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## Genetic Diversity in Nigerian Small Ruminants: A Review

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**Abstract** Sustainability of animal agriculture depends on genetic diversity of livestock. Therefore, species in general and breeds in particular should be characterized to prioritize their value for conservation. This paper reviews studies on the characterization of Nigerian small ruminants based on microsatellite markers, blood protein polymorphism and morphological traits. In Maradi and West African Dwarf (WAD) goats, 21 microsatellite markers have been found to be highly polymorphic and heterozygosity ranged from 0.46 to 0.55 while genetic distance between the two breeds was 0.39 confirming ecological divergence. In Yankasa, Uda and Balami sheep, 15 microsatellite markers showed high polymorphism and heterozygosity ranged from 0.405 to 0.563 while analysis of molecular variance showed greater variation within individuals than among breeds. Genetic distance estimates based on allelic frequencies of blood protein loci indicated that Balami sheep is more closely related to Yankasa as compared to Uda. There was also similarity in the heterozygosities in goats and sheep suggesting similar proportions of heterozygotes. Based on genetic distance estimates from qualitative trait loci, there is phylogenetic relationship between Maradi and WAD goats and also among Yankasa, Uda and Balami while there is also differentiation indication by some loci which could be used to classify breeds into distinct populations. Genetic variation in Nigerian sheep and goats is wide enough to provide tool for genetic improvement. This should be maintained through formulation of appropriate conservation policies and more comprehensive studies on animal genetic resources.

**Keywords** small ruminants, genetic diversity, microsatellite markers, blood polymorphism, morphological traits

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### Introduction

Nigerian economy is dominated by Agriculture which contributes an average of 41% of the GDP [1]. Nigerian small ruminants constitute of 35.2 and 56.5 million sheep and goats respectively which make 63% of the livestock population [1]. The Nigerian population is estimated at 170 million and in order to meet the FAO recommended 34g/capita daily meat consumption more should be done to improve livestock production. Genetic diversity is required to meet current production needs in various environments to allow sustained genetic improvement and facilitate rapid adaptation changes in breeding objectives [2].

Sustainability of agricultural production depends on genetic diversity of livestock. Currently, a large proportion of breeds is in danger of extinction and resources available for conservation activities are limited [2]. Therefore species in general and breeds in particular should be characterized to prioritize their value of conservation. The aim of this paper is to review studies on the characterization of Nigerian sheep and goats based on microsatellite DNA markers, blood protein polymorphism and morphological features.

### Genetic Diversity of Goats and Sheep Based on Microsatellite Marker

DNA makers have received particular attention in diversity studies because of their possible use in determining the chronology of evolutionary events. The development of molecular techniques in detection of DNA



polymorphism in coding and non-coding regions of chromosomes enable the description of the genetic uniqueness by breeds more accurately [2].

DNA based makers are increasingly employed for diversity studies; advanced molecular techniques led to the introduction of many new types of markers which estimate DNA sequence polymorphism or DNA sequence variation. The general description, applicability for population studies and comparison has been made by several authors [3-5]. These techniques include:

- RFLP (restriction fragment length polymorphism).
- RAPD (random amplified polymorphic DNA)
- Microsatellites DNA sequencing
- SNPs (Single nucleotide polymorphism as individual or micro arrays).

In Nigeria, heterozygosity and genetic distance between maradi and WAD goats was [6] determined using an panel of 21 microsatellite markers selected from bovine and caprine makers recommended by ISAG/FAO advisory group animal genetic diversity for use in chicken diversity studies. The markers were all polymorphic with disparate diversities given by the microsatellites which were shown to be highly polymorphic with allele sizes ranging from 5 to 24 in goats (table 1) percentage heterozygosity ranged between 0.46 to 0.55 among the goats (table 2) while the ecological divergence of the breeds was confirmed with the WAD being genetically distant from the maradi by the value of 0.39 (table 3).

Based on microsatellite DNA polymorphisms, Adebambo *et al.* [7] reported a high degree of heterozygosity (0.57 to 0.72) in 285 alleles in the Nigerian sheep and genetic distances of 0.356 between the Yankasa and Uda, and 0.432, 0.534 and 0.665 between the WAD and the Yankasa, Uda and Balami respectively.

**Table 1:** Range of alleles detected and allele numbers in Nigerian goats [7]

S/N	Marker	Range	Allele No
1	ETH 225	148-158	10
2	INRA 35	114-120	6
3	ILST 5	129-194	11
4	ETH 152	191-203	5
5	ETH 10-2	203-213	8
6	INRA 63	164-185	10
7	INRA 5-2	137-145	7
8	HEL 9	96-104	5
9	HEL 1	103-165	24
10	CSSM 66	184-237	23
11	MM 12	91-119	22
12	ETH 3	98-126	16
13	BM 2113	124-148	15
14	BM 1824	171-180	10
15	CSRM 60	78-95	14
16	TGLA 122	132-146	12
17	SPS 115	237-252	6
18	BM 1818	252-272	17
19	INRA 37	109-149	18
20	TGLA 53	135-161	22
21	HAUT 27	137-151	15

**Table 2:** Number of alleles and heterozygosity for the goat breeds [7]

Goat breeds	Maradi	West African Dwarf	Maradi X West African Dwarf
N	61	43	34
Allele no	10.6	6.52	3.57
Heterozygosity	0.46	0.55	0.49

**Table 3:** Genetic distances between Nigerian goat breeds [7]

	Maradi	West African Dwarf
Maradi		
West African Dwarf	0.39	



From the study by Agaviezor *et al.* [8], polymorphism information content (PIC) and F statistics ( $F_{IS}$ ,  $F_{IT}$ ,  $F_{ST}$ ), and  $G_{ST}$  and Shannon index values for 15 microsatellite markers analyzed in Nigerian sheep, all the 15 microsatellite loci showed high polymorphism in the study sheep population with PIC values ranging from 0.751 to 0.927 (table 4). This lends support to the use of this panel of markers for assessing Nigerian sheep genetic diversity. The highest  $F_{ST}$  value (0.146) was observed in BM8125 while the lowest was seen in DYMS1. The population differences examined by global analysis of  $F_{ST}$  (coefficient of multilocus genetic differentiation fixation index) for each of the 15 microsatellites bin across the four sheep breeds showed that most of the total genetic variation corresponds with differences among individuals within breeds (91.2%) while 8.8% results from differences among breeds.  $G_{ST}$  also revealed that gene variation among breeds is low.

Effective number of alleles ranged from 17.330 in Yankasa to 7.200 in WAD with a similar trend in allelic richness with Yankasa having 10.51 and WAD with 6.59. Expected heterozygosity followed the same pattern while observed heterozygosity across the reeds ranged from 0.405 in Uda to 0.563 in Yankasa (Table5).

**Table 4:** Polymorphism Information Content (PIC), F statistics ( $F_{IS}$ ,  $F_{IT}$ ,  $F_{ST}$ ),  $G_{ST}$  and shannon index values for 15 microsatellite markers analyzed in Nigerian sheep breeds [8]

Locus	PIC	$F_{IS}$	$F_{IT}$	$F_{ST}$	$G_{ST}$	Shannon index
DYMS 1	0.927	0.442	0.454	0.022	0.125	2.964
OarCP34	0.751	0.373	0.436	0.099	0.106	2.203
OarFCB193	0.845	0.220	0.329	0.140	0.163	2.321
BM8125	0.808	0.316	0.416	0.146	0.130	2.082
OarJMP29	0.904	0.287	0.352	0.092	0.084	2.854
OarJMP58	0.899	0.318	0.361	0.063	0.079	2.325
OarFCB128	0.782	0.534	0.593	0.126	0.187	2.212
OarFCB304	0.901	0.319	0.339	0.029	0.033	2.882
SRCRSP1	0.787	0.251	0.301	0.066	0.046	2.263
OarAE129	0.792	0.325	0.365	0.059	0.130	1.653
OarVH72	0.853	0.171	0.278	0.129	0.146	2.375
SRCRSP5	0.896	0.406	0.472	0.111	0.175	2.914
MCM140	0.872	0.428	0.459	0.055	0.069	2.332
OarHH47	0.825	0.387	0.436	0.079	0.211	2.172
SRCRSP9	0.857	0.245	0.320	0.099	0.122	2.268
Mean	0.846	0.335	0.394	0.088	0.120	2.388

**Table 5:** AMOVA design and results (average over 15 loci) [8]

Source of variation	Sum of squares	Variance components	Percentage variation
Among populations	172.808	0.585	8.739
Among individuals within populations	1432.042	2.04	30.545
Within individuals	759.500	4.063	60.716
Total	2364.350	6.692	

Based on AMOVA, greatest variation (60.716%) is within individuals, 30.545 is among individuals within populations and 8.739 among populations.

### Genetic Diversity Based on Blood Protein Polymorphism

The genetic relationship among Nigerian Yankasa Uda and Balami sheep populations based on blood protein polymorphism has been reported [9]. A total of 11 alleles were observed in the investigated three blood protein loci (Haemoglobin (Hb), Transferrin (Tf) and carbonic anhydrase (Ca) with Tf locus having 7 alleles, and the Hb and Ca loci having 2 each. At the Tf locus, A,B,C and E alleles were present in all the breeds with allele G and P occurred only in Yankasa and Balami respectively. Hb<sup>B</sup> and CA<sup>S</sup> occurred at high frequency among all the breeds. TfA was the most frequent in yakasa and uda sheep (table 6).

Mean heterozygosities were similar in the three breeds with 0.383, 0.283 and 0.383 in Balami, Uda and Yankasa respectively. This is an individual of the similar number of occurring alleles in each breed. Genetic distance estimates between each pair of breeds (table 7) and the dendrogram generated showed that Balami was more closely related to Yankasa compared to Uda sheep. (Table 8, figure 1).



Salako *et al.* [10] and Alphonsus *et al.* [11] have reported the presence of 4 haemoglobin phenotypes A, B, AB and AC in Red Sokoto goats (Table 9). Salako *et al.* [10] reported genotype frequencies of 0.4, 0.17, 0.4 and for AA, AB and BB and AC at the haemoglobin locus of West African Dwarf (WAD) sheep, and 0.13, 0.36, 0.50 and 0.01 for AA, AB, BB and AC for the Red Sokoto goats. The heterozygosities of the WAD sheep and the Red Sokoto goats were reported to be 0.483 and 0.435 respectively. The similarity in the heterozygosities suggests that proportions of heterozygotes in the goats and sheep are similar and it could be regarded as the measure of genetic diversity at the Hb locus of the populations.

**Table 6:** Distributions of genotypes in Balami, Uda and Yankasa sheep breeds [9]

Loci	Genotype	Breed		
		Balami	Uda	Yankasa
Haemoglobin	AA	-	-	2
	AB	20	4	11
	BB	20	36	27
Carbonic Anhydrase	SS	33	26	22
	FS	5	11	12
	FF	2	3	6
Transferrin	AA	1	14	10
	AB	3	3	6
	AC	-	3	3
	AB	-	3	3
	AE	4	2	1
	AZ	-	-	1
	BB	10	5	9
	BC	5	3	2
	BB	-	3	1
	BE	5	-	1
	BP	2	-	-
	CC	4	4	1
	CD	-	-	1
	CE	1	-	-
	CP	2	-	-
EE	3	-	1	
GD	-	-	1	

**Table 7:** Allele frequencies of blood protein variants in Balami, Uda and Yankasa sheep breeds [9]

Loci	Alleles	Breed		
		Balami	Uda	Yankasa
Haemoglobin	A	0.25	0.10	0.19
	B	0.75	0.90	0.81
Carbonic Anhydrase	F	0.11	0.21	0.30
	S	0.89	0.79	0.70
Transferrin	A	0.11	0.49	0.42
	B	0.44	0.23	0.38
	C	0.20	0.18	0.04
	D	-	0.08	0.09
	E	0.20	0.02	0.05
	G	-	-	0.02
	P	0.05	-	-

**Table 8:** Genetic distance values among three indigenous breeds (above the diagonal and Euclidean genetic distance below the diagonal) [9]

Breed	Breed		
	Balami	Uda	Yankasa
Balami	***	0.015	0.008
Uda	0.175	***	0.003
Yankasa	0.11	0.08	***



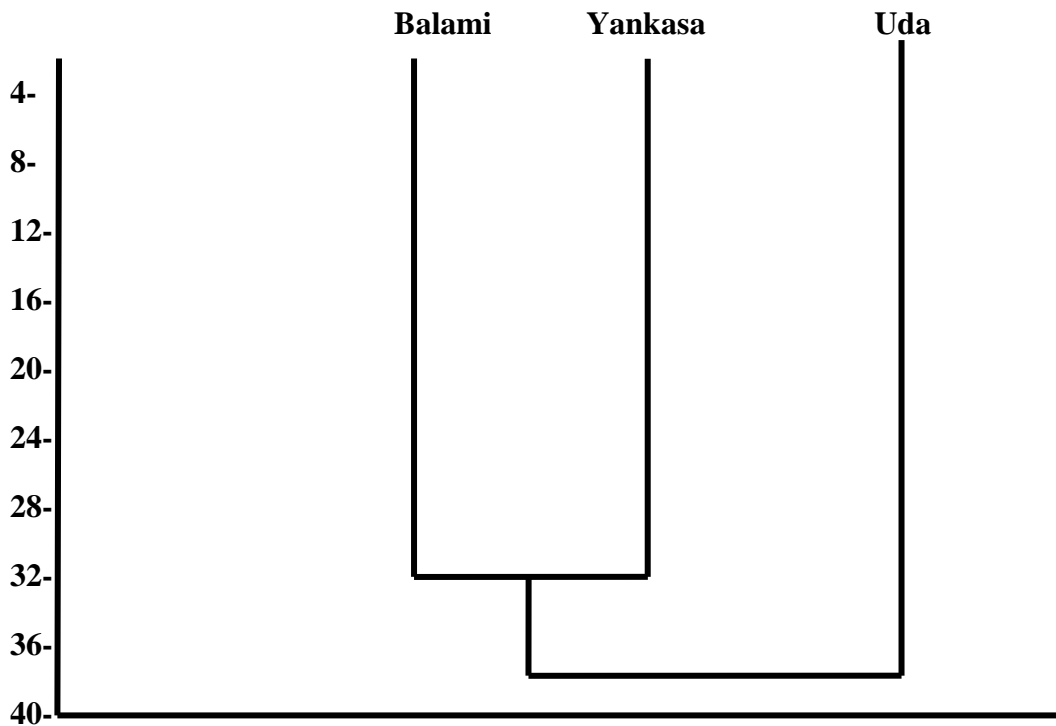


Figure 1: Dendrogram of the relationship among three Nigerian sheep breeds drawn from Euclidean genetic distance matrix (pooled for three loci studied) [9]

**Table 9:** Allele and genotype frequency at heamoglobin locus in Red Sokoto Goats [11]

Genotype	Number of Genotype	Genotype frequency	Alleles	Allele frequency
AA	30	0.3191	A	0.601
AB	41	0.4362	B	0.335
BB	11	0.11	C	0.064
AC	12	0.1277		

**Genetic Diversity of Nigerian Sheep and Goats Based on Qualitative traits.**

Studies on diversity of sheep breeds on the basis of quantitative (morphostructural) and qualitative (morphological) variables have been carried out in Nigeria [8, 12-15]. Yakubu *et al.* [15] reported a frequencies of the dominant alleles for both WAD and Red Sokoto goats to be 0.09 and 0.02 ( $Wa^w$ ); 0.05 and 0.12 ( $Br^b$ ); 0.00 and 0.00 ( $Ho^p$ ), and 0.20 and 0.63 ( $A^{wt}$ ) which were lower than the expected Mendelian value of 0.75; with exception of  $A^{wt}$  of Red Sokoto goats which occurrence was not significantly ( $p>0.05$ ) different from the Mendelian ratio of 3:1 concurring with the report of Adedeji *et al.* [16] on how occurrence of beardedness and polledness (Table 10).

**Table 10:** Gene frequencies of some qualitative traits in indigenous goats and sheep [15]

Traits	alleles	Goats							
		West African dwarf				Red Sokoto			
		Expected	Observed	Gene frequency	$\chi^2$ test	Expected	Observed	Gene frequency	$\chi^2$ test
Wattle	$Wa^w$	301.5	69	0.09	*	316.5	11	0.02	*
	$Wa^+$	100.5	333	0.05		105.5	411	0.98	
Beard	$Br^b$	301.5	42	0.05	*	316.5	91	0.12	*
	$Br^+$	100.5	360	0.95		105.5	331	0.88	
Horn	$Ho^p$	301.5	0	0.00	*	316.5	0	0.00	*
	$Ho^+$	100.5	402	1.00		105.5	422	1.00	



Phaeomelanin standard pigmentation	A <sup>wt</sup>	287.25	136	0.20	*	316.5	364	0.63	ns
Eumelanin standard pigmentation	A <sup>a</sup>	95.75	247	0.80		105.5	58	0.37	

### Sheep

Traits	Alleles	Yankasa				Uda				Balami			
		Expected	Observed	Gene frequency	$\chi^2$ test	Expected	Observed	Gene frequency	$\chi^2$ test	Expected	Observed	Gene frequency	$\chi^2$ test
Wattle	Wa <sup>w</sup>	174	34	0.08	*	153	10	0.02	*	150	33	0.09	*
	Wa <sup>+</sup>	58	198	0.92		51	194	0.98		50	167	0.91	
Beard	Br <sup>b</sup>	174	0	0.00	*	153	0	0.00	*	150	0	0.00	*
	Br <sup>+</sup>	58	232	1.00		51	204	1.00		50	200	1.00	

**Table 11:** Matrix of genetic distances of goat and sheep populations [15]

Traits	WAD Vs Red Sokoto	Yankasa vs. Uda	Yankasa vs. Balami	Uda vs. Balami
Wattle	0.005	0.004	0.001	0.005
Beard	0.005	-	-	-
Coat colour	0.18	-	-	-

In sheep, the observed frequencies ( $W_a^w$ ) were 0.08, 0.02 and 0.09 for Yankasa, Uda and Balami respectively and beards were virtually non existent. However, Ozoje and Kadri (2001) reported an estimated frequency of 0.39 for the wattle gene is at the risk of extinction and so there is need to take right steps to conserve it.

Estimate of genetic distance [15] between WAD and Red Sokoto goats were 0.005, 0.005 and 0.18 at the Wattle, beard and coat colour loci respectively (Table 11). At the wattle locus estimates ranging from 0.0001 and 0.005 were observed between pairs of sheep populations.

The minuscule values obtained at the Wa and Br loci of goats are indications of phylogenetic relationship between the two breeds while the higher value of A<sup>wt</sup> locus is indicative of genetic differentiation which could be used to classify the breeds into distinct populations.

The same applies to sheep where the low values obtained show high similarity of alleles at the wattle locus.

### Conclusions

- Heterozygosity estimates in Nigerian small ruminants using information from microsatellite markers, protein loci and morphological features meet the requirement for measuring genetic variation among the breeds of these species.
- Balami and Yankasa are more closely related than Uda and crossing Yankasa and Uda may give a better heterotic advantage than with Balami
- Crossing maradi and WAD goats presents enough diversity to generate good heterotic advantage also
- The wattle gene is at the risk of extriction in Nigerian sheep
- Genetic variation in Nigeria small ruminants is good enough to provide tool for genetic improvement

### Recommendations

- More studies should be conducted on genetic diversity of Nigerian small ruminants using DNA markers, greater number of blood proteins for all breeds and their crosses.
- Efforts should be made to preserve the wattle gene which is at the brink of extinction in sheep.
- Livestock conservation policies should be formulated and adhered to, especially to avoid indiscriminate mating and crossing of various breeds.



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