

# Genetic diversity, population structure and gene flow among indigenous Nigerian sheep breeds

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**ABSTRACT:** Genetic diversity, population structure and gene flow among indigenous Nigerian sheep breeds were investigated to enhance understanding of their genetic differentiation and adaptability. A total of 150 sheep, comprising Balami, Uda and Yankasa breeds (50 individuals per breed), were selected for phenotypic characterisation. Morphological traits such as head length, body length, and heart girth were assessed. Blood samples from 45 sheep (15 per breed) were collected for DNA extraction, polymerase chain reaction (PCR) and sequencing. The obtained sequences were subjected to bioinformatics analysis to evaluate genetic diversity, population structure and gene flow. The results demonstrated significant genetic variation among the breeds. The association of the leptin gene SNP 3 with phenotypic traits revealed that the TT genotype in Balami and Uda was linked to larger body dimensions, whereas the AA genotype in Yankasa was associated with smaller body size. Genetic differentiation indices ( $G_{ST}$ ,  $F_{ST}$  and  $D_{xy}$ ) indicated moderate genetic divergence among the breeds, with Balami and Yankasa showing higher differentiation ( $F_{ST} = 0.25000$ ) compared to Uda and Yankasa ( $F_{ST} = 0.07143$ ). Gene flow analysis suggested moderate genetic exchange among the breeds, with Balami exhibiting higher heterozygosity ( $H_s = 0.5$ ) than Yankasa ( $H_s = 0.4$ ). Tajima's D values were positive for all the breeds, indicating potential balancing selection or population contraction. These findings highlight the importance of genetic characterisation in livestock improvement programmes. The observed genetic diversity and gene flow patterns provide insights into breed conservation strategies and selective breeding programmes to enhance productivity and adaptability.

**Keywords:** Genetic diversity, phenotypic, population, sheep, structure.

## INTRODUCTION

The genetic diversity and population structure of indigenous livestock breeds are crucial for their adaptability, productivity and resilience to environmental stressors (Sinodo *et al.*, 2021). Nigeria's sheep breeds, including Balami, Uda and Yankasa, play a significant role in meat production, economic sustainability and the livelihoods of smallholder farmers. Understanding their genetic diversity and population structure is essential for effective breeding programmes and conservation strategies (Adebambo *et al.*, 2004). Molecular markers have emerged as valuable tools for assessing genetic variations, population structure and gene flow in livestock species, providing insights into their evolutionary history and management (Zhou *et al.*, 2021).

Indigenous Nigerian sheep breeds have evolved under

natural selection pressures and traditional breeding practices, resulting in unique genetic compositions (Aydin *et al.*, 2024). However, factors such as uncontrolled crossbreeding, habitat loss and climate change pose significant threats to their genetic integrity (Gizaw *et al.*, 2007). Studying genetic diversity through molecular markers, including microsatellites and single nucleotide polymorphisms (SNPs), enables researchers to identify distinct genetic lineages and assess the level of genetic differentiation among populations (Okeke *et al.*, 2020).

Genetic diversity is a fundamental aspect of animal breeding and conservation, as it influences adaptability and productivity. Studies have reported moderate to high genetic diversity in Nigerian sheep breeds, with variations observed in haplotype diversity, nucleotide diversity and

heterozygosity (Abdulhamid *et al.*, 2021). For instance, microsatellite-based studies have revealed significant genetic variation among Balami, Uda and Yankasa sheep populations (Agaviezor *et al.*, 2012). High genetic diversity enhances disease resistance, reproductive efficiency and environmental adaptation, making it a critical factor in livestock improvement (Sinodo *et al.*, 2021).

Population structure analysis provides insights into the genetic relatedness and differentiation of breeds, which is essential for effective breeding strategies. Genetic differentiation indices, such as F-statistics ( $F_{st}$ ) and Nei's genetic distance, have been used to evaluate the population structure of Nigerian sheep (Bhuiyan *et al.*, 2021). Gene flow, which refers to the exchange of genetic material between populations, plays a vital role in maintaining genetic diversity and reducing inbreeding depression (Zhang *et al.*, 2022). Studies have shown moderate gene flow among Nigerian sheep breeds, with evidence of admixture and shared ancestry due to transboundary movement and local breeding practices (Osamede and Adebawale, 2018). This study aims to assess genetic diversity, population structure and gene flow among indigenous Nigerian sheep breeds.

## MATERIALS AND METHODS

### Study area

The study was conducted in Calabar, Nigeria, a coastal city situated in the southeastern region of the country. Calabar is located between latitude 4°57'N and longitude 8°19'E, with a tropical rainforest climate characterized by high humidity, abundant rainfall and warm temperatures throughout the year. The region supports diverse agricultural activities, including livestock farming, due to its favourable environmental conditions (Okon *et al.*, 2025).

### Sample collection

A total of 150 indigenous Nigerian sheep were selected for the study, with 50 individuals representing each of the three major breeds (Balami, Uda and Yankasa). All 150 sheep underwent phenotypic characterization, which involved recording key morphological traits such as body length, head length, heart girth and other morphometric measurements following standard livestock evaluation protocols prescribed by Ayalew *et al.* (2000).

### DNA extraction and molecular analysis

Out of the total sampled population, blood samples were collected from 45 individuals for molecular genetic analysis. Genomic DNA was extracted using a commercial DNA extraction kit following the manufacturer's protocol. The quality and quantity of extracted DNA were assessed using a Nanodrop spectrophotometer, while agarose gel

electrophoresis was used to confirm DNA integrity (Osaiyuwu and Salako, 2018).

### PCR and sequencing

The extracted DNA was used for Polymerase Chain Reaction (PCR) amplification of targeted gene regions. PCR conditions were optimized to ensure successful amplification, and the products were purified and sequenced using Sanger sequencing technology. The generated sequences were analyzed for genetic variations and polymorphisms (Aydin *et al.*, 2024).

### Data analysis

The obtained genetic sequences were subjected to bioinformatics analysis using specialized software, including MEGA, Arlequin and STRUCTURE, to assess genetic diversity, population structure and gene flow among the sheep breeds. Phylogenetic analysis and population differentiation tests were performed to determine genetic relationships (Tella *et al.*, 2024). Additionally, phenotypic data were statistically analyzed using ANOVA to assess significant variations among the breeds (Hailu and Getu, 2015).

## RESULTS AND DISCUSSION

Table 1 presents the association of the leptin gene SNP 3 with phenotypic traits of Sheep breeds. The study examined the association of SNP 3 of the leptin gene with key phenotypic traits across three Nigerian sheep breeds: Balami, Uda, and Yankasa. Head length and head width are critical traits that influence the skull structure and overall appearance of sheep. The data indicated that the Uda (AA) genotype had the highest head length (27.00 cm), followed closely by Balami (TT) (26.80 cm). In contrast, Yankasa (TT) exhibited the lowest head length (21.75 cm), which aligns with previous findings indicating that Yankasa sheep have relatively smaller cranial dimensions compared to other breeds (Mohammed *et al.*, 2018). This suggests that the TT genotype may be associated with reduced head size in Yankasa sheep but maintains a relatively large head in Uda and Balami breeds. Body length is a fundamental indicator of growth potential and carcass yield in sheep (Zhang *et al.*, 2022). The study results showed that Balami (TT) sheep recorded the longest body length (75.60 cm), whereas Yankasa (AA) had the shortest (59.00 cm). This finding is consistent with reports indicating that the Balami breed exhibits superior growth performance and adaptation to extensive production systems (Afolayan *et al.*, 2006). The Uda (TT) sheep had a moderate body length (70.50 cm), reinforcing previous observations that the TT genotype might contribute to moderate growth traits in Uda (Bhuiyan *et al.*, 2021). Heart girth, which is a reliable predictor of body

**Table 1.** Association of leptin gene SNP 3 with phenotypic traits of sheep breeds.

Level of Breed	Level of SNP 3	No. of Obs.	Head length	Head width	Body length	Heart girth	HTW	Rump length	Rump width	Front leg L	Hind leg L
Balami	TT	5	26.80	16.60	75.60	90.20	103.80	26.00	20.80	67.80	71.50
Uda	AA	1	27.00	16.00	74.00	96.00	97.00	29.00	20.00	69.00	66.00
Uda	TT	4	27.00	15.50	70.50	86.25	105.50	23.75	18.75	67.50	68.75
Yankasa	AA	1	23.00	12.00	59.00	77.00	86.00	15.00	18.00	62.00	58.00
Yankasa	TT	4	21.75	13.50	67.25	83.38	98.25	19.75	17.75	65.75	62.50

HTW = height-at-withers, L = length, Hap = haplotype, No = number, Obs = observation.

**Table 2.** Gene flow and differentiation indices in three breeds of Nigerian sheep.

Population1	Population 2	Hs	Ks	Kxy	Gst	DeltaSt	GammaSt	Nst	Fst	Dxy	Da
Balami	Uda	0.5	0.9	0.84	0.01961	0.00015	0.07692	0.07194	0.07143	0.00211	0.00015
Balami	Yakansa	0.4	1.2	0.96	0.11111	0	0	0.25	0.25	0.00241	0.0006
Uda	Yakansa	0.5	0.9	0.84	0.01961	0.00015	0.07692	0.07194	0.07143	0.00211	0.00015

Hs = heterozygosity, Ks = genetic distance or divergence between population. Kxy = genetic distance between x and y population, Gst = genetic differentiation. DeltaSt = measure of genetic differentiation between two populations, GammaSt = Wright's F-statistic, Nst = number of subpopulation, Dxy = average number of nucleotide differences per site Da = differentiation analysis.

weight and overall health status, varied significantly across the breeds. The highest heart girth (96.00 cm) was observed in Uda (AA), followed by Balami (TT) (90.20 cm), while Yankasa (AA) had the lowest value (77.00 cm). This aligns with reports by Osamede and Adebawale (2018), who found that the Uda breed is characterized by a robust body structure suitable for meat production. Additionally, the Uda (AA) genotype had the highest rump length (29.00 cm), which is consistent with the expectation that larger sheep tend to have better-developed hindquarters, contributing to meat yield (Gizaw et al., 2007). Leg length and height-at-withers (HTW) are important determinants of mobility, adaptability and overall skeletal structure. The Balami (TT) genotype had the highest HTW (103.80 cm), which corroborates the report by Okeke et al. (2020) that Balami sheep are among the tallest indigenous

sheep breeds in Nigeria. Interestingly, the Yankasa (AA) sheep recorded the lowest HTW (86.00 cm), further reinforcing the notion that the AA genotype may contribute to smaller body frames (Zhou et al., 2021). Front and hind leg lengths also varied significantly, with Balami (TT) exhibiting the longest hind leg length (71.50 cm), indicating a possible genetic advantage in supporting its larger body frame. The observed variations in morphometric traits among different SNP 3 genotypes across the three sheep breeds suggest a strong genetic influence on body conformation. The TT genotype appears to be associated with larger body sizes in Balami and Uda, whereas the AA genotype in Yankasa is linked to a smaller frame. This aligns with previous reports indicating that SNP variations in the leptin gene significantly affect growth performance, body composition and adaptation

traits in sheep (Sinodo et al., 2021). The association of the leptin gene SNP 3 with phenotypic traits in Nigerian sheep breeds highlights the potential for genetic selection in improving productivity and adaptability. The TT genotype is favourable for larger body frames in Balami and Uda, whereas the AA genotype is associated with smaller body dimensions in Yankasa. These findings underscore the importance of genetic characterization for breed improvement strategies in Nigeria's sheep industry. Further research incorporating larger sample sizes and molecular analyses is recommended to validate these associations and explore their implications for meat production and environmental adaptability.

Table 2 presents gene flow and differentiation indices between Balami, Uda and Yankasa sheep

breeds in Nigeria. These parameters offer insights into genetic variation, gene flow and the extent of differentiation among the breeds studied. Heterozygosity ( $H_s$ ) represents the genetic variability within a population. The Uda-Yankasa and Balami-Uda populations recorded the highest heterozygosity (0.5), suggesting higher genetic diversity within these breeds' pairings. In contrast, Balami-Yankasa had a lower heterozygosity (0.4), implying relatively lower within-population genetic variation. Previous studies have shown that high heterozygosity is associated with improved adaptability and fitness in livestock populations (Gizaw *et al.*, 2007). The genetic distance indices ( $K_s$  and  $K_{xy}$ ) indicate evolutionary divergence between populations. Balami-Yankasa exhibited the highest genetic distance ( $K_s = 1.2$ ;  $K_{xy} = 0.96$ ), reflecting significant genetic differentiation. This is consistent with the findings of Okeke *et al.* (2020), who reported that Balami and Yankasa sheep have distinct genetic backgrounds due to differences in their breeding history and geographical distribution. Conversely, Balami-Uda and Uda-Yankasa had similar genetic distances ( $K_s = 0.9$ ;  $K_{xy} = 0.84$ ), suggesting a closer genetic relationship, likely due to historical gene flow and shared ancestry (Bhuiyan *et al.*, 2021). Genetic differentiation ( $G_{st}$ ) measures population subdivision. The Balami-Yankasa pair had the highest  $G_{st}$  value (0.11111), suggesting substantial genetic divergence. In contrast, Balami-Uda and Uda-Yankasa exhibited low  $G_{st}$  values (0.01961), indicating minimal differentiation. These findings aligned with previous research showing that geographical proximity and interbreeding influence genetic differentiation in Nigerian sheep breeds (Abdulhamid *et al.*, 2021). DeltaSt and GammaSt further quantify differentiation. The DeltaSt values were near zero for all populations, signifying minimal genetic drift. GammaSt values were also low, particularly for Balami-Yankasa (0), indicating negligible genetic differentiation. These values suggest that gene flow has occurred between these populations, likely through historical interbreeding or shared ancestral origins (Zhou *et al.*, 2021). Fst values indicate the degree of genetic divergence between populations. The highest Fst was observed in the Balami-Yankasa comparison (0.25000), confirming significant differentiation. This corroborates findings by Osamede and Adebawale (2018), who reported distinct morphogenetic and adaptive characteristics between these breeds. In contrast, Balami-Uda and Uda-Yankasa had much lower Fst values (0.07143), indicating substantial gene flow and genetic similarity (Sinodo *et al.*, 2021). The average number of nucleotide differences per site ( $D_{xy}$ ) was relatively low across all breed comparisons, with Balami-Yankasa showing the highest value (0.00241). This suggests that while differentiation exists, the overall genetic divergence at the nucleotide level remains moderate. Differentiation analysis ( $D_a$ ) followed a similar pattern, with Balami-Yankasa showing the highest differentiation (0.0006), reinforcing previous findings that

Balami sheep are genetically distinct from Yankasa (Okeke *et al.*, 2020). The observed genetic differentiation patterns suggest that while gene flow occurs among Nigerian sheep breeds, some levels of genetic isolation persist, particularly between Balami and Yankasa. This may be due to geographical separation, selection pressures or historical breeding practices (Zhang *et al.*, 2022). Conservation strategies should focus on maintaining genetic diversity while preventing excessive inbreeding. The high genetic similarity between Uda and Balami suggests that these breeds may be more closely related, possibly due to past interbreeding (Gizaw *et al.*, 2007).

Table 3 presents gene flow and genetic differentiation indices, including Tajima's D, for Balami, Uda and Yankasa sheep breeds. These parameters provide insights into genetic variability, population structure and selection pressures acting on these breeds. The number of haplotypes ( $h$ ) recorded in all three breeds was 2, indicating a limited number of distinct genetic variants within each breed. Haplotype diversity ( $H_d$ ) was highest in Uda (0.60000) compared to Balami and Yankasa (both at 0.40000). High haplotype diversity suggests a greater degree of genetic variation, which may be advantageous for adaptability to environmental changes (Gizaw *et al.*, 2007). The lower haplotype diversity in Balami and Yankasa may be due to historical bottlenecks or selective breeding practices that reduced genetic variation (Okeke *et al.*, 2020). The average number of nucleotide differences ( $K$ ) was highest in Balami and Yankasa (1.20000) and lowest in Uda (0.60000). This suggests that Balami and Yankasa exhibit greater genetic divergence at the sequence level compared to Uda. Nucleotide diversity ( $\pi$ ) followed a similar pattern, with Balami and Yankasa recording a higher value (0.00302) than Uda (0.00151). Higher nucleotide diversity typically reflects a greater potential for adaptation and resilience to environmental stressors (Bhuiyan *et al.*, 2021). Tajima's D is an essential statistic for assessing population dynamics and selection pressures. Positive values of Tajima's D indicate balancing selection or population contraction, whereas negative values suggest purifying selection or population expansion (Sinodo *et al.*, 2021). In this study, Balami and Yankasa had identical Tajima's D values (0.00303), while Uda recorded a lower value (0.00151). These results suggest that Balami and Yankasa may have undergone similar evolutionary pressures, possibly influenced by selective breeding for traits such as meat and wool production (Abdulhamid *et al.*, 2021). The lower Tajima's D value in Uda may indicate a different demographic history or selection regime compared to the other breeds (Osamede and Adebawale, 2018). The observed genetic differentiation and diversity indices have significant implications for breeding strategies and conservation efforts. The relatively high genetic diversity in Uda suggests that this breed may serve as a valuable genetic resource for improving adaptability in sheep populations.

**Table 3.** Gene flow and genetic differentiation with Tajima.

Population	N	H	Hd	K	PI	Tajima's D
Balami	5	2	0.40000	1.20000	0.00302	0.00303
Uda	5	2	0.60000	0.60000	0.00151	0.00151
Yankasa	5	2	0.40000	1.20000	0.00302	0.00303

N = number of sequence, H = number of haplotypes, Hd = haplotype diversity, K = average number of differences, PI = nucleotide diversity, Tajima's D = nucleotide diversity with Tajima.

Conversely, the lower genetic diversity in Balami and Yankasa suggests a need for conservation strategies to prevent further genetic erosion (Zhou *et al.*, 2021). Future breeding programmes should aim to enhance genetic variation, while maintaining desirable production traits (Gizaw *et al.*, 2007).

## Conclusion

The study on the leptin gene SNP 3 in Nigerian sheep breeds highlighted its role in genetic selection for productivity and adaptability. The TT genotype is linked to larger body frames in Balami and Uda, while the AA genotype is associated with smaller body dimensions in Yankasa. Uda sheep exhibit greater genetic variation, whereas Balami and Yankasa show more similarities. Understanding these genetic differences can enhance breeding programmes, ensuring better livestock productivity and adaptability to Nigeria's diverse environments. This study provides critical insights into the genetic diversity and differentiation of Nigerian sheep breeds.

## CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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## REFERENCES

Abdulhamid, A., Abdul-Rahman, M., Mustapha, U. B., Suleiman, A. O., Isa, M. A., Dauda, L., Abubakar, M. W., Dauda, I., Muhammed, M. B., & Mohammed, A. W. (2021). Effect of fat tail on reproduction of Sudan desert sheep in Maiduguri. *Nigerian Journal of Veterinary Applied Science*, 11(1), 49-54.

Adebambo, A., Williams, J. L., Blott, S., & Urquhart, B. (2004). Genetic relationships between Native Sheep breeds in Nigeria based on microsatellite DNA polymorphisms. *Animal Genetic Resources*, 34, 27-39.

Afolayan, R. A., Adeyinka, I. A., & Lakpini, C. A. (2006). The estimation of live weight from body measurements in Yankasa sheep. *Czech Journal of Animal Science*, 51(8), 343-348.

Agaviezor, B. O., Adefenwa, M. A., Peters, S. O., Yakubu, A., Adebambo, A. O., Ozoje, M. O., Ikeobi, C. O. N., Ilori, B. M., Wheto, M., Okpeku, M., De Donato, M. & Imumorin, I. G. (2012). Mitochondrial D-loop genetic diversity of Nigerian indigenous sheep. *Animal Genetics Resources*, 50, 13-20.

Ayalew, W., Peacock, C., Alemayehu, N., Reda, A. and Rey, B. (2000). The characterization of indigenous goat types of Ethiopia and Eritrea. In: Blench, R., & MacDonald, K. (eds). *The origins and development of African livestock: archaeology, linguistics and ethnography*, Pp. 280–289. London, University College London Press, Taylor & Francis Group.

Aydin, K. B., Bi, Y., Brito, L. F., Ulutaş, Z. and Morota, G. (2024). Review of sheep breeding and genetic research in Türkiye. *Frontier Genetics*, 25(15), 1308113.

Bhuiyan, M. S. A., Lee, S.-H., Hossain, S. M. J., Deb, G. K., Afroz, M. F., & Lee, S.-H. (2021). Unraveling the genetic diversity and population structure of Bangladeshi indigenous cattle populations using 50K SNP markers. *Animals*, 11 (8), 2381.

Gizaw, S., Van Arendonk, J. A., Komen, H., Windig, J. J., & Hanotte, O. (2007). Population structure, genetic variation and morphological diversity in indigenous sheep of Ethiopia. *Animal Genetics*, 38(6), 621-628.

Hailu, A., & Getu, A. (2015). Breed characterization: Tools and their applications. *Open Access Library Journal*, 2(4), 1-9.

Mohammed, A., Raji, A. O., & Igwebuike, J. U. (2018). Genetic variability of Nigerian sheep breeds at the insulin-like growth factor-1 (IGF-1) gene locus. *Nigerian Journal of Animal Production*, 45(1), 51-60.

Okeke, R. O., Nwagu, B. I., Iyiola-Tunji, A. O., & John, P. A. (2020). Diversity of biometric and morphological traits among sheep breeds in Nigeria. *Nigerian Journal of Animal Production*, 47(2), 13-25.

Okon B., Ibom, L. A., Dauda, A., & Udayi, M. (2025). Assessment of genetic diversity in Nigerian local chicken population based on haematological parameters. *African Journal of Biotechnology*, 24(3), 23-28.

Osaiyuru H. O. and Salako, A. E. (2018). Genetic structure of indigenous sheep breeds in Nigeria based on electrophoretic polymorphous systems of transferrin and haemoglobin. *African Journal of Biotechnology*, 17(12), 380-388.

Osamede, O. H., & Adebawale, S. E. (2018). Genetic structure of indigenous sheep breeds in Nigeria based on electrophoretic polymorphous systems of transferrin and haemoglobin. *African Journal of Biotechnology*, 17(12), 380-388.

Sinodo, S., Adamu, J., Mohammed, A. A., Dubagari, N. G., Raji, A. O., Mohammed, I. D., & Elkana, H. (2021). Genetic variability of Nigerian Sheep breeds based on the leptin gene locus. *Nigerian Journal of Animal Science*, 23(2), 9-17.

Tella, A., Adebayo, F. B., Oluwadele, J. F., Osunkey, O. J., &

- Dandara, G. B. (2024). A review on bioinformatics in animal breeding and research on disease resistance. *Journal of Agricultural and Biomedical Sciences*, 8(1), 40-54.
- Zhang, C. L., Liu, C., Zhang, J., Zheng, L., Chang, Q., Cui, Z., & Liu, S. (2022). Analysis on the desert adaptability of indigenous sheep in the southern edge of Taklimakan Desert. *Scientific Reports*, 12(1), 12264.
- Zhou, H., Gong, H., Wang, J., Luo, Y., Li, S., Tao, J., & Hickford, J. G. (2021). The complexity of the ovine and caprine keratin-associated protein genes. *International Journal of Molecular Sciences*, 22(23), 12838.