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COMPARISON STUDY OF THE GENETIC DIVERSITY OF NIGERIAN INDIGENOUS CATTLE BREEDS BASED ON VARIATION OF HAEMOGLOBIN AND TRANFERRIN POLYMORPHISM

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Key Words:
Cattle, Genetic diversity, Haemoglobin, Transferrin

Abstract

This study was undertaken to evaluate and compare the genetic diversities of some selected breeds of cattle (Sokoto Gudali, Red Bororo and White Fulani) using Transferrin and Haemoglobin. Blood samples were collected from 300 cattle comprising males and females of 100 Sokoto Gudali, 100 Red Bororo and 100 White Fulani inan heparinized bottle and the protein polymorphism was investigated using cellulose acetate electrophoresis. The observed allele frequencies and genotypes (%) were tested with Hardy-Weinberg's Equilibrium (χ^2), from the three breeds, only White Fulani was observed to be significant ($p<0.05$) while Sokoto Gudali and Red Bororo were not significant ($p>0.05$) Four alleles Tf^A, Tf^B, Tf^C and Tf^D controlling ninee genotypes were observed at the Transferrin locus while two Haemoglobin alleles (Hb^A and Hb^B) controlling three genotypes were observed in haemoglobin. The values for the observed heterozygosity in

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Sokoto Gudali, Red Bororo and White Fulani were 0.609, 0.527 and 0.678 respectively. The value of the expected heterozygosity for Sokoto Gudali, Red Bororo and White Fulani were 0.589, 0.557 and 0.573 respectively, while the gene diversity (D) for Sokoto Gudali, Red Bororo and White Fulani were 0.587, 0.557 and 0.569 respectively. The values of the examined fixation indices for F_{IS}, F_{IT} and F_{ST} were -0.029, 0.017 and -0.048 respectively. The Genetic distance estimate in this study ranged from 0.008-0.050. Using protein loci, the genetic distance indicated that the Red Bororo and White Fulani were the most genetically similar while Sokoto Gudali was farther from the two breeds indicating that Sokoto Gudali may have had different historical origins or prehistoric migration route.

INTRODUCTION

Genetic diversity plays a crucial role in the survival and enhancement of livestock across diverse environments (Olaoluwa *et al.,* 2018). In the context of domestic animals, studying genetic diversity aims to assess variations within and between breeds, with breeds being the managed units where factors like inbreeding are controlled (Tapio *et al.,* 2005). However, the conventional breed definition by the Food and Agricultural Organization (FAO) often doesn't capture the underlying genetic population structure (Osaiyuwu *et al.,* 2018). Thus, delving into the molecular genetics of population diversity and structure becomes essential to grasp the true genetic resources at hand.

Domestic animal biodiversity arises from a blend of genetic and environmental factors, leading to the development of diverse physical, physiological, and productive traits. These traits are vital for all production systems as they offer the basis for breed enhancement and adaptation to changing conditions (Ceriotti *et al.,* 2003). Characterizing Farm Animal Genetic Resources (FAGR) involves activities that identify, quantitatively

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and qualitatively describe, and document breed populations in their natural habitats and related production systems (Gizaw *et al.,* 2011).

The genetic resources of livestock face threats from erosion (Ajmone-Marson, 2010), which is particularly concerning in developing nations. Native breeds, with unique disease resistance and local environmental adaptations, often give way to industrial breeds. Unfortunately, due to lack of information, local breed development is sidelined in favor of introducing germplasm from exotic breeds, which have more available data (Ajmone-Marson, 2010). It is imperative to characterize breeds both in terms of physical attributes and their interaction with production systems, as well as genetically (FAO, 2011).

DNA-based technologies have become the preferred method for genetic characterization of livestock (Arora *et al.,* 2011). Nevertheless, alternative techniques like protein/allozyme polymorphism remain highly valuable, particularly in developing countries due to their practicality, affordability, information yield, and ease of interpretation (Rege and Okeyo, 2006). These methods, including blood protein polymorphism, hold significance in regions where genetic research is less advanced (Mwacharo *et al.,* 2002).

Blood protein polymorphism, detected through electrophoresis, has been instrumental in assessing genetic differences between breeds and in phylogenetic studies (Ibeagha-Awemu and Erhardt, 2004; Camoglu and Elmaci, 2005). These protein variants have aided in understanding genetic relationships within farm animals (Shahrbabak *et al.,* 2010). However, many past livestock variation studies primarily relied on morphological distinctions, which can underestimate true genetic variation due to their complex inheritance and environmental influence (Yakubu and Akinyemi, 2010; Yakubu and Ibrahim, 2011).

To gain better insights into cattle breeding and effective conservation strategies, investigating their genetic diversity through blood protein polymorphism is essential. This approach can enhance the expertise of local

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scientists, strengthen institutional capabilities, and prioritize conservation measures. Examining the possible connections between ecological and genetic profiles can validate the adaptive theory of allozymic variation. If genetic structures are linked to ecological determinants on various levels, it reinforces the idea of adaptive variation. This study focuses on the genetic diversity of Indigenous cattle in Ogun State, Nigeria.

METHODOLOGY

Animal and Experimental Procedure

In the study, three distinct cattle populations from Nigeria—White Fulani, Red Bororo, and Sokoto Gudali, were sampled across various regions of Ogun State, including Ijebu, Remo, Yewa, and Egba. A total of 300 blood samples were collected, with each breed contributing 100 samples, encompassing both male and female individuals. For sample collection, approximately 5ml of blood was drawn from each animal's vein into heparinized tubes. Following a method outlined by Riken (2006), red blood cells (RBCs) were isolated from the erythrocyte fraction of the heparinized blood. This isolation process involved centrifugation at speeds ranging from 2500 to 3000 revolutions per minute for 10 minutes at a temperature of 40 degrees Celsius. The RBCs were then treated with distilled water at a fourfold volume to release carbonic anhydrase. Separation of the plasma fraction from the erythrocyte fraction was carried out. In the next step, cellulose acetate plates were immersed in the same buffer used as the electrode buffer. Using an applicator, the samples were applied onto the plate, and once loaded, the plates were positioned on the wicks within the tank. The loaded zone, containing the samples, was positioned at the cathodal end of the tank, which facilitated an anodal migration. Upon completion of the gel run, the plates were taken out of the tank and placed into an empty Petri dish.

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To enhance visualization, the plates were stained with Ponceau stain before drying out. After approximately 20 minutes of staining, the plates were sufficiently stained. Subsequently, destaining was performed multiple times until distinct and clear bands emerged. These bands were evaluated visually, considering their migratory pattern as described by Riken (2006). Gene frequencies were calculated by means of direct counting. In summary, the research involved sampling three Nigerian cattle populations in different regions of Ogun State: White Fulani, Red Bororo, and Sokoto Gudali. A total of 300 blood samples, 100 from each breed, were collected from both male and female cattle. The study protocol included isolating red blood cells (RBCs) from the heparinized blood, separating plasma from the erythrocyte fraction, applying samples onto cellulose acetate plates, and running the gel for migration. After staining and destaining, distinct bands were visually assessed to calculate gene frequencies. The study aimed to analyze genetic diversity among these cattle populations using this methodology.

Statistical Analysis

The allele and genotype frequency, observed and expected heterozygosity, Hardyweinberg's Equilibrium coefficient, Wright F_{IS}, F_{IT} and F_{ST} estimated and drawing Unpaired Group Method of Algorithm (UPGMA) dendogram as well as the genetic distance according to (Nei's, 1972) were generated using Tools for Population Genetics Analyses (TFPGA) software.

RESULTS

Gene Frequency

The two loci that were studied in the cattle populations were found to be polymorphic in all the breeds. Allele frequencies ranged from 0.006 for Tf^D in Red Bororo to 0.587 for Hb^A in Sokoto Gudali. The transferrin locus had four alleles while Haemogloin had two alleles.

Table 1: Allele frequencies of blood protein variants in cattle population

Locus	Allele	SokotoGudali	Red Bororo	White Fulani
Tf	Tf^A	0.374	0.235	0.322
	Tf^B	0.313	0.524	0.467
	Tf^C	0.275	0.235	0.195
	Tf^D	0.039	0.006	0.017
Hb	Hb^A	0.587	0.491	0.466
	Hb^B	0.413	0.509	0.534

~~Tf~~ → Transferrin, ~~Hb~~ → Haemoglobin.

Genotype Frequency

The Transferrin locus was more polymorphic than haemoglobin locus with nine genotypes controlled by four codominant alleles. The genotype frequency ranged from 0.011 for Tf^{DC} and Tf^{AA} in Sokoto Gudali and White Fulani to 0.527 for Hb in White Fulani. Genotype Tf^{AD} Tf^{AB} Tf^{CC} Tf^{DC} Tf^{DD} does not exist in Sokoto Gudali, Red Bororo, White Fulani and White Fuani respectively.

Table 2: Genotype Frequencies for the Loci Across the Breeds

Locus	Genotypes	Sokoto Gudali	Red Bororo	White Fulani
Transferrin	AA	0.109	0.306	0.011
	AB	0.319	0.000	0.402
	BB	0.066	0.306	0.161
	AC	0.209	0.153	0.184
	BC	0.176	0.129	0.207
	CC	0.077	0.094	0.000
	DC	0.011	0.000	0.000
	DD	0.033	0.000	0.000
	AD	0.000	0.012	0.034
X^2		81.106	17.951	23.179

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Significance		N.S	N.S	N.S
Haemoglobin	AA	0.349	0.264	0.203
	AB	0.476	0.453	0.527
	BB	0.175	0.283	0.270
X^2		0.041	0.568	0.200
Significance		N.S	N.S	N.S

X^2: chi-square and Sig values are significant when P<0.05

Heterozygosity

In table 3 observed and expected heterozygosity (H_O and H_E) ranged from 0.453 for haemoglobin in Sokoto Gudali to 0.741 for Tf in Sokoto Gudali and 0.689 for Tf in Sokoto Gudali respectively, while the mean ranged from 0.527 for Red Bororo to 0.678 for White Fulani and 0.562 for Red Bororo to 0.589 for Sokoto Gudali respectively. The gene diversity (D) ranged from 0.489 for Haemoglobin in Sokoto Gudali to 0.685 for Tf in Sokoto Gudali.

Table: 3 Heterozygosity and polymorphism by population for codominant data

Population	Locus	n	HO_O	HE_O	HO_E*	HE_E*	Nei**	Av. H
SokotoGudali	Tf	182	0.286	0.741	0.311	0.689	0.685	0.627
	HB	126	0.524	0.476	0.511	0.489	0.489	0.494
	Mean		0.405	0.609	0.411	0.589	0.587	0.561
Red Bororo	Tf	170	0.400	0.600	0.381	0.619	0.615	0.627
	HB	106	0.547	0.453	0.495	0.505	0.499	0.494
	Mean		0.474	0.527	0.438	0.562	0.557	0.561
White Fulani	Tf	174	0.172	0.828	0.355	0.645	0.641	0.627

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	HB	148	0.473	0.527	0.499	0.501	0.498	0.494
	Mean		0.323	0.678	0.427	0.573	0.569	0.561
Overall	Tf	526	0.286	0.723	0.349	0.645	0.647	0.627
	HB	380	0.511	0.489	0.499	0.501	0.499	0.494
	Mean		0.399	0.606	0.424	0.573	0.573	0.561

n= sample size, HO_O= Observed homozygosity, HE_O= Observed heterozygosity

HO_E= Expected homozygosity, HE_E= Expected heterozygosity, H= Heterozygosity

***Expected homozygosity and heterozygosity were computed using Levene (1949)**

****Nei's (1973) expected heterozygosity**

Genetic Distance and Genetic Identity

The distance between populations ranged from 0.008 to 0.050. The smallest genetic distance was observed between Red Bororo and White Fulani populations while the farthest distance was observed between Sokoto Gudali and Red Bororo populations. Results of genetic identity are presented in Table 4. It showed that the Red Bororo and White Fulani populations are more genetically alike (0.992) while the Red Bororo and Sokoto Gudali populations were the least genetically identical (0.951).

Table 4: Nei's Original Measures of Genetic Identity and Genetic distance

Population	Sokoto Gudali	Red Bororo	White Fulani
SOKOTO GUDALI	****	0.951	0.964
RED BORORO	0.050	****	0.992
WHITE FULANI	0.037	0.008	****

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Nei's genetic identity (above diagonal) and genetic distance (below diagonal)

F-Statistics and Gene Flow

Population differentiation revealed by fixation indices F_{IS}, F_{IT} and F_{ST} for each of the loci studied across three Nigerian cattle population are shown in Table 5 The global heterozygosity deficit (F_{IT}) was estimated at 0.017 and the within-breed deficit in heterozygote evaluated by F_{IS} was 0.026 for Hb and -0.721 for Tf with a total mean of -0.029 for both loci. Global breed differentiation evaluated by F_{ST}, was estimated at -0.048. The mean gene flow over all loci was -5.458.

Table 5: F-Statistics and Gene Flow for all population in each locus

Locus	F_{IS}	F_{IT}	F_{ST}	Nm*
Tf	-0.721	0.023	-0.097	-2.827
Hb	0.026	0.009	0.017	14.456
Mean	-0.029	0.017	-0.048	-5.458

Nm*= Gene flow estimated from F_{ST} = 0.25(1 - Fst)/F_{ST}

n= Sample size

Chi square (X^2) Test of Hardy-Weinberg Equilibrium

The test of Hardy-Weinberg equilibrium (HWE) for single locus was conducted for the cattle populations within the two protein loci. Tables 6 revealed that all the breeds had no significant deviation from HWE (P<0.05), except the Tranferrin locus of White Fulani which deviated with the value 0.0365.

Table 6: Summary of Chi– Square Tests for Hardy Weinberg Equilibrium

Population	Locus	ChiSq	Prob	
Sokoto Gudali	Tf	1.466	0.226	N.S
	Hb	0.020	0.889	N.S

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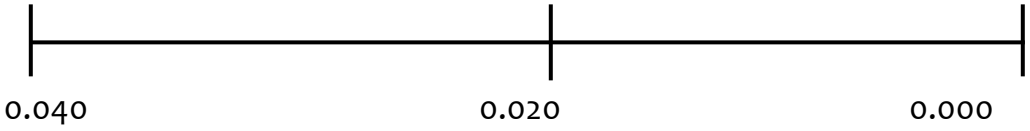
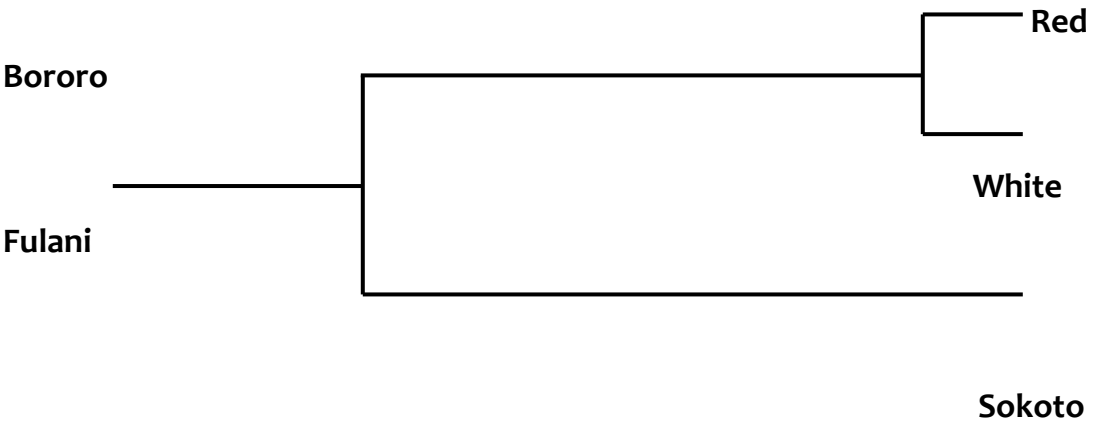
Red Bororo	Tf	1.381	0.239	N.S
	Hb	0.469	0.394	N.S
White Fulani	Tf	4.374	0.037	*
	Hb	0.259	0.613	N.S

Dendrogram

The genetic distance estimates were used to construct dendrogram based on individual locus and the pooled distances for the loci. The dendogram showed White Fulani and Red Bororo branched from the same root while Sokoto Gudali branched from another root





Discussions

Gene and Genotype Frequencies

A total of 6 alleles were observed in the investigated loci. All loci sampled were found to be polymorphic. The Transferrin locus produce four alleles

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and the Haemoglobin locus had two alleles; each of the allele observed is present in all the populations sampled. The frequencies of Hb^{B} allele were considerably higher than that of Hb^{B} in Red Bororo and White Fulani except for Sokoto Gudali. Osaiyuwu and Salako (2018), Shahrbabak et al. (2010) and Boujenane et al. (2008), reported similar results that Hb^{B} is generally the most occurring allele in most sheep breeds. In contrary to this, the Hb^{A} was higher in the Sokoto Gudali population in this study; this variation may be attributed to the selective advantages of Hb in different geographical regions. Tella et al. (2000) in a study of West African Dwarf and Yankassa sheep in South West Nigeria reported that Hb^{A} occur at higher frequency in the two breeds with Hb^{A} occurring in 98.8% of the WAD population and 78.78% of the Yankassa population sampled.

The two loci in this study were polymorphic in the populations. Hb^{AA}, Hb^{AB} and Hb^{BB} in this study was similar to the report of Essien *et al.,* (2011) on Bunaji cattle in Zaria, Nigeria, with frequencies of heterozygote Hb^{AB} considerably higher than either of the homozygote Hb^{AA} and Hb^{BB}. Gwaza *et al.,* (2019) also observed the genotypes Hb^{AA}, Hb^{AB} and Hb^{BB} in his work on West Africa dwarf goat, and among the three genotypes of the haemoglobin reported, the genotype Hb^{AB} has the highest frequency. This increased frequency may be due to an improved advantage of the heterozygote (Hb^{AB}) genotype that favoured it survival, fitness and adaptation to enviromental challenges compared to the homozygotes (Hb^{AA} and Hb^{BB}) genotypes.

In the Gudali breed, gene frequency of Hb^{A} is more consistent than the Hb^{B} variant with values 0.587 and 0.412 respectively, this is in agreement with Tawah and Rege, 1996 that Hemoglobin (Hb) gene frequencies are similar in the zebus, with a substantial presence of both Hb^{A} and Hb^{B} with the former usually more than the latter i.e. (Hb^{A}= 0.52-0.60), (Hb^{B}=0.32-0.44). The overall frequency shows that the Hb^{A} type is the most consistent among zebu type animals even when the White Fulani and Red Bororo breeds

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showed a contrasting feature for the gene frequency as the Hb^B was considerably higher than the Hb^A variant which was common among the taurine breeds.

The four alleles observed at the Transferrin locus were dispersed, in terms of their frequencies and number within each breed, and in respect of their distributions among breeds. The differences observed at the Tf alleles indicate clear genetic differentiation between the cattle breeds studied.

The gene frequencies at Transferrin locus were compared with those reported by other researchers in term of the degree of divergence between breeds. Nguyen *et al.,* (1992) published results on these alleles in Spanish Merino. Osaiyuwu and Salako, (2018) also observed Tf^A, Tf^B, Tf^C, and Tf^D in their work on Genetic structure of indigenous sheep breeds in Nigeria based on electrophoretic polymorphous systems. The presence of Tf^B, and Tf^D alleles in this study was also reported by Ibeagha-Awemu and Erhardt (2004). Some alleles where observed by other researchers which were not present in this study, Ibeagha-Awemu and Erhardt (2004) posited that the absence of these alleles may not totally exclude their occurrence in the breeds but may have exposed the limitation of the method of starch gel electrophoresis in separating Tf variants.

Observation at Transferrin locus are generally difficult to compare with the result obtained in other studies because of the different electrophoresis media used by other researchers and subsequently different resolution power, that is, starch gel and poly acrylamide gel electrophoresis (Akinyemi and Salako, 2012). However, significant deviations of allele frequencies may occur owing to crossing and linking, inbreeding, sample error, population bottlenecks and random genetic drift.

The transferrin locus was more polymorphic than the haemoglobin locus, as it has four alleles and nine genotypes while the haemoglobin locus has two alleles and three genotypes. The haemoglobin locus has the highest allele frequencies in Sokoto Gudali and White Fulani breeds while the transferrin

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locus has the highest allele frequency only in the Red Bororo breed. All of the three genotypes in the haemogobin were present in the three breeds while only five of the genotypes in the transferrin locus were present in all the breeds. Bunjah (2016) reported a similar result on his work on Bunaji, Gudali and Friesian X Bunaji crossbreed as he observed two alleles (Hb^A and Hb^B) and three genotypes (Hb^{AA} Hb^{AB} and Hb^{BB}) in the three breeds while he reported two alleles (Tf^A and Tf^B) and three genotypes (Tf^{AA} Tf^{AB} and Tf^{BB}). Awobajo *et al.,* (2018) also reported two haemoglobin alleles (Hb^A and Hb^B) and three genotypes (Hb^{AA} Hb^{AB} and Hb^{BB}) as well as two transferring alleles (Tf^A and Tf^B) and three genotypes (Tf^{AA} Tf^{AB} and Tf^{BB}) in the genetic relationship among Nigerian west african dwarf goats.

Heterozygosity and Gene Diversity

The observed heterozygosity (H_O) was higher than the expected heterozygosty in Sokoto Gudali and White Fulani while observed heterozygosity was lower than the expected heterozygosty in Red Bororo. This means that there is high variability as well as a lot of cross breeding in Sokoto Gudali and White Fulani, while the Red Bororo breed has a lot of inbreeding in its population. The values of the gene diversity (Nei's expected heterozygosity) were higher than the observed heterozygosity in all the breeds and markers except in Sokoto Gudali breed with Hb and White Fulani with Hb. This mean that the gene diversity is low indicating or implying inbreeding is taking place within the Sokoto Gudali and White Fulani breeds. Awobajo *et al.,* (2016) reported that the average H_O was more than the H_E West African Dwarf goats by allozyme markers, and the average expected gene diversity (Nei, 1973) within the population ranged from 0.34 (Hb) to 0.50 (Tf) with an overall mean of 0.44 ± 0.09. Ajayi *et al.,* (2016) reported that Sokoto Gudali recorded the highest average heterozygosity of 0.583. Pandey *et al.,* (2006) reported the mean observed heterozygosity of 0.574 and 0.540 for Khergarh and Kenkatha cattle. Demir and Balcioglu

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(2019) reported observed heterozygosity ranged from 0.30 to 0.98 with a mean of 0.63, while the expected heterozygosity ange from 0.51 to 0.88 with a mean of 0.74. Generally the observed heterozygosity was lower than expected heterozygosity, which may be due to the presence of more homozygous individuals in the analysed samples.

Hardy-Weinberg's Equilibrium

The tests of deviation from Hardy-Weinberg proportions are frequently made to check on random mating in populations, and the deviations from expectation are used to estimate inbreeding coefficients. The significant deviations observed in white fulani population at the Transferrin locus ($P<0.05$) is similar with the report of Sargent et al. (1999) who established deviations from HWE at protein loci in Southern Africa Sheep. The significant deviations from HWE could be as a result of any one or a combination of unobserved null alleles, excess of heterozygote, migration, high mutation rate and artificial selection (Aminafshar *et al.,* 2008), crossing and linking, inbreeding, sample error, population bottlenecks and random genetic drift. Ideal Hardy-Weinberg populations do not actually occur in nature owing to various factors, which can shift the equilibrium and disrupt the stability of a population, giving rise to change in the genetic structure (Sargent et al. 1999).

Genetic Distance, Genetic Identity and Dendogram

The Nei (1972) standard genetic distance was used to determine the genetic relationship between populations that is genetic distance and identity between the populations. The genetic distance obtained in this study (0.008-0.050) indicates the level of genetic differentiation between the breeds, and this was similar to 0.001 - 0.055 reported for Spanish sheep breeds (Ordas and Primitivo, 1986). 0.01 - 0.22 reported by Nigussie et al. (2016) for eastern Ethiopia sheep breeds, was higher than 0.008 – 0.050 of

this study. Zanotti et al. (2008) reported genetic distance ranging between 0.012 and 0.060 in five Italian sheep breeds. Boujenane et al. (2008) reported a genetic distance range of 0.006 to 0.026. Distances obtained in this study between breeds were also higher to that of Akinyemi and Salako (2012) who reported a range of 0.003 to 0.015. The distance estimate in this current study revealed a closer relationship between Red Bororo and White Fulani. From the dendogram constructed, Sokoto Gudali branched from another root aside from the one Red Bororo and White Fulani branched from. Signifying prehistoric separation of origin in the Gudali breed. The genetic relationship between the Red Bororo and White Fulani breed may be attributed to possible interbreeding between these two populations which are predominantly Northern breeds to form a homogenous population separated by administrative boundaries. According to Mwacharo *et al.,* (2002) the close genetic relationship between the breeds may also be ascribed to similarity in ecological zones and production systems as well as the incidents of cross border livestock rustling contributing to the migration and movement of livestock and subsequent interbreeding between such livestock.

Gene Flow and F- Statistics

F-Statistic values of F_{ST} and F_{IT} are measures of deviation from Hardy-Weinberg's proportions and total populations respectively. Positive values indicate a deficiency in heterozygotes and negative values indicate an excess of heterozygotes. F_{IS} can be interpreted as a measure of inbreeding (the measure of allelic fixation of individuals relative to the subpopulations). Thus, the negative values of F_{IS} observed at the Tf locus in the three breeds studied and the overall value of -0.029 showed excess heterozygosity in the populations and that mate were less related in comparison with the average relationship of the population. This observed excess of heterozygotes could be due to non-random mating and genetic exchange between populations.

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The global heterozygosity deficit (F_{IT}) was estimated at 0.017, which indicates there excess of homozygotes in the populations and that mate were less related in comparison with the average relationship of the population. Estimated F_{ST}, which corresponds to the proportion of genetic variability accounted for by the differences among breeds, was -0.048. Thus, a large part of the total genetic diversity can be explained by the variation within breeds and to a smaller extent by the variation among breeds. This result indicates that genetic diversity quantified by allozyme markers shows little genetic differentiation among the breeds studied. The degree of differentiation observed between the cattle breeds could be due to geographic proximity, similarities in environment and breeding practices, but most likely due to past genetic exchange among them since average gene flow over all loci was -5.458. The Mean estimate of F-statistics; F_{IS} (0.193, within population inbreeding estimate), F_{ST} (0.123, estimate of population differentiation) and F_{IT} (-0.047 , overall global heterozygote deficit across population) reported by Osaiyuwu and Salako (2018) and 0.44, 0.03 and 0.46 for F_{IS}, F_{ST} and F_{IT} respectively reported by Awobajo *et al.*, (2016) were different from the values in the current study. According to Hartle (1980), F_{ST} values up to 0.05 indicate negligible genetic variations while values greater than 0.25 indicate large genetic differentiation amongst populations. The current study reported moderate level of genetic differentiation among the three populations of cattle studied.

Conclusion

The populations in this study were characterized with the existence of four transferrin alleles Tf^A, Tf^B, Tf^C, and Tf^D with ten genotypes, four of which were homozygous and six heterozygous. Two haemoglobin alleles, Hb^A and Hb^B controlling 3 genotypes were found. Two of the haemoglobin genotypes were homozygous. As revealed by the Chi square test of Hardy Weinberg Equilibrium, all breeds in the transferrin locus were not significant

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except for White Fulani. In the haemoglobin locus all the breeds were not significant.

Based on the estimate of the genetic distance in this study using protein loci, the Sokoto Gudali breed was observed to have branched from another root of the phylogenetic tree while Red Bororo and White Fulani were nearly genetically similar as they branched from a different route from that of Sokoto Gudali. This is indicating that Sokoto Gudali may have had different historical origins or prehistoric migration route.

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