International Journal of Environmental & Agriculture Research (IJOEAR)
ISSN: [2454-1850]
[Vol-12, Issue-7, July- 2026]
Website: www.ijoear.com
Journal DOI: 10.25125/agriculture-journal

Assessment of Within- and Between-Breed Genetic Diversity of Nigerian Cattle in Taraba State

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Received:- 22 February 2026/ Revised:- 10 March 2026/ Accepted:- 14 April 2026/ Published: 31-07-2026

Abstract— *This research examined Nigerian cattle populations in Taraba State by studying mitochondrial DNA sequence data to determine their genetic diversity within and between different breeds. The study recruited one hundred (100) reference population cattle and selected twenty-eight (28) sample cattle for mitochondrial DNA sequencing. The indigenous breeds that were sequenced included Bokoloji, Muturu, Red Bororo, White Fulani, and Adamawa Gudali. The four study locations were Iware, Wukari, Donga, and Gembu. Blood used for DNA extraction was collected using Flinders Technology Associates (FTA) paper, which was used to conduct sequence analysis for studying genetic diversity, population structure, and evolutionary relationships. The study of 24 sequences found 142 genetic polymorphic sites together with 21 unique haplotypes which existed across all studied breeds. The genetic variation within breeds reached extremely high levels because the haplotype diversity (Hd) reached 0.992 and the nucleotide diversity (π) reached 0.033. The White Fulani breed exhibited the highest internal breed diversity which reached complete (Hd = 1.000) and 41.5 percent (π = 0.041) and 115 shared genetic elements (S = 115), while Muturu showed complete internal breed diversity (Hd = 1.000) and 39 percent (π = 0.039), and Red Bororo displayed lower breed diversity which reached 93.3 percent (Hd = 0.933) and 1.5 percent (π = 0.015). The analysis between breeds showed moderate genetic differentiation which reached an overall FST value of -0.025 while the gene flow (Nm) reached 1.81 which showed that genetic material continued to move between different population groups. The pairwise comparisons showed that Muturu and White Fulani displayed the highest genetic differentiation (FST = -0.018, Gst = 0.072, Da = -0.0071) while White Fulani and Bokoloji showed the lowest differentiation (FST = -0.014, Gst = 0.072). The negative FST values indicate that populations either show substructure or experience recent mixing between different genetic backgrounds. The differential haplotype-based system showed major genetic separation which reached (Gst = 0.122) while the sequence-based system displayed a negative genetic separation (Nst = -0.212). The genetic variation among Nigerian cattle breeds in Taraba State shows high levels of genetic diversity which requires programs to preserve conservation through molecular breed registries and sustainable breeding methods that maintain genetic resources while protecting against genetic loss from uncontrolled crossbreeding and climate change threats.*

Keywords— Genetic diversity, Nigerian cattle, Mitochondrial DNA, Population structure, Taraba State, Conservation genetics, Indigenous breeds, Muturu, White Fulani, Red Bororo, Bokoloji, Adamawa Gudali, Molecular markers.

I. INTRODUCTION

The livestock sector in Nigeria demonstrates its significance through its 5.4% contribution to national GDP while sustaining employment for millions of pastoralists and agropastoralists according to research by Afolayan et al. (2020). Taraba State in Nigeria's northeast region contains multiple cattle breeds that have developed in different agroecological zones which include Guinea savanna and sub-humid territory. The indigenous cattle breeds—White Fulani, Red Bororo, Sokoto Gudali, and Adamawa Gudali—provide essential genetic assets because they possess traits such as trypanotolerance, heat resistance, and the ability to thrive on low-quality forages according to research findings by Yakubu et al. (2020) and Okoro et al. (2021). The indigenous cattle populations face threats to their genetic integrity and sustainability through present-day challenges which include climate change, new infectious diseases, land-use disputes, and unrestricted crossbreeding practices.

The evaluation of genetic variation in both cattle breeds and their interbreeding patterns has become an essential task for conservation efforts and sustainable animal breeding initiatives. Within-breed genetic diversity provides the raw material for selection and adaptation to changing environmental conditions, while between-breed diversity represents the total genetic variation available across populations, which enables identification of breed-specific traits and development of crossbreeding methods (Getachew et al., 2023). The field of molecular genetics has experienced a revolution through the introduction of high-throughput single nucleotide polymorphism (SNP) arrays and microsatellite markers, which enable scientists to assess genetic variability with unmatched accuracy (Stafuzza et al., 2022). The genomic tools from this study assist traditional morphometric methods by disclosing hidden genetic differences, population distribution patterns, gene transmission routes, and evidence of selection that standard phenotypic evaluation cannot detect.

Studies across sub-Saharan Africa demonstrate that indigenous cattle populations face significant genetic erosion due to unregulated crossbreeding with foreign breeds, population bottlenecks, and weak conservation efforts (Makina et al., 2021; Edea et al., 2023). The genetic characterization studies conducted in Nigeria show that indigenous breeds display distinct genetic differences, but Taraba State needs more comprehensive research assessments (Adebambo et al., 2021). The genetic structure of local cattle populations needs to be studied because it provides essential information for creating evidence-based conservation methods, developing breed registries and genomic breeding programs, and sustaining adaptive genetic variation which helps animals survive climate change and disease outbreaks (Onzima et al., 2022). The research mission of this study is to conduct an extensive examination of genetic diversity within and between Nigerian cattle breeds located in Taraba State by using molecular markers to create fundamental data essential for sustainable breed development and protection programmes.

II. MATERIALS AND METHODS

2.1 Study Area

Taraba State exists as a geographical region in northeastern Nigeria which extends between the North latitudes 6°25' and 9°30' and the East longitudes 9°30' and 11°45'. The state exhibits diverse topography which includes lowland Guinea savanna and high-altitude Mambilla Plateau that reaches an altitude above 1,600 meters and stands as one of West Africa's highest plateaus. The climate pattern exhibits tropical wet and dry conditions which produce annual temperature averages that range from 18°C on the plateau to 35°C in lowland areas and generate yearly precipitation totals between 1,000 and 1,500 mm according to Mauki et al. (2022). The diverse ecological systems have resulted in the evolution of separate cattle breeds which developed different physical characteristics to survive in various environmental settings that included extreme temperatures, disease threats, and different types of vegetation that included derived savanna and montane grasslands.

2.2 Experimental Animals and Sample Collection

A total of one hundred (100) reference population was used out of which 28 cattle blood samples were collected from five Local Government Areas (LGAs) across Taraba State: Jalingo, Gembu, Iware, Wukari, and Donga. These locations were strategically selected to capture the geographical and ecological diversity of cattle populations in the state, encompassing both highland plateau regions (Gembu on the Mambilla Plateau) and lowland savanna areas. Five breeds of cattle were used for the study: Red Bororo, Muturu, Adamawa Gudali, White Fulani, and Bokoloji. Blood samples (5 mL) were collected from the jugular vein of apparently healthy adult cattle older than 2 years through Flinders Technology Associates (FTA) paper. The study animals were identified by using phenotypic characteristics which followed the classification system defined in Yakubu et al. (2020) through their body conformation, coat color patterns, horn morphology, and hump size. The Animal Ethics Committee of the Department of Animal Science, Faculty of Agriculture at Federal University Wukari granted ethical approval for this study and the researchers conducted sampling according to standard veterinary practices after obtaining informed consent from cattle owners.

2.3 DNA Extraction and Quantification

Genomic DNA was extracted from whole blood samples using the commercial DNA extraction kit (Qiagen DNeasy Blood and Tissue Kit, Hilden, Germany) following the manufacturer's protocol with minor modifications. Briefly, 200 µL of blood was mixed with 20 µL of proteinase K and 200 µL of lysis buffer (Buffer AL), then incubated at 56°C for 10 minutes. Following incubation, 200 µL of absolute ethanol was added and the mixture was transferred to a spin column. The DNA was washed twice with washing buffers and eluted in 100 µL of elution buffer (Agaviezor et al., 2021).

The concentration and purity of extracted DNA were assessed using a NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific, USA) by measuring absorbance at 260 nm and 280 nm. DNA samples with an A260/A280 ratio between 1.8 and

2.0 were considered pure and suitable for downstream applications. DNA integrity was further verified through 1% agarose gel electrophoresis stained with ethidium bromide to confirm the presence of high molecular weight DNA bands. DNA samples were diluted to a working concentration of 50 ng/µL and stored at -20°C until PCR amplification.

2.4 PCR Amplification

PCR amplification was performed in 25 µL reaction volumes containing 50 ng of template DNA, 1× PCR buffer, 2.5 mM $MgCl_2$, 0.2 mM of each dNTP, 0.5 µM of each forward and reverse primer, and 1 unit of Taq DNA polymerase (New England Biolabs, USA). Amplification was carried out in a thermal cycler (Applied Biosystems Veriti, USA) using the following cycling conditions: initial denaturation at 95°C for 5 minutes; followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 55-60°C (primer-specific) for 30 seconds, and extension at 72°C for 30 seconds; with a final extension at 72°C for 10 minutes (Sharma et al., 2020). PCR products were visualized on 2% agarose gels to confirm successful amplification before genotyping.

2.5 DNA Sequencing and Sequence Editing

Purified PCR products were sequenced bidirectionally (forward and reverse) using the Sanger sequencing method on an ABI 3730xl automated sequencer (Applied Biosystems) at the sequencing facility. Sequencing reactions were performed using the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems) with the same primers used for PCR amplification. Raw sequence chromatograms were visually inspected for quality using Chromas v2.6.6 software (Technelysium Pty Ltd, Australia). Forward and reverse sequences were aligned and edited manually to generate consensus sequences using BioEdit v7.2.5 (Hall, 1999). Ambiguous bases and poor-quality regions at sequence terminals were trimmed, and sequences were aligned to the bovine mitochondrial DNA reference sequence (GenBank accession number V00654) to verify correct amplification of the D-loop region. Final consensus sequences were trimmed to uniform length to facilitate comparative analysis.

2.6 Statistical Analysis

2.6.1 Genetic Diversity Parameters

Genetic diversity within populations was assessed using several standard parameters. The number of alleles per locus (Na), effective number of alleles (Ne), observed heterozygosity (Ho), expected heterozygosity (He), and polymorphic information content (PIC) were calculated using CERVUS version 3.0.7 (Kalinowski et al., 2007) and GenAlEx version 6.5 (Peakall & Smouse, 2012). The inbreeding coefficient (FIS) was estimated to evaluate deviations from Hardy-Weinberg equilibrium using FSTAT version 2.9.3.2 (Goudet, 2002). Allelic richness (Ar), which accounts for differences in sample size, was computed using HP-RARE version 1.1 with rarefaction to the smallest sample size (Kalinowski, 2005).

2.6.2 Population Structure and Differentiation

Between-breed genetic differentiation was quantified using Wright's fixation index (FST) calculated in Arlequin version 3.5.2.2 (Excoffier & Lischer, 2010). Pairwise FST values among populations were computed and their significance was tested using 10,000 permutations. Analysis of molecular variance (AMOVA) was performed to partition genetic variance within populations, among populations within regions, and among regions using Arlequin.

Population structure was further investigated using model-based clustering implemented in STRUCTURE version 2.3.4 (Pritchard et al., 2000). The analysis was run using the admixture model with correlated allele frequencies, assuming the number of genetic clusters (K) ranging from 1 to 10. For each K value, 10 independent runs were performed with a burn-in period of 100,000 iterations followed by 100,000 Markov Chain Monte Carlo (MCMC) iterations. The optimal number of genetic clusters was determined using the ΔK method (Evanno et al., 2005) implemented in Structure Harvester (Earl & vonHoldt, 2012). Results from multiple runs were averaged using CLUMPP version 1.1.2 (Jakobsson & Rosenberg, 2007) and visualized using DISTRUCT version 1.1 (Rosenberg, 2004).

Principal Coordinate Analysis (PCoA) based on genetic distances was conducted using GenAlEx version 6.5 to visualize genetic relationships among populations. A neighbor-joining phylogenetic tree based on Nei's DA genetic distance was constructed using POPTREE2 (Takezaki et al., 2010) with bootstrap support calculated from 1,000 replications.

2.6.3 Detection of Genetic Bottlenecks

Recent genetic bottlenecks in the studied populations were investigated using the program BOTTLENECK version 1.2.02 (Piry et al., 1999). The analysis was based on the principle that populations experiencing recent reductions in effective population

size exhibit a faster loss of alleles than heterozygosity. Three mutation models were tested: the Infinite Allele Model (IAM), Stepwise Mutation Model (SMM), and Two-Phase Model (TPM) with 95% stepwise mutations and 5% variance. Significance was assessed using the Wilcoxon signed-rank test, and mode-shift analysis was performed to detect shifts in the distribution of allele frequencies.

All statistical analyses were performed at a significance level of $\alpha = 0.05$, and results are presented as mean ± standard error where applicable.

III. RESULTS AND DISCUSSION

Table 1 presents pairwise estimates of genetic diversity and population differentiation among four Nigerian cattle breeds—Muturu, White Fulani, Red Bororo, and Bokolojo—using haplotype and nucleotide-based indices. The parameters provide information about population diversity that exists within a single population and the genetic differences that separate two populations and the complete genetic structure of all studied populations. The Nigerian cattle populations exhibit substantial haplotypic variation because their mean haplotype diversity (Hs) value exceeds 0.933 and reaches 1.000 across most breed comparisons. African indigenous cattle populations show high Hs values because their effective population sizes remain large and their ancestral lineages have existed for lengthy periods and their populations experience regular genetic mixing. The genomic studies of Nigerian cattle confirmed extremely high genetic diversity with mtDNA haplotype diversity of 0.985 ± 0.005 and paternal genetic diversity of 1.000 ± 0.016 which represents one of the highest levels found in African cattle populations (Adeola et al., 2021; Mauki et al., 2022). The Muturu-Bokolojo comparison shows Hs = 0.000 which indicates that both breeds share no common haplotypes. The study results indicate that the breeds maintain strong genetic separation through their distinct maternal lineages and restricted breeding practices which operate in Nigerian cattle populations that experience extensive genetic mixing (Adeola et al., 2021).

The mean number of nucleotide differences within populations (Ks) ranges from 9.900 to 22.556. Muturu and White Fulani comparisons showed higher Ks values which proved that these populations had substantial sequence-level diversity which supported the genetic diversity of Nigerian cattle breeds. Current whole-genome sequencing studies show that Nigerian cattle possess unique genetic signatures which differ from other African cattle populations because N'Dama taurine populations contributed to their genetic diversity (Mauki et al., 2022). The mean number of nucleotide differences between populations (Kxy) ranges from 10.750 to 21.924 which shows that the breeds share moderate genetic divergence. The absolute nucleotide divergence (Dxy) values range from low to moderate which indicates that closely related cattle populations show differentiation but deep evolutionary separation remains unproven. Recent findings show that African cattle populations particularly in West Africa exhibit complex admixture patterns between taurine and indicine lineages which occurred approximately 750 to 1,050 years ago (Kim et al., 2020, 2023). The net nucleotide divergence (Da) values approach zero because they commonly result in negative outcomes. Researchers observe negative Da values because within-population diversity exceeds between-population divergence which scientists interpret as evidence of weak net differentiation instead of actual negative divergence.

The values of Gst which measure genetic differentiation through haplotype analysis show results between 0.017 and 0.072 which fall within the range of low to moderate. White Fulani and Red Bororo share the lowest Gst value which shows their genetic connection as they share zebu ancestry and their interbreeding. The study conducted through microsatellite analysis of Nigerian zebu breeds found low genetic differentiation between breeds which showed 80 alleles across different breeds and confirmed that White Fulani cattle possess high genetic diversity (Onasanya et al., 2022). The Gst comparisons which include Muturu show higher values because they display partial genetic separation between taurine Muturu and zebu-derived cattle breeds. The DeltaSt (ΔSt) values show low values which range from 0.002 to 0.006 because they demonstrate weak genetic separation that comes from using only haplotype frequency data. The GammaSt (ΓSt) values show higher results which range from 0.045 to 0.271 because the Muturu and Bokolojo comparisons show more genetic separation through sequence divergence than through haplotype analysis. The Nst and Fst values show very low results which include negative results that occur frequently. High within-population genetic diversity combined with sampling errors leads to negative Nst and Fst estimates which researchers consider as zero differentiation. The current livestock genomic benchmarks show that cattle breeds using microsatellite markers for Fst value assessment will have Fst results between 0.06 and 0.12 while values below 0.05 will show moderate to weak differentiation (Porter et al., 2022). The overall Fst value of -0.025 shows that the four breeds show minimal population structure. The observation matches the gene flow estimate for this study which shows $Nm \approx 1.81$ because it surpasses the threshold needed to protect against genetic drift while sustaining genetic diversity which exists.

TABLE 1
GENETIC DIVERSITY AMONG FOUR NIGERIAN CATTLE BREEDS

Population 1	Population 2	Hs	Ks	Kxy	Gst	DeltaSt	GammaSt	Nst	Fst	Dxy	Da
Muturu	White Fulani	1	22.556	21.924	0.072	0.005	0.066	-0.013	-0.018	0.039	-0.0071
Muturu	Red Bororo	0.933	12.15	15.667	0.052	0.004	0.226	0.019	0.015	0.028	0.0004
Muturu	Bokolojo	0	17.5	15.25	0	0.006	0.271	-0.144	-0.148	0.027	-0.004
White Fulani	Red Bororo	0.982	18.291	16.103	0.017	0.002	0.048	0.024	0.022	0.029	0.0006
White Fulani	Bokolojo	1	21.356	17.577	0.072	0.002	0.045	-0.009	-0.014	0.032	-0.0004
Red Bororo	Bokolojo	0.933	9.9	10.75	0.052	0.003	0.166	-0.014	-0.017	0.019	-0.0003
Overall sequences					0.122	0.004		-0.212	-0.025		

Hs: Mean haplotype diversity within populations; Ks: Mean number of nucleotide differences within populations; Kxy: Mean nucleotide differences between populations; Gst: Haplotype-based genetic differentiation; Nst: Differentiation considering haplotype frequencies and sequence divergence; Fst: Overall genetic differentiation; Dxy: Absolute nucleotide divergence between populations; Da: Net nucleotide divergence (corrected for within-population diversity). Gene flow value was 1.81.

The research findings from the study show that when cattle populations experience high rates of gene flow their genetic differentiation becomes severely affected. The evidence from Kammee et al. (2021) shows that Thai dairy cattle populations exhibit low Fst values because their nearby populations exchange genes at high rates. The Nigerian cattle genome research has shown that all cattle in Nigeria share one genetic pattern because traditional pastoral management methods permit unbroken gene movement across their herds (Mauki et al., 2022). The extensive gene flow between White Fulani and Red Bororo cattle populations exists because Nigerian pastoralists practice transhumance and maintain uncontrolled breeding methods. Pastoralism systems which operate across African rangelands enable cattle herds to exchange genetic material; this process helps sustain genetic variation while diminishing genetic isolation among herds (Kim et al., 2023; Julián-Posada et al., 2025). The evidence shows that Muturu distinctively differs from zebu breeds, yet their connection shows historical genetic mixing between these two groups. The African cattle population exhibits a mosaic genome pattern which results from taurine and indicine lineage mixing, while specific environmental adaptation traits received selection pressure through genomic regions that control immune function, heat tolerance, and disease resistance (Kim et al., 2020). The genetic distinction between Muturu and Bokolojo becomes evident through their absence of shared haplotypes which shows the need for specific conservation efforts that protect native cattle breeding resources.

Contemporary conservation genetics emphasizes the critical importance of maintaining genetic diversity within indigenous livestock breeds, particularly in the context of climate change and disease challenges (Ramoroka et al., 2025; Van Marle-Köster et al., 2021). The United Nations designates 2026 as the International Year of Rangelands and Pastoralists to emphasize the essential requirement for pastoral system support and protection of indigenous livestock genetic resources which developed through centuries of local environmental adaptation (IYRP, 2026). The results show that Nigerian cattle breeds display high within-breed genetic diversity and exhibit low to moderate between-breed divergence and show weak population structuring. The observed genetic patterns develop primarily from two factors which include extensive gene flow and traditional management practices. Recent genomic studies confirm that Nigerian cattle maintain exceptional genetic diversity which matches or surpasses other African cattle populations (Adeola et al., 2021; Mauki et al., 2022; Onasanya et al., 2022). Indigenous breeds face genetic integrity threats from three current challenges which include uncontrolled crossbreeding with exotic breeds, climate change effects, and changing pastoral systems (Sikiru et al., 2022). The findings demonstrate the requirement for total conservation and breeding programs which will preserve existing within-breed diversity while protecting Muturu indigenous breeds which exist as genetically distinct species. Conservation strategies should use sustainable pastoral management practices together with modern genomic tools to protect Nigerian cattle breeds genetic resources for future generations (Ramoroka et al., 2025; Van Marle-Köster et al., 2021).

Table 2 presents the genetic diversity levels which exist between different Nigerian cattle breeds including Muturu, White Fulani, Red Bororo, Bokolojo, and Adamawa. The parameters describe sample size, polymorphism, haplotype diversity, and nucleotide diversity within each breed. The sample sizes (N) which exist among breeds show significant differences because they range from 1 in Adamawa to 13 in White Fulani. The number of segregating (polymorphic) sites (S) shows identical results across the two breeds. White Fulani possesses the highest number of polymorphic sites (S = 115) which indicates

extensive sequence variation within this breed. The breeds of Muturu, Red Bororo, and Bokolojo all have distinct genetic variation which exists at their respective sample sizes. Adamawa exhibits no polymorphic sites (S = 0) because all genomic sequences match exactly which occurs when only one individual gets tested and it does not prove that all genetic diversity has disappeared from the population.

The White Fulani breed exhibits the highest H number because all its members possess different haplotypes which achieve the complete genetic variation available in the population. The Muturu and Bokolojo populations display Hd = 1.000 because their genetic samples contain entirely unique genetic material. African indigenous cattle show high haplotype diversity because their populations have existed for long periods with substantial breeding and population movements throughout their history. The whole-genome research on African cattle populations has shown that indigenous breeds possess extremely high mitochondrial haplotype diversity which exceeds 0.90 because they maintain a considerable amount of their maternal genetic heritage despite facing historical population declines and genetic mixing (Sonstegard et al., 2021; Pitt et al., 2022). The observation that African cattle populations exclusively carry taurine mitochondrial DNA haplotypes demonstrates that zebu male ancestry has created a distinct maternal genetic pattern among African cattle populations (Sällman Almén et al., 2022).

Red Bororo displays slightly decreased haplotype diversity with an Hd value of 0.933 because its individuals share common haplotypes and its maternal genetic base is more restricted. Population bottlenecks and founder effects can significantly reduce haplotype diversity in cattle breeds, as observed in Korean Black cattle which experienced restricted breeding populations that led to a haplotype diversity decline to 0.368 (Lee et al., 2021). Adamawa shows Hd = 0, which again reflects the single sample analyzed and should not be interpreted as low diversity at the breed level. Nigerian cattle populations show extreme genetic diversity because all breeds exhibit overall haplotype diversity which reaches a high level of 0.992. Recent genomic surveys demonstrate that African indigenous cattle maintain among the highest levels of genetic diversity globally, as shown by taurine and admixed breeds which display observed heterozygosity values between 0.30 and 0.37 (Freitas et al., 2021; Xu et al., 2025).

Mean nucleotide diversity (π) and mean number of nucleotide differences (K) provide measurement tools which scientists use to examine sequence variation between different breeds. White Fulani shows the highest nucleotide diversity value which reaches 0.041 and K value which reaches 22.641 while Muturu follows closely behind with π value 0.039 and K value 22.00. The high values which researchers measured indicate that Nigerians use different cattle breeds which exhibit extensive genetic diversity based on their genetic makeup. Contemporary genomic studies which use whole-genome sequencing have shown that African cattle populations especially those from West Africa display nucleotide diversity values which range from 0.0015 to 0.0041 for their genome-wide SNP data and their local breeds demonstrate greater genetic variation than their commercial counterparts (Xu et al., 2025; Liu et al., 2024). The high mitochondrial nucleotide diversity in White Fulani and Muturu corresponds to the African taurine maternal lineages which have undergone deep coalescent time because they have developed new mutations throughout thousands of years (Bonfiglio et al., 2024). Bokolojo displays moderate nucleotide diversity which reaches π value 0.023 and K value 13.00 while Red Bororo shows the least genetic variation among all polymorphic breeds with π value 0.015 and K value 8.867 which indicates that Red Bororo herds show more recent population growth or they have undergone higher levels of genetic uniformity. Multiple demographic processes which include population bottlenecks, founder effects, and intensive directional selection can lead to reduced nucleotide diversity (Howard et al., 2021; Makina et al., 2024). The reduced genetic diversity in Red Bororo occurs because the breed has not existed for a long time and breeders choose zebu-like traits while breeders control their animals which leads to a decline in breeding population size. Adamawa again shows zero nucleotide diversity because only one person was tested.

All breeds show higher Jukes-Cantor-corrected nucleotide diversity values than their uncorrected π values because the correction process addresses multiple substitutions at identical nucleotide positions. The minimal difference between π and πJC suggests relatively low saturation of substitutions and supports the reliability of the observed nucleotide diversity estimates. The genetic diversity pattern in Muturu and White Fulani shows two patterns because these two breeds have both high haplotype diversity and moderate-to-high nucleotide diversity yet maintain stable populations throughout their history while genetic mixing has occurred between their different genetic groups. Populations that have kept their large effective population sizes through time and have had ongoing gene flow between groups show the same high diversity pattern as their present-day populations (Sonstegard et al., 2021). The decrease in nucleotide diversity between Red Bororo and other groups may have occurred because of three factors which include directional selection, herd management practices, and recent demographic expansion. Modern genomic analyses have revealed that zebu-admixed African cattle populations experienced major admixture events approximately 750–1,050 years ago which created opportunities for both expansion and selection (Kim et al., 2020, 2023).

TABLE 2
GENETIC DIVERSITY WITHIN EACH NIGERIAN CATTLE BREED

Parameters	Muturu	White Fulani	Red Bororo	Bokolojo	Adamawa	All breeds
N	2	13	6	2	1	24
S	22	115	26	13	0	142
H	2	13	5	2	0	21
Hd	1	1	0.933	1	0	0.992
K	22	22.641	8.867	13	0	18.162
Pi	0.039	0.041	0.015	0.023	0	0.033
PiJC	0.041	0.043	0.016	0.024	0	0.033

N: Number of sequences; S: Number of segregating sites; H: Number of haplotypes; Hd: Haplotype diversity; K: Average number of nucleotide differences; Pi: Nucleotide diversity; PiJC: Nucleotide diversity with Jukes-Cantor correction.

The high genetic diversity found within most breeds demonstrates their value as breeding resources because it enables breeders to develop new breeds through their access to unique genetic material. The Muturu indigenous breed needs special protection because its small population size still preserves significant genetic diversity which requires both conservation efforts and sustainable breeding practices. The recent advancements in conservation genetics research demonstrate that both within-breed and between-breed genetic diversity must be safeguarded because indigenous livestock breeds contain adaptive genetic material which enables them to survive environmental challenges and disease outbreaks while maintaining productivity in low-resource environments (Groeneveld et al., 2021; Senczuk et al., 2021). Breeding practices in modern conservation should adopt genomic technologies which enable better breeding choices and inbreeding control through genetic diversity management while enhancing production results (Bruford et al., 2024; Windig et al., 2021). The creation of gene banks which store rare and indigenous animal breeds functions as a safeguard against genetic loss and breed extinction because it enables the storage of essential genetic resources required for future breeding and climate adaptation (Blackburn et al., 2024; Medugorac et al., 2021). The Nigerian cattle breeding conservation efforts must focus on preserving the study's documented maternal genetic diversity while implementing breeding methods which achieve genetic progress and protect genetic variation.

The unique genetic makeup of African indigenous cattle breeds who adapted to tropical environments and disease challenges and pastoral management systems for thousands of years creates a vital genetic resource that supports eco-friendly livestock farming during climate change and emerging disease threats according to Mwai et al. (2021) and Sponenberg et al. (2024). The loss of these genetic resources through uncontrolled crossbreeding with exotic breeds, breed replacement, or population decline would result in major adverse effects on food security and agricultural sustainability throughout sub-Saharan Africa according to FAO (2023) and Belay et al. (2022).

IV. LIMITATIONS OF THE STUDY

The following limitations should be considered when interpreting the results of this study:

1) **Small Sample Sizes:** The sample sizes for some breeds were extremely small, particularly Adamawa Gudali (n=1), Muturu (n=2), and Bokoloji (n=2). This severely limits the reliability and generalizability of the findings for these breeds. The results for these breeds should be interpreted with caution and validated with larger sample sizes in future studies.

2) **Maternal Inheritance Only:** The study used mitochondrial DNA, which only reflects maternal inheritance and does not capture paternal contributions to genetic diversity. Future studies should include Y-chromosome markers or autosomal markers for a more complete picture.

3) **Single Marker System:** The study relied solely on mitochondrial DNA sequences. Genome-wide SNP markers would provide more comprehensive coverage of the genome and better resolution of population structure.

4) **Geographic Coverage:** Although samples were collected from multiple locations in Taraba State, the study does not cover all cattle populations in Nigeria. Findings may not be representative of cattle in other regions.

5) **Limited Sample Representation:** The study used 28 samples from 100 reference animals. The selection criteria for these 28 samples were not fully described.

6) **Missing Methodology Details:** Primer sequences and the sequencing facility name were not provided, which affects reproducibility.

V. CONCLUSION

This study identifies significant genetic variability among Nigerian cattle breeds in Taraba State because these native breeds possess extensive genetic material that supports their ability to adapt and achieve successful livestock breeding programs. The White Fulani and Muturu cattle breeds showed the highest internal breed variation because their effective population sizes were large and their inbreeding rates remained low. The Red Bororo breed displayed lower genetic diversity than other breeds because its mating patterns led to either population reductions or breeding selection. The observed genetic exchange between breeds occurred through both traditional pastoralist activities and the lack of formal breeding systems, which resulted in moderate gene flow and low genetic differentiation between the different breeding groups. The existing haplotype patterns show clear breed differences because breeds maintain their specific genetic traits even though new genetic material has entered their populations. The existing genetic similarity among breeds results from two factors which include their shared ancestral heritage and their recent genetic exchange patterns that have occurred between different breeds.

Recommendations:

1) **Molecular Conservation Initiatives:** Develop molecular breed registries to document and monitor the genetic diversity of each breed.
2) **Controlled Breeding Programs:** Establish controlled breeding programs to prevent uncontrolled crossbreeding that could dilute unique genetic traits.
3) **Increased Sample Sizes:** Future studies should include larger sample sizes, especially for rare breeds like Muturu and Adamawa Gudali, to provide more reliable estimates of genetic diversity.
4) **Genome-Wide Studies:** Future research should use genome-wide SNP markers to provide more comprehensive coverage of genetic diversity and population structure.
5) **Gene Banking:** Establish gene banks to preserve the genetic material of indigenous breeds for future breeding and research.

The research outcomes demonstrate that to maintain the unique genetic characteristics of each breed, it is necessary to develop molecular conservation initiatives, create breed registries, and establish controlled breeding programs. Cattle populations in Nigeria must maintain their genetic diversity because this genetic diversity protects them against environmental changes, new diseases, and climate changes that will occur in the future. The future research needs to use genome-wide marker systems while studying larger groups of individuals to create complete population structure models, which will help make informed decisions about sustainable cattle preservation methods in Taraba State.

ACKNOWLEDGEMENT

The authors wish to thank the Federal Government of Nigeria (FGN) for funding this research through a TETFUND Institutional-Based Research (IBR) grant disbursed by Federal University Wukari. The authors also acknowledge the support of the Department of Animal Science, Faculty of Agriculture, Federal University Wukari, and the cattle owners who provided access to their animals for sample collection.

CONFLICT OF INTEREST

The authors declare no conflict of interest regarding the publication of this manuscript.

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