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REGULAR ARTICLES

Morphological characterisation of small East African Zebu and Tyrolean Grey Zebu crosses under on-station conditions in Uganda

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Abstract
The Small East African Zebu (SEAZ) is an indigenous Ugandan cattle breed valued for disease resistance but characterised by low milk production. To enhance productivity, Uganda introduced Tyrolean Grey cattle semen from Austria in 2009 to crossbreed with SEAZ, resulting in the Tyrolean Grey Zebu crosses (TGZ). This study aimed to morphologically characterise SEAZ and TGZ cattle to inform future breeding and conservation programmes. A sample of 214 SEAZ and TGZ was randomly selected from Aswa Ranch and Lusenke Stock Farm. The two genotypes exhibited distinct phenotypic differences, particularly in coat colour, coat hair, dewlap size, hump shape, horn characteristics, back profile, and tail length. SEAZ cattle predominantly expressed darker coat colours (brown, dark brown, and black), whereas TGZ cattle were mainly grey and light brown. Multivariate analyses revealed that most morphological traits varied significantly across genotype, location, sex, and age ($p < 0.05$), while rump shape showed no significant variation. Discriminant function analysis demonstrated a high classification accuracy between SEAZ and TGZ, confirming clear phenotypic differentiation between the two genotypes. These findings indicate that genetic background and environmental adaptation strongly influence cattle morphology and highlight the need for complementary production, reproductive, and genomic studies to support targeted breeding strategies in Uganda.

Keywords Genotype · Phenotypic characterisation · Coat colour · Phenotypes · Structural traits

Introduction

The global cattle population currently stands at 1.5 billion heads, encompassing 1109 well-defined breeds that reflect the rich diversity within the cattle species (Ahmed et al. 2024). The Food and Agriculture Organisation of the United Nations (FAO) suggests that livestock contribute 40% of global agricultural output value, supporting the livelihoods and food security of 1.3 billion people (Bonilla-Cedrez et al. 2023). The decline in livestock genetic diversity, particularly in indigenous cattle populations, poses threats to food security and community livelihoods (Leroy et al. 2024). The livestock sector is valuable to Uganda's food security and agricultural economy, providing livelihoods for a significant portion of the rural population (Waiswa et al. 2021). With an annual milk production of 3.85 million tons, the production system is dominated by smallholders (Ndambi et al. 2008; Sanchez-Molano et al. 2025) and characterised by a mix of indigenous, exotic, and crossbred cattle.

Despite their resilience, productivity remains relatively low; for example, indigenous Zebu cattle may take up to four years to reach saleable weight, often yielding limited economic returns(Greenwood 2021). These limitations have prompted interest in strategic crossbreeding to enhance productivity while retaining adaptive traits. Exploring genetic diversity requires an understanding of phenotypic and genomic variations (Panigrahi et al. 2025). Phenotypic variation in cattle breeds may indicate genetic diversity (Houessou et al. 2022; Yakubu et al. 2024). Morphological traits, including coat colour, coat characteristics, and body conformation, are widely recognised indicators of genetic

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variation, environmental adaptation, and suitability for breeding programmes.

The TGZ are crosses between Tyrolean Grey and SEAZ cattle. They were introduced in Uganda to improve meat and milk production while maintaining adaptability to local conditions (Acila et al. 2023). In this study, morphological characterisation was undertaken to describe and compare SEAZ and TGZ crosses. Currently, TGZ are hosted at Aswa Ranch, Lusenke Stock Farm, and in the neighbourhood of the farm. Uganda has a population of about 410 TGZ, with the majority in Lusenke Stock Farm (central Uganda). Although crossbreeding initiatives have been implemented, limited information exists on the phenotypic characteristics of TGZ crosses. No comprehensive morphological characterisation has been conducted to support breed improvement, selection, and conservation strategies. This knowledge gap shows the importance of the present study. It aimed at characterising the phenotypes of SEAZ and TGZ crosses to inform breeding programmes.

Methodology

Study area

The study was conducted at Aswa Ranch in Pader District (northern Uganda) and Lusenke Stock Farm in Kayunga District (central Uganda). These sites represent contrasting agro-ecological zones under on-station cattle management systems. Aswa Ranch lies between latitude 2°45′ N and longitude 32°15′ E, within the northern savannah zone. The area experiences a bimodal rainfall pattern with an average annual rainfall of approximately 1,300 mm. Mean annual temperatures range from 24 to 31 °C, and the average relative humidity is about 60–65%. The ranch is characterised by open grasslands and seasonal variability in forage availability, conditions suitable for indigenous zebu cattle rearing. Lusenke Stock Farm is located in the Lake Victoria Crescent agro-ecological zone at an altitude ranging from 914 to 1,800 m above sea level. The area receives 1,125–1,300 mm of rainfall annually, with temperatures ranging from 15 to 32.5 °C. Average relative humidity is higher than in Aswa, ranging between 70 and 80%. The farm lies within a humid environment influenced by proximity to the River Nile and supports relatively lush pasture growth throughout the year. The map of Uganda showing the study areas is presented in Fig. 1.

Study design

This study adopted a cross-sectional observational design to phenotypically characterize Small East African Zebu (SEAZ) and Tyrolean Grey Zebu crosses (TGZ). Morphological traits were recorded at a single point in time under on-station conditions, without experimental manipulation, and comparisons were made across genotypes, locations, sex, and age groups between April 2025 and September 2025.

Description of study animals

The study involved Small East African Zebu (SEAZ) and Tyrolean Grey Zebu (TGZ) cattle maintained under on-station conditions at Aswa Ranch and Lusenke Stock Farm. Individual animals were identified using ear tag numbers to ensure accurate monitoring and recording. All cattle were raised exclusively on natural pastures. Morphological observations were conducted with animals restrained in a confinement crush while remaining free-standing as much as possible to ensure precision and consistency of measurements. Observations were made by calmly approaching animals from the appropriate side to minimise disturbance and stress.

Tyrolean grey breed

The Tyrolean Grey is one of the oldest Alpine cattle breeds, originating from Austria and traditionally managed in mountainous regions (Kühl et al. 2020). The breed is classified as dual-purpose, with reported average milk yields of approximately 4,900 kg per lactation, containing about 4.0% fat and 3.3% protein. Tyrolean Grey cattle are predominantly kept in smallholder systems, with over 80% of farms located at altitudes above 1,000 m (Acila et al. 2024). The breed is considered rare, representing about 1% of the total cattle population in Austria, and is maintained by approximately 1,300 breeder families managing around 5,000 registered cows. These cattle are valued for their hardiness, moderate productivity, and adaptability to challenging environments, characteristics that motivated their use in crossbreeding programmes with indigenous cattle such as the SEAZ.

Small East African Zebu (SEAZ)

The SEAZ is the dominant indigenous cattle breed in Uganda and forms the backbone of livestock production in the north-eastern savannah grasslands and semi-arid dryland regions. Over centuries, SEAZ cattle have evolved adaptive traits that enable survival under harsh environmental conditions, including small body size, drought tolerance, disease resistance, and the ability to perform under low-input management systems(Acila et al. 2023). Beyond their role in meat and milk production, SEAZ cattle contribute

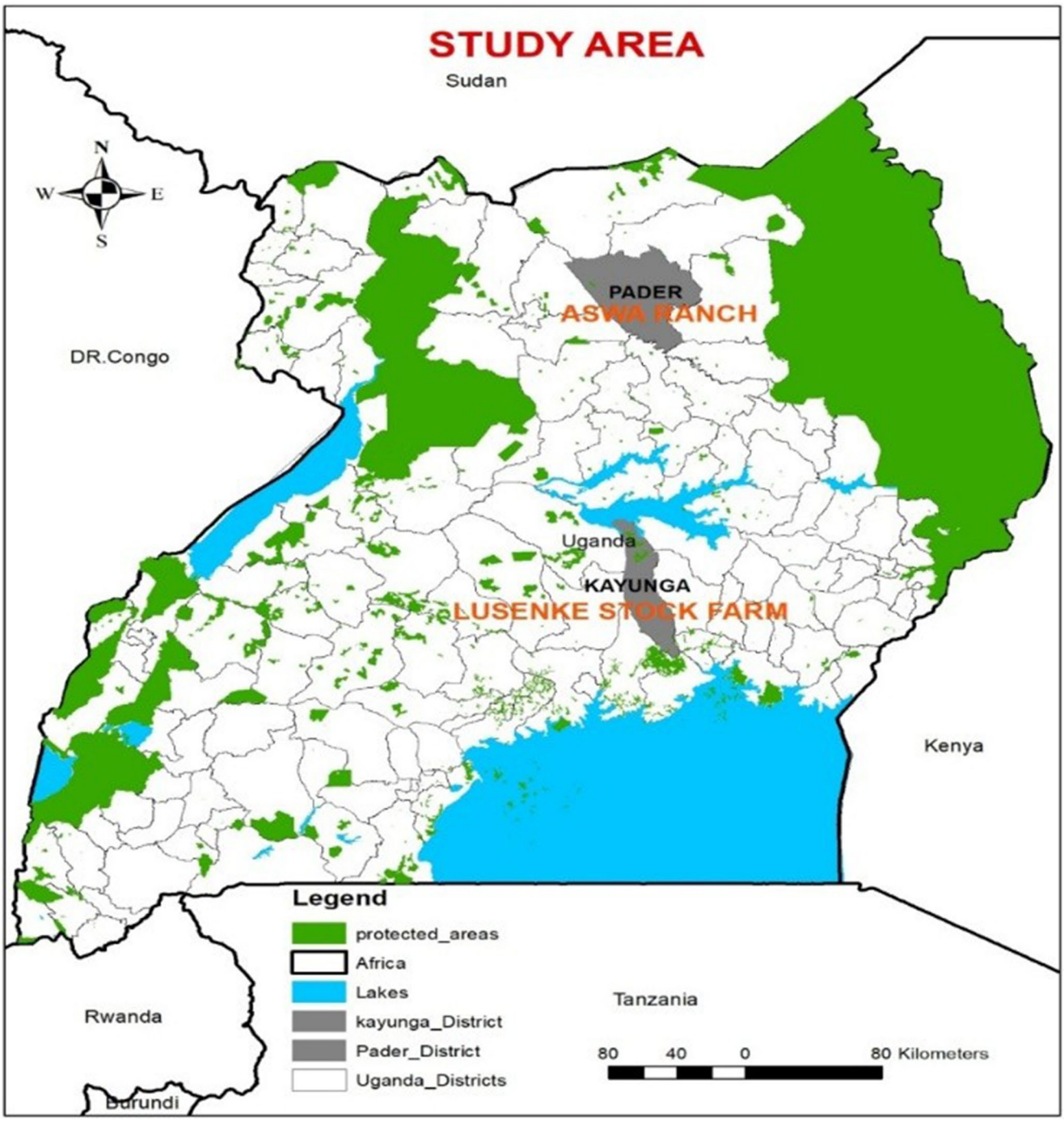

Fig. 1 Map showing the study area

significantly to household livelihoods through draft power and socio-cultural functions (Fig. 2).

Sampling

Animals were purposively selected for this study based on clearly defined phenotypic and demographic criteria consistent with zebu cattle characterisation guidelines (Rege and Tawah, 1999). Purposive sampling was adopted to ensure adequate representation of the two target genotypes. The Small East African Zebu (SEAZ) and Tyrolean Grey Zebu (TGZ) were classified across key classification factors, namely genotype, location, sex, age, and parity.

A total of 214 animals (SEAZ and TGZ combined) were included in the study. The sample comprised calves below 1 year and cows in 2nd and 3rd parity, categories selected to



Fig. 2 Tyrolean Grey Zebu Crosses (TGZ) and Small East African Zebu (SEAZ)

minimise confounding effects of extreme age and reproductive status on morphological traits. Ear tag numbers were used to identify animals and facilitate accurate monitoring and data recording. All sampled cattle were maintained under on-station conditions and raised exclusively on natural pastures.

Sampling procedures followed the FAO (2012) guidelines for phenotypic characterisation of animal genetic resources, which recommend approximately 10–30 males and 100–300 females for reliable morphological description. Accordingly, both males and females meeting the inclusion criteria were considered.

Exclusion criteria included bulls and cows in late pregnancy, animals of parity greater than three, and individuals exhibiting physical abnormalities, illness, or injuries that could bias morphological assessment. These exclusions were applied to ensure sample uniformity and improve the reliability of phenotypic comparisons.

Data collection

Morphological characterisation of SEAZ and TGZ

Morphological characterization of Small East African Zebu (SEAZ) and Tyrolean Grey Zebu (TGZ) was conducted under on-station conditions using standardized visual assessment procedures for breed identification as recommended by FAO (2012). Traits were recorded separately for males and females using an observation guide and structured checklist. The recorded traits included coat colour and coat colour pattern, coat hair length and type, and a range of structural characteristics. Dewlap size, hump presence, size, shape, and position, facial profile, back profile, and rump shape were visually assessed. Horn characteristics recorded included presence or absence, shape, spacing, orientation, and shaping. Tail length was also recorded. All traits were categorized according to predefined phenotypic classes to ensure consistency across observations.

Statistical analysis

STATA (Version 16.0) was used in the analysis of the data. To classify cattle into their respective genotypes, Discriminant Function Analysis (DFA) was conducted to identify morphological traits that best distinguished the two cattle genotypes, SEAZ and TGZ. The analysis included traits measured up to Tail length, encompassing coat colour, coat pattern, hair type, dewlap size, hump characteristics, tail length, horn traits, and udder/testis size, selected based on their biological relevance and common use in phenotypic characterization. To meet the assumptions of DFA, categorical traits were converted into dummy variables, allowing the analysis to accommodate non-normal distributions, while homogeneity of covariance matrices across genotypes was assessed using Box's M test, which indicated no severe violations. Standardized canonical discriminant function coefficients were examined to identify the traits contributing most to genotype separation, and a leave-one-out cross-validation procedure was implemented to evaluate classification accuracy, ensuring robust predictive performance.

The model applied in this analysis follows the classical linear discriminant function form:

$$D = a + b_1X_1 + b_2X_2 + ... + b_nX_n$$

Where

- D is the discriminant score
- a is the constant term
- b_1, b_2, …, b_n are the discriminant coefficients, and
- X_1, X_2,…, X_n are the independent variables (morphological traits such as shape, dewlap, tail length, etc.).

The analysis tested the hypothesis that "these morphological traits significantly differentiate between SEAZ and TGZ genotypes (Johnson and Wichern 2002). The DFA produced Wilks' Lambda, eigenvalues, canonical correlations, and classification results to assess the discriminatory power of the traits. The statistical significance of individual traits was evaluated using F-statistics based on Wilks' Lambda.

Following DFA, Multiple Correspondence Analysis (MCA) was applied to the same set of categorical traits to explore underlying patterns of association and to visualize multidimensional relationships among traits and genotypes. The MCA reduced the high-dimensional trait dataset to principal components, providing complementary insights into phenotypic variation and enabling further interpretation of trait clustering. To statistically evaluate the separation of genotypes based on DFA and MCA results, univariate Analysis of Variance (ANOVA) was performed on individual traits, while Multivariate Analysis of Variance (MANOVA) assessed differences across multiple traits simultaneously, accounting for correlations between traits. This combined approach enabled the identification of both the key discriminating traits and the broader patterns of morphological variation between SEAZ and TGZ cattle.

The robustness of the model was supported by high tolerance values for most variables, close to one. This indicates low multicollinearity and confirms that the traits included in the analysis had contributed unique information to the discriminant function. This strengthens the reliability and validity of the results and emphasises the distinct role of each significant variable in genotype classification. The model strength was further examined through canonical correlation and classification accuracy, including cross-validation.

Results

Coat colour characteristics of the genotypes by location, sex, and age

The results presented in Table 1 describe the distribution of morphological characteristics, specifically coat colour, coat colour pattern, hair, and hair type across locations (Aswa and Lusenke), genotypes (SEAZ and TGZ), sex (male and female), and age groups (<1 year and >1 year). Chi-square tests were used to find out whether variations are statistically significant across the different categories.

Coat colour varied highly significantly across location (χ^2 = 115.161, $p<0.001$) and genotype (χ^2 = 73.981, $p<0.001$) (Table 1). Significant differences were also observed across sex (χ^2 = 13.909, $p<0.05$) and age groups (χ^2 = 18.805, $p<0.01$), although these effects were comparatively smaller.

Coat colour pattern showed significant variation across location (χ^2 = 17.414, $p<0.001$) and genotype (χ^2 = 13.011, $p<0.01$), but not across sex or age (Table 1).

Hair length differed significantly by location (χ^2 = 23.881, $p<0.001$), genotype (χ^2 = 10.660, $p<0.01$), and sex (χ^2 = 15.590, $p<0.001$), but showed no significant variation across age groups (Table 1).

Hair type exhibited highly significant differences across location (χ^2 = 42.619, $p<0.001$) and genotype (χ^2 = 20.853, $p<0.001$), as well as significant variation by sex (χ^2 = 6.922, $p<0.01$), while age-related differences were not significant (Table 1).

Morphological characteristics of the genotypes by location, sex, and age

The association between morphological characteristics and location, genotype, sex, and age was assessed using chi-square (χ^2) tests (Table 2). Several traits showed significant variation across location and genotype, while others exhibited limited or no differentiation.

Dewlap size varied significantly across location (χ^2 = 15.082, $p<0.001$) and genotype (χ^2 = 6.446, $p<0.05$), but not across sex ($p>0.05$) (Table 2).

Hump characteristics showed marked variation. Hump size differed significantly by location (χ^2 = 10.970, $p<0.01$) and genotype (χ^2 = 6.999, $p=0.01$), while differences by sex and age were not significant (Table 2). Hump shape exhibited highly significant variation across both location (χ^2 = 84.896, $p<0.001$) and genotype (χ^2 = 57.780, $p<0.001$). Hump position showed marginal variation by location ($p=0.051$) but no significant differences across genotype, sex, or age.

Back profile differed significantly across location (χ^2 = 3.932, $p<0.05$), sex (χ^2 = 6.258, $p<0.05$), and age (χ^2 = 46.129, $p<0.001$), but not by genotype ($p=0.949$) (Table 2).

Rump shape showed no statistically significant differences across location, genotype, sex, or age ($p>0.05$ for all comparisons) (Table 2).

Horn characteristics exhibited limited variation. Horn presence, shape, and spacing did not differ significantly across location, genotype, sex, or age ($p>0.05$). However, horn orientation varied significantly by location (χ^2 = 33.852,

Table 1 Coat colour characteristics of SEAZ and TGZ by location, sex, and age

Characteristics		Location			Genotype			Sex			Age of animal		
	Variables	Aswa	Lusenke	X2 (*p*-values)	SEAZ	TGZ	X2 (*p*-values)	Male	Female	X2 (*p*-values)	Calves (<1 year)	Adults (>1 year)	X2 (*p*-values)
Coat colour				115.161*** (0.000)			73.981*** (0.000)			13.909* (0.016)			18.805**(0.002)
	Brown	57 (40.7)	10 (13.5)		44 (40.4)	23 (21.9)		14 (22.6)	53 (34.9)		47 (32.0)	20 (29.9)	
	White	7 (5.0)	1 (1.4)		5 (4.6)	3 (2.9)		2 (3.2)	6 (3.9)		7 (4.8)	1 (1.5)	
	Black	19 (13.6)	2 (2.7)		18 (16.5)	3 (2.9)		4 (6.5)	17 (11.2)		8 (5.4)	13 (19.4)	
	Dark brown	35 (25.0)	1 (1.4)		28 (25.7)	8 (7.6)		17 (27.4)	19 (12.5)		30 (20.4)	6 (9.0)	
	Grey	0 (0.0)	41 (55.4)		0 (0.0)	41 (39.0)		17 (27.4)	24 (15.8)		32 (21.8)	9 (13.4)	
	Light brown	22 (15.7)	19 (25.7)		14 (12.8)	27 (25.7)		8 (12.9)	33 (21.7)		23 (15.6)	18 (26.9)	
Coat colour pattern				17.414** (0.001)			13.011** (0.005)			4.895ns (0.180)			4.474ns (0.215)
	Uniform	111 (79.3)	57 (77.0)		88 (80.7)	80 (76.2)		50 (80.6)	118 (77.6)		119 (81.0)	49 (73.1)	
	Spotted	16 (11.4)	4 (5.4)		11 (10.1)	9 (8.6)		8 (12.9)	12 (7.9)		14 (9.5)	6 (9.0)	
	Shaded	5 (3.6)	13 (17.6)		3 (2.8)	15 (14.3)		4 (6.5)	14 (9.2)		11 (7.5)	7 (10.4)	
	Pied	8 (5.7)	0 (0.0)		7 (6.4)	1 (1.0)		0 (0.0)	8 (5.3)		3 (2.0)	5 (7.5)	
Coat hair				23.881*** (0.000)			10.660** (0.005)			15.590*** (0.000)			3.108ns (0.211)
	Short	131 (93.6)	51 (68.9)		101 (92.7)	81 (77.1)		44 (71.0)	138 (90.8)		121 (82.3)	61 (91.0)	
	Medium	9 (6.4)	21 (28.4)		8 (7.3)	22 (21.0)		16 (25.8)	14 (9.2)		24 (16.3)	6 (9.0)	
	Long	0 (0.0)	2 (2.7)		0 (0.0)	2 (1.9)		2 (3.2)	0 (0.0)		2 (1.4)	0 (0.0)	
Coat hair type				42.619*** (0.000)			20.853*** (0.000)			6.922** (0.009)			1.462ns (0.227)
	straight	137 (97.9)	49 (66.2)		106 (97.2)	80 (76.2)		48 (77.4)	138 (90.8)		125 (85.0)	61 (91.0)	
	curly	3 (2.1)	25 (33.8)		3 (2.8)	25 (23.8)		14 (22.6)	14 (9.2)		22 (15.0)	6 (9.0)	

Values in parentheses are percentages and p-values in the chi-square test column

***$P<0.001$; **$P<0.01$; *$P<0.05$

$p<0.001$), while differences by genotype ($p=0.081$), sex, and age were not statistically significant (Table 2).

Tail length showed significant variation across all examined factors, including location ($\chi^2 = 21.119$, $p<0.001$), genotype ($\chi^2 = 15.478$, $p<0.001$), sex ($\chi^2 = 24.394$, $p<0.001$), and age ($\chi^2 = 41.332$, $p<0.001$) (Table 2).

Determining morphological characteristics used to distinguish between the genotypes

The discriminant analysis results presented in Table 3 revealed that the model was statistically significant, as indicated by a Wilks' Lambda value of 0.884 and an associated F-value of 7.979 with a p-value of 0.006. This result suggests that the linear combination of the included morphological variables significantly differentiates between the two genotypes. The canonical correlation coefficient of 0.340 implies that approximately 11.6% of the variation in genotype can be explained by the discriminant function. Although this represents a moderate level of explanatory power, it is considered acceptable in studies involving biological traits where overlapping characteristics are common.

Among the traits analysed, three variables: Shape, Shape A, and Tail Length, were statistically significant in distinguishing between the genotypes. Shape had the highest discriminative power, with a Wilks' Lambda of 0.884 and a highly significant F-value of 7.979 ($p=0.006$), indicating that this trait contributed most strongly to genotype classification. Shape A also demonstrated significant differentiation between the genotypes, with SEAZ animals showing a lower mean score (1.19) compared to TGZ animals (1.49), and an associated p-value of 0.025. Tail Length was similarly significant ($p=0.048$), with TGZ animals generally exhibiting longer tails than their SEAZ counterparts. These traits emerge as valuable indicators for classifying cattle into their respective genotypes using observable phenotypic characteristics.

Conversely, several morphological traits were statistically non-significant and did not contribute meaningfully to the discriminant function. These included Coat Colour, Coat Hair, Hair Type, Back, Rump, Teats, Udder Size, and Navel Flap. Despite some differences in mean values across the genotypes, the associated F-values were low, and p-values exceeded 0.05, indicating that these traits did not significantly distinguish between SEAZ and TGZ cattle. For example, Coat Colour had means of 2.92 for SEAZ and 4.03 for TGZ, yet it was not statistically significant ($p=0.127$), reflecting either high variability within groups or minimal biological differentiation.

The robustness of the model was supported by high tolerance values for most variables, which were close to one. This indicates low multicollinearity and confirms that the traits included in the analysis contributed unique information to the discriminant function. This strengthens the reliability of the results and emphasises the distinct role of each significant variable in genotype classification.

Biologically, the results confirm that TGZ cattle are characterized by more distinct physical features, such as longer tails, more defined body shape, and a pronounced morphological trait coded as Shape A. These findings are consistent with field observations and can be particularly useful for livestock experts, breeders, and extension workers who may not have access to genetic testing but require reliable phenotypic indicators to differentiate between genotypes.

Multiple correspondence analysis (MCA) of coat colour characteristics and structural morphological characteristics

The multiple correspondence analysis (MCA) of coat colour and structural morphological traits revealed distinct patterns of phenotypic variation in the cattle population. For coat colour traits, the first two dimensions captured 80.28% of the total inertia, with Dim 1 (65.95%) primarily differentiating grey and curly-haired individuals from brown and straight-haired animals, while Dim 2 (14.32%) separated pied and spotted coat patterns from uniform and shaded patterns. This indicates that coat colour and pattern are major sources of phenotypic differentiation.

Linking these dimensions to the animal factors revealed that genotype strongly influences coat colour and pattern. SEAZ cattle predominantly exhibited brown and dark brown colours with straight hair, while TGZ were characterised by grey coat colour, pied, spotted patterns, and curly hair Table 4. Sex differences were also evident, with males showing deeper pigmentation and more pronounced curly hair in TGZ crosses, consistent with sexual dimorphism and breeder selection preferences. The effect of age was less pronounced for coat colour but contributed to some variation in hair type and pattern expression, particularly in calves versus adults. Location significantly influenced Dim 1 (MANOVA Wilks' lambda $p<0.001$), indicating site-specific variation in coat traits, likely reflecting environmental adaptation and management practices.

For structural traits, the first two dimensions explained 60.53% of the total inertia, with Dim 1 (48.41%) distinguishing individuals with large dewlaps, medium humps, dropping hump shapes, sloping rumps, and curved horns, while Dim 2 (12.13%) captured variation in small to medium dewlaps, small humps, erect humps, and tail length. MANOVA results showed that location significantly influenced these structural traits, with cattle at different sites exhibiting variation in dewlap size, hump shape, and tail length, reflecting environmental adaptation. Sex also had a significant effect

Table 2 Morphological characteristics of SEAZ and TGZ by location, sex and age

Characteristics		Location			Genotype			Sex			Age of animal		
	Variables	Aswa	Lusenke	X2 (*p*-values)	SEAZ	TGZ	X2 (*p*-values)	Male	Female	X2 (*p*-values)	Calves (< 1 year)	Adults (> 1 year)	X2 (*p*-values)
Dewlap	**Dewlap**			15.082*** (0.000)			6.446* (0.040			2.575ns (0.276)			13.614*** (0.000)
	Small	133 (95.0	66 (89.2)		104 (95.4)	95 (90.5)		59 (95.2)	140 (92.1)		141 (95.9)	58 (86.6)	
	Medium	1 (0.7)	8 (10.8)		1 (0.9)	8 (7.6)		3 (4.8)	6 (3.9)		6 (4.1)	3 (4.5)	
	Large	6 (4.3)	0 (0.0)		4 (3.7)	2 (1.9)		0 (0.0)	6 (3.9)		0 (0.0)	6 (9.0)	
Hump	**Hump**			10.970** (0.001)			6.999** (0.008)			0.022ns (0.883)			3.269ns (0.071)
	Small	137 (97.9)	64 (86.5)		107 (98.2)	94 (89.5)		58 (93.5)	143 (94.1)		141 (95.9)	60 (89.6)	
	Medium	3 (2.1)	10 (13.5)		2 (1.8)	11 (10.5)		4 (6.5)	9 (5.9)		6 (4.1)	7 (10.4)	
	Large	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)	
	Shape			84.896*** (0.000)			57.780*** (0.000)			0.330ns (0.566)			1.353ns (0.245)
	Erect	133 (95.0)	28 (37.8)		106 (97.2)	55 (52.4)		45 (72.6)	116 (76.3)		114 (77.6)	47 (70.1)	
	Dropping	7 (5.0)	46 (62.6)		3 (2.8)	50 (47.6)		17 (27.4)	36 (23.7)		33 (22.4)	20 (29.9)	
	Position			3.819ns (0.051)			2.096ns (0.148)			4.949* (0.026)			0.920ns (0.337)
	Thoracic	140 (100.0)	72 (97.3)		109 (100.0)	103 (98.1)		60 (96.8)	152 (100.0)		145 (98.6)	67 (100.0)	
	Cervicothoracic	0 (0.0)	2 (2.7)		0 (0.0)	2 (1.9)		2 (3.2)	0 (0.0)		2 (1.4)	0 (0.0)	
Profile	**Face**			-			-			-			-
	Flat	140 (100.0)	74 (100.0)		109 (100.0)	105 (100.0)		62 (100.0)	152 (100.0)		147 (100.0)	67 (100.0)	
	Convex	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)	
	Concave				0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)				
	Back			3.932* (0.047)			0.004ns (0.949)			6.258* (0.012)			46.129*** (0.000)
	Curved	28 (20.0)	7 (9.5)		18 (16.5)	17 (16.2)		4 (6.5)	31 (20.4)		7 (4.8)	28 (41.8)	
	Straight	112 (80.0)	67 (90.5)		91 (83.5)	88(83.8)		58 (93.5)	121 (79.6)		140 (95.2)	39 (58.2)	
	Rump			4.837ns (0.089)			5.747ns (0.056)			2.101ns (0.350)			1.496ns (0.473)
	Flat	131 (93.6)	66 (89.2)		102 (93.6)	95 (90.5)		56 (90.3)	141 (92.8)		135 (91.8)	62 (92.5)	
	Sloping	6 (4.3)	8 (10.8)		4 (3.7)	10 (9.5)		4 (6.5)	10 (6.6)		9 (6.1)	5 (7.0)	
	Roofy	3 (2.1)	0 (0.0)		3 (2.8)	0 (0.0)		2 (3.2)	1 (0.7)		3 (2.0)	0 (0.0)	
Horns	**Present**			0.545ns (0.460)			0.714ns (0.398)			-			
	Polled	1 (2.4)	0 (97.3)		0 (0.0)	1 (2.7)		0 (0.0)	1 (1.6)		0 (0.0)	1 (1.6)	
	Horned	40 (97.6)	22 (100.0)		26 (100.0)	36 (97.3)		0 (0.0)	62 (98.4)		0 (0.0)	62 (68.4)	
	Dehorned			-			-			-			
	Yes	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)	
	No	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)	

Table 2 (continued)

Characteristics		Location			Genotype			Sex			Age of animal		
	Shape			3.022ns (0.221)			5.019ns (0.081)			-			
	Straight	29 (70.7)	12 (54.5)		21 (80.8)	20 (54.1)		0 (0.0)	41 (65.1)		0 (0.0)	41 (65.1)	
	Curved	12 (29.3)	9 (40.9)		5 (19.2)	16 (43.2)		0 (0.0)	21 (33.3)		0 (0.0)	21 (33.3)	
	Lyre-shaped	0 (0.0)	1 (4.5)		0 (0.0)	0 (0.0)		0 (0.0)	1 (1.6)		0 (0.0)	1 (1.6)	
	Spacing			1.167ns (0.280)			0.068ns (0.794)			-			
	Narrow	13 (31.7)	10 (45.5)		9 (34.6)	14 (37.8)		0 (0.0)	23 (36.5)		0 (0.0)	23 (36.5)	
	Wide	28 (68.3)	12 (54.5)		17 (65.4)	23 (62.2)		0 (0.0)	40 (63.5)		0 (0.0)	40 (63.5)	
	Orientation			33.852*** (0.000)			5.023ns (0.081)			-			
	Forward	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	13 (20.6)		0 (0.0)	13 (19.7)	
	Lateral	1 (2.4)	15 (68.2)		3 (11.5)	13 (35.1)		0 (0.0)	3 (4.8)		0 (0.0)	3 (4.5)	
	Upward	40 (97.6)	7 (31.8)		23 (88.5)	24 (64.9)		0 (0.0)	47 (74.6)		0 (0.0)	47 (74.6)	
	Horn shaping			-			-			-			
	Natural	41 (100.0)	22 (100.0)		26 (100.0)	37 (100.0)		0 (0.0)	63 (100.0)		0 (0.0)	63 (100.0)	
	Modified	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)	
Tail	**Tail length**			21.119*** (0.000)			15.478*** (0.000)			24.394*** (0.000)			41.332*** (0.000)
	Short	62 (44.3)	17 (23.0)		50 (45.9)	29 (27.6)		38 (61.3)	41 (27.0)		60 (40.8)	19 (28.4)	
	Medium	69 (49.3)	37 (50.0)		53 (48.6)	53 (50.5)		22 (35.5)	84 (55.3)		82 (55.8)	24 (35.8)	
	Long	9 (6.4)	20 (27.0)		6 (5.5)	23 (21.9)		2 (3.2)	27 (17.8)		5 (3.4)	24 (35.8)	

Values in parentheses are percentages, and p-values in the chi-square test column

***$P<0.001$; **$P<0.01$; *$P<0.05$

Table 3 Discriminant analysis to determine morphological characteristics used to distinguish between the genotypes

Variable	SEAZ	TGZ	Total	Test of equality of group means			Variables not in the analysis		
	Means (SD)	Means (SD)		Wilks' Lambda	$F_{1, 61}$	Sig.	Tolerance	Sig. of F to Enter	Wilks' Lambda
Coat colour	2.92 (1.742)	4.03 (2.088	3.57 (2.014)	0.926	4.876	0.031	0.957	0.127	0.85
Coat colour pattern	1.46 (1.029)	1.49 (0.837	1.48 (0.913)	1.00	0.011	0.916	0.994	0.923	0.884
Coat Hair	1.08 (0.272)	1.11 (0.315	1.1 (0.296)	0.997	0.167	0.684	0.983	0.97	0.884
Hair type	1.12 (0.326)	1.08 (0.277	1.1 (0.296)	0.997	0.203	0.654	0.957	0.9	0.884
Dewlap	1.27 (0.667)	1.16 (0.501	1.21 (0.572)	0.991	0.53	0.469	0.992	0.661	0.881
Hump	1.08 (0.272)	1.14 (0.347	1.11 (0.317)	0.992	0.512	0.477	0.707	0.37	0.872
Shape	1.12 (0.326)	1.43 (0.502	1.3 (0.463)	0.884	7.979	0.006	-	- -	
Back	1.5 (0.51)	1.65 (0.484	1.59 (0.596)	0.978	1.378	0.245	0.993	0.385	0.873
Rump	1.08 (0.272)	1.08 (0.277	1.08 (0.272)	1.00	0.003	0.953	0.96	0.631	0.881
Present	2.00 (0.000)	1.97 (0.164	1.98 (0.126)	0.989	0.699	0.406	0.984	0.265	0.866
Shape A	1.19 (0.402)	1.49 (0.559	1.37 (0.517)	0.92	5.275	0.025	0.754	0.34	0.871
Spacing	1.65 (0.485)	1.62 (0.492	1.63 (0.485)	0.999	0.066	0.798	0.995	0.954	0.884
Orientation	2.77 (0.652)	2.38 (0.893	2.54 (0.820)	0.944	3.619	0.062	0.996	0.113	0.848
Tail length	1.81 (0.749)	2.22 (0.821	2.05 (0.812)	0.938	4.058	0.048	0.942	0.205	0.861

Wilks' lambda = 0.884, $\chi^2 = 7.437$; Exact $F_{1,61} = 7.979$, $p = 0.006$; canonical correlation = 0.340

Eigen value = 0.131; Values in parentheses are standard deviations

(Wilks' lambda $p = 0.0396$), with males generally showing larger and more pronounced humps and dewlaps. Genotype had a smaller but observable effect, with TGZ crosses showing greater variability in structural traits compared to the more uniform SEAZ cattle. Age effects were minimal for structural traits, suggesting that many of these features are largely established early in life, with only minor changes through maturation.

Overall, the MCA combined with ANOVA and MANOVA confirms that genotype is the primary determinant of coat colour traits, while location and sex shape structural morphological traits. These analyses highlight the joint contribution of multiple categorical traits in differentiating cattle, demonstrating that coat colour, pattern, hair type, and structural features can be used together for breed characterization, selection, and adaptation studies.

Effects of location, breed, age group, and sex on the first two MCA dimensions (ANOVA results)

The analysis of variance for the first MCA dimension (mca_dim1) shows that the model explains a substantial proportion of the variability in the data ($R^2 = 0.509$; adjusted $R^2 = 0.499$), indicating that nearly half of the structural variation captured by this dimension is accounted for by location, breed, age group, and sex. The overall model is highly significant ($F = 54.13$, $p < 0.001$), confirming that these factors jointly influence the primary phenotypic axis identified by the MCA (Table 5).

Among the explanatory variables, location emerges as the dominant factor, contributing the largest share of explained variance ($F = 78.86$, $p < 0.001$). This indicates strong spatial differentiation in the structural trait combinations summarized by MCA Dimension 1, suggesting that animals from different locations exhibit markedly distinct morphological profiles. Breed also has a statistically significant effect on this dimension ($F = 4.72$, $p = 0.031$), implying that genetic background contributes to the major axis of phenotypic variation, although to a lesser extent than location. Sex is likewise significant ($F = 6.42$, $p = 0.012$), reflecting sexual dimorphism in the structural traits represented along this axis. In contrast, age group does not significantly influence Dimension 1 ($p = 0.405$), indicating that the dominant morphological pattern captured by this dimension is relatively stable across age categories.

Overall, MCA Dimension 1 can therefore be interpreted as a major phenotypic gradient primarily structured by geographic location, with additional contributions from breed and sex.

In contrast, the ANOVA results for the second MCA dimension (mca_dim2) show that the explanatory variables collectively account for very little variation in this axis ($R^2 = 0.014$; adjusted $R^2 = -0.005$). The overall model is not statistically significant ($F = 0.72$, $p = 0.578$), indicating that location, breed, age group, and sex do not meaningfully explain variation along this dimension.

None of the individual factors show a significant effect on MCA Dimension 2 (all p-values > 0.36). This suggests that the second dimension captures minor or residual variation in trait associations that is not systematically structured by the major biological or demographic factors considered in the study. Consequently, Dimension 2 appears to represent within-group heterogeneity or subtle morphological

Table 4 Multiple correspondence analysis (MCA) of coat colour characteristics and morphological characteristics

Panel A: Inertia explained by MCA dimensions				
MCA block	Dimension	Inertia	Percentage of inertia (%)	Cumulative inertia (%)
Coat colour traits	Dim 1	0.0811	65.95	65.95
	Dim 2	0.0176	14.32	80.28
	Dim 3	0.0070	5.67	85.95
	Dim 4	0.0001	0.06	86.01
	Total	0.1229	100.00	
Structural traits	Dim 1	0.0337	48.41	48.41
	Dim 2	0.0084	12.13	60.53
	Dim 3	0.0047	6.71	67.24
	Dim 4	0.0026	3.68	70.92
	Total	0.0696	100.00	

Panel B: Category coordinates and contributions on the first two MCA dimensions								
Trait group	Variable	Category	Mass	Quality	Dim 1 coord.	Dim 1 contrib.	Dim 2 coord.	Dim 2 contrib.
Coat colour traits	Coat colour	Brown	0.104	0.777	0.715	0.053	1.409	0.207
		White	0.012	0.653	0.078	0.000	−2.248	0.063
		Black	0.033	0.430	1.106	0.040	0.239	0.002
		Dark brown	0.056	0.697	0.707	0.028	−1.705	0.163
		Grey	0.064	0.861	−2.139	0.292	0.508	0.016
		Light brown	0.064	0.648	−0.232	0.003	−0.997	0.064
	Coat colour pattern	Uniform	0.262	0.757	0.027	0.000	−0.593	0.092
		Spotted	0.031	0.657	1.040	0.034	2.478	0.191
		Shaded	0.028	1.054	−2.382	0.159	1.294	0.047
		Pied	0.012	0.641	2.192	0.060	3.346	0.140
	Hair type	Straight	0.290	0.899	0.386	0.043	−0.083	0.002
		Curly	0.044	0.899	−2.565	0.287	0.548	0.013
Structural traits	Dewlap	Small	0.087	0.670	0.249	0.005	0.388	0.013
		Medium	0.005	0.385	1.747	0.015	−1.226	0.007
		Large	0.008	0.756	−3.792	0.114	−3.529	0.099
	Hump	Small	0.089	0.704	−0.364	0.012	0.494	0.022
		Medium	0.011	0.704	2.916	0.094	−3.949	0.173
	Hump shape	Erect	0.070	0.737	−0.925	0.060	0.412	0.012
		Dropping	0.030	0.737	2.142	0.138	−0.953	0.027
	Back profile	Curved	0.041	0.601	−0.854	0.030	−1.744	0.126
		Straight	0.059	0.601	0.600	0.021	1.226	0.088
	Rump	Flat	0.092	0.621	−0.235	0.005	0.371	0.013
		Sloping	0.008	0.621	2.722	0.059	−4.302	0.147
	Horn shape	Straight	0.065	0.799	−1.031	0.069	0.436	0.012
		Curved	0.033	0.790	1.843	0.113	−0.882	0.026
	Tail length	Short	0.030	0.759	−1.624	0.080	−1.889	0.108
		Medium	0.035	0.230	0.410	0.006	0.452	0.007
		Long	0.035	0.685	0.993	0.034	1.179	0.049

Table 5 Effects of location, breed, age group, and sex on the first two MCA dimensions (ANOVA results)

Source	df	Dimension 1 F	Dimension 1 *p*-value	Dimension 2 F	Dimension 2 *p*-value
Location	1	78.86	<0.001 ***	0.82	0.366
Breed	1	4.72	0.031 *	0.02	0.882
Age group	1	0.70	0.405	0.66	0.416
Sex	1	6.42	0.012 *	0.31	0.576
Model	4	54.13	<0.001 ***	0.72	0.578
Residual	209	—	—	—	—
R^2	—	0.509	—	0.014	—
Adj. R^2	—	0.499	—	−0.005	—

variation rather than clear differentiation among locations, breeds, sexes, or age groups.

Interpretation of MANOVA results (joint analysis of MCA dimensions 1 and 2)

The multivariate analysis of variance (MANOVA), which jointly considers MCA Dimensions 1 and 2, provides a more integrated assessment of phenotypic differentiation. The overall MANOVA model is highly significant across all test statistics (Wilks' $\lambda = 0.483$; Pillai's trace = 0.523;

Table 6 Multivariate analysis of variance (MANOVA) of MCA dimensions by location, breed, age group, and sex

Source	Test statistic	Value	Approx. F	df (hypothesis)	df (error)	*p*-value
Model	Wilks' Lambda	0.4829	22.83	8	416	< 0.001 ***
	Pillai's Trace	0.5225	18.48	8	418	< 0.001 ***
	Lawley–Hotelling Trace	1.0599	27.42	8	414	< 0.001 ***
	Roy's Largest Root	1.0494	54.83	4	209	< 0.001 ***
Location	Wilks' Lambda	0.7210	40.24	2	208	< 0.001 ***
	Pillai's Trace	0.2790	40.24	2	208	< 0.001 ***
	Lawley–Hotelling Trace	0.3869	40.24	2	208	< 0.001 ***
	Roy's Largest Root	0.3869	40.24	2	208	< 0.001 ***
Breed	Wilks' Lambda	0.9779	2.35	2	208	0.098 ns
	Pillai's Trace	0.0221	2.35	2	208	0.098 ns
	Lawley–Hotelling Trace	0.0226	2.35	2	208	0.098 ns
	Roy's Largest Root	0.0226	2.35	2	208	0.098 ns
Age group	Wilks' Lambda	0.9939	0.64	2	208	0.528 ns
	Pillai's Trace	0.0061	0.64	2	208	0.528 ns
	Lawley–Hotelling Trace	0.0062	0.64	2	208	0.528 ns
	Roy's Largest Root	0.0062	0.64	2	208	0.528 ns
Sex	Wilks' Lambda	0.9694	3.28	2	208	0.040 *
	Pillai's Trace	0.0306	3.28	2	208	0.040 *
	Lawley–Hotelling Trace	0.0315	3.28	2	208	0.040 *
	Roy's Largest Root	0.0315	3.28	2	208	0.040 *

Lawley–Hotelling trace = 1.060; Roy's largest root = 1.049; all $p < 0.001$). This confirms that, taken together, the two MCA dimensions are significantly associated with the set of explanatory variables (Table 6).

Consistent with the univariate ANOVA results, location has a very strong multivariate effect on the combined MCA dimensions (Wilks' $\lambda = 0.721$, $p < 0.001$). This indicates pronounced spatial structuring of overall phenotypic variation, reinforcing the conclusion that geographic context plays a central role in shaping morphological trait combinations. Sex also shows a significant multivariate effect (Wilks' $\lambda = 0.969$, $p = 0.040$), confirming that sexual dimorphism influences the joint distribution of structural traits across the two dimensions.

Breed shows a marginal but non-significant multivariate effect ($p = 0.098$), suggesting that while breed influences the primary axis of variation (as seen in Dimension 1), its overall contribution across both dimensions combined is weaker. Age group does not exhibit a significant multivariate effect ($p = 0.528$), further supporting the inference that age-related differences are not a major driver of the phenotypic structure captured by the MCA.

Integrated interpretation and biological meaning

Taken together, the ANOVA and MANOVA results demonstrate that the first MCA dimension captures biologically meaningful and structured phenotypic variation, largely driven by location, with additional effects of breed and sex. This dimension represents the principal axis of morphological differentiation in the population. The second MCA dimension, by contrast, reflects minor variation that is not systematically explained by the studied factors.

The MANOVA confirms that phenotypic differentiation is primarily multivariate and location-dependent, with sex playing a secondary but significant role, while breed contributes modestly and age group contributes minimally. These findings validate the use of MCA as a dimensionality-reduction tool and justify subsequent inferential analyses based on the extracted dimensions, as they successfully link complex morphological trait patterns to key biological and environmental determinants.

Discussion

The morphological characterisation of Small East African Zebu (SEAZ) and Tyrolean Grey Zebu (TGZ) demonstrates that phenotypic differentiation between the two genotypes reflects a structured interaction between genetic inheritance, environmental context, and age. By applying standardised trait definitions consistent with FAO (2012) and subsequent empirical studies, this study avoids subjective interpretation and provides biologically meaningful comparisons relevant for breed classification, selection, and conservation.

Coat colour and environmental context

Coat colour was one of the most discriminating traits between genotypes and locations. SEAZ cattle were predominantly brown, dark brown, and black, whereas TGZ cattle were largely grey and light brown. Brown and dark

brown coats were more frequent in Aswa Ranch and SEAZ cattle, while grey and light brown coats were more common in Lusenke Stock Farm and TGZ animals. These patterns reflect genetic inheritance, particularly the influence of Tyrolean Grey ancestry in TGZ crosses, but they may interact with environmental conditions. Studies across eastern and southern Africa indicate that lighter coats enhance solar reflectance and reduce heat load, while darker coats persist due to cultural preference, camouflage, or long-term stabilisation within indigenous populations (Terefe et al. 2015; Kunene et al. 2022). The observed location-related differences, therefore, likely reflect both environmental filtering and management history rather than direct climatic adaptation alone.

Coat pattern as a genetically stable trait

Coat pattern varied significantly across genotype and location but not across sex or age, confirming its genetic stability. Uniform coat patterns predominated across both locations and genotypes, while pied, shaded, and spotted patterns occurred at low frequencies and were confined to specific location–genotype combinations. Uniform coats predominated in both genotypes, while shaded and spotted patterns were more frequent in TGZ cattle, consistent with increased phenotypic heterogeneity following crossbreeding (Gelaye et al. 2022; Shahid et al. 2022). In contrast, some indigenous populations show reduced pattern diversity under prolonged selection or controlled mating (Ahmed et al. 2024), suggesting that the diversity observed in TGZ reflects relatively recent introgression rather than long-term stabilisation.

Hair length and type: defined ranges and adaptive implications

Hair length differed clearly between genotypes and age groups when classified using standard ranges. Following FAO (2012) and Gelaye et al. (2022), hair length was defined as short (≤2 cm), medium (2.1–5 cm), and long (>5 cm). Short hair was the dominant category overall, with medium and long hair contributing to discrimination between genotypes and between males and females. SEAZ cattle predominantly exhibited short hair within this defined range, a characteristic associated with enhanced convective heat loss in tropical environments. TGZ cattle showed a higher frequency of medium and long hair, reflecting temperate-adapted Tyrolean Grey ancestry. Younger animals in both genotypes tended to fall within the upper limits of the short to medium range, with hair length decreasing or stabilising as animals matured, a pattern also reported for indigenous cattle in Ethiopia (Getaneh et al. 2019). These findings indicate that hair length is shaped primarily by genotype, with age acting as a secondary modifier rather than an independent driver.

Hair type further reinforced genotypic differentiation. Straight hair was predominant overall, whereas curly hair contributed strongly to differentiation between locations and genotypes. Straight hair dominated in SEAZ, while TGZ cattle exhibited a higher frequency of curly hair. Hair type is considered a genetically controlled trait with limited environmental plasticity (FAO 2012), although its functional implications differ across production systems. Curly hair may confer insulation benefits in cooler climates but may reduce heat dissipation under tropical grazing conditions, highlighting a potential trade-off introduced through crossbreeding (Gebremedhin et al. 2023).

Dewlap size: quantified categories and biological relevance

Dewlap size was interpreted using defined measurement ranges to avoid subjectivity. Based on FAO (2012) and Getachew et al. (2020), dewlaps were categorised as small (≤15 cm), medium (16–25 cm), and large (>25 cm), measured as the vertical extension of the dewlap from the neck. SEAZ cattle predominantly fell within the small category, while TGZ cattle were more frequently classified as having medium dewlaps, with only a small proportion exceeding 25 cm. Minimal variation across sex and age supports previous findings that dewlap size is largely genetically determined and weakly influenced by post-maturity growth. Age-related differences were observed descriptively, although the overall test by age was not statistically significant. Small dewlaps predominated across all categories. Although larger dewlaps are often associated with thermoregulation, some studies caution that their functional role may be secondary to genetic conformation and body size (Yakubu et al. 2024).

Hump size and shape: standardised measurements

Hump morphology showed clear genotypic and age-related differentiation when assessed using standard size classes. Following FAO (2012) and Getaneh et al. (2019), hump size was categorised as small (≤10 cm), medium (11–20 cm), and large (>20 cm), measured from the base to the apex of the hump. Most SEAZ cattle exhibited small, erect humps, whereas TGZ cattle more frequently showed medium-sized humps, with occasional drooping shapes. Age influenced hump size, with calves predominantly classified in the small category and adults shifting towards the medium range, consistent with fat deposition and muscular development over time (Gelaye et al. 2022). The predominance of erect

humps in SEAZ aligns with classic zebu morphology, while the variability observed in TGZ reflects exotic genetic influence rather than environmental pressure alone.

Overall, among the evaluated morphological traits, coat colour, hair length, and hair type showed the strongest discriminatory power across locations and genotypes, as indicated by consistently high chi-square values and significance levels (Table 1). In contrast, variation attributable to sex and age was limited and trait-specific.

Structurally conserved traits

Facial and back profiles showed minimal variation across genotypes and environments, indicating strong structural conservation. Straight backs were predominant overall, with curvature occurring more frequently in specific categories. Such traits are widely recognised as being under stabilising selection and are less responsive to environmental variability, making them less informative for adaptive differentiation (FAO 2012; Ibrahim et al. 2024).

Horn and tail traits: quantified functional variation

Horn traits showed limited differentiation, suggesting weak selective pressure across genotypes. In contrast, tail length exhibited pronounced variation when defined using standard anatomical landmarks. Following FAO (2012) and Getaneh et al. (2019), tail length was classified as short (terminating above the hock joint), medium (reaching the hock), and long (extending below the hock). SEAZ cattle predominantly exhibited short tails, while TGZ cattle more frequently displayed medium to long tails. Short and medium tail lengths were most common, with clear differentiation among groups. Age-related progression was evident, with calves largely in the short category and adults shifting toward longer tails. Location-related differences, particularly the higher frequency of long tails in Lusenke Stock Farm cattle, may reflect management conditions or parasite pressure rather than direct climatic adaptation. Similar functional associations between long tails and fly-swatting efficiency have been reported in Ethiopian and Eritrean cattle populations (Banerjee et al. 2014; Goitom et al. 2019).

Implications for selection and crossbreeding

Overall, the findings confirm the study hypothesis that morphological differentiation between SEAZ and TGZ cattle is primarily driven by genetic background, with environment and age acting as modifying factors. The most informative traits—coat colour, hair length and type, dewlap size, hump morphology, and tail length—were interpreted using defined measurement ranges, strengthening the objectivity and biological relevance of the analysis. From a breeding perspective, these results highlight the need to balance productivity gains from exotic introgression with the preservation of adaptive traits characteristic of indigenous SEAZ cattle. Integrating standardised phenotypic characterisation, as advocated by FAO (2012), into breeding and conservation programmes can therefore support sustainable cattle improvement across Uganda's diverse agro-ecological zones.

Overall, the results in Table 2 indicate that hump characteristics, dewlap size, horn orientation, and tail length were the most discriminating morphological traits across locations and genotypes. In contrast, rump shape and most horn traits showed minimal variation. Age-related differences were biggest for back profile and tail length, while sex effects were limited.

Conclusion and recommendations

The morphological characterisation of the Small East African Zebu (SEAZ) and Tyrolean Grey Zebu crosses (TGZ) reveals clear genotype-specific differences in the expression of phenotypic traits, with these differences further influenced by the animal's sex, age, and location. The implications of the findings on coat colour distinctions align with genotype differentiation, which could serve as useful indicators for genotype selection and breed characterisation under different environmental and cattle production systems. These variations provide valuable information for breed classification and conservation strategies, particularly for improving cattle productivity and resilience in diverse agro-ecological zones. There is a need for an mtDNA study to help explain the observed phenotypic variations.

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Author contributions MGA, DRK (Lead) contributed: data collection, MGA (Lead) methodology, SO, DRK, DRM (Lead) validation, MGA (Lead) investigation, writing original draft, formal analysis; DRM, DRK, SO, DKN, SA, MGNM, DK (Lead) review and editing.

Data availability The original data generated in the research was shared alongside the publication.

Declarations

Compliance with ethical requirements The study was conducted in accordance with the institutional requirements. Ethical approval (ref: SVAR- IACUC/238/2025) was obtained from the Institutional Animal Care and Use Committee (IACUC) of the School of Veterinary Medicine and Animal Resources of Makerere University.

Conflict of interest The authors declared no conflict of interest.

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