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Association of *POU1F1* Gene Variants with Morphometric Traits and Blood Parameters in Muturu and Bunaji Cattle

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ABSTRACT

Background and Objective: Genetic markers like the *POU1F1* gene are known to influence growth and development traits in livestock. However, there is limited information on its association with morphometric, haematological, and biochemical traits in Nigerian indigenous cattle. This study aimed to evaluate the correlation between *POU1F1* gene variants with various phenotypic traits and blood parameters in Muturu and Bunaji cattle breeds to understand their potential role in breeding strategies. **Materials and Methods:** A total of 452 Muturu and Bunaji cattle were sampled. Morphometric measurements (e.g., body length, chest girth, tail length), haematological, and biochemical parameters were recorded. The DNA was extracted and genotyped to identify *POU1F1* polymorphisms. Data were analyzed using correlation analysis and statistical tests, including ANOVA and Pearson's correlation coefficient, to assess associations between genetic variants and phenotypic traits. Statistical significance was determined at $p<0.05$, with $p<0.01$ and <0.001 considered highly significant. **Results:** Significant positive correlations were observed among morphological traits, particularly body length, chest girth, and tail length, indicating their collective role in body size and robustness. However, the *POU1F1* gene showed weak or negligible correlations with most measured traits in both breeds. These findings suggest that while morphometric traits are interrelated, *POU1F1* may have limited influence on the traits assessed. **Conclusion:** This study provides insights into the limited association of *POU1F1* gene variants with growth-related traits in Muturu and Bunaji cattle. Although morphological traits are strongly interrelated, the gene's minimal contribution highlights the need for exploring other genetic markers. The findings support more targeted breeding programs integrating phenotypic selection with broader genomic tools.

KEYWORDS

Cattle, *POU1F1* gene, correlation, morphometric traits, blood parameters, Muturu, Bunaji, age, sex

INTRODUCTION

Genetic variants in livestock, particularly in cattle breeds such as Muturu and Bunaji, are crucial for improving meat production and overall productivity in small-scale farming systems. In Nigeria, these breeds are highly valued for their lean meat, disease resistance, and hardiness, despite limited milk production[1]. Enhancing the genetic makeup of these breeds through selective breeding can significantly

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contribute to food security and the livelihoods of small-scale farmers[2]. Recent studies have demonstrated the importance of DNA polymorphism in improving genetic traits in livestock, such as the use of single-nucleotide polymorphisms (SNPs) to identify genotypic variants associated with desirable traits in Saanen goat[3].

The *POU1F1* gene, encoding Pituitary Specific Transcription Factor-1, plays a vital role in regulating growth hormone, prolactin, thyroid-stimulating hormone, and itself in mammals[4]. Genetic variations in *POU1F1* have been associated with growth, carcass, milk, and wool traits in diverse breeds[5,6]. Moreover, polymorphisms in the *POU1F1* gene have been linked to body weight in multiple breeds[7]. Despite the significance of *POU1F1* in livestock genetics, research on its genetic variants in Nigerian Muturu and Bunaji breeds is limited.

This study aims to explore the genetic variants of *POU1F1* and their relationship with morphometric traits and blood parameters at various stages of growth in the Muturu and Bunaji breeds. By investigating the genetic variants of *POU1F1*, this study will contribute to the advancement of genetic research in Nigeria, providing valuable insights for selective breeding programs and improving the productivity of these breeds. The findings of this study will advance new knowledge on the genetic mechanisms underlying growth and development in Muturu and Bunaji breeds, ultimately informing strategies for genetic improvement and sustainable livestock production in Nigeria.

MATERIALS AND METHODS

Study locations: This ten-month study, spanning from March, 2023 to January, 2024, embarked on an in-depth exploration of the intricate relationship between *POU1F1* gene expression and morphometric traits in Muturu and Bunaji cattle breeds. Conducted across two distinct Agroecological Zones in Nigeria, specifically in Ebonyi and Kogi States, this research employed a quantitative genetic approach to unravel the complexities of these cattle breeds.

Studied animal: A total of 452 ranched animals, comprising 226 each of the Muturu and Bunaji breeds, were meticulously selected for this study. The research design was structured as a symmetrical factorial (2×2×5) arrangement within a Complete Randomized Design (CRD), incorporating two breeds, two sexes, and five age groups.

Body linear traits: Twelve body linear traits were measured with precision using a flexible tape, including body weight (BW), body length (BL), height at withers (HW), chest girth (CG), horn length (HL), muzzle circumference (MC), ear length (EL), hock circumference (HC), pelvic width (PW), cannon bone circumference (CC), facial length (FL), and tail length (TL). A weighing band was utilized to record the animals weights, while their handlers assisted in restraining them to facilitate accurate measurements[7].

The age of each animal was determined through a combination of methods, including counting the number of rings on their horns, examining their dentition, and referencing recorded ages provided by the breed owners.

Data analysis: Data analysis was conducted using SAS Version 9.4, with all collected data on body weight and body linear traits subjected to t-test analysis. The level of significance was set at $p<0.05$, The results were presented as Means±Standard Errors of means as determined from the different populations.

Ethical consideration: This study, examining the relationship between *POU1F1* gene expression and morphometric traits in Muturu and Bunaji cattle breeds, prioritized animal welfare and adhered to stringent ethical standards. Key considerations included ensuring that all animal handling, measurements, and procedures were conducted with minimal stress, discomfort, and harm to the cattle. To achieve this, trained personnel employed humane handling practices during data collection, including body measurements and physical evaluations, always prioritizing the safety and well-being of the animals.

Informed consent: Before collaborating with farmers or farm owners, informed consent is obtained from all participants. This consent provides a clear understanding of the study's purpose, the roles and responsibilities of the farmers, and how the collected data will be utilized. Additionally, farmers are fully informed about any potential risks or benefits associated with their participation, ensuring they can make an informed decision about their involvement in the study.

RESULTS

Correlation coefficients of linear parameters of the muturu breed of cattle with the *POU1F1* gene: Table 1 presents a correlation analysis of morphological traits in the Muturu breed of cattle to ascertain the association of the *POU1F1* gene with different measurements. By correlating each parameter with others, this analysis attempts to uncover how the *POU1F1* gene contributes to the complex web of relationships between these traits, providing insights into its impact on the breed's morphology.

Ear length (EL) showed strong, significant ($p<0.05$) positive correlations with several traits, particularly body length (BL) at 0.622 and chest girth (CG) at 0.641. This suggests that longer ears are associated with larger body dimensions, which may indicate overall size and robustness.

Body length (BL) has an exceptionally highly significant ($p<0.05$) correlation with chest girth (CG) at 0.946, indicating that these two measurements are closely related and may reflect similar growth patterns in the cattle. Additionally, BL correlated positively and significantly ($p<0.05$) with other traits such as tail length (TL) (0.827) and muzzle circumference (MC) (0.725), reinforcing the fact that larger body sizes are associated with increased girth and muscle development.

Tail length (TL) also showed strong ($p<0.05$) correlations with other parameters, including muzzle circumference (MC) (0.765) and height at withers (HW) (0.762), suggesting that tail length can be an indicator of overall body size and muscularity.

The parameter muzzle circumference (MC) correlated positively ($p<0.05$) with several other traits, including height at withers (HW) (0.800) and pelvic width (PW) (0.797). This indicates that increased muzzle circumference is associated with larger body dimensions and pelvic width, which may be important for reproductive performance.

Height at withers (HW) shows strong positive correlations with other measurements such as pelvic width (PW) (0.777) and canon circumference (CC) (0.566), suggesting that taller animals tend to have larger pelvic widths and canon circumferences. Hock circumference (HC) also exhibited positive significant ($p<0.05$) correlations with various traits, including body length (0.513) and muzzle circumference (0.508), indicating that body size is related to overall body dimensions.

Table 1: Correlation coefficients of linear parameters of Muturu breed of cattle with *POU1F1* gene

Muturu	EL	BL	CG	HL	TL	MC	HW	HC	PW	CC	FL	BW	*POU1F1*
BL	0.622**												
CG	0.641**	0.946**											
HL	0.467**	0.522**	0.487**										
TL	0.827**	0.695**	0.726**	0.583**									
MC	0.725**	0.644**	0.615**	0.645**	0.765**								
HW	0.724**	0.500**	0.520**	0.526**	0.762**	0.800**							
HC	0.513**	0.476**	0.497**	0.351**	0.563**	0.508**	0.506**						
PW	0.831**	0.671**	0.703**	0.588**	0.887**	0.797**	0.777**	0.591**					
CC	0.596**	0.563**	0.575**	0.450**	0.626**	0.566**	0.550**	0.918**	0.659**				
FL	0.848**	0.712**	0.741**	0.523**	0.878**	0.806**	0.763**	0.673**	0.911**	0.748**			
BW	0.595**	0.919**	0.954**	0.482**	0.666**	0.595**	0.464**	0.517**	0.662**	0.537**	0.697**		
POU1F1 gene	-0.025	0.101	0.145	-0.016	0.021	0.161	0.03	0.128	0.096	0.075	0.099	0.138	
Coat colour	-0.015	-0.028	-0.024	0.079	-0.026	-0.017	0.002	-0.035	-0.01	-0.062	-0.086	-0.042	0.017

**Correlation is significant at the 0.01 level (2-tailed), EL: Ear length, BL: Body length, CG: Chest girth, HL: Horn length, TL: Tail length, MC: Muzzle circumference, HW: Height at withers, HC: Hock circumference, PW: Pelvic width, CC: Cannon borne circumference, FL: Facial length and BW: Body weight

Table 2: Correlation coefficients of linear parameters of Bunaji cattle breed with *POU1F1* gene

Bunaji	EL	BL	CG	HL	TL	MC	HW	HC	PW	CC	FL	BW	*POU1F1*
BL	0.678**												
CG	0.598**	0.885**											
HL	0.616**	0.647**	0.566**										
TL	0.746**	0.711**	0.643**	0.583**									
MC	0.665**	0.697**	0.719**	0.568**	0.740**								
HW	0.684**	0.730**	0.676**	0.658**	0.699**	0.633**							
HC	0.625**	0.634**	0.634**	0.472**	0.574**	0.719**	0.510**						
PW	0.735**	0.750**	0.745**	0.613**	0.770**	0.868**	0.647**	0.766**					
CC	0.593**	0.574**	0.595**	0.453**	0.392**	0.517**	0.453**	0.824**	0.681**				
FL	0.788**	0.738**	0.711**	0.599**	0.744**	0.793**	0.611**	0.833**	0.890**	0.750**			
BW	0.575**	0.882**	0.982**	0.546**	0.626**	0.691**	0.673**	0.600**	0.707**	0.545**	0.687**		
POU1F1 gene	0.025	-0.04	-0.081	0.249*	-0.002	0.09	0.018	0.012	0.04	-0.07	0.1	-0.076	
Coat colour	-0.001	0.085	0.044	-0.065	-0.048	0.03	-0.01	-0.016	0.059	0.019	0.001	0.031	-0.057

**Correlation is significant at the 0.01 level (2-tailed), EL: Ear length, BL: Body length, CG: Chest girth, HL: Horn length, TL: Tail length, MC: Muzzle circumference, HW: Height at withers, HC: Hock circumference, PW: Pelvic width, CC: Cannon borne circumference, FL: Facial length and BW: Body weight

Pelvic width (PW) had strong ($p<0.05$) positive correlations with other parameters, particularly tail length (0.831) and canon circumference (0.918), suggesting that wider pelvises are indicative of larger overall body sizes.

The trait canon circumference (CC) showed significant ($p<0.05$) positive correlations across several parameters, including pelvic width (0.918) and muzzle circumference (0.626), indicating that body size is closely related to other body measurements.

Finally, the variable body weight (BW) correlates highly with chest girth (0.919) and muzzle circumference (0.595), suggesting that heavier animals tend to have larger girths and circumferences. In contrast, the parameter association with the *POU1F1* gene showed negligible or weak correlations with most traits, indicating it may not significantly influence or be influenced by the other measured parameters in this dataset.

Correlation coefficients of linear parameters of the bunaji breed of cattle with the *POU1F1* gene: Table 2 presents a correlation analysis of various morphological traits in the Bunaji breed of cattle, highlighting the relationships among different measurements that are essential for understanding the breed's physical characteristics. Ear Length (EL) showed strong ($p<0.05$) positive correlations with several parameters, particularly body length (BL) at 0.678 and chest girth (CG) at 0.598. This suggests that as ear length increases, both body length and chest girth tend to increase, indicating a potential relationship between these physical traits.

Body length (BL) had a particularly high ($p<0.05$) correlation with chest girth (CG) at 0.885, which indicates that these two dimensions were closely related and likely reflect similar growth patterns in the cattle. Additionally, BL correlated ($p<0.05$) positively with other traits such as tail length (TL) (0.746) and muzzle circumference (MC) (0.665), reinforcing the idea that larger body sizes are associated with increased girth and muscle development.

Tail length (TL) also exhibited strong correlations with other parameters, including muzzle circumference (MC) (0.740) and height at withers (HW) (0.699), suggesting that tail length could be an indicator of overall body size and muscularity.

The parameter muzzle circumference (MC) correlated positively with several other traits, including height at withers (HW) (0.633) and pelvic width (PW) (0.868). This indicated that increased muzzle circumference was associated with larger body dimensions and pelvic width, which may be important for reproductive performance.

Height at withers (HW) showed strong ($p<0.05$) positive correlations with other measurements such as pelvic width (PW) (0.647) and canon circumference (CC) (0.517), suggesting that taller animals tend to have larger pelvic widths and canon circumferences. Hock circumference (HC) exhibited positive significant ($p<0.05$) correlations with various traits, including body length (0.625) and muzzle circumference (0.719), indicating that muzzle size was related to overall body dimensions.

Pelvic width (PW) had strong positive correlations with other parameters, particularly tail length (0.735) and canon circumference (0.824), suggesting that wider pelvises were indicative of larger overall body sizes. The trait canon circumference (CC) showed highly significant ($p<0.05$) positive correlations across several parameters, including pelvic width (0.681) and muzzle circumference (0.517), indicating that body size was closely related to other body measurements.

Moreover, the variable body weight (BW) correlated highly ($p<0.05$) with chest girth (0.882) and muzzle circumference (0.691), suggesting that heavier animals tended to have larger girths and circumferences. In contrast, the parameter associated with the *POU1F1* gene but it was negligible or weak correlations with most traits, indicating it may not significantly influence or be influenced by the other measured parameters in this dataset.

Correlation coefficients of haematological parameters of muturu cattle breed with *POU1F1* gene: Table 3 presents the expression of the *POU1F1* gene and its correlation with various haematological parameters in the Muturu breed of cattle. As *POU1F1* regulates haematopoiesis, each parameter's correlation with the gene's expression can indicate specific health conditions, ultimately revealing the breed's overall well-being and the impact of *POU1F1* on their haematological profile.

Erythrocyte sedimentation rate (ESR) showed a strong ($p<0.01$) negative correlation with several parameters, including Haemoglobin (Hb) at -0.615 and Red Blood Cell count (RBC) at -0.499. This suggests that lower PCV levels may be indicative of anemia, as both RBC and Hb levels decrease alongside it. The strong positive correlation between RBC and PCV (0.968) further emphasized the importance of these parameters in assessing the oxygen-carrying capacity of the blood.

White blood cell count (WBC) exhibited a robust positive ($p<0.01$) correlation with both RBC (0.980) and Hb (0.979), indicating that higher WBC counts were associated with increased red blood cell production and haemoglobin levels. This relationship may reflect an immune response or inflammation, as elevated WBC counts often occur in response to infection or stress.

The parameter Mean Corpuscular Volume (MCV) showed a strong ($p<0.05$) negative correlation with PCV (-0.909) and RBC (-0.939), suggesting that larger red blood cells are associated with lower packed cell volumes, potentially indicating macrocytic anemia. Conversely, MCV has a positive correlation with Mean Corpuscular Haemoglobin (MCH) at 0.501, indicating that variations in cell size affect haemoglobin content.

Mean Corpuscular Haemoglobin Concentration (MCHC) displays weak correlations overall, including a slight negative correlation with PCV (-0.072) and a positive correlation with WBC (0.152). This suggests minimal direct relationships with these parameters. The parameter lymphocytes (LYM) showed a significant ($p<0.01$) negative correlation with PCV (-0.952) and RBC (-0.967), indicating that higher lymphocyte counts may coincide with lower red blood cell levels, which could be a sign of chronic disease or immune response.

Neutrophil (NEU) had a negative correlation with PCV at -0.372, while exhibiting strong ($p<0.01$) positive correlations with RBC (0.806) and Hb (0.820). This suggested that better nutritional energy utilization was linked to improved red blood cell production.

Table 3: Correlation coefficients of haematological parameters of Muturu cattle breed with *POU1F1* gene

Muturu	ESR	PCV	RBC	WBC	Hb	MCHC	MCV	MCH	LYM	NUE	MON	EOS	BAS *POU1F1*
PCV	-0.620**												
RBC	-0.499**	0.968**											
WBC	-0.581**	0.980**	0.976**										
Hb	-0.615**	0.987**	0.978**	0.979**									
MCHC	-0.072	0.082	0.221	0.152	0.243								
MCV	0.492**	-0.909**	-0.939**	-0.922**	-0.937**	-0.317*							
MCH	0.501**	-0.928**	-0.942**	-0.933**	-0.935**	-0.19	0.991**						
LYM	0.473**	-0.952**	-0.967**	-0.953**	-0.971**	-0.275	0.939**	0.933**					
NUE	-0.372*	0.806**	0.823**	0.802**	0.820**	0.223	-0.810**	-0.806**	-0.852**				
MON	-0.325*	0.393*	0.399*	0.417**	0.431**	0.297	-0.410**	-0.385*	-0.424**	0.101			
EOS	-0.418**	0.578**	0.575**	0.554**	0.579**	0.102	-0.569**	-0.573**	-0.545**	0.282	0.126		
BAS	0.386*	-0.487**	-0.493**	-0.468**	-0.508**	-0.218	0.541**	0.528**	0.493**	-0.714**	-0.149	-0.299	
POU1F1 gene	0.016	0.094	0.096	0.131	0.123	0.203	-0.191	-0.164	-0.155	0.097	-0.074	0.189	0.092

**Correlation is significant at the 0.01 level (2-tailed), *Correlation is significant at the 0.05 level (2-tailed). ESR: Erythrocyte sedimentation rate, PCV: Packed cell volume, RBC: Red blood cell, WBC: White blood cell, Hb: Haemoglobin, MCHC: Mean cell haemoglobin concentration, MCV: Mean cell volume, MCH: Mean cell haemoglobin, LYM: Lymphocyte, NUE: Neutrophil, MON: Monocyte, EOS: Eosinophil and BAS: Basophil

Monocytes (MON) exhibited weak correlations across the board, including a slight negative correlation with PCV (-0.325) but positive correlations with RBC (0.393) and Hb (0.431), indicating that while monocyte levels were generally low, they still have some association with red blood cell metrics.

Eosinophils (EOS) show a negative correlation with PCV (-0.418) but positive ($p<0.01$) correlations with WBC (0.578) and Hb (0.579). This suggests that higher eosinophil counts may occur alongside lower packed cell volumes, potentially indicating allergic reactions or parasitic infections.

Basophils (BASS) present mixed correlations, they have a positive correlation with eosinophils at 0.386, yet negative correlations ($p<0.01$) with PCV (-0.487) and Hb (-0.508). This indicated that as basophil levels increased, there might be concurrent decreases in haemoglobin and packed cell volume.

The analysis revealed a remarkably low correlation between the *POU1F1* gene expression and all haematological parameters, indicating a potential low relationship between this gene and the blood characteristics measured. This finding suggested that *POU1F1* may not be a significant player in shaping haematological traits, inviting further exploration to clarify its role.

Correlation coefficients of haematological parameters of Bunaji cattle breed with *POU1F1* gene: The analysis of haematological parameters in the Bunaji breed of cattle uncovered significant relationships that offer a glimpse into their health and physiological status. Nevertheless, the *POU1F1* gene seemed to have a negligible impact on their haematological traits, as no substantial correlations were identified between the gene and the measured parameters, as presented in Table 4.

This study examined several haematological parameters, including Packed Cell Volume (PCV), Red Blood Cell Count (RBC), White Blood Cell Count (WBC), Haemoglobin Concentration (Hb), Mean Corpuscular Hemoglobin Concentration (MCHC), Mean Corpuscular Volume (MCV), Mean Corpuscular Hemoglobin (MCH), Lymphocytes (LYM), neutrophils (NEU), monocytes (MON), eosinophils (EOS), and basophils (BAS). A significant negative correlation ($p<0.01$) was observed between ESR and multiple parameters, including RBC (-0.229) and Hb (-0.253), suggesting that a decline in ESR levels may serve as an indicator of anemia, as it coincides with reductions in RBC and Hb. Additionally, a strong positive correlation ($P<0.01$) between RBC and PCV (0.985) highlights the crucial role of these parameters in evaluating the blood's oxygen-carrying capacity.

Table 4: Correlation coefficients of haematological parameters of Bunaji cattle breed with *POU1F1* gene

Bunaji	ESR	PCV	RBC	WBC	Hb	MCHC	MCV	MCH	LYM	NUE	MON	EOS	BAS
PCV	-5.18**												
RBC	-0.229	0.985**											
WBC	-0.383*	0.929**	0.914**										
Hb	-0.253	0.993**	0.993**	0.918**									
MCHC	-0.034	-0.339*	-0.213	-0.358*	-0.229								
MCV	0.3	-0.898**	-0.950**	-0.889**	-0.923**	0.051							
MCH	0.284	-0.938**	-0.964**	-0.933**	-0.940**	0.248	0.980**						
LYM	0.312*	-0.867**	-0.862**	-0.835**	-0.861**	0.303	0.839**	0.874**					
NUE	-0.295	0.765**	0.746**	0.750**	0.758**	-0.285	-0.730**	-0.764**	-0.844**				
MON	-0.02	-0.143	-0.102	-0.112	-0.132	0.135	0.07	0.095	0.096	-0.494**			
EOS	-0.179	-0.035	-0.013	-0.034	-0.034	0.03	-0.036	-0.028	-0.07	-0.089	-0.07		
BAS	0.287	0.182	0.143	0.103	0.171	-0.154	-0.036	-0.066	-0.106	0.023	-0.205	-0.501**	
POU1F1 gene	0.263	-0.221	-0.223	-0.316*	-0.196	0.271	0.247	0.293	0.264	-0.224	0.002	-0.025	0.015

*Correlation is significant at the 0.05 level (2-tailed), **Correlation is significant at the 0.01 level (2-tailed). ESR: Erythrocyte sedimentation rate, PCV: Packed cell volume, RBC: Red blood cell, WBC: White blood cell, Hb: Haemoglobin, MCHC: Mean cell haemoglobin concentration, MCV: Mean cell volume, MCH: Mean cell haemoglobin, LYM: Lymphocyte, NUE: Neutrophil, MON: Monocyte, EOS: Eosinophil and BAS: Basophil

White Blood Cell count (WBC) showed a robust positive ($p<0.01$) correlation with RBC at 0.929 and Hb at 0.918, indicating that higher WBC counts were associated with increased red blood cell production and haemoglobin levels. This relationship may reflect an immune response or inflammation, as elevated WBC counts often occur in response to infection or stress.

The parameter Mean Corpuscular Volume (MCV) exhibited a strong ($p<0.01$) negative correlation with PCV at -0.898 and RBC at -0.950, suggesting that larger red blood cells were associated with lower packed cell volumes, potentially indicating macrocytic anemia. Conversely, MCV had a positive ($p<0.01$) correlation with Mean Corpuscular Haemoglobin (MCH) at 0.284, indicating that variations in cell size affect haemoglobin content.

Mean Corpuscular Haemoglobin Concentration (MCHC) displayed weak correlations overall, including a slight negative correlation with PCV at -0.034 and a negative correlation with WBC at -0.358. This suggests minimal direct relationships with these parameters.

The parameter Lymphocytes (LYM) showed a significant ($p<0.01$) negative correlation with PCV at -0.867 and RBC at -0.862, indicating that higher lymphocyte counts may coincide with lower red blood cell levels, which could be a sign of chronic disease or immune response.

Neutrophil (NEU) had a negative correlation with PCV at -0.295, while exhibiting strong ($p<0.01$) positive correlations with RBC (0.765) and Hb (0.758). This suggested that better nutritional energy utilization was linked to improved red blood cell production.

Monocytes (MON) exhibited weak correlations across the board, including a slight negative correlation with PCV (-0.325) but positive correlations with RBC (0.393) and Hb (0.431), indicating that while monocyte levels were generally low, they still had some association with red blood cell metrics. Eosinophils (EOS) showed weak correlations overall, indicating they may not significantly influence or be influenced by other parameters in this dataset.

Basophils (BAS) presented mixed correlations; they had a positive correlation with eosinophils at 0.386, yet negative correlations with PCV (-0.487) and Hb (-0.508). This indicates that as basophil levels increase, there may be concurrent decreases in hemoglobin and packed cell volume.

Aside from these, the *POU1F1* gene expression demonstrated very low correlations with all haematological markers in this dataset, suggesting that it was unlikely to have a significant impact on, or be influenced by, the blood-related processes represented by these markers. In essence, the *POU1F1* gene appeared to be lowly associated with regards to the haematological parameters examined in this study.

Correlation coefficients of biochemical parameters of the Muturu cattle breed with the *POU1F1* gene: The biochemical parameters analyzed in the Muturu breed of cattle, which are influenced by the *POU1F1* gene, provided crucial insights into their health and metabolic status. Each parameter, shaped by the *POU1F1* gene's expression, reflected specific physiological functions and can indicate various health conditions, contributing to a comprehensive understanding of the breed's overall well-being and the impact of the *POU1F1* gene on their health, as shown in Table 5.

The ALT (Alanine Aminotransferase) is, enzyme primarily found in the liver and serves as a key marker for liver health. In the Muturu cattle, ALT showed a strong ($p<0.01$) positive correlation with AST (Aspartate Aminotransferase) at 0.661. This suggested that as ALT levels increased, AST levels also tend to rise, indicating potential liver or muscle damage.

Total protein (T.P) measures the total amount of protein in the blood, which includes both albumin and globulin. In this breed, T.P. exhibited weak negative correlations with both ALT (-0.084) and AST (-0.045), indicating that variations in total protein levels may not significantly affect these liver enzymes.

Albumin (ALB) is another critical protein that helps maintain oncotic pressure and transport substances in the blood. It showed a slight positive correlation with AST at 0.14, but its relationship with T.P was weakly negative (-0.016). This suggests that albumin levels remain relatively stable despite fluctuations in other parameters.

Globulin (Glo) plays an essential role in immune function and exhibits a very strong positive correlation with total protein at 0.973. This indicates that higher globulin levels were associated with increased total protein levels. However, it also showed a negative correlation with calcium (-0.171), suggesting an inverse relationship between these two parameters.

Calcium (Ca) is vital for various physiological functions, including muscle contraction and nerve transmission. In Muturu cattle, calcium correlated ($p<0.01$) positively with both AST (0.615) and ALT (0.506), indicating that higher calcium levels may relate to increased liver enzyme activity.

Table 5: Correlation coefficients of biochemical parameters of the Muturu cattle breed with the *POU1F1* gene

Muturu	ALT (U/L)	AST (U/L)	T.P (mg/dL)	ALB (mg/dL)	Glo (mg/dL)	Ca (mg/dL)	P (mg/dL)	K (mg/dL)	Zn (mg/dL)	Na (mg/dL)	AlP (U/L)
AST (U/L)	0.661**										
T.P (mg/dL)	-0.084	-0.045									
ALB (mg/dL)	-0.016	0.14	0.061								
Glo (mg/dL)	-0.079	-0.077	0.973**	-0.171							
Ca (mg/dL)	0.615**	0.506**	-0.312	0.015	-0.311						
P (mg/dL)	0.231	0.085	0.112	0.067	0.095	0.018					
K (mg/dL)	0.259	0.103	0.09	0.226	0.037	0.013	0.887**				
Zn (mg/dL)	0.549**	0.392*	-0.176	0.011	-0.177	0.863**	0.14	0.172			
Na (mg/dL)	-0.693**	-0.582**	0.172	0.05	0.158	-0.864**	-0.094	-0.077	-0.733**		
ALP (U/L)	1.000**	0.661**	-0.084	-0.016	-0.079	0.615**	0.231	0.259	0.549**	-0.693**	
POU1F1 gene	-0.049	0.02	0.131	0.155	0.094	-0.265	-0.135	-0.217	-0.229	0.195	-0.049

**Correlation is significant at the 0.01 level (2-tailed), *Correlation is significant at the 0.05 level (2-tailed). ALT: Alanine transaminase, AST: Aspartate transaminase, T.P: Total protein, ALB: Albumin, Glo: Globulin, Ca: Calcium, P: Phosphorus, K: Potassium, Zn: Zinc, Na: Sodium and ALP: Alkaline phosphatase

Phosphorus (P) is essential for energy metabolism and bone health but exhibited weak correlations across the board, with the highest being a positive correlation of 0.231 with potassium (K). This suggested minimal interaction with other biochemical parameters.

Potassium plays a crucial role in maintaining cellular function and fluid balance. It showed a strong ($p<0.01$) positive correlation with zinc at 0.887, indicating that as potassium levels rise, zinc levels also tend to increase significantly.

Zinc is critical for immune function and enzyme activity, correlated ($p<0.01$) positively with both AST at 0.549 and calcium at 0.863. This suggests that higher zinc levels may be associated with increased enzyme activity and better mineral status.

Sodium (Na) is essential for maintaining fluid balance and nerve function, exhibiting ($p<0.01$) strong negative correlations with alkaline phosphatase (ALP) at -0.693 and AST at -0.582. This indicated that elevated sodium levels may correlate with lower enzyme activity, potentially suggesting health issues or dietary imbalances.

The *POU1F1* gene-associated variable exhibited a strikingly low correlation with all biochemical markers in this dataset, suggesting a minimal impact on, or response to, these physiological indicators. This finding implied that the *POU1F1* gene may not play a substantial role in modulating the biochemical processes represented in this dataset.

Correlation coefficients of biochemical parameters of the Bunaji cattle breed with the *POU1F1* gene: The biochemical parameters in the Bunaji breed of cattle, which are associated with the *POU1F1* gene, are interconnected and interdependent. The correlation analysis of these parameters offers a unique perspective on how the *POU1F1* gene contributes to the breed's health and metabolic status, providing valuable insights into the gene's role in maintaining their overall well-being, as presented in Table 6. AST (Aspartate Aminotransferase) showed positive ($p<0.01$) correlation with ALT (Alanine Aminotransferase) at 0.318, suggesting that increases in AST levels may be associated with liver health issues, as both enzymes are commonly used to assess liver function.

Total Protein (T.P) had weak negative correlations with AST (-0.081) and ALT (-0.076), indicating that variations in total protein levels may not significantly impact liver enzyme activities. Similarly, Albumin (ALB) displayed a slight positive correlation with AST (0.168) but a more notable negative correlation with globulin (-0.359), suggesting that higher albumin levels might coincide with lower globulin levels. Globulin

Table 6: Correlation coefficients of biochemical parameters of the Bunaji cattle breed with the *POU1F1* gene

Bunaji	ALT (U/L)	AST (U/L)	T.P (mg/dL)	ALB (mg/dL)	Glo (mg/dL)	Ca (mg/dL)	P (mg/dL)	K (mg/dL)	Zn (mg/dL)	Na (mg/dL)	ALP (U/L)
AST (U/L)	0.318*										
T.P (mg/dL)	-0.081	-0.076									
ALB (mg/dL)	0.168	0.022	-0.359*								
Glo (mg/dL)	-0.152	-0.059	0.822**	-0.827**							
Ca (mg/dL)	0.216	-0.004	-0.297	0.688**	-0.599**						
P (mg/dL)	-0.195	-0.116	0.862**	-0.353*	0.735**	-0.295					
K (mg/dL)	-0.304	-0.153	0.833**	-0.29	0.679**	-0.255	0.940**				
Zn (mg/dL)	0.216	-0.004	-0.297	0.688**	-0.599**	1.000**	-0.295	-0.255			
Na (mg/dL)	-0.216	0.004	0.297	-0.688**	0.599**	-1.000**	0.295	0.255	-1.000**		
ALP (U/L)	1.000**	0.318*	-0.081	0.168	-0.152	0.216	-0.195	-0.304	0.216	-0.216	
POU1F1 gene	0.123	0.282	-0.049	-0.318*	0.164	-0.309	-0.067	-0.093	-0.309	0.309	0.123

**Correlation is significant at the 0.01 level (2-tailed), *Correlation is significant at the 0.05 level (2-tailed). ALT: Alanine transaminase, AST: Aspartate transaminase, T.P: Total protein, ALB: Albumin, Glo: Globulin, Ca: Calcium, P: Phosphorus, K: Potassium, Zn: Zinc, Na: Sodium and ALP: Alkaline phosphatase

(Glo) plays a crucial role in immune function and showed a strong ($p<0.01$) positive correlation with total protein at 0.822, indicating that higher globulin levels were associated with increased total protein levels. However, it also had a significant ($p<0.01$) negative correlation with calcium (-0.827), suggesting that as globulin levels rise, calcium levels may decline.

Calcium (Ca) is vital for numerous physiological processes, including muscle contraction and nerve function. It showed a moderate positive correlation with AST (0.216) and a strong ($P<0.01$) positive correlation with potassium (0.688). However, it also exhibited a negative correlation with globulin (-0.599), indicating an inverse relationship between these two parameters. Phosphorus (P) demonstrated a strong ($P<0.01$) positive correlation with globulin at 0.862, suggesting that higher phosphorus levels might be linked to increased globulin concentrations, which could reflect nutritional status or metabolic health.

Potassium (K) is essential for maintaining cellular function and fluid balance. It showed a strong ($p<0.01$) positive correlation with zinc (0.940) and high correlations with other parameters like globulin (0.833). This indicated that higher potassium levels were associated with increased zinc levels, which is important for various metabolic processes.

Zinc (Zn) also correlated positively with AST at 0.549, suggesting that higher zinc levels may be associated with increased enzyme activity, reflecting better mineral status in the cattle.

Sodium (Na) exhibited strong ($p<0.01$) negative correlations with both AST (-0.582) and ALP (-0.693), indicating that elevated sodium levels may correlate with lower enzyme activity, potentially pointing to health issues or dietary imbalances.

The analysis reveals a remarkably low correlation between the *POU1F1* gene-associated variable and all biochemical parameters, indicating a potential low association of the physiological processes measured in this study. This finding suggested that the *POU1F1* gene may not be a significant contributor to, or influenced by, these biochemical markers, and its role in this experimental context is likely to be minimal.

DISCUSSION

The correlation analysis between linear parameters of the Muturu breed of cattle and the *POU1F1* gene provided valuable insights into the relationships among morphological traits and the potential influence of the *POU1F1* gene on these traits. The current study's findings were corroborated by previous research on the Polled Hereford Cattle. Bullock *et al.*[8]. reported a significant positive correlation between body length and chest girth, mirroring the strong correlation observed in this study. Similarly, Hoffmann[9] found a significant relationship between body weight and chest girth, consistent with the correlation obtained in the present study. Adebambo[10] documented a positive correlation between muzzle circumference and body length, aligning with the correlation found in this investigation. Furthermore, Huai *et al.*[11] revealed a strong association between muzzle circumference and pelvic width, supporting the correlation observed in the present study. Jalil-Sarghale *et al.*[7] demonstrated a significant correlation between pelvic width and reproductive performance, which was consistent with the correlation between pelvic width and muzzle circumference in this study. Huai *et al.*[11] investigated the genetic influence of the *POU1F1* gene and found minimal correlations with various traits, echoing the negligible correlations observed in this study. Jalil-Sarghale *et al.*[7] reported that coat colour had a low impact on morphological traits, supporting the observation of negligible correlations in this investigation. These findings contributed to the existing body of knowledge on the Muturu breed's morphological characteristics, reinforcing the importance of considering body measurements and body conformation in breeding programs.

A comprehensive correlation analysis of morphological traits in the Bunaji breed of cattle (Bos indicus) revealed significant interrelationships among various body measurements, corroborating findings in previous studies, Iranian Zel and Lori-Bakhtiari sheep, Jalil-Sarghale *et al.*[7], and Hoffmann[9]. Ear Length (EL) strong positive correlations were observed with body length (bl) and chest girth (cg), which were consistent with reports in Muturu cattle[10]. Body length (bl) high correlation with chest girth (CG), reflecting similar growth patterns observed in pastoral cattle[1]. Tail length (TL) shows strong correlations with muscle circumference (MC) and height at withers (HW), supporting its importance as an indicator of body size and muscularity[10]. Muscle circumference (MC) positive correlations with height at withers (HW) and pelvic width (PW), highlighted its importance for reproductive performance[10]. Height at withers (HW), strong positive correlations with pelvic width (pw) and canon circumference (CC) were consistent with observations in Iranian Zel and Lori-Bakhtiari sheep[7]. Body weight (BW) has high correlations with chest girth (CG) and muscle circumference (MC), supporting the relationship between body weight and body measurements. *POU1F1* Gene negligible correlations with most traits, aligning with findings of minimal impact on morphological traits[9]. Coat colour has minimal correlations with other morphological traits, consistent with reports on production traits[10]. These findings contributed to our understanding of the morphological characteristics of Bunaji cattle and provided valuable insights for breeding programs and production management.

A comprehensive analysis of haematological parameters revealed significant correlations, providing valuable insights into Polled Hereford cattle health status[8,12]. A strong negative correlation between packed cell volume (PCV) and haemoglobin (Hb) was observed. This was consistent with anemia indications reported by Adebambo[10] and Li *et al.*[13] PCV-red blood cell count (RBC) correlation supported findings by Hoffmann[9]. while RBC-PCV correlation confirmed results from Lopes *et al.*[14]. White blood cell count (WBC)-RBC correlation was stronger than that reported by Adebambo[10]. WBC-Hb correlation was similar to Lee *et al.*[12]. Mean corpuscular volume (MCV)-PCV correlation was consistent with macrocytic anemia, supporting Hoffmann[9]. MCV-RBC correlation aligned with Li *et al.*[13], while MCV-mean corpuscular haemoglobin (MCH) correlation confirmed Hoffmann[9]. Lymphocytes (LYM)-PCV correlation was stronger than Lopes *et al.*[14] and LYM-RBC correlation was similar to Bullock *et al.*[8]. NEU-PCV correlation was weaker than Lan *et al.*[15], while NEU-RBC correlation was stronger than Li *et al.*[13]. Monocytes (MON)-PCV correlation was similar to Bullock *et al.*[8], and eosinophils (EOS)-PCV correlation was consistent with Lan *et al*[15]. A study examining the relationship between the *POU1F1* gene and haematological parameters yielded negligible correlations, implying that *POU1F1* gene did not directly regulate haematopoiesis. The gene's primary function is associated with growth and development. Hematological traits are influenced by a complex interplay of genetic and environmental factors. These findings aligned with Lan *et al.*[15], who reported no significant associations between *POU1F1* gene variants and haematological traits in cattle.

Research on Bunaji cattle's haematological parameters uncovered significant correlations, offering valuable insights into their health and physiological status[8,12]. Notably Packed cell volume (PCV) and red blood cell count (RBC) showed a negative correlation. The PCV and haemoglobin (Hb) also exhibited a negative correlation. These findings suggested anemia in Bunaji cattle, consistent with previous studies on Chinese goats[13]. Strong positive RBC-PCV correlation confirmed results in Simmental cattle in Nellore cattle[14]. White blood cell count (WBC)-RBC correlation and WBC-Hb correlation indicated immune response or inflammation, similar to cattle[12]. Mean corpuscular volume (MCV)-PCV correlation and MCV-RBC correlation suggested macrocytic anemia, consistent with Polled Hereford cattle Bullock *et al.*[8]. The MCV-mean corpuscular haemoglobin (MCH) correlation confirmed results in Nellore cattle[14]. (NEU)-PCV correlation and NEU-RBC correlation indicated improved red blood cell production with better nutritional energy utilization, similar in cattle[16]. Lymphocytes (LYM)-PCV correlation and LYM-RBC correlation suggested chronic disease or immune response, consistent with findings of Lee *et al.*[12]. Monocytes (MON) and eosinophils (EOS) showed weak correlations, while basophils (BAS) presented mixed correlations. Negligible correlations of the *POU1F1* gene with haematological parameters were consistent with findings in goat by Lan *et al*[15].

The biochemical parameters analyzed in the Muturu breed of cattle provided crucial insights into their health and metabolic status[8,15]. Each parameter reflected specific physiological functions and can indicate various health conditions, contributing to a comprehensive understanding of the breed's overall well-being. ALT (alanine aminotransferase), an enzyme primarily found in the liver, serves as a key marker for liver health by Lan *et al.*[15]. In Muturu cattle, ALT showed a strong positive correlation with AST (aspartate aminotransferase), indicating potential liver or muscle damage consistent with Lee *et al.*[12], Bullock *et al.* [8], and Lan *et al.*[15]. The AST is another enzyme associated with liver health, and its correlation with ALT suggested that liver enzyme activity may be linked to muscle function by Lopes *et al.*[14]. Total protein (T.P.) measures the total amount of protein in the blood, including albumin and globulin[12]. In this breed, T.P. exhibited weak negative correlations with both ALT and AST, indicating minimal impact on liver enzymes as confirmed by Lan *et al.*[15]. Albumin (ALB) helps maintain oncotic pressure and transport substances in the blood[8] Its slight positive correlation with AST suggested a potential link between albumin and liver health, supported by Lan *et al.*[15]. Globulin (Glo) played an essential role in immune function and exhibited a very strong positive correlation with total protein, indicating that higher globulin levels were associated with increased total protein levels confirmed by Lee *et al.*[12] and Li *et al.*[13]. Calcium (Ca) is vital for muscle contraction and nerve transmission Bullock *et al.*[8]. In Polled Hereford cattle, calcium correlated positively with both AST and, indicating potential links between calcium levels and liver enzyme activity consistent with Bullock *et al.*[8] Phosphorus (P) is essential for energy metabolism and bone health, but exhibited weak correlations across the board, weaker than that reported by Lan *et al.*[15]. Potassium (K) plays a crucial role in maintaining cellular function and fluid balance, showing a strong positive correlation with zinc, stronger than that reported by Lopez *et al.*[16] Zinc is critical for immune function and enzyme activity, correlated positively with both AST and calcium supported by Li *et al.*[13] and Lan *et al.*[15]. Sodium (Na) is essential for maintaining fluid balance and nerve function, exhibited strong negative correlations with alkaline phosphatase (ALP) and AST similar to Bullock *et al.*[8] and Lee *et al.*[12]. suggesting potential health issues. The variation associated with the *POU1F1* gene showed negligible correlations across all parameters, indicating it may not significantly influence or be influenced by the biochemical markers measured in this dataset, and this was consistent with Lan *et al.*[15].

The correlation analysis of biochemical parameters in the Bunaji breed of cattle provided valuable insight into their health and metabolic status[12,13]. Each parameter reflected specific physiological functions and can indicate various health conditions. The AST (Aspartate Aminotransferase) showed positive correlation with ALT (Alanine Aminotransferase), suggesting liver health issues[12]. Enzymes AST and ALT are commonly utilized to evaluate liver function in Bunaji cattle, as noted[17]. Similarly, research on Angus cattle by Lee *et al.*[12] revealed weak negative correlations between Total Protein (T.P.) and both AST and ALT. Albumin (ALB) displayed a slight positive correlation with AST but a more notable negative correlation with globulin, suggesting higher albumin levels might coincide with lower globulin levels[18]. Calcium (Ca) is vital for muscle contraction and nerve transmission V It showed moderate positive correlations with AST and potassium. Calcium also exhibited a negative correlation with globulin, indicating an inverse relationship[13]. Phosphorus (P) demonstrated a strong positive correlation with globulin, suggesting higher phosphorus levels might be linked to increased globulin concentrations Lee *et al.*[15]. Potassium (K) is essential for maintaining cellular function and fluid balance, showed strong positive correlations with zinc and globulin Kluska *et al.*[18]. Globulin (Glo) played a crucial role in immune function and shows a strong positive correlation with total protein[9]. Zinc (Zn) correlated positively with AST, suggesting higher zinc levels may be associated with increased enzyme activity[18]. Sodium (Na) exhibited strong negative correlations with AST and ALP, indicating elevated sodium levels may correlate with lower enzyme activity[12]. The variable associated with the *POU1F1* gene showed negligible correlations across all parameters, indicating it may not significantly influence or be influenced by the biochemical markers measured in this experiment[19].

CONCLUSION

This study demonstrates that *POU1F1* gene variants have minimal influence on growth-related traits in Muturu and Bunaji cattle breeds. Despite strong correlations among key morphological traits such as body length, chest girth, and tail length, the gene showed weak associations with these parameters. These findings underscore the complexity of genetic control over growth traits and point to the need for further research into alternative genetic markers. Incorporating phenotypic data with broader genomic tools may enhance the effectiveness of future breeding programs aimed at improving productivity in indigenous cattle breeds.

SIGNIFICANCE STATEMENT

This study identified key body traits in Muturu and Bunaji cattle breeds, which could be beneficial for improving selective breeding strategies. This study will assist researchers in uncovering critical areas of genetic influence on cattle traits that have remained unexplored by many. Consequently, a new theory on heritable traits in livestock breeding may be developed.

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