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Heritability and sexual dimorphisms on morphometric parameters of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades

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Abstract

The study evaluated the effect of sexual dimorphisms on the morphometric and genetic parameters of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrade. This study was carried out in the Teaching and Research farm of FUNAAB. Nigerian Indigenous: Normal feathered (N), Frizzle-feathered (Fz) and Naked neck (Nk) chickens were crossed with Marshall Exotic breed (M) to obtain F1 (MN, MNk and MFz) and F2 upgrade (MMN, MMFz, MMNk) used for the study. Sex was regarded treatment. The design of the experiment was CRD. Data were collected on growth traits: body weight (BW, body length (BL), breast girth (BG), wing length (WL), wing span (WS), thigh length (TL), shank length (SL) and keel length (KL) from day old to 8 weeks of termination. AL Data were analyzed using the General Linear Model of Statistical Analysis System. Results showed that sex significantly ($p<0.001$) affected BW and linear body parameters in this study. Males had higher means than their female counterparts on BW and linear body parameters measured at all ages except at weeks 0 to 3 that WL, WS, THL, SL and KL were statistically ($p>0.001$) similar in mean on both sexes studied. Heritability estimate ranged from low to high with values from 0.02±0.05 to 0.64±0.05 s studied. Shank length had the least heritability estimate value while keel length had the highest in this study. Phenotypic correlations showed positive correlations which ranged from 0.01 to 0.83 for the growth traits measured in this study. In conclusion, Males performed better than their female counterparts in this study.

Keywords: Chicken; Correlation; Genetic; Heritability; Morphometric; Parameters

1 Introduction

Sexual dimorphism is a natural process in all growing animals characterized by manifestation of some physical changes between male and female species. Sexual differences in external morphology are of interest in studies of reproductive biology and descriptively to analyze population composition [1]. This can be used to detect the amount and distribution of genetic variation within and between populations of the indigenous chicken thereby increasing the understanding of the historical processes underlying the genetic diversity [2]. This can also, provide important information for selection and breeding programmed.

Chicken which has a significant impact on fundamental biology is a major source of protein worldwide. It is a widely acceptable livestock which serves as an ideal model for examining animal growth trait development and for sufficient supply of animal protein to the humans [3]. The rational of conservation and sustainable use of indigenous chicken (IC) resources require their morph biometrical characterization [4]. Morphometric measurements is useful in contrasting size and shape of animals [5; 6]. Chicken has some interesting economic traits such as short reproductive cycle and highly prolific which greatly increased productivity. Nigerian indigenous chickens with their slow growth rate and small bodied size which may be due to their production systems (free-range low input, backyard and semi-intensive) [7] when compared to the exotic breeds which are reared intensively and had been selected for fast growth rate over time need

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some improvement measures to be adopted such as selection, crossbreeding as well as intensive system of production in order to transform Nigerian poultry industry [8]. Crossbreeding is a major feature of current broiler breeding programmes [9]. The performance of lines and strains in cross combinations can be evaluated in terms of general and specific combining ability. The performance of the indigenous crossbred chicken was due to heterotic advantage as a result of the genetic difference existing between the parents. Adebambo et al., [10] reported that the genetic determination of crossbred performance permits for the observation between offspring and maternal heterosis and also for particular combination of genes which only show up to advantage when they are crossed to other populations. Marker-assisted selection (MAS) which increase selection efficiency can linked with quantitative traits loci and serves in direct selection of genotype which further improves production traits. In traits where heritability is low to medium, crossbreeding provides an opportunity to make reasonable progress in one generation as a result of positive heterosis. The dominant genes normally mask the recessive genes to produce hybrid vigour (heterosis), where the offspring performs better than the average of both parents.

2 Materials And Methods

2.1 Experimental site

The research was carried out at the Poultry Breeding Unit of the University Teaching and Research Farm, Federal University of Agriculture, Abeokuta, Alabama Road, Abeokuta. Alabama is at latitude 7o10`N and longitude 3o2`E in Odeda Local Government Area of Ogun State, Nigeria. It has a mean annual rainfall of about 1037mm. The mean monthly ambient temperature ranged from 28- 36oC and 34oC on average. Relative humidity ranged from 60-94%, 82% on the average. The vegetation represents an inter-phase between the tropical rainforest and the derived savannah [11].

2.2 Experimental stock

2.2.1 Parents

The parent stock of the chickens used for the study includes

Pure indigenous chicken genotypes reared in the breeding unit of the University's Research Farm were used to generate the offspring for this research. The parent stock was basically Normal-feathered (N) of two cocks and ten hens, Frizzled-Feathered (Fz) of one Cock and seven hens and naked neck chicken (NK) of two 2 Cocks and ten hens and Marshall (M) of three Cocks and hens and ten Dihybrid cross of ten hens which were cross through artificial insemination method. The combination of these four genotypes at different bloodlines resulted in ten genotypes used in this study: 100% pure breeds, 50:50% M: Ind (di-hybrid) 75:25% M: Ind (F2 upgrade) fifty chickens per genotype (sample size) making five hundred chickens altogether. The genotypes are presented below:

2.2.2 Mating design

Sires Dams 100% bloodline (purebreds)

1. M X M = M

2. N X N = N

3. Fz X Fz = Fz

4. NK X NK = NK

50%:50% (M: Ind) bloodline (F1crosses)

5. M X N = MN (F1)

6. M X Fz = MFZ (F1)

7. M X NK =MNK (F1)

75%:25% (M: Ind) bloodline (F2 upgrades)

8. M X MN =MMN (F2)

9. M X MF =MMFZ (F2)

10. M X MNK =MMNK (F2)

M- Marshall Exotic breed, N-Normal-Feathered, Fz-Frizzle-Feathered,

NK-Naked Neck chicken genotype, M: Ind = Marshall: indigenous.

2.3 Matings, egg collection and hatching.

Artificial insemination was carried out on the chickens three times a week. It was done by introducing semen collected from Exotic Marshall cocks (sires) into the reproductive tracts of both exotic and indigenous hens (dams), also, indigenous cock to Indigenous hens following the above mating design to produce the 10 different genotypes of birds studied in this research. The parent stock was housed in the battery cage system according to their mating group fed ad libitum with constant water supplied. The pure Marshall genotype served as control. Then the same exotic cocks (Marshal) were crossed to all the genotypes to obtain F1 birds with 50%: 50% M: Ind bloodline (dihybrid crosses) and F2 birds with 75%:25% M: Ind bloodline (F2 upgrades).

2.4 Egg collection, incubation and hatching

Eggs from each mating group were collected daily and labelled accordingly. The eggs were then transferred to the University Teaching and Research Farm, Federal University of Agriculture, Abeokuta, hatchery unit for incubation and hatching. Assortment of eggs for incubation was done by selecting cracked, discolored or odd- shaped eggs before setting. The eggs were fumigated so as to destroy microbes using fumes from mixture of 35g potassium permanganate in 53cc formalin per cubic meters. Circular air movement in the cabinet and speedy gas removal after 20 minutes fumigation was ascertained. Three-day egg collections were set along sire-lines at a temperature of 38-39°C and humidity of 55-66% for the first eighteen days. On the 18th day of incubation, candling was conducted and number of fertile eggs were recorded. The eggs were transferred into the hatcher; the temperature was set to 39-40°C and humidity to 70-75%. The eggs were turned automatically hourly through 90°C in the incubator. On the 21st day chicks were collected and the number of hatched chicks was recorded.

2.5 Housing, feeding and management

Chicks obtained were identified by wing-tagging immediately after hatching in respects to their sire line and sex were separated. From the hatchery, the chicks were transferred to the already disinfected brooding pens according to the genetic groups. The chicks were brooded for 3 weeks. Adequate management and health care were followed as shown in Table 1. The chicks were fed with commercial starter ration that contain 23% crude protein and 2850 kcal/kg metabolizable energy (ME) for up to four weeks of age. At four weeks of age, chicks were transferred to already compartmentalize rearing pens of 48.5 x 37 x 41.5 cm deep litter system to accommodate 50 birds per genotype. Placement into each compartment was randomly done according to sex by sire line (genotype). Water was constantly supplied to the chicks and fed ad libitum with commercial broiler finisher ration that supplied 19.5% CP and 3080kcal/kg (ME) from five weeks to eight weeks of age when the project terminated. The chicks were vaccinated: Newcastle vaccine given at day old, NDV-Komorov at 9ay and 17 days, Gumboro at 16-and 26-day, fowl Pox rugs at 6eeks and Coccidiostat at two weeks interval

3 Data collection

3.1 Growth

The chicks body weights (BW) were weighed weekly from day old to 8 weeks of age with the use of a weighing scale with 0.1g limit of sensitivity in the morning before feeding. Other linear body measurements were taken from day-old to 8 weeks using tape rule.

- **Shank length (SL)**: The distance between the hock joint and the tarso-metatarsus on the left leg was measured using tape rule.
- **Thigh length (TL)** was measured as the distance between the patella (knee cap) and the posterior end of the tibia joining the taros-metatarsus using tape rule.
- **Wing length (WL)**: The distance between the tip of the phalanges and the coracoid-humerus joint of the left wing with was measured with tape rule.

- **Wing span (WS)**: Tape rule was used to measure the distance between the tips of left phalanges to the tip of the right phalanx's phalanges.
- **Body length (BL)** was measured with tape rule as the length from the vertebral region, to the base of neck to the hollow part at the base of the tail.
- **Keel length (KL)**: It was measured as the length of the bird's sternum or breast plate from the hollow of the V-bone with a tape rule.
- **Breast girth (BG)** was measured as the bird's circumference around the deepest region of the breast; excluding the wings with tape rule.

3.2 Statistical analyses

Analysis of variance for the body parameters was carried out with [12] software using General Linear Model. Means were separated using Duncans Multiple Range Test at probability of 5% level.

3.3 Experimental models

3.3.1 Model 1

YIJK = μ + Si + ƐIJ

YIJK = Observation of the itch sex on the jet bird

μ = Overall mean

Si = Effect of the jet sex (j = 1-2)

ƐIJ = Error due to individual observation

3.4 Heritability and phenotypic correlations

Heritability and phenotypic correlations and their standard errors were carried out using IML (Integrated matrix language) in [12] software. Means was separated using Duncans Multiple Range test.

$$\text{Heritability (h2)} = \frac{4\hat{o}2S}{\delta 2S + \delta 2D + \delta 2W}$$

Were

- δ2S = Variance component of Sire (MSS - MSD/K3)
- δ2D = Variance component of Dam (MSD-MSW/k1)
- δ2W = Variance component of within offspring (SSW/DFW = MSW)
- k1 = number of offspring per dam
- k3 = number of offspring per sire

$$\text{Phenotypic correlation} = \frac{COVW + COVS}{\sqrt{(\delta 2w(x) + \delta 2S(x))\,(\delta 2w(y) + \delta 2S(y))}}$$

Were

- COVS = COVERIANCE of sire for x and y trait
- COVW = COVERIANCE of within progeny for x and y trait
- δ2S(x) = variance component of sire for x trait
- δ2S(y) = variance component of sire for y trait
- δ2w(x) = variance component of within progeny for x trait
- δ2w (y) = variance component of within progeny for y trait.

4 Result and Discussion

4.1 Effect of sex on growth traits

4.1.1 Effect of sex on body weight

Result showed that sex significantly ($p<0.01$ to $p<0.0001$) affected body weight (BW) at all ages. The least square means of body weight as affected by sex showed that males generally had higher body weight statistically ($p<0.0001$) different from the female's counterpart at all ages.

4.1.2 Effect of sex on linear body measurements

Result showed that sex significantly ($p<0.01$ to $p<0.0001$) affected all linear body parameters measured in this study at all ages. The least square means of all linear body parameters as affected by sex revealed that males consistently had higher mean values than females at all ages except at weeks 0 to 3 that wing length, wing span, thigh length, shank length and keel length that males and females recorded statistically ($P>0.0001$) similar mean values, Table 2.

The results of the present study showed that sex significantly affected ($p<0.0001$) growth traits from 0 to 8 weeks of age. Males performed better than females on body weight and other body parameters measured such as body length, breast girth, wing length, wing span, thigh length, shank length and keel length. This could be attributed to the level of aggressiveness, dominance of male over female while feeding and hormonal influence in male as also reported by[13; 14]. Male sex hormones testosterone leads to sexual dimorphism in favor of the males over females due to this hormonal profile as reported by [15;16]. Dana et al. [17] as well observed that males were taller and heavier than the female counterparts in research involving five different chicken genotypes which is in accordance to the trend of the result of this study. The results of the present study showed that the genotype by sex interactively affected growth traits from 0 to 8 weeks of age.

The trend of the results of this study showed that Males of the F2 upgrades came first followed by F1 crosses while the purebred indigenous had the least mean values in both body weight and all the linear body traits measured at all ages in this study.

Table 1 Effect of sex on the body parameters of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades (LSM±SE) (cm)

			Weeks								
Sex	N	Parameter	0	1	2	3	4	5	6	7	8
M	244	BW(g)	35.65±0.41^{a}	83.80± 1.30^{a}	150.42±3.56^{a}	237.65±5.39^{a}	379.05±6.19^{a}	497.07±8.84^{a}	642.13±11.41^{a}	834.42±14.44^{a}	1039.47±18.51^{a}
F	242		34.49±0.33^{b}	74.41±1.53^{b}	139.45±3.17^{b}	228.97±5.49^{a}	282.23±8.84^{b}	389.82±7.91^{b}	500.92±9.54^{b}	650.89±10.89^{b}	796.00±14.02^{b}
M	244	BL (cm)	4.71±0.03^{a}	5.69±0.04^{a}	6.69±0.06^{a}	7.76±0.07^{a}	9.47±0.08^{a}	10.57±0.10^{a}	12.50±0.11^{a}	13.82±0.14^{a}	15.62±0.18^{a}
F	242		4.60±0.04^{b}	5.56±0.05^{b}	6.77±0.05^{a}	7.85±0.07^{a}	8.72±0.09^{b}	10.21±0.10^{b}	11.18±0.11^{b}	13.23±0.11^{b}	15.03±0.13^{b}
M	244	BG(cm)	6.63±0.08^{a}	7.70±0.08^{a}	9.02±0.09^{a}	10.43±0.11^{a}	12.09±0.12^{a}	13.79±0.15^{a}	15.54±0.19^{a}	18.00±0.24^{a}	21.90±0.26^{a}
F	242		6.42±0.10^{b}	7.55±0.07^{a}	8.94±0.08^{a}	10.25±0.10^{a}	11.81±0.10^{b}	13.32±0.15^{b}	15.36±0.17^{b}	17.20±0.19^{b}	18.21±0.21^{b}
M	244	WL (cm)	4.82±0.04^{a}	6.13±0.05^{a}	7.80±0.06^{a}	9.11±0.08^{a}	10.83±0.08^{a}	12.37±0.10^{a}	14.83±0.10^{a}	17.01±0.12^{a}	18.58±0.17 ^{a}
F	242		4.90±0.05^{a}	6.25±0.05^{a}	7.70± 0.06^{a}	8.97±0.07^{a}	10.63±0.09^{b}	12.15±0.10^{b}	13.36±0.10^{b}	15.37±0.11^{b}	17.94±0.15^{b}

a, b Means within the same column with same superscripts are not significantly different; F- female, M-male, BW-body weight, BL- body length, BG- breast girth, WL- wing length

Table 2 Coned: Effect of sex on the body parameters of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades (LSM±SE) (cm)

			Weeks								
Sex	**N**	**Parameter**	**0**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**
M	244	WS (cm)	10.80±0.09^{a}	13.94±0.12^{a}	17.28±0.15^{a}	20.13±0.19^{a}	24.91±0.17^{a}	27.29±0.23^{a}	31.38±0.24^{a}	37.51±0.26^{a}	42.41±0.32^{a}
F	242		10.92±0.09^{a}	13.80±0.12^{a}	17.26±0.14^{a}	20.29±0.16^{a}	22.44±0.18^{b}	26.74±0.23^{b}	30.72±0.27^{b}	33.63±0.25^{b}	37.51±0.28^{b}
M	244	TL (cm)	5.17±0.02^{a}	6.18±0.03^{a}	7.56±0.29^{a}	8.394±0.07^{a}	10.20±0.08^{a}	11.08±0.10^{a}	13.05±0.11^{a}	14.95±0.11^{a}	17.09±0.13^{a}
F	242		5.13±0.02^{a}	6.20±0.03^{a}	7.56±0.29^{a}	8.29±0.06^{a}	9.12±0.07^{b}	10.71±0.10^{b}	11.67±0.09^{b}	13.27±0.10^{b}	14.75±0.09^{b}
M	244	SL (cm)	4.28±0.02^{a}	5.01±0.03^{a}	5.80±0.05^{a}	6.76±0.06^{a}	8.26±0.07^{a}	10.98±0.10^{a}	10.51±0.10^{a}	11.89±0.13^{a}	13.90±0.13^{a}
F	242		4.32±0.17^{a}	5.02±0.03^{a}	5.84±0.05^{a}	6.76±0.06^{a}	7.26±0.07^{b}	10.56±0.09^{b}	9.54±0.09^{b}	10.80±0.11^{b}	11.99±0.11^{b}
M	244	KL (cm)	1.26±0.04^{a}	2.26±0.10^{a}	3.03±0.03^{a}	3.88±0.04^{a}	4.86±0.05^{a}	5.76±0.07^{a}	6.66±0.07^{a}	7.97±0.08^{a}	9.37±0.10^{a}
F	242		1.26±0.02^{a}	2.18±0.02^{a}	3.03±0.03^{a}	3.87±0.05^{a}	4.67±0.06^{b}	5.60±0.07^{b}	6.52±0.07^{b}	7.12±0.08^{b}	7.95±0.08^{b}

a, b Means within the same column with same superscripts are not significantly different; WS- wing span, TL- thigh length, SL- shank length, KL- keel length

5 Heritability

5.1 Heritability estimates for body weight and other linear measurements at all ages are presented in Tables 3 to 7

The heritability for all growth parameters ranged from low to high. Heritability estimates for body weight increased gradually in a steady trend at weeks 0, 2, 4 and 6 with the values of 0.34±0.10, 0.54±0.07, 0.61±0.10, 0.62±0.10 and dropped to 0.57±0.12 at 8th week. Heritability estimates for body length were increasing in a steady trend with the values of 0.22±0.10, 0.43±0.10, 0.50±0.15, 0.55±0.10 and 0.59±0.11 for weeks 0, 2, 4, 6 and 8, respectively. Breast girth had the heritability values of 0.37±0.20, 0.48±0.10, 0.55±0.15, 0.60±0.09 and 0.59±0.07 for weeks 0, 2, 4, 6 and 8, respectively. It increased from weeks 0, 2, 4 and 6 but had a little drop at week 8.

Wing length had the heritability values of 0.38±0.15, 0.38±0.08, 0.39±0.10, 0. 48±0.11 for weeks 0, 2, 4 and 6, respectively. The trend was in a steady increment but slightly dropped at week 8 to 0.46±0.14. Heritability estimates for wing span had a low to high trend with the values of 0.37±0.10, 0.47±0.10, 0.46±0.15, 0.59±0.09 and 0.60±0.05 for weeks 0, 2, 4, 6 and 8, respectively. Thigh length had the heritability values of 0.11±0.05 at week 0, then dropped to 0.10±0.03 at week 2 and increased again for weeks 4 and 6 (0.48±0.10 and 0.59±0.06) and dropped again at week 8 to 0.29±0.05. It had no specific trend this parameter. Heritability estimates for shank length was low to high with the values 0.02±0.05, 0.37±0.03, 0.58±10, 0.60±0.07 for weeks 0, 2, 4 and 6 respectively, then dropped to 0.53±0.10 at week 8. Keel length had the heritability values that increased from 0.21±0.04 at week 0 to 4. 0.53±0.06 at week 2 and also increased to 0.64±0.04 at week 4 where it was constant up to week 6 (0.64±0.05) then dropped to 0.57±0.07 at weeks 8.

5.2 Generally, in this study the trend of heritability estimate for growth traits in all the chickens breed and genotypes used for the study were observed to have a steady increment in values from 0 to 6 weeks but dropped at week 8.

The heritability (h2) of body weight and linear parameters estimated in this study revealed low to high trend of heritability which suggested that the appreciable additive genetic variance exist for this trait in the indigenous chicken population and hence, good response to selection can be expected. The amount of additive genetic variance in any population is largely a function of the level of selection that had been done in that population. Selection depletes additive genetic variance. The heritability estimate range obtained for some of the body parameters in this study were lower in values than as observed by [8]. However, the low values observed in the heritability estimate studied were only at day old, thereafter improved which suggested selection of these chickens can be done for their genetic improvement. This report was in agreement with the result of Ebangi and Ibe [18] who reported sixth week body weight heritability of 0.40 while Demeure et al [19] reported low to high heritability of 0.32 to 0.63 in F2 chickens population measured at 3 to 7 weeks between the intercross of lean and fat lines chicken population which agrees with the findings of in this study. Similarly, Adebambo et al.[20] (2010) reported weekly high heritability estimates which is in consonance with this study.

5.3 Phenotypic Correlation Coefficient

The results of phenotypic correlation coefficients (rp) among body weights and other body measurements are shown in Table 3 to 7.

Phenotypic correlations among growth traits obtained in this study ranged from low to very high values of 0.01±0.00 to 0.99±0.02 and all the values were positive. At day old the least values in phenotypic correlation were recorded for wing length and thigh length, breast girth and wing length and body length and wing length, relationship with the values of 0.02±0.01, 0.04±0.02 and 0.14±0.09 while body weight and shank length, breast girth and shank length and body weight and keel length relationship had the highest phenotypic values of 0.99±0.03 and 0.99±0.43 and 0.92±0.07, respectively (Table 3)

The phenotypic correlation generally increases from week 0 till week 8. At week 2 all the growth traits were highly correlated with the range of 0.93±0.05 to 0.99±0.02 as shown in Table 4. At week 4 the values obtained for the relationship between body length and breast girth, body length and wing length, body length and wing span, body length and thigh length, body length and shank length and body length and keel length slightly declined in values to 0.92±0.01, 0.79±0.14, 0.74±0.16, 0.77±0.10, 0.91±0.06 and 83±0.11 though it was still high. It gradually increased again from week 6 to 8 as shown in Tables 6 and 7. Generally, the trend of the relationship in this study was low to high and positively correlated for all the growth studied.

The result on phenotypic correlation was observed to be from low to high. This was in line with the observation made by Ezzeldin et al.[21] who had similar observation in these findings. Similarly, Peters (2000) reported medium to high genetic correlation in the Nigerian indigenous chicken which is in line with the result of this study. The present result also showed that body weight and linear parameters were positively correlated which suggests direct selection for improvement in one trait would bring about a corresponding improvement in the other trait. This was in consonance with Ebangi and Ibe[18] who observed positive correlation between body weight and the linear parameters measured in the experiment.

Table 3 Heritability and phenotypic correlations and ± standard error of growth traits of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades at day old (0 week)

	BW	**BL**	**BG**	**WL**	**WS**	**TL**	**SL**	**KL**
BW	0.34±0.10							
BL	0.41±0.03	0.22±0.10						
BG	0.30±0.04	0.29±0.04	0.37±0.20					
WL	0.25±0.04	0.25±0.05	0.13±0.04	0.38±0.15				
WS	0.28±0.04	0.29±0.05	0.21±0.04	0.82±0.02	0.37±0.10			
TL	0.33±0.04	0.30±0.04	0.26±0.03	0.26±0.05	0.35±0.04	0.11±0.05		
SL	0.11±0.01	0.04±0.02	0.10±0.02	0.01±0.00	0.10±0.02	0.04±0.01	0.02±0.01	
KL	0.32±0.02	0.23±0.04	0.14±0.04	0.150±0.04	0.17±0.04	0.012±0.04	0.08±0.02	0.21±0.04

Heritability in bold and phenotypic correlation above the diagonal. BW - Body weight, BL- Body length, BG - Breast girth, WL - Wing length, WS-Wing span, TL - Thigh length, SL – Shank length and Keel-length.

Table 4 Heritability and phenotypic correlations and ± standard error of growth traits of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades at two weeks of age

	BW	**BL**	**BG**	**WL**	**WS**	**TL**	**SL**	**KL**
BW	0.54 ±0.0							
BL	0.51±0.02	0.43±0.10						
BG	0.56±0.01	0.59±0.01	0.48±0.10					
WL	0.45±0.02	0.42±0.01	0.45±0.01	0.38±0.08				
WS	0.54±0.02	0.51±0.01	0.57±0.01	0.10±0.03	0.47±0.10			
TL	0.01±0.00	0.10±0.01	0.10±0.02	0.11±0.01	0.11±0.03	0.10±0.03		
SL	0.51±0.01	0.51±0.01	0.10±0.02	0.39±0.01	0.50±0.01	0.10±0.01	0.37±0.10	
KL	0.49±0.02	0.52±0.01	0.50±0.01	0.51±0.01	0.55±0.01	0.10±0.01	0.39±0.01	0.53±0.06

Heritability in bold and phenotypic correlation below the diagonal.BW - Body weight, BL- Body length, BG - Breast girth, WL - Wing length, WS-Wing span, TL - Thigh length, SL – Shank length and Keel-length.

Table 5 Heritability and phenotypic correlations and ± standard error of growth traits of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades at four weeks of age

	BW	**BL**	**BG**	**WL**	**WS**	**TL**	**SL**	**KL**
BW	0.61±0.10							
BL	0.69±0.03	0.50±0.15						
BG	0.60±0.01	0.57±0.02	0.55±0.15					
WL	0.52±0.01	0.43±0.03	0.52±0.01	0.39±0.10				
WS	0.70 ±0.02	0.49±0.03	0.54±0.01	0.10±001	0.46±0.15			
TL	0.74±0.02	0.60±0.03	0.54±0.02	0.52±0.01	0.68±0.01	0.48±0.10		
SL	0.77±0.01	0.61±0.02	0.60±001	0.47±0.02	0.63±0.02	0.70±0.01	0.58 ±0.06	
KL	0.68±0.00	0.55±0.02	0.71±001	0.55±0.01	0.61±0.01	0.62±0.01	0.62±0.01	0.64±0.04

Heritability in bold and phenotypic correlation below the diagonal. BW - Body weight, BL- Body length, BG - Breast girth, WL - Wing length, WS-Wing span, TL - Thigh length, SL – Shank length and Keel-length.

Table 6 Heritability and phenotypic correlations and ± standard error of growth traits of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades at six weeks of age

	BW	**BL**	**BG**	**WL**	**WS**	**TL**	**SL**	**KL**
BW	0.62±10							
BL	0.64±0.01	0.55±0.10						
BG	0.67±0.01	0.10±0.01	0.60±0.09					
WL	0.60±0.02	0.58±0.01	0.61±0.01	0.48±0.11				
WS	0.60±0.02	0.66±0,01	0.67±0.01	0.57±0.01	0.59±0.09			
TL	0.72±0.01	0.61±0.01	0.61±0.01	0.66±0.01	0.51±0.02	0.53±0.07		
SL	0.71±0.02	0.63±0.01	0.63±0.01	0.67±0.02	0.55±0.02	0.76±0.01	0.60±0.10	
KL	0.67±0.01	0.67±0.01	0.67±0.01	0.58±0.01	0.60±0.01	0.58±0.01	0.67±0.01	0.64±0.05

Heritability in bold and phenotypic correlation below the diagonal. BW - Body weight, BL- Body length, BG - Breast girth, WL - Wing length, WS-Wing span, TL - Thigh length, SL – Shank length and Keel-length.

Table 7 Heritability and phenotypic correlations and± standard error of growth traits of Nigerian indigenous chicken genotypes, exotic breed and their crosses to F2 upgrades at eight weeks of age

	BW	**BL**	**BG**	**WL**	**WS**	**TL**	**SL**	**KL**
BW	0.57±0.12							
BL	0.75±0.01	0.59±0.11						
BG	0.72±0.01	0.68±0.01	0.64±0.07					
WL	0.66±0.01	0.71±0.01	0.63±0.01	0.46±0.14				
WS	0.82±0.01	0.70±0.01	0.83±0.01	0.10±0.01	0.60±0.05			
TL	0.65±0.02	0.50±0.02	0.67±0.01	0.44±0.02	0.70±0.01	0.29±0.10		
SL	0.73±0.01	0.63±0.00	0.77±0.01	0.59±0.01	0.79±0.01	0.61±0.03	0.53±0.09	
KL	0.77±0.01	0.67±0.02	0.64±0.01	0.58±0.01	0.78±0.01	0.63±0.02	0.76±0.01	0.57±0.07

Heritability in bold and phenotypic correlation below the diagonal BW - Body weight, BL- Body length, BG - Breast girth, WL - Wing length, WS-Wing span, TL - Thigh length, SL – Shank length and KL- keel length.

6 Conclusion

The results of this study showed that sex significantly affected body weight and all the linear parameters measured from 0 to 8 weeks of age. Males performed better than females on body weight and linear body parameters (body length, breast girth, wing length, wing span, thigh length, shank length and keel length) measured in this study at all ages. The heritability estimates for all the morphometric parameters ranged from low to high values of 0.01±0.00 to 0.99±0.02. This indicated that there was existence of heritability within these chickens. Phenotypic correlation Coefficient for the morphometric parameters measured showed a low to high trend. The relationship among the morphometric parameters measured showed positive correlations.

Compliance with ethical standards

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Disclosure of conflict of interest

The author declares that there are no competing interests.

Statement of ethical approval

This research was carried out according to the ethical guidelines of the Institutional Animal Care and Use Committee (IACUC) of the International Livestock Research Institute as per the ethics application approval numbers 2014.15 and 2014.16.

Author declaration

The author declared that this article is original article submitted for publication which has not been published anywhere in the world.

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