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## GENETIC DISTANCE AND IDENTITY AT IGF-1 GENE LOCUS OF SOME INDIGENOUS CATTLE BREEDS IN NIGERIA

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### ABSTRACT

*An experiment was conducted to determine the genetic distance and identity at insulin-like growth factor 1 (IGF-1) gene locus in some indigenous cattle breeds in Nigeria. One (1) Local Government Area (LGA) each from Adamawa, Taraba, Gombe and Sokoto States was purposively selected which include Mubi North, Yorro, Balanga, and Wurno Local Government Areas, respectively. The snowball method was used to sample (96) cattle consisting of (24) Adamawa Gudali, (24) Sokoto Gudali, (24) Bunaji and (24) Rahaji cattle from pastoralists in many communities of the LGAs. Blood samples were collected from the animals through jugular venepuncture. DNA extraction was done using Zymo Quick DNA™ Mini prep kit. NanoDrop 1000 spectrophotometer was used for the determination of DNA quality and quantity using DNA purification kit. Genetic distances among the breeds of cattle were calculated using distance measures with the aid of Gen AEx software package. The highest level of genetic distance estimate was observed between Rahaji and Bunaji cattle breeds (0.085) while the closest genetic distance (0.001) was observed between Sokoto Gudali and Bunaji. The highest genetic identities were recorded between Sokoto Gudali and Bunaji (0.999) cattle breeds whereas the closest matrix of genetic identity (0.904) was recorded between Rahaji and Sokoto Gudali cattle. Cluster analysis using UPMGA revealed that Bunaji and Sokoto Gudali cattle formed the first cluster which is separate from Adamawa, which formed the second cluster. Rahaji cattle formed the third cluster, which is far and distant from the first and second clusters at IGF-1 gene locus. Rahaji cattle had the longest genetic distance with other three breeds of cattle. High genetic distance and identity existed among some indigenous breeds of cattle studied.*

**Keywords: Insulin-Like growth factor 1 gene, Indigenous, breeds, genetic distance and cattle**

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### INTRODUCTION

One of the ways of characterizing livestock breeds is to determine genetic distance among contemporary populations (Metta *et al.*, 2004). The existence of substantial genetic differentiation between cattle populations has been considered by many scholars to be advantageous for selection and conservation purpose (Tally, 2004). When the value of genetic distance is high, it is an indication of high genetic difference between populations. The genetic distance between a pair population help to evaluate the relationship within breed Blott *et al.* (1998). FAO (2003) established that genetic distance gives a genetic similarity between any pair of populations. Insulin-like Growth Factor I (IGF-1) is known to play an important role in various aspects of muscle growth and development (Davis and Simmen, 2006). Due to the effect of IGF-1 on the hypertrophy of muscle cells, muscle fiber diameter can be affected by IGF-1. This study was designed to determine the genetic distance and identity among some indigenous breeds of cattle in Nigeria at Insulin-like growth factor 1 gene locus.

### MATERIALS AND METHODS

#### Experimental location

The experiment was conducted in four States, which are Adamawa, Gombe, Taraba and Sokoto States in Nigeria. One (1) Local Government Area (LGA) each from each of the States was purposively selected. The LGAs were Mubi North, Balanga, Yorro, and Wurno, respectively.

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### Sample size and sampling techniques

A multistage (three stages) approach was used to select the breeds of cattle from the States with large population of pastoralists that rear Adamawa Gudali, Sokoto Gudali, Bunaji and Rahaji cattle breeds. Four States were selected for the purpose of this study. The snowball sampling method was used to sample 96 cattle consisting of 24 Adamawa Gudali, 24 Sokoto Gudali, 24 Bunaji and 24 Rahaji cattle from pastoralists in many communities of the LGAs using random sampling technique.

### Data Collection

#### Blood sample collection

Blood sample of two milliliter were collected from each animal through jugular vein from 96 cattle, consisting of 24 Adamawa Gudali, 24 Sokoto Gudali, 24 Bunaji and 24 Rahaji cattle into a ten milliliter (10mL) heparinized vacutainer tubes containing Ethylene Diamine Tetra Acetic Acid (EDTA) to prevent coagulation. The blood samples were properly labelled and kept cold by placing them in an ice packs and care was taken to prevent exposure to extreme temperatures and thereafter carried to the laboratory of the Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Ogun State, Nigeria for analysis.

#### Genomic DNA Extraction

Deoxyribonucleic Acid (DNA) was extracted using Zymo Quick DNA <sup>TM</sup>Mini prep kit. NanoDrop 1000 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).

#### Statistical Analysis

##### Measurement of genetic distance

Genetic distances among the breeds of cattle were calculated using distance measures with the aid of Gen AIEx (2012) software package according to (Hammer *et al.*, 2001). The unbiased standard Nei distance  $D_s$  was calculated as follows:

$$D_s = (1 - J_{xy}) - 1/2 \{ (1 - J_x) + (1 - J_y) \}$$

$$D_s = \ln (J_{xy} / \sqrt{J_x J_y})$$

$$\text{Where } J_x = 2n_x \sum x^2 i - 1 / (2n_x - 1)$$

$$J_y = 2n_y \sum y^2 i - 1 / (2n_y - 1)$$

$$J_x = \sum xy$$

n = Population size (number of individuals in the sample)

$x_i, y_i$  = Allele frequencies for  $x^{\text{th}}$  allele in population x and y

##### Cluster analysis

Genetic diversity among the four cattle breeds were determined using Unweighted Pairs Group Method (UPMGA), which were used for clustering of the breeds using dendrogram in order to determine the relationships among cattle breeds based on the protein structural loci of IGF-1 gene. Distances were used to construct a dendrogram using the Unweighted Pairs Group Method analysis implemented in R 2.13.0 (R Development Core Team, 2015) package TREE procedure that prints the dendrogram based on the distances between the clusters introduced in PROC CLUSTER procedure.

## RESULTS AND DISCUSSION

Pairwise population matrix of genetic distance among some indigenous breeds of cattle are presented in Table 1. The genetic distance estimate obtained in this study ranged between (0.001) and (0.101) which indicate a large genetic differentiation between the breeds. The closest genetic distance (0.001) observed in this study between Sokoto Gudali and Bunaji is in agreement with the findings of Ajayi *et al.* (2016) who reported the shortest genetic distance (0.0010) between Bunaji and Rahaji. Similarly, the highest genetic distance (0.085) recorded between Rahaji and Bunaji in this study is similar to the findings of Citek *et al.* (2006), who reported the highest genetic distance (0.0850) between Czech Red and German Red cattle breeds. The high genetic distance observed in this study between Rahaji and Bunaji revealed that there is a wider genetic relationship among the breeds.

**Table 1. Pairwise population matrix of genetic distance among some indigenous breeds of cattle**

Adamawa Gudali	Bunaji	Rahaji	Sokoto Gudali	Breeds
0.000				Adamawa Gudali
0.010	0.000			Bunaji
0.036	0.085	0.000		Rahaji
0.015	0.001	0.101	0.000	Sokoto Gudali

Pairwise population matrix of genetic identity among some indigenous breeds of cattle is shown in Table 2. Genetic identity between Sokoto Gudali and Bunaji (0.999) were the highest, followed by the distance between Rahaji and Adamawa Gudali (0.991). This could be attributed to differences in breed and genetic make-up of the animals. Ajayi *et al.* (2016) reported the highest genetic identities between Bunaji and Sokoto Gudali (0.9990), which agrees with the value of genetic identity between Sokoto Gudali and Bunaji (0.999) reported in this study.

**Table 2. Pairwise population matrix of genetic identity among some indigenous breeds of cattle**

Adamawa Gudali	Bunaji	Rahaji	Sokoto Gudali	Breeds
1.000				Adamawa Gudali
0.991	1.000			Bunaji
0.964	0.919	1.000		Rahaji
0.985	0.999	0.904	1.000	Sokoto Gudali

The phylogeny showing genetic relationships among Bunaji, Sokoto Gudali, Adamawa Gudali and Rahaji cattle breeds at IGF-1 gene locus are shown in Figure 1. The Cluster analysis using UPMGA revealed that Bunaji and Sokoto Gudali cattle formed the first cluster which is separate from Adamawa Gudali, which formed the second cluster. Rahaji cattle formed the third cluster, which is far and distant from the first and second clusters at IGF-1 gene locus. Rahaji cattle had the longest genetic distance compared to the other breeds of cattle. The dendrogram based on phylogenetic distance estimates showed that the breeds were clearly separated genetically from each other. The distances observed in this study among indigenous cattle breeds revealed wider genetic relationship among the breeds. This could serve as criteria in selection for genetic improvement of the animals. Kim *et al.* (2002) evaluated genetic diversity based on 13 microsatellites using DA distance and N J tree, found the group of Chinese, Korean cattle and the Japanese Black cattle was clearly distinct, which corroborate the results of this study.

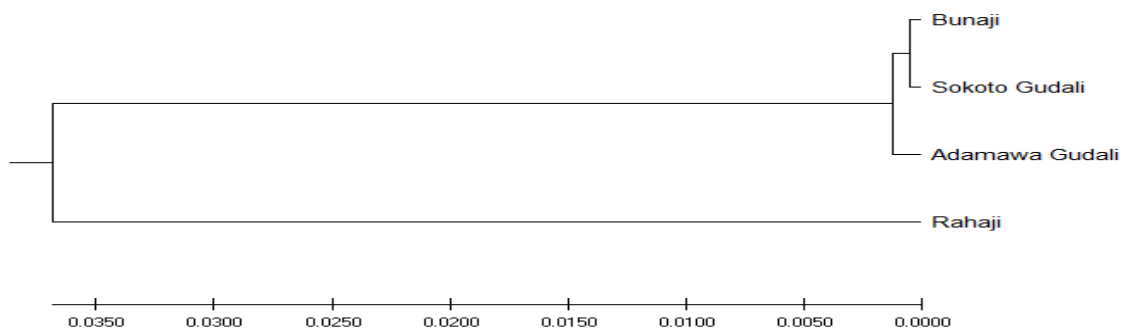


Figure 1. Dendrogram showing phylogenetic relationships among some indigenous breeds of cattle at IGF-1 gene locus

**CONCLUSION AND RECOMMENDATION**

The highest level of genetic distance estimate was observed between Rahaji and Bunaji cattle breeds (0.085) whereas the highest genetic identity was recorded between Sokoto Gudali and Bunaji (0.999) cattle breeds.

Cluster analysis using UPMGA revealed that Rahaji cattle had the highest genetic distance with other three breeds of cattle at IGF-1 gene locus.

Further study should be carried out to determine the genetic distance and identity among other indigenous cattle breeds in Nigeria.

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