GENETIC DISTANCE MEASURES AMONG FIVE INDIGENOUS CATTLE BREEDS IN NIGERIA

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ABSTRACT

Genetic variation is the basis of effective 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 selected indigenous cattle breeds have not been fully documented. Therefore, blood protein electrophoretic patterns of selected indigenous cattle breeds in Nigeria were assessed. Blood samples (5mL) were taken underneath the tail by venipuncture from 200 cattle (40/breed) randomly selected from the five indigenous cattle breeds. The samples were subjected to cellulose acetate electrophoresis to determine the genetic variants of haemoglobin (Hb), carbonic anhydrase (CA) and transferrin (Tf). Data were analysed using Euclidean genetic distance and cluster analysis. Two main clusters from the dendrogram were observed for each of Hb, CA and Tf. Euclidean genetic distance at the Hb locus between WF and SG, WF and RB, WF and BK, WF and Muturu were 15.3, 15.7, 23.9 and 35.1 respectively, while the corresponding values at CA locus were 3.9, 3.3, 29.1 and 36.2, similarly, the corresponding values at Tf locus were 22.8, 25.8, 94.3 and 102.7. Genetic distance estimates were found to be higher between non-related breeds than between breeds which had common ancestors.

Keywords: Blood protein polymorphism, Breed differentiation, Indigenous cattle

INTRODUCTION

One of the ways of characterizing livestock breeds is to determine genetic distance among contemporary populations (Metta *et al.,* 2004). It is however worthy to note that full extent of molecular variations and diversity of the Nigerian indigenous cattle remains largely unknown. Studies based on these molecular markers capable of unraveling phylogenetic history of biodiversity and development to better understand the genetic structure of the Nigerian cattle population is therefore necessary. Available literatures on characterization of these breeds using their blood protein polymorphism and reliable molecular markers are scanty and are yet to achieve full documentation. Also, one of the priorities of FAO global strategy for improvement of livestock is the identification and characterization of all breeds of livestock (AGRI, 2006).

This study is designed to unveil the genotypic diversity among the selected Nigeria indigenous cattle breeds using data obtained from markers extracted from blood to assess diversity of the selected indigenous populations in order to update published variations as well as document genetic distances between the populations. This will help to better understanding the genetics of Nigeria breeds of cattle for improvement and conservation goals and unravel the biodiversity that exist among the breeds using biochemical analysis. It will also provide a quantitative assessment of the diversity among the selected indigenous cattle breeds in Nigeria and thereafter provides light for objectives prediction and pave way for a better improvement in planning for a productive genetic improvement.

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 within the country. Blood sample of five milliliter (5mL) was collected from each animal underneath the tail by venipuncture into a ten milliliter (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 2500-3000rpm for 10mins at 4^0C. The RBC were washed in saline (0.155M NaCl) three times and centrifuged at 2500-3000rpm for 5mins at 4^0C. 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 2500-3000rpm. The supernatant was used. Similar standard method was used for carbonic anhydrase and transferrin. The method used was as described by RIKEN (2006). Data obtained were analysed for genetic distances among the breeds at the three structural loci (haemoglobin, carbonic anhydrase and transferrin) using D_A Euclidean genetic distance measure and cluster analysis was constructed with the aid of PaST software (Hammer *et al.*, 2001).

RESULTS AND DISCUSSION

Genetic distance estimates between each pair of cattle breeds investigated at Hb locus are shown in Table 1. The genetic distance estimates obtained from Euclidean genetic measure showed that genetic distance estimates between White Fulani and Sokoto Gudali, White Fulani and Red Bororo, White Fulani and Bornu Kuri; and White Fulani and Muturu at Hb locus were 15.30, 15.72, 23.86 and 35.11, respectively, while the corresponding values at CA locus were 3.9, 3.3, 29.1 and 36.2 (Table 2). Similarly, the corresponding values at Tf locus were 22.8, 25.8, 94.3 and 102.7 (Table 3). The dendrogram based on the pooled Euclidean genetic distance estimates (Fig. 1) showed that the breeds were clearly separated genetically from each other. The existence of substantial genetic differentiation between cattle populations has been considered by many scholars to be advantageous for selection and conservation purpose (Talle, 2004). When the value of genetic distance is high, it is an indication of high genetic difference between populations. Euclidean genetic distance (DA) estimate obtained in this study ranged between 3.162 and 104.2 which indicate a large genetic differentiation between the breeds. A shorter distance obtained between White Fulani and Sokoto Gudali suggest a close genetic relationship between the breeds while the longer genetic distances observed in this study between White Fulani and Muturu, Borno Kuri and Muturu, Sokoto Gudali and Muturu; and Red Bororo and Muturu suggests that there is a wider genetic relationship among the breeds.

CONCLUSION

The value of genetic distance estimates in this study using blood proteins polymorphism were higher between non-related breeds than between breeds which had common ancestors and the existence of the substantial genetic differentiation among the cattle populations has been considered by many scholars to be advantageous for selection and conservation purpose.

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Table 1: Genetic distance estimates of the five cattle breeds at haemoglobin locus (WF=White Fulani,Sokoto Gudali, RB Red Bororo BK= Bornu kuri MU=Muturu)

DISTANCE MEASURE		WF	SG	RB	BK	MU
	WF	0				
	SG	15.297	0			
EUCLIDEAN	RB	15.716	3.606	0		
	BK	23.854	28.443	28.531	0	
	MU	35.114	34.161	36.304	32.311	0

Table 2 Genetic distance estimates of the cattle breeds at carbonic anhydrase locus (WF=White Fulani,Sokoto Gudali, RB=Red Bororo,BK= Bornu kuri, U=Muturu)

DISTANCE MEASURE		WF	SG	RB	BK	MU
	WF	0				
	SG	3.873	0			
EUCLIDEAN	RB	3.317	3.162	0		
	BK	29.086	30.185	30.935	0	
	MU	36.166	36.756	37.643	35.242	0

Table 3: Genetic distance estimates of the five cattle breeds at transferrin locus (WF=White Fulani,Sokoto Gudali RB=Red Bororo,BK= Bornu kuri, MU=Muturu)

DISTANCE MEASURE		WF	SG	RB	BK	MU
	WF	0				
	SG	22.847	0			
EUCLIDEAN	RB	25.846	18.111	0		
	BK	94.324	95.797	92.849	0	
	MU	102.710	104.470	104.200	66.204	0

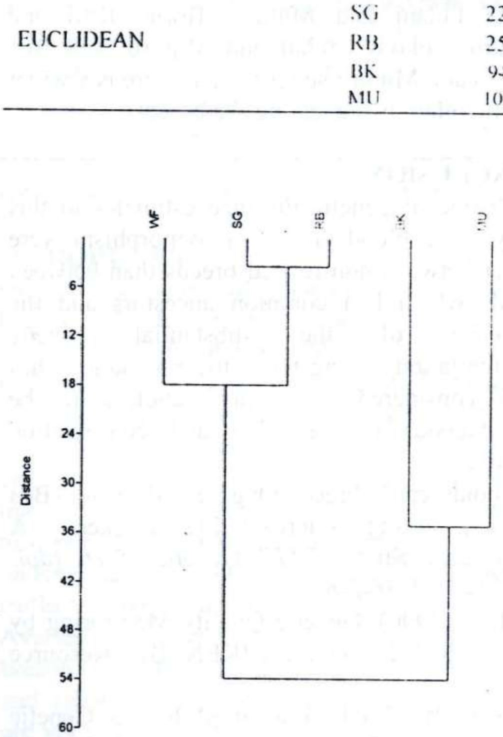

Fig. 1: Dendrogram showing genetic relationship among White Fulani(WF), Sokoto Gudali(SG), Red Bororo(RB), Bornu Kuri(BK) and Muturu(MU) Breeds of cattle based on the pooled Euclidean genetic distance estimates