ABG -08

Biochemical Differentiation of Selected Indigenous Cattle Breeds in Nigeria

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Abstract
Variations in genetic resources are the basis for effective genetic improvement in farm animals. Population differentiation is used for objective choice of parental genotypes that constitutes new hybrids in crossbreeding. In Nigeria, population characteristics of some selected indigenous cattle breeds have not been fully documented. Therefore, biochemical differentiation of some selected indigenous cattle breeds in Nigeria was assessed using their blood protein polymorphism. Blood samples (5mL) were taken underneath the tail by venipuncture from 40 cattle randomly selected from each of the five selected breeds. The samples were subjected to cellulose acetate electrophoresis to determine the genetic variants of haemoglobin (Hb), carbonic anhydrase (CA) and transferrin (Tf) following standard procedure. Data were analyzed using allele frequencies and cluster analysis. Allele frequencies ranged between0.10 (Hb^{A+}) and 0.90 (Hb^{B+}), 0.11 (CA^{F+}) and 0.89 (CA^{FS}) and 0.02 (Tf^{A+}) and 0.49 (Tf^{AE}) across the breed. Two main clusters from the dendrogram were observed for each of Hb, CA and Tf. Genetic variants of transferrin were largest within breed which indicated the potential for selection.

Keywords: Carbonic anhydrase, cattle, differentiation, haemoglobin, transferrin.

Introduction

The initial step however, in characterization is the identification of distinct populations using information on their geographic and ecological isolation, traditional nomenclature (traditionally, recognized populations), phenotypic distinctness and level of genetic differentiation among the population (Gizaw *et al.*, 2011). The concern with the conservation of genetic variation of livestock breeds has been present in the last decades and genetic markers are being used to assess the level of genetic variation within breeds (Pablo-Gomez *et al.*, 2016). Available literatures on differentiation of these breeds using their biochemical characteristics are yet to achieve full documentation. Moreso, the Global Plan of Action for Animal Genetic Resources recognizes that a better understanding of the characteristics of livestock breeds is necessary for guiding decision making in the development of breeding programs (FAO, 2007).

This study is designed to provide indices for ascertaining the diversity among the selected indigenous cattle breeds in Nigeria and it will also help to better understanding the genetics of Nigeria breeds of cattle and unravel the biodiversity that exist among the breeds using biochemical analysis.

Materials and Methods

Two hundred animals (forty from each breed of White Fulani, Sokoto Gudali, Red Bororo, Bornu Kuri and Muturu) were randomly selected ignoring sex from areas where they were found abundant in the country. Blood sample of 5mL was collected from each animal from underneath the tail by venipuncture into a 10mL heparinized vacutainer tubes to prevent coagulation. The blood samples were kept cold by placing them in ice packs and care was taken to prevent exposure to extreme temperatures. Red blood cells (RBC) were prepared from the erythrocyte fraction of heparinized blood by centrifuging at 2500-3000 rpm for 10 mins at 4°C. The RBC were washed in saline (0.155 M NaCl) three times and centrifuged at 2500-3000 rpm for 5 mins at 4°C. The RBCs were lysed with a fourfold volume of distilled H_20 to release haemoglobin. The plasma fraction was separated from the erythrocyte fraction of heparinized blood by centrifuging at 2500 – 3000 rpm. The supernatant was used. The method used was as described by RIKEN (2006). Once plates have been removed from the tank, they were stained immediately with appropriate stain before they dried out. Once the plate had stained sufficiently to resolve the band, the stain was removed by washing and rinsing the gel plate several times with the specified destaining solution until sharp bands were visible. The bands were scored visually based on their migratory pattern as described by RIKEN (2006). Direct counting was used for calculating gene frequencies. Frequencies generated were used to compute genotypic frequencies. PAST– Paleontological statistics software package (Hammer *et al.*, 2001) was used to analyze data obtained from the electrophoretic analysis in order to generate dendrogram at each of the locus investigated.

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Results and Discussion

At the three blood protein loci (haemoglobin, carbonic anhydrase and transferrin), two different alleles were observed for each of haemoglobin and carbonic anhydrase, while seven alleles were observed for transferrin. Thus, at the haemoglobin (Hb) locus, the two different alleles observed were A and B. Similarly, at the carbonic anhydrase (CA) locus, the two different alleles observed were S and F, However, at the transferrin (Tf) locus, seven different alleles observed were A, B, C, D, E, G and P. The allele frequencies for the three blood protein loci were presented in Table 1. All loci were polymorphic. Haemoglobin B allele occurred at a higher frequency in all the five cattle breeds investigated: 0.64, 0.74, 0.75, 0.77 and 0.70 in White Fulani, Sokoto Gudali, Red Bororo, Bornu Kuri and Muturu respectively (Table 1). All the five cattle breeds investigated had F and S alleles at the carbonic anhydrase locus. The S allele at the CA locus occurred at the higher frequencies in all the five cattle breeds investigated, 0.79, 0.86, 0.85, 0.81 and 0.88 in White Fulani, Sokoto Gudali, Red Bororo, Bornu Kuri and Muturu respectively(Table 1).

Seven co-dominant alleles namely, A, B, C, D, E, G and P controlling genotypes were observed at the transferrin locus. The A, B, C and P alleles were present in all the breeds sampled. The D allele was found only in Sokoto Gudali, Red Bororo, Bornu Kuri and Muturu; E allele was found in White Fulani, Red Bororo, and Bornu Kuri while G allele was found in Sokoto Gudali, Red Bororo and Muturu.The dendrograms at heamoglobin locus (Figure I) showed that the breeds were clearly separated from each other.The HbB type has a very high frequency in cattle of northern savannah zone, the region in which the White Fulani, Red Bororo, Bornu Kuri and Sokoto Gudali are predominantly found. The breeds have HbB conferred on them for survival in the drier savannah regions where the breeds are found. This predominance appears to be of adaptive significance in the arid regions to which these breeds fit. This is due to the decreased haematocrit values, lower blood viscosity and higher availability of water associated with HbB blood types compared to HbA types. This seems to be of adaptive significance in habitats characterized by the aridity of the climate such as the northern zone of Nigeria.

The five breeds in this current study were polymorphic at CA locus. The CA^S was the most common in all the breeds. This current investigation was at variant with what Ibeagha-Awemu *et al.* (2004) reported, they discovered that Muturu showed monomorphism at CA locus. The distribution of alleles at the transferrin locus among the five cattle breeds and their number within each breed were dispersed. The observed differences at the transferrin alleles indicate a clear genetic differentiation among the selected indigenous cattle breeds of Nigeria studied. This showed that genetic variants of transferrin within breed were largest and this is an indication of the potential for selection. In this study, Muturu exhibited high frequency of homozygotes genotypes of $Tf^{EE}$and Tf^{BB} while White Fulani, Red Bororo and Sokoto Gudali had higher frequencies of Tf^{DD} and Tf^{AA} than other genotypes; this is an indication that these breeds could be selected for the economic trait associated with these genotypes. Observation at Transferrin locus are generally difficult to compare with the result obtained in other studies because of the different electrophoretic media used by other researchers and subsequently different resolution power, that is, starch gel and polyacrylamide gel electrophoresis (Akinyemi and Salako, 2012). There was a closer genetic relationship among White Fulani, Red Bororo and Sokoto Gudali compare to a wider genetic relationship between any of these breeds with Bornu Kuri. Muturu breeds were relatively distantly related from the other indigenous breeds selected for this study. This finding can be attributed to the different ancestral origin of Muturu breed (a taurine),

Table 1: Allele frequencies at the haemoglobin, carbonic anhydrase and transferrin loci of White Fulani, Sokoto Gudali, Red Bororo, Bornu Kuri and Muturu cattle breeds

Locus	Allele	White Fulani	Sokoto Gudali	Red Bororo	Bornu Kuri	Muturu
Hb	A	0.36	0.26	0.25	0.23	0.30
	B	0.64	0.74	0.75	0.77	0.70
CA	S	0.79	0.86	0.85	0.81	0.88
	F	0.21	0.14	0.15	0.91	0.12
Tf	A	0.14	0.36	0.43	0.29	0.38
	B	0.39	0.30	0.20	0.28	0.23
	C	0.29	0.19	0.05	0.24	0.08
	D	-	0.03	0.08	0.66	0.11
	E	0.17	-	0.11	0.09	0.09
	G	-	0.03	0.05	-	0.08
	P	0.045	0.08	0.08	0.04	0.03

Hb = Haemoglobin; CA = Carbonic anhydrase, Tf = Transferrin

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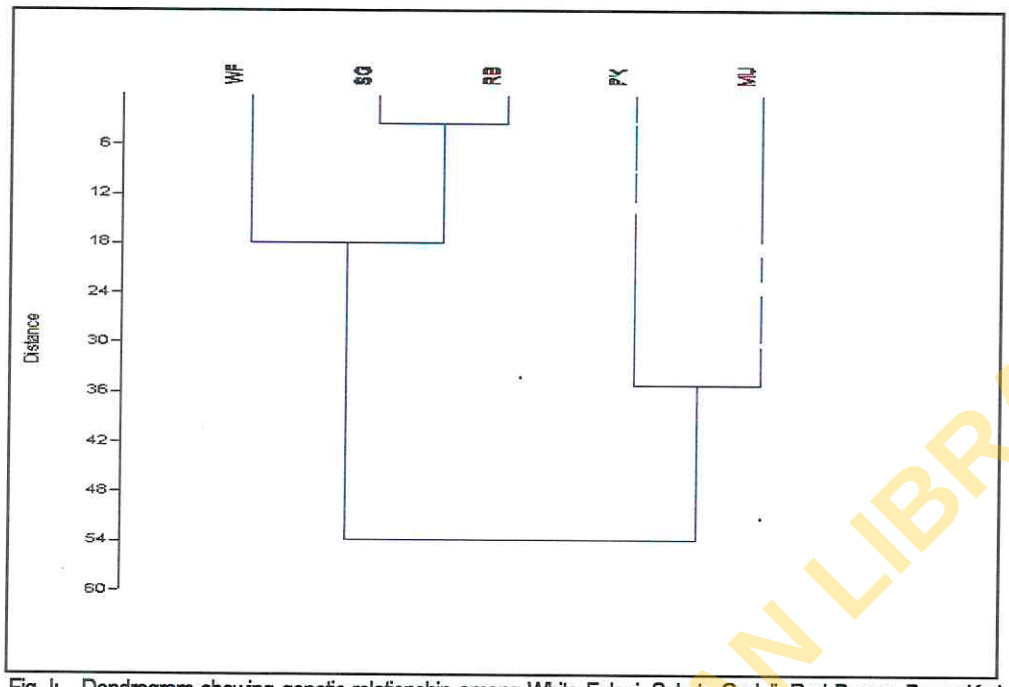

Fig. I: Dendrogram showing genetic relationship among White Fulani, Sokoto Gudali, Red Bororo, Bornu Kuri and Muturu Breed of cattle at haemoglobin locus.

Conclusion

Three blood proteins were analysed electrophoretically to reveal their polymorphisms for inherent variants. The three proteins were polymorphic with haemoglobin and carbonic anhydrase exhibiting two alleles each ($Hb^{A \text{ and } B}$, $CA^{S \text{ and } F}$) while transferrin revealed seven alleles ($Tf^{A, B, C, D, E, G \text{ and } P}$). The frequency of Hb^{B} was significantly higher than Hb^{A} in all the five breeds investigated while at the CA locus, CA^{S} exhibited higher frequency than CA^{F}. Genetic variants of transferrin were largest within breed which indicated potential for selection.

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