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Original scientific article

GENETIC DIVERSITY AND DIFFERENTIATION OF SOME NIGERIAN INDIGENOUS CATTLE BREEDS AT IGF-1 GENE LOCUS

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A study was conducted to determine the genetic diversity and differentiation in selected in digenous breeds of cattle in Nigeria at Insulin-Like Growth Factor 1 gene locus. Ninety-six (96) cattle (n = 24 per breed) were sampled purposively across Adamawa, Taraba, Gombe and Sokoto States. Blood samples were collected from the animals via jugular venipuncture. DNA was extracted using a DNA purification kit, and quality and quantity were assessed with a NanoDrop-1000 UV spectrophotometer. Genomic DNA was extracted from whole blood and genotyped for an IGF-1 fragment using PCR–RFLP with the SnaBI restriction enzyme using Zymo Quick DNA ™Mini prep kit. Data collected were subjected to F Statistics analysis using GenAIEx software package. Analysis of Molecular Variance (AMOVA) of cattle revealed 61% of within population, 30% of the variance was attributed to among individuals and 9% was due to among population. The TT genotype appeared to be the highest, followed by CT genotype whereas the CC genotype was the least. Complete polymorphism was observed at the IGF-1 gene locus

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and the gene flow N (nm) over all populations for each locus was (2.595) and within population inbreeding coefficient (F_{IS}) per population was (0.310). The expected heterozygosity (0.444) and unbiased expected heterozygosity (0.454) also appeared to be preponderant in Sokoto Gudali cattle breed compared to others breeds. Restriction Fragment Length Polymorphism (RFLP) marker revealed high level of genetic variations and diversity at IGF-1 gene locus among the population of cattle studied.

Keywords: Breed, IGF-1 gene, Cattle, Differentiation, Genetic diversity, Indigenous

INTRODUCTION

Nigeria has several indigenous breeds of cattle but major ones include Muturu, Ndama, Sokoto Gudali and White Fulani also known as Bunaji (ONASANYA *et al*., 2020). These indigenous cattle breeds, over the years, have evolved characteristics that shaped their adaptation, survival and productivity under local environmental conditions, and traditional management systems characterized by limited feed resources, stressful weather and climatic factors, endemic diseases, parasites, pests (TABOR *et al*., 2017; NWACHUKWU *et al*., 2020; PAGUEM *et al*., 2020). In addition to the limited studies based on genetic diversity and differentiation in some Nigerian indigenous breeds of cattle, most of the reports did not cover the major cattle breeds in Nigeria.

Genetic variation is the basis of effective improvement in farm animals. One way to characterize livestock breeds is by measuring the genetic distance between current populations (METTA *et al*., 2004). In Africa, there are different breeds that represent a rich source of genetic diversity that has not been well studied and exploited. This is reflected in differences in morphology, physiology and behavioural attributes between individuals, breeds and populations (FRANKHAM *et al*., 2002). The advent of molecular techniques has led to an increase in the studies that focus on the genetic characterization of domestic breeds using genetic markers (GIOVAMBATTISTA *et al*., 2001). In addition, genetic assessment is also of interest for the design of genetic improvement programs including appropriate choice of breeds for crossbreeding (MWACHARO *et al*., 2006).

Insulin-like Growth Factor I (IGF1) gene plays a key role in multiple aspects of muscle growth and development (DAVIS and SIMMEN, 2006), and because it promotes hypertrophy of muscle cells, IGF1 can influence muscle fiber diameter, which in turn may affect tenderness as larger fiber diameter has been associated with decreased tenderness (HERRING *et al*., 2009). However, it is worthy to note that full extent of molecular variations and diversity of the Nigerian indigenous cattle remain largely unknown. Studies based on other molecular markers capable of unraveling phylogenetic history of biodiversity and development to better understand the genetic architecture of the Nigerian cattle population is therefore necessary, which is the focus of this study. The aim of this study is to determine the genetic diversity and differentiation in some indigenous breeds of cattle in Nigeria at IGF-1 gene locus.

MATERIALS AND METHODS

Experimental site

The experiment was carried out in four States, including Adamawa, Gombe, Sokoto and Taraba. These States were purposively selected because the high existence of breeds of cattle

owned by pastoralists. The semi-arid zone of Nigeria starts from about 11°N latitude and ends at the Nigeria-Niger frontier. It encompasses the Sudan and Sahel Savanna and part of the Northern Guinea Savanna. The mean annual temperature runs between 26 and 28°C. There is single rainy season from May to October, with mean annual rainfall ranging from 1016mm in the wettest parts to less than 508mm in the driest parts. The length of growing period is about 100-150 days which makes it possible to cultivate a wide variety of crops (OGUNGBILE *et al*., 1998). The semi-arid zone has a land mass of 113,530km^2 and a population of over 35 million people (NPC, 2006). The major inhabitants of this area are Hausa and Fulani who are predominantly mixed crop-livestock farmers and livestock herders respectively.

Data collection

Two milliliters of blood sample were collected from each animal via jugular venipuncture from 96 cattle, 24 each of Adamawa Gudali, Sokoto Gudali, Bunaji and Rahaji cattle into a ten milliliter (10mL) Ethylenediaminetetraacetic acid (EDTA) heparinized vacutainer tubes to prevent clotting. The blood samples were properly labelled and kept cold by placing them on ice block and care was taken to prevent exposure to extreme temperatures and thereafter, transported to the laboratory of the Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria for analysis.

Deoxyribonucleic Acid (DNA) extraction

DNA was extracted from 96 blood samples that were collected from 4 different breeds of cattle in each of the 4 States using Zymo Quick DNA ™Mini prep kit. NanoDrop™ ND-1000 UV spectrophotometer was used for the determination of DNA quality and quantity using DNA purification kit according to the manufacturer's instructions (BERTANI *et al*., 1999). Four hundred (400 µl) of genomic lysis buffer was added to 100 µl of whole blood in a ratio of (4:1). It was mixed completely by vortexing for 4-6 seconds, then stands for 5-10 minutes at room temperature. The mixture was transferred to a Zymo-Spin ™ Column in a collection tube. It was centrifuge at 10,000 x g for one minute. The collection tube with the flow through was discarded. The Zymo-Spin™ Column was transferred to a new collection tube. 200 µl of DNA Pre-Wash Buffer was transferred to the spin column. It was then centrifuge at 10,000 x g for one minute. 500 µl of g-DNA Wash Buffer was added to the spin column. It was centrifuge at 10,000 x g for one minute. The spin column was transferred to a clean micro centrifuge tube. ≥50 ul DNA Elution Buffer was added to the spin column. It was incubated for 2-5 minutes at room temperature and then centrifuge at top speed for 30 seconds to elide the DNA. DNA extraction was carried using Zymo Quick DNA ™Mini prep kit. The eluded DNA were immediately stored for molecular based applications at ≤-20^{o}C for future use.

Polymerase chain reaction (PCR) standardization

Four (4) primers were placed in a centrifuge machine and removed after spinning the samples for 5 minutes. Ninety-sex (96) samples were used for the purpose of this experiment. The mixture was submitted to initial denaturation at 94^{o}C for 4 minutes followed by 30 cycles, 94^{o}C for 30 seconds, 56^{o}C for 30 seconds, 72^{o}C for 2 minutes, and a final extension step of 72^{o}C for 5 minutes. Each PCR reaction was carried out in 50µl final volume and contained 20 ng

genomic DNA, 1μM primers, 2m $MgCl_2$, 1 U platinum® Taq polymerase, and 1 × PCR buffer (RAMUNNO *et al*., 2000). The PCR fragments obtained were separated in 1.5% agarose gel, stained with ethidium bromide and observed under ultraviolet light.

Agarose Gel Electrophoresis

Two (2) grams of agarose powder was added into 200 liters of Ethylenediaminetetraacetic acid (EDTA) and 6μl of Ethidium Bromide into 100 liters of EDTA. Little amount of loading dye was added to a PCR tube containing DNA. A drop was added into an electrophoretic tank with the use of micropipette. A drop of a DNA ladder was added at both ends of the bands. The amplified products were electrophoresed on 1.5% (w/v) agarose gels in Tris-Borate-Ethylene Diamine Tetra Acetic Acid (TBE) buffer for allelic differentiation, DNA fragments separation, visualization and purification. DNA was stained in a 3 ng/ml Synergy Brands (SYBR) Safe-DNA Gel Stain. Gel analysis was then performed on a Bio-Rad Ultra illuminator 2000. Allele size was determined using a Molecular Mass Ruler of 100bp fragment size

Determination of genetic diversity in the indigenous cattle populations in Nigeria

Genetic diversity within each population was determined by estimating the expected heterozygosity (HE) or gene diversity and Wright's F*IS* (WRIGHT, 1978).

Expected Heterozygosity: The gene diversity or expected heterozygosity (HE) was used to estimate the probability that two randomly-chosen alleles from the breed are different. The unbiased estimator of HE provided by WEIR (1996) at the l-th locus is hereby defined as

$$H_E = \frac{1-\sum_{l=1}^{n} Pi^2}{1-\frac{1+f}{n}}$$

Where *Pi* is the frequency of the l-th of *k* alleles and *f* is the inbreeding coefficient across animals (*n*).

Gene flow: Was determined by the private allele method by SLATKIN (1993).

Thus, Gene flow (N(nm)) = $\frac{1}{4}\left(\frac{1}{FST}-1\right)$

Where; *FST* is the genetic differentiation among the sub-populations

Inbreeding coefficient (FIS): The significance of *FIS* estimates was determined by genotypes within the total population (GOUDET, 2002) i.e, $F_{IS} = 1 - \frac{Hi}{Hs}$

Where: HI = intra population gene diversity or average observed heterozygosity in a group of populations

HS = average expected heterozygosity estimated from each subpopulation

Analysis of molecular variance (AMOVA)

The analysis of molecular variance (AMOVA) was use to partition genetic diversity within and between populations, or among groups of populations, based on molecular markers. In *F* statistics, gene frequencies were compared among breeds. However, from molecular data, the within and among molecular variances of cattle were determined. The analysis of molecular

variance (AMOVA) was performed using the GenAlEx 6.5 software package (PEAKALL and SMOUSE, 2012).

Determination of polymorphism of igf-1 gene of cattle

Determination of IGF-1 gene polymorphism (a growth control gene) in cattle was carried out using PCR-RFLP technique. The PCR fragment of IGF-1 gene was analyzed using RFLP by digestion of fragment with SnaB1 enzyme. The PCR product was digested with SnaB1 endonuclease at 37 ^{o}C for 3 hours, which recognized TAC/GTA sequence within the PCR product.

Primers, polymorphism, primer sequencing, annealing temperature, length of base products and restriction enzyme for the Insulin-like Growth Factor 1 gene (IGF-1) gene for growth trait in cattle is shown in the Table 1.

Table 1. Sequence of PCR primers, position of the primers (f = forward; r = reverse), position of RT-PCR product

Polymorphism	Primer	Primer sequencing	T_a(^{o} C)	Length of PCR product (bp)	Restriction enzyme
IGF-1/SnaB1	IGF677F	5'-ATTACAAAGCTGCCTGCCCC-3'	62	20	SnaB1 TAC/GTA
	IGF897R	5'-ACCTTACCCGTATGAAAGGAA TATACGT-3'		28	
	IGFP1F	5'-TCATCCAGCTGAGAGATTTGAAT-3'	58	23	
	IGFPIR	5'-TGTGTGTGTGTGTGTGTGTGAAT-3'		23	

T_a=Annealing temperature.
SZEWCZUK *et al*. (2013).

Ethical

The study "Genetic diversity and differentiation of some Nigerian indigenous cattle breeds at IGF-1 gene locus" was conducted according to the Ethical Guideline of Animal Research Ethical Committee of the Department of Animal Science, Faculty of Agriculture, Ahmadu Bello University, Zaria, Nigeria.

RESULTS

Percentages of molecular variance of cattle

The Analysis of Molecular variance of IGF1 gene in cattle is shown in Table 2. AMOVA partitioned molecular variance as 9% among populations, 30% among individuals within populations, and 61% within individuals. Permutation tests revealed among population component to be small but statistically detectable ($p< 0.05$), consistent with modest population differentiation.

Table 2. Analysis of molecular variance of IGF-1 gene in cattle

Source	df	SS	MS	Est. Var. Component	% Variation
Among Populations	3	2.932	0.977	0.016	9%
Among Individuals	92	19.938	0.217	0.054	30%
Within Individuals	96	10.500	0.109	0.109	61%
Total	191	33.370		0.179	100%

df: Degree of freedom, SS: Sum of square, MS: Mean square, %: Percent, Est. Var. =estimated variance.

Genotype frequencies in some indigenous breeds of cattle

Number and frequencies of genotypes in some indigenous breeds of cattle is presented in Table 3. Across breeds TT was the most common genotype, CT intermediate, and CC least common. The IGF-1/SnaBI locus was 100% polymorphic in all sampled breeds, with TT genotype predominance and low CC frequency. Rahaji cattle exhibited the highest frequency of genotype TT (0.9583), followed by Adamawa Gudali (0.6667), whereas the Sokoto Gudali (0.5417) and Bunaji (0.500) showed moderate frequency of occurrence.

Table 3. Number and frequencies of genotypes in some indigenous breeds of cattle

Breed	Genotypes		
Adamawa Gudali	CC	CT	TT
N	3	5	16
Frequency	0.1250	0.2083	0.6667
Sokoto Gudali			
N	5	6	13
Frequency	0.2083	0.2500	0.5417
Bunaji			
N	3	9	12
Frequency	0.125	0.375	0.500
Rahaji			
N	-	1	23
Frequency	NA	0.0417	0.9583

CC: Homozygous CC genotype, CT: Heterozygous CT genotype, TT: Homozygous TT genotype, C: Allele C, T: Allele T, N: Number.

Allele frequency distribution at IGF-1 gene locus of cattle breeds

The allele frequency distributions among breeds of cattle are presented in Figure 1. Allele frequency distributions among breeds of cattle showed that Rahaji had the highest frequency for T allele, followed by Adamawa Gudali cattle breed whereas Bunaji and Sokoto Gudali breeds had similar pattern of frequency of occurrence. Sokoto Gudali and Bunaji cattle had high frequency of occurrence of C allele than Adamawa Gudali whereas Rahaji showed the least C allele.

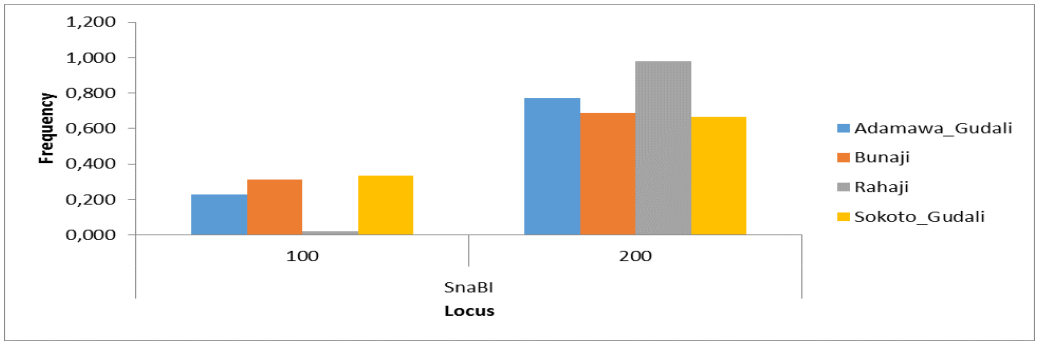

Figure 1. Allele frequency distributions among breeds of cattle

100-Allele C; 200: Allele T

Genetic differentiation and diversity at IGF-1 gene locus of some breeds of cattle

Heterozygosity, F-Statistics and polymorphism by populations of cattle breeds is shown in Table 4. All the four breeds showed two alleles at the IGF-1 locus (Na = 2), giving 100% polymorphic status for this locus across populations (Table 2). Effective allele numbers (Ne), Shannon's index (I), observed and expected heterozygosity, and unbiased He varied by breed. Sokoto Gudali exhibited the highest He (0.444) and uHe (0.454), whereas Rahaji had the lowest (He = 0.041; uHe = 0.042). Observed heterozygosity was highest in Bunaji (Ho = 0.375).

Table 4. Heterozygosity, F-Statistics and polymorphism by populations of cattle breeds

Population	Locus	N	Na	Ne	I	Ho	He	uHe	F	% P	Nm
Adamawa Gudali	IGF-1 gene	24	2.000	1.546	0.538	0.208	0.353	0.361	0.410	100	
Sokoto Gudali	IGF-1 gene	24	2.000	1.800	0.637	0.250	0.444	0.454	0.438	100	
Bunaji	IGF-1 gene	24	2.000	1.753	0.621	0.375	0.430	0.439	0.127	100	
Rahaji	IGF-1 gene	24	2.000	1.043	0.101	0.042	0.041	0.042	0.021	100	
Grand mean and SE over loci and populations											
		N	Na	Ne	**I**	Ho	He	uHe	F		
Total	Mean	24.000	2.000	1.536	0.474	0.219	0.317	0.324	0.238	100	2.595
	SE	0.000	0.000	0.173	0.126	0.069	0.094	0.096	0.111	0.00	
F-Statistics and estimates of Nm over populations for each locus											
All populations	Locus	Fis	Fit	Fst							
	IGF-1gene	0.310	0.371	0.088							

N: Number, Na: Number of different Alleles, Ne: Number of Effective Alleles, I: Shannon's Information Index, Ho: Observed Heterozygosity, He: Expected Heterozygosity, uHe: Unbiased Expected Heterozygosity, F: Fixation Index, Nm: Gene flow, Fis: Average inbreeding coefficient within subpopulation, Fit: Overall inbreeding within the entire population, Fst: Genetic differentiation among subpopulations, IGF-1: Insulin-like growth factor 1 gene, %P: Percentage of polymorphic locus, SE: Standard error, %: Percent

The gene flow N (nm) value combining all the four (4) breeds, amounted to (2.595). When gene flow was examined within breed, gene migration among cattle breeds population ranged from (0.041) in Rahaji to 0.444 in Sokoto Gudali cattle breed. The average inbreeding coefficient (FIS) within subpopulation was (0.310) whereas the overall inbreeding (FIT) within the entire population was (0.371). The genetic differentiation among subpopulations (FST) was (0.088), that is, the genetic makeup which differs between population.

DISCUSSION

Analysis of molecular variance of cattle revealed that a large population of the observed variance occurred within individuals than among individuals and variation among population. Similar to the results of this study, BORA *et al*. (2023) reported genetic variability of (84%) among individual, (13%) among population and (3%) within individual. ZANG *et al*. (2021) also reported higher genetic variance within population (81.7%) than among populations (18.3%), indicating low degree of genetic differentiation between populations. The between breed variation of 9% observed in this study is higher compared to 1.14% reported by ADIDO *et al.* (2019), 2.6% by GREMA *et al.* (2017) in Niger cattle, and 6.1% by EMA *et al*. (2014) in Cameroonian cattle, suggesting significant genetic differentiation between the studied populations. The results of this study corroborate the findings of NWACHUKWU *et al.* (2022) who also reported high genetic variation within population as 79% within populations and 21% among populations. The higher within population variation depict considerable level of isolation as the animals were likely kept separately on the farm. The closeness of the breeds reported in this study showed similar proximity of geographical location.

The IGF-1/SnaBI locus was 100% polymorphic in all sampled breeds, with TT genotype predominance and low CC frequency. The results of this study agreed with the findings of SZEWCZUK *et al.* (2011) who reported high allele frequency of T than C. The differences in allele differences reported could be attributed to the differences in breeds or genetic constitution of the animals. This allele configuration frequent T allele and less frequent C allele reflects patterns reported in other breeds and regions where the IGF-1 SnaBI/TasI polymorphisms have been screened (SZEWCZUK *et al*., 2013).

F-statistics across all populations at the IGF-1 locus were FIS = 0.310, FIT = 0.371, and FST = 0.088, indicating a moderate average inbreeding within subpopulations and low–moderate differentiation among subpopulations. Using the standard island model approximation, Nm across the combined populations was (2.595), suggesting sufficient gene flow to limit strong differentiation. The observed heterozygosity varied: Bunaji exhibited the highest Ho (0.375) while Rahaji had the lowest (0.042). Expected heterozygosity was highest in Sokoto Gudali (He = 0.444).

The mean FIS of (0.310) indicates a moderate excess of homozygosity within subpopulations; possible causes include assortative mating, population substructure, or sampling of related individuals. The detection of polymorphism at IGF-1 and moderate heterozygosity in Sokoto Gudali and Bunaji suggests available genetic variation that selection programs could exploit if favorable allele–trait relationships are established. In this study, the F_{IS} (0.310) estimated using RFLP was close to zero, which indicates very little admixture among the breeds. Genetic characterization of Ethiopian cattle breeds using microsatellite reported within

population inbreeding of (0.071) and a total of inbreeding of (0.083) (DADI *et al*., 2008). The differences observed in the results reported might be attributed to the differences in breeds, genetic make-up of an animals and the techniques used in the study. A hundred percent 100% polymorphic loci were recorded in this study. AJAYI *et al*. (2016) similarly reported (100%) polymorphic loci among breeds of cattle in Nigeria. The similarities observed in the result reported might be as a results of breed similarities and over lapse of habitat or Agro ecological zone. However, the (100%) polymorphic value obtained in this study is at variance with the earlier reports of (75%) and (98%) respectively by NGUYEN *et al*. (2007) and MAKKAWI *et al*. (2007). The differences observed in the polymorphic loci reported might be attributed to breed differences or the genetic constitutions of the animals.

The average observed heterozygosity in this study is within the range reported in seven Italian cattle breeds (0.06-0.68; DEL BO *et al*., 2001) and five Swiss cattle breeds (0.60-0.69; SCHMID *et al*., 1999). Lower level (0.59) of heterozygosity was reported in Deoni cattle breed of India (MUKESH *et al*., 2004). Sokoto Gudali and Bunaji had higher expected heterozygosity values in this study. AJAYI *et al*. (2016) reported the highest average heterozygosity of (0.5833) at B allele for Sokoto Gudali cattle breed. The mean heterozygosity value reported in this study is lower than the previous findings of AJAYI *et al*. (2016) who reported average heterozygosity value (0.6119) in the entire population of White Fulani, Red Bororo and Sokoto Gudali cattle breeds respectively. The heterozygosity values in Adamawa Gudali, Sokoto Gudali and Bunaji cattle breeds respectively reported in this study is similar to the (0.574) and (0.5401) reported by PANDEY *et al*. (2006) for Kherigarh and Kenkatha cattle respectively.

The mean Allelic patterns across populations of cattle breeds revealed that the average numbers of effective alleles were predominant in Sokoto Gudali, followed by Bunaji, with the least in Rahaji cattle breed. The Shannon's information index was also high in Sokoto Gudali whereas Rahaji had the least. The expected heterozygosity and unbiased expected heterozygosity also appeared to be preponderant in Sokoto Gudali cattle breed compared to others breeds. The heterozygosity value recorded in Adamawa Gudali cattle in this study is similar to the heterozygosity value (0.332) observed in Angus breed (CARRUTHERS *et al*., 2011), and heterozygosity values (He) of (0.25) for African cattle and (0.30) for European originated breeds, respectively based on SNP analysis (GAUTIER *et al*., 2007). This could be attributed the similarities in breeds studied. The mean number of effective alleles observed in this study across the breeds were generally lower than (2.50±0.32) in Sokoto Gudali to 3.25±0.29 in White Fulani with a mean of 2.82±0.13 across the four breeds reported by NWACHUKWU *et al*., (2022). The differences observed could be as a result of the genetic constitution of the animals.

CONCLUSIONS

Analysis of molecular variance (AMOVA) of breeds of cattle revealed that a larger percentage (61%) of the observed variance occurred within the breeds (30%) compared with among individuals (30%) and among populations (9%). Genetic differentiation and diversity at IGF-1 gene locus of some cattle breeds revealed high genetic variations among the cattle breeds populations studied. The entire gene locus was found to be 100% polymorphic and the gene flow

N(nm) over all populations for each locus was (2.595) and within population inbreeding coefficient (F_{IS}) per population was (0.310).

Genetic differentiation and diversity at IGF-1 gene locus revealed variations in allelic (C and T) and genotypic (CC, CT and TT) frequencies across the breeds. T allele had the higher proportion or frequency of occurrence than C allele in all the breed. Restriction Fragment Length Polymorphism (RFLP) marker of IGF-1 gene revealed high level of genetic variations among the population of cattle breeds studied.

RECOMMENDATION

Restriction Fragment Length Polymorphism (RFLP) marker can provide more insight for differentiation of cattle breeds because of the high levels of genetic variations observed. Cattle with T allele should be considered over the ones with C allele for differentiation because of their higher level of frequency of occurrence. The cattle carrying CT and TT genotypes of the IGF-1 gene polymorphism should be preferred in selection for improving these traits compared to the ones with CC because they had better association with performance.

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DATA AVAILABILTY

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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GENETSKA RAZNOVRSNOST I DIFERENCIJACIJA NEKIH NIGERIJSKIH AUTOHTONIH RASA GOVEDA NA GENSKOM LOKUSU IGF-1

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Izvod

Studija je sprovedena radi utvrđivanja genetske raznolikosti i diferencijacije kod odabranih autohtonih rasa goveda u Nigeriji na lokusu gena insulin-sličnog faktora rasta 1. Devedeset šest (96) goveda (n = 24 po rasi) je namerno uzorkovano u državama Adamava, Taraba, Gombe i Sokoto. Uzorci krvi su prikupljeni od životinja putem jugularne venepunkcije. DNK je ekstrahovana pomoću kompleta za prečišćavanje DNK, a kvalitet i količina su procenjeni pomoću NanoDrop-1000 UV spektrofotometra. Genomska DNK je ekstrahovana iz pune krvi i genotipizovana za IGF-1 fragment korišćenjem PCR-RFLP sa SnaBI restrikcionim enzimom korišćenjem Zymo Quick DNA TMMini prep kompleta. Prikupljeni podaci su podvrgnuti F statističkoj analizi korišćenjem softverskog paketa GenAIEx. Analiza molekularne varijanse (AMOVA) goveda otkrila je 61% varijanse unutar populacije, 30% varijanse je pripisano među pojedincima, a 9% među populacijama. Genotip TT je bio najviši, zatim genotip CT, dok je genotip CC bio najmanji. Kompletan polimorfizam je primećen na lokusu gena IGF-1, a protok gena N (nm) kroz sve populacije za svaki lokus je bio (2,595), a koeficijent inbridinga unutar populacije (FIS) po populaciji je bio (0,310). Očekivana heterozigotnost (0,444) i nepristrasna očekivana heterozigotnost (0,454) su takođe izgledale preovlađujuće kod rase goveda Sokoto Gudali u poređenju sa drugim rasama. Marker polimorfizma dužine restrikcionih fragmenata (RFLP) otkrio je visok nivo genetskih varijacija i raznolikosti na lokusu gena IGF-1 među populacijom proučavanih goveda.

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