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RESEARCH ARTICLE

GENETIC DISTANCE AND RELATIONSHIP AMONG INDIGENOUS GOATS USING BLOOD BIOCHEMICAL POLYMORPHISM

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ABSTRACT

Quantitative description of genetic diversity of some Nigerian indigenous goat population is scanty. Biochemical characters were used to determine the relationship among Red Sokoto, Sahel and West Africa Dwarf .Equal numbers of breed (Red Sokoto, Sahel and WAD from Sokoto, Borno and Ogun state were sampled for blood biochemical polymorphic traits (Haemoglobin (Hb), Transferrin (Tf) and Carbonic anhydrase (CA) loci) using a total of 900 goats. Generally, genetic distance analysis based blood biochemical indicators indicated closer relationship between the Red Sokoto and Sahel with both breeds being distant from the WAD. Also there were high degrees of similarity in genetic relationship among the three breeds indicating a high rate of dilution of the breeds which may lead to loss of genetic resources. It is recommended that efforts should be made to conserve genetic resources and reduce dilution of the gene pool through indiscriminate mating among the breeds.

INTRODUCTION

The characterization of domestic animal diversity is essential to meet future needs in Africa and Nigeria in particular. In order to cope with unpredictable future, genetic reserves capable of readily responding to directional forces imposed by broad spectrum of environment must be maintained. Maintaining genetic diversity is an insurance package against future adverse conditions. Due to diversity among environments, nutritional standards and challenges from infectious agents, a variety of breeds and populations are required. These act as store houses of genetic variation which form the basis for selection and may be drawn upon in times of biological stress such as famine, drought or disease epidemics. The wide range of breeds and species are each specifically adapted to a different set of conditions. In recent years, analysis of genetic markers based on blood protein polymorphism (detected by the electrophoretic method) has become a tool for studying genetic differentiation among population or phylogenetic and evolutionary studies. Studies on blood protein polymorphism have revealed that the phenotype of an individual with respect to these traits does not change throughout life except in extreme condition, for example haemoglobin switching which can be identified by objective methods of analysis e.g. electrophoresis (Van Vliet and Huisman, 1964). Blood groups and proteins have been widely used to assess genetic diversity (Dossa *et al.,* 2007; Missohou, 1990; Ndamukong, 1995; Nyamsamba *et al*., 2003). Thus an objective quantification of the magnitude of the genetic differences among a set of breeds can be obtained from allele frequency data for each breed.

Although DNA – based technologies are now the method of choice, several alternative assays, such as protein/allozyme polymorphisms, remain tremendously useful, especially in developing countries like Nigeria, because of their utility, ease, cost, and amount of genetic information accessed or simplicity of data interpretation. The role or potential of these alternative approaches in animal genetic diversity studies' should not be underplayed. Polymorphism of blood protein first offered the possibility to study genetic differentiation before the advent of molecular markers. Consequently several livestock breeds including the domestic sheep and goat have been characterized for variations in major blood proteins (Di Stasio, 1997). In addition to several important functions of blood proteins, several studies in sheep have already linked these markers to production traits and environmental adaptations (Vicovan and Rascu, 1989; Charon *et al*., 1996, Akpa*et al.,* 2011). Information on blood protein has also been used to study genetic relationship among breeds (Nwacharo *et al.,* 2002; Ibeagha-Awemu and Erhardt, 2004; Esharatkhah

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et al., 2007). To re-examine the degree of relationship and distance between indigenous goat breeds becomes imperative in the light of the need for conservation of genetic resources and is therefore the goal of this study.

identity indicated a great deal of similarity between the breeds for these genes. Figures 1, 2 and 3 reveal the Dendogram for the blood biochemical polymorphism traits studied.

Table 4.12. Genetic Distance and Identities between Population at Haemogblobin Transferin and Carbonic Anhydrase Loci

Population	Hb locus		Tf locus		CA locus	
	Distance	Identities	Distance	Identities	Distance	Identities
Red Sokoto	0.086	0.913	0.089	0.9113	0.0001	0.9999
Sahel	0.002	0.999	0.0003	0.9997	0.0000	1.0000
WAD	0.079	0.92	0.0998	0.9002	0.0000	1.0000

Hb: Haemoglobin, Tf: Transferrin, CA: Carbonic Anhydrase

Table 4.13. UPMGA Cluster Showing relationship between Populations at Hb, Tf and CA locus in Nigerian Indigenous Breed of Goats

NodeHbTf			CA			
	Distance	Population	Distance	Population	Distance	Population
1	0.0020	1, 3	0.0003	1, 3	0.0000	1, 2
2	0.0830	1, 2, 3	0.0942	1, 2, 3	0.0000	1, 2, 3

Hb: Haemoglobin, Tf: Transferrin, CA: Carbonic Anhydrase

MATERIALS AND METHODS

Experimental Animals and Management

Animals used for this study were sampled in the abattoir, of Borno, Sokoto and Ogun states when brought for slaughter either by the owner or by the slaughter man. It is believed that all animals find their way into the abattoir from villages and local markets, where they are kept in small numbers by local farmers; they are raised under the extensive system of management.

Sampling Size and Sampling Structure

A total of nine hundred (900) goats comprising of three hundred Sahel goats from Borno state, three hundred Red Sokoto goats from Sokoto state and three hundred West African Dwarf goats from Ogun state were used for the study. Each breed consisted of three hundred goats each, made up of fifty males and fifty females distributed in the following age groups <1, 1-2 and 2-3 years.

Blood Collection and sample preparation

Blood was collected from each animal by means of jugular venipuncture and placed in heparinized tubes to prevent coagulation. It was then refrigerated at 8^0C for two hours and thereafter carried into the laboratory. Samples were prepared and analyzed according to RIKEN (2006).

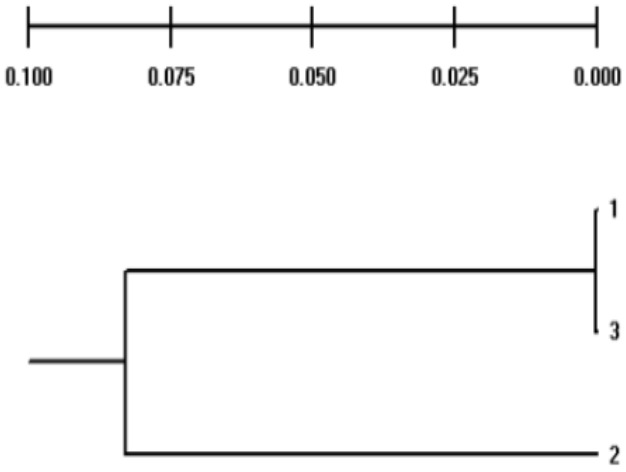
Measurement of Genetic Distance

Gene frequency, Genotypic frequency and Genetic distances among the breeds (estimated from gene frequencies) were calculated using Tools for Population Genetics Analyses Software, Version 1.3 (Copyright, Mark, P. Miller).

RESULTS AND DISCUSSIONS

Table 1 and 2 presents the observed distances and UPMGA cluster based on Hb, Tf and CA loci were 0.086, 0.089 and 0.0001 in the Red Sokoto, 0.002, 0.0003 and 0in the Sahel and 0.079, 0.0998 and 0 in the WAD. The converse which is the

In Figure 4, the Sahel and Red Sokoto in node 1 were similar in the Hb locus but differed greatly (0.079) from the WAD in node 2. In the transferrin locus depicted in Figure 5, similar trend was observed among the breeds for this locus.

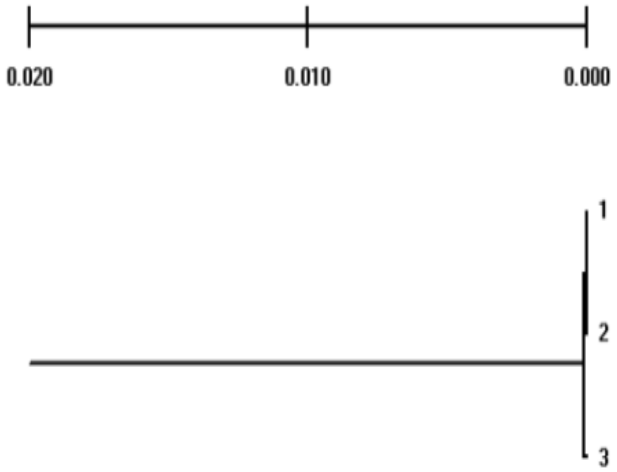


Key 1: Sahel; 2: WAD; 3: Red Sokoto

Figure 1. Dendogram Showing Similarity among Red Sokoto, Sahel and WAD at the Haemoglobin locus

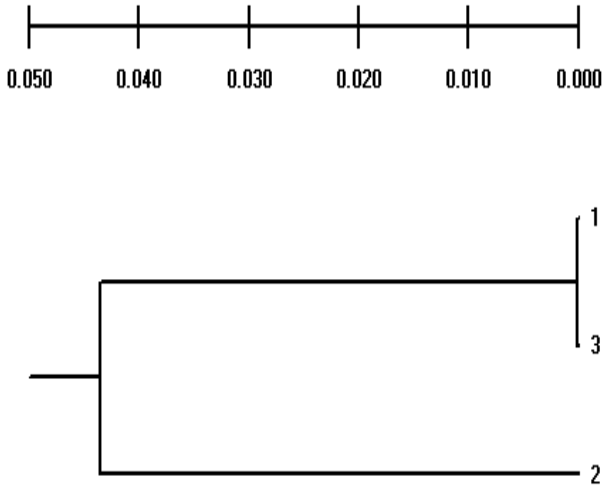
Key 1: Sahel; 2: WAD; 3: Red Sokoto

Figure 2. Dendogram Showing Similarity among Red Sokoto, Sahel and WAD at the Transferrin locus



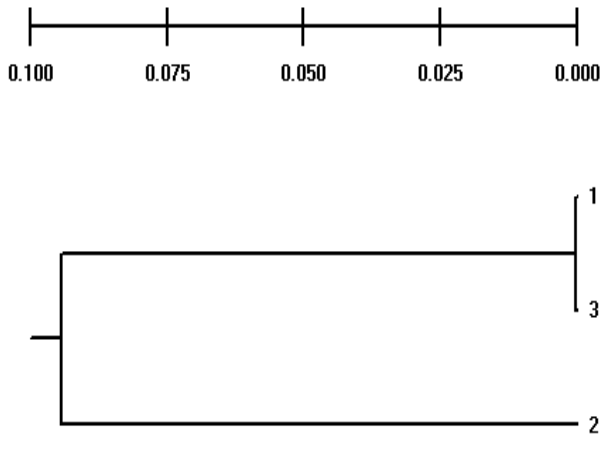
Key 1: Sahel; 2: WAD; 3: Red Sokoto

Figure 3. Dendogram Showing Similarity among Red Sokoto, Sahel and WAD at the Carbonic Anhydrase locus



Key 1: Sahel; 2: WAD; 3: Red Sokoto

Figure 4. Dendogram Showing Similarity among Red Sokoto, Sahel and WAD Pooled for all loci studied

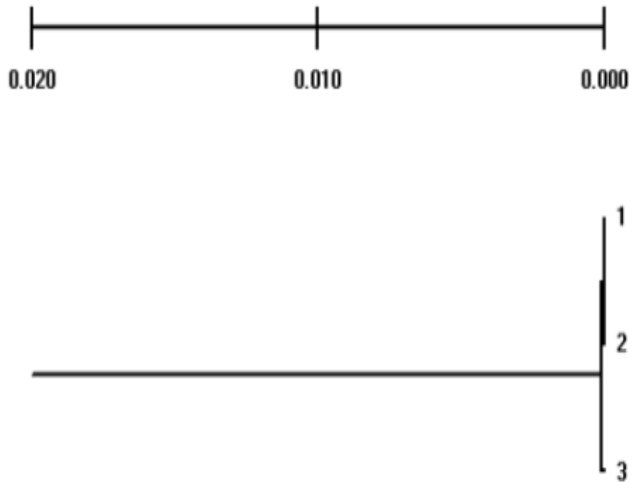


Key 1: Sahel; 2: WAD; 3: Red Sokoto

Figure 5. Dendogram Showing Similarity among Red Sokoto, Sahel and WAD at the Transferrin locus

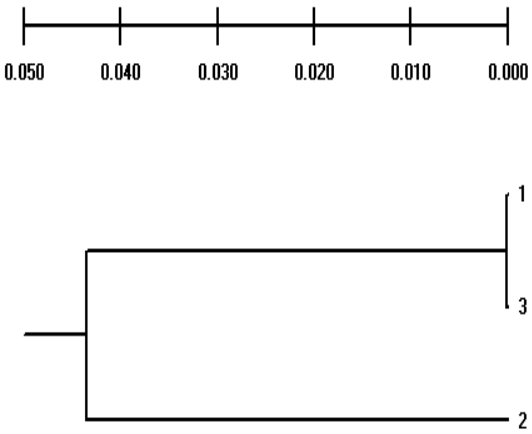
All breeds were nearly not different in the Carbonic anhydrase locus as revealed by the near margin of the two nodes in Figure 6.

But the Sahel and WAD were closer in this locus than the Red Sokoto. Figure 4 shows the pooled chart for all studied loci, the Sahel and WAD were similar on node 1, but were farther (about 0.045) away from the WAD in genetic similarity.



Key 1: Sahel; 2: WAD; 3: Red Sokoto

Figure 6. Dendogram Showing Similarity among Red Sokoto, Sahel and WAD at the Carbonic Anhydrase locus



Key 1: Sahel; 2: WAD; 3: Red Sokoto

Figure 7. Dendogram Showing Similarity among Red Sokoto, Sahel and WAD Pooled for all loci studied

Genetic Distance and Association of the breeds of Goats

The pattern of variations observed in the gene and genotypic frequencies of the CA locus above and reported literature accounts of the same locus in sheep makes comparison for genetic distance based on blood biochemical polymorphism difficult, genetic distance has been carried out in goats based on other phenotypic traits but not blood biochemical polymorphism, however, observed distances of 0.086, 0.089 in Red Sokoto; 0.002 and 0.0003 in the Sahel and 0.079 and 0.0998 in the WAD for Hb and TF locus were similar to the values of 0.015, 0.008 and 0.003 (Nei distance) reported by Akinyemi and Salako (2012) in sheep breeds and 0.027, 0.076 and 0.102 in breeds of horses (Jiskrova *et al*., 2002). Distance for the CA locus was non-existent as shown by values in the UPMGA cluster and further confirms the report on mean heterozygosity for this locus. The Dendogram showing similarity among breeds for all loci studied however shows

that there exist closer similarity between the Red Sokoto and Sahel and both differed from the WAD this observation is similar to what was obtained by Adebambo *et al*. (2011) when they compared the WAD, Red Sokoto and their crosses, however, value was dissimilar been higher (0.39) in the reports of these authors than obtained in this study (0.045). Variations in reported genetic distances among breeds of goats is trait dependent, thus it can be safely declared that for better heterosis in cross breeding experiments based on blood biochemical polymorphism, the WAD and the Sahel or Red Sokoto would be most suitable but not crosses between Red Sokoto and Sahel.

Conclusions

Generally, genetic distance analysis based on the morphological loci of hair structure, tail shape and wattle gene along with blood biochemical indicators indicated closer relationship between the Red Sokoto and Sahel with both breeds being distant from the WAD. These may indicate a high rate of dilution of the breeds through indiscriminate breeding across the breeds, which may lead to loss of genetic resources.

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