Multivariate analysis of morphostructural characteristics in Nigerian indigenous sheep

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Abstract

The population variability of three breeds of Nigerian sheep was investigated using multivariate discriminant analysis. The sampled populations comprised mature 331 Yankasa, 296 Uda and 166 Balami sheep kept by traditional farmers in northern Nigeria. A total of ten morphological traits (withers height, rump height, body length, face length, rump length, tail length, chest circumference, head width, shoulder width and rump width) were collected on each animal. The univariate analysis revealed that the body measures of Balami sheep were significantly larger (P<0.05) than others with the exception of tail length. Uda sheep also had higher mean values (P<0.05) than their Yankasa counterparts in all the morphological traits analysed. However, the stepwise discriminant analysis revealed that head width chronologically followed by tail length, chest circumference and body length were more discriminating in separating the three sheep populations. The Mahalanobis distance of the morphological traits between Yankasa and Balami sheep was longest (4.83) while the least differentiation was observed between Yankasa and Balami sheep, 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.

The issue of farm animal genetic resources conservation has gained momentum in the last few decades and has become a major activity of regional bodies like European Association of Animal Production (EAAP) and the African Union (AU) and global bodies like the FAO. Documentation of existing genetic resources, including the description of the population phenotypic characteristics, cultural importance and genetic uniqueness is one of the main areas of the livestock conservation activities (Ruane, 1999; Duchev and Groeneveld, 2006). The first phase of characterization involves the identification of populations based on morphological descriptors (Gizaw et al., 2007). Phenotypic comparison based on morphological characters can provide to an extent a reasonable representation of genetic differences among populations. Body measurement can also be used routinely in weight estimation and selection programmes based on its utility in determining breed evolution trends (Sarti et al., 2003; Riva et al., 2004; Araujo et al., 2006).

Materials and methods

Environmental setting of the study location and sheep population

Sampling of sheep was done in Nasarawa, Kaduna, Kano and Borno States, respectively. Nasarawa state falls within the guinea savanna agro-ecological zone of north central Nigeria. It is found between latitudes 7°52’N and 8°56’N and longitudes 7°25’E and 9°37’E, respectively (Lyam, 2000). Kaduna state is found in the sudan savanna zone of north western Nigeria which characteristically experiences the tropical wet-dry climate. Kano state is located in the sudan savanna zone of north western Nigeria. Borno State lies between latitudes 10°N and 13°N and longitudes 12°E and 15°E, respectively.

Morphological measurements were taken on randomly selected 793 sheep comprising 331 Yankasa (102 females and 229 males), 296 Uda (89 females and 207 males) and 166 Balami (65 females and 101 males) sheep of both sexes. They were up to twenty-two months of age as determined by dentition (presence of 4-8 permanent incisors). The animals were subjected to the traditional extensive management system, with little or no provision for shelter in the night. They grazed during the day on natural pasture containing forages such as northern gamba grass (Andropogon gayanus), stylo (Stylosanthes gravis) and leucaena (Leucaena leucocephala). Occasionally, supplements such as cassava and yam peels, cereal offal and crop residues were provided prior and/or after grazing of natural pastures.

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Key words: Sheep, Morphological traits, Discriminant analysis, Conservation, Nigeria.

Received for publication: 26 August 2010.
Revision received: 12 February 2011.
Accepted for publication: 18 February 2011.

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Italian Journal of Animal Science 2011; 10:e17
doi:10.4081/ijas.2011.e17
Adequate health care was virtually non-existent while non-directional breeding was the practice.

Morphological variables measured

The ten morphometric traits measured were withers height (WH), rump height (RH), body length (BL), face length (FL), rump length (RL), tail length (TL), chest circumference (CC), head width (HW), shoulder width (SW) and rump width (RW). The height measurement (cm) was done using a graduated measuring stick. To achieve this, animals were placed on a flat ground and held by two field assistants. The length and circumference measurements (cm) were effected using a tape rule while the width measurements (cm) were taken using a calibrated wooden calliper. Measurements were done in the morning before the animals were released for grazing. All measurements were carried out by the same person, in order to avoid inter-individual variations.

Statistical analysis

Basic statistics for the morphological traits were obtained using PROC UNIVARIATE procedure of SAS (1999), with breed of sheep included 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:

$$Y_{ij} = \mu + \tau_i + c_{it} + e_{ij}$$

where,

- $Y_{ij}$ = record of morphological traits of each animal
- $\tau_i$ = fixed effect of the $i$th breed ($i$ = Yankasa, Uda, Balami)
- $c_{it}$ = random residual error associated with record of each animal

Stepwise discriminant procedure was applied using PROC STEPDISC to determine which morphological traits have more discriminant power than others. The relative importance of the morphometric variables in discriminating the three breeds of sheep was assessed using the level of significance ($P<0.05$) and partial $R^2$ values $\geq 0.01$. The CAN- DISC procedure was used for univariate and multivariate one-way analysis that calculated the Mahalanobis distances of the morphological traits, and derived canonical functions (linear combinations of the continuous variables that summarize variation between the three sheep breeds). The ability of these canonical functions to assign each individual sheep to its breed was calculated as the percentage of correct assignment of each breed using the DISC procedure (Nearest Neighbour Discriminant Analysis).

Results and discussion

Descriptive statistics of the linear body measurements of the sheep are presented in Table 1. The body measures of Balami sheep were consistently larger ($P<0.05$) than the two other breeds apart from TL. Uda sheep also had significantly higher ($P<0.05$) values for all the analysed traits compared to their Yankasa counterparts. This indicates that the Balami sheep is bigger than the two other northern sheep breeds of Nigeria. Sheep breeds exhibit an unusual intra-species polymorphism (Alpak et al., 2009). The present morphological differences as revealed by the univariate analysis are 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 WH and CC values obtained in this study were larger than WHs of 67.4 and 68.0 cm and CCs of 80.0 and 81.3 cm, respectively reported for mature Zulu sheep in South Africa (Kunene et al., 2007). The values were also larger than the 52.7 and 47.0 cm recorded for WH and BL of the Nigerian West African Dwarf (WAD) sheep (Sowande and Sobola, 2008). This is not surprising as the WAD sheep, which occupies mainly the humid zones of southern parts of the country are smaller in stature, although with a comparative advantage of being trypanotolerant.

The result of the stepwise discriminant analysis is presented in Table 2. Seven of the measured variables were found to be significant ($P<0.01$-$P<0.0001$). However, WH chronologically followed by TL, CC and BL had more discriminant power than the others as revealed by their higher $R^2$ and F-values. Therefore, all other variables were removed from the final model. It was done following the method of Dossa et al. (2007). This implies that taking these four basic measurements (HW, TL, CC and BL) consistently could be more important in differentiating between the three Nigerian sheep breeds than acquiring numerous additional measurements. Some of the discriminating variables obtained in the
present study are similar to those reported by earlier workers (Herrera et al., 1996; Dossa et al., 2007; Yakubu and Akinyemi, 2010; Yakubu et al. 2010c) in the morphostructural differentiation of sheep and goats respectively.

The between-breeds Mahalanobis distance matrix is presented in Table 3. Mahalanobis distance was estimated from the mean values of HW, TL, CC and BL. All pairwise distances were significant (P<0.0001). However, the largest distance (4.83) was found between Balami and Yankasa sheep while the smallest distance (1.79) was recorded for Uda and Yankasa sheep. Phenotypic differences are maintained in part by the reduction of gene flow among populations separated by large distances. Adaptive divergence in morphological traits was higher between Balami and Yankasa sheep, and lower between Uda and Yankasa sheep. This indicates that the genetic exchange that has taken place overtime between the latter 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 cross-breeding among local populations. Gizaw et al. (2007) obtained a strong indication of adaptive divergence in morphological characters during the morphometric differentiation of Ethiopian sheep into nine breeds. It could therefore be predicted from the foregoing that a cross between Balami and Yankasa sheep breeds may yield appreciable heterosis, while the mating between their Uda and Yankasa counterparts might not give desirable heterotic gains with regard to most economic traits. In a related study, Traore et al. (2008) reported low differentiation between the Sudan (Djallonke) and Sudan-Sahel (Mossi) sheep using Mahalanobis distance, and attributed this to sustained introgression of the Sahelian sheep.

This is similar to the report of Yakubu et al. (2010b) in the morphometric differentiation of West African Dwarf goats from three agro-ecological zones. Discriminant analysis however, has been used to separate West African Dwarf and Red Sokoto goats into distinct genetic groups with a long Mahalanobis distance of 72.3 (Yakubu et al., 2010a).

The classification of the three breeds into their genetic source is presented in Table 4. Most Balami sheep (61.5%) were classified into their source population. However, the reverse was the case of their Uda and Yankasa counterparts. While 41.2% of Uda sheep were misclassified as Yankasa sheep, 35.4% of Yankasa were wrongly assigned as Uda sheep. The reason that could be adduced for these misclassifications is high degree of intermingling between the two sheep breeds. The genetic admixture could have been brought about mainly by the activities of Fulani pastoralists (Transhumance) of northern Nigeria who moved from one place to another with their flocks in search of pasture and water. Such transhumance has been cited as a dynamic factor of gene exchange (Draganescu, 1997).

Animal genetic resources are components of biological diversity and are important in meeting the food requirement of countries of the world. Between-breed diversity is classically considered as a major criterion to be taken into account when setting priorities for conservation of domestic animal breeds. A comprehensive phenotypic description of Nigerian sheep kept under extensive management conditions would enable their accurate comparison with other sheep breeds, thereby assisting in the development of conservation and improvement programmes. However, further characterization using genetic analyses will consolidate information arising from morphological differentiation. According to Kunene et al. (2009), such phenotypic and genetic data when sensibly combined into a single database could be critical for decisions regarding indigenous sheep breeds’ exploitation and conservation.

Conclusions

The study revealed that HW, TL, CC and BL could best be used to show morphological variation in Yankasa, Uda and Balami sheep. However, the low Mahalanobis distance between Uda and Yankasa at the morphological level could be attributed to the genetic exchange that has taken place between the two populations. The morphological variations obtained in this study should be consolidated with more evidence drawn from genetic analyses using protein and microsatellite markers. The present morphometric information could aid future decision on the management, conservation and improvement of the indigenous sheep genetic resources.

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Table 3. Mahalanobis distance between the three sheep breeds.

| Breed   | Yankasa | Uda | Balami |
|---------|---------|-----|--------|
| Balami  | 4.83    | 2.35|        |
| Uda     | 1.79    |     |        |

Table 4. Percentage of individual sheep classified into genetic group.

| Breed   | Yankasa | Uda | Balami |
|---------|---------|-----|--------|
| Yankasa |          |     |        |
| Uda     |          |     |        |
| Balami  |          |     |        |

[Ital J Anim Sci vol.10:e17, 2011]
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