



Phylogenetic Relationship Between West African Dwarf Goat and Red Sokoto Goat in Anambra, Nigerian

VC Ejogugua and JC Okonkwo*

Department of Animal Science and Technology, Nnamdi Azikiwe University, Awka, Nigeria

*Corresponding Author: JC Okonkwo, Department of Animal Science and Technology, Nnamdi Azikiwe University, Awka, Nigeria.

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Abstract

Phylogenetic Relationship between Nigerian Goat Breeds and Ecotypes Using Growth Hormone (GH) gene was studied using fifty goats. DNA extraction and amplification using PCR-RFLP were carried out at Molecular Genetics Laboratory of the Department of Animal Science, University of Port Harcourt, Port-Harcourt, River State, and DNA sequencing at International Institute for Tropical Agriculture (IITA), Ibadan, Nigeria. Using standard protocols, the phylogenetic tree was established. Tracing the line of evolutionary descent of West Africa Dwarf (WAD) goat and Red Sokoto (RS) goat from a common ancestor, the phylogenetic tree showed two major divergences indicating that there are high genetic diversity and similarity of Nigerian goat sub populations. Greater genetic bind between was observed between the WAD from Onitsha axis and RS goats from Anambra, Awka and Onitsha areas. The first divergence was between WAD goats from Anambra area and those from Onitsha, and RS goat breed. In the second divergence, WAD goats from Awka axis differed out-rightly from other WAD goat ecotypes and RS breed, indicating that there is an indigenous breed or line at Awka axis which are different from the WAD goats. The study revealed more similarity among RS goats than WAD goat breed. Obviously, the WAD goats are not true breed, rather, conglomeration of all the midgets and bantam found in the tropics.

Keywords: DNA Extraction; Amplification and Sequencing; PCR-RFLP; Unweighted Pair Group

Introduction

The Nigerian indigenous goat populations exhibit great phenotypic variation due to lack of selection in both qualitative and quantitative traits and there is need to differentiate strains [1,2]. Of several breeds of goats in the world, Sahel (S), Red Sokoto (RS), and West African dwarf (WAD) goats are the most predominant breeds of goat in Nigeria. The Sahel goats (Borno White or Kyalla and kano brown) are common in the arid or Sahel region of the country. It is medium to large in size, long legged, and covered with coat of short fine hair and ears are long and droppy. The Red Sokoto (Maradi) goat is the most numerous goat breed in Nigeria.

It was originally confined to the Niger Republic and Sokoto province, but has now spread throughout the Savannah belt. The skin of Maradi goat is among the most valuable of all goat skins in the leather industry locally and internationally. While West African Dwarf goat is predominant breed in humid forest belt of the southern Nigerian. WADG breed is characterized by short legs and blocky body, very hardy, good meat and prolific, frequently twins and triplet, with low growth rate and milk yield [3-5]. They are also highly trypano-tolerant and haermoncho-tolerant.

Goats constitute the largest group of ruminant livestock in Nigeria, 53.8 million and also account for 6.2 percent of the world goat

population [4]. Surveys by FDLPCS [6] reported that 85 percent of rural households, poor farmers and small-time business people of all age groups and sexes keep goats. The majority of Nigerian goats are breed under traditional management, and have significant role in the livelihoods of the rural households and farmers. Importance of goat can never be overemphasized, thus as source of animal protein and immediate cash, and have a variety of socio-cultural values in different regions in Nigeria. Improvement of Nigerian goat breeds can easily be achieved by selection superior genotypes using genetic markers. Different ecotypes have emerged among Nigerian goat breeds, under varying selection pressures and diversified climate and topography in different places [7].

Nwachukwu., *et al.* [2] and Ojo [8] reported that molecular variations among Sahel, WAD, Red Sokoto and Kano Brown goats were higher within Populations (96%) than among populations (4%), suggested higher heterozygosity within population, thus "Admixture" due to extensive cross-breeding and high gene flow amongst the breeds. The phenotypic characterization of polymorphisms in genes that control economically important traits such as growth and so on in Nigerian goats should be examine pointing to their potential application for genetic improvement for these traits. The goat genetic variability assessment is necessary to achieve current production needs and sustain genetic improvement and adaptation to adverse weather of Nigeria.

Growth is a complexly detailed biological process that consist of the regulated coordination of a wide diversity of neuro-endocrine pathways, including a coordination of several hormones like growth, thyroxine, insulin, and prolactin hormones, secreted by the endocrine glands and controlled by the action of their corresponding genes [9-13]. It is reported that animals with high levels of these hormones exhibit enhanced growth performance [14-16]. Therefore, selection of breeding animals based on their performance helps to explore individuals of superior growth traits, which could be a result of receiving active gene variant(s) from their ancestors. The molecular genetic study of breeding populations can help to determine the genetic similarity and variation they possess (Mahrous., *et al.* 2018). Several techniques have been established to estimate the genetic variance or polymorphism within and among populations [2,17]. One of the most commonly used techniques is polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP). It is a powerful method for detecting nucleotide sequence variance in the amplified deoxyribonucleic acid (DNA).

The study aimed at assessing the taxonomic relationship between Nigerian Goat breeds using GH gene.

Materials and Methods

The study was carried out at three agricultural zones in Anambra state namely Anambra, Awka and Onitsha. Fifty goats comprising 25 each of RS and WAD goat breeds were randomly selected from rural goat farmers and markets in three agricultural zones in Anambra state. Three (3) mLs of blood was collected from each goat from the jugular vein in a 5mL bottle gently mixed with the EDTA to prevent coagulation. The bottles were kept in an ice pack and transferred to the Molecular Genetics Laboratory of the Department of Animal Science, University of Port Harcourt, Port-Harcourt, River State where they were preserved at -4 C until DNA extraction. DNA was extracted from the blood of the goats using Quick-DNA Mini-prep Plus kit by Zymo Research, following the manufacturer's instruction. Amplification using Polymerase Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) was done using the DNA and GH gene primer. 2.5 ul of 10x PCR buffer, 1.0 ul of 25 Mm MgCl₂, 1.0 ul of 5pMol forward primer (TCA GCA GAG TCT TCA CCA AC) and 1.0 ul of 5pMol reverse primer (CCA CAA CGC CAT CCT CAC). Also to be added is 1.0 ul DMSO, 2.0 ul of 2.5Mm DNTPs, 0.1 ul Taq 5 u/ul, 3.0 ul of 10 ng/ul DNA and 13.4 ul water. A touch down PCR condition that involves initial denaturation at 94°C for 5 minutes, 9 Cycles of denaturation at 94°C for 15seconds, annealing temperature at 62°C at 20seconds and extension at 72°C for 30 seconds was carried out. This was followed by 35 cycles of denaturation at 94°C for 15seconds, annealing temperature at 58°C for 20b seconds and extension at 72°C for 30seconds and a final extension at 72°C for 7 minutes. PCR products of GH gene of the goats were sent for sequencing at the International Institute for Tropical Agriculture (IITA), Ibadan, Nigeria.

Result and Discussion

The phylogenetic tree using unweighted pair group method with arithmetic mean (UPGMA) between the various ecotypes and breeds studied are shown in figure 1. The dendrogram revealed three major clusters. The WAD goat from Awka and Anambra were completely separated from others. The WAD from Onitsha and RS Anambra Agricultural zone goats were most closely related at the Growth Hormone (GH) gene. These ecotypes (WAD from Onitsha and RS Anambra Agricultural zone) were closer to RS goats from Awka, then RS goats from Onitsha. The WAD goats from Awka zone are farthest.

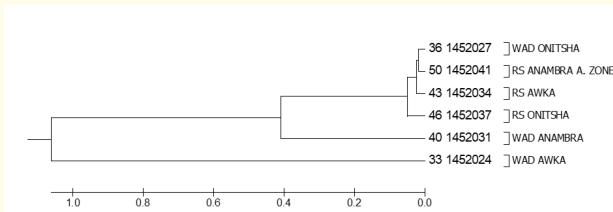


Figure 1: Phylogenetic tree using unweighted pair group method with arithmetic mean (UPGMA) between goat breeds from Onitsha, Awka and Anambra.

Tracing the line of evolutionary descent of WAD goat and RS goat from a common ancestor, the phylogenetic tree showed two major divergences. The phylogenetic tree supported the high genetic diversity and similarity of Nigerian sub populations, it reveal insight on genetic bind WAD Onitsha goat have with RS goats from Anambra, Awka and Onitsha Agricultural zones. The first divergence was between WAD goats from Anambra area and those from Onitsha, and RS goat breed. Obviously, the so-called WAD goats are not true breed, rather, conglomeration of all the midgets and bantam found in the tropics.

Conversely, RS goats appear to come from the same descent, and shared many genetic identities. The result demonstrate the similar genetic backgrounds of goats in Anambra state and suggests that natural and artificial selection pressure from similar rearing and production systems of the Nigerian goats and those from Northern ecotype versus Southern ecotype populations explains some of this genetic homogeneity. Due to high number of RS goat population must have led to most of the crossbreeding with other breeds in Nigeria.

In the second divergence, WAD goats from Awka axis differed out-rightly from other WAD goat ecotypes and RS breed. This might be that there is an indigenous breed or line at Awka axis which are different from WAD goats. Equally, it confirmed the wide genetic diversity often reported among WAD goats [1,8]. So, earlier researchers simply grouped all the small stature and miniature goats found in the tropics as WAD goat breed [3,8]. With molecular study, the differences within this so-called WAD goat breed are unveiled. However, those found in Awka differ remarkably from other eco-

types which shared common descent with WAD goats from Onitsha.

The studied populations was observed to be significantly differentiated into different groups, and showed fairly high level of inbreeding and global heterozygote deficit among RS goats while WAD goats show high crossbreeding and global heterozygote surplus. There's more similarity among RS goats than WAD goat breed. The within breed genetic variation in Nigerian goats is higher than between-breeds [8], and that the higher genetic variability in WAD suggests the presence of unique ancestry alleles reflecting the presence of certain functional genes which may result in better adaptability in most agro-ecological zones of Nigeria [18-20].

Conclusion

The study evinced greater disparity among WADGs compared to RSG.

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