

## Diversity of biometric and morphological traits among sheep breeds in Nigeria

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### Abstract

*Towards assessment of variations within and between sheep; biometric and morphological data of the four breeds of sheep found in Nigeria were collected using multi-stage sampling method. A total of 46 Balami, 30 Uda, 36 Yankasa and 37 WAD were sampled. Stepwise multiple regression procedure was used to find the best linear combination of metric variables that best predict the body weight. Principal component analysis of biometric and morphological traits was carried out. Simple discriminant analysis procedure was used to classify the breeds. Cluster analysis was done using the model building specification interface. Head length (HL), chest girth (CG), leg length (LL), and tail length were the only linear body measurements that were significant ( $P < 0.01$ ) in predicting body weight of sheep in the overall prediction equation. Body weight and all the linear body measurements had their highest loadings on principal component 1 (PC1). Tassel was the only variable that had its highest loading on PC2. Tail type and state (location) were the variables that best describes the third component (PC3). Sex and hair type were variables that best described the forth component (PC4). Discriminant analysis showed that 70.59% of sheep sampled as Balami were classified as pure breed. Sheep sampled as WAD and Yankasa had 100% conformation while Balami and Uda had 70.59% and 60%, respectively in conformation to the classifying features of their breed based on discriminant analysis. The farthest genetic distance (5.48) was observed between Balami and WAD while the shortest genetic distance (1.26) was observed between Balami and Uda. Improvement of growth traits of sheep breeds in Nigeria is recommended through the use of either Balami or Uda as sire and either WAD or Yankasa as dam.*

**Keywords:** Sheep breeds, multivariate analysis, biometric traits; morphological traits

### Introduction

Domestic animal diversity is an important component of global biodiversity (FAO, 2001). Domesticated livestock (sheep inclusive) have spread with human migrations and trading to all inhabited continents. Broad distinction between sheep importance and ubiquity in the north and the more dispersed populations of the humid zone has made it easy for sheep to be raised all over Nigeria (Iyiola-Tunji, 2012). Ecological factors influence genetic diversity (Brehem *et al.*, 2001; Via, 2002; Whiteley *et al.*, 2004) through morphological adaptation to local

conditions (Brown and Thorpe, 1991). These factors cause favorable variation. Genetic diversity in genes has resulted in variation and this is necessary to allow sheep to adapt to ever-changing environments (Orr and Unckless, 2014), thus providing a range of products and functions (Salako and Ngere, 2002). Also, genetic exchange between different ecological zones in Nigeria has made breed identification a difficult task, and increase inbreeding and reduction in reproductive fitness in animal husbandry (Frankham *et al.*, 2002; Willi *et al.*, 2006). This gives breeders an opportunity to expand and

### *Diversity of biometric and morphological traits among sheep breeds in Nigeria*

preserve genetic diversity of their stock. Genetic diversity is defined as the sum of genetic differences in multiple loci among individuals in a population, and is most readily reflected in the phenotypic variations seen in many populations. It is a valuable asset towards adaptability of a population (Woolliams *et al.*, 2005). Loss of diversity among domestic species including sheep has far reaching economic, ecological, scientific and social implications. Accurate classification of Nigerian sheep population will not only have impact on management of these animals but also reduce mis-identification by livestock traders. It will equally help in the conservation of genetic resources. Conservation of indigenous animal resources can help to slow down the loss of genetic diversity in livestock breeds through extinction. This is because it could be a resource for novel genes that can permit sustained genetic improvement as

well as enabling adaptation to changing breeding objectives and environments (Notter, 1999). Proper conservation and utilization of indigenous breeds can be achieved by evaluation of genetic variations that exist among these breeds (Kunene *et al.*, 2009). Assessment of variations within and between sheep breeds in Nigeria was therefore the major objective of this study.

#### **Materials and methods**

Biometric and morphological data of the four breeds of sheep found in Nigeria were collected from Bauchi, Kastina, Nasarawa and Anambra States (Table 1) for Balami, Uda, Yankasa and West Africa Dwarf sheep, respectively using multi-stage sampling method. Majority of animals sampled were reared through the semi-extensive management system and originated from different herds. A total of 46 Balami, 30 Uda, 36 Yankasa and 37 WAD were sampled.

**Table 1: Breeds specification of sampled sheep by State, LGAs and sex**

State	LGA	Breed	Sex		No of adult	No of yearling	No of weaner	Sub-total
			Male	Female				
Bauchi	Misau	Balami	3	4	4	0	3	7
	Jamaire	Balami	3	5	3	3	2	8
	Ganjuwa	Balami	3	4	3	2	2	7
	Alkaleri	Balami	4	3	0	3	4	7
	Bauchi	Balami	1	5	3	0	3	6
Kastina	Maiadua	Balami	4	7	7	1	3	11
		Uda	0	5	5	0	0	5
	Daura	Uda	5	20	12	6	7	25
Nasarawa	Wamba	Yankasa	1	8	5	1	3	9
	Akwanga	Yankasa	4	7	3	8	0	11
	Keffi	Yankasa	3	6	4	5	0	9
	Karu	Yankasa	1	6	3	4	0	7
Anambra	Isuanaocha	WAD	2	2	0	3	1	4
	Aguata	WAD	2	6	3	3	2	8
	Njikaoka	WAD	1	4	2	2	1	5
	Awkasouth	WAD	1	3	1	1	2	4
	Aniocha	WAD	0	7	1	1	5	7
	Idemili	WAD	1	8	1	3	5	9
<b>Total</b>								<b>149</b>

Morphological features described by Adu and Ngere (1979) were used as baseline markers to ascribe sampled animals to a breed. Individuals that do not conform strictly to primary breed characters and visibly pregnant animals were excluded. Sheep were grouped into three age groups through the use of dentition counts as described by Solomon (1995). The age groups were 6 months to 11 months (weaner), 12 months to 23 months (yearling) and 24 months and above as adult. Anatomical reference points for linear body measurements according to the method of Salako and Ngere (2002) were used. All measurements were obtained using a flexible tape rule calibrated in centimeter (cm). Measurements were taken after restraining and holding the animals while standing on a flat surface with head held up in an unforced position. Cautions were taken to avoid animal movement and variation in hair cover which may have reduced the accuracy with which measurements were recorded. All measurements were carried out by the researcher in order to avoid errors due to individual variations. A total number of 12 biometric traits were measured and the following measurements were obtained from each animal: Body weight (BWT) was measured (in kg) using an Avery® weighing scale (bathroom weighing scale). Head length (HL) was measured as the distance from between the base of the horn to the upper lip; Neck length (NL) was measured as the distance between the bases of the skull to the first thoracic bone; Height at withers (WH) was measured as the highest point from the scapulae vertical to the ground. This was taken using a graduated measuring stick. Chest girth (CH) was measured as the circumference of the body at the narrowest point just behind the shoulder perpendicular to the circumference of the body. Loin girth (LG)

was measured as body circumference round the sheep just before the hind legs. Back length (BL) was measured diagonally from the lateral tuberosity on the scapula to the pin bone. Leg length (LL) was measured as the distance from the scapula bone to the distal phalanges. Neck Circumference (NC) was measured as the circumference of the neck at the midpoint.

Scrotal Circumference (SC) was measured as the maximum dimension around the pendulous scrotum after pushing the testes firmly into the scrotum (Akpa *et al.*, 2006). Ear length (EL) was measured as the distance from the base to the zygomatic arch to the tip of the ear. Tail length (TL) was measured from the base of the tail to the tip (Coccygeal vertebrae). Morphological characters that were observed on each animal include: tassels, wattle, hair type (HT), tail shape (TS) and coat color. Wattle was observed as the presence of the loose fold of skin hanging from the throat. Tassel was observed as the presence of the hair at the lower jaw. Hair type was determined through touch and feel of the hair. This was observed and categorized into short-smooth (SS), short-rough (SR) and long-curly (LC) woolly hair type based on length and texture.

Tail shape was observed and categorized as thin long and thin short tail. Coat color was observed as white, black with white, brown with white, white with black patches, white with brown patches and black (Adalsteinsson *et al.*, 1994). **Statistical analysis**

Stepwise multiple regression procedure was used to find the best linear combination of metric variables that best predict the body weight. This was performed for each breed. The following linear multiple regression models were applied:

$$Y = a + b_1 X_1 + b_2 X_2 + b_3 X_3 + \dots + b_i X_i$$

Where:

### *Diversity of biometric and morphological traits among sheep breeds in Nigeria*

Y = the dependent variable (Body weight)

a = the intercept of regression curve on y – axis and was the value of the dependent variable y when all independent variables were Zero.

$b_i$  = the partial regression coefficient associated with respective independent variable  $X_i$ .

$X_i$  = the independent variables (body measurement) the regression assumes that the independent variable has no measurement error.

And that the above errors about the regression line were equal. The regression analysis was carried out using SAS (SAS, 2004). Comparison of regression equations were based on coefficient of determination ( $R^2$ ).

Principal component analysis of biometric and morphological traits was carried out using data reduction procedure of SPSS Version 21 (SPSS, 2015). During the evaluation, factors were rotated with Varimax rotation of Kaiser. The aim of the Varimax rotation was to maximize the sum of variances of  $a_{ij}^2$  quadratic weight. Anti-image correlations, Kaiser-Meyer Olkin measures of sampling adequacy and Barlett's Test of Sphericity were computed to test the validity of the factor analysis of the data sets. The appropriateness of the factor analysis was further tested using communalities and ratio of cases to variables.

The data were subjected to discriminant analysis using the equation below:

$$D = v_1X_1 + v_2X_2 + v_3X_3 + \dots + v_iX_i + a$$

Where

D = discriminate function

v = discriminant coefficient or weight for that variable

X = respondent's score for that variable

a = a constant

i = number of prediction variables

For the classification of Balami, Uda, Yankasa, and WAD sheep, the Euclidean as the distance measurement, single linkage, average linkage, and complete linkage were applied while the obtained results were compared. Simple discriminant analysis procedure was used to classify the breeds using SAS JMP (SAS JMP, 2012). Mahalanobis distances, the canonical coefficients and a scatter diagram for visual interpretation of the different groups were also generated during the canonical discriminant analysis.

Cluster analysis was done using the model building specification interface of SAS JMP (2012) statistical software. All the traits were screened using the stepwise regression procedure and only traits that were selected as covariate of the target variable were used to build the cluster matrix. The distances were used to construct a dendrogram using the un-weighted pair group method analysis implemented in SAS JMP (2012) statistical software that prints the dendrogram based on the data of distances between the clusters introduced in Proc cluster procedure.

### **Results and discussion**

#### ***Prediction of body weight using linear body measurements of sheep***

Table 2 shows prediction equations for body weight of sheep in Nigeria. Head length (HL), chest girth (CG), leg length (LL), and tail length were the only linear body measurements that were significant ( $P < 0.01$ ) in predicting body weight of sheep in the overall prediction equation (irrespective of sex, age class and breed). The  $R^2$  value for the prediction equation is 0.834. This means that the model is efficient to predict the body weight of sheep irrespective of the breed. The equation generated for Balami sheep (irrespective of age class and sex) had chest girth, leg

length, tail length, ear length and tail circumference as the significant ( $P<0.01$ ) contributors to body weight with  $R^2$  value of 0.786. Only chest girth ( $R^2 = 0.731$ ;  $P<0.01$ ) was significant for predicting body weight of Uda sheep (irrespective of age class and sex). The significant linear body measurements for the prediction of body weight of WAD sheep (irrespective of age class and sex) were head length, neck length, height at withers, leg length and tail length. The  $R^2$  value obtained for the equation was 0.819. The body weight of Yankasa sheep (irrespective of age class and sex) had head length, height at withers

and tail circumference as the best predictor of body weight with  $R^2$  value of 0.78. The high  $R^2$  values obtained for prediction equation for each breed indicated that the model is efficient to predict body weight of sheep.

#### **Prediction equations for body weight of Balami sheep**

Table 3 shows prediction equation for different age class and sex of Balami sheep. Coefficient of determination for the prediction equations ranged from  $R^2 = 0.259$  - 0.98. Highest coefficient of determination  $R^2=0.98$  was obtained for weaner males. Yearling females had the least  $R^2=0.259$ .

**Table 2: Prediction equation for body weight of sheep**

Breeds	Prediction equation	$R^2$
Overall	$BWT = -43.88 + 0.94HL + 0.42CG + 0.57LL - 0.18TL$	0.834**
Balami	$BWT = -111.81 + 0.57CH + 0.66LL - 0.36TL + 0.73EL + 2.00TC$	0.786**
Uda	$BWT = -33.93 + 0.85CG$	0.731**
WAD	$BWT = -56.76 + 1.09HL + 1.24NL + 0.35HW + 0.43LG - 0.52TL$	0.819**
Yankasa	$BWT = -40.01 + 0.95HL + 0.34HW + 2.73TC$	0.78**

BWT = body weight, HL = head length, NL = neck length, HW = height at withers, CH = chest girth, LG = lion girth, LL = leg length, TL = tail length, EL = ear length, TC = tail circumference, WAD = West African Dwarf,  $R^2$  = coefficient of determination, \*\* $p<0.01$

**Table 3: Prediction equation for body weight of Balami sheep at different age class and sex**

Variables	Prediction equation	$R^2$
Adult Balami	$BWT = -101.36 + 1.76NL + 0.55LG + 1.03EL$	0.857**
Weaner Balami	$BWT = -102.84 + 0.95CG + 1.95LL - 0.90TL - 1.27EL + 3.45TC$	0.960**
Yearling Balami	$BWT = -49.20 + 1.03HL + 1.17LL$	0.551**
Adult female	$BWT = -50.16 + 1.77NL + 0.56LG - 0.66TL$	0.848**
Weaner male	$BWT = -89.05 + 0.82HW + 0.65LG$	0.98**
Yearling female	$BWT = -42.83 + 1.62LG$	0.259*
Yearling male	$BWT = -27.24 + 2.27HL$	0.786*

BWT = body weight, HL = head length, NL = neck length, HW = height at withers, CH = chest girth, LG = lion girth, LL = leg length, TL = tail length, EL = ear length, TC = tail circumference, WAD = West African Dwarf,  $R^2$  = coefficient of determination, \* $p<0.05$ , \*\* $p<0.01$

#### **Prediction equation for body weight of Uda sheep**

Table 4 shows prediction equation for body weight of Uda sheep at different age class and sex. The coefficient of determinations for the prediction equations ranged from 0.99 - 0.94. Weaner male recorded highest

$R^2=0.99$ , this indicates that the model is efficient for prediction of body weight. All age class and sex had high coefficient of determination ( $R^2$ ). The values for coefficient of determination observed by adult Uda  $R^2=0.94$  and adult female  $R^2=0.94$  were the same.



## *Diversity of biometric and morphological traits among sheep breeds in Nigeria*

### ***Prediction equation for body weight of West African dwarf sheep***

Table 5 shows prediction equation for body weight of West African dwarf sheep at different age class and sex. The coefficient of determination for the prediction equations ranged from 0.513 to 0.998. Weaner females recorded highest  $R^2=0.99$ . All age class and sex had high coefficient of determination ( $R^2$ ). Least  $R^2$  (0.513) was recorded by yearling female WAD. The high  $R^2$  values observed indicate that the model is efficient for prediction of body weight of WAD sheep at different age class and sex.

### ***Prediction equation for body weight of Yankasa sheep***

Table 6 shows prediction equations for body weight of Yankasa sheep at different age class and sex. The coefficient of determination for the prediction equations ranged from 0.531 - 0.986. Highest values of  $R^2=0.99$  was recorded by weaner male.

Least coefficient of determination  $R^2=0.53$ ;  $R^2=0.53$  was recorded by adult Yankasa and adult females sheep respectively. The implication of high  $R^2$  values obtained indicates that the model is efficient for prediction of body weight of the Yankasa sheep irrespective of age and sex.

The prediction equation for values of  $R^2$  in breeds of sheep obtained for regression model was within the range reported by several researchers (Salako and Ngere, 2002, Atta and Elkhidir, 2004; Adeyinka and Mohammed, 2006; Okpeku *et al.*, 2013). Overall regression for breeds of sheep was modeled at  $R^2=0.83$  which was similar with regression  $R^2=0.78$  recorded by Fajemilehin and Salako (2008). However, regression for breeds of sheep was lower than what was recorded by several research works by Oke and Ogbonnaya (2011), Iyiola-Tunji (2012) and Agaviezor *et al.* (2012b). Reason for low  $R^2$  for breeds of sheep could be due to chance.

**Table 4: Prediction equation for different age class and sex of Uda sheep**

Variables	Prediction equation	$R^2$
Adult Uda	BWT= -43.41+1.92HL+ 0.21LG+ 0.67EL	0.944**
Weaner Uda	BWT= -44.10+ 0.18HW+ 1.35LL	0.995**
Yearling Uda	BWT= -11.99+ 0.61NL- 1.17HW+ 1.08CG+ 0.27LG	0.976**
Adult female	BWT= -43.41+ 1.92HL+ 0.21LG+ 0.67EL	0.944**
Weaner female	BWT= -8.52+ 0.49CG	0.997**
Weaner male	BWT= -48.59-0.03LG+ 1.81LL	0.99**
Yearling female	BWT= -66.16+ 0.52NL+ 0.83CG+ 2.04EL- 2.87TC	0.984**

BWT = body weight, HL = head length, NL = neck length, HW = height at withers, CH = chest girth, LG = lion girth, LL = leg length, EL = ear length, TC = tail circumference,  $R^2$  = coefficient of determination, \*\* $p<0.01$

**Table 5: Prediction equation for different age class and sex of West African dwarf (WAD) sheep**

Variables	Prediction equation	$R^2$
Adult WAD	BWT=-5.15+2.11HL- 0.44NL-0.19LL+0.48TL	0.996**
Weaner WAD	BWT=-19.14+1.24CG-0.55LG	0.777*
Yearling WAD	BWT=-31.79+1.15NL+0.61BL	0.564**
Adult female	BWT=-5.15+2.11HL- 0.44HW- 0.19LL+ 0.48TL	0.996**
Weaner female	BWT= -75.00+4.00NL	0.998**
Weaner male	BWT= -28.84- 0.60BL	0.756*
Yearling female	BWT= -17.87- 0.62HL- 0.54CG+ 0.64LG	0.513*

BWT = body weight, HL = head length, NL = neck length, HW = height at withers, CH = chest girth, LG = lion girth, LL = leg length, TL = tail length, EL = ear length, BL = back length,  $R^2$  = coefficient of determination,

\* $p<0.05$ , \*\* $p<0.01$

**Table 6: Prediction equation for different age class and sex of Yankasa sheep**

Variables	Prediction equation	R <sup>2</sup>
Adult Yankasa	BWT= -16.76+1.06LL	0.531**
Yearling Yankasa	BWT= -42.78+ 0.66HL+ 0.33HW+ 3.89TC	0.715**
Adult female	BWT= -16.76+1.06LL	0.531**
Yearling female	BWT= -9.61+0.28TL+3.09TC	0.656**
Yearling male	BWT= -15.93+1.81HL+0.71HW+0.20CG-0.69LG- 0.39BL+0.18EL	0.986**

BWT = body weight, HL = head length, HW = height at wither, CH = chest girth, LG = lion girth, LL = leg length, TL = tail length, EL = ear length, TC = tail circumference, R<sup>2</sup> = coefficient of determination, \*\*p<0.01

### ***Rotated component loadings and communality for breeds of sheep***

Presented on Table 7 were the rotated component loadings, eigen values, %variance and communalities for biometric and morphological traits of sheep. Body weight and all the linear body measurements had their highest loadings on principal component 1 (PC1). Tassel was the only variable that had its highest loading on PC2. Tail type and state (location) were the variables that best describes the third component (PC3). Sex and hair type were variables that best described the forth component (PC4). The first component can be named growth characteristics, the second component was related to tassel, the third component was related to location of environment where the sheep were living and the fourth component was related to sex of sheep. However, each of the variance % for PC1 which is 45.23%, PC2; 12.55%, PC3; 10.71%, PC4; 8.37% contributed to the 76.86% of the total variance of the four principal component.

The Principal Component Analysis (PCA) obtained was in line with previous studies on sheep of Nigeria (Yakubu and Ayoade, 2009; Yakubu *et al.*, 2009). Principal component analysis had a total of 77% variance which explained variation in the population studied, this was similar to PCA of 78% recorded by Yakubu *et al.* (2009) for adult Fulani cattle. The PCA for breeds of sheep was lower than what was recorded by Yakubu *et al.* (2009) in young Fulani cattle.

The possible reason for higher PCA for indigenous breeds of sheep as obtained could be due to differences in morphological structure and location (genotype and environment interaction). Mavule *et al.* (2013) recorded lower PCA (66.85%) for Zulu sheep in Northern South Africa. Very high communalities were obtained for each of the variables studied with the exception of sex which had moderate value (0.422). The high values of communalities are an indication of good relationship (correlations) among most of the variables. Communality is the total amount of variance an original variable shares with all other variables included in the analysis (Hair *et al.*, 2007).

### ***Re-substitution summary using linear discriminant function***

Table 8 shows the linear discriminant function of sheep. Discriminant analysis showed that 70.59% of sheep were classified as pure Balami. Breeds of sheep classified as pure Uda had 60% while West African dwarf and Yankasa breeds were classified as 100% pure, respectively. Discriminant analysis for breeds of sheep obtained was in line with earlier studies of Yakubu *et al.* (2010a); Agaviezor *et al.* (2012b) and Yunusa *et al.* (2013) on breeds of sheep in Nigeria. Based on the results of all morphometric measurements in this study, the Yankasa and the WAD were purely classified into distinct breeds. The result obtained was similar to the previous research of Yakubu *et al.* (2010a) who reported 99.4% in WAD goats and 100% in

*Diversity of biometric and morphological traits among sheep breeds in Nigeria*

**Table 7: Rotated component loadings and communality for breeds of sheep**

Variables	PC1	PC2	PC3	PC4	Communality
BWT	<b>0.907</b>	0.011	0.076	-0.021	0.829
HL	<b>0.891</b>	0.192	0.093	-0.030	0.840
NL	<b>0.875</b>	0.221	-0.125	0.015	0.830
HW	<b>0.958</b>	0.187	-0.071	-0.053	0.960
CG	<b>0.951</b>	0.178	-0.080	0.008	0.943
LG	<b>0.928</b>	0.157	-0.040	-0.011	0.888
BL	<b>0.913</b>	0.203	-0.023	0.010	0.876
LL	<b>0.938</b>	0.207	-0.025	-0.029	0.925
TL	<b>0.915</b>	0.105	-0.147	-0.066	0.897
ER	<b>0.894</b>	0.085	0.080	-0.288	0.895
TC	<b>0.882</b>	0.156	0.088	-0.110	0.822
Breed	<b>-0.621</b>	0.285	-0.495	0.372	0.851
Sex	0.067	0.227	0.093	<b>0.598</b>	0.422
Wattle	0.110	0.042	0.019	0.239	0.621
Tassel	0.126	<b>0.716</b>	0.014	0.295	0.615
Hair type	-0.201	0.148	-0.154	<b>0.766</b>	0.673
Tail type	-0.210	-0.033	<b>0.860</b>	0.292	0.870
Hair color	0.657	0.274	-0.358	-0.444	0.833
State/location	0.645	0.046	<b>-0.608</b>	0.149	0.810
Eigenvalue	10.85	3.01	2.57	2.01	
% variance	45.23	12.55	10.71	8.37	76.86

BWT=body weight, HL= head length, NL =neck length, HW= height at withers, C G= chest girth, LG= lion girth, BL= back length, LL=leg length, TL = tail length, EL= ear length, TC= tail circumference, SC= scrotal circumference, PC1= principal component 1, PC2= principal component 2, PC3= principal component 3, PC4=Principal component 4

Red Sokoto goat but was not in concordance with the previous work of Agaviezor *et al.* (2012a) who reported values of 93.3% and 63.9% for WAD and Yankasa sheep, respectively. The possible reason for the variations could be due to chance and to influence of environment and location. Balami and Uda sheep were expected to have shared the highest number of traits 29.41%. This explains that, there is room for improvement of indigenous breeds of sheep especially between Southern and Northern breeds.

***Canonical clusters among populations of sheep***

The classification of breeds of sheep into clustering groups is presented in Figure 1. The canonical loading by breed in the entire study was 82.65%. The accuracy for Balami ( $X_1$ ), Uda ( $X_2$ ), WAD ( $X_3$ ), and Yankasa ( $X_4$ ) were 70.59%, 60%, 100% and 100%, respectively. Among the breeds, WAD and

Yankasa had the highest accuracy for classification into distinct genetic groups (100%) while Uda had the least accuracy (60%). Cluster analysis for the indigenous breeds of sheep obtained was in line with the previous study on sheep in Nigeria (Adebambo *et al.*, 2004; Agaviezor *et al.*, 2012a). However, the percentage of clustering for WAD and Yankasa sheep were higher than what was recorded by Agaviezor *et al.* (2012a). The possible reason for higher percentage for WAD and Yankasa breeds as recorded could be due to genotype by environment interaction. Breeds used for the study were sampled only in Anambra and Nasarawa States. The sampled animals were known to be more purified in these locations. Moreover, there were several levels of admixtures (quantitative traits) between Balami and Uda in the genome of these animals that constitute the clusters. The possible reason



for these admixtures could be attributed to indiscriminate crossbreeding practices of the farm-owners and gene flow between these breeds due to geographical proximity. WAD and Yankasa were the only breeds

with minimal case of admixtures. This was in line with the report of Agaviezor *et al.* (2012a) that obtained lower percentage for the four breeds carried out his experiment across the country.

**Table 8: Re-substitution summary using linear discriminant function**

Observations and percent classified into breeds					
Breeds	Balami	Uda	WAD	Yankasa	Total
Balami	70.59	29.41	0.00	0.00	100.00
Uda	40.00	60.00	0.00	0.00	100.00
WAD	0.00	0.00	100.00	0.00	100.00
Yankasa	0.00	0.00	0.00	100.00	100.00
Total	36.84	21.05	18.42	23.68	100.00
Priors	0.25	0.25	0.25	0.25	-

WAD = West African dwarf

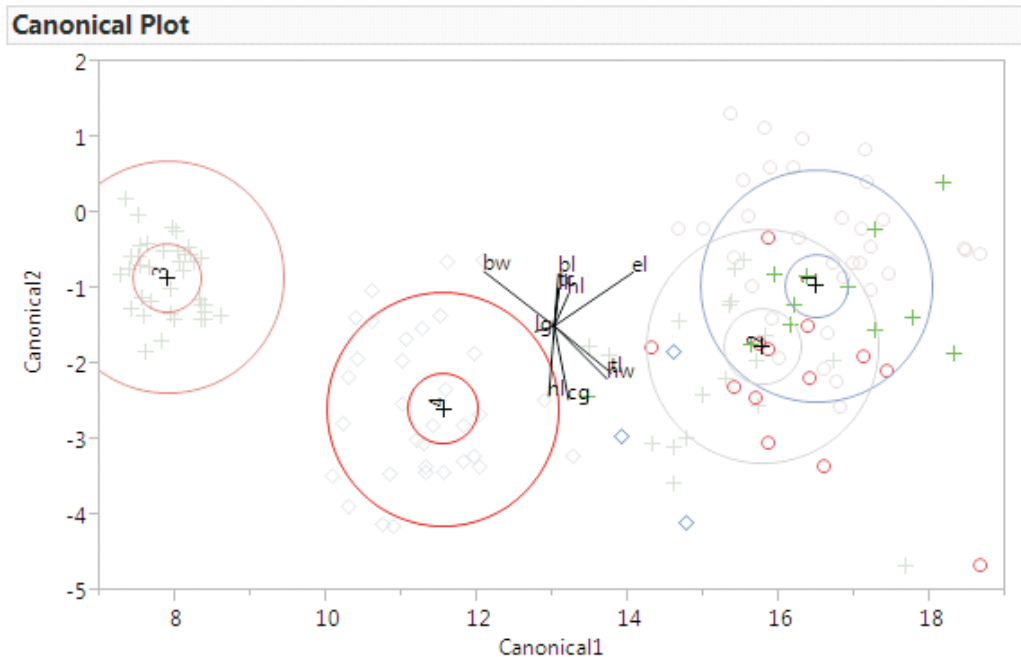


Figure 1: Canonical cluster analysis describing the loading of indigenous sheep

### ***Phylogenetic of the four breeds of sheep in Nigeria***

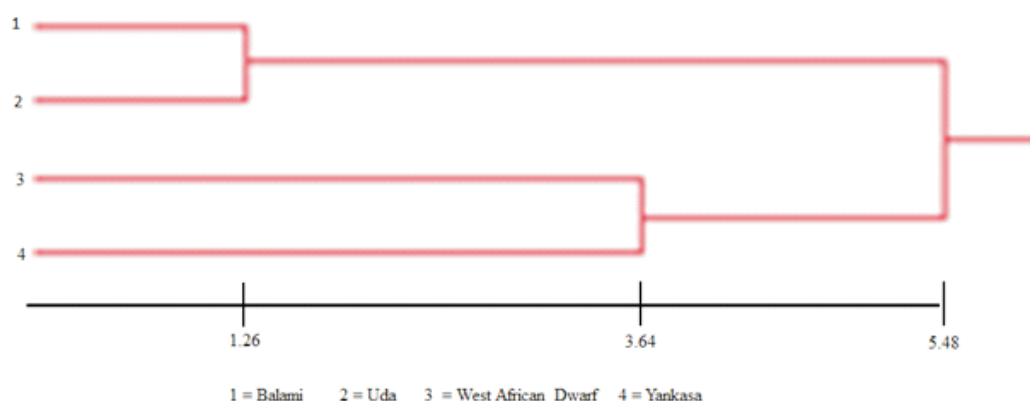
Figure 2 showed the phylogenetic association of breeds of sheep in Nigeria. Genetic distance (degree of genomic differences within and between animal populations) was derived from the

dendrogram. Genetic distance of 5.48 was recorded between Balami and WAD and this was the farthest among the breeds of sheep. Genetic distance of 1.26 was recorded between Balami and Uda. However, genetic distance of 3.64 was recorded between WAD and Yankasa. Phylogenetic tree (dendrogram) for the

### *Diversity of biometric and morphological traits among sheep breeds in Nigeria*

indigenous breeds of sheep obtained was in line with the previous study on sheep in Nigeria (Adebambo *et al.*, 2004; Agaviezor *et al.*, 2012b). However, the genetic distances recorded were higher than what was obtained by (Agaviezor *et al.*, 2012b). Breeds used were sampled only at Northern, central and Eastern States. The sampled animals in these States were known to have evolutionary divergence which makes them distinct entities. However, Balami and Uda had close genetic distances, which could partly be attributed to geographical proximity. The

reason for the wider genetic distance between Balami and WAD sheep could be attributed to lack of substantial gene flow between these breeds. Adebambo *et al.* (2004) who obtained lower genetic distances for the four breeds carried out his experiment at South-west middle-belt and North-west of Nigeria. The genetic distance obtained between Balami and WAD sheep showed greater variability and conserving the genes for these breed will result to higher hybrids and faster genetic improvement for meat production.



**Figure 2: Dendrogram showing phylogenetic association of four breeds of sheep in Nigeria**

#### **Conclusion and recommendation**

Sheep sampled as WAD and Yankasa had 100% conformation while Balami and Uda had 70.59% and 60%, respectively as conformation to the classifying features of their breed based on discriminant analysis. The farthest genetic distance (5.48) was observed between Balami and WAD while the shortest genetic distance (1.26) was observed between Balami and Uda. Improvement of growth traits of sheep breeds in Nigeria is recommended through the use of either Balami or Uda as sire and either WAD or Yankasa as dam.

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*Received: 11<sup>th</sup> October, 2019*

*Accepted: 17<sup>th</sup> February, 2020*