Principal component and cluster analyses of somatometric traits in four varieties of guinea fowls, *Numidea meleagris galeata* pallas, found in Sokoto State, Nigeria

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Abstract - The population variability of four varieties of guinea fowl (pearl, lavender, black and white) was investigated using principal component and cluster analyses to assess the magnitude of genetic diversity and interdependence of morphological traits. A total of 1,272 adult guinea fowls: 425 pearl, 313 lavender, 271 black and 263 white varieties sourced from smallholders in Sokoto, Balle, Bodinga, Shagari, Goronyo, and Illela villages in Sokoto State, Nigeria were used for the study. Data on body weight (BW), head thickness (HT), helmet length (HL), helmet width (HW), wattle length (WL), wattle width (WW), keel length (KL), body circumference (BC), shank length (SL), shank thickness (ST), drumstick length (DL), thigh length (TL) and wing length (WGL) were collected and analyzed using Principal Component Analysis (PCA) procedure and cluster analysis. The PCA showed extraction of three patterns of variation in lavender, two in each of pearl and black and one in white variety. In lavender, the first principal component explained 61.16% of the generalized variance; in pearl, the first principal component explained 73.38% of the generalized variance; in black, the first principal component explained 67.09% of the generalized variance while the only PCA extracted for the white variety explained 84.48% of the generalized variance. The cluster analysis generated showed close similarities (85%) between the pairs of white and lavender and white and black. The black and lavender are 72% similar; white and pearl 65% similar; lavender and pearl 58% similar and black and white 45% similar. The similarities indices of 58%, 65%, 72% and 85% are sufficient to classify these varieties as one.

Key words: cluster analysis, genetic diversity, guinea fowl varieties, morphometric traits, population variability, principal component, smallholders, Sokoto State

1 INTRODUCTION

Skeletal and muscular increments in size and conformation are twin complex traits under genetic and non genetic factors for assessing growth in farm animals. These biological phenomena in most cases are correlated due to pleiotropic effect of genes and loci linkages [1]. Correlations between body dimensions may be different if the dimensions are treated as bivariates rather than multivariates because of the lack of orthogonality of the explanatory traits. To address this constraint, multivariate analysis of data sets such as the use of principal component factor technique which is a current trend in livestock classification [2], [3] becomes imperative.

Multivariate statistical tools which could be Principal Component or Cluster analyses is a form of statistics encompassing the simultaneous observation and analysis of more than one statistical outcome variable at a time. It is the best way to summarize a data table with many variables by creating a few new variables containing most of the information [4] which has been proved suitable in assessing genetic variation within and between populations [5].

Principal components which is the simplest of the true eigenvector-based multivariate analyses [6] is a mathematical procedure that transforms a number of possibly correlated

variables into a smaller number of uncorrelated variables known as principal components which are ordered so that the first few components retain most of the variation present in the original variables [7]. The results of a PCA are usually discussed in terms of component scores, sometimes called factor scores (the transformed variable values corresponding to a particular data point), and loadings (the weight by which each standardized original variable should be multiplied to get the component score) [8].

Several workers have used Principal component analysis to estimate body weight [9], to establish relationships between body weights and body measurements and among body measurements in different species of poultry [10], [11], [12], [13], [14. Others have used it to determine functional traits [15], as a selection criterion for the improvement of body size [16] and to reduce the number of independent variables in the prediction of genomic breeding values [17].

[18] posited that there are four varieties of Nigeria helmeted guinea fowl: pearl, lavender/ash, black and white based on plumage colour/pattern. Clustering of the morphological traits of the different varieties and the genetic distance will classify the varieties accordingly not only from conservation point of view, but also for using them in population studies.

Cluster analysis (CA) is an exploratory data analysis tool for organizing observed data into meaningful taxonomies, groups, or clusters, based on combinations of variables, which maximizes the similarity of cases within each cluster while maximizing the dissimilarity between groups that are initially unknown. In this sense, cluster analysis creates new groupings without any preconceived notion of what clusters may arise. Cluster analysis provides no explanation as to why the clusters exist neither is any interpretation made. Each cluster thus describes, in terms of the data collected, the class to which its members belong.

Genetic distance refers to the genetic divergence between species or between populations within a species. Smaller genetic distances indicate a close genetic relationship whereas large genetic distances indicate a more distant genetic relationship. Within a species genetic distance can be used to measure the divergence between different sub-species. In its simplest form, the genetic distance between two populations is the difference in frequencies of a trait. The genetic distance of several individual traits can then be averaged to compute an overall genetic distance [19]. Genetic distance varies between 0 and 1. A value of 0 indicates that two populations are genetically identical whereas a value of 1 indicates that two populations are different species. The study is carried out to determine the most important morphometric traits causing variation and to establish the magnitude of genetic diversity in varieties of helmeted guinea fowl for genetic and breeding purposes.

MATERIALS AND METHODS

Description of study areas

The study was carried out in Sokoto State, Nigeria. Sokoto State is located in the extreme northwest of Nigeria, near to the confluence of the Sokoto River and the Rima River. Sokoto State shares its borders with Niger Republic to the North, Zamfara State to the East, Kebbi State to the South-East and Benin Republic to the West.

Research Design

A cross – sectional research design was employed in this study and purposive sampling method was used in selection of sampling sites and sampling. The selected sample sites were Sokoto, Bodinga, Goronyo, Balle, Shagari and Illela.

Animals and management

The indigenous guinea fowl populations were managed under the traditional semi-intensive systems at the backyards of the smallholders. At night, the birds were housed and fed grains like millet, rice, corn, other cereals and broken beans in the morning, just before they were allowed to go out to scavenge for feed. During the day, the birds roam freely finding their own food consisting of insects, leaves, bulbs, seeds, worms etc around the owners' house. No routine health management was administered to the birds.

Data collection

Data were collected on 1,272 adult guinea fowls comprising 425 pearl, 313 lavender, 271 black and 263 white varieties. Data on quantitative traits: body weight (BWT), head thickness (HT), helmet length (HML), helmet width (HMW), wattle length (WL), wattle width (WW), body length (BL), keel length (KL), body circumference (BC), shank length (SL), shank thickness (ST), drumstick length (DL), thigh length (TL) and wing length (WGL) were taken on each of the birds. All measurements were taken in the mornings before the animals were fed and allowed to leave the shelter to scavenge. Each measurement was taken at least twice and the average of the measurements recorded as the value for the trait.

Body weight of individual birds was determined using Mettler Toledo® top loading scale sensitive at 1g. Somatometric traits were determined in *cm* using a measuring tape and vernier caliper. The anatomical reference points for the somatometric traits were the standard procedures in [20], [21], [22]

Body weight: the total weight of the live fowl
Head thickness: the circumference at the middle of the head
Helmet length: the distance between the base of the head to the tip of the helmet
Helmet width: the distance between the broadest part of the helmet
Wattle length: the distance between the base of the beak and the tip of the wattle
Wattle width: the distance between the broadest part of the wattle
Body length: the distance between the posterior end of the pygostyle and the anterior of the nasal openings.
Keel length: the anterior point of keel to the posterior end.
Body circumference: the circumference of the body around the breast region
Shank length: the distance between the foot pad and the hock joint when the tibio-tarsus and tarsometa-tarsus were held at right angles to each other
Shank thickness: the circumference at the middle of the shank
Drumstick length: the hock joint to the tibio-fibula-femora joint.
High length: the distance between the knee and the hip
Wing length: the distance between the tip of the phalanges and the coracoids-humerous joint

Data analysis.

The data were subjected to principal component analysis performed in a single step using the Factor programme of the SPSS – Version 18, 25 Statistical Package. A KMO measure of 0.60 and above was considered adequate [23]. The general form for the formula to compute scores on the components extracted in a principal component analysis were:

$C_1 = b_{11}(X_1) + b_{12}(X_2) + \ldots b_{1p}(X_p)$

$C_2 = b_{21}(X_1) + b_{22}(X_2) + \ldots b_{2p}(X_p)$

$C_3 = b_{31}(X_1) + b_{32}(X_2) + \ldots b_{3p}(X_p)$

Where:

C_1, C_2, C_3 = Decreasing proportions of the total variance in the original variables

b_{11}-b_{1p}, b_{21}- b_{2p} and b_{31}- b_{3p} = the regression coefficient for observed variable p, as used in creating Principal components 1, 2 and 3

x_1 - x_p = The subject's score on observed variable p.

Hierarchical cluster method was used to describe qualitative variables that were similar between varieties of helmeted

guinea fowl with the aid of dendrogram.

RESULTS

Rotated component matrix of Principal Component Analysis (PCA) of guinea fowl varieties

Rotated component matrix of the PCA showing the factor solution of the somaometric traits of guinea fowl is presented in Table 1. Kaiser-Meyer- Olkin measure of sampling adequacy ($p<0.01$) were 0.91, 0.95, 0.89 and 0.95 for lavender, pearl, black and white varieties, respectively. The communalities ranged from 0.42-0.92, 0.46-0.94, 0.73-0.94 and 0.54-0.93 for lavender, pearl, black and white varieties, respectively. The PCA revealed extraction of three discernable patterns of variation by the factor solution in the lavender variety, two in each of pearl and black variety and one in white variety.

In lavender, the first principal component was positive and explained 61.16% of the generalized variance in the body measurements giving emphasis ranging from 0.642 to 0.908 to each body measurement except wing length which gave emphases of 0.374. The second principal components accounted for 10.15% of the generalized variances while the third principal components accounted for 6.25 % of the generalized variances. In lavender, PC 2 had negative loadings in head thickness, helmet length, helmet width, wattle length, body length, body circumference, shank thickness and shank circumference and PC 3 had negative loadings in helmet length, helmet width, keel length, body circumference, shank length, shank thickness, shank circumference, wing length and thigh length.

In pearl, the first principal component explained 73.38% of the generalized variance in the body measurements giving emphasis ranging from 0.89-0.97 to each of the body measurements except shank circumference and drumstick length with emphases of 0.54 and 0.71, respectively. The second principal components accounted for 7.81%. The PC 2 had negative loadings in head thickness, helmet length, helmet width, wattle length and shank thickness.

In black, the first principal component explained 67.09% of the generalized variance in the body measurements giving nearly equal emphasis to each body measurement (0.85-0.97). The second principal components accounted for 19.30% of the generalized variance with negative loadings in keel length, body circumference, shank length, thickness and circumference, drumstick length, wing and thigh lengths.

The only PCA extracted for the white variety was positive and explained 84.48% of the generalized variances giving emphasis of between 0.85 and 0.97 as loading strengths of all the original variables.

DISCUSSION

Kaiser-Meyer- Olkin measure of sampling adequacy which reveals the proportion of the variance in the body measurements caused by the underlying factor was high for all the morphometric traits (0.91, 0.95, 0,89 and 0.95 for lavender, pearl, black and white varieties of guinea fowl, respectively) indicating that true factors existed in the data sets. The Bartlett's Test of Sphericity for the body measurements of the four varieties were significant ($p<0.01$) thus providing additional support for the validity of the factor analysis of the data sets. The communalities, which represent the proportion of the variance in the original variables that is accounted for by the factor solution ranged from 0.42-0.92 , 0.46-0.94, 0.73-0.94 and 0.54-0.93 for the lavender, pearl, black and white varieties, respectively. The high communalities obtained for the four varieties of guinea fowl indicated that PCA was appropriate for the data sets thus permitting all the measurements into reasonable factor analysis. The adequate values obtained in this study may probably be related to the different associations of each measurement with bone, environmental components or the time taken to reach maturity [24].

Positive loadings indicate that a variable and a principal component are positively correlated: an increase in one results

in an increase in the other. Negative loadings indicate the reverse, a negative correlation. The magnitude of variation for a given character dictates the kind of breeding plan that would be employed for the improvement [10]. Thus genetic improvement in body weight can be achieved faster by selecting for head circumference, head thickness, helmet length, helmet width, wattle length, body length, keel length, body circumference, shank length, and thigh length in all the varieties which have direct and positive relationship with body weight.

The present results agree with those reported by [25] in rabbits, [26] in musk ducks, [24] in immature Uda Sheep, [13] in Muscovy duck, [27], [9] in ruminants, [28] in Nigerian indigenous chickens, [11] in Arbor Acre broilers, [29] in Ross 308 broilers and [30] in guinea fowl who reported that the first factor accounted for the largest variance with high positive loadings and reduced percentage of variance explained with subsequent loadings. However, this result disagrees with the report of [30] that body length, neck length shank length and wing span are the common variability in indigenous guinea fowl.

The factor pattern coefficients were used to assess the relative contributions of the various body measurements in determining the numerical value of the principal components. The three principal components obtained for pearl and white varieties and the two components for each of pearl and black could equally be important as one obtained for white variety in appraising animals for breeding and selection purposes. This is partly because the elements present in each component probably have common genomic sites for their genetic control and also because the correlation between principal components is perpendicular or orthogonal, therefore selection of animals for any principal component will not cause correlated response in terms of other principal components [16].

Morphological cluster analysis of the four varieties of guinea fowl

The morphological parameters of the four varieties were used to generate a dendrogram by means of UPGMA cluster analysis and the results are presented in Figures 1-3. The cluster analysis generated showed similarity coefficients which ranged from 0.45 to 0.85. The highest similarity index occurred between white and lavender varieties and between white and black varieties with a coefficient value of 0.85 and the lowest index of similarity occurred between black and white varieties with a coefficient value of 0.45. The detailed similarity index between black and pearl; white and lavender; lavender and pearl; white and black; black and lavender and white and pearl were 0.45, 0.85, 0.58, 0.85, 0.72 and 0.65, respectively as encapsulated in the figures below.

The result of this study thus show close similarities (85%) between the pairs of white and Lavender and White and Black. The Black and Lavender are 72% similar; White and Pearl 65% similar; Lavender and Pearl 58% similar and Black and White 45% similar. The similarities indices of 58%, 65%, 72% and 85% are sufficient to classify these varieties as one. This finding is inconsistent with the report of [31] that the varieties of helmeted guinea fowl were clearly separated from one another. It also disagrees with the reports of several other authors that plumage colour is the basis for classification of helmeted guinea fowl [32], [33], [34], [35], [36].

Conclusion

i. The aggregation of morphometric traits into factors was variety dependent. In lavender, three factors were obtained which contributed 77.56% of the total variance, in pearl two factors were obtained which contributed 81.19% of the total variance, in black, two factors were obtained which contributed 86.39% of

the total variance and in white, only one factor was obtained which contributed 84.48% of the total variance.

ii. The close similarity among the varieties suggests that they are similar only differing in plumage colour.

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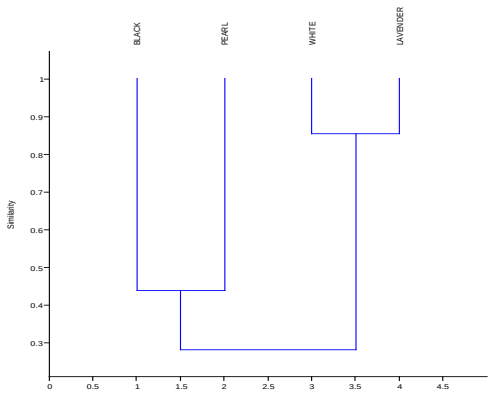

Figure 1. Cluster analysis of the morphometrical variables showing genetic relationship between Black and Pearl and between White and Lavender varieties

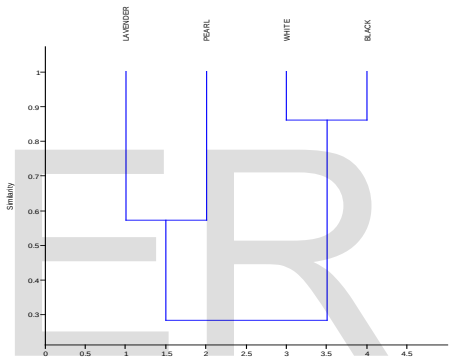

Figure 2. Cluster analysis of the morphometrical variables showing genetic relationship between Lavender and Pearl varieties and between White and Black varieties

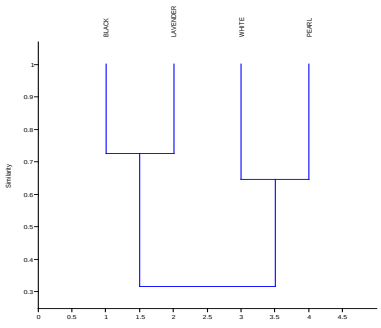

Figure 3: Cluster analysis of the morphometrical variables showing genetic relationship between Black and Lavender varieties and between White and Pearl varieties

Table 1. Rotated component matrix of the PCA showing the factor solution of the biometric traits of guinea fowl

	Lavender			Pearl		Black		White
Parameters	**PC 1**	**PC 2**	**PC 3**	**PC1**	**PC 2**	**PC1**	**PC2**	**PC 1**
Body weight	**0.908**	**0.262**	**0.021**	**0.93**	**0.26**	**0.76**	**0.39**	**0.93**
Head circumference	**0.862**	**0.398**	**0.021**	**0.97**	**0.00**	**0.76**	**0.46**	**0.93**
Head thickness	**0.802**	**-0.362**	**0.050**	**0.91**	**-0.27**	**0.73**	**0.64**	**0.85**
Helmet length	**0.901**	**-0.258**	**-0.006**	**0.90**	**-0.34**	**0.85**	**0.48**	**0.97**
Helmet width	**0.799**	**-0.510**	**-0.010**	**0.89**	**-0.32**	**0.80**	**0.44**	**0.85**
Wattle length	**0.805**	**-0.226**	**0.059**	**0.90**	**-.294**	**0.74**	**0.62**	**0.88**
Body length	**0.818**	**-0.457**	**0.013**	**0.91**	**0.32**	**0.84**	**0.51**	**0.93**
Keel length	**0.767**	**0.563**	**-0.017**	**0.94**	**0.12**	**0.83**	**-0.42**	**0.90**
Body circumference	**0.786**	**-0.023**	**-0.037**	**0.92**	**0.28**	**0.87**	**-0.33**	**0.93**
Shank length	**0.908**	**0.308**	**-0.002**	**0.91.**	**017**	**0.86**	**-0.40**	**0.95**
Shank thickness	**0.796**	**-0.152**	**-0.025**	**0.89**	**-0.31**	**0.84**	**-0.49**	**0.90**
Shank circumference	**0.893**	**-0.133**	**-0.063**	**0.54**	**0.41**	**0.81**	**-0.30**	**0.92**
Drumstick length	**0.642**	**0.060**	**0.045**	**0.71**	**0.21**	**0.84**	**-0.32**	**0.91**
Wing length	**0.374**	**0.326**	**-0.366**	**0.90**	**0.23**	**0.89**	**-0.18**	**0.97**
Thigh length	**0.881**	**0.305**	**-0.027**	**0.92**	**0.26**	**0.88**	**-0.33**	**0.95**