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Research Article
Morphological Characterization of Nigerian Chicken Genotypes Using Multivariate Analyses

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Abstract

Background and Objective: Nigerian indigenous chickens play a vital role in food security. This study aimed to determine the relationship between morphometric traits, predict body weight and classify three Nigerian indigenous chicken genotypes using multivariate analyses. **Methodology:** Data were obtained from a total of 808 randomly selected, matured and extensively reared Nigerian indigenous chickens, comprised of 490 normal feathered (NF), 170 frizzle feathered (FF) and 148 naked neck (NN) genotypes. **Results:** The phenotypic correlation between the morphometric traits ranged from 0.08-0.74, -0.11-0.76 and 0.03-0.77 for NF, FF and NN, respectively, with breast girth and tibia length being the most correlated to body weight. Three principal components from the factor analysis of morphometric traits explained about 75-84% of the total variance across genotypes. Regression models using original morphometric traits as predictors explained 44-65% of the variation in body weight across the genotypes, while orthogonal traits explained 29-62%. The discriminant analysis revealed some intermingling between the NF and NN genotypes, while NF and FF were almost distinct. **Conclusion:** We concluded that some morphometric traits could serve as markers for body weight but are genotype specific. The intermingling between NF and NN suggests that there is unrestricted gene flow and intermingling between NF and NN, which may pose a threat regarding genetic conservation.

Competing Interest: The author has declared that no competing interest exists.

Data Availability: All relevant data are within the paper and its supporting information files.

INTRODUCTION

Indigenous chickens play a vital role in rural economies of developing countries[1]. Although, they are inferior in body weight, egg production and feed conversion compared to exotic chickens[2], they are preferred for their adaptation to local climatic conditions, disease resistance, meat quality and scavenging ability[1]. Due to their enormous variations in performance traits, Horst[3] and Padhi[4] described indigenous chickens as genetic reservoirs that could be used to develop genetic stocks with improved disease resistance, growth, reproductive and morphological traits.

Improvement in growth traits (e.g., body weight) of indigenous chickens is necessary due to climate change and the inability of exotic chickens to adapt to harsh tropical environmental conditions. According to FAO[5], the rate of genetic gain depends on the amount of genetic variability (diversity) in the population, generation interval, selection criteria and intensity. Therefore, evaluation of the genetic diversity of indigenous chickens is crucial and forms the basis for designing breeding programmes and making rational decisions on the sustainable use of animal genetic resources[6].

Genetic diversity is evaluated using morphological, biochemical and molecular characterisation methods. Morphological characterisation is inexpensive and assesses the environmental influence on traits[7]. Also, some morphological characters, such as morphometric traits, are correlated with body weight[8,9]. Thus, such morphometric traits could be used as markers in body weight improvement programmes and as body weight predictors. Traditional linear regression yields less reliable results in characterisation and prediction under the univariate assumption due to multicollinearity. On the other hand, multivariate techniques (e.g., principal component, multivariate regression and canonical correlation analyses) yield more reliable predictions and classification.

Many studies on multivariate analyses in Nigerian indigenous chickens have been conducted at various locations[8,9]; however, there is lack of information on similar studies in the Adavi Local Government Area (LGA) of Kogi State. Consequently, there is a need for more information, as every ecological niche is peculiar. Therefore, the present study was designed to ascertain the magnitude of genetic diversity in Nigerian indigenous chicken genotypes in Adavi LGA and predict the body weight from some morphometric traits in Nigerian indigenous chickens. The results of this study could be useful in indigenous chicken conservation and body weight improvement programmes in tropical conditions.

MATERIALS AND METHODS

Experimental location and design: The present study was carried out at Adavi LGA of Kogi State, Nigeria. Adavi is located between 7°36' north longitude and 6°12' east latitude in the southern Guinea savannah ecological zone of Nigeria. Data were collected during the same time period using a cross-sectional research design and study areas were chosen using a purposive sampling method.

Data collection: Morphological data were collected from a total of 808 male and female chickens, comprised of three genotypes: normal feathered (NF), frizzle feathered (FF) and naked neck (NN). The birds were randomly selected, extensively reared and more than five months of age. The birds were sampled from the Nagazi, Ogaminana, Inoziomi, Osisi and Kuroko areas of Adavi LGA of Kogi State, Nigeria. Body weight of individual birds was determined using a top loading scale sensitive at 1 g. All morphometric traits were measured in centimetres using a tape ruler as used by Gueye *et al*.[10] and Fayeye *et al*.[11]:

- **Breast girth (BG):** The circumference of the chest from under the wings
- **Wing length (WINGL):** The distance from the scapula joints to the last digit of the wing
- **Tibia length (TL):** The length between posterior aspects of the hock joint to the foot pad
- **Comb length (CL):** The horizontal distance from the beginning to the end of the comb
- **Comb height (CH):** The highest vertical distance from the comb attachment point to the tip
- **Wattle length (WL):** The horizontal distance from the beginning to the end of the wattle
- **Wattle height (WH):** the vertical distance from the attachment point to the tip

Statistical analysis: A preliminary analysis was performed to determine the homogeneity of variances using a Levene's test. All variances were unequal between groups. Hence, multiple one-way analyses of variances were performed and a Welch robust test was used to identify the effect of genotype and sex on the morphometric traits at the 5% level of significance. A Games-Howell post hoc test was used, due to unequal sample sizes, to identify significant differences between groups[12].

After data for both sexes were pooled, the strength of the linear relationship between morphometric traits was estimated using Pearson's coefficient of correlation. Principal

component analysis (PCA) was performed to determine the morphometric traits that explain the highest percentage of the total phenotypic variance. Principal component analysis linearly transforms a set of original variables into new sets of variables, called principal components (PC)[13]. These new sets of variables are ordered in such a way that they explain the percentage of the total phenotypic variance in a decreasing order[13]. PCA, in matrix notation, can be defined as:

$$Y = A' X$$

where, Y contains the new sets of variables (PC), A contains the standardized weights and X contains the original variables. Bartlett's test was used to determine the significance of the relationship between the traits.

We performed stepwise multiple regressions to predict body weight from the morphometric traits and PC factor scores using the following models:

$$BW = a + b_i X_i + ... + b_n X_n$$

$$BW = c + d_i PC_i + ... + d_n PC_n$$

where, BW is the body weight, a and c are the intercepts, b_i and d_i are the ith partial regression coefficients of the ith morphometric trait and principal component and X_i and PC_i are the ith morphometric trait and principal component, respectively.

All the morphometric traits were subjected to a stepwise discriminant procedure to determine which combinations of morphometric traits best separate the three genotypes[12]. A stepwise discriminant procedure builds a discrimination model step by step and a morphometric trait that contributes the most to the discrimination between the chicken genotypes is added at each step. The discriminating ability of each morphometric trait was evaluated using p-value and F-to-remove statistics, while the collinearity between the traits

was estimated by tolerance statistics. Then the chickens were separated into genotype groups using the discriminant model. The ratio of genotypes predicted by the discriminant model to the actual genotype was multiplied by 100 to obtain the percentage of correctly classified individuals. The accuracy of classification was obtained by cross-validation. All analyses were carried out using SPSS[14].

RESULTS

Results of the present study showed that significant variation exists in body weight and some morphometric traits. It was also observed that genotype and sex significantly (p<0.05) affected the morphometric traits of indigenous chickens (Table 1). The NF chickens had significantly higher means for the morphometric traits compared to NN, while FF chickens had the least (Table 1). Values for all the morphometric traits were significantly (p<0.05) higher in males than females (Table 1).

The correlation coefficients between body weight and morphometric traits varied significantly in magnitude and across the genotypes (Table 2). Among all morphometric traits, BG had the highest correlation with BW, with a coefficient of 0.65, 0.74 and 0.72 in NF, FF and NN genotypes, respectively. TL followed BG and was consistent across all genotypes. However, the correlation between BW and the other morphometric traits were not consistent across genotypes.

Table 3 shows the PCA for Nigerian indigenous chicken genotypes. The communalities (column 5) for NF, FF and NN genotypes ranged from 0.73-0.90, 0.46-0.96 and 0.79-0.93, respectively. The three principal components extracted explained 80.66, 74.49 and 83.81% of the total variation in NF, FF and NN genotypes, respectively. Each PC showed variation across the genotypes regarding loadings. For instance, PC1 loaded BG, TL and WL in the NF genotype (column 2); CH, CL and WH in the FF genotype and WINGL and CH in the NN

Table 1: Least square means ($\pm$standard error) of morphometric traits of Nigerian indigenous chickens

Traits	Genotypes			Sex	
	Normal feathered (n = 490)	Frizzle feathered (n = 170)	Naked neck (n = 148)	Male (n = 545)	Female (263)
Body weight (g)	1317.68±19.95ᵃ	920.58±30.32ᶜ	1050.75±31.18ᵇ	1199.55±20.46ᵃ	993.12±24.39ᵇ
Breast girth (cm)	24.41±0.21ᵃ	18.90±0.31ᶜ	21.76±0.32ᵇ	22.88±0.21ᵃ	20.50±0.25ᵇ
Tibia length (cm)	8.85±0.08ᵃ	7.60±0.13ᶜ	8.51±0.13ᵇ	8.83±0.09ᵃ	7.81±0.10ᵇ
Wing length (cm)	19.51±0.12ᵃ	17.66±0.18ᶜ	17.75±0.18ᵇ	20.03±0.12ᵃ	16.57±0.144ᵇ
Wattle height (cm)	2.48±0.04ᵃ	1.13±0.06ᶜ	1.37±0.06ᵇ	2.29±0.03ᵃ	1.03±0.05ᵇ
Wattle length (cm)	4.11±0.06ᵃ	1.68±0.09ᶜ	2.15±0.09ᵇ	2.96±0.06ᵃ	2.33±0.07ᵇ
Comb height (cm)	4.58±0.14ᵃ	2.23±0.21ᶜ	2.59±0.22ᵇ	5.05±0.14ᵃ	1.12±0.17ᵇ
Comb length (cm)	5.54±0.08ᵃ	3.09±0.13ᶜ	2.99±0.13ᵇ	4.82±0.09ᵃ	2.92±0.10ᵇ

Means with different superscripts in the same row are significantly (p<0.05) different, n: No. of observations

Table 2: Coefficient of correlation between body weight and linear parameters of Nigerian indigenous chicken genotypes

Traits	Body weight	Breast girth	Tibia length	Wing length	Wattle height	Wattle length	Comb height
Normal feathered							
Breast girth	0.74*						
Tibia length	0.64*	0.72*					
Wing length	0.38*	0.34*	0.42*				
Wattle height	0.32*	0.27*	0.19*	0.11			
Wattle length	0.16*	0.08	0.12	0.14	0.21*		
Comb height	0.26*	0.30*	0.27*	0.27*	0.68*	0.25*	
Comb length	0.25*	0.22*	0.10	0.28*	0.50*	0.16*	0.59*
Frizzle feathered							
Breast girth	0.65*						
Tibia length	0.63*	0.56*					
Wing length	0.34*	0.53*	0.60*				
Wattle height	0.50*	0.35*	0.22*	0.44*			
Wattle length	-0.08	0.24*	0.35*	0.41*	0.12*		
Comb height	-0.11*	0.25*	0.48*	0.58*	0.26*	0.67*	
Comb length	0.46*	0.22*	0.07	0.29*	0.76*	0.27*	0.22*
Naked neck							
Breast girth	0.72*						
Tibia length	0.50*	0.69*					
Wing length	0.39*	0.42*	0.59*				
Wattle height	0.48*	0.31*	0.40*	0.62*			
Wattle length	0.35*	0.44*	0.33*	0.37*	0.45*		
Comb height	0.41*	0.48*	0.63*	0.75*	0.77*	0.35*	
Comb length	0.33*	0.05	0.03	0.15	0.64*	0.31*	0.19*

*p<0.05

Table 3: Factor loadings, communalities, eigenvalues and proportion of total variance of factors

	PC 1	PC2	PC 3	Communality
Normal feathered				
Breast girth	**0.83**	-0.01	0.21	0.72
Tibia length	**0.78**	0.34	-0.06	0.73
Wing length	**0.72**	0.41	0.26	0.75
Wattle length	0.11	**0.90**	0.10	0.82
Comb height	0.29	**0.85**	0.11	0.83
Comb length	0.01	0.18	**0.93**	0.90
Wattle height	0.28	0.04	**0.90**	0.89
Eigen values	3.26	1.41	0.98	
Percentage of total variance (%)	46.56	20.10	14.01	
Cumulative (%)	46.56	66.66	80.67	
Frizzle feathered				
Breast girth	0.19	**0.85**	-0.08	0.77
Tibia length	0.06	**0.91**	0.02	0.83
Wing length	0.14	0.63	0.21	0.46
Wattle length	0.14	0.07	**0.97**	0.97
Comb height	**0.85**	0.22	0.14	0.79
Comb length	**0.81**	0.09	0.05	0.67
Wattle height	**0.85**	0.11	0.06	0.73
Eigen values	2.85	1.45	0.91	
Percentage of total variance (%)	40.77	20.67	13.05	
Cumulative (%)	40.77	61.44	74.50	
Naked neck				
Breast girth	0.35	**0.83**	-0.08	0.82
Tibia length	0.65	0.59	-0.14	0.79
Wing length	**0.85**	0.21	0.13	0.79
Wattle length	0.07	**0.74**	0.48	0.79
Comb height	**0.90**	0.22	0.19	0.89
Comb length	0.07	0.02	**0.92**	0.86
Wattle height	0.67	0.13	0.68	0.93
Eigen values	3.69	1.34	0.83	
Percentage of total variance (%)	52.76	19.13	11.92	
Cumulative (%)	52.76	71.89	83.81	

PC1, PC2, PC3: Principal components 1, 2 and 3, respectively. Variables with strong associations (r>0.70) with the principal components are in bold

genotype. PC2 (column 3) loaded WL and CH in NF, BG and TL in the FF genotype and BG and TL in the NN genotype. PC3 (column 4) mainly loaded CL and WH in the NF genotype but loaded WL and CL in the FF and NN genotypes.

BG explained most of the variation in body weight (ranging from 42-55%) across the genotypes when morphometric traits were used as predictors (Table 4). The proportion of explained variance increased (ranging from 58-65%) with the addition of other morphometric traits to the models. On the other hand, PC1 explained 28-49% of the variation in BW across genotypes when principal component factor scores were used as predictors. The proportion of explained variance improved (range of 44-62%) with the addition of other factor scores to the model.

The result of the stepwise discriminant analysis revealed that the combination of WL, WH, CH, BG, CL and TL, in decreasing order of discriminating ability (as shown by the Wilk's Lambda and F-to-remove value), constituted the discriminant model used to separate the chickens into genotypes (Table 5).

Table 6 presents the classification of Nigerian indigenous chickens into genotypes using discriminant analysis. The

Table 4: Stepwise multiple regression of body weight on morphometric traits and their principal component (PC) factor scores in chickens

Models	SE	R^2
Normal feathered chickens (Morphometric traits as predictors)		
• BW= -450.91+72.91BG	3.85	0.42
• BW= -688.65+64.63BG+72.32CL	7.00	0.53
• BW = -728.51+73.19BG+85.90CL-44.35CH	3.47	0.65
Orthogonal traits as predictors		
• BW = 1386.35+237.14PC1	16.62	0.29
• BW = 1386.35+237.14PC1+209.74PC2	13.66	0.53
• BW = 1386.35+237.14PC1+209.74PC2-134.33PC3	12.24	0.62
Frizzle feathered chickens (Morphometric traits as predictors)		
• BW = -60.90+50.36BG	3.55	0.55
• BW = -114.21+39.70BG+33.92TL	11.36	0.57
• BW = -110.98+37.17BG+34.15TL+57.99WH	22.80	0.58
Orthogonal traits as predictors		
• BW = 850.148+158.02PC1	12.34	0.49
• BW = 850.148+158.02PC1+49.25PC2	11.78	0.54
Naked neck chickens (Morphometric traits as predictors)		
• BW = 110.58+44.33BG	3.58	0.51
• BW = -55.89+43.42BG+54.01CL	9.84	0.60
• BW = -16.40+40.73BG+35.88CL+49.61WH	23.51	0.61
Orthogonal traits as predictors		
• BW = 1100.96+144.51PC1	19.11	0.28
• BW = 1100.96+144.51PC1+91.94PC2	17.59	0.40
• BW = 1100.96+144.51PC1+91.94PC2+59.47PC3	16.94	0.44

PC1, PC2, PC3: Principal components 1, 2 and 3, respectively, BG: Breast girth, TL: Tibia length, CH: Comb height, CL: Comb length; WH: Wattle height

Table 5: Stepwise discriminant analysis of Nigerian indigenous chicken genotypes

Variables	Wilk's Lambda	F-to-remove	Tolerance
Wattle length	0.38	160.61	0.52
Wattle height	0.32	62.16	0.38
Comb height	0.29	19.28	0.46
Breast girth	0.28	10.98	0.66
Comb length	0.28	4.69	0.42
Tibia length	0.28	3.86	0.58

Table 6: Classification of Nigerian indigenous chicken into genotypes using discriminant analyses

| Genotypes | Predicted group membership | | | |
	Normal feathered	Frizzle feathered	Naked neck	Total
Original count (%)				
Normal feathered	87.6	0.0	12.4	100.0
Frizzle feathered	1.8	83.9	14.3	100.0
Naked neck	28.4	7.4	64.2	100.0
Cross-validated count (%)				
Normal feathered	87.6	0.0	12.4	100.0
Frizzle feathered	2.0	83.3	14.7	100.0
Naked neck	29.1	7.4	63.5	100.0

81.1% of original grouped and 80.6% of the cross-validated grouped cases were correctly classified
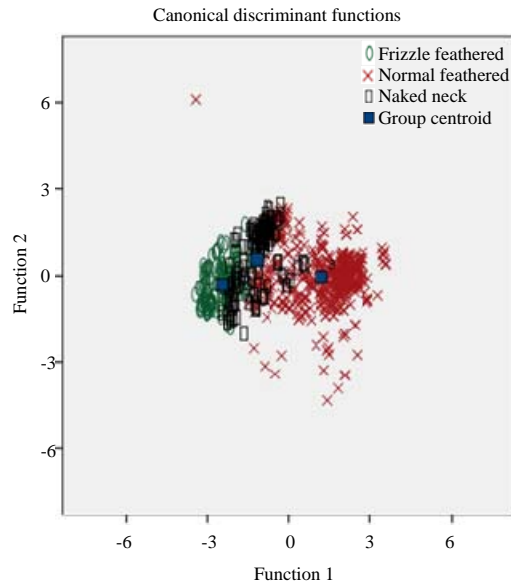
Fig. 1: Discriminant function showing the relationship and distribution between Nigerian chicken genotypes

discriminant function correctly classified 87.6, 83.3 and 63.5% of NF, FF and NN genotypes, respectively. For the NF genotype, 87.6% of the NF chickens were correctly classified while 0 and 12.4% were misclassified as FF and NN genotypes, respectively. However, for the NN genotype, 29.1% was misclassified as NF while 7.4% was misclassified as FF. The results suggest that the NF and NN genotypes are similar in morphometric traits while the NF and FF genotypes are almost distinct as depicted in Fig. 1.

DISCUSSION

The observed higher body weight in the NF than in the NN and FF genotypes (Table 1) agrees with earlier reports[15,16] for adult birds but disagrees with the report of Ajayi *et al.*[8]. The discrepancy in these results could be attributed to the difference in age, location and sample size of the birds. We expected animals with the FF and NN genotypes to have higher body weights than those with the NN genotype because several studies suggest that naked neck and frizzle genes are associated with the potential for faster growth[15,16]. However, Olutunmogun[16] reported that despite the fast initial growth in the NN and FF genotypes, the NF genotype overtakes the NN and FF genotypes beyond 20 weeks of age. This trend was observed when these genotypes were studied from 0-32 weeks of age and could not have been observed at 12 weeks of age as studied by Ajayi *et al.*[8]. The higher values

recorded for morphometric traits in NF genotypes point out that they have larger body frames. Therefore, the choice of genotype for genetic improvement programmes depends on the breeding purpose. The observed higher body weight in males agrees with earlier reports[8,11], as well as the principle of sexual dimorphism in Gallus birds, where males are bigger than their female counterparts.

High and significant correlations in BG and TL with BW were observed (Table 2). Therefore, selecting birds based on BG and TL will invariably improve BW. Also, BG and TL may provide a more realistic prediction of body weight compared to other morphometric traits studied.

The measure of sampling adequacy, which determines the reliability of the PCA, was above the recommended limit of 0.50[17]. The high communality values obtained in this study (Table 3) are similar to those obtained by Egena *et al.*[18] in extensively raised Nigerian indigenous chickens. Like other phenotypic studies[8,19,20] in poultry that utilized PCA, PC 1 explained the largest percentage of the variance in all of the genotypes. The application of principal component analysis helped to reduce the dimension of the predictors (morphometric traits) into three principal components. This provided a better understanding of the magnitude of the relationship between traits as many of the morphometric traits could be redundant due to multicollinearity. The variations in the morphometric traits loaded on the PCs across the genotypes suggests that care should be taken when making selection decisions, given that these traits are genotype specific.

Our finding that BG explained most of the variation in BW across the genotypes when morphometric traits are used as predictors (Table 4) agrees with the findings of Ajayi *et al.*[8]. However, the amount of variance in body weight explained by BG in this study (ranging from 42-51%) were lower than 71% and 84% reported for the FF and NN genotypes[8]. The discrepancy in results could be due to age and method of rearing the birds. Although the use of principal component factor scores led to a reduction in the explained variance, we believe these results are more realistic than those from the original morphometric traits, given the tendency of original variables to be correlated. Principal component factor scores transform interdependent original measurements into uncorrelated variables, thus eliminating multicollinearity associated with interdependent predictors[13].

The findings of the present study that WL and WH were the most discriminating variables disagrees with Ajayi *et al.*[8], who reported breast girth and keel length as the most discriminating variables in intensively reared Nigerian

indigenous chicken genotypes (Table 5). The discrepancy observed in discriminating variables could be due to differences in age, method of raising the birds, sample size and the number of variables measured.

The high accuracy of the discriminant function used to correctly classify the chickens into genotypes suggests its suitability in phenotypic characterisation of breeds and strains. It could be particularly useful in differentiating strains or nondescript breeds. The similarity between NF and NN genotypes points to the absence of selection, unrestricted gene flow and random mating (Table 6 and Fig. 1). According to the inhabitants of the study areas, the NF and NN genotypes were the most preferred and predominant genotypes. Thus, the chances of mating between the NF and NN genotypes are higher compared to the FF genotype, which has a much smaller population size. Unrestricted gene flow and random mating, if unaddressed, could pose a threat regarding genetic conservation[21] and could also erode the genetic variability between these genotypes, thereby reducing heterosis in breeding programmes.

We acknowledge that recent genetic diversity studies use biochemical and molecular characterisation methods, rather than morphological characterisation methods. Morphological characterisation methods are inexpensive and are required to detect variable traits between and within genotypes. These variable traits are then exploited to identify key genes and their mode of inheritance, to increase the rate of genetic gain. In developing countries, trait improvement programmes rely on morphological characterisation methods because biochemical and molecular characterisation methods are expensive. Nevertheless, genetic diversity of Nigerian indigenous chickens using biochemical and molecular characterisation methods awaits evaluation. Although several multivariate studies have been carried out on Nigerian indigenous chicken genotypes, the results of this study confirm that animals in each environment are unique and discoveries from other environments may be inapplicable.

CONCLUSION

The present study revealed significant variation in body weight and the interdependency of seven original morphometric traits in normal, frizzle and naked neck Nigerian indigenous chicken genotypes. It was observed that some morphometric traits could serve as markers for body weight but are genotype specific. Therefore, management decisions based on these traits should be cautious. Also, wattle length

and height were the most discriminating variables between the genotypes. The findings of this study could be applied in developing countries to develop strains with improved body weight and tolerance to tropical conditions. Morphometric methods could be combined with genomic selection to increase the rate of genetic gain.

SIGNIFICANCE STATEMENT

This study discovers the possible genetic diversity of Nigerian indigenous chicken genotypes that can be beneficial for body weight improvement. This study will help researchers to uncover the critical areas in the use of multivariate analysis in the genetic evaluation that many researchers were not able to explore. Thus, a new theory on management, characterisation and conservation of chicken genetic resources may be developed.

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