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Genetic Relationship between Indigenous Cattle of Nigeria

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Abstract

This study was undertaken to asess the genetic relationship of selected breeds of cattle (Sokoto Gudali Red Bororo and White Fulani) using Transferrin, Carbonic anhydrase and Haemoglobin. Blood samples were collected from 300 cattle comprising of 100 Sokoto Gudali, 100 Red Bororo and 100 White Fulani into heparinized bottles and the protein polymorphism were investigated using cellulose acetate electrophoresis. The Genetic distance estimated for the three loci ranged from 0.006 to 0.047 while the genetic identity between the cattle at the three loci ranged from 0.954 to 0.994. 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. the dendrogram of the three cattle shows that 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. Based on the results of this study, it is recommended that distant breeds are a good fit for improved animal population. Hence, the crossing of Sokoto Gudali with either White Fulani or Red Bororo breeds will produce a better improved population of animals, since the breeds are heterogeneous and distinctly different in their genetic and origin relationship.

Key words: Cattle, Blood protein, Genetic Distance, Genetic identity and Dendrogram

Introduction

The loss of genetic diversity in native livestock populations has been a significant worldwide concern. In an effort to lay the groundwork for the preservation of these potentially valuable germplasms, research into the genetic diversity of livestock species has been conducted (Arora *et al.,* 2011). The loss of genetic variation within and between breeds is detrimental, not only from the perspectives of culture and conservation but also from the standpoint of usefulness, since lost genes may be economically significant in the future. Breed survival prospects are limited by high rates of genetic diversity loss within the breed because inbreeding depression lowers fitness. Therefore, it is essential to describe breeds in terms of both the traits of the animals and the genetic relationships they have with production.

Genetic divergence between breeds can be used to characterize using Allelic variation the difference in entities (Egahi, 2020). The degree of genetic relationship and variations among populations or species is quantified by a numerical value. Genetic divergence studies can be performed to assess how genotypes behave in various settings and determine which genotypes are superior to others. Genetic distance is crucial for determining which genotypes are divergent enough to be parents in breeding programs and for establishing the connection between genetic divergence and heterosis. According to Bruchi *et al.,* (2003), the rate of gene flow between populations determines how genetic diversity is distributed both within and between populations. These authors further reported that the extent of gene flow in a population depends on the distribution of the habitat it occupies and the size and degree of isolation.

Mutation, genetic drift, selection, and migration all influence the genetic distances between breeds or populations. A distance of zero denotes that there is no genetic variation across groups, whereas a maximum value denotes the fixation of alternative alleles. According to FAO, characterization comprises defining precisely the genetic characteristics of a breed or species of animal that gives it a distinct identity as well as the habitat that the populations of that breed or species have adapted to (FAO, 1984). The findings of Salako & Ngere (2001) supported this, stating that morphological distance can serve as a reliable basis and point of reference for the methodical assessment and characterization of native species. It can also reduce the cost of experimental materials by reducing the number of animals that may be needed for assessment. Several authors have reported on the estimation of distance between populations in goats Salako & Ngere) and in fish (Salako & Ngere, 2001; Joan *et al.*, 2006). However, there is scarcity of information as to the genetic distance estimation in Cattle, especially the Nigerian indigenous chicken. In the current study, the genetic diversity between Red Bororo, Sokoto Gudali and White Fulani indigenous cattle of Nigeria is evaluated using traits that show continuous variation.

Methodology

White Fulani, Red Bororo and Sokoto Gudali were sampled in Ijebu, Remo, Yew and Egba zones in Nigeria. 300 blood samples were collected, comprising 100 samples from each breed. 5ml of blood samples were collected from each animal into heparinised tubes by vein puncture. Based on Riken (2006), Red blood cell (RBC) was prepared from the erythrocyte fraction of heparinized blood by centrifuging at 2500 – 3000rpm for 10mins at 4^0C. The RBCs were lysed with a fourfold volume of distilled water to release the carbonic anhydrase. The plasma fraction was separated from the erythrocyte fraction of heparinized blood. Cellulose acetate plates were soaked in the same buffer as the electrode buffer. Samples were applied on to the plate using the applicator and once loaded; plates are rested on the wicks in the tank. The loaded zone on the plate was positioned for migration to take place. After the completion of the gel run, the plates were stained with Ponceau stain in Petri dish before they dry out. After 20 min the plates were sufficiently stained, they were destained several times until clear and sharp bands appear, the bands were scored visually based on their migratory pattern as described by RIKEN (2006) and direct counting was used for calculating gene frequencies. 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

Genetic Distance and Genetic Identity at single locus

Table 1 presents the genetic characteristics at the transferrin, carbonic anhydrase, and haemoglobin loci. The genetic distance and identity values varied across populations. For the transferrin locus, the genetic distance ranged from 0.015 to 0.094, with corresponding identity values ranging from 0.910 to 0.984. Notably, the Red Bororo and White Fulani populations exhibited the closest genetic distance (0.015) and highest genetic identity (0.984), while the Red Bororo and Sokoto Gudali populations showed the farthest distance (0.094) and the lowest genetic identity (0.910). At the carbonic anhydrase locus, the genetic distance varied between 0.003 and 0.036, and the identity ranged from 0.965 to 0.998. The smallest genetic distance (0.003) occurred between White Fulani and Red Bororo populations, whereas the largest distance (0.036) was observed between Red Bororo and Sokoto Gudali populations. The highest genetic identity (0.998) was found between White Fulani and Red Bororo populations, contrasting with the lowest identity (0.965) between Red Bororo and Sokoto Gudali populations. Regarding the haemoglobin locus, the genetic distance values fell between 0.01 and 0.029, accompanied by identity values ranging from 0.971 to 0.998. The minimum genetic distance (0.001) was noted between White Fulani and Red Bororo populations, while the maximum distance (0.029) was observed between White Fulani and Sokoto Gudali populations. The highest genetic identity (0.998) was documented between White Fulani and Red Bororo populations, while the lowest identity (0.971) was found between White Fulani and Sokoto Gudali populations.

Table 1: Measures of Genetic Identity and Genetic distance at Single locus

Locus	Population	Sokoto Gudali	Red Bororo	White Fulani
Tranferrin	**Sokoto Gudali**	****	0.910	0.954
	Red Bororo	0.094	****	0.984
	White Fulani	0.046	0.015	****
Carbonic Anhydrase	**Sokoto Gudali**	****	0.965	0.980
	Red Bororo	0.036	****	0.998
	White Fulani	0.020	0.003	****
Haemoglobin	**Sokoto Gudali**	****	0.981	0.971
	Red Bororo	0.019	****	0.999
	White Fulani	0.029	0.001	****

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

Genetic Distance and Genetic Identity at two loci

Genetic distancing estimates of the Nei's (1972/1978) were calculated and presented in Table 2. The distance between populations at the Haemoglobin/Carbonic anhydrase loci ranged from 0.003 to 0.031. The smallest genetic distance (0.003) was observed between White Fulani and Red Bororo populations while the farthest (0.031) was between Red Bororo and Sokoto Gudali populations. The farthest genetic identity (0.970) was observed between Red Bororo and Sokoto Gudali while the closest in genetic identity (0.997) was observed between White Fulani and Red Bororo. At the Haemoglobin/Transferrin loci, 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 2. 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). At Carbonic anhydrase/transferrin loci Genetic distance estimates of the Nei's (1972) shows that the smallest genetic distance (0.009) was observed between White Fulani and Red Bororo populations while the farthest (0.063) was between Red Bororo and Sokoto Gudali populations. The farthest genetic identity (0.939) was observed between Red Bororo and Sokoto Gudali while the closest in genetic identity (0.991) was observed between White Fulani and Red Bororo.

Table 2: Nei's Measures of Genetic Identity and Genetic distance at Two loci

Locus	Population	Sokoto Gudali	Red Bororo	White Fulani
Haemoglobin/Carbonic anhydrase loci	**Sokoto Gudali**	****	0.970	0.976
	Red Bororo	0.031	****	0.997
	White Fulani	0.025	0.003	****
Haemoglobin/Transferrin loci	**Sokoto Gudali**	****	0.951	0.964
	Red Bororo	0.050	****	0.992
	White Fulani	0.037	0.008	****
Transferrin/Carbonic anhydrase loci	**Sokoto Gudali**	****	0.939	0.969
	Red Bororo	0.063	****	0.991
	White Fulani	0.031	0.009	****

Nei's genetic identity (above diagonal) and genetic distance (below diagonal) among Nigerian three cattle populations.

Genetic Identity and Genetic Distance in all Loci

Genetic distancing estimates of the Nei's (1972/1978) were calculated using alleles frequency and presented in Table 3. The distance between populations ranged from 0.006 to 0.047. The smallest genetic distance (0.006) was observed between White Fulani and Red Bororo populations while the farthest (0.047) was between Red Bororo and Sokoto Gudali populations. The farthest genetic identity (0.954) was observed between Red Bororo and Sokoto Gudali while the closest in genetic identity (0.994) was observed between White Fulani and Red Bororo.

Table 3: Nei's Measures of Genetic Identity and Genetic distance at the three loci

Population	Sokoto Gudali	Red Bororo	White Fulani
Sokoto Gudali	****	0.954	0.970
Red Bororo	0.047	****	0.994
White Fulani	0.031	0.006	****

Nei's genetic identity (above diagonal) and genetic distance (below diagonal) among Nigerian three cattle populations.

Dendrogram of Three Nigerian Indigenous Cattle

The tree below showed the relationship among the three Nigerian cattle breeds. The dendrogram showed Red Bororo and White Fulani branched from the same root while Sokoto Gudali branched from another root.

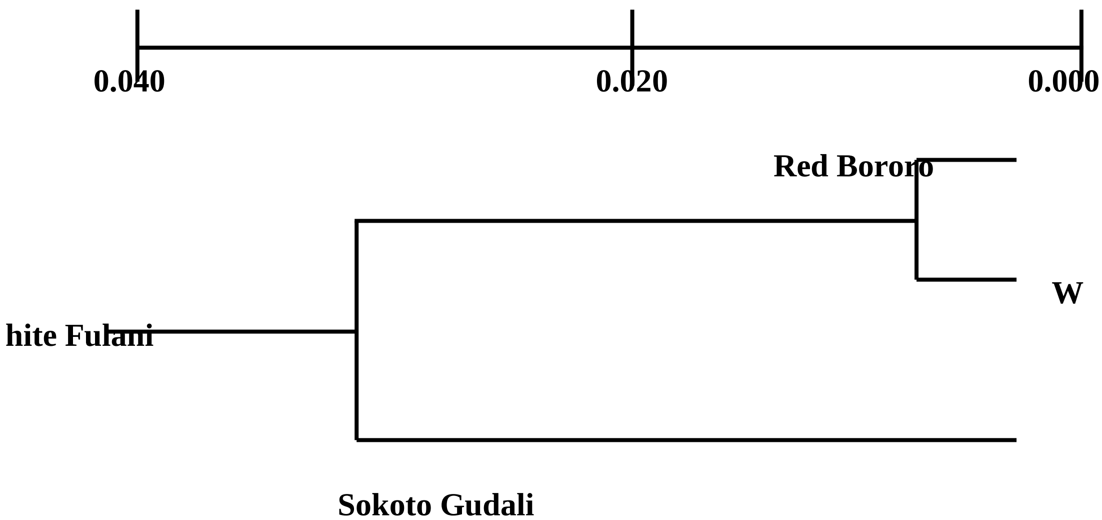

Figure 1: Dendrogram of Nigerian Indigenous Cattle

Discussion

Genetic Distance, Genetic Identity and Dendrogram

The genetic relationship between populations was assessed using the Nei (1972) standard genetic distance, measuring both genetic distance and identity. The genetic distances observed across three loci in this study (ranging from 0.006 to 0.047) denote the degree of genetic differentiation between breeds. This range is comparable to the 0.001 to 0.055 reported for Spanish sheep breeds (Ordas and Primitivo, 1986). However, it is higher than the 0.01 to 0.22 range reported for eastern Ethiopia sheep breeds by Nigussie *et al.,* (2016). Additionally, our findings surpass the genetic distance reported by Zanotti *et al.*, (1990) for five Italian sheep breeds (ranging from 0.012 to 0.060), as well as the range (0.006 to 0.026) reported by Boujenane *et al.*, (2008). The distances in our study are also greater than those reported by Akinyemi and Salako (2012), who found a range of 0.003 to 0.015.

Notably, the analysis revealed a closer genetic relationship between Red Bororo and White Fulani breeds. The constructed dendrogram showed Sokoto Gudali branching from a separate root, distinct from the root of Red Bororo and White Fulani. This suggests a prehistoric divergence in the origin of the Gudali breed. The proximity observed between Red Bororo and White Fulani breeds may be attributed to potential interbreeding, especially given their common Northern origin, forming a genetically homogeneous population despite administrative boundaries. According to Mwacharo *et al.*, (2002), the close genetic relationship could also result from similarities in ecological zones, production systems, and incidents of cross-border livestock rustling, facilitating the migration, movement, and subsequent interbreeding of livestock between these populations.

Conclusion and Recommendation

The findings concerning cattle breeds are crucial for future monitoring of gene flow within populations, providing insights into the levels of inbreeding and crossbreeding in each breed. This information is vital for enhancing the overall understanding of domestic animal diversity. The genetic distance estimates obtained in this study, utilizing protein loci, revealed that Red Bororo and White Fulani are the most genetically similar breeds, whereas Sokoto Gudali stands farther from the two, suggesting potential differences in historical origins or prehistoric migration routes for Sokoto Gudali.

Based on these results, it is recommended that distant breeds be considered for enhancing animal populations. The statistical analyses, indicating significant differences, support the idea that crossbreeding involving Sokoto Gudali with either White Fulani or Red Bororo breeds has the potential to yield an improved population. Given the heterogeneity and distinct genetic and origin relationships among these breeds, such crossbreeding is anticipated to result in vigor (positive heterosis) in the hybrid, contributing to the overall improvement of the animal population.

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