# PHYLOGENETIC (DENDROGRAM) ANALYSIS OF THREE INDIGENOUS BREEDS OF GOAT IN NORTHERN NIGERIA

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**ABSTRACT**
Phylogenetic (Dendrogram) Analysis of three indigenous breeds of goat in northern Nigeria namely Red Sokoto, Borno White and West African Dwarf goats (40 animals each) were evaluated using Random Amplified Polymorphic DNA (RAPD) marker. This study was conducted in three states of northern Nigeria namely Jigawa, Yobe and Nasarawa States. Ten RAPD markers were initially used for the analysis, 1 of the 10 markers was discarded based on the band pattern quality. The Laboratory analysis was conducted at the Molecular Laboratory, National Institute of Trypanosomiasis Research (NITR), Kaduna. Results were analyzed using GenALEX 6.5 software. Phylogenetic tree constructed using the boostrapped data and neighbor-joining method grouped all the three breeds into two clusters indicating an agreement with phenotypic similarities. The result indicated that West African dwarf goat is most genetically distant from Red Sokoto and Borno white. The information obtained indicates that these breeds are genetically different which provide a good background about the breeds for genetic improvement and conservation of our local goat breed in the feature. The present study suggests that RAPD-PCR can effectively be used to determine the Phylogenetic relationship among the goat breeds.
**Keywords: Dendrogram, DNA, PCR, Polymorphism and RAPD**

## INTRODUCTION

Goat production has been given a pride of place in animal production in Nigeria in view of its multipurpose roles. They are a very prominent feature of the subsistence rural economy in most West African homes, even in places where cattle are not commonly kept (Tweneboah, 2000). They also occupy a unique responsibility in the food chain and overall livelihoods of rural households. Goats can be reared for various reasons such as income generation, religious purposes, household consumption, hobby and as security against crop failure (Ozung *et al*., 2011). The most notable goat populations in Nigeria are the Red Sokoto (Maradi), Sahel (Borno white goat), West African dwarf and the Kano brown goats. Despite their importance to human, information on the genetic variability is required to meet current production needs in different ecosystem, to allow maintained genetic improvement, and to facilitate fast adaptation to extreme weather conditions, resistance to diseases and rapid adaptation to change in breeding purpose (El-Hanafy *et al*., 2010). With the advent of molecular techniques, the use of molecular markers in revealing polymorphism at the DNA level has been playing an increasing part in animal genetic studies (Zhao *et al*., 2011). However, this study was designed to determine the phylogenetic analysis of three indigenous breeds of goat in northern Nigeria.

## MATERIALS AND METHODS

### Experimental location

The study was conducted in Jigawa, Yobe and Nasarawa States. Dutse the state capital is situated between latitude $11^0$N and longitude $8^0$ E $10^0$ 35'E, at an altitude of 485m above the sea level. Yobe State on the other hand is located in Northeastern Nigeria. The state borders four states: Bauchi, Borno, Gombe and Jigawa. Nasarawa State is a state in the North Central region of Nigeria, bordered to the east by the states of Taraba and Plateau, north, by Kaduna State, south, by Kogi and Benue States, west by the Federal Capital Territory. The laboratory analysis was conducted at the Molecular Laboratory, National Institute of Trypanosomiasis Research (NITR), Kaduna State. All samples were properly prepared before been transported to the laboratory.

**Experimental materials**

For the purpose of genotyping analysis, ten (10) distinct Random Amplified Polymorphic DNA markers recommended by previous researches were initially used. Of the 10 markers used, 9 were selected and one (1) was discarded because of its poor band pattern quality (Table 3).

**Table 3.: Selected RAPD Markers used in the Study**

| N | Marker | Sequences (F /R: 5'→3') | Base pair (bp) | TM°C | Source |
|---|---|---|---|---|---|
| 1. | OPA3 | AGTCAGCCAC | 10 | 30 | Yousif and Aram, 2017 |
| 2. | OPA10 | GTGATCGCAG | 10 | 28 | Yousif and Aram, 2017 |
| 3. | OPB8 | GTCCACACGG | 10 | 30 | Yousif and Aram, 2017 |
| 4. | OPA8 | TTCGAGCCAG | 10 | 31 | Yadav and Yadav, 2007 |
| 5. | OPC1 | TTCGAGCCAG | 10 | 31 | Sulaiman, 2012 |
| 6. | OPC20 | ACTTCGCCAC | 10 | 28 | Sulaiman, 2012 |
| 7. | RAPD7 | GCAGCTGTGC | 10 | 28 | Kumari *et al*., 2013 |
| 8. | RAPD8 | ACGGTGTACC | 10 | 30 | Kumari *et al*., 2013 |
| 9. | RP11 | GGACCTGTGC | 10 | 30 | Kumari *et al*., 2013 |

RAPD = Randomly Amplified Polymorphic DNA, TM = Annealing Temperature, bp = Base Pair

**Experimental animals**

A total of forty (40) randomly selected samples of indigenous goats from three (3) breeds (Sokoto Red, Borno white and West African dwarf goat) were used for the experiment. The numbers of samples were 13, 13, and 14 for Red Sokoto, Borno white and West African dwarf goats respectively. Unrelated animals were sampled (different ages and sexes) as recommended by International Society for Agriculture/Food and Agriculture Organization (ISAG/FAO, 2004).

**Data collection**

Data were collected through polymerase chain reaction (PCR) process in the laboratory; 5 ml of blood sample was drawn from each animal and then transferred immediately into a labeled sterile EDTA anticoagulant tube which was immediately stored at 4°C before being process for the DNA isolation. Genomic DNA was isolated from the sample using Zymo Research quick-gDNA™ Mini Prep plus Kit (Cat. No.: D4068) according to the manufacturer's instructions. DNA templates were used for PCR. All PCR reactions were carried out in a conventional thermo cycler PCR machine based on the recommended procedures. Following amplification, the PCR products were electrophoresed on a 1.5 percent agarose gel, stained with DNA intercalating dye (Ethidium Bromide) and viewed under ultraviolet light. The clear images from the gel were taken for the construction of Phylogenetic tree (dendrogram) according to Nei (1978).

**Statistical analysis**

The statistical programme Gen AlEX 6.5, genetic analysis package of Peakall and Smouse (2012) was used for the estimation of phylogeny according to Nei (1978).

**RESULTS**

**Phylogenetic (Dendrogram) Analysis**

The phylogenetic tree obtained by using the genetic distance is the standard Neigbour-Joining (NJ) methods applied for obtaining the tree. Dendrogram obtained from RAPD data showed a single lineage pattern (Figure 1). The phylogenetic tree supports the genetic distance estimate when the West African goat diverged first and is the most genetically distinct. This was followed by Borno white and then Red Sokoto goats, although separated, but having almost similar genetic base.

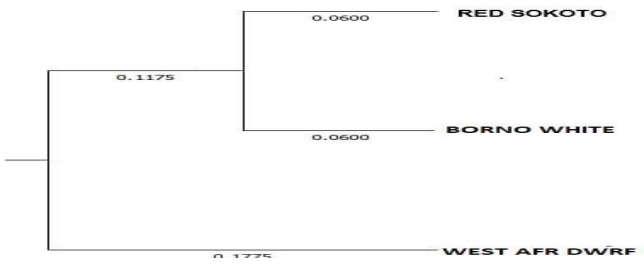


Figure 1: UPGMA Phylogenetic Tree (Dendrograms) Showing Differentiation between three Goat Breeds based on Nei's (1978) Genetic Distance and Neighbor-Joining methods.

**DISCUSSION**

The Dendrogram was conducted from Nei's genetic distance matrix using unweighted pair group method. The Neighbour-Joining method grouped goat into cluster. The phylogenetic/ Dendrogram of the three breeds based on Neighbour-joining methods (Nei's genetic distance analysis) showed that breeds were grouped in to cluster. In the present study, the descended two breeds (Red Sokoto and Borno white goats) were reflective of a common possible ancestor.. These results further indicated that the West African dwarf goats is the most genetically distinct from both Red Sokoto and Borno white goat in the second cluster indicating a close relationship between them. The Dendrogram showed that there is genetic diversity among goat breeds. This result is in agreement with the report of Ojo (2015) and Udeh *et al*. (2020) who reported that Dendrogram based on Nei genetic distance using UPGMA method indicated segregation of Borno white and Red Sokoto from the West African dwarf goat. The result of this study demonstrated that geographically, populations were more genetically related, probably due to founder effect and inbreeding, especially around bordering areas.

**CONCLUSION**

Conclusively, Red Sokoto and Borno white goats based on RAPD markers are the most closely related, indicating that the genetic distance between these breeds were small. The study revealed that the molecular genetic techniques such as RAPD-PCR can be efficiently used not only to establish phylogenetic analysis among breeds but also to develop marker for genetic improvement.

**RECOMMENDATION**

It is therefore recommended that conservation Strategy should be carried out so as to conserve the uniqueness and distinctness of the Nigerian Indigenous goat breeds.

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