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Genetic Correlations and Genotype Effect on the Growth Traits of Nigerian Broiler Genotypes

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ABSTRACT

The study evaluated genotype effect on growth traits and genetic correlations of Nigerian indigenous chicken (NIC) broiler genotypes at the T&R farm of FUNAAB. NICs- Normal feathered(N), Frizzle-feathered(Fz) and Naked neck(Nk) chickens were crossed with Marshall(M) Exotic breed to obtain F_1(MN, MNk, MFz) and F_2 upgrades(MMN, MMFz, MMNk) for the study. The design of the experiment was RCBD. Growth traits data on 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) were easured for 8 weeks. Data were analyzed using the GLM of SAS ver. 9.2. Results showed that genotype significantly ($p<0.001$) affected BW and linear body parameters studied. At 8 weeks, BW were 1,252.25±40.94g, 1,172.66±39.51g, 1,110.23±29.42g, 1,055.88±26.67g, respectively for M, MMFz, MMNk, MMN and 904.38±25.16g, 816.52±23.89g, 805.24±21.68g for MNk, MFz and MN genotypes, respectively while 791.92±17.95g, 637.05±17.96g and 619.71±19.18g were recorded for Fz, Nk, N, respectively. For F_2 upgrades, MMFz upgrade recorded highest BW (1,172.66±39.51g); for F_1 crosses, MNk recorded highest BW(904.38±25.16g) while Fz was the heaviest (791.92±17.95g) amongst purebreds. Marshall (control) led in all the linear body measurements, except for TL and SL studied. Heritability ranged was low to high with 0.02±0.05 to 0.64±0.05. SL had lowest h^2 value while KL recorded the highest as measured. Genetic correlations showed low to high positive relationships of 0.01 to 0.83 range. In conclusion, F_2 upgrades performed best in growth performance, regarded as NIC broilers genotypes. MMFz and MMNK upgrades performed the best for growth traits measured in NIC broiler genotypes of this study.

KEYWORDS: Chicken, Correlation, Genetic, Heritability, Morphometric, Parameters.

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INTRODUCTION

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 (Xu *et al.*, 2013). It has some interesting economic traits such as a short reproductive cycle and is highly prolific which greatly increases productivity. Nigerian indigenous chickens with their small body size compared to the exotic breeds of chicken reared intensively which had been selected for fast growth rate over time as such need some improvement measures to adopt such as selection, crossbreeding in intensive system of production to transform Nigerian poultry industry (Peters *et al.*, 2000). Marker-assisted selection (MAS) which increases selection efficiency can be linked with quantitative traits loci and serves in direct selection of genotype which further improves productive traits (Lamont *et al.*, 1996). A good mating combination of the breeding stock should produce offspring which are improved in growth rate, efficiency of feed conversion and reproductive traits with less production cost. A programme which will allow a successful selection when associating productive traits of interest are carefully selected or improved few traits at a time rather than all at once, will be expected of greater genetic progress in any meat chicken (Adebambo *et al*., 1999). Understanding the genetic control of growth in chickens will provide an opportunity for the genetic improvement of production performance and physiology (Li *et al*., 2003). The rationale of conservation and sustainable use of indigenous chicken (IC) resources requires their Morph biometrical characterization Habimana *et al*. (2020)

Hence, this study aimed at evaluation of genotype effect on the morphometric and genetic parameters of Nigerian Indigenous Chickens broilers.

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 of Federal University of Agriculture, Abeokuta, Alabata Road, Abeokuta. Alabata is at latitude 7°10`N and longitude 3°2`E in Odeda Local Government Area of Ogun State, Nigeria. The area is characterized with a tropical climate with a mean annual rainfall of about 1037mm. The mean monthly ambient temperature ranged from 28- 36°C and 34°C 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 (University Meteorological Unit, 2023).

2.2 Experimental stock

2.2.1. Parents

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 were 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 crossed 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 (F_2 upgrade) fifty chickens per genotype (sample size) making five hundred chickens altogether. The genotypes are presented below:

3.2.2 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 (F_1crosses)

5. M X N = MN (F_1)
6. M X Fz = MFz (F_1)
7. M X Nk =MNk (F_1)

75%:25% (M: Ind) bloodline (F_2 upgrades)

8. M X MN =MMN (F_2)
9. M X MF =MMFz (F_2)
10. M X MNk =MMNk (F_2)

M- Marshall Exotic breed, N-Normal-Feathered, Fz-Frizzle-Feathered,
Nk-Naked Neck chicken genotype, M: Ind = Marshall: indigenous.

3.3 Inseminations, 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 singly and 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 F_1 birds with 50%: 50% M: Ind bloodline (dihybrid crosses) and F_2 birds with 75%:25% M: Ind bloodline (F_2 upgrades).

3.3.1 Egg collection, incubation and hatching

Eggs from each mating group were collected daily and labelled according to sire-line. The eggs were then transferred to the University's Teaching and Research farm 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 a mixture of 35g potassium permanganate in 53cc formalin per cubic meter. 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 the 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.

3.4 Housing, feeding and management

Chicks obtained were identified by wing-tagged immediately after hatching in respect to their sire line. 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 three weeks of age. At four weeks of age, chicks were transferred to already compartmentalized rearing pens of 48.5 x 37 x 41.5 cm deep litter system to accommodate 50 birds per genotype and fed with grower mash (20 CP and 3000Kcal/Kg (ME)) till six weeks. Placement into each compartment was randomly done. Water was constantly supplied to the chicks and fed *ad libitum* with commercial broiler feed then switched to finisher ration that supplied 19.5% CP and 3080kcal/kg (ME) from six weeks to eight weeks of age when the project terminated. Routine vaccinations and drug administration were administered: Newcastle vaccine on day one, NDV-Komorov on the 9th and 17th day, Gumboro on 16 and 26th day, Fowl Pox on the 6th week and Coccidiostat at 2 weeks interval.

3.5 Data collection

3.5.1 Growth

The chicks body weights (BW) were weighed weekly from day old to 8 weeks of age with 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 tailor's tape: **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 tarso-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 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 phalanges 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.

3.5.2 Statistical analyses

Analysis of variance for the body parameters was done with (2010, v. 9.2) software Package using General Linear Model. Means were separated using Duncans Multiple Range Test at a probability of 5% level.

Experimental models:

Model 1

$Y_{ijk} = \mu + G_i + \varepsilon_{ij}$

Y_{ijk} = Observation of the $_i$th genotype on the $_j$th bird

μ = Overall mean

G_i = Effect of the $_i$th chick genotype ($_i$ = 1, 2 …10)

ε_{ij} = Error due to individual observation

3.5.3 Heritability, Genetic Correlations

Heritability, genetic correlations and their standard errors were carried out using IML (Integrated matrix language) in SAS [8] (2010, v.9.2) software. Means was separated using Duncans Multiple Range test.

$$\text{Heritability } (h^{2)} = \frac{4\hat{\delta}^2_S}{\delta^2_S + \delta^2_D + \delta^2_W}$$

Where,

δ^2_S = Variance component of Sire (MS_S - MS_D/K_3)

δ^2_D = Variance component of Dam (MS_D-MSw/k_1)
δ^2_W = Variance component of within offspring ($SS_w/df_w = MS_w$)
k_1 = number of offspring per dam
k_3 = number of offspring per sire

$$\text{Genetic correlation} = \frac{4Covs_{(XY)}}{\sqrt{\delta^2_{S(x)} \times \delta^2_{S(y)}}}$$

Where:
Cov_s = Covariance of sire for x and y trait
Cov_w = covariance of within progeny for x and y trait
$\delta^2_{S(x)}$ = variance component of sire for x trait
$\delta^2_{S(y)}$ = variance component of sire for y trait
$\delta^2_{w(x)}$ = variance component of within progeny for x trait
$\delta^2_{w(y)}$ = variance component of within progeny for y trait.

3. RESULTS AND DISCUSSION

Effect of genotype on the growth traits

Genotype significantly ($p<0.0001$) affected body weight and all the linear body parameters measured at weeks 0 to 8 in this study. The least square means of body weights (BW) as affected by genotype are presented in Table 1. The least square means of linear body parameters as affected by genotypes are presented in Tables 2 to 7.

Effect of genotype on body weight

M breed had the highest body weight from 0 to 8 weeks as the control. Amongst the purebred, the body weight of purebred indigenous chickens were not significantly ($p>0.0001$) different from each other from 0 to 3 weeks. At weeks 4 to 8 purebred Fz genotype had means statistically ($p<0.0001$) higher (243.05±10.21 g, 342.31±13.44 g, 497.93 g±12.45 g, 632.69±15.58 g, 791.92±17.95 g) than Nk (217.35±8.72 g, 289.08±10.98 g, 371.62±12.36 g, 543.86±12.56 g, 637.05±17.69) and N (207.89±7.60 g, 276.44±8.88 g, 345.67±12.22 g, 519.40±12.35 g, 619.71±19.18 g) genotypes.

Comparison of means of the F_1 crossbreds revealed that the body weights of MN, MFz and MNk were not significantly different at all ages except at 3rd and 8th week in which the MNk chickens with 251.12±4.81 g, 904.38±25.16 g were statistically ($p< 0.0001$) higher than MFz (225.26±6.72 g, 816.52 g±23.89 g) and MN (214.038.65 g, 805.24±21.68 g) but at 0 week (day old) MFz (35.53±0.39 g) was statistically ($p< 0.0001$) higher than MN (33.50±0.73 g) and MNk (32.23±0.53 g) genotypes.

Comparison of means of the F_2 upgrades showed that, the body weights of MMN, MMFz and MMNk were not significantly ($p>0.0001$) different at all ages except at weeks 2, 3, 4, and 8 that MMFz with 193.07±7.86 g, 322.90±10.53 g, 419.47±11.39g, 1172.66±39.51 g were statistically ($p< 0.0001$) different from MMNk (159.93±4.43 g, 264.25±7.08 g, 400.64±9.97 g, 1110.23±29.42 g) and MMN (157.28±4.95 g, 262.41±8.25 g, 379.10±8.89 g, 1055.88±26.67 g) genotypes. Also at weeks 1 and 7 MMFz with 89.74±1.83 g, 915.57±25.25 g were statistically ($p< 0.0001$) higher than MMN with 81.65±1.98 g, 867.15±19.82 g. Generally, the values obtained for body weights (Table 1) showed that the F_2 upgrades had the highest mean body weights while purebreds indigenous were the least.

Effect of genotypes on linear body measurements

The results of the analysis revealed that genotype significantly ($p<0.0001$) affected all linear parameters (body length (BL), breast girth (BG), wing length (WL), wing span (WS), thigh length (TL), shank length (SL) and keel length (KL)) from 0 to 8 weeks measured.

The mean values for BL, BG, WL, WS, TL, SL and KL followed the same pattern noticed for body weights at all ages. Between the Nigerian indigenous purebred chickens, Fz had higher values significantly ($p<0.0001$) different from others at different ages from weeks 6 to 8 in BG, WL, WS and TL as shown in Tables 2 to 7.

The least square means of BL at all ages (Table 2) showed that F_2 upgrades had values comparatively similar to M breed (control). However, MMFz had the highest mean values in body length at all ages though statistically ($p>0.0001$) similar to MMNk. Similarly, from weeks 1, 4, 6 to 8 MMFz had the higher values of 6.17±0.10 cm, 10.36±0.18 cm, 13.31±0.18 cm, 15.14±0.20 cm and 17.55±0.26 cm statistically ($p<0.0001$) different from MMN (5.71±0.09 cm, 9.92±0.14 cm, 12.79±0.12 cm, 14.24±0.13 cm and 15.98±0.19 cm) though at 0 week MMN (5.19±0.09 cm) was statistically ($p<0.0001$) higher than MMNk upgrade (4.72±0.05 cm) and MMF(4.51±0.07 cm). Among the F_2 upgrades, MMFz performed best in BL while MMN upgrade was the least.

Comparison between the F_1 crosses showed that MNk had values in BL statistically ($p>0.0001$) similar to MFz except at day-old and week 4 that MFz had 4.70±0.06 cm, 9.50±0.09 cm significantly ($p<0.0001$) higher than 4.35±0.11 cm, 9.44±0.13 cm of MNk. However, MNk had higher values from 3 to 8 weeks of age with 8.12±40.13 cm, 9.44±0.13 cm, 10.77±0.09 cm, 12.09±0.11 cm, 13.60±0.16 cm, 15.49±0.16 cm significantly ($p<0.0001$) different from MN cross (7.25±0.12 cm, 7.69±0.13 cm, 9.38±0.15 cm, 10.73±0.18 cm, 12.52±0.20 cm and 14.53±0.22 cm) although at day old MN with 4.60±0.05 cm was statistically ($p<0.0001$) different from MNk (4.35±0.11 cm) genotypes. MNk cross had the highest values in BL among the F_1 crosses while MN performance was the least.

Comparison between indigenous purebreds revealed that Fz purebred were not statistically ($p>0.0001$) different from the other purebreds except at weeks 1, 5 to 8, that, the Fz purebred chickens (5.30±0.09 cm, 9.12±0.21 cm, 10.57±0.16 cm, 12.28±0.19 cm and 13.90±0.21 cm) were statistically ($p<0.0001$) higher than N purebred of 5.04±0.07 cm, 8.46±0.16 cm, 9.72±0.16 cm, 11.08±0.14 cm and 12.42±0.16 cm. Fz genotype performed best of all the indigenous purebreds while N genotype was the least. Generally, the F_2 upgrades had the highest in BL while purebred indigenous were the least (Table 2).

The least square means of BG at all ages (Table 3) showed that F_2 upgrades had values statistically ($p>0.0001$) similar to M breed. Similarly, MMFz had higher values in BG at all ages though statistically ($p>0.0001$) similar to the other counterparts in some weeks. Result showed that MMFz from weeks 0, 1, 5 to 8 had means of 7.41±0.37 cm, 8.54±0.11 cm, 15.62±0.18 cm, 18.27±0.27 cm, 21.38±0.29 cm, 25.12±0.36 cm statistically ($p<0.0001$) higher than MMNk (5.31±0.12 cm, 8.11±0.13 cm, 14.97±0.25 cm, 17.15±0.28 cm, 20.00±0.36 cm, 22.59±0.40 cm) and MMN with 6.42±0.11 cm, 8.02±0.15 cm,14.80±0.23 cm, 16.72±0.27 cm, 18.97±0.29 cm, 21.31±0.33 cm. Likewise, 3rd and 4th week that MMFz were statistically ($p<0.0001$) higher with 11.71±0.15, 13.45±0.15 than MMN with 11.22±0.13 cm, 12.76±0.16 cm.

Comparison between F_1 Crosses revealed that MNk had the widest BG of 9.18±0.12 cm, 10.55±0.13 cm, 14.26±0.23 cm, 16.24±0.24 cm,18.38±0.27 cm, 20.94±0.33 cm for weeks 2, 3, 5 to 8 statistically ($p<0.0001$) different from MF (8.77±0.12 cm, 9.91±0.16 cm, 13.66±0.17 cm, 15.36±0.19 cm, 17.13±0.24 cm, 19.21±0.28 cm) and MN (8.37±0.15 cm, 9.49±0.18 cm, 12.07±0.23 cm, 14.01±0.25 cm, 16.32±0.31 cm, 18.61±0.37 cm) as well as week 4 of 10.93±0.22 while MFz of 12.37±0.16 cm was higher, respectively but similar at weeks 0 and 4.

Among the Nigerian purebred indigenous, Fz genotype had the widest ($p<0.0001$) BG mean values in weeks 1, 5 and 8 of 7.07±0.09 cm, 12.01±0.19 cm, 16.77±0.22 cm than Nk (6.62±0.07 cm, 11.39±0.29 cm, 16.00±0.38 cm) and N chickens (6.59±0.13 cm, 10.66±0.17 cm, 15.33±0.26) cm, also Fz was higher ($p<0.0001$) significantly in values at weeks 2, 3, 4, 6, 7 (8.15±0.14 cm, 9.57±0.14 cm, 10.90±0.17 cm, 13.19±0.20 cm, 14.81±0.21 cm) than N with 7.45±0.07 cm, 8.36±0.11 cm, 9.37±0.14 cm, 11.97±0.19 cm, 13.32±0.20 cm but relatively similar to Nk genotype. Similarly, Frizzle-feathered upgrade had the widest breast girth while the purebred indigenous came least.

The least square mean values for WL in Table 4 showed that, among the F_2 upgrades, MMFz at weeks 1, 3, 6, 8 of age had higher mean values of 6.79±0.09 cm, 9.91±0.09 cm, 15.36±0.16 cm, 20.05±0.21 cm for WL significantly ($p<0.0001$) different from MMNk upgrade with 6.15±0.11 cm, 9.45±0.14 cm, 14.87±0.23 cm, 19.25±0.26 cm and MMN with 6.13±0.10 cm, 9.15±0.16 cm, 14.87±0.15 cm, 19.27±0.36 cm. Also, at weeks 2, 4, 5 and 7 MMFz (8.48±0.15 cm, 11.46±0.08 cm, 13.13±0.14 cm, 17.73±0.02 cm) was significantly ($p<0.0001$) different from MMN (7.81±0.03 cm, 10.69±0.16 cm, 12.67±0.18 cm, 16.86±0.18 cm) although at day old MMN (5.44±0.08 cm) was significantly higher than MMFz upgrade (4.46±0.06 cm).

Within the F_1 crosses MNk values in WL were statistically ($p<0.0001$) different (7.86±0.10 cm, 12.27±0.19 cm, 14.54±0.18 cm) at weeks 2, 5 and 6 from MFz (7.58±0.10 cm, 11.92±0.15 cm, 14.06±0.13 cm). Similarly, MNk with (4.39±0.06 cm, 6.14±0.06 cm) were significantly ($p<0.0001$) lower than MN cross (4.72±0.05 cm, 6.48±0.11 cm) at weeks 0 and 1 but at weeks 5 to 7 MNk had values (12.57±0.19 cm, 14.54±0.18 cm, 16.35±0.17 cm) higher ($p<0.0001$) than MN (11.92±0.15 cm, 13.38±0.18 cm, 15.81±cm) but similar in all other ages (Table 4).

Comparison among the purebreds indigenous revealed that Fz purebred was statistically ($p<0.0001$) higher in WL mean values than other purebreds at weeks 1, 2 and 6 with the values 5.79±0.10 cm, 7.48±0.13 cm, 12.85±0.26 cm and Nk (5.62±0.12 cm, 6.81±0.10 cm, 13.30±0.20 cm) then N purebred (5.43±0.07 cm, 6.78±0.08 cm, 11.80±0.17 cm). Also, at weeks 4, 5, 7, 8 Fz had mean of 10.27±0.12 cm, 11.52±0.15 cm, 15.28±0.21 cm, 17.14±0.22 cm statistically ($p<0.0001$) higher than N chickens with 9.13±0.13 cm, 10.22±0.14 cm, 13.44±0.19 cm, 15.00±0.17 cm but similar to Nk Nigerian purebred.

The least square mean values of TL (Table 5) were significantly ($p<0.0001$) similar in all the upgrades at all ages except at weeks 4, 5 and 8 that MMFz upgrade was significantly ($p<0.0001$) higher in values 10.90±0.14 cm, 12.86±0.22 cm, 17.90±0.43 cm than MMNk (9.92±0.12 cm, 11.55±0.12 cm, 17.09±0.25 cm) and MMN with 9.77±0.10 cm, 11.15±0.15 cm, 16.57±0.22 cm. Also, MMFz was significantly ($p<0.0001$) higher (9.48±0.11 cm, 13.63±0.17 cm, 15.42±0.43 cm) than MMN (8.47±0.12 cm, 12.78±0.18 cm, 14.68±0.14 cm) at weeks 3, 6, 7 but similar to MMNk and other ages they were similar in means.

Comparison between all the F_1 genotypes were similar in TL values at all ages except at 4 and 6 weeks that MNk with 92.92±0.14 cm and 12.48±0.16 cm were significantly ($p<0.0001$) higher than MFz (9.36±0.13 cm, 11.62±0.16 cm) and MN (9.37±0.11 cm, 11.45±0.20 cm). Also, at weeks 0, 2, 3, 5, 7, 8 MNk genotype with 5.23±0.03 cm, 7.34±0.08 cm, 8.02±0.10 cm, 10.97±0.08 cm, 13.96±0.18 cm and

16.17±0.19 cm were significantly ($p<0.0001$) higher in values than MN cross (5.05±0.04 cm, 7.21±0.09 cm, 8.11±0.11 cm, 10.31±0.13 cm, 13.41±0.17 cm and 15.33±0.16 cm).

Among the purebreds indigenous Fz was significantly ($p<0.0001$) different from Nk and N genotypes at weeks 6, 7 and 8 (Table 5).

The least square means of SL as affected by genotype presented in Table 6 showed that comparison between M breed and the F_2 upgrades, revealed that, the MMFz had values in SL relatively similar to M breed in all ages except at weeks 4, 6 and 7 that MMFz had values lower than M breed but statistically higher (12.88±0.22 cm, 16.07±0.28 cm) than Marshall genotype (10.85±0.22 cm, 13.39±0.22 cm) at week 5 and 8, respectively.

Within the F_2 upgrades, MMFz upgrade was statistically ($p<0.0001$) higher in values than other counterparts at weeks 0, 3, 4, 5, 7 and 8 but similar at weeks 1, 2 and 6 (Table 6).

Among the F_1 crosses, MNk had values of 6.04±0.06 cm, 7.00±0.08 cm, 11.35±0.14 cm significantly ($p<0.0001$) higher than MFz with 5.53±0.06 cm, 6.63±0.09 cm, 10.74±0.18 cm and MN (5.52±0.08 cm, 6.27±0.11 cm and 10.25±0.19 cm) at weeks 2, 3, and 7 but similar in all other ages. However, of all the indigenous purebreds the shank length values were statistically similar at all ages in this study. Generally, MMFz upgrade had the highest mean values in SL measurement while indigenous purebreds had the lowest.

The least square means of KL as affected by genotype presented in Table 7 showed that, on comparing F_2 upgrades, MMFz upgrade was significantly ($p<0.0001$) higher in mean values of 4.46±0.17 cm, 5.49±0.07 cm, 10.14±0.23 cm than MMN upgrade (4.14±0.04 cm, 5.19±0.05 cm, 9.07±0.14 cm) at weeks 3, 4 and 8 but similar to MMNk. MMFz and MMN were similar at all ages except at week 8 that MMNk (9.11±0.13 cm) was statistically ($p<0.0001$) lower than MMFz with 10.14±0.23 cm (Table 7).

Within F_1 crosses, Marshall Naked Neck was statistically ($p<0.0001$) higher than other F_1 crosses at weeks 2, 4, 7 and 8 (Table 8). Fz purebreds were significantly ($p<0.0001$) higher at weeks 2, 3, 4 and 5 than the Nk and NM purebreds as presented in Table 7.

Generally, the performance in this study reflected this trend of 75:25% Marshall: Indigenous bloodline (F_2 upgrades) being the leading genotype followed by 50:50% Marshall: Indigenous bloodline (di-hybrid) while the least was the purebred indigenous genotype. And from all indications in this study, at the 75:25% Marshall: Indigenous bloodline (F_2 upgrades) our chicken genotypes can be addressed as Nigerian broiler chickens since they compete comparatively similar to the Marshall exotic chicken.

The results of BW as affected by genotype showed that M breed as a control performed slightly better than F_2 (75:25% M: Ind) upgrades followed by F_1 (50:50% M: Ind) cross then purebred indigenous as the least. The M breed being exotic which was known for intense selection for fast growth rate over time was expected to have the highest weight. Nevertheless, F_2 upgrades (75:25% M: Ind) performed comparatively similar to Marshall in body weight but performed better than the F_1 cross while indigenous purebreds were the least in performance. The reason could be as a result of heterosis, also due to the high percentage of exotic blood incorporation compared to the indigenous in the genotype. The di-hybrid being next to the F_2 upgrade could be due to the same reason of exotic blood present in the genotype which transferred the fast growth rate and high meat yield qualities to the progenies. This improved the slow growth rate and light breed qualities of the Nigerian indigenous chicken. This higher performance of the offspring when traced back to the performance of the stock confirmed the existence of heterosis as was also observed by Peters (2005).

Within the F_2 upgrades, the Frizzle-feathered upgrade had highest mean values superior to Naked Neck upgrade while Normal feathered upgrade was the least, hence, Frizzle-feathered upgrade emerged the best performing genotype in this study. From the result of this study Frizzle-feathered was the heaviest genotype of all the three purebred Nigerian indigenous chicken genotypes followed by Naked Neck and then the Normal feathered Adedeji *et al.* (2004) corroborated this result that Naked Neck and Frizzled-Feathered chickens performed better than Normal feathered types in body weight and linear body measurement traits.

Exotic genotype performed best in all the linear body parameters as expected of the control, but the values were quite similar to those of F_2 upgrades except in shank length and thigh length. The better performance found in shank and thigh lengths observed in the upgrades could be attributed to the presence of indigenous blood in the genotype of the F_2 upgrades. Long thigh and shank length is one of the adaptive features which served the Nigerian indigenous chickens from environmental stress both in feeding and escaping of some environmental dangers while the shortness of the shank and the thigh lengths of exotic breed were for better support of its heavy bodied weight preventing the birds from paralyzing. The short shank and thigh lengths observed for Marshall Breed was in concurrent with the observation of Deeb and Lamout (2002) who reported that the shortness of the shank and thigh lengths of the exotic breed were to support its heavy-bodied weight. This was supported by Adebambo *et al.* (2010) who reported the long shank and thigh lengths in Nigerian chickens.

It was also observed that there was a steady and gradual increment in growth rate both in body weight and other body parameters at all ages. This findings is in consonance with the observation by Peters (2005); Adebambo *et al.* (2010) who observed the growth pattern of Nigerian chickens to be in a steady and gradual increment. The steady and gradual growth increment of Nigerian birds observed in the present study was also observed by Adedeji *et al.* (2008). At a late age of between 6 and 8 weeks the rate of growth increment was rapid, this could be attributed to sex dimorphism as corroborated by Ikeobi *et al*. (1996) who stated the onset of sexual dimorphism to be visible from week 6 to 8.

Frizzle-feathered upgrade performance in breast girth and keel length was quite similar to those of the Marshall, although the Marshall mean values were slightly higher. Marshall exotic (Control) had superior values in breast girth and keel lengths on considering the number of the genotypes involved in this study, the fact remains the same that Marshall exotic breed had been developed and selected over time for meat potentials and fast growth quality.

However, considering the Nigerian chickens genotypes in this study, MMFz upgrade had the widest breast girth and the longest keel lengths which are the choice parts in broiler meat production. Among the F_2 upgrades, MMFz upgrade was the best while MMNk was next and MMNF had the least means for the breast girth and keel lengths. This was due to the same reason of having the 75% and 50% exotic genetic contribution which impacted the fast growth rate and high meat yield. This result further proved that crossbreeding is a tool for genetic improvement of Nigerian indigenous breeds. This finding confirmed the conclusion of Adebambo *et al.* (1996) and Peters (2005); Peters *et al*. (2008) and Adeleke *et al.* (2011) that Nigerian indigenous chicken has the potential for genetic improvement.

Table 1: Effect of genotype on body weight (LSM±SE) (g)

		Weeks								
Genotype	N	0	1	2	3	4	5	6	7	8
M	50	39.25± 0.60^{a}	122.28±3.56^{a}	222.56±8.43^{a}	335.31±9.62^{a}	454.45±12.78^{a}	617.57±17.80^{a}	803.56±23.12^{a}	1037.45±34.20^{a}	1252.25±40.94^{a}
NXN	50	30.82±0.72^{de}	61.44±1.69^{f}	97.20±2.96^{f}	148.05±8.55^{d}	207.89±7.60^{g}	276.44±8.88^{f}	345.67±12.22^{e}	519.40±12.35^{f}	619.71±19.18^{f}
FzXFz	46	29.87± 0.30^{e}	68.87±1.99^{e}	109.92±3.56^{ef}	154.93±5.95^{d}	243.05±10.21^{f}	342.31±13.44^{e}	497.93±12.45^{d}	632.69±15.58^{e}	791.92±17.95^{e}
NKXNK	48	33.97±1.29^{bc}	64.78±1.40^{ef}	107.30±5.69^{ef}	149.75±8.13^{d}	217.35±8.72^{g}	289.08±10.98^{f}	371.62±12.36^{e}	543.86±12.56^{f}	637.05±17.96^{f}
MXN	49	33.50±0.73^{c}	69.02±2.43^{e}	117.89±3.91^{e}	214.03±8.65^{c}	318.18±9.03^{e}	425.59±12.87^{d}	522.49±9.94^{cd}	657.48±16.76$^{d e}$	805.24±21.68^{e}
MXFz	48	35.53±0.39 ^{b}	70.30±1.80^{de}	133.86±3.25^{d}	225.26±6.72^{c}	327.02±11.29^{e}	428.05± 8.61^{d}	548.34±15.69^{c}	669.14±20.94$^{d e}$	816.52±23.89^{e}
MXNK	50	32.23±0.53^{cd}	75.14±1.73^{d}	147.66±4.39^{cd}	251.12±4.81^{b}	334.46±6.28^{e}	435.57±13.53^{d}	548.29±16.30^{c}	700.89±19.97^{d}	904.38±25.16^{d}
MXMXN	50	37.61±0.51^{a}	81.65±1.98^{c}	157.28±4.95^{c}	262.41±8.25^{b}	379.10±8.89^{d}	518.89±12.69^{c}	683.22±18.63^{b}	867.15±19.82^{c}	1055.88±26.67^{c}
MXMXFz	47	38.54±0.52^{a}	89.74± 1.83^{b}	193.07±7.86^{b}	322.90±10.53^{a}	419.47±11.39^{b}	553.99±12.45^{b}	699.70±15.38^{b}	915.57±25.25^{b}	1172.66±39.51^{b}
MXMXNK	50	39.18±0.79 ^{a}	86.49±1.31^{bc}	159.93±4.43^{c}	264.25±7.08^{b}	400.64±9.97^{c}	539.95±13.88^{bc}	688.22±16.75^{b}	872.6±23.75^{bc}	1110.23±29.42^{c}

$^{a, b, c, d, e, f, g}$ Means within the same column with the same superscripts are not significantly different. MxM-Pure Marshall, NxN- Pure Normal-feathered, Fzx Fz-Pure Frizzle-feathered, NKxNK-Pure naked neck, MxN-Dihybrid Normal-Feathered, MxFz-dihybrid Frizzle-Feathered, MxNK-dihybrid Naked Neck, MxMxN-Normal-Neathered upgrade, MxMxFz-Frizzle upgrade, MxMxNK-Naked Neck upgrade.

Table 2: Effect of genotype on body length (LSM±SE) (cm)

		Weeks								
Genotype	N	0	1	2	3	4	5	6	7	8
MXM	50	5.02±0.07^{a}	6.30±0.09^{a}	7.41±0.13^{a}	8.78±0.13^{a}	9.81±0.14^{bc}	11.53±0.20^{a}	13.81±0.21^{a}	16.17±0.25^{a}	18.76±0.28^{a}
NXN	50	4.39±0.05^{cd}	5.04±0.07^{g}	5.82±0.07^{c}	6.61±0.10^{f}	8.18±0.14^{e}	8.46±0.16^{d}	9.72±0.16^{g}	11.08±0.14^{g}	12.42±0.16^{g}
FzXFz	46	4.46±0.06^{cd}	5.30±0.09^{ef}	6.0±0.10^{c}	6.92±0.13^{ef}	8.06±0.16^{e}	9.12±0.21^{c}	10.57±0.16^{ef}	12.28±0.19^{ef}	13.90±0.21^{ef}

NKXNK	48	4.60 ± 0.07^{bc}	5.17 ± 0.06^{fg}	6.08 ± 0.12^{c}	6.99 ± 0.16^{e}	8.08 ± 0.17^{e}	9.17 ± 0.17^{c}	10.30 ± 0.23^{f}	11.93 ± 0.25^{f}	13.34 ± 0.28^{f}
MXN	49	4.60 ± 0.05^{bc}	5.42 ± 0.07^{de}	6.52 ± 0.09^{b}	7.25 ± 0.12^{e}	7.69 ± 0.13^{f}	9.38 ± 0.15^{c}	10.73 ± 0.18^{e}	12.52 ± 0.20^{e}	14.53 ± 0.22^{e}
MXFz	46	4.70 ± 0.06^{b}	5.46 ± 0.08^{de}	6.69 ± 0.11^{b}	7.97 ± 0.12^{d}	9.50 ± 0.09^{c}	10.66 ± 0.16^{b}	12.04 ± 0.17^{d}	13.50 ± 0.16^{d}	14.90 ± 0.29^{d}
MXNK	50	4.35 ± 0.11^{d}	5.54 ± 0.09^{cd}	6.75 ± 0.09^{b}	8.12 ± 40.13^{cd}	9.44 ± 0.13^{d}	10.77 ± 0.09^{b}	12.09 ± 0.11^{d}	13.60 ± 0.16^{d}	15.49 ± 0.16^{d}
MXMXN	50	5.19 ± 0.09^{a}	5.71 ± 0.06^{c}	7.17 ± 0.079^{a}	8.36 ± 0.10^{bc}	9.92 ± 0.14^{b}	10.36 ± 0.18	12.79 ± 0.12^{c}	14.24 ± 0.13^{c}	15.98 ± 0.19^{c}
MXMXFz	47	4.51 ± 0.07^{bcd}	6.17 ± 0.10^{ab}	7.38 ± 0.11^{a}	8.67 ± 0.12^{ab}	10.36 ± 0.18^{a}	11.82 ± 0.19^{a}	13.31 ± 0.18^{b}	15.14 ± 0.20^{b}	17.55 ± 0.26^{b}
MXMXNK	50	4.72 ± 0.05^{b}	6.07 ± 0.07^{b}	7.30 ± 0.07^{a}	8.35 ± 0.09^{bc}	9.91 ± 0.09^{a}	11.55 ± 0.15^{a}	12.96 ± 0.19^{bc}	14.74 ± 0.18^{b}	16.26 ± 0.18^{b}

[a, b, c, d, e, f, g, h] Means within the same column with same superscripts are not significantly different; MxM-Pure Marshall, NxN- Pure Normal-Feathered, Fzx Fz-Pure Frizzle-Feathered, NKxNK-Pure Naked Neck, MxN-Dihybrid Normal-Feathered, MxFz-dihybrid Frizzle-Feathered, MxNK-dihybrid Naked Neck, MxMxN-Normal-Feathered upgrade, MxMxFz-Frizzle upgrade, MxMxNK-Naked Neck upgrade.

Table 3: Effect of genotype on breast girth (LSM±SE) (cm)

						Weeks				
Genotype	N	0	1	2	3	4	5	6	7	8
MXM	50	7.99 ± 0.24^{a}	9.16 ± 0.24^{a}	10.53 ± 0.20^{a}	11.96 ± 0.18^{a}	13.59 ± 0.23^{a}	15.98 ± 0.23^{a}	18.67 ± 0.26^{a}	21.11 ± 0.38^{a}	24.53 ± 0.62^{a}
NXN	50	6.17 ± 0.08^{cd}	6.59 ± 0.13^{f}	7.45 ± 0.07^{f}	8.36 ± 0.11^{g}	9.37 ± 0.14^{d}	10.66 ± 0.17^{g}	11.97 ± 0.19^{g}	13.32 ± 0.20^{g}	15.33 ± 0.26^{f}
FzXFz	46	5.80 ± 0.08^{de}	7.07 ± 0.09^{de}	8.15 ± 0.14^{e}	9.57 ± 0.14^{ef}	10.90 ± 0.17^{c}	12.01 ± 0.19^{e}	13.19 ± 0.20	14.81 ± 0.21^{f}	16.77 ± 0.22^{e}
NKXNK	48	6.31 ± 0.08^{c}	6.62 ± 0.07^{f}	8.06 ± 0.14^{e}	9.23 ± 0.19^{e}	10.43 ± 0.24^{c}	11.39 ± 0.29^{f}	12.80 ± 0.31^{f}	14.45 ± 0.35^{f}	16.00 ± 0.38^{f}
MXN	49	6.31 ± 0.07^{c}	7.16 ± 0.11^{de}	8.37 ± 0.15^{e}	9.49 ± 0.18^{ef}	10.93 ± 0.22^{c}	12.07 ± 0.23^{e}	14.01 ± 0.25^{e}	16.32 ± 0.31^{e}	18.61 ± 0.37^{d}
MXFz	46	7.58 ± 0.09^{ab}	7.42 ± 0.08^{de}	8.77 ± 0.12^{d}	9.91 ± 0.16^{e}	12.24 ± 0.15^{b}	13.66 ± 0.17^{d}	15.36 ± 0.19^{d}	17.13 ± 0.24^{d}	19.21 ± 0.28^{d}
MXNK	50	6.01 ± 0.09^{cd}	7.51 ± 0.10^{d}	9.18 ± 0.12^{c}	10.55 ± 0.13^{d}	12.37 ± 0.16^{b}	14.26 ± 0.23^{c}	16.24 ± 0.24^{c}	18.38 ± 0.27^{c}	20.94 ± 0.33^{c}
MXMXN	50	6.42 ± 0.11^{c}	8.02 ± 0.15^{c}	9.63 ± 0.18^{b}	11.22 ± 0.13^{c}	12.76 ± 0.16^{b}	$14.80\pm0.23^{b\,c}$	16.72 ± 0.27^{bc}	18.97 ± 0.29^{c}	21.31 ± 0.33^{c}
MXMXFz	47	7.41 ± 0.37^{b}	8.54 ± 0.11^{b}	9.91 ± 0.13^{b}	11.71 ± 0.15^{ab}	13.45 ± 0.15^{a}	15.62 ± 0.18^{a}	18.27 ± 0.27^{a}	21.38 ± 0.29^{a}	25.12 ± 0.36^{a}
MXMXNK	50	5.31 ± 0.12^{e}	8.11 ± 0.13^{c}	9.63 ± 0.13^{b}	11.32 ± 0.25^{bc}	13.43 ± 0.22^{a}	14.97 ± 0.25^{b}	17.15 ± 0.28^{b}	20.00 ± 0.36^{b}	22.59 ± 0.40^{b}

[a, b, c, d, e, f, g, h] Means within the same column with same superscripts are not significantly different. MxM-Pure Marshall, NxN- Pure Normal-feathered, Fzx Fz-Pure Frizzle-Feathered, NKxNK-Pure Naked Neck, MxN-Dihybrid Normal-Feathered, MxFz-dihybrid Frizzle-Feathered, MxNK-dihybrid Naked Neck, MxMxN-Normal-Feathered upgrade, MxMxFz-Frizzle upgrade, MxMxNK-Naked Neck upgrade.

Table 4: Effect of genotype on wing length (LSM±SE) (cm)

						Weeks				
Genotype	N	0	1	2	3	4	5	6	7	8
M x M	50	4.75±0.08^{cd}	6.93±0.08^{a}	8.49±0.09^{a}	10.32±0.13^{a}	12.26±015 ^{a}	14.06±0.16^{a}	15.90±0.19^{a}	17.87±0.22 ^{a}	20.86±0.31^{a}
NxN	50	4.93±0.06^{cd}	5.43±0.07^{f}	6.78±0.08^{f}	7.93±0.12^{e}	9.13±0.13^{f}	10.22±0.14^{f}	11.80±0.17^{g}	13.44±0.19^{h}	15.00±0.17^{g}
Fz x Fz	46	5.02±0.09^{c}	5.79±0.10^{e}	7.48±0.13^{e}	7.95±0.12^{e}	10.27±0.12^{de}	11.52±0.15^{de}	12.85±0.26^{f}	15.28±0.21^{g}	17.14±0.22^{ef}
Nk x Nk	48	4.87±0.13^{cd}	5.62±0.12^{f}	6.81±0.10^{f}	8.30±0.10^{e}	10.08±0.18^{e}	11.23±0.21^{e}	13.30±0.20^{e}	14.84±0.20^{a}	16.68±0.29^{f}
M x N	49	4.72±0.05^{d}	6.48±0.11^{c}	8.02±0.01^{c}	9.22±0.11^{cd}	10.98±0.19^{c}	11.85±0.18^{d}	13.38±0.18^{e}	15.81±0.23^{f}	17.78±0.36^{d}
M x Fz	46	4.26±0.10^{e}	6.04±0.09^{de}	7.58±0.10^{e}	9.05±0.16^{d}	10.34±0.15^{de}	11.92±0.15^{d}	14.06±0.13^{d}	16.41±0.22^{de}	18.22±0.29^{d}
M x Nk	50	4.39±0.06^{e}	6.14±0.06^{d}	7.86±0.10^{cd}	9.09±0.14^{cd}	10.65±0.16^{cd}	12.57±0.19^{c}	14.54±0.18^{c}	16.35±0.17 ^{e}	18.29±0.22^{d}
MxMxN	50	5.44±0.08^{b}	6.13±0.10^{de}	7.81±0.03^{d}	9.15±0.16^{c}	10.69±0.16^{cd}	12.67±0.18^{c}	14.87±0.15^{c}	16.86±0.18^{cd}	19.27±0.28^{c}
MxMxFz	47	4.46±0.06^{e}	6.79±0.09^{b}	8.48±0.15^{a}	9.91±0.09^{b}	11.46±0.08^{b}	13.33±0.14^{b}	15.36±0.16^{b}	17.73±0.26^{ab}	20.05±0.21^{b}
MxMxNk	50	5.75±0.10^{a}	6.51±0.11^{c}	8.19±0.09^{ab}	9.45±0.14^{c}	11.41±0.14^{b}	13.13±0.11^{b}	14.87±0.23^{c}	17.31±0.16^{bc}	19.25±0.26^{c}

$^{a,\ b,\ c,\ d,\ e,\ f,\ g,\ h}$ Means within the same column with same superscripts are not significantly different, MxM-Pure Marshall, NxN- Pure Normal-feathered, Fzx Fz-Pure Frizzle-Feathered, NKxNK-Pure Naked Neck, MxN-Dihybrid Normal-Feathered, MxFz-dihybrid Frizzle-Feathered, MxNK-dihybrid Naked Neck, MxMxN-Normal-Neathered upgrade, MxMxFz-Frizzle-Feathered upgrade, MxMxNK-Naked Neck upgrade

Table 5: Effect of genotype on thigh length (LSM±SE)(cm)

		Weeks								
Genotype	N	0	1	2	3	4	5	6	7	8
M x M	50	5.31±0.04^{a}	6.57±0.07^{a}	9.30±1.97^{a}	9.43±0.15 ^{a}	11.14±0.17^{a}	12.24±0.16^{b}	14.80±0.26^{a}	16.31±0.31^{a}	16.49±0.24^{cd}
N x N	50	5.18±0.03^{abc}	5.70±0.07^{f}	6.87±0.09^{b}	7.23±0.09^{g}	8.15±0.10^{e}	9.39±0.17^{g}	10.65±0.15^{f}	12.33±0.17^{f}	14.00±0.17^{g}
Fz x Fz	46	4.87±0.04^{d}	6.03±0.05^{de}	7.05±0.06^{b}	7.97±0.12^{f}	9.10±0.15^{cd}	9.86±0.18^{f}	11.73±0.12^{d}	13.37±0.23^{e}	15.21±0.31^{e}
Nk x Nk	48	5.17±0.06^{abc}	5.93±0.07^{e}	7.02±0.08^{b}	7.89±0.11^{f}	8.95±0.13^{d}	9.77±0.20^{fg}	11.09±0.19^{e}	12.77±0.22^{f}	14.55±0.22^{f}
M x N	49	5.05±0.04^{c}	6.06±0.06^{de}	7.21±0.09^{b}	8.11±0.11^{ef}	9.37±0.11^{d}	10.31±0.13^{e}	11.45±0.20^{de}	13.41±0.17^{e}	15.33±0.16^{e}
M x Fz	46	5.26±0.06^{ab}	6.14±0.06^{d}	7.28±0.10^{ab}	8.09±0.11^{def}	9.36±0.13^{d}	10.81±0.14^{d}	11.62±0.16^{d}	13.62±0.23$^{d e}$	15.98±0.18^{d}
M x Nk	50	5.23±0.03^{ab}	6.16±0.16^{cd}	7.34±0.08^{a}	8.02±0.10^{d}	9.92±0.14^{c}	10.97±0.08^{d}	12.48±0.16^{c}	13.96±0.18^{d}	16.17±0.19^{cd}
MxMxN	50	5.18±0.04^{abc}	6.55±0.02^{a}	7.46±0.06^{ab}	8.47±0.12^{cd}	9.77±0.10^{c}	11.15±0.15^{cd}	12.78±0.18^{c}	14.68±0.14^{c}	16.57±0.22^{c}
MxMxFz	47	5.14±0.06^{bc}	6.44±0.08^{ab}	8.06±0.10^{ab}	9.48±0.11^{b}	10.9±0.14^{b}	12.86±0.22^{a}	13.63±0.17^{b}	15.42±0.42^{b}	17.90±0.43^{a}
MxMxNk	50	5.12±0.06$^{b c}$	6.31±0.05^{bc}	7.98±0.11^{ab}	8.70±0.08^{bc}	9.92±0.12^{c}	11.55±0.12^{c}	13.31±0.10^{b}	15.18±0.17^{b}	17.09±0.25^{b}

$^{a, b, c, d, e, f, g, h}$ Means within the same column with same superscripts are not significantly different, MxM-Pure Marshall, NxN- Pure Normal-Feathered, Fzx Fz-Pure Frizzle-Feathered, NKxNK-Pure Naked Neck, MxN-Dihybrid Normal-Feathered, MxFz-dihybrid Frizzle-Feathered, MxNK-dihybrid Naked Neck, MxMxN Normal-Feathered upgrade, MxMxFz-frizzle-Feathered upgrade, MxMxNK-Naked Neck upgrade.

Table 6: Effect of genotype on shank length (LSM±SE)(cm)

		Weeks								
Genotype	N	0	1	2	3	4	5	6	7	8
M x M	50	4.69±0.06^{ab}	5.74±0.07^{b}	6.51±0.17^{a}	7.80±0.08^{a}	9.25±017^{a}	10.85±0.26^{c}	12.55±0.22^{a}	13.97±0.30^{a}	13.39±0.22^{c}
N x N	50	4.13±0.04^{b}	4.40±0.04^{f}	5.05±0.05^{d}	5.82±0.09^{f}	6.63±0.10^{f}	9.52±0.20^{e}	8.63±0.18^{e}	9.87±0.26^{g}	10.93±0.19^{e}
Fz x Fz	46	3.86±0.04^{b}	4.78±0.05$^{d e}$	5.47±0.14^{d}	6.11±0.08^{e}	6.66±0.10 ^{f}	9.86±0.18^{de}	8.92±0.19$^{d e}$	10.08±0.17^{g}	11.34±0.17^{e}
Nk x Nk	48	4.15±0.04^{b}	4.71±0.05^{e}	5.40±0.07^{d}	6.04±0.10^{ef}	6.81±0.13^{f}	9.77±0.20^{e}	8.60±0.12^{e}	9.87±0.20^{g}	11.34±0.21^{e}
M x N	49	4.26±0.03^{b}	4.85±0.07$^{d e}$	5.52±0.08^{d}	6.27±0.11^{e}	7.06±0.14^{e}	10.31±0.13^{d}	9.12±0.15^{d}	10.25±0.19^{g}	12.63±0.15^{d}
M x Fz	46	4.30±0.04^{b}	4.93±0.03^{cd}	5.53±0.06^{d}	6.63±0.09^{d}	8.01±0.12^{d}	10.82±0.14^{c}	10.08±0.12^{c}	10.74±0.18^{f}	12.63±0.17^{d}
M x Nk	50	4.22±0.03^{b}	5.05±0.05^{c}	6.04±0.06^{c}	7.00±0.08^{c}	8.02±0.09^{d}	10.96±0.08^{c}	10.13±0.04^{c}	11.35±0.14^{e}	12.86±0.12^{d}
MxMxN	50	4.25±0.04^{b}	5.20±0.06^{b}	6.05±0.06^{c}	7.02±0.07^{bc}	7.90±0.10^{d}	11.15±0.15^{bc}	10.30±0.12^{c}	11.86±0.12^{d}	14.48±0.22^{b}
MxMxFz	47	5.19±0.87^{a}	5.23±0.05^{b}	6.40±0.09^{ab}	7.68±0.13^{a}	8.89±0.10^{b}	12.88±0.22^{a}	10.94±0.14^{b}	12.96±0.16^{b}	16.07±0.28^{a}
MxMxNk	50	4.19±0.03^{b}	5.22±0.05^{b}	6.21±0.04^{bc}	7.23±0.07^{b}	8.33±0.07^{c}	11.59±0.12^{b}	10.93±0.10^{b}	12.35±0.14^{c}	12.86±0.12^{c}

$^{a , b , c, d ,e, f ,g , h}$ Means within the same column with same superscripts are not significantly different, MxM-Pure Marshall, NxN- Pure Normal-Feathered, Fzx Fz-Pure Frizzle-Feathered, NKxNK-Pure Naked Neck, MxN-Dihybrid Normal-Feathered, MxFz-dihybridFfrizzle-Feathered, MxNK-dihybrid Naked Neck, MxMxN-Normal-Feathered upgrade, MxMxFz-Frizzle-Feathered upgrade, MxMxNK-Naked Neck upgrade.

Table 7: Effect of genotype on keel length (LSM±SE) (cm)

		Weeks								
Genotype	N	0	1	2	3	4	5	6	7	8
M x M	50	1.45±0.01^{a}	2.87±0.52^{a}	3.48±0.05^{a}	4.64±0.07^{a}	5.79±0.08^{a}	7.02±0.10^{a}	8.03±0.12^{a}	9.65±0.18^{a}	10.83±0.20^{a}
N x N	50	0.96±0.01^{c}	1.67±0.03^{c}	2.33±0.05^{e}	2.94±0.07^{f}	3.62±0.08^{h}	4.47±0.11^{f}	5.34±0.13^{e}	6.06±0.14^{g}	7.10±0.12^{f}
Fz x Fz	46	1.18±0.18^{b}	2.01±0.03$^{b c}$	2.84±0.05^{c}	3.50±0.06^{d}	4.25±0.08^{g}	4.86±0.08^{e}	5.57±0.12^{e}	6.42±0.10^{f}	7.33±0.17^{f}
Nk x Nk	48	1.05±0.02^{bc}	1.94±0.03^{bc}	2.60±0.05^{d}	3.24±0.07^{e}	3.95±0.10^{f}	4.55±0.12^{f}	5.46±0.08^{e}	6.36±0.16^{f}	7.22±0.10^{f}
M x N	49	1.16±0.01^{b}	2.04±0.02^{bc}	2.88±0.06^{c}	3.70±0.07^{cd}	4.57±0.09^{e}	5.36±0.10^{d}	6.50±0.09^{d}	7.10±0.13^{e}	8.23±0.10^{e}
M x Fz	46	1.40±0.02^{a}	2.02±0.04^{bc}	2.90±0.07^{c}	3.75±0.07^{c}	4.56±0.09^{e}	5.50±0.11^{cd}	6.57±0.08^{d}	7.45±0.08^{d}	8.59±0.13^{d}
M x Nk	50	1.20±0.01^{b}	2.31±0.02^{b}	3.13±0.04^{b}	3.91±0.04^{c}	4.79±0.07^{d}	5.71±0.07^{c}	6.65±0.11^{d}	7.91±0.08^{c}	8.93±0.15^{c}
MxMxN	50	1.46±0.01^{a}	2.36±0.03^{ab}	3.35±0.03^{a}	4.14±0.04^{b}	5.19±0.05^{c}	6.29±0.07^{b}	7.11±0.04^{c}	8.01±0.07^{c}	9.07±0.14^{c}
MxMxFz	47	1.49±0.01^{a}	2.46±0.03^{ab}	3.39±0.07^{a}	4.46±0.17^{a}	5.49±0.07^{b}	6.51±0.09^{b}	7.41±0.10^{b}	8.10±0.03^{bc}	10.14±0.23^{b}
MxMxNk	50	1.53±0.01^{a}	2.44±0.04^{ab}	3.35±0.03^{a}	4.44±0.06^{a}	5.41±0.04^{b}	6.44±0.03^{b}	7.15±0.03^{bc}	8.30±0.06^{b}	9.11±0.13^{c}

$^{a, b, c, d, e, f, g, h}$ Means within the same column with same superscripts are not significantly different, MxM-Pure Marshall, NxN- Pure Normal-Feathered, Fzx Fz-Pure Frizzle-Feathered, NKxNK-Pure Naked Neck, MxN-Dihybrid Normal-Feathered, MxFz-dihybrid Frizzle-Feathered, MxNK-dihybrid Naked Neck, MxMxN-Normal-Feathered upgrade, MxMxFz-Frizzle- Feathered upgrade, MxMxNK-Naked Neck upgrade.

4.6 Heritability

Heritability estimates for body weight and other linear measurements at all ages are presented in Tables 8 to 12.

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 in 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 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.

The heritability (h^2) of body weight and linear parameters estimated in this study revealed a low to high range 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 was lower than in values observed by Peters (2000). However, the low values observed in the heritability study 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 (1994) who reported sixth week body weight heritability of 0.40 while Demeure *et al.* (2013) reported low to high heritability of 0.32-0.63 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 in this study. Similarly, Adebambo *et al*. (2010) reported weekly high heritability estimates.

Genetic correlation of the Nigerian Chickens genotypes

Results of the genetic correlations are presented in Tables 8 to 12.The genetic correlation coefficients obtained among body weight and all other linear body measurements were positive. The least values were recorded in weeks 0 and 2 while the highest values were recorded at week 3 and 8. The trend of genetic correlation between the body weight and the growth parameters relationship studied showed a low to high trend. The relationship between BW and WS was 0.99±0.01 as the highest value while the lowest value was recorded for SL and WL (0.01±0.00)

The relationship between wing length and shank length had the least value of 0.01±0.00, followed by thigh length and shank length with 0.04±0.01 at week 0 and 0.01±0.00 for the body weight and thigh length at week 2 and the highest value was 0.82±0.02 for wing length and wing span relationship at day old. Also, 0.82±0.01 was recorded for body weight and wing span, then 0.83±0.01 for breast girth and wing span relationship at week 8 but the rest of the ages had low to high correlations amongst the body traits. Generally the genetic correlation ranged from 0.01±0.00 to 0.99±0.01 (Table 8 to 12).

The genetic correlation coefficients of body weight and linear body measurements were significant ($P<0.05$) and ranged from medium to high. Similarly Peters[2] (2000) reported medium to high genetic correlation in the Nigerian indigenous chicken. 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 (1994) who observed positive correlation between body weight and the linear parameters measured in the experiment. Likewise, Adebambo *et al*. (2010) observed medium to high range in genetic correlation coefficient in body weight and linear parameters of chicken crosses. 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*. (1994) who had similar observations in these findings.

Table 8: Heritability, genetic and phenotypic correlations and ± standard error of growth traits of chickens at day old (0 week).

	BW	BL	BG	WL	WS	TL	SL	KL
BW	**0.34±0.10**	0.71±0.18	0.45±0.27	0.21±0.10	0.30±0.20	0.50±0.27	0.99±0.30	0.92±0.07
BL		**0.22±0.10**	0.36±0.20	0.14±0.09	0.28±0.18	0.37±0.20	0.49±0.24	0.64±0.22
BG			**0.37±0.20**	0.10±0.03	0.04±0.02	0.62±0.05	0.99±0.43	0.36±0.18
WL				**0.38±0.15**	0.90±0.06	0.02±0.01	0.50±0.05	0.30±0.04
WS					**0.37±0.10**	0.28±0.10	0.04±0.02	0.33±0.05
TL						**0.11±0.05**	0.71±0.43	0.26±0.05
SL							**0.02±0.01**	0.82±0.35
KL								**0.21±0.04**

Heritability in bold, genetic 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 9: Heritability and genetic correlations and ± standard error of growth traits of chickens at two weeks of age.

	BW	BL	BG	WL	WS	TL	SL	KL
BW	**0.54±0.07**	0.94±0.04	0.99±0.02	0.93±0.05	0.94±0.05	0.99±0.05	0.97±0.03	0.91±0.06
BL		**0.43±0.10**	0.99±0.01	0.98±0.02	0.98±0.02	0.99±0.02	0.98±0.03	0.99±0.02
BG			**0.48±0.10**	0.97±0.03	0.98±0.02	0.99±0.02	0.99±0.02	0.99±0.02
WL				**0.38±0.08**	0.99±0.02	0.99±0.02	0.96±0.02	0.98±0.02
WS					**0.47±0.10**	0.99±0.02	0.98±0.01	0.99±0.02
TL						**0.10±0.03**	0.99±0.02	0.99±0.01
SL							**0.37±0.10**	0.99±0.01
KL								**0.53±0.06**

Heritability in bold, genetic 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 10: Heritability and genetic correlations and ± standard error of growth traits of chickens at four weeks of age.

	BW	BL	BG	WL	WS	TL	SL	KL
BW	**0.61±0.10**	0.84±0.10	0.97±0.03	0.96±0.03	0.94±0.04	0.93±0.05	0.95±0.03	0.99±0.01
BL		**0.50±0.15**	0.92±0.06	0.79±0.14	0.74±0.16	0.77±0.14	0.91±0.06	0.83±0.11
BG			**0.55±0.15**	0.97 ±003	0.95±0.04	0.93±0.05	0.95±0.04	0.97±0.02
WL				**0.39±0.10**	0.99±0.02	0.97±0.03	0.94±0.05	0.98±0.02
WS					**0.46±0.15**	0.97±0.02	0.90±0.07	0.98±0.02
TL						**0.48±0.10**	0.94±0.02	0.96±0.03
SL							**0.58±0.0**	0.94±0.05
KL								**0.64±0.04**

Heritability in bold, genetic 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 11: Heritability and genetic phenotypic correlations and ± standard error of growth traits of chickens at six weeks of age.

	BW	BL	BG	WL	WS	TL	SL	KL
BW	**0.62±10**	0.94±0.02	0.97±0.03	0.98±0.04	0.88±0.08	0.96±0.03	0.94±0.04	0.97±0.03
BL		**0.55±0.10**	0.99±0.01	0.99±0.01	0.97±0.02	0.96±0.03	0.96±0.03	0.97±0.02
BG			**0.60±0.09**	0.99±0.01	0.97±0.03	0.96±0.03	0.96±0.03	0.98±0.02
WL				**0.48±0.11**	0.96±0.03	0.94±0.05	0.93±0.05	0.96±0.03
WS					**0.59±0.09**	0.88±0.08	0.92±0.06	0.95±0.04
TL						**0.53±0.07**	0.97±0.03	0.94±0.05
SL							**0.60±0.10**	0.96±0.03
KL								**0.64±0.05**

Heritability in bold, genetic 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 12: Heritability and genetic correlations and ± standard error of growth traits of chickens at eight weeks of age.

	BW	BL	BG	WL	WS	TL	SL	KL
BW	**0.57±0.12**	0.98±0.02	0.96±0.03	0.97±0.03	0.99±0.01	0.92±0.06	0.96±0.02	0.95±0.03
BL		**0.59±0.11**	0.98±0.02	0.91±0.01	0.99±0.01	0.89±0.08	0.99±0.01	0.99±0.01
B			**0.64±0.07**	0.97±0.03	0.97±0.02	0.96±0.04	0.95±0.03	0.02±0.02
WL				**0.46±0.14**	0.99±0.02	0.92±0.06	0.97±0.03	0.97±0.03
WS					**0.60±0.05**	0.93±0.05	0.96±0.01	0.96±0.03
TL						**0.29±0.10**	0.81±0.12	0.86±0.09
SL							**0.53±0.09**	0.99±0.01
KL								**0.57±0.07**

Heritability in bold, genetic 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 KL- keel length.

CONCLUSION

The result of this study showed that genotype significantly influenced all the morphometric parameters measured at all ages.

The 75:25% Marshall: Indigenous bloodline (F_2 upgrades) was the leading genotype followed by 50:50% Marshall: Indigenous bloodline (di-hybrid) next while the least was the purebred indigenous in the general performance. Within the F_2 upgrades, the Frizzle-feathered upgrade had highest mean values superior to Naked neck upgrade while Normal feathered upgrade was the least

Frizzle-feathered upgrades emerged as the best performed genotype in both body weight and the linear body parameters measured at all ages in this study. Frizzle-feathered was the heaviest genotype of all the three purebred Nigerian indigenous chicken genotypes followed by Naked Neck and then the Normal feathered.The F_2 upgrades had similar mean values to the Marshall exotic breed used except in shank length and thigh length. It was also observed that there was a steady and gradual increment in growth rate both in body weight and other body parameters at all ages. Considering the Nigerian broiler chickens in this study, Frizzle-feathered upgrades had the widest breast girth and the longest keel lengths followed by Naked neck and next was Normal-Feathered upgrades.

The heritability for all growth parameters measured in this study ranged from low to high with the values 0.01 to 0.64 for 8 weeks. Generally, in this study the trend of heritability estimate for growth traits in all the chicken genotypes 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.

Genetic correlations coefficient ranged from between 0.10 to 0.99 for the growth traits measured which confirmed that improvement of one trait leads to improvement of the other.

Conflict of Interests

All authors declare that there is no conflict of interests.

Ethics 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

All authors declare that this article is an original article submitted for publication which has not been published anywhere in the world.

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