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Research Article

Morphometric Characterization and Discrimination of Three Broiler Chickens Using Canonical Discriminant Analysis

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Abstract: This study was conducted to assess morphometric traits of three commercial broiler strains. A total of 300 day-old chicks, 100 each of Arbor Acre, Cobb 500, and Ross 308, were used for this study. Data were obtained on body weight (BW) and biometric traits, including, body length (BL), chest girth (CG), thigh length (TL), shank length (SL), wing length (WL), and keel length (KL). Analysis revealed significant ($p<0.01$) variations between strains for shank length, wing length, and keel length, with Cobb 500 exhibiting higher body weight than Arbor Acre and Ross 308. CG had the strongest positive relationship with body weight ($r=0.886$), indicating its usefulness in predicting body weight. The Mahalanobis distance analysis revealed that Arbor Acre and Cobb 500 were most closely related based on shank length ($D^2=0.247$), while Arbor Acre and Ross 308 were closely related in WL, CG, and KL. Stepwise Canonical Discriminant Analysis identified SL, WL, CG, and KL as the most discriminating traits among the strains. The discriminant functions classified 64.8% of the chickens into their respective strains after cross-validation, with Cobb 500 exhibiting the highest accuracy (67.3%). Information obtained from current research demonstrates the potential of morphometric traits in distinguishing broiler strains.

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1. Introduction

Poultry rearing play vital role in the sustenance of household economy, besides being healthy and nutritious source of protein, it contributes significantly in dietary security, specially, of the young ones (Mohammed et al., 2020). Broilers are bred for rapid growth, high feed efficiency, and good carcass yield and meat quality. Broiler production is a business in which volume is necessary to offset the small unit of profit. In Nigeria, four commonly used broiler strains used for commercial production are Arbor Acre, Cobb 500, Marshall and Ross 308.

Quantitative traits are good indicators of the growth and market value of broilers (Isaac et al., 2023). Ajayi et al. (2012) and N'dri et al. (2016) reported that quantitative traits serve as the basis for characterization, classification, and selection for improvement of poultry breeds. Variations in morphological traits within species are of great biological interest for descriptive and analytical tools (Rotimi and Ati, 2020).

Discriminant analysis is a statistical procedure to classify species or breeds that are morphologically distinct (Setiaji et al., 2012; Kambur and Kekeçoğlu, 2020; Rotimi et al., 2021).

Canonical discriminant analysis is a multivariate technique that describes the relationship between two or more variables through linear combinations that are maximally correlated (Kambur and Kekeçoğlu, 2020; Ogah, 2013). Barbosa (2005) reported that the techniques of discriminant analysis have been successfully employed as a means of identifying developing genotypes and better utilizing the advantages provided by heterosis. The use of a stepwise approach in multivariate discriminant analysis is essential for the reduction of interdependency among a set of traits that are correlated (Isaac and Adeolu, 2023). The discriminant analysis uses a set of prediction equations based on independent variables that are used to classify individuals into groups, thereby reducing errors of selection for improvement programs in livestock (Yakubu et al., 2010). Researchers have used discriminant analysis procedures to classify various farm animals into groups using; morphometric parameters on West African Dwarf and Red Sokoto goats (Yakubu et al., 2010), body weight, and linear body measurements on three Saudi goat types (Aziz and Al-Hur, 2013), morphometric on West African Dwarf Goats in south-eastern Nigeria (Ebegbulem et al., 2011) and morphometric characterization of Nigerian indigenous sheep (Yunusa et al., 2013). According to the report of Abdelqader et al. (2010), body weight, body length, heart girth, and height at the hip are the best discriminatory variables between the three Jordanian chicken genotypes.

Rotimi and Ati (2020) also reported that abdominal circumference was the most discriminating variable in the sex of rabbits. The discriminant analysis allows us to understand the differences between populations and predict the class or group to which individuals belong. Rotimi et al. (2021) applied discriminant analysis to correctly classify three goat breeds in Nigeria.

There exist many strains of broilers developed for table meat production in Nigeria. The distinctiveness of each strain is necessary for proper identification and utilization by poultry farmers. There is a need to discriminate today's broiler strains into distinct genetic groups and at the same time group related strains together based on their common attributes. The objective of the study was to discriminate three broiler strains into distinct genetic groups and to determine the best traits for discriminating among the three strains of broiler chickens based on their morphological traits. The information obtained from this study will provide a basis for effective identification, conservation, management, and utilization of the strains of broilers.

2. Material and Methods

2.1. Study location

The experiment was carried out at Prof. Lawal Abdul Saulawa Livestock Teaching and Research Farm of the Department of Animal Science, Federal University Dutsin-Ma. The description of the study location was as earlier done by Rotimi (2023).

2.2. Experimental birds

Three hundred (300) commercial strains of day-old broiler chicks, including one hundred each of; Arbor Acre, Cobb 500, and Ross 308 were used for this study. The chicks were managed intensively in a deep litter, open-sided, dwarf-walled house. Feed and water were given to the chickens *ad libitum*. All routine management, medications, and vaccinations were carried out.

2.3. Data Collection and Statistical Analysis

Data were taken on individual broiler chickens on body weight (BW), body length (BL), Chest girth (CG), Thigh length (TL), Shank length (SL), Shank girth (SG), Wing length (WL) and Keel length (KL). All measurements were taken according to Isaac et al. (2022). Data obtained were subjected to statistical analysis using IBM SPSS Statistical Package version 27.0.0. Mean, standard error, and standard deviation were obtained to evaluate the effect of strains on the parameters studied. Stepwise canonical discriminant analysis was conducted. The general model of the linear discriminant function was given in the expression;

$$Y = a + D_1X_1 + D_2L_2 + \ldots + D_iL_i \qquad (1)$$

Where;
Y = Discriminant z score of discriminant function,

a = Intercept
D = Discriminant coefficient for a quantitative trait
X = Quantitative trait

2.3.1. Tolerance

Tolerance determines the amount of multicollinearity existing among the measured traits. High tolerance indicates that a variable or trait is quite independent of other variables and contributes much information to a model. Tolerance was computed as;

$$1 - R^2 \tag{2}$$

Where; R^2 = Coefficient of determination, which is the percentage contribution of a particular quantitative trait to the total variation in performance (Yakubu et al., 2022; Isaac and Adeolu, 2023).

2.3.2. Mahalanobis distance

This was calculated as a squared distance between any two strains in terms of a given trait studied. Mahalanobis distance was calculated according to Isaac (2020) as adapted from Mahalanobis (1936).

2.3.3. Wilks' lambda

This was evaluated as the proportion of the total variance in the discriminant scores not explained by differences among the strains. The value ranges between 0 and 1. Values close to 0 indicate that group means are different.

3. Results and Discussion

Descriptive statistics of body weight and the linear body measurements of the three strains of broiler chickens are revealed in Table 1. Strains show a non-significant ($p>0.05$) effect on BW, BL, CC, TL, and SG. Cobb 500 recorded higher body weight than Arbor Acre and Ross 308 (2950.00±13.21, 2830.23±11.37 and 2850.07±11.30 respectively). Cobb 500 recorded higher non-significant ($p>0.05$) values in most of the other linear body parameters except in WL, where Arbor Acre had significantly ($p<0.01$) higher values than Cobb 500 and Ross 308 (11.49±0.17 and 10.68±0.17, respectively). Results show significant ($p<0.01$) effects of strains on SL, WL, and KL. This result is similar to the reports of other authors (Udeh and Ogbu, 2011; Sam and Okon, 2022).

Table 1. Least square means (±SE) of body weight (g) and linear body measurements (cm) of the three broiler strains

Traits	Strains	N	Mean (±SE)	Std. Deviation	Sig.
Body weight	Arbor Acre	56	2,830.23±11.37	85.10	0.767
	Cobb 500	49	2,950.00±13.21	92.49	
	Ross 308	60	2,850.07±11.30	87.51	
	Overall	165	2,870.39±6.84	87.82	
Body length	Arbor Acre	56	15.76±0.23	1.74	0.119
	Cobb 500	49	18.74±2.53	17.72	
	Ross 308	60	14.99±0.23	1.76	
	Overall	165	16.36±0.77	9.83	
Chest girth	Arbor Acre	56	14.55±0.28	2.08	0.175
	Cobb 500	49	15.15±0.28	1.96	
	Ross 308	60	14.45±0.28	2.14	
	Overall	165	14.69±0.16	2.08	
Thigh length	Arbor Acre	56	9.73±0.16	1.21	0.585
	Cobb 500	49	9.86±0.22	1.53	
	Ross 308	60	9.60±0.15	1.19	
	Overall	165	9.72±0.10	1.30	

Table 1. Least square means (±SE) of body weight (g) and linear body measurements (cm) of the three broiler strains (continued)

Traits	Strains	N	Mean (±SE)	Std. Deviation	Sig.
Shank length	Arbor Acre	56	4.07±0.08^{a}	0.60	0.000
	Cobb 500	49	4.35±0.07^{b}	0.48	
	Ross 308	60	3.76^{c}±0.08	0.60	
	Overall	165	4.04±0.05	0.61	
Shank girth	Arbor Acre	56	2.89±0.07	0.55	0.325
	Cobb 500	49	3.01±0.08	0.54	
	Ross 308	59	2.87±0.06	0.46	
	Overall	164	2.92±0.04	0.52	
Wing length	Arbor Acre	56	11.49±0.17^{a}	1.30	0.000
	Cobb 500	49	10.68±0.17^{b}	1.16	
	Ross 308	60	10.53±0.17^{b}	1.34	
	Overall	165	10.90±0.10	1.34	
Keel length	Arbor Acre	56	7.24±0.16^{b}	1.23	0.000
	Cobb 500	49	7.74±0.16^{a}	1.11	
	Ross 308	60	6.63±0.15^{c}	1.13	
	Overall	165	7.16±0.10	1.24	

The result of the correlation matrices obtained from the pooled data on the three strains from the discriminant analysis is presented in Table 2. Correlation results for individual strain are, therefore, not presented. Positive and significant (p<0.01) correlations were obtained between body weight and biometric traits except with BL (r = 0.016^{NS}). Positive correlations exist among the body measurements studied, meaning that improvement of any of these traits can positively affect others through correlated responses. However, negative correlations were observed between CG and TL with BL (r = -0.027 and r = -0.009 respectively). Low correlations were observed between all the traits with BL. The highest correlation between BWT and CG (r = 0.886). This result implies that indirect selection for broilers with larger CG can greatly lead to improvement of body weight. This observation is similar to the observations of other authors (Ojedapo et al., 2012; Fayeye et al., 2014; Isaac, 2020; Isaac et al., 2024). These authors affirmed the use of breast width as an important estimator of body weight and selection criterion for meat type birds. Lowest correlation exists between BL and TL (r = -0.009).

Table 2. Correlation coefficient between traits Pooled Within-Groups strains

	BW	BL	CG	TL	SL	SC	WL
BL	0.016	1.000					
CG	0.886**	-0.027	1.000				
TL	0.735**	-0.009	0.747**	1.000			
SL	0.608**	0.045	0.695**	0.637**	1.000		
SG	0.563*	0.046	0.668**	0.572**	0.676**	1.000	
WL	0.709**	0.076	0.725**	0.684**	0.649**	0.649**	1.000
KL	0.707**	0.012	0.752**	0.668**	0.692**	0.643**	0.709**

BW = Body weight, BL = Body length, CG = Chest girth, TL = Thigh length, SL = Shank length, SG = Shank girth, WL = Wing length, KL = Keel length, *Correlation is significant (p < 0.05), **Correlation is significant (p < 0.01).

The results of the stepwise discriminant analysis are presented in Table 3. Results revealed the traits of the three strains that maximized the Mahalanobis distance. From the analysis, Arbor Acre and Cobb 500 were more closely related in SL (Min. D Sq. = 0.247). This result is close to the observation of Isaac et al. (2024), who recorded the closest distance between Arbor Acre and Marshall in shank length (2.006). Arbor Acre and Ross 308 were closely related in WL (Min. D Sq. = =0.558), CG (Min. D Sq. = 1.279) and KL (Min. D Sq. = 1.358). Contrary to this study, Isaac et al. (2024) reported that Arbor Acre and Marshall were closely related at wing length (5.704), body girth (6.002), and thigh circumstance (6.314). While Arbor Acre and Ross 308 were closely related only in body length (4.212).

This result shows the genetic similarity between Arbor Acre and Ross 308 which is closer than between Arbor Acre and Cobb 500. This suggests the existence of a common genetic origin for Arbor Acre and Ross 308 broiler chickens, thereby affirming the usefulness of Mahalanobis distance analysis for establishing genetic differences between broiler strains (Li et al., 2019; Isaac et al., 2024).

The shank length which minimizes the distance between Arbor Acre and Cobb 500 may be used as a reliable body measurement in broilers for classifications of strains into similar groups (Mushi et al., 2020; Isaac et al., 2024).

Table 3. Traits that maximize the Mahalanobis distance between the two closest strains by stepwise discriminant analysis

Step	Traits	Min. D Sq.	Between Groups	Exact F Statistic	df1	df2	Sig.
1	Shank length	0.247	Arbor Acre and Cobb 500	6.458	1	161.000	0.012
2	Wing length	0.558	Arbor Acre and Ross 308	7.966	2	160.000	0.001
3	Chest girth	1.279	Arbor Acre and Ross 308	12.100	3	159.000	3.556×10^{-7}
4	Keel length	1.358	Arbor Acre and Ross 308	9.575	4	158.000	5.869×10^{-7}

Min. D Sq. = Minimum Distance squared, F = Fisher, df1, df2 = degrees of freedom 1 and 2 respectively, LOS = Level of significance.

Table 4 shows the traits selected by stepwise discriminant analysis for classifying strains into closely related groups. The tolerance values were also presented in the table. Stepwise discriminant analysis selected four traits out of the seven traits involved. These traits were used as variables for discriminatory tools for the three strains of broilers involved in this study. The traits selected as the best discriminating variables are shank length (SL), wing length (WL), chest girth (CG), and keel length (KL). The stepwise multivariate discriminant analysis helps to exclude redundant variables that are capable of increasing multi-colinearity issues among a set of independent variables as multi-colinearity reduces the accuracy of analysis and may lead to wrong inference on variables that did not contribute much to the overall variation in the performance of animals (Kim, 2019; Rotimi et al., 2020 and 2021; Isaac et al., 2022 and 2024). This result was confirmed by the report of Ajayi et al. (2012), who also reported that shank length, wing length, breast girth, and keel length were among some of the variables selected as the best discriminatory variables used in classifying chickens into distinct populations. However, the present result of this study was different from the report of other authors; such as; Ogah (2013) who reported that body weight, thigh length, and body width as the most discriminant variables for discriminating between normal feathered, frizzled, and naked neck chickens, Isaac et al. (2024) who selected body length, breast girth and shank length as the best discriminatory traits in the study with three strains of broilers. Worth noting that the variations observed may be due to the differences in size, age, strains, and method of discriminant analysis employed by these authors.

The high tolerance value (1.00) of shank length obtained in step 1 revealed that SL contributed the highest discriminatory power and variability independent of other traits. This confirmed the reason why SL has been recommended for the phenotypic characterization of indigenous chickens (Maharani et al., 2021; Isaac et al., 2024).

Table 4. Traits selected by stepwise discriminant analysis for classifying strains into closely related groups

Step	Traits	Tolerance	F to Remove	Min. D Sq.	Between Groups
1	Shank length	1.000	14.368	-	-
2	Shank length	0.578	25.875	0.011	Cobb 500 and Ross 308
	Wing length	0.578	19.981	0.247	Arbor Acre and Cobb 500
3	Shank length	0.472	19.754	0.141	Cobb 500 and Ross 308
	Wing length	0.433	26.418	0.253	Arbor Acre and Cobb 500
	Chest girth	0.387	9.794	0.558	Arbor Acre and Ross 308
4	Shank length	0.434	8.967	1.249	Arbor Acre and Ross 308
	Wing length	0.398	29.325	0.287	Arbor Acre and Cobb 500
	Chest girth	0.333	10.357	0.561	Arbor Acre and Ross 308
	Keel length	0.348	8.400	1.279	Arbor Acre and Ross 308

F = Fisher, Min. D Sq. = Minimum Distance squared.

Table 5 presents the canonical discriminant function analysis summary. The provision of functions 1 and 2 in the summary of the canonical discriminant function is due to the three strains involved in the analysis, as the number of functions is usually one less than the number of discriminating groups (Ogah, 2013; Rotimi *et al*., 2021; Isaac *et al*., 2024). From function 1, the strains were genetically different. Low Wilks' Lambda value (0.546) was obtained and the Chi-square test (P<0.001), validated the discriminant analysis done. Lower values of Wilks' lambda indicated a better discriminatory power (Ariza *et al*., 2022). This trend is in consonant with the report of Rotimi *et al.* (2021). Results also indicated that function 1 had better discriminatory power based on its higher eigenvalue/variance ratio (0.474) and percentage variance (66.20%) compared to function 2 with lower eigenvalue (0.242) and percentage variance (33.80%).

Table 5. Summary of canonical discriminant function analysis

Parameters	**Function**	**Function 2**
Eigenvalue	0.474	0.242
Variances (%)	66.20	33.80
Canonical correlation	0.567	0.441
Wilks' Lambda	0.546	0.805
Chi-square	96.405	34.514
Df	8	3
Sig.	0.000	0.000

Df = degree of freedom, Sig. = Significance.

Table 6 presents the results of functions at the group centroid. The centroid was considered as the group means of the predictor variables or morphometric traits of chickens in each strain. Group centroids are therefore important statistics for the accurate classification of individuals. Chickens with scores near a centroid are regarded as belonging to one group (Ogbogo, 2019; Isaac et al., 2024).

The negative signs for Arbor Acre and Ross 308 indicated that Arbor Acre and Ross 308 are in one direction and opposite to Cobb 500 with the positive sign in function 1. This observation indicated that Arbor Acre and Ross 308 are genetically closely related and can be classified into similar groups, but different from Cobb 500 based on the biometric traits measured.

Table 6. Functions at group centroid

Strain	**Function 1**	**Function 2**
Arbor Acre	-0.494	0.577
Cobb 500	1.043	0.044
Ross 308	-0.398	-0.584

The coefficients of the function are shown in the Table 7. From the table, the best reduced discriminant models for discriminating among the strains are as follows.

Arbor Acre: $D = -43.667 + 0.371CG + 4.809SL + 6.287WL - 1.671KL$
Cobb 500: $D = -40.602 + 0.680CG + 6.406SL + 4.382WL - 0.769KL$
Ross 308: $D = -37.873 + 1.120CG + 3.929SL + 5.346WL - 2.081KL$

The coefficients indicated the contributions of each morphometric trait to the discriminant function (equation). WL had the highest contribution in each strain (6.287, 4.382, and 5.346 respectively). This indicated that WL is the best trait for strain separation or discrimination. This is contrary to the report of Isaac et al. (2024), who observed that Shank length had the highest contribution and the best trait for strain separation in Arbor Acre, Marshal, and Ross 308.

Table 7. Classification function coefficients

Parameter	**Strain**		
	Arbor Acre	Cobb 500	Ross 308
CG	0.371	0.680	1.120
SL	4.809	6.406	3.929
WL	6.287	4.382	5.346
KL	-1.671	-0.769	-2.081
(Constant)	-43.667	-40.602	-37.873

Table 8 shows the classification results. The table revealed that 37 (66.10%), 35 (71.40%), and 41 (68.30%) out of 56, 49, and 60 original cases were correctly classified as Arbor Acre, Cobb 500, and

Ross 308 respectively. However, after cross-validation, 34 (60.70%), 33 (67.30%), and 40 (66.70%) cases were correctly classified as Arbor Acre, Cobb 500 and Ross 308 strains of broiler. The cross-validation procedure provides a more honest presentation of the discriminant function out of 56, 49, and 60 of the total cases. Cobb 500 had the highest accuracy of prediction (67.30% after cross-validation) compared to the other strains. This indicates that Cobb 500 are more unique in the traits measured, implying that Cobb 500 can easily be identified in a mixed population and classified with high fidelity based on their morphometric traits. Classification results are an essential tool for discriminating animals in mixed populations for effective management and conservation (Kadurumba et al., 2014; Isaac et al., 2024). Discriminant function classification has been employed by other researchers in; rabbits (Rotimi and Ati, 2020), three indigenous goat breeds in Nigeria (Rotimi et al., 2021), West African Dwarf and Red Sokoto goats in Nigeria (Yakubu et al., 2010) and village goat production systems in South Africa (Mdladla et al., 2017).

Table 8. Classification results

		Strain	**Predicted Group Membership**			**Total**
			Arbor Acre	Cobb 500	Ross 308	
Original	Count	1	37	8	11	56
		2	8	35	6	49
		3	12	7	41	60
	%	1	66.1	14.3	19.6	100.0
		2	16.3	71.4	12.2	100.0
		3	20.0	11.7	68.3	100.0
Cross-validated	Count	1	34	9	13	56
		2	9	33	7	49
		3	12	8	40	60
	%	1	60.7	16.1	23.2	100.0
		2	18.4	67.3	14.3	100.0
		3	20.0	13.3	66.7	100.0

Strain 1 = Arbor Acre, Strain 2 = Cobb 500, Strain 3 = Ross 308.

Conclusion

The use of canonical discriminant analysis to assess morphometric traits among the three broiler strains has helped to determine their genetic differences and identify the best traits for distinguishing these strains. It was observed that Cobb 500 exhibited higher body weight and superior performance in most linear body parameters compared to Arbor Acre and Ross 308. Significant differences were noted in shank length (SL), wing length (WL), and keel length (KL) between the strains. Arbor Acre and Ross 308 were more closely related, sharing genetic similarities, while Cobb 500 was distinct. Shank length minimized the Mahalanobis distance between Arbor Acre and Cobb 500, indicating its reliability for strain classification. Wing length contributed most to strain classification, indicating its potential as a key trait for identifying genetic differences. Cobb 500 showed the highest accuracy of prediction (67.3%) after cross-validation, indicating that it can be identified and classified with high fidelity in a mixed population.

Ethical Statement

Ethical approval is not required for this study because the methods of the study does not require review by an ethics committee.

Conflict of Interest

The author declares that there are no conflicts of interest.

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Author Contributions

The author confirms sole responsibility for the study from conception, design, data collection, analysis and interpretation of results, and manuscript preparation.

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