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Application of Multifactorial Discriminant Analysis of Morphostructural Differentiation of Sheep

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ABSTRACT

A study on phenotypic variation was carried out with a total of 905 sheep comprising 250 Koroji (120 males and 130 females), 233 Balami (115 males and 118 females), 202 Uda (98 males and 104 females) and 220 Yankasa (108 males and 112 females). The animals were selected based of alertness, health and absence of deformity. Theparameters measured were body weight (BW),body length (BL), height at wither (HTW), chestcircumference (CC), head length (HDL), headwide (HDW), ear length (EL), horn length(HNL), horn circumference (HNC), tail length(TL), rump wide (RW), rump length (RL),height at rump (HR), foreleg (FLG), hind leg(HLG), height at rump (HTR) and neck length(NL).The data were analyzed with SPSS. The results revealed that breed had significant (P<0.05) effect on phenotypic traits. This study revealed highest genetic distance between Balami and Yankasa (27.57) than followed by distance between Balami and Koroji (18.36) and the least is between Koroji and Uda (7.22). Eigen value revealed share variance (69.6) of function 1 and 19.3 and 11.1% in function 2 and 3 respectively. The result of structure matrix revealed EL has the highest loading (0.73) followed by RW (0.18) in function 1. RL has the highest loading (0.46) followed by HDL (0.43) in function 2. HDW has the highest loading (0.91) followed by BW (0.76) in function 3. Beside, standardized canonical discriminate coefficients revealed that the highest EL (1.04) and HDL (0.85) were in function 1, RL (1.26), HDL (0.89) in function 2 and HDW (1.02) and RW (0.37) in function 3. The study concluded that breeds had effect on phenotypic traits of sheep. The genetic distance showed large distance between Balami and Yankasa and low distance between Koroji and Uda. Eigenvalue showed 69.6% variations that exist between the four breeds populations. The structure matrix and standard canonical discriminant coefficient revealed EL, HDL, HDW and RW as the discriminators and predictors of variations in sheep (Balami, Koroji, Uda.

KEYWORDS: *Discriminant, Sheep, Traits, Morphological*

INTRODUCTION

The relative contribution of livestock to agricultural gross domestic product (GDP) is higher in the developed regions but the trend has been slightly downwards over the past 30 years, whereas in most developing regions, there has been a rise in the importance of livestock (FAO, 2001). Within the livestock industry in Nigeria, small ruminants represent a very important national resource. Sheep are reared primarily for meat and play significant socio-economic roles in the lives of rural dwellers (Yakubu and Ibrahim, 2011).Adequate knowledge of diversities within and between animal populations will not only help in reducing misidentification in animal husbandry but also aid conservation of many important endangered alleles. Sub-Saharan Africa is an important source of farm animal genetic resources as most of the alleles coding for traits which are implicated for resistance to stress, resistance to diseases, ability to thrive on low quality feed can be found in this region (Yunusa *et al*., 2013). Genetic diversity in animal breeds allows for the existence of livestock in all but few environments globally, providing a range of products and functions (Salako and Ngere, 2002). It is the diversity in genetic characteristics that enable different animal races to survive in different climatic zones of the world (Yunusa *et al*., 2013).The characterization of indigenous sheepbreeds and breed diversity are essential forconservation of their genes sources andattainment of the flocks position for breedingpurposes as well as to meet future needs (Yilmaz *et al*., 2013; Khan *et al*., 2014; Dauda *et al*., 2018b). A good description comparison orcharacterization based on morphologicalproperties can provide to some extent areasonable representation of the differencesamong the breeds, though not exhaustive, itserves as the foundation upon whichdeoxyribonucleic acid (DNA) analysis can bebuilt (Yunusa *et al* 2013). Knowledge of morphometriccharacteristics marks the first step inclassification of farm animal genetic resources (FAnGR) (Delgado *et al* 2001). In Nigeria previously, effort on morphometric differentiation of Nigerian breeds of sheep have been restricted to the use of analysis of variance, whereas the current trend in livestockclassification involves the use of multivariatestatistical tools (Zaitoun *et al*., 2005; Dossa *et al*., 2007). Multifactorial analyses of morphological traits have been proved to be suitable inassessing genetic variation within andbetween populations when all morphologicalvariables are considered simultaneously (Yakubu and Ibrahim, 2011). The general objective of this study is to characterize four local sheep breeds of Nigeria based on morphological differences using multifactorial discriminant analysis.

MATERIALS AND METHODS

Study Area

The study was carried out at Maidugurimetropolis. Maiduguri is the capital and thelargest urban center of Borno State, NorthEastern Nigeria. The state lies between latitude11°32′ North and 11°40′ North and latitude13°20′ East and 13°25′ East between the Sudan Savanna and Sahel Savanna vegetation zones,characterized by short rainy season of 3-4months (June-September) followed by aprolonged dry season of about 8 monthsduration (BMLS, 2016).

Management of Experimental Animal

The animals were managed underextensive management where they weresubjected to the traditional extensivemanagement system, with little or no provisionfor shelter in the day and night. They grazedduring the day on natural pasture containingforages such as Northern Gamba grass(*Andropogon gayanus*), Stylo (*Stylosanthesgracilis*) and Leucaena (*Leucaenaleucocephala*). Occasionally, supplements suchas groundnut haulm, beans shell, cereal offal and crop residues were sometimes providedprior and/or after grazing of natural pastures. Adequate health care was virtually nonexistent while uncontrolled breeding was thepractice.

Phenotypic Traits Measured

The morphological measurements were taken from selected 905 sheep comprising 250 Koroji (120 males and 130 females), 233 Balami (115 males and 118 females), 202 Uda (98 males and 104 females) and 220 Yankasa (108 males and 112 females). The animals were selected based of alertness, health and absence of deformity. The parameters measured were body weight (BW),body length (BL), height at wither (HTW), chestcircum ference (CC), head length (HDL), head wide (HDW), ear length (EL), horn length(HNL), horn circumference (HNC), tail length(TL), rump wide (RW), rump length (RL),height at rump (HR), foreleg (FLG), hind leg(HLG), height at rump (HTR) and neck length(NL). The weight (Kg) was measured by using of glas fiber band with model number WJ515and the height measurement (cm) was done using a ruler. This was achieved by placing the animals on a flatground and held by two field assistants. The length and circumference measurements (cm)were carried out using a graduated tape. Measurements were done in the every morning before the animals were released for grazing throughout the period of morphometric measurement. All measurements were carried out by the same person, in order to avoid inter-individual variations.

Data Analysis

The statistical analysisfor the phenotypic traitswere obtained using PROC UNIVARIATE procedure of SAS (2004), with breed of sheepincluded in the model as the source of variation. Means separation was done using Duncan’s Multiple Range Test of the same statistical package at probability level of 5%. The linear model employed was:

$Yij=\mu+\alpha i+ e_{ij}$

where,

Yij=record of morphological traits of each animal

μ=overall mean

αi=fixed effect of the ith breed (i = Balami, Koroji, Uda, Yankasa)

eij=random residual error associated with record of each animal.

The Estimation of Mahalanobis squared distances (D2) between different breeds in same location were obtained using Candisc procedure of SAS (1999). Squared distance (D2) between the different breeds in same location was estimated by the following relationship D2 (i/j) = (xi – xj) cov-1 (xi - xj).

Where D2 = genetic distance between populations in an m- dimensional space. I/j = the element of the ith row and the jth column of the inverse matrix.

xi–xj= mean sets of original variables Cov = covariance of the original data set.

RESULTS AND DISCUSSION

The results of effect of breeds on phenotypic traits are presented in Table 1. The result showed that all the phenotypic traits were significantly (P<0.05) different except BW, HDW and NL. BW, HTW, CC, TL, HL, FL, HTR showed high values 64.12, 84.87, 84.41, 47.24, 66.26, 56.56 and 76.37 respectively in Koroji except El and RL value 24.11 and 22.18 is high in Balami sheep. Balami sheep also had significantly higher (P<0.05) values for all the phenotypic traits measured compared to Yankasa and Uda counterparts. This indicates that Koroji sheep is bigger than the three other sheep found in the northern Nigeria. The present phenotypic variations as showed in this study could be an indication of the inherent genetic constitution of each sheep breed. Morphological variation could be quite attractive for screening overall adaptive genetic diversity (Toro and Caballero, 2005).The value of HTW, CC obtained in this study were higher the value 76.01 and 79.40 reported for mature Balami sheep (Yunusa *et al*., 2013). The HTW and CC obtained in this study were also higher than HTWs of 67.4 and 68.0cm and CCs of 80.0 and 81.3cm respectively for mature Zulu sheep in South Africa (Kunene *et al*., 2007).The variation in CC and HTW could be due to breeds, management or environment.Productivity of sheep is affected by many factors, such as breed improvement programs based on the maximum utilization of genetic variation, but these features may also vary due to certain environmental factors (Petrovic *et al*., 2011)

Table1.*Effect of Breeds on Phenotypic Traits*

	Balami		Koroji		Uda		Yankasa	
Traits	Mean	Std Dev	Mean	Std Dev	Mean	Std Dev	Mean	Std Dev
BW	60.87^{a}	14.31	64.12^{a}	16.42	57.83^{a}	17.76	51.09^{b}	8.47
BL	52.80	5.81	53.17	5.91	50.48	8.14	50.67	5.12
HTW	81.51^{b}	6.26	84.87^{a}	8.11	79.27^{bc}	7.04	76.84^{c}	6.83
CC	82.12^{ab}	8.42	84.41^{a}	9.23	79.39^{bc}	12.46	76.96^{c}	5.63
HDL	23.91^{a}	9.72	23.37^{ab}	3.37	22.34^{ab}	2.73	21.09^{b}	3.06
HDW	12.31	1.81	12.35	1.57	11.93	2.22	12.00	3.22
EL	24.11^{a}	3.29	20.50^{c}	2.65	22.43^{b}	2.87	18.09^{d}	1.98
TL	45.62^{ab}	6.80	47.24^{a}	5.64	44.27^{b}	5.47	45.72^{ab}	7.19
RL	22.18^{a}	3.35	21.78^{a}	2.93	18.82^{b}	4.66	20.88^{a}	3.83
RW	16.42^{bc}	2.10	17.67^{a}	2.01	15.80^{c}	3.11	17.44^{ab}	2.53
HTR	74.86^{ab}	6.58	76.37^{a}	7.51	72.88^{b}	6.06	69.53^{c}	6.32
FL	53.93^{b}	5.07	56.56^{a}	5.89	53.77^{b}	3.67	51.56^{b}	7.77
HL	62.98^{b}	4.98	66.26^{a}	5.67	63.57^{b}	5.69	60.00^{c}	7.31
NL	31.51	3.44	32.94	6.96	33.16	4.70	32.47	6.77

BW=body weight, BL=body length, HTW=height-at-wither, CC=chest circumference, HDL=head length, HDW=head width, EL=ear length, TL=tail length, RL=rump length, RW=rump width, HTR=height-at-rump, FL=fore leg length, HL=hind leg length, NL=neck length. Std Dev=standard deviation

The results of Mahalanobis distance between Balami, Koroji, Uda and Yankasa are presented in Table 2.Genetic distance which is the degree of genetic difference (genomic difference) between breeds/species or populations are measured by some numerical method (Dauda *et al*., 2018b). Thus, the average number ofcodon or nucleotide differences per gene is a measure of genetic distance.It is theoretically obtained as difference in allele frequencies for all loci in animal genome (Yunusa et al., 2013; Dauda *et al*., 2018b).Genetic distance is important to determine the hybrid vigour (heterosis) expected during crossbreeding (Yunusa *et al*., 2013). Since, to exploit animal genetic resources it is pertinent to have background knowledge of the amount of genetic variation that exists between and within the species (Dauda *et al*., 2018b). This study revealed highest genetic distance between Balami and Yankasa (27.57) than followed by distance between Balami and Koroji (18.36) and the least is between Koroji and Uda (7.22).The high genetic distance observed between Balami and Yankasa could be due to natural selection, artificial selection and adaptation to environmental conditions whereas the lower genetic distance between koroji and Uda could be due to genetic exchange that has taken place overtime and has reduced the genetic distance that would have theoretically described their differences. This could have been facilitated by geographical proximity, whereby there was unrestricted and indiscriminate crossbreeding among local populations (Yakubu and Ibrahim, 2011). Thus, crossbreeding between Balami and Yankasa may produce good heterosis, while the crossbreeding between Koroji and Uda might not produce desirable heterosis with regard to traits of economic importance.Animal genetic diversity is essential in meeting the protein shortage in the developing countries such as Nigeria. Genetic diversity of livestock species allows animal production to be practiced in a range of environments and with a range of different objectives. It provides the raw material for survival and adaptability of a species.

Table2.*Mahalanobis Distance between Balami, Koroji, Uda and Yankasa*

	Balami	Koroji	Uda
Balami			
Koroji	18.36		
Uda	11.94	7.22	
Yankasa	27.57	8.53	15.72

The results Eigen value, Canonical correlation, Cumulative and Variance Percentage are presented in Table 3. The percentage of share variance (69.6) of function 1 is higher than 19.3 and 11.1% in function 2 and 3 respectively. The canonical correlation of function 1 is also higher (0.712) than 0.471 and 0.375 in function 1 and 2 respectively. The high percentage of the shared variance (eigenvalue) and the total variation in the grouping of discriminant function 1 in this study could be attributed to the differences among the four sheep populations in their phenotypic traits and evidence of high genetic variability among them. The results of Structure Matrix for Discriminant Functions are presented in Table 4. The result revealed that EL has the highest loading (0.73) and followed by RW (0.18) in function 1. RL has the highest loading (0.46) followed by HDL (0.43) in function 2. HDW has the highest loading (0.91) followed by BW (0.76) in function 3. The structure matrix showed the correlation of each variable with each discriminant function (Gwaza and Igbayima, 2015). The highest loading of EL and RW suggested that the correlation between EL and RW was the function that discriminated between the populations in discriminant function 1. In discriminate function 2, high loading of RL and HDL suggested that the correlation between these was the function that discriminated between the populations in discriminant function 2 and correlation between HDW and BW in function 3 also implies are the traits that discriminated between the populations. These traits are the most powerful predictors of variation in body dimension of four breeds of sheep between populations. The results of standardized canonical discriminant coefficients are presented in Table 5. The results revealed that EL (1.04) and HDL (0.85) in their standardized canonical discriminant coefficients in function 1, RL (1.26) showed highest followed by HDL (0.89) in function 2 and HDW (1.02) showed highest and followed by RW (0.37) in function 3. The standardized canonical discriminant coefficient provides information on the importance and strength of each predictor to the discriminant function (Meritexell *et al.*, 2003). The aforementioned traits are adequate to be use in discriminating and identifying phenotypic variation between the populations of four breeds of sheep (Balami, Koroji, Uda and Yankasa).

Table 3.*Eigen value, Canonical correlation, Cumulative and Variance Percentage*

Function	Eigenvalue	% of Variance	Cumulative %	Canonical correlation
1	1.026	69.6	69.6	0.712
2	0.285	19.3	88.9	0.471
3	0.164	11.1	100.0	0.375

Table 4.*Structure Matrix for Discriminant Functions*

	Function		
Traits	1	2	3
EL	0.73	0.20	-0.04
HDW	0.09	0.20	0.91

BW	0.06	0.07	0.76
CC	0.10	0.10	0.74
HTR	0.17	0.21	0.71
BL	0.02	0.08	0.68
RL	0.07	0.46	0.67
HDL	0.05	0.43	0.63
FLG	0.10	0.27	0.60
HTW	0.14	0.03	0.50
RW	0.18	-0.19	0.47
TL	0.03	0.11	0.28
HNL	0.15	0.02	0.26
NL	0.15	0.07	0.20

Table 5.*Standardized Canonical Discriminant Coefficients*

Function			
Traits	1	2	3
HDW	0.26	0.33	1.02
EL	1.04	0.53	-0.27
RL	0.35	1.26	0.36
RW	0.74	0.10	0.37
HTR	0.65	-0.09	0.17
HDL	0.85	0.89	-0.20

CONCLUSION

The study concludes that breeds had effect on phenotypic traits of sheep. The genetic distance showed large distance between Balami and Yankasa and low distance between Koroji and Uda. Eigenvalue showed 69.6% variations that exist between the four breeds populations. The structure matrix and standard canonical discriminant coefficient revealed EL, HDL, HDW and RW as the powerful discriminators and predictors of variations in sheep (Balami, Koroji, Uda and Yankasa) populations. Information emanating from this study will aid in future conservation, selection and planning of breeding programmes.

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