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PHENOTYPIC, GENETIC AND ENVIRONMENTAL CORRELATIONS BETWEEN BODY WEIGHT AND LINEAR BODY TRAITS OF CHICKEN GENOTYPES

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ABSTRACT

Data from 123, 49, 116, 137, 42 and 64 chickens belonging to Isa Brown x frizzle feathered (IBxF), Isa Brown x naked neck (IBxNa), Isa Brown x normal feathered (IBxN), frizzle feathered x Isa Brown (FxIB), naked neck x Isa Brown (NaxIB) and normal feathered x Isa Brown (NxIB) genotypes, respectively were used to establish phenotypic (r_P), genetic (r_G) and environmental (r_E) correlations between body weight and linear body traits at 2, 10 and 20 weeks of age. Phenotypic correlations were analyzed by Pearson's Product Moment method. Genetic and environmental correlations were estimated by covariance analysis. The highest r_P estimates were obtained between body weight and shank length (SL) in IBxF (0.84) and NxIB (0.87) at 10 weeks, body width (BW) in IBxNa (0.84) and IBxN (0.72), drumstick length (DL) in FxIB (0.71) and NaxIB (0.88) at 20 weeks. Body weight had highest r_G estimates with SL in NxIB (0.99), BW in IBxF (2.40), wing length (WL) in 1BxNa (0.91) and FxIB (7.39) at 10 weeks, body girth (BG) in IBxN (0.97) and BW of NaxIB (4.73) at 20 weeks. However, SL of IBxNa (-5.15), BG of NaxIB (-0.53), keel length (KL) of NxIB (0.35), WL of IBxF (-0.38) and FxIB (-1.41) at 2 weeks and WL of IBxN (-0.43) at 20 weeks had the least r_E with body weight. Indirect selection of body weight using the highest phenotypic, genetic and lowest environmental correlated linear traits will result in rapid genetic improvement in these chickens.

***Keywords*:** Correlations, Body weight, Linear body traits, Genotypes, Chicken

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1. INTRODUCTION

Correlation is an association between two independent traits which may be positive or negative. The statistic that measures the magnitude or strength of a correlation is known as correlation coefficient. Phenotypic, genetic and environmental correlations are common in animal breeding. Phenotypic correlation is the sum total of genetic and environmental correlations. According to Ibe (1998), phenotypic correlation between any two traits is the correlation of their observed values. Genetic correlation is the correlation of additive genes governing any two traits while environmental correction is the correlation between environmental deviations, including all non-additive deviations. These non-additive deviations include dominance, epistasis and maternal effects (Bolormaa et al. 2015). Hill (2013) also defined genetic correlation as the correlation of breeding value. The primary causes of genetic correlation are pleiotropy and linkage disequilibrium. According to Roff (1997), the ability of one gene to control two or more traits is a phenomenon known as pleiotropy, and linkage disequilibrium occurs when traits, which may be controlled by two independent genes, are associated due to non-random mating, selection or drift. When correlation of traits is controlled by pleiotropic gene action, Ebangi and Ibe (1994) and Agu et al. (2012) explained that by indirect selection for one trait, genetic improvement in the other trait will be realized through correlated response. Very high genetic correlation implies less environmental effect on a trait such that the phenotype is a true reflection of the genotype (Hazel 1943; Hill et al. 2007; Okpeku et al. 2019).

Estimates of phenotypic correlation are useful in examining the relationship between measurements of size and shape in chicken (Ibe 1989; Yakubu et al. 2009; Habimana et al. 2021). Genetic correlation estimates reveal the amount of additive genetic variance for a trait, enable response to selection to be predicted and aid in selection decision. Environmental correlation estimates, on the other hand, indicate much about the influence of environmental factors such as feed on performance of animals. Negative and low positive environmental correlation suggests less environmental but high genotypic effect on the phenotype.

The phenotypic and genetic correlations of body weight with other economic characters in poultry are well established in literature. Adeleke et al. (2011) reported phenotypic correlation coefficients of 0.73, 0.70, 0.74, 0.74,

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0.70, 0.83 and 0.79 between body weight and each of wing length, wing span, shank length, thigh length, body length, breast girth and keel length, respectively at 8 weeks in chicken. At the same age, the authors also reported genetic correlation coefficients of 0.69, 0.73, 0.97, 0.93, 0.62, 0.99 and 0.99 for the same pairs of traits, respectively. Ebangi and Ibe (1994) reported positive and high genetic correlation coefficients between body weight and each of shank length (0.99), keel length (1.13) and breast width (1.09) of local chickens at 6 weeks of age. Adebambo et al. (2006) and Adedeji et al. (2008) reported low to high positive phenotypic correlation coefficients between body weight and linear body traits in chickens. Phenotypic, genetic and environmental correlations had been reported on semen (Kabir 2006) and egg production and partial recording (El-Labban et al. 2011) traits in chicken and plant (Hebert et al. 1994; Amabile et al. 2015). However, reports on the three correlations between body weight and linear body traits in chickens are quite rare in available literature. There is need for more information on the three correlations between growth traits for good management and genetic improvement of chickens. The goal of the present study was to establish phenotypic, genetic and environmental correlations between body weight and linear body traits in crossbred Isa Brown and local chickens of Nigeria.

2. MATERIALS AND METHODS

2.1. Ethics Statement

Animals were reared and handled perfectly well in agreement with the Ethics Committee or Bioethics/Biosecurity Committee/Institutional Bioethics Committee guidelines.

2.2. Experimental stock and management

A total of 69 parents consisting of exotic Isa Brown (9 males and 27 females) and local chickens namely frizzle feathered (3 males and 8 females), naked neck (3 males and 7 females) and normal feathered (3 males and 9 females) strains were used in the experiment. The chickens were naturally mated in main and reciprocal order with Isa Brown cocks in the main cross and the local cocks in the reciprocal. Eggs were collected and their pedigree identified with permanent markers. They were stored in cool, dry place. A total of 531 first filial generation unsexed chickens were produced in 12 consecutive hatches at weekly intervals. Their number and genotype were 123, 49, 116, 137, 42 and 64 for Isa Brown x frizzle feathered (IBxF), Isa Brown x naked neck (IBxNa), Isa Brown x normal feathered (IBxN), frizzle feathered x Isa Brown (FxIB), naked neck x Isa Brown (NaxIB) and normal feathered x Isa Brown (NxIB), respectively. The pedigree and progeny number of the genotypes is shown in Table 1.

The chicks were vaccinated at day-old against Newcastle Disease and brooded together in cages of 79 x 67 x 61 cm^3 dimension each, constructed on deep litter pens of 2.65 x 1.67 m^2 dimension. Brooding lasted for 4 weeks per hatch. Standard commercial feeds together with water were given both to the parents and F_1 chickens *ad libitum*. Appropriate antibiotics were administered to the birds to control bacterial diseases. The experiment lasted for 60 weeks and 4 days between 2012 and 2013.

2.3. Data Collection and measurement of traits

All data on body weight and linear body traits namely shank length, drumstick length, body width, body girth, body length, keel length and wing length were collected on individual chickens at 2, 10 and 20 weeks on both sexes. Body weight (BWT) was measured in grams (g), using Ohaus electronic sensitive weighing scale (Model CS5, 000) with sensitivity of 2.00g. All linear body traits were measured in centimeter (cm) using measuring tape. Shank length (SL) was measured as the length of the leg from the hock joint to the tarso- metatarsus pad. Drumstick length (DL) was measured as the length of the femur bone. Body width (BW) was measured as the circumference of the widest part of the body. Body girth (BG) was measured as the circumference of the breast around the deepest region. Body length (BL) was measured as the distance between the comb and pygostyle towards the tail. Keel length (KL) was measured as the length of the keel bone from the V-joint to the end of the sternum. Wing length (WL) was measured as the length of the wing from the scapular joint to the last digit of the wing.

2.4. Statistical Analysis

2.4.1. Analysis of covariance (ANCOVA) for estimation of genetic and environmental correlations

Analysis of covariance (ANCOVA) between any two measured traits was performed with SAS (1999) software. The analysis yielded sire, dam and error components, which were estimated by equating them to their respective expected mean cross products and solving. The equations for their solutions were obtained using expressions (1), (2) and (3), respectively (Becker 1984).

$$COV_e = MCP_e \quad \ldots \quad (1)$$
$$COVd = (MCP_d - MCP_e)/k_1 \quad \ldots \quad (2)$$
$$COV_s = MCP_s - (MCP_e + k_2Cov_d/k_3 \quad \ldots \quad (3)$$

Table 1: Pedigree and progeny number of main and reciprocal crossbred chickens produced at day-old in 12 hatches

Main cross					Reciprocal cross					
Genotype	Pedigree				Genotype	Pedigree				Total
	Sire	Dam	DT	ST		Sire	Dam	DT	ST	
IBxF	IB$_1$	F$_1$	21		FxIB	F$_1$	IB$_1$	13		
		F$_2$	20				IB$_2$	13		
		F$_3$	19	60			IB$_3$	11	37	
	IB$_2$	F$_4$	15			F$_2$	IB$_4$	9		
		F$_5$	9				IB$_5$	27		
		F$_6$	15	39			IB$_6$	11	47	
	IB$_3$	F$_7$	15			F$_3$	IB$_7$	16		
		F$_8$	9	34			IB$_8$	19		
	Total			123			IB$_9$	18	53	
IBxNa	IB$_4$	Na$_1$	7			Total			137	
		Na$_2$	6		NaxIB	Na$_1$	IB$_{10}$	4		
		Na$_3$	10	23			IB$_{11}$	4		
	IB$_5$	Na$_4$	4				IB$_{12}$	3	11	
		Na$_5$	5	9		Na$_2$	IB$_{13}$	2		
	IB$_6$	Na$_6$	6				IB$_{14}$	9		
		Na$_7$	11	17			IB$_{15}$	4	15	
	Total			49		Na$_3$	IB$_{16}$	2		
IBxN	IB$_7$	N$_1$	13				IB$_{17}$	7		
		N$_2$	11				IB$_{18}$	7	16	
		N$_3$	15	39		Total			42	
	IB$_8$	N$_4$	11		NxIB	N$_1$	IB$_{19}$	8		
		N$_5$	14				IB$_{20}$	6		
		N$_6$	14	39			IB$_{21}$	7	21	
	IB$_9$	N$_7$	15			N$_2$	IB$_{22}$	10		
		N$_8$	15				IB$_{23}$	5		
		N$_9$	8	38			IB$_{24}$	8	23	
	Total			116		N$_3$	IB$_{25}$	1		
							IB$_{26}$	8		
							IB$_{27}$	11	19	
						Total			64	
	Main cross Total			288		Reciprocal cross Total			243	531

DT=Dam total, ST=Sire total, IBxF=Isa Brown x frizzle feathered, IBxNa=Isa Brown x naked neck: IBxN=Isa Brown x normal feathered, FxIB=frizzle feathered x Isa Brown, NaxIB=naked neck x Isa Brown: NxIB=normal feathered x Isa Brown

Table 2: Summary of analysis of covariance (ANCOVA)

Source of variation	df	Sum of cross products	Mean cross products	[E(MCP)]
Between Sires, S	s-1	SCP$_s$	MCPs	COVe+k$_2$COV$_d$+k$_3$COV$_s$
Dams within sires	d-s	SCP$_d$	MCP$_d$	COVe+k$_1$COV$_d$
Progeny/dam/sire	n..-d	SCP$_e$	MCP$_e$	COV$_e$

df=Degree of freedom; s=number of sires; d=number of dams; n=total number of progenies; SCPs, SCP$_d$ and SCPe=Sums of cross products due to sire, dam and error, respectively; MCPs, MCP$_d$, MCP$_e$, COVs, COV$_d$ and COV$_e$ are as defined below; E(MCP)=Expected mean cross products.

Where COV$_s$, COV$_d$ and COV$_e$ are covariance components due to sire, dam and error, respectively. MCPs, MCP$_d$ and MCP$_e$ are mean cross products due to sire, dam and error, respectively. The summary of ANCOVA involving s sires, d dams within sire and n total progeny in the full-sib family is shown in Table 2. The ANCOVA was derived according to Becker (1984). The sums of cross products were calculated by the formulae below:

$$SCP_s = \sum_i \frac{X_{i..}\ Y_{i..}}{n_{i.}} - CF$$

$$SCP_d = \sum_i \sum_j \frac{X_{ij.}\ Y_{ij.}}{n_{ij}} - \sum_j \frac{X_{i..}\ Y_{i..}}{n_{i.}}$$

$$SCP_e = \sum_i \sum_j \sum_k X_{ijk}\ Y_{ijk} - \sum_i \sum_j \frac{X_{ij.}\ Y_{ij.}}{n_{ij}}$$

Where $\sum$ = summation, $X_{i..}$ and $Y_{i..}$ = total of all observations of X and Y correlated traits for sire i, $X_{ij.}$ and $Y_{ij.}$ = total of all observations of X and Y correlated traits for dam j mated to sire i, X_{ijk} and Y_{ijk} = total of all observations of X and Y correlated traits for progeny k of dam j mated to sire i, $n_{i.}$ = total number of progeny of sire i, n_{ij} = total number of progeny of dam j mated to sire i, CF = correction factor for the mean (= y^2.. /n..), y^2.. = grand total of all observations, and n = total number of progenies. Ibe (2019) noted that in a full-sib unbalanced nested design as is the case of this study, where there are unequal number of progeny per dam within sire, dams per sire and progeny per dam, the coefficient $k_1 \neq k_2$. The formulae for calculating the three coefficients k_1, k_2 and k_3 in the ANCOVA table are given by Becker (1984) as expressed in equations (4), (5) and (6) respectively.

$$k_1 = (n_{..} - \sum_i \frac{\sum n_{ij}{}^2}{n_{i.}})/\text{d.f (dams)} \quad \dots \quad (4)$$

$$k_2 = (\sum_i \frac{\sum n_{ij}{}^2}{n_{i.}} - \frac{\sum\sum n_{ij}{}^2}{n_{..}})/\text{d.f (sires)} \quad \dots \quad (5)$$

$$k_3 = (n_{..} - \frac{\sum n_{i.}{}^2}{n_{..}})/\text{ d.f (sires)} \quad \dots \quad (6)$$

where n.. is the total number of progeny per genotype, $n_{i.}$ is the number of progenies per sire and n_{ij} is the number of progeny per dam with their numerical values being provided in Table 1.

2.4.2. Estimation of phenotypic correlation

Phenotypic correlation (r_P) between any two traits, say X and Y, was estimated as the correlation of their observed values using expression (7).

$$r_P = \frac{COV(P_X P_Y)}{\sqrt{[\sigma^2_{(X)}\sigma^2_{(Y)}]}} \quad \dots \quad (7)$$

2.4.3. Estimation of genetic correlation

Genetic correlation (r_G) was estimated as the correlation of additive genes governing any two traits from sire (r_{GS}) and dam (r_{Gd}) variance and covariance components using the expressions (8) and (9), respectively.

$$r_{G\,(s)} = \frac{COV_S}{\sqrt{[\sigma^2_{s(X)}][\sigma^2_{s}]}} \quad \dots \quad (8)$$

$$r_{G\,(d)} = \frac{COV_d}{\sqrt{[\sigma^2_{d(X)}][\sigma^2_{d(Y)}]}} \quad \dots \quad (9)$$

where cov_S and cov_d are sire and dam covariance components respectively. The standard error of estimate of genetic correlation, SE (r_G), was computed with expression (10) according to Becker (1984).

$$SE\,(r_G) = \frac{COV_{XY}}{\sigma^2_{(X)} \cdot \sigma^2_{(Y)}} \quad \dots \quad (10)$$

where COV_{XY} is covariance between trait X and Y, $\sigma^2_{(X)}$ and $\sigma^2_{(Y)}$ are population variances of traits X and Y respectively.

The sample variance, S^2 of any trait was computed with expression (11).

$$S^2 = \frac{\Sigma x_i^2 - (\Sigma x_i)^2/n}{n-1} \quad \dots \quad (11)$$

Where x_i is any trait with i = 1, 2,…, n measurements or observations. The covariance between any two traits was computed using expression (13)

$$Cov(X, Y) = [(\Sigma xy - (\Sigma x_i)(\Sigma y_i)/n] /(n - 1) \quad \dots \quad (13)$$

Where X and Y are any two traits with measurements, x_1, x_2, …,x_n and y_1, y_2, …, y_n respectively.

2.4.4. Estimation of environmental correlation

Environmental correction (r_E) was estimated from sire (r_{Es}) and dam (r_{Ed}) variance (σ^2) and covariance (cov) components as the correlation between environmental deviations, including all non-additive deviations with expressions (14) and (15), respectively.

$$r_{E(s)} = \frac{Cov_e - 2Cov_s}{[\sigma^2_{e(X)} - \sigma^2_{s(X)}][\sigma^2_{e(Y)} - \sigma^2_{s(Y)}]} \quad \dots \quad (14)$$

$$r_{E(d)} = \frac{Cov_e - 2Cov_d}{[\sigma^2_{e(X)} - \sigma^2_{d(X)}][\sigma^2_{e(Y)} - \sigma^2_{d(Y)}]} \quad \dots \quad (15)$$

3. RESULTS

3.1. Phenotypic correlations between body weight and linear body traits of crossbred chickens (sexes combined) at 2, 10 and 20 weeks

The estimates of phenotypic correlation between body weight and linear body traits are presented in Tables 3-8. The estimates generally increased with age with the highest values obtained at 20 weeks in all genotypes except for NxIB which recorded slightly higher values at 10 weeks of age. Estimates of phenotypic correlation increased consistently with age between body weight and shank length in IBxN and IBxN; drumstick length in IBxF, IBxNa, IBxN and NaxIB; body girth in IBxNa and NaxIB; body width in IBxF, IBxNa, FxIB and NaxIB; keel length in IBxF and NxIB; body length in IBxF, IBxNa and NaxIB and wing length in IBxF, IBxNa and NaxIB genotypes. Estimates obtained for IBxN progeny at 2 weeks were quite higher than those of other genotypes at the same age.

Body weight had highest positive phenotypic correlation with shank length in IBxF (0.84) at 10 weeks; body width in IBxNa (0.84) and IBxN (0.72) at 20 weeks, drumstick length in FxIB (0.71) and NaxIB (0.88) at 20 weeks. Highest positive estimates of phenotypic correlation of 0.85 existed between body weight and each of SL and KL in NxIB genotype at 20 weeks.

3.2. Genetic correlations between body weight and linear body traits of crossbred chickens (sexes combined) at 2, 10 and 20 weeks

Genetic correlation estimates between body weight and linear body traits of the different genotypes are presented in Tables 3-8. The estimates generally showed moderate to high positive ranged values from sire variance component in IBxF (0.23±0.66 – 2.40±0.28) at 2 and10 weeks and IBxN (0.18±0.01 – 0.97±0.01) at 10 and 20 weeks.

Low positive estimate between body weight and drumstick length (0.05±0.02) at 10 weeks and negative estimates between body weight and body length at 2 (-0.22 ±0.11) and 10 (-0.37±0.51) weeks were also obtained in IBxF. Negative genetic correlation was observed between body weight and body length (-0.81±0.02) at 10 weeks in IBxN. Low to high range of positive genetic correlations (0.003±0.00 – 0.91±0.09) was observed in IBxNa from sire variance components at 2 to10 weeks while negative estimate occurred between body weight and body width (-0.34) at 2 weeks old. In FxIB genotype, positive estimates ranged from low to high from sire (0.15±0.12–1.00±0.03) and moderate to high from dam (0.28±0.16–1.83±0.08) variance components at 2 to 20 weeks. Negative estimates occurred in FxIB genotype between body weight and each of keel length (-0.26±0.45) and body length (-0.56±0.00) at 2 weeks and wing length (-0.75±0.02) at 20 weeks. Body weight correlated negatively with drumstick

Table 3: Estimates of phenotypic, genetic and environmental correlations between body weight and linear body traits of IBxF genotype at 2, 10 and 20 weeks of age

Age (weeks)	Trait	Phenotypic	Genetic	Environmental	
				E_{r_s}	E_{r_d}
2	SL	0.50	0.51±0.73	0.26	0.52
	DL	0.43	0.45±0.31	0.18	0.30
	BG	0.37	1.14±0.68	-0.11	0.71
	BW	0.13	0.24±0.10	-0.11	0.14
	KL	0.22	0.23±0.66	0.16	0.19
	BL	-0.02	-0.22±0.11	0.23	0.10
	WL	0.03	0.47±0.24	-0.38	0.12
10	SL	0.84	1.30±0.94	0.53	0.71
	DL	0.46	0.05±0.02	0.77	0.71
	BG	0.49	2.01±0.25	0.63	0.78
	BW	0.48	2.40±0.28	0.40	0.74
	KL	0.33	1.05±0.44	0.38	0.54
	BL	0.38	-0.37±0.51	0.62	0.64
	WL	0.45	-	0.48	0.85
20	SL	0.44	-	0.09	0.12
	DL	0.52	-	0.93	1.08
	BG	0.14		1.09	0.82
	BW	0.74	-	1.03	1.03
	KL	0.42	-	0.94	1.01
	BL	0.59	-	0.89	0.99
	WL	0.59	-	0.75	0.93

SL=Shank length, DL=Drumstick length, BG=Body girth, BW=Body width, KL=Keel length, BL=Body length, WL=Wing length, - =not estimable, IBxF=Isa Brown x frizzle feathered.

Table 4: Estimates of phenotypic, genetic and environmental correlations between body weight and linear body traits in IBxNa genotype at different ages

Age (weeks)	Trait	Phenotypic	Genetic	Environmental	
				E_{r_e}	E_{r_A}
2	SL	0.26	0.71±.17	-5.15	0.02
	DL	0.12	0.21±0.07	-	-0.32
	BG	0.08	0.24±0.16	-2.86	-0.80
	BW	-0.05	-0.34±0.18	2.85	-
	KL	0.18	0.37±0.27	-	-0.09
	BL	0.16	0.22±0.06	-	-0.09
	WL	0.21	0.38±0.10	-	-0.25
10	SL	0.37	0.003±0.00	0.86	0.79
	DL	0.35	0.38±0.04	0.75	0.94
	BG	0.32	0.03±0.00		0.43
	BW	0.41	0.29±0.02	0.73	0.58
	KL	0.18	0.17±0.03		-0.34
	BL	0.39	0.47±0.03	0.45	0.67
	WL	0.37	0.91 ±0.09	0.39	1.03
20	SL	0.83	-	0.93	1.05
	DL	0.81	-	0.93	1.08
	BG	0.79	-	1.09	0.82
	BW	0.84	-	1.03	1.03
	KL	0.82	-	0.94	1.01
	BL	0.81	-	0.89	0.99
	WL	0.77	-	0.75	0.93

SL=Shank length, DL=Drumstick length, BG=Body girth, BW=Body width, KL=Keel length, BL=Body length, WL=Wing length, - =not estimable, IBxNa=Isa Brown x naked neck.

Table 5: Estimates of phenotypic, genetic and environmental correlations between body weight and linear body traits in IBxN genotype at different ages

Age (weeks)	Trait	Phenotypic	Genetic	Environmental	
				E_{r_e}	E_{r_A}
2	SL	0.45	-	0.56	-0.002
	DL	0.52	-	0.60	0.49
	BG	0.59	-	0.68	0.63
	BW	0.62	-	0.63	0.14
	KL	0.47	-	0.61	0.47
	BL	0.52	-	0.53	0.71
	WL	0.53	-	0.56	-0.002
10	SL	0.68	0.62±0.11	0.68	0.88
	DL	0.66	0.34±0.04	0.69	0.72
	BG	0.53	0.59±0.02	0.34	0.42
	BW	0.57	0.18±0.01	0.79	0.96
	KL	0.61	0.42±0.10	0.62	0.61
	BL	0.11	-0.81±0.02	0.23	0.21
	WL	0.58	0.62±0.11	0.68	0.88
20	SL	0.67	0.49±0.02	0.59	0.65
	DL	0.67	0.26±0.01	0.69	0.69
	BG	0.70	0.97±0.01	0.52	0.86
	BW	0.72	0.93±0.02	0.60	0.93
	KL	0.61	-	0.52	0.95
	BL	0.68	0.21±0.00	0.80	0.91
	WL	-0.11	-0.12±0.00	-0.43	-0.85

SL=Shank length, DL=Drumstick length, BG=Body girth, BW=Body width, KL=Keel length, BL=Body length, WL=Wing length, - =not estimable, IBxN=Isa Brown x normal feathered

length (-0.03±0.00), body girth (-0.12±0.03) and keel length (-0.03±0.02) at 2 weeks and body length (-0.81±0.02) at 10 weeks in NaxIB genotype. All other estimates between body weight and linear body traits were positive and ranged from low to high (0.15±0.15 – 4. 73±0.05) at 2 to 20 weeks in NaxIB genotype. In NxIB genotype, negative genetic correlations existed between body weight and drumstick (-0.41±0.19), body girth (-0.33±0.12), body width

(-0.53±0.31), body length (-0.41±0.15) and wing length (-0.06±0.03) at 2 weeks whereas positive correlation occurred only between body weight and shank length. At 10 and 20 weeks in the same genotype, body weight correlated positively with all the linear traits and the estimates ranged from low to high (0.16±0.19 – 0.99±0.13).

Highest positive genetic correlation estimates were obtained at 10 weeks between body weight and each of body width (2.40±0.28) and wing length (0.91±0.09) in IBxF and IBxNa genotypes, respectively. Highest positive estimates were also obtained between body weight and body girth (0.97±0.01) at 20 weeks in IBxN, wing length (7.39±5.19) from dam variance component at 10 weeks in FxIB, body width (4.73±0.50) at 20 weeks in NaxIB and shank length (0.99±0.13) at 10 weeks in NxIB genotypes. Shank length correlated positively with body weight in all genotypes and at all ages studied. The genetic correlation estimates of the traits generally increased with age in the genotypes.

3.3. Environmental correlations between body weight and linear body traits of crossbred chickens (sexes combined) at 2, 10 and 20 weeks

Estimates of environmental correlation between body weight and linear body traits of the various genotypes at different ages are presented in Tables 3-8. The estimates were obtained from both sire and dam variance components in all genotypes at the three ages studied. The estimates ranged from -5.15 to 2.85 and -1.41 to 4.18 from sire and dam variance components, respectively at the entire ages of the genotypes. Negative and positive environmental correlation estimates existed between body weight and shank length (-5.15 to 4.18, 0.23 to 0.96 and, 0.09 to 1.05), drumstick length (-0.32 to 0.94, 0.43 to 0.95, 0.18 to 1.11), body girth (-2.86 to 0.88, 0.05 to 1.11, 0.09 to 1.09), body width (-0.42 to 2.85, 0.24 to 0.98 and -0.51 to 1.03), keel length (-0.09 to 0.79, -0.51 to 0.96 and 0.10 to 1.01), body length (-0.49 to 0.71, -0.50 to 0.80 and -0.07 to 1.39) and wing length (-1.41 to 0.57, 0.11 to 1.03 and -0.85 to 1.06) at 2, 10 and 20 weeks, respectively from both variance components in all genotypes. More negative estimates occurred, especially between body girth and body weight at 2 weeks while higher positive estimates were mostly obtained at 20 weeks from dam variance component of the genotypes. However, shank length had highest positive (4.18) environmental correlation estimate with body weight from dam variance component in NaxIB genotype at 2 weeks. Estimates in NxIB genotype were all positive compared to other genotypes where both negative and positive values occurred.

4. DISCUSSION

4.1. Phenotypic correlation

The estimates of phenotypic correlation between body weight and linear body traits obtained in this study were slightly lower in magnitude compared to 0.13 - 0.99 and 0.3 – 0.98 ranges of phenotypic correlation coefficients reported by Ige (2013) in crossbred Fulani ecotype chickens at 2 and 10 weeks old, respectively. The estimates increased with age similar to those reported by Adeleke et al. (2011) between body weight and shank length, thigh length, breast girth and keel length at 4 and 20 weeks of age in pure and crossbred progeny of Nigerian indigenous chickens.

The increasing magnitude of the phenotypic correlations implies that maximum response to selection could be achieved at 20 weeks of age in these chickens. The positive phenotypic correlation estimates observed between most of the linear traits and body weight indicate that there was increase in body weight with corresponding increase in the linear body traits of the genotypes. According to Ebangi and Ibe (1994) and Ige (2013), they observed high positive phenotypic correlations also indicate that genetic improvement in body weight can be realized by indirect selection of any one of the linear body traits using their observed values. Ojo (2010) noted that traits with positive correlation can be collectively included in a selection index for multiple traits selection. The negative estimates of phenotypic correlation between body weight and some of the linear body traits obtained in this study were similar to those reported by Fayeye et al. (2014) in Isa Brown and Ilorin ecotype chickens. Negative correlations simply implied that body weight decreased as linear body traits increased in size. Assan (2015) explained that environmental factors including disease could cause such negative correlation between traits. Indirect selection of body weight based on negative correlation response from the linear traits will adversely affect body weight. Hence, Tongsiri et al. (2014) suggested that traits exerting such negative correlated responses should be considered separately for selection program as a way of circumventing their adverse effect on body weight.

The highest positive phenotypic correlation estimates of body weight obtained with shank length at 10 weeks in IBxF, body width at 20 weeks in IBxNa and IBxN, drumstick length in FxIB at 20 weeks, keel length and shank length at 20 weeks in NxIB genotypes suggest that these traits could serve as best predictors and indirect selection criteria for body weight at these ages in their respective genotypes. Similarly, Ukwu et al. (2014) and Nwaogwugwu et al. (2018) had reported shank length and thigh length in chicken and quail, respectively as the best predictors of body weight based on their positive relationship. Kabir et al. (2006) also obtained high and positive phenotypic correlation between shank length and body weight and opined that it was possible to predict body weight of live Rhode Island chickens on the basis of their shank length measurement. The higher phenotypic correlation estimates of reciprocal crosses than the main crosses suggest that the former may have faster growth rate than the later. This result agrees with the findings of Nwachukwu at al. (2006).

Table 6: Estimates of phenotypic, genetic and environmental correlations between body weight and linear body traits in FxIB genotype at different ages

Age (weeks)	Traits	Phenotypic	Genetic		Environmental	
			G_{r_c}	G_{r_A}	E_{r_c}	E_{r_A}
2	SL	0.28	0.19±0.33	-	0.33	0.44
	DL	0.18	0.15±0.12	0.28±0.16	0.15	-0.17
	BG	0.32	0.40±0.14	-	-0.20	-0.05
	BW	0.34	0.61±0.27	-	-	0.09
	KL	0.35	-0.26±0.45	0.56±0.29	0.67	-
	BL	0.34	0.34±0.17	0.85±0.52	0.13	-0.32
	WL	0.49	0.51±0.49	0.71±0.28	0.14	-1.41
10	SL	0.65	0.95±0.14	0.80±0.11	0.23	0.28
	DL	0.66	0.82±0.08	0.91±0.22	0.43	0.62
	BG	0.60	0.88±0.03	0.22±0.01	0.05	0.69
	BW	0.55	0.68±0.03	0.88±0.05	0.26	0.24
	KL	0.56	0.93±0.07	0.62±0.06	-0.51	0.13
	BL	0.02	-0.56±00	-	0.06	-0.50
	WL	0.52	0.84±0.05	7.39±5.17	0.11	0.18
20	SL	0.59	0.69±0.04	0.81±0.02	0.61	0.28
	DL	0.71	1.00±0.03	1.06±0.02	0.46	0.18
	BG	0.50	0.25±0.01	1.73±0.03	0.50	0.09
	BW	0.67	0.93±0.02	1.17±0.01	0.38	-0.25
	KL	0.48	0.78±0.02	0.89±0.03	0.10	0.16
	BL	0.40	0.47±0.00	0.96±0.01	0.28	-0.07
	WL	0.46	-0.75±0.02	1.83±0.08	1.06	0.27

SL=Shank length, DL=Drumstick length, BG=Body girth, BW=Body width, KL=Keel length, BL=Body length, WL=Wing length, - =not estimable, FxIB=Frizzle feathered x Isa Brown.

Table 7: Estimates of phenotypic, genetic and environmental correlations between body weight and linear body traits in NaxIB genotype at different ages

Age (weeks)	Trait	Phenotypic	Genetic	Environmental	
				E_{r_c}	E_{r_A}
2	SL	0.14	0.15±0.15	0.58	4.18
	DL	0.07	-0.03±0.00	-	-
	BG	0.17	-0.12±0.03	0.88	-0.53
	BW	0.21	0.40±0.08	-0.42	0.36
	KL	0.15	-0.03±0.02	0.79	0.53
	BL	0.16	0.24±0.05	-0.49	0.08
	WL	0.23	0.27±0.12	-0.08	0.04
10	SL	0.75	0.62±0.11	0.68	0.88
	DL	0.71	0.34±0.04	0.69	0.72
	BG	0.69	0.59±0.02	0.34	0.42
	BW	0.66	0.19±0.01	0.79	0.96
	KL	0.47	0.42±0.10	0.62	0.61
	BL	0.53	-0.81±0.02	0.23	0.21
	WL	0.54	0.26±0.03	0.71	0.88
20	SL	0.67	0.96±0.06	-	-
	DL	0.88	0.47±0.01	0.92	1.11
	BG	0.82	0.39±0.00	0.83	0.91
	BW	0.76	4.73±0.05	-0.51	1.00
	KL	0.80	1.13±0.07	0.75	0.99
	BL	0.80	1.32±0.02	0.51	1.39
	WL	0.63	0.49±0.01	0.85	0.98

SL = Shank length, DL =Drumstick length, BG =Body girth, BW =Body width, KL =Keel length, BL Body length, WL =Wing length, - = not estimable, NaxIB =Naked neck x Isa Brown.

Table 8: Estimates of phenotypic, genetic and environmental correlations between body weight and linear body traits in NxIB genotype at different ages

Age (weeks)	Trait	Phenotypic	Genetic	Environmental	
				E_{r_e}	E_{r_a}
2	SL	0.39	0.16±0.19	0.84	1.09
	DL	0.33	-0.41±0.19	0.94	0.79
	BG	0.41	-0.33±0.12	0.81	0.61
	BW	0.40	-0.53±0.31	0.69	0.73
	KL	0.34	-	0.35	-
	BL	0.33	-0.41±0.15	0.56	0.47
	WL	0.36	-0.06±0.03	0.57	0.52
10	SL	0.87	0.99±0.13	0.74	0.96
	DL	0.84	0.89±0.05	0.68	0.95
	BG	0.80	0.95±0.04	0.74	1.11
	BW	0.78	0.84±0.02	0.64	0.98
	KL	0.67	0.73±0.10	0.68	0.96
	BL	0.67	0.39±0.01	0.73	0.80
	WL	0.65	0.80±0.05	0.54	0.64
20	SL	0.85	0.89±0.04	0.81	0.93
	DL	0.80	0.64±0.02	0.86	1.02
	BG	0.66	0.45±0.00	0.78	1.01
	BW	0.76	0.49±0.00	0.77	0.91
	KL	0.85	0.72±0.03	0.85	0.97
	BL	0.67	0.50±0.01	0.79	1.04
	WL	0.61	0.41±0.01	0.72	0.86

SL = Shank length, DL =Drumstick length, BG =Body girth, BW =Body width, KL =Keel length, BL =Body length, WL =Wing length, - = not estimable, Normal feathered x Isa Brown.

4.2. Genetic correlation

The low to high positive estimates of genetic correlation obtained in IBxNa, FxIB, NaxIB and NxIB genotypes between 2 and 20 weeks agree with the findings of Udeh (2017) while the moderate to high estimates found in IBxF and IBxN at the same age range are similar to those of Kabir et al. (2006). The different ranges of the genetic correlation estimates obtained in the genotypes are an indication that different proportions of additive genetic variances existed in these genotypes, thus supporting the claim that the genotype of an animal contributes to variation in additive genes for traits (Hill 2010). The high positive genetic correlation estimates obtained between body weight and shank length, body girth, body width and wing length in this study are similar to the estimates between body weight and shank length, keel length and breast girth reported by Ebangi and Ibe (1994) in chicken. Adebambo et al. (2006) and Agu et al. (2012) noted that these higher estimates indicate strong pleiotropic genes controlling the traits. The implication is that by indirect selection for any of these linear traits, genetic improvement in body weight will be realized as correlated response. Pleiotropy could be antagonistic as noted by Zoltán and Gerdien de (2004), and this is the cause of negative correlation between two traits. There were favorable relationships among shank length, body girth, body width and wing length which had high positive correlations. This is in line with the report of Ojo (2010). These traits could be improved simultaneously in a selection index. The negative correlation estimates occurring more at 2 weeks for drumstick length, body girth, keel length, body width, body length and wing length and later changed to positive at later stages of growth of the chickens is similar to the pattern of the genetic correlation estimates reported by Manjula et al. (2018) in Korean native chicken and Barbato (1991) in mice. Tongsiri et al. (2019) and Tongsiri et al. (2020) suggested that traits with negative correlations should not be included in selection index program but selected independently for improvement.

The increasing genetic correlation estimates with age found in this study is in contrast with the observations of Adeyinka et al. (2006) but agrees with the findings of Adeleke et al. (2011). This difference may be attributed to differences in breeding method as pointed out by Kabir (2006). The increasing genetic correlation estimates suggests that greater additive genetic variance and pleiotropic genes controlling these traits existed at 20 weeks than at 2 or 10 weeks. This suggests that greater response to selection can be achieved at 20 weeks of age in line with the report of Dana et al. (2011). The consistent increase of the genetic correlation estimates reveals that there was a constant growth in body weight with corresponding growth in the linear body traits throughout the 2-20 weeks period of growth. This implies that the linear body traits can serve as indicators for high body weight at any time within the ages studied. Shank length which had positive correlation with body weight at all ages in the genotypes may serve as the best predictor and index of selection for body weight in chicken throughout 2 to 20 weeks period.

This result is affirmed by Nosike et al. (2020) who reported shank length as a predictor of body weight in broiler chickens.

4.3. Environmental correlation

The ranges of environmental correlations indicated that highest positive estimates were obtained with shank length and body width at 2 weeks, drumstick length at 10 weeks and body girth, keel length, body length and wing length at 20 weeks. Lowest negative estimates were obtained from shank length, drumstick length, body girth and wing length at 2 weeks, keel length and body length at 10 weeks and body width at 20 weeks. The positive estimates indicated that body weight of the chickens increased with increase in linear body traits with greatest effect from environmental and non- additive deviations. The lowest negative estimates indicated that increase in body weight with corresponding increase in linear body traits resulted from least environmental effects. The negative environmental correlations implied large additive genetic variance for the traits. Hence indirect selection of body weight using shank length, drumstick length, body girth and wing length at 2 weeks, keel length and body length at 10 weeks and body width at 20 weeks will result in rapid genetic improvement. Higher environmental correlation estimates obtained from dam than sire variance component, especially in IBxF genotype, is an indication that resistance to negative environmental effects was offered more from the sire. In other words, higher environmental effect on the chickens was contributed more by dam variance component. Since additive genetic variance due to dam is more biased than that of sire in animal breeding (Ibe 1998), sires should therefore be selected for hardiness and survivability of chickens. The inestimable genetic and environmental correlations obtained in the different Tables indicated negligible additive genetic variances and environmental deviations for the affected traits. This was possibly due to method of estimation or data size (Ibe 2019).

Conflict of Interest: The author declares that there was no conflict of interest in the Study.

Conclusion: The high genetic and phenotypic correlation estimates of body weight with shank length, body width and wing length at 10 weeks, drumstick length and body girth at 20 weeks indicated that these traits could be included in selection index for multiple selection and improvement of body weight through correlated responses. The negative environmental correlations obtained between body weight and shank length, drumstick length, body girth and wing length at 2 weeks, keel length and body length at 10 weeks and body width at 20 weeks implied less environmental deviations with large additive genetic variances on the traits. Genetic improvement of the linear body traits can be realized at these ages with less adverse environmental effects.

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