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BODY WEIGHT AS A DISCRIMINANT FACTOR AMONG THREE BREEDS OF THE NIGERIAN LOCAL CHICKEN

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ABSTRACT

The body weights (BWT) of three different breeds of the Nigerian local chicken were monitored in order to ascertain their validity as markers and genotype discriminants. 139 day-old local chickens comprising of 45, 42 and 52 naked neck, frizzle and normal genotypes respectively generated from 36 adult local chickens of three different genotypes, were used in a 24 – weeks experiment. Results showed that the normal genotypes had significantly ($p < 0.05$) highest mean values and were superior to the frizzle and naked neck genotypes. Breed centroid obtained were opposing (-.386, .372 and .564) BWT, which indicate that the genotypes were different and were rightly classified as different varieties/breeds. The classification results indicated that 49.9% and 60.8% based on BWT of original cases for naked neck frizzle and normal, respectively were correctly classified. The results of this study indicate that the naked neck, frizzle and normal genotypes are distinctly different from each other and could be classified as different varieties using body weight as a discriminating factor..

KEYWORDS: Body weight, discriminant, Frizzle, Naked neck and Normal.

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INTRODUCTION

Growth rate is expressed as changes in body weight over time and is highly heritable. Growth is a compound trait influenced by genetic and management especially nutrition and health. The recognized importance of local chickens in providing meat, cash income and socio-cultural values to rural people and their efficient scavenging system has led to increased research on the species during the past 10 years [4], little or no investment into the system, cost of production of local chicken is low, makes use of by-products resources and is thus efficient [1]. The Nigerian local chicken is characterized by poor growth and small body size which are not desirable in competitive economic situation [6, 11]. The village scavenging condition is variable without standard husbandry system [7]. Performance of local chickens is thus also variable under traditional production system and knowledge of their production potential is also essential [13]. this knowledge can guide sound formulation of strategies to improve local chickens. As a result of indiscriminate random mating and unconscious upgrading between the local chickens and the exotic ones, a pool of heterogeneous individuals that differ in adult body size, weight and plumage have resulted. In spite of their large population, the local chickens have been abandoned in the hands of resource poor rural farmers who rear them under the traditional management system where they scavenge for food for survival. Efforts to characterize them into different breeds or strains to assess their growth and production potential have been difficult due to indiscriminate random mating among the local chickens and their exotic counterparts. This has led to existence of morphologically different types of the local chickens, which are non-descript. Animal Breeders can achieve very little in terms of genetic improvement, thus some categorical characterization of these chickens is

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desirable to change their genetic profile through different breeding strategies due to the existence of genetic variation. Thus the objective of this work is to determine body growth as a factor in discriminating among the three genotypes of the Nigerian local chickens.

MATERIALS AND METHODS

The experiment was carried out at the Poultry Unit of the Teaching and Research Farm, Michael Okpara University of Agriculture, Umudike, Abia State of Nigeria. Umudike lies between latitude 5°29'N and longitude 7°33' E on an altitude of 122m above sea level. Located within the tropical rainforest zone with a bimodal rainfall pattern and total rainfall range of 1700mm – 2100mm. Umudike has maximum and minimum daily temperature of 26.0 – 36.0°C and 18.0 – 23.0°C respectively and relative humidity of 57.0 – 91.0%. The environment is characterized by an annual rainfall of about 2177m [8]. The experiment lasted for a period of 8 weeks. A total of 139 day – old chicks comprising 45, 42 and 52 of the naked neck frizzle normal feathered birds respectively, were produced from the base population chickens. Eggs produced, were set in the incubator on weekly basis and hatched in six consecutive batches. The resulting progeny chicks were properly identified on hatching and were brooded in three small metal cages, each hatch for a period of 2 weeks after which they were transferred to deep litter pens. Commercial feed and fresh clean water were given *ad libitum* to the chicks during this period.

Data on body weight were taken weekly using a weighing balance, and was subjected to analysis of variance (ANOVA) in a randomized complete block design (RCBD). Means were separated using Duncans Multiple Range test [3] to detect significant difference in means of various genotypes. Discriminant analysis was performed using parameters that showed significant difference with genotype as the discriminating factor. Discrimination models and group centroids were determined and used for discrimination and [14] was used for the analysis.

RESULTS AND DISCUSSIONS

Univariate analysis of variance (ANOVA) revealed significant ($P < 0.05$) differences in all the body weight measurements, except for week 5 with higher means recorded for the normal genotype (Table 1). The frizzle and naked neck genotypes did not differ significantly ($p > 0.05$) in body weights in all the weeks except in week 8. The body weight gain recorded for frizzle and naked neck individuals may be as a consequence of their direct effect on efficiency of thermoregulation in hot environments. The values got are in accordance with [5] who reported superiority of the normal feathering birds over their naked neck and frizzle counterparts. However, body weights recorded in this study are in agreement with earlier reports by [9, 12] that indigenous chickens are relatively small in body weights. The major setback in improvement of indigenous chickens is their poor genetic profile which is due to lack of purposeful selection of the local chickens unlike their exotic counterparts [10]. The significant differences ($p < 0.05$) recorded in all the weeks indicates that BWT as a trait can be used to discriminate effectively among the genotypes.

Table 1: Descriptive Statistics of body weight for local chickens

Age (weeks)	Genotype		
	Naked neck	Frizzle	Normal
2	53.64 ± 2.23	51.57 ± 8.58	50.10 ± 2.78
3	80.75 ± 2.77 ^b	80.86 ± 1.52 ^b	88.90 ± 2.68 ^a
4	113.0 ± 1.61 ^b	111.93 ± 4.46 ^b	127.81 ± 1.27 ^a
5	161.19 ± 4.09 ^b	166.85 ± 4.75 ^{ab}	173.67 ± 2.77 ^a
6	202.80 ± 4.80 ^b	198.18 ± 3.76 ^b	220.17 ± 3.80 ^a
7	247.68 ± 3.31 ^b	235.11 ± 5.33 ^b	274.52 ± 5.06 ^a
8	308.10 ± 3.76 ^b	292.35 ± 4.23 ^c	345.90 ± 4.54 ^a
9	337.68 ± 4.31 ^b	335.05 ± 5.68 ^b	376.98 ± 3.45 ^a

^{a-c} Means in the same row with different superscripts are significantly different ($p < 0.05$).

Stepwise procedure allowed the selection of the most discriminating variables that enable a clear separation between the three genotypes. Although the univariate statistics showed normal genotype to be significantly higher in all

measurements, the multivariate technique provided better resolution. The varying coefficients of variation in this study could be attributed to breed differences, influence of the environment on the parameters and absence of controlled selection.

Results of the stepwise discriminant analysis showing Wilk’s Lambda values, eigenvalues, percentage variance and canonical correlation are presented in Table 2. The unstandardized stepwise discriminant function was used to classify individual genotypes. The variables included in the discriminant (D) equation which gave the best discrimination models obtained from this study is given as follows:

$$D = 1.000BWT \text{ for weeks 3 to 9 respectively.}$$

The variance ratio (eigenvalue) of each of the discriminant functions is all highly significant except for week 5. The percentage of total variance gave 100% in all the weeks.

Table 2: Canonical Discriminant Function Statistics for Body Weights

Age (weeks)	Eigenvalue	% variance	Canonical correlation	Wilk’s lambda	Significance
3	0.057	100.0	0.233	0.946	0.024
4	0.188	100.0	0.398	0.842	0.000
5	0.044	100.0	0.206	0.958	0.060
6	0.129	100.0	0.338	0.886	0.000
7	0.298	100.0	0.497	0.771	0.000
8	0.677	100.0	0.635	0.596	0.000
9	0.482	100.0	0.570	0.675	0.000

The group centroids generated from the model was used to discriminate between the three genotypes at weeks 3 - 9 of age. The magnitude and signs of the group centroids indicate that the three genotypes are distinctly different from one another when body weight is used as the discriminant factor in weeks 3, 4, 5,6,7,8 and 9 respectively. At week 3, 4 and 9, the naked neck frizzle genotypes had close values with same sign, this indicate that the two genotypes are not distinct.

Table 3: Group Centroids for Body Weight

Genotype	Age (weeks)						
	3	4	5	6	7	8	9
Naked neck	-.190	-.307	-.255	-.199	-.231	-.376	-.512
Frizzle	-.183	-.369	-.031	-.368	-.633	-.933	-.603
Normal	.301	.544	.239	.433	.629	.960	.845

The classification results (Table 4) indicate that 36.8 %, 49.9% and 60.8% of original cases for naked neck, frizzle and normal, respectively were correctly classified. There was 63.2% error in correctly classifying naked neck individuals, 50.1% error in correctly classifying normal individuals. This means that 15 out of 41 naked neck individuals were correctly classified, 19 out of 39 frizzle were correctly classified. 31 out of 51 normal individuals were correctly classified. 13 naked necks and 13 naked necks were wrongly classified as frizzle and normal individuals respectively. 10 frizzle and 10 frizzle were wrongly classified as naked neck and normal individuals respectively while fourteen normal and six normal individuals were wrongly classified as naked neck and frizzle individuals respectively. These errors in classification maybe due to measurement errors. This result indicates that body weight maybe a reliable classification criterion for discrimination among the genotypes except in weeks 3, 4 and 9.

The present classification function is the first tool available to differentiate between the three genotypes under field conditions, which could aid their effective management and conservation. This is important because the potential

capacity of populations to adapt and evolve as independent biological entities in different environmental conditions is restricted by the exchange of individuals between populations [16]. In a related investigation, [2] was able to correctly allocate more than 70% of individual goats into their different groups while [15] used discriminant analysis to correctly classify most Sudan and Sudan-Sahel goat populations of Burkina Faso into their source population (79.3% and 82.7%, respectively). The function provides important and informative variables (racial markers) that could be used to assign the breeds into distinct populations, thereby reducing the errors of selection in future breeding programmes [16].

Table 4: Classification Results for Body Weights

Age (weeks)	Predicted Group Membership												
	Na			F			Nor			Total			
	Na	F	Nor	Na	F	Nor	Na	F	Nor	Na	F	Nor	
3	Count	22	2	19	22	6	13	23	0	29	43	41	52
	Count %	51.2	43.7	44.2	53.7	14.6	31.7	44.2	0	55.8	100	100	100
4	Count	8	26	10	0	29	11	6	3	43	44	40	52
	Count %	18.2	59.1	22.7	0	72.5	27.5	11.5	5.8	82.7	100	100	100
5	Count	25	3	15	12	7	20	12	15	24	43	39	51
	Count %	58.1	7.0	34.9	30.8	17.9	51.3	23.5	29.4	47.1	100	100	100
6	Count	4	20	17	14	20	17	3	24	25	41	39	52
	Count %	9.8	48.8	11.5	35.9	51.5	12.8	5.8	46.2	48.1	100	100	100
7	Count	9	15	16	0	29	8	29	3	20	40	37	52
	Count %	22.5	37.5	40.0	0	78.4	21.6	55.8	5.8	38.5	100	100	100
8	Count	14	17	10	15	22	0	15	0	37	41	37	52
	Count %	34.1	41.5	24.4	40.5	59.5	0	28.8	0	71.2	100	71.2	100
9	Count	26	41.5	24.4	40.5	59.5	0	28.8	0	71.2	100	100	100
	Count %	63.4	10	5	11	21	6	10	0	42	41	38	52

CONCLUSION

This study showed that body weight maybe a reliable classification criterion for discrimination among the genotypes. The present findings could aid field assessment, management and conservation of the three chicken populations, where the goal is to obtain phenotypically pure local genetic resources for sale and/or for future selection and breeding strategies.

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