

Full Length Research Paper

Morphometric characterization of Nigerian indigenous sheep using multifactorial discriminant analysis

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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. A total number of 1195 animals comprising 380 Yankasa sheep, 414 Uda sheep, 224 Balami sheep and 177 West African Dwarf (WAD) sheep were sampled from Osun and Oyo states, South Western Nigeria. Yankasa and WAD were sampled from traditionally managed flock while Balami and Uda sheep were obtained from markets in these states. Seventeen (17) morphometric characters were measured to study their phenotypic variations. The characters measured include rump width (RW), rump length (RL), tail length (TL), wither height (WH), heart girth (HG), paunch girth (PG), rump height (RH), ear length (EL), foreleg length (FLL), rear-leg length (RLL), body length (BL), shoulder width (SW), neck circumference (NC), head length (HeL), head width (HW), horn length (HL) and hock length (HoL). Stepwise multifactorial discriminant analysis was explored to check traits that best differentiate the Nigerian sheep. Length of tail was the most discriminating character among the eight distinguishing traits found. Longest genetic distance was found between WAD and Uda sheep while the closest breeds were Balami and Uda, as indicated by the Euclidian distance. The large Euclidian distance obtained for genetic gap between Uda and WAD sheep gives prospect for improvement if they are crossbred. Since Uda and WAD have been reared successfully in the arid Northern region and trypano-endemic region of Southern humid Nigeria, respectively, crossing WAD with Uda will produce a relatively large, heat tolerant and trypanotolerant hybrid.

Key word: Phenotypic variation, Nigerian sheep, discriminant analysis.

INTRODUCTION

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. 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. Ability of Merino sheep and Uda sheep to thrive in the cold region of Australia and hot region of Northern Nigeria respectively is due to genetic diversity. The high survivability of West African dwarf (WAD) sheep in this trypano-endemic region of humid southern Nigeria is also due to the genetic diversity. Genetic improvement of

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caprine races has formally been achieved through the crossing of exotic and indigenous sheep to the disadvantage of the latter (Salako and Ngere, 2002). When these animals are been crossed with their exotic counterpart, their genetic properties that contributes greatly to their survivability tend to be eroded. This trend is currently being reversed with greater attention focused on the indigenous breeds (Maijala, 1993). Characterization of Farm Animal Genetic Resources (FAnGR) encompasses all activities associated with the identification, quantitative and qualitative description, and documentation of breed populations and the natural habitats and production systems to which they are or are not adapted (Gizaw et al., 2011).

The characterisation of domestic animal diversity is essential to meet future needs in Nigeria and sub-Saharan Africa in general. Comparison or characterization based on morphological properties can provide to some extent a reasonable representation of the differences among the breeds, though not exhaustive, it serves as the foundation upon which DNA analysis can be built. Domestic animal diversity is critical for food security and essential to meet unpredictable future demand of population increase, climate change and more virulent disease pathogens, thus, a reservoir not only depends on the number of breeds but also on the genetic diversity within and between these breeds (Crepaldi et al., 2001). Agaviezor et al. (2012a) noted that 740 breeds are recorded as extinct, with 1,335 (32% of the estimated total breeds) being classified at high risk of loss or under threat of extinction

Knowledge of morphometric characteristics marks the first step in classification of FAnGR (Delgado et al., 2001). Discriminant analysis of morphostructure of sheep and other livestock of same ecological zone has been done extensively with two or three breeds in the discriminant analysis model (Salako and Ngere, 2002; Yakubu et al., 2010a, b; Yakubu and Ibrahim, 2011). Movements by Fulani pastoralists and trading of livestock between South and Northern Nigeria have encouraged introgression. This genetic exchange between different ecological zones in Nigeria has made breed identification a difficult task in animal husbandry as any of the breeds can be mistaken for another.

This study identified traits that best distinguish Nigerian breeds of sheep, including the four major breeds namely Yankasa, Uda, Balami and WAD for proper classification. Accurate classification of Nigeria sheep population will not only have impact on management of these animals but also reduce misidentification by livestock traders and help in the conservation of genetic resources.

MATERIALS AND METHODS

A total number of 1195 animals comprising 380 Yankasa sheep, 414 Uda sheep, 224 Balami sheep and 177 West African Dwarf sheep were sampled from the traditionally managed flocks in Osun

and Oyo states of South Western Nigeria. Balami and Uda sheep were obtained from markets in these states. Animals were reared semi-intensively. No special shelter was provided for them at night. Routine medications were also provided for some of the animals. Body measurements were taken when the animals were in standing position with head raised and weight on all four feet without body movement. Physical restraint was sometimes applied to limit movement. Measurements were taken with a measuring tape. The methods used for the measurements are as described by FAO (2012). Anatomic reference points for the measurements are as described by Salako and Ngere (2002). Seventeen metric traits were measured on each animal using the identification marks already documented; rump width (RW), rump length (RL), tail length (TL), Wither Height (WH), heart girth (HG), paunch girth (PG), rump height (RH), ear length (EL), foreleg length (FLL), rear-leg length (RLL), body length (BL), shoulder width (SW), neck circumference (NC), head length (HeL), head width (HW), horn length (HL) and hock length (HoL) were the traits measured.

Statistical analysis

Descriptive statistics for the variables were generated for each breed showing means and standard error for the means. Data were adjusted for variations in age and sex. Univariate analysis of variance (ANOVA) was done to examine whether there are significant differences in the morphometric characters between the breeds. Duncan multiple range test was used to group the means (Steel and Torrie, 1980) Table 1. Stepwise discriminant analysis was performed to identify morphometric parameters that best serve as racial marker between the breeds of sheep investigated. This was accomplished with discriminant analysis option of variable classification using the Statistical Package for Social Science (Version 19). Euclidian genetic distance was also generated with the dendrogram plot.

RESULTS AND DISCUSSION

A discriminant analysis was conducted to predict any of the seventeen traits measured that best distinguish the four breeds into separate categories. The result of Box's M is presented in Table 2 which was expected not to be significant especially when small sample size is used. In ANOVA, the assumption is that the variances are equivalent for each group but in discriminant analysis the basic assumption is that the variance-co-variance matrices are equivalent. Box's M tests the null hypothesis that the covariance matrices do not differ between groups. The result of this study violated the assumption; however, this problem was not regarded important given the large sample size.

Results of the stepwise discriminant analysis displaying Wilk's lambda values, F-values and probabilities are presented in Table 3. Out of 17 variables considered, 8 were included in the analysis. Tail length (TL) was found to be the most discriminating character followed by ear length (EL), rump width (RW), hock length (HoL), rear leg length (RLL), heart girth (HG), wither height (WH) and shoulder width (SW) in decreasing order of discriminating power. This result was in harmony with Salako and Ngere(2002) where tail length was obtained to be the most discriminating variable between Yankasa and WAD

Table 1. Duncan multiple range separation of means for the univariate ANOVA of morphometric characters of Nigerian sheep (Mean±SEM).

Parameter	Yankasa	Uda	Balami	WAD
Body length	66.93±0.43 ^b	69.97±0.42 ^a	71.06±0.67 ^a	57.82±0.53 ^c
Wither height	71.99±0.39 ^c	77.41±0.42 ^a	76.01±0.58 ^b	61.66±0.28 ^d
Heart girth	75.99±0.42 ^c	81.65±0.47 ^a	79.40±0.64 ^b	68.66±0.61 ^d
Paunch girth	86.12±0.58 ^b	93.46±0.59 ^a	92.24±0.75 ^a	75.72±0.78 ^c
Rump height	70.48±0.35 ^c	75.14±0.46 ^a	73.58±0.53 ^b	61.14±0.66 ^d
Rump width	19.14±0.32 ^b	18.70±0.20 ^b	21.14±0.64 ^a	14.72±0.19 ^c
Rump length	23.21±0.16 ^b	24.61±0.17 ^a	24.77±0.24 ^a	19.97±0.25 ^c
Tail length	38.81±0.38 ^c	43.20±0.35 ^a	41.28±0.58 ^b	26.39±0.54 ^d
Ear Length	13.84±0.11 ^b	16.94±0.20 ^a	16.47±0.24 ^a	11.47±0.15 ^c
Foreleg length	47.96±0.35 ^b	50.81±0.35 ^a	51.40±0.52 ^a	42.45±0.50 ^c
Rear leg length	54.74±0.34 ^b	57.87±0.37 ^a	57.55±0.53 ^a	50.11±0.48 ^c
Shoulder width	22.55±0.20 ^b	24.57±0.20 ^a	23.88±0.34 ^a	18.22±0.34 ^c
Neck circumference	42.57±0.38 ^b	45.13±0.35 ^a	45.84±0.55 ^a	35.53±0.51 ^c
Head length	24.36±0.15 ^b	26.36±0.19 ^a	25.91±0.26 ^a	21.21±0.23 ^c
Head width	14.66±0.12 ^c	15.30±0.11 ^b	15.85±0.19 ^a	12.63±0.17 ^d
Horn length	22.73±0.47 ^c	25.02±0.47 ^b	25.67±0.66 ^a	16.67±0.60 ^d
Hock length	30.51±0.16 ^c	32.57±0.14 ^a	32.45±0.27 ^a	26.84±0.11 ^c

^{abcd}Means along same row with different superscripts are significantly different ($p < 0.05$) DMRT = Duncan multiple range test.

Table 2. Result of Box'M.

Box's M	982.049
F-Approx.	8.898
Df1	108
Df2	331887.684
Sig	0.000

Table 3. Summary of discriminant analysis for WAD, Balami, Uda and Yankasa Sheep.

Variable	Wilk's Lampda	F-remove	P-Level
Tail length	0.76	95.87	0.0001
Ear length	0.68	64.85	0.0001
Rump width	0.65	48.31	0.0001
Hock length	0.63	38.94	0.0001
Rear leg length	0.62	32.55	0.0001
Heart girth	0.60	28.69	0.0001
Wither height	0.59	25.92	0.0001
Shoulder width	0.58	23.56	0.0001

sheep. However, a considerable proportion of cross-classification errors between Uda and Balami, also between WAD and Yankasa were evaluated using discriminant analysis thus confirming the introgression of

the Northern sheep southwards. The introgression observed in these sheep could be explained with various reasons. Massive migration of rams from North to South during festivals and trans-human activities in the country where northern animals move southwards during dry season encourage interbreeding of sheep of different agro ecological zones. Farmers in the South occasionally procure the northern rams for breeding purpose, crossing these rams with southern ewes encouraged introgression. Yakubu et al. (2010b) opined that the increasing activities of Fulani pastoralists lead to indiscriminate flock movement and traditional livestock movement. Similar gene movement was reported by Traore et al. (2008) between the Sahelian and Sudan-Sahelian (Mossi) sheep of Burkina-Faso. This result corroborates the findings of Agiviezor et al. (2012b) who reported a low genetic differentiation fixation index (F_{st}) among the four breeds of sheep, they further attributed this to indiscriminate breeding and shrinkage of grazing area.

Categorising the phenotypic groups based on the discriminating characters is presented in Tables 4 and 5. Rump width (RW) was the only character that was apart between Uda and Balami, it also differentiated between Yankasa and WAD. Distinguishing Yankasa and WAD from Balami, so also distinguishing Yankasa and WAD from Uda could be done with the remaining seven (7) dis-

Table 4. Structure matrix for discriminant functions.

Variables	Functions	
	1	2
Tail length	0.762*	0.094
Hock length	0.703*	0.259
Wither height	0.702*	0.174
Ear length	0.691*	-0.165
Heart girth	0.538*	-0.061
Shoulder width	0.538*	0.087
Rear-leg length	0.376*	0.105
Rump width	0.236	0.677*

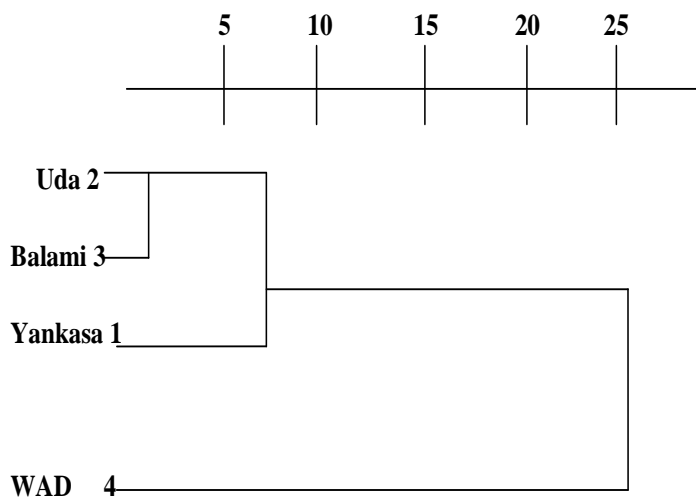
*Functions with significant loadings.

Table 5. Functions at group centroids.

Breed	Function	
	1	2
Yankasa	-0.368	0.256
Uda	0.556	-0.298
Balami	0.319	0.341
WAD	-1.964	-0.417

Table 6. Euclidean genetic distances between phenotypic groups.

	Yankasa	Uda	Balami	WAD
Yankasa	0.00			
Uda	15.07	0.00		
Balami	12.82	4.94	0.00	
WAD	28.18	42.69	40.66	0.00

**Figure 1.** Dendrogram showing diversity and similarity among Nigerian breeds of sheep.

criminating variables in the analysis, which are TL, HoL, WH, EL, HG, SW and RLL. The highest discriminating power of TL here brought to light that the Northern and Southern sheep of Nigeria can best be distinguished with TL. This result is partly in variance with the findings of Salako and Ngere (2002) where TL was obtained as the most discriminating character between Yankasa and WAD sheep but RW was not included in the aforementioned study. Agievezor et al. (2012) also reported tail length, rump height, chest girth, ear length and chest depth as the most discriminating variables to separate WAD, Yankasa, Uda and Balami sheep.

The Euclidian distance is presented in Table 6. Genetic distance is the degree of genomic differences within and between animal populations. It is theoretically obtained as difference in allele frequencies for all loci in animal genome. In this study, genetic distances were derived from the Euclidian distances between the breeds investigated. Longest genetic distance was found between WAD and Uda sheep. The smallest distance of 4.94 was obtained for genetic gap between Uda and Balami sheep. Genetic distance is important to determine the hybrid vigour (heterosis) expected during cross-breeding. The farther two genotypes are the more the improvement that should be expected when they are crossed. From the result of this study, there is room for improvement of the indigenous breeds of sheep especially between Southern and Northern breeds. Uda and Balami sheep were closer to each other than Yankasa and WAD.

This study reveals that greatest improvement should be expected from the cross between Uda and WAD sheep. Though Uda sheep is the second largest breed of sheep in Nigeria Table 1, the highest hypotype diversity reported by Agaviezor et al. (2012b) for this breed shows the prospect of the sheep in response to selection. The pattern of differentiation revealed by the matrix of Nei's genetic distances and the tree topology reflected the evolutionary history, geographical distributions and the gene flow among breeds. Genetic structure of a breed at any time is the result of a balance between genetic drift (founder effect and selection) and gene flow (Farid et al., 2000). Based on the result of this morphometric analysis, Uda and Balami sheep were expected to have shared the highest number of allele while Uda and WAD were expected to share the least number of allele Figure 1. Validating the result of this study with molecular genetics study is critically necessary because many authors have reported deviations from morphological findings when genetic studies were carried out (Ndumu et al., 2008; Agaviezor et al., 2012a).

Conclusion

Distinguishing between breeds of sheep that are indigenous to Nigeria could be best done with length of tail because of the high discriminating power of this cha-

racter. Furthermore, large Euclidian distance obtained for genetic gap between Uda and WAD sheep gives prospect for improvement if they are cross bred. Uda sheep with its large body size has been reared successfully in the hot arid region of Nigeria, thriving under the high ambient temperature. WAD sheep as well thrives in the trypano-endemic region of Southern humid Nigeria. With the wide genetic distance between the two populations, size of the body and trypanotolerance being mediocre in WAD and Uda respectively would be expected to improve in the hybrid.

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