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Research Article

Phenotypic characterization and Multivariate analysis of Bali cattle in East Nusa Tenggara, Indonesia

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Abstract
Bali cattle (*Bos javanicus*) are well known for their high adaptive capacity to harsh environmental conditions, and low-input management ystems. Despite these adaptive advantages, its productivity is relatively low and varies between areas largely due to seasonal drought. In such a conditons, phenotypic characteristics can be used for developing appropriate improvement strategies for smallholder production systems in the region. This study aimed to characterize phenotypic variations of Bali cattle in East Nusa Tenggara (NTT), Indonesia, by integrating quantitative and qualitative traits using multivariate statistical approaches. Phenotypic data were collected from cattle raised under traditional management systems across several districts. Quantitative measurements included body weight, shoulder height, body length, chest circumference, chest width, and tail length, while qualitative traits encompassed coat color and horn shape. Descriptive statistics and Pearson's correlation analysis were employed to assess relationships among traits, followed by Principal Component Analysis (PCA), Factor Analysis, and hierarchical cluster analysis to explore the underlying structure of phenotypic variation. The results revealed a strong positive correlation between body weight and chest circumference (r = 0.81), indicating that chest girth is a reliable proxy for overall body size. PCA demonstrated that the first principal component accounted for the majority of phenotypic variability, primarily influenced by body weight, body length, and chest circumference. Cluster analysis grouped cattle populations by regional origin, suggesting phenotypic differentiation potentially shaped by environmental conditions and management practices. This study provides baseline phenotypic information to support selection strategies and sustainable breeding programs for Bali cattle in tropical environments.

Keywords: Bali cattle, Morphometric analysis, Phenotypic traits, Principal component analysis, Tropical livestock

INTRODUCTION

Livestock production plays a crucial role in supporting food security and sustaining rural livelihoods in tropical regions, particularly in developing countries that continue to rely on indigenous livestock breeds as primary genetic resources. Phenotypic characterization of local livestock is a fundamental approach to understanding the interactions between genetic background and environmental conditions, especially under low-input production systems. Such information provides a critical scientific basis for developing sustainable breeding and livestock management strategies to improve productivity while maintaining the adaptive capacity of animals in tropical environments (Barendse, 2017; Cooke *et al*., 2020a; 2020b). East Nusa Tenggara Province (NTT) is recognized as one of the major centers for the development of local cattle in Indonesia, particularly Bali cattle, which play a strategic role in smallholder livestock production systems. Bali cattle (*Bos javanicus*) are well known for their high adaptive capacity to harsh environmental conditions, including elevated ambient temperatures, limited feed availability, and traditional low-input management systems. These characteristics make Bali cattle a valuable genetic resource for sustainable livestock development in tropical environments (Firman and Nono, 2021; Widyas *et al.,* 2022). Despite these adaptive advantages, the productivity of Bali cattle in this region remains relatively low, largely due to poor feed quality, traditional husbandry practices, and environmental constraints, particularly seasonal drought. These challenges highlight the need for a comprehensive understanding of Bali cattle's phenotypic characteristics as a basis for developing appropriate improvement strategies for tropical smallholder production systems (Montgomery *et al*., 2010; Hariyono *et al*., 2025).

Morphometric traits such as body weight, withers height, body length, and chest girth have been widely used as indicators of growth performance, body structural development, and overall livestock productivity. Numerous studies have demonstrated that these morphometric measurements are closely associated with production performance and physiological status, indicating their potential use as selection criteria in local cattle breeding programs (Berry *et al.,* 2021; Lomillos and Alonso, 2020). In locally raised cattle under extensive production systems, morphometric traits also reflect adaptation to environmental conditions and the efficiency with which low-quality feed resources are utilized (Velado-Alonso *et a*l., 2022; Bayssa *et al*., 2021). Nevertheless, information regarding phenotypic variation and population structure of Bali cattle in East Nusa Tenggara remains limited and has not yet been comprehensively integrated (Adinata *et al*., 2023).

Multivariate statistical approaches, such as Principal Component Analysis (PCA), Factor Analysis (FA), and cluster analysis, have been widely applied to analyze complex phenotypic data in livestock populations. These methods allow for the reduction of redundant variables and the identification of key traits that explain a substantial proportion of phenotypic variation within a population (Chen *et al*., 2020; Baliarti *et al*., 2023). In addition, cluster analysis based on phenotypic traits can classify livestock populations according to similarities in body characteristics and geographic origin, thereby providing important insights into phenotypic differences among production regions (FAO. 2012; Suryaka *et al*., 2024; Musdalifah *et al*., 2025; Okoh *et al.* 2025). Therefore, the present study aimed to characterize the phenotypic variation of Bali cattle in NTT Province, Indonesia based on qualitative and quantitative traits using multivariate statistical approaches.

MATERIALS AND METHODS

Study area and period

The study was conducted in eight districts of NTT Province, Indonesia: Kupang City, districts of Kupang, South Central Timor, Rote Ndao, North Central Timor, Belu, Ende and Nagekeo. Ende Districts, located on Flores Island, were selected to represent the overall population, as it is one of the major development areas for Bali cattle. The study area is characterized by a tropical climate with an average temperature of approximately 29°C and seasonal fluctuations in feed availability. The management system of Bali cattle in this region is predominantly traditional, with natural forages and agricultural by-products serving as the primary feed resources, as commonly observed in smallholder livestock production systems in NTT (Firman and Nono, 2021; Hariyono *et al*., 2025). These environmental and management conditions were considered potential factors influencing the expression of phenotypic traits in the cattle population.

Materials and sampling procedure

The research materials consisted of Bali cattle reared by smallholder farmers across the eight districts. A total of 120 Bali cattle were included in the study. Animals were randomly selected from herds that met predefined inclusion criteria (clinically healthy, free of deformities, and with typical management exposure). No visual selection based on body size or body condition score was performed, thereby minimizing sampling bias. This approach has been widely applied in phenotypic characterization studies of local cattle under traditional production systems (Lomillos and Alonso, 2020; Baliarti *et al*., 2023). All animals included in the study were clinically healthy at the time of data collection. The sampled population comprised 26 males aged 1-6 years (mean age = 3.04 years) and 94 females aged 1-10 years (mean age = 4.48 years), based on information provided by the farmers. Each animal was treated as an independent observational unit during clustering analysis.

Phenotypic data collection

Phenotypic data were obtained through direct observation and morphometric measurements of each animal. Quantitative parameters measured were body weight (kg), withers height (cm), body length (cm), chest girth (cm), chest width (cm), tail length (cm), age (years), and sex (male, female). All measurements

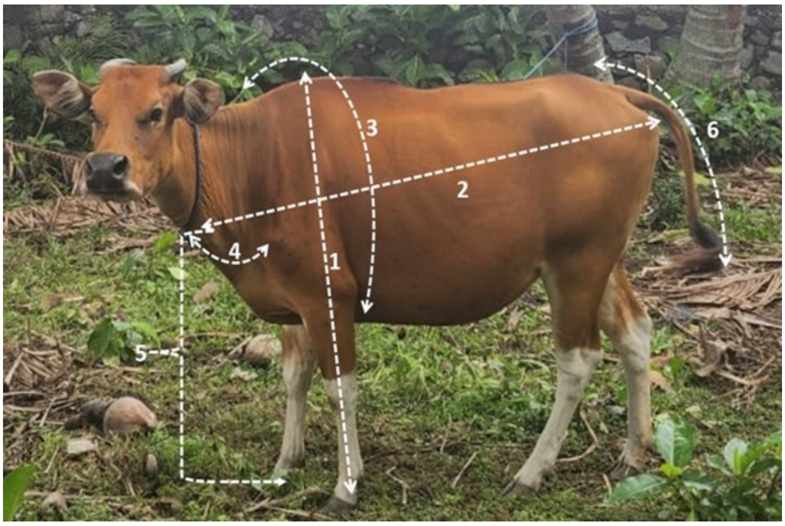


Fig. 1. *Phenotypic characteristics of cattle measured*

were conducted using standard tools, such as measuring tapes and livestock measuring sticks, following established procedures for morphometric characterization of local cattle (Lomillos and Alonso, 2020; Bayssa *et al*., 2021).

Body weight was directly measured for 40 animals using a livestock scale. For 80 animals where weighing facilities were unavailable, body weight was estimated using the following equation adapted from Hartati and Putra (2021):

BW(kg)=a+b×(Chest Girth)2BW (kg) = a + b \times (Chest\ Girth)^2BW(kg)=a+b×(Chest Girth)2

where BW is body weight (kg) and chest girth is expressed in centimeters (Berry et al., 2021).

In addition to quantitative traits, qualitative characteristics—coat color, body color pattern, horn shape, and facial profile were visually assessed and classified according to standard descriptors commonly applied in local cattle studies (FAO, 2012; Baliarti *et al*., 2023; Suryaka *et al.*, 2024; Musdalifah *et al*., 2025; Okoh *et al.,* 2025).

Supplementary information regarding feed types, management systems, and environmental conditions was obtained through brief interviews with farmers. These data provided contextual insights into the observed phenotypic variation, as recommended in studies of local cattle under smallholder production systems (Widyas *et al*., 2022).

Data analysis

Statistical analyses were conducted to describe variation and relationships among phenotypic traits of Bali cattle. Descriptive statistics were used to summarize the basic characteristics of the data, including means, standard deviations, and ranges for quantitative variables, and frequency distributions for qualitative variables. The normality of quantitative data was assessed using the Shapiro–Wilk test prior to parametric analysis. Normality was assessed within sex groups using Shapiro–Wilk tests and verified using Q–Q plots. Mild multimodality was observed in pooled data due to demographic heterogeneity.

Relationships among morphometric traits were evaluated using Pearson's correlation coefficients to determine the strength and direction of associations between variables. Principal Component Analysis (PCA) and Factor Analysis (FA) with Varimax rotation were subsequently applied to reduce data dimensionality and to identify the underlying structure of phenotypic variation. Hierarchical cluster analysis using Ward's method was performed on standardized data to classify cattle based on similarities in phenotypic characteristics and geographic origin. The results of the cluster analysis were presented in the form of a dendrogram.

Statistical analysis

All statistical analyses were performed using R software version 4.1.0 and SPSS version 25.0. PCA, FA, and cluster analysis were conducted using the FactoMineR and cluster packages in R, whereas descriptive statistics and Pearson's correlation analysis were carried out using SPSS, consistent with approaches commonly applied in phenotypic and morphometric studies of local cattle (Pundir *et al*., 2015; Chen *et al*., 2020; Baliarti *et al*., 2023). The level of statistical significance was set at p<0.05.

To control for demographic confounding, morphometric traits were adjusted for age and sex effects prior to multivariate analysis. A General Linear Model (GLM) was fitted for each quantitative trait using the following model:

Yijk=μ+Si+Aj+eijkY_{ijk} = \mu + S_i + A_j + e_{ijk}Yijk =μ+Si+Aj+eijk   Eq.1

where:

YijkY_{ijk}Yijk = observed morphometric trait,

μ\muμ = overall mean,
SiS_iSi = fixed effect of sex (male, female),
AjA_jAj = covariate effect of age (years),
eijke_{ijk}eijk = residual error.

Residuals derived from this model were extracted and used as adjusted values for Principal Component Analysis (PCA) and hierarchical clustering. This approach ensures that multivariate structure reflects phenotypic variation independent of age and sex composition.

RESULTS

Qualitative phenotypic characteristics

Observations results indicated that the Bali cattle examined exhibited relatively uniform qualitative phenotypic characteristics. Coat color was predominantly brick red to brown, with typical features including white markings on the distal parts of the legs and a distinct dark dorsal stripe. All individuals displayed a straight facial profile, while horn shape ranged from short to long. Given the limited sample size per district (approximately 15 animals), districts were grouped into broader agro-ecological zones based on climatic similarity to increase statistical robustness. Multivariate analyses were re-conducted at the zone level.

Phenotypic variation among Bali cattle from different regions of NTT Province is illustrated in Fig. 2. The fig. highlights the general uniformity of the main qualitative characteristics of Bali cattle, with only minor variations observed among individual animals

Quantitative phenotypic characteristics

Descriptive analysis revealed considerable variation in the morphometric traits of Bali cattle, particularly in body weight, withers height, body length, and chest girth. Among these traits, body weight exhibited the widest range of variation, whereas tail length showed relatively low variability (Appendix 1).

The distribution and variability of morphometric traits across the different regions of NTT Province are illustrated in Fig. 3 through boxplots and distribution graphs. These visualizations highlight differences in body size variability among regions, reflecting heterogeneity in phenotypic expression across production areas.

Relationships among morphometric traits

Pearson's correlation analysis between directly measured body weight (n = 120) and chest girth revealed a significant positive association ($r = 0.81$ $p < 0.05$), confirming the robustness of chest girth as a predictor of body size independent of estimation procedures. Positive correlations were also observed between body length and chest girth, as well as between chest width and chest girth. In contrast, tail length exhibited relatively weak correlations with other

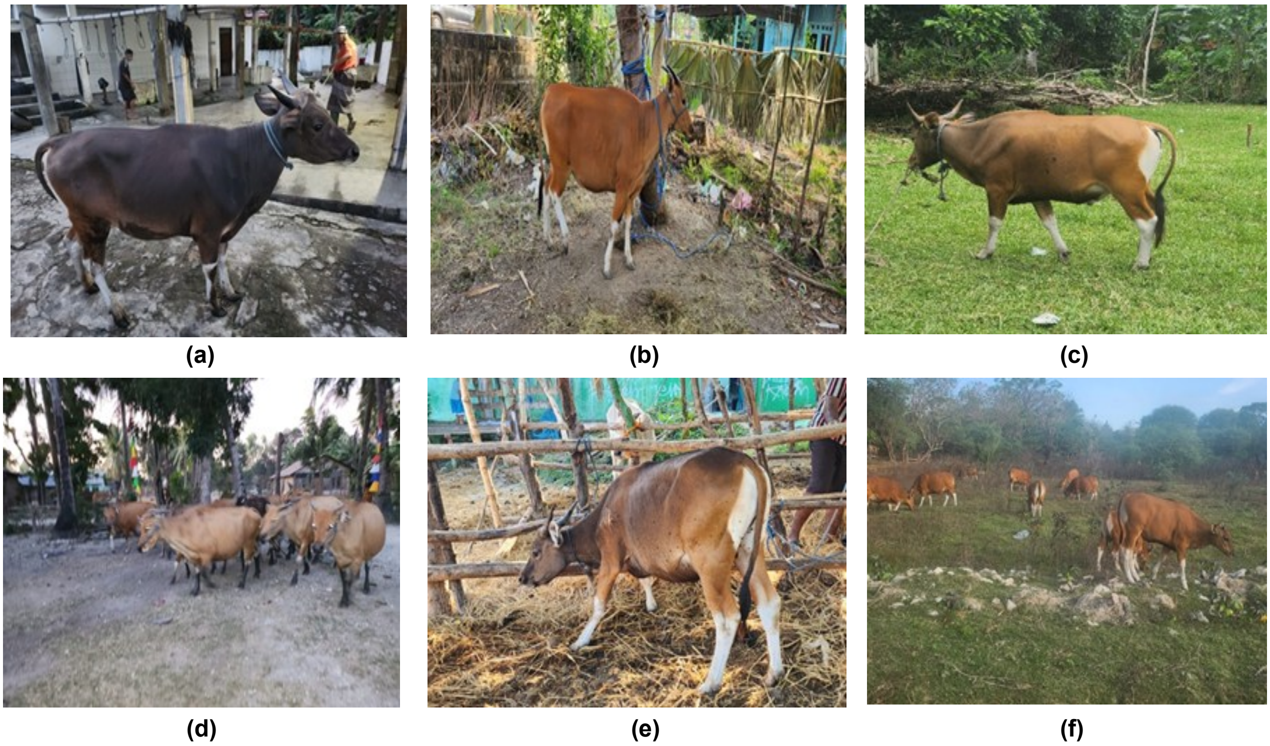
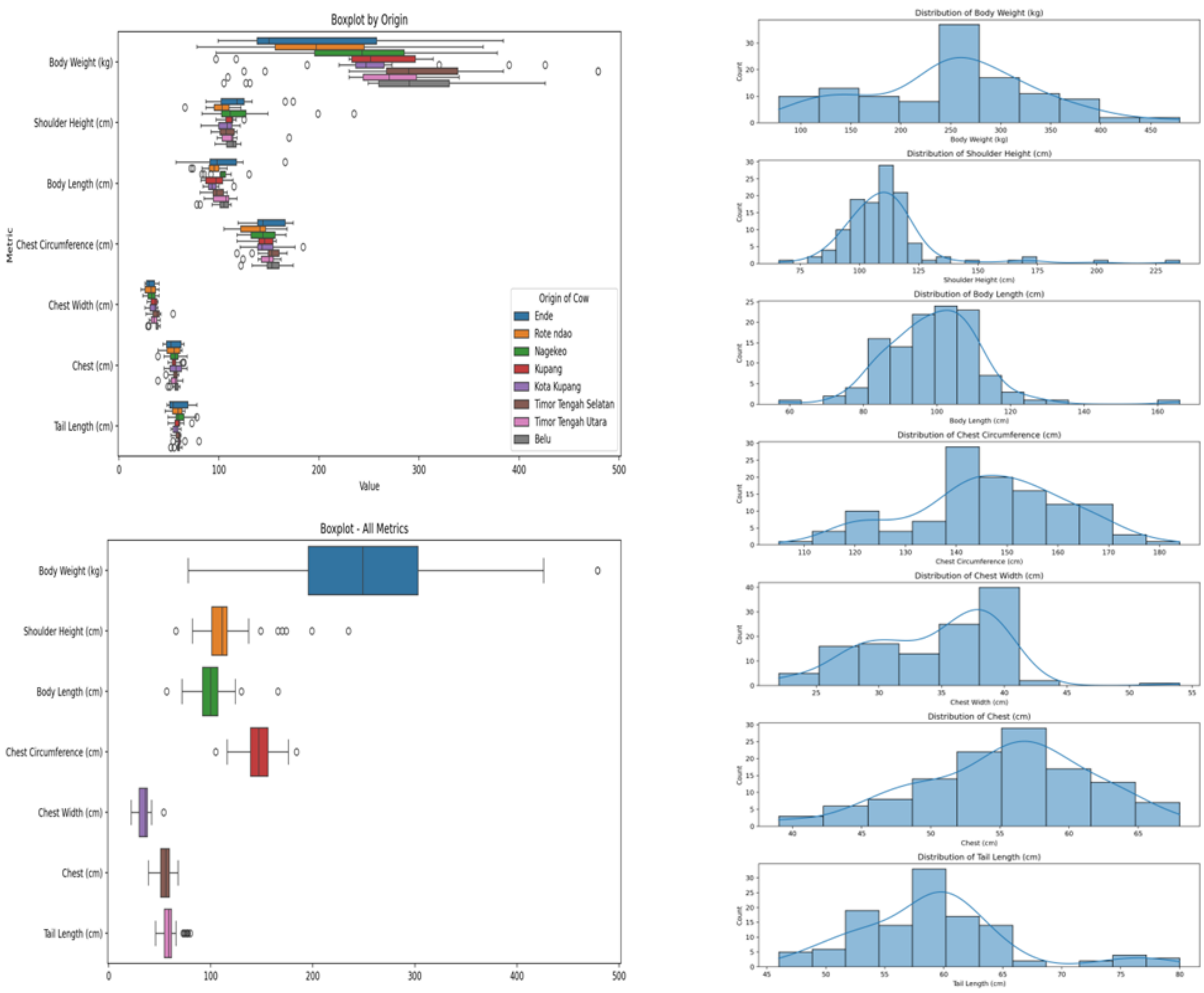


Fig. 2. *Bali cattle from various regencies in East Nusa Tenggara Province: (a) Ende, (b) Kupang, (c) Nagekeo, (d) Belu, (e) Rote Ndao, and (f) South Central Timor; Cluster analysis was performed based on individual animal data rather than regional mean values; therefore, each animal was treated as a single observational unit.*



(A) **(B)**

Fig. 3. *(a). Boxplot of origin and phenotypic characters of cattle, (b). Distribution of each phenotypic character*

morphometric traits.

The patterns of relationships among morphometric traits are visualized in Fig. 3 using a correlation heatmap (Fig.4) and pairwise scatter plots. These visualizations highlight the strength and direction of trait associations, providing insights into the structural relationships underlying phenotypic variation in Bali cattle.

Principal component analysis and factor analysis

Principal Component Analysis (PCA) was conducted using age- and sex-adjusted residual values derived from the GLM. The first principal component (PC1) accounted for 59% of the adjusted phenotypic variance and was primarily associated with body weight, body length, and chest girth. The variables contributing most strongly to PC1 were body weight, body length, and chest girth. The second principal component (PC2) was primarily associated with variation in withers height and tail length.

The PCA results are presented in Fig. 5 as a scree plot and a biplot, which illustrate the relative contributions of morphometric traits to the principal components. Furthermore, Factor Analysis (FA) with Varimax rotation grouped the morphometric traits into two main factors, as visualized in Fig. 6 and 7. These factors highlight the clustering of traits according to their shared variance, providing insights into the structural dimensions of phenotypic variation in Bali cattle.

Cluster analysis based on regional origin

Hierarchical cluster analysis using Ward's method grouped Bali cattle according to similarities in phenotypic traits and regional origin. The clustering results are presented in Fig. 8 as a dendrogram, which reveals several regional clusters with varying levels of phenotypic similarity. These clusters highlight the influence of geographic origin and local management practices on phenotypic differentiation within the Bali cattle population. Hierarchical clustering was performed using individual animal data (n = 120). Branches are

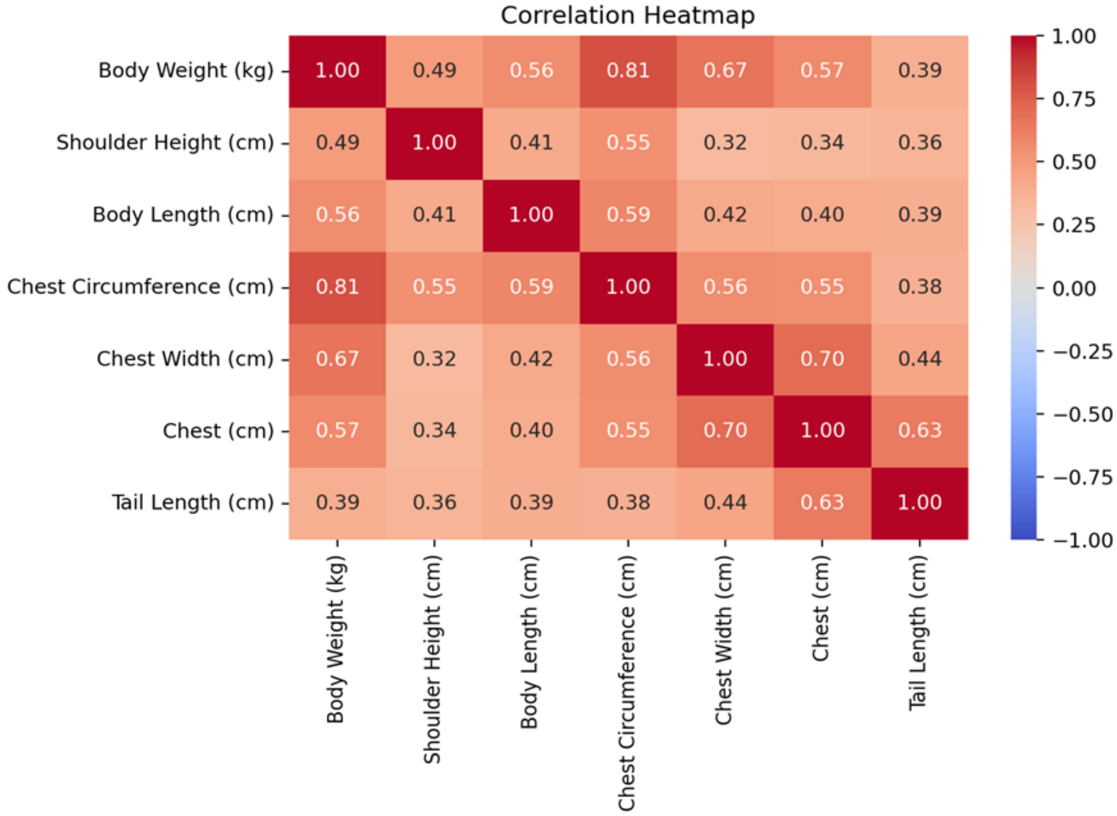


Fig. 4. *Heatmap of phenotypic character correlation*

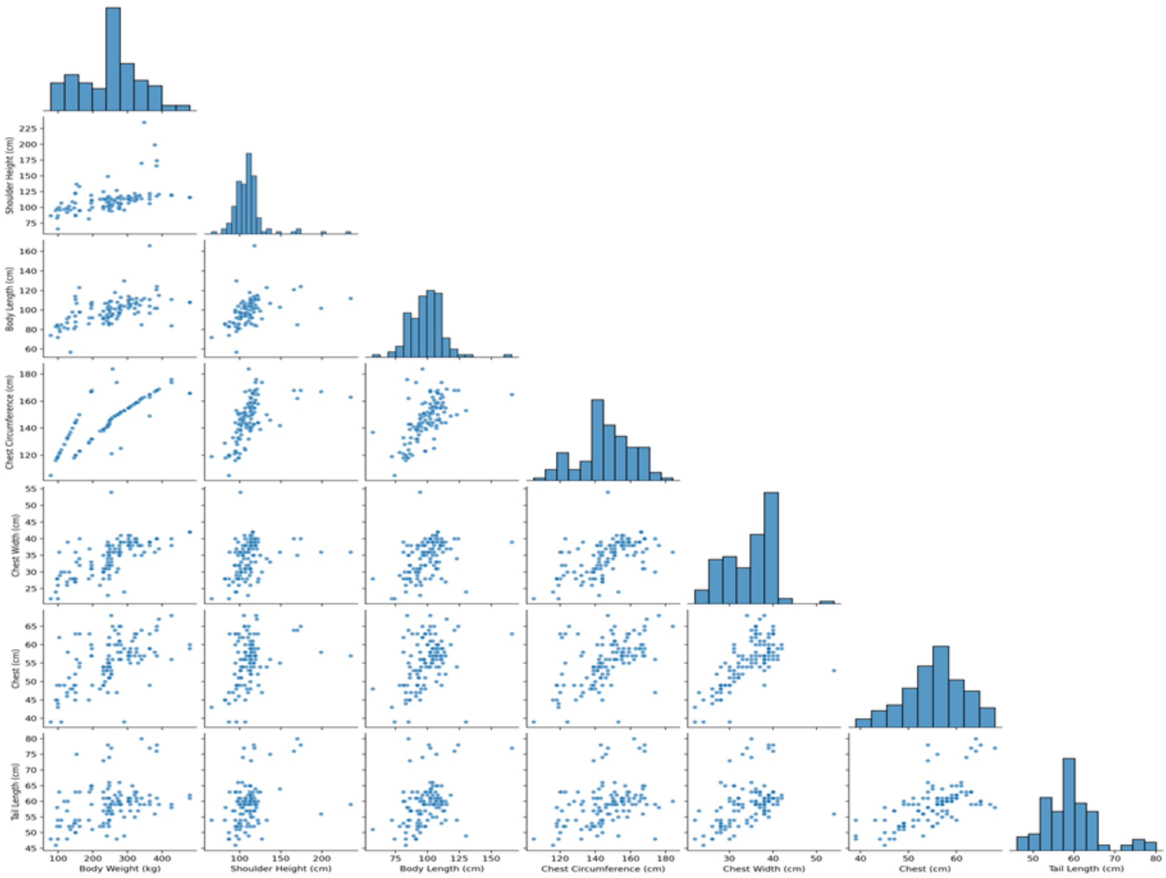


Fig. 5. *Pairplot of the distribution of each phenotypic character of cattle*

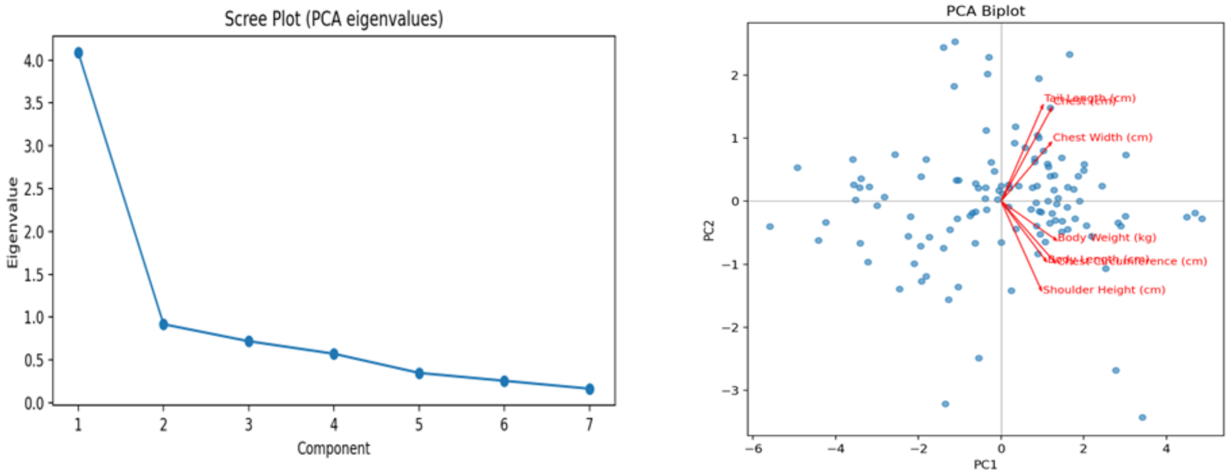


Fig. 6. *Multivariate analysis of phenotypic characters of cattle*

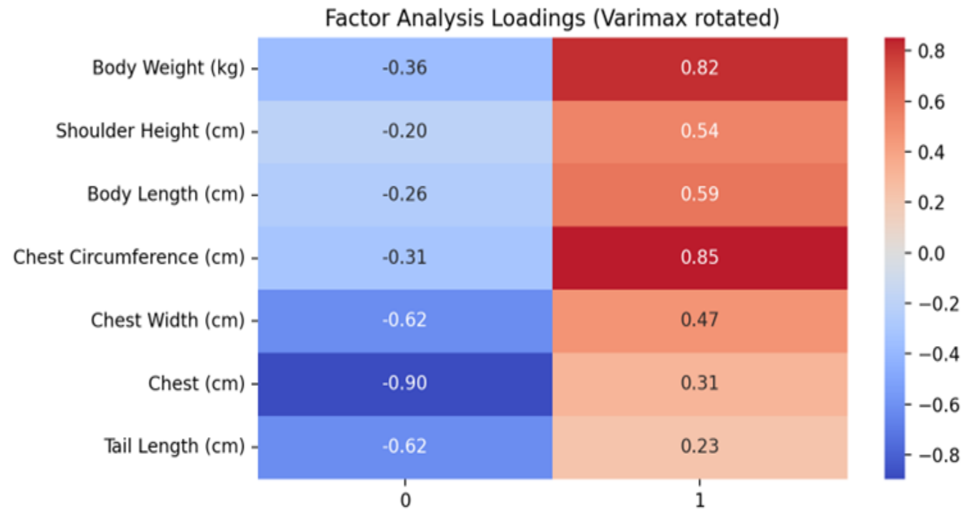


Fig. 7. *Analysis of phenotypic character factors of cattle*

labelled by district affiliation for visualization purposes only.

DISCUSSION

The qualitative phenotypic characteristics observed in this study for Bali cattle are consistent with the breed's typical traits previously reported by Baliarti *et al.* (2023). The predominance of brick red to brown coat color, combined with white markings on the lower legs and the presence of a dark dorsal stripe, represents stable phenotypic features that are commonly used as visual identifiers of Bali cattle (FAO. 2012; Baliarti *et al.,* 2023; Suryaka *et al.,* 2024; Musdalifah *et al.,* 2025; Okoh *et al.,* 2025). The uniformity of these qualitative traits suggests that the Bali cattle population in the study area has largely maintained its breed-specific characteristics.

The clustering of Bali cattle based on phenotypic traits reflects similarity in external morphology rather than genetic differentiation. Environmental conditions, feeding systems, management practices, and demographic factors such as age structure and sex composition likely influence regional differences in phenotypic expression. In the absence of genetic data or a common-garden experimental design, genetic interpretation of the observed clustering patterns could not be reliably inferred.

Variation in morphometric traits, particularly body weight and chest girth, reflects the combined influence of environmental factors and management practices. Body weight, which exhibited the widest range of variation, appears highly sensitive to differences in feed availability and production systems, consistent with findings from studies of local cattle in other tropical regions (Kebede *et al.,* 2021; Bayssa *et al.,* 2021; Lomillos and Alonso, 2020; Adinata *et al.,* 2023). Since age and sex were not included as covariates, demographic structure may have partially contributed to the observed variation. Tail length showed weak correlations with the main morphometric traits, suggesting a limited role in explaining overall body size variation in Bali cattle.

The strong positive correlation between body weight and chest girth confirms that chest girth is a reliable

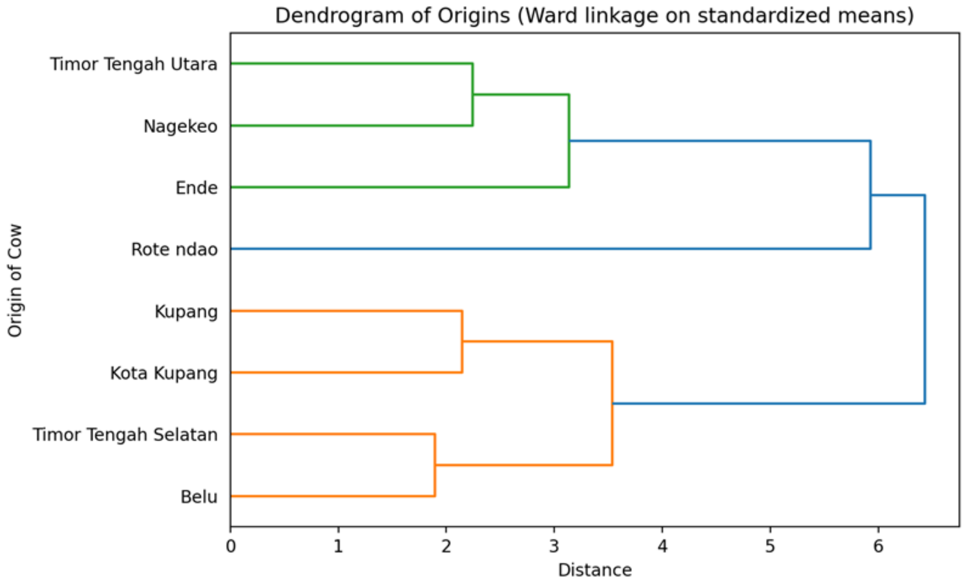


Fig. 8. *Dendrogram of cattle grouping based on phenotypic characters according to region of origin (district).*

proxy for estimating body weight in Bali cattle, particularly under smallholder production systems where weighing facilities are limited. This finding aligns with the reports of Berry *et al*. (2021) and Hartati and Putra (2021), who demonstrated that specific body measurements can serve as practical predictors of body weight in cattle. Conversely, the weak association between tail length and other morphometric traits suggests that this trait is relatively independent of overall body size. Tail length, therefore, appears less relevant as a selection criterion in body size–based breeding programs, consistent with previous studies on local cattle morphology (Mancin *et al*., 2021).

Overall, the phenotypic clustering observed in this study likely reflects environmental plasticity rather than genetic differentiation. Regional differences may reflect environmental variation, although specific environmental parameters were not quantitatively measured in this study. Therefore, environmental influences should be interpreted as hypotheses rather than confirmed causal factors. The results of PCA and FA indicated that phenotypic variation in Bali cattle was largely explained by a single major factor associated with body size, particularly body weight, body length, and chest girth. This pattern is consistent with previous findings (Pundir *et al*., 2015; Kebede, *et al*., 2021; Chen *et al*., 2020; Baliarti *et al*., 2023) that a primary body size dimension generally dominates the phenotypic structure of local cattle populations.

The clustering of Bali cattle based on phenotypic traits suggests that variation is influenced not only by genetic factors but also by environmental conditions and management systems prevailing in different regions. This supports the concept that phenotypic adaptation in local cattle results from interactions between genetic background and environmental influences (Velado-Alonso *et al*., 2022; Adinata *et al*., 2023). The physiological status of female cattle (e.g., pregnancy or lactation stage) was not recorded during sampling and may have influenced body weight and girth measurements. This represents a potential source of uncontrolled variation.

The present findings confirm that body weight, chest girth, and body length are the principal traits contributing to body size variation in Bali cattle. These traits demonstrate strong potential as practical selection criteria for Bali cattle development programs in tropical regions. However, this study has several limitations, including the lack of control for age, sex, and management system as separate factors, as well as the ab-

Appendix 1. Table showing descriptive statistics of morphometric traits by sex (Mean ± SD)

Trait	Male (n = 26)	Female (n = 94)
Body weight (kg)	222.19 ± 18.78	196.33 ± 15.23
Withers height (cm)	112.45 ± 4.12	108.37 ± 3.85
Body length (cm)	121.68 ± 5.34	116.92 ± 4.76
Chest girth (cm)	156.72 ± 6.21	148.85 ± 5.44
Chest width (cm)	37.84 ± 2.15	35.96 ± 1.98
Tail length (cm)	77.52 ± 3.88	74.63 ± 3.47

sence of genetic data. Consequently, the results primarily reflect phenotypic variation under smallholder farming conditions and should be interpreted with caution in the context of genetic improvement programs. The relatively small number of animals per district limits the strength of sub-regional inference. Therefore, clustering patterns should be interpreted cautiously and validated using larger population samples. Future research should integrate genomic tools such as SNP genotyping to validate phenotypic clustering patterns. Estimation of heritability and genetic correlations for key morphometric traits will be essential to distinguish environmental plasticity from genetic differentiation. Controlled experimental designs are also recommended to isolate environmental effects.

Conclusion

This study provides a phenotypic characterization of Bali cattle (Bos javanicus) in East Nusa Tenggara under smallholder conditions. After adjusting morphometric traits for age and sex effects using a General Linear Model, multivariate analyses indicated that body weight, chest girth, and body length constitute the primary axis of structural body size variation. Although regional clustering patterns were observed, these results reflect adjusted phenotypic structure rather than confirmed genetic differentiation. Therefore, while key morphometric traits may serve as practical field indicators, their use in breeding programs requires further validation through genetic parameter estimation and genomic analysis.

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Data availability
The data used in this study are available from the corresponding author upon reasonable request.

Conflict of interest
The authors declare that they have no conflict of interest.

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