

HERITABILITY OF BODY WEIGHT AND LINEAR BODY MEASUREMENTS OF ISA BROWN x LOCAL CHICKEN GENOTYPES

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ABSTRACT

Heritability of growth traits was studied at 2, 10 and 20 weeks using 531 day-old unsexed crossbred chickens belonging to six genotypes. Heritability estimates were obtained from variance components of sire (σ_s^2), dam (σ_d^2) and sire plus dam (σ_{s+d}^2) by analysis of variance in a nested design. The heritability of body weight was high (0.43-0.66) in frizzle feathered x Isa Brown (FxIB), Isa Brown x frizzle feathered (IBxF), Isa Brown x normal feathered (IBxN) and normal feathered x Isa Brown (NxIB) at 10 and 20 weeks, but low to moderate (0.02-0.38) in Isa Brown x naked neck (IBxNa) and naked neck x Isa Brown (NaxIB) at all ages from different variance components. The heritability of shank length was high at weeks 2 (0.45) in NaxIB, 10 (0.53-0.90) in IBxF, IBxN and NaxIB and 20 (0.40 - 0.53) in IBxNa and IBxN from σ_s^2 . The heritability of drumstick length (0.40 - 0.46), body girth (0.54 - 0.62), body width (0.50 - 0.81) and keel length (0.72 - 1.50) was also high from different variance components and ages. Body length was highly heritable only in IBxN (0.50) from σ_s^2 at 20 weeks. Wing length was lowly to moderately heritable (0.01 - 0.36) at all ages of the genotypes. There was large additive genetic variance for most of the traits in different genotypes and ages. Rapid genetic improvement of growth can be made in these chickens by individual selection, especially using shank length of IBxN from sire lines between 10 and 20 weeks of age.

Keywords: Chicken, Genotype, Body measurements, Heritability, Variance components.

1. INTRODUCTION

The productivity of local chickens is quite low compared to their improved exotic counterparts (Ajayi, 2010). This is due mainly to their low genetic profile and lack of improved production environment (Leenstra and Cahaner, 1992; Adetayo and Babafunso, 2001). This problem has resulted in insufficient animal production and concomitant low animal protein consumption in developing countries like Nigeria. The level of animal protein consumption in Nigeria is put at 5 g/caput/day, which is far below the Food and Agriculture Organization recommended level of 35 g/caput/day (Ojo, 2003). On the other hand, there is not only huge foreign exchange implication (Ibe, 1990) but also health and environmental problems associated with importation of exotic stock as well as genotype-environment interaction which causes loss of fitness (Ebangi and Ibe, 1994). The productivity of the local chickens must therefore be improved to address the problem of low animal protein consumption in the country. Previous

studies have shown that estimation of genetic parameters is a prerequisite to genetic improvement in chicken (Oleforuh-Okoleh, 2011; Niknafs *et al.*, 2012). Heritability is a genetic parameter which enables prediction of breeding value and selection decision to be made (Zhang *et al.*, 2005; El-Labban *et al.*, 2011). Estimates of heritability may be high, moderate or low with corresponding values of 0 to 19%, 20 to 39% and 40 % and above, respectively (Falconer, 1989).

Heritability estimate for a trait is dependent upon the population and environment from where it was estimated (Ranjan and Guatam, 2018). This accounts for a wide range of differences in heritability estimates for a trait in literature. Le Bihan-Duval *et al.* (1998), Argentaño *et al.* (2002) and Sanda *et al.* (2014) reported low to high estimates of heritability for body weight and linear body measurements at different ages in commercial strains of broiler chickens. Momoh and Nwosu (2008) reported moderate to high heritability estimates for body weight at different ages of local chicken. Ebangi and Ibe (1994) reported moderate to high heritability estimates for body weight, shank length, keel length and breast width of local chickens at 6 weeks of age and concluded that appreciable genetic variance existed in the local chicken population. Ibe (1993), on the other hand, noted that growth traits are useful in quantifying size and shape which have direct relationship with the economic value of animals.

Extensive research has not been carried out on the heritability of growth traits from the three variance components of crossbred local chickens except perhaps the work done by Nwosu and Asuquo (1984) and Roff, (2006). Therefore, the present study will not only assist in bridging the research gap but give opportunity to compare the level of bias in the three variance estimates as to know the best source from which heritability can be estimated for fast genetic improvement in chicken (Roff, 2008; Ibe, 2019; Bal *et al.* 2019). The objective of this study was to estimate the heritability of body weight and some linear body measurements of main and reciprocal crossbred Isa Brown and local chickens.

2. MATERIAL AND METHODS

2.1 Experimental animals and management

The parent stocks used in the study consisted of Isa Brown strain of layers and three strains of local chickens namely frizzle feathered, naked neck and normal feathered. The Isa Brown chickens consisted of 9 cocks and 27 hens. Each strain of local chicken consisted of 3 cocks. The hens were made up of 8 frizzle, 7 naked neck and 9 normal feathered chickens. These were randomly allotted in nested design and mated in main and reciprocal order using Isa Brown cocks and local chicken cocks, respectively. A total of 531 F₁ day-old chicks were produced in 12 hatches at weekly interval. The chicks were made up of 123 Isa Brown x frizzle feathered (IBxF), 49 Isa Brown x naked neck (IBxNa), 116 Isa Brown x normal feathered (IBxN), 137 frizzle feathered x Isa Brown (FxIB), 42 naked neck x Isa Brown (NaxIB) and 64 normal feathered x Isa Brown (NxIB) genotypes.

The chickens were brooded for four weeks. Water and feed were given to them *ad libitum*. They were fed with starter mash containing 2800 kcal ME/kg and 20% CP at 0 - 6 weeks and grower mash containing 2550 kcal ME/kg and 15% CP at 6-20 weeks. The birds were administered antibiotics and coccidiostats against diseases. The experiment lasted for twenty weeks.

2.2 Data collection and traits measurement

Data were collected from individual chicken of mixed sexes at 2, 10 and 20 weeks on the body weight and linear body measurements, namely shank length, drumstick length, body width, body girth, body length, keel length, and wing length. The descriptions of these traits are reported by Isaac (2020).

2.3 Experimental design and statistical analytical procedures

Unbalanced nested design was employed in the experiment. The design has a mixed model involving fixed (hatch) and random (sire and dam) effects. There were 12 hatches, 18 sires and 54 dams. The model was specified in (1).

$$Y_{ijkl} = \mu + H_i + S_j + D_{kj} + \epsilon_{ijkl}, \dots (1)$$

where Y_{ijkl} is observation made on the l^{th} progeny of k^{th} dam mated to j^{th} sire in i^{th} hatch, μ is overall mean, H_i is fixed effect of hatch ($i = 1, \dots, 12$), S_j is random effect of sire ($k = 1, \dots, 18$), D_{kj} is random effect of dam mated to sire ($l = 1, \dots, 51$) and ϵ_{ijkl} is random error, assumed to be independently and identically, normally distributed with zero mean and constant variance [$iind(0, \sigma^2)$].

Analysis of variance (ANOVA) for unbalanced data was employed as a method of estimation of variance components (Table 1). By unbalanced data it meant that number of dams per sire, number of progeny per dam and number of progeny per sire were not equal in each case. All analysis was carried out using SAS (1999) computer programme.

Table 1: Analysis of variance for estimation of variance components.

Source variance	Df	SS	MS	E(MS)
Sires	s-1	SS _s	MS _s	$\sigma_e^2 + k_2\sigma_d^2 + k_3\sigma_s^2$
Dams/Sire	d-s	SS _d	MS _d	$\sigma_e^2 + k_1\sigma_d^2$
Progeny/dam/sire	n..-d	SS _e	MS _e	σ_e^2
Total	n..-1	SS _t		

df= Degree of freedom; SS= Sum of squares; MS = Mean square; E(MS) = Expected mean square; SS_t = total sum of squares; s = number of sires; d = number of dams; n.. = total number of progeny; $\sigma_e^2, \sigma_d^2, \sigma_s^2$ = error, dam and sire variances components, respectively.

The correction factor and sums of squares in Table 1 were calculated with expressions (2), (3), (4), (5) and (6), respectively according to Becker (1984) and Ibe (2019).

$$CF = \frac{y^2 \dots}{n} \dots (2)$$

$$SS_t = \sum_{i=1}^n \sum_{j=1}^d \sum_{k=1}^{n_{ij}} y_{ijk}^2 - \dots (3)$$

$$SS_s = \sum_i \frac{y_{i..}^2}{n_i} - CF \dots (4)$$

$$SS_d = \sum_i \sum_j \frac{y_{ij.}^2}{n_{ij}} - \sum_i \frac{y_{i..}^2}{n_i} \dots (5)$$

$$SS_e = SS_t - SS_d \quad \dots \quad (6)$$

where $y_{...}$ is the grand total of all observations, y_{ijk} is a single progeny record, y_i is the total for sire i , y_{ij} is the total for dam j mated to sire i , s is the total number of sires, d is the total number of dams, n_i is the number of progeny produced by sire i , and n_{ij} is the number of progeny produced by dam j mated to sire i . From Table 1, the coefficients of σ_d^2 in the dams/sire and sire lines are not equal i.e $k_1 \neq k_2$ because of the unbalanced data used. Therefore, the three coefficients were determined by using expressions (7) – (9), respectively.

$$k_1 = (n_{..} - \sum_i \frac{\sum n_{ij}^2}{n_i}) / d.f. (dams) \quad \dots \quad (7)$$

$$k_2 = (\sum_i \frac{\sum n_{ij}^2}{n_i} - \frac{\sum \sum n_{ij}^2}{n_{..}}) / d.f. (sires) \quad \dots \quad (8)$$

$$k_3 = (n_{..} - \frac{\sum n_i^2}{n_{..}}) / d.f. (sires) \quad \dots \quad (9)$$

where $n_{..}$ is the total number of progeny per genotype, n_i is the number of progeny per sire and n_{ij} is the number of progeny per dam. The ANOVA yielded variance components of sire (σ_s^2), dam (σ_d^2) and error (σ_e^2) which were estimated by equating the mean squares to their expectations and solving. Solutions were obtained as expressed in (10), (11) and (12), respectively (Becker, 1984).

$$\sigma_e^2 = MS_e \quad \dots \quad (10)$$

$$\sigma_d^2 = (MS_d - MS_e) / k_1 \quad \dots \quad (11)$$

$$\sigma_s^2 = MS_s - (MS_e + k_2 \sigma_d^2) / k_3 \quad \dots \quad (12)$$

The three variance components were summed to obtain the total phenotypic variance (σ_p^2) for any trait as shown in expression (13).

$$\sigma_p^2 = \sigma_s^2 + \sigma_d^2 + \sigma_e^2 \quad \dots \quad (13)$$

Heritability was computed from paternal half-sib (h_s^2), maternal half-sib (h_d^2) and full-sib (h_{s+d}^2) correlations as the ratio of sire, dam and combined sire and dam variance components to total phenotypic variance, respectively according to Becker (1984). The corresponding formulae used to compute the three heritabilities were as follows:

$$h_s^2 = 4\sigma_s^2 / \sigma_p^2$$

$$h_d^2 = 4\sigma_d^2 / \sigma_p^2$$

$$h_{s+d}^2 = 2(\sigma_s^2 + \sigma_d^2) / \sigma_p^2$$

Standard errors of the heritability estimates were computed according to Becker (1984).

3. RESULTS

In Table 2, heritability of body weight from sire and sire plus dam variance components (0.08 and 0.02, respectively) were low at 2 weeks and those from the three variance components ranged from low to high (0.07-0.50) at 20 weeks in IBxF. The heritability estimates were high for shank length at 10 and 20 weeks and for body width at 20 weeks from sire, sire plus dam and dam variance components, respectively in IBxF. At other ages, heritability of shank length, body width and other linear body measurements ranged from low to moderate (0.02 to 0.36) from all

variance components. Table 3 presents the heritability estimates of body weight and linear body measurements from sire, dam and sire plus dam variance components of IBxNa genotype at different ages. The estimates for body weight were moderate (0.19-0.31) at 2 weeks; low to moderate at 10 (0.07- 0.38) and 20 (0.11-0.33) weeks from sire, dam and sire plus dam variance components, respectively. The estimates for the linear body measurements ranged from low to moderate (0.02 -0.38) from all variance components at all ages except for drumstick length from sire plus dam variance component at 2 weeks, shank length from sire variance component and keel length from dam variance component each at 20 weeks which had high estimates (0.40 - 0.46). In Table 4, heritability of body weight was low (0.04) from sire variance component at 2 weeks, moderate to high (0.21-0.48) from sire and sire plus dam variance components at 10 weeks and high (0.44-0.54) from the three variance components at 20 weeks. The heritability estimates were high for shank length at all ages, drumstick length at 2 weeks, body girth and keel length at 10 and 20 weeks, respectively from different variance components in IBxN genotype. The heritability estimates for the other traits ranged from low to moderate (0.01-0.39) from different variance components at all ages. In Table 5, heritability estimates for body weight of FxIB ranged from low to moderate (0.11-0.22) from the three variance components at 2 weeks, moderate to high (0.21-0.46) from sire variance component at 10 weeks and low to moderate (0.17-0.36) from sire plus dam variance components at 20 weeks. High heritability estimate (0.52) existed only for body width from sire variance components at 20 weeks in FxIB. The heritability estimates for the other linear measurements ranged from low to moderate (0.01 - 0.36) in this genotype. Heritabilities of many traits were inestimable from dam and sire plus dam variance components in this genotype.

Table 6 showed that heritability of body weight in NaxIB genotype was very low at 2 (0.00-0.11) and 10 weeks (0.02-0.03) and moderate at 20 weeks (0.17 -0.20) from the three variance components. High heritability estimates were obtained for shank length at 2 and 10 weeks, drumstick length and body width each at 10 weeks from sire variance component. Estimates for shank length, drumstick length, body width and other linear traits from different variance components at other ages ranged from low to moderate (0.01-0.37). Heritabilities of many traits from dam variance components were inestimable. The heritability of body weight and linear body measurements from sire, dam and sire plus dam variance components of NxIB genotype at different ages are presented in Table 7. The estimates for body weight were low (0.04-0.13) both at 2 and 10 weeks and ranged from moderate to high (0.27-0.66) at 20 weeks from the three variance components. The heritability estimates for the linear measurements ranged from low to moderate (0.01-0.28) at all ages from the three variance components except for body width which was high (0.81) from sire variance component at 20 weeks. The heritability was inestimable for most of the linear measurements at 2 weeks from sire and sire plus dam variance components.

Table 2: Heritability estimates for body weight and linear body measurements from sire, dam and sire plus dam variance components in IBxF genotype at different ages

Age (weeks)	Trait	h_s^2	h_d^2	h_{s+d}^2
2	Body weight (g)	0.08±0.00		0.02±0.00
	Shank length (cm)	0.12±0.02		0.04±0.00
	Drumstick Length (cm)	0.08±0.00		0.02±0.00
	Body girth (cm)		0.03±0.00	0.02±0.02
	Body width (cm)	0.17±0.05		0.08±0.00
	Keel length (cm)	0.13±0.03	0.18±0.06	0.00
	Body length (cm)	0.20±0.06	0.06±0.00	0.13±0.02
	Wing length (cm)		0.04±0.00	0.02±0.00
10	Shank length (cm)	0.90±0.69	0.07±0.00	0.08±0.00
	Drumstick length (cm)	0.03±0.00	0.05±0.00	0.04±0.00
	Body girth (cm)		0.02±0.00	
	Body width (cm)		0.50±0.30	
	Wing length (cm)	0.11±0.01	0.03±0.03	0.07±0.00
20	Body weight (g)	0.07±0.00	0.50±0.30	0.28±0.10
	Shank length	0.40±0.20	0.41±0.22	0.22±0.08
	Drumstick length (cm)	0.08±0.00	0.33±0.16	0.20±0.07
	Body width (cm)	0.00	0.36±0.19	0.18±0.05
	Keel length (cm)	0.03±0.00	0.11±0.01	0.07±0.00
	Body length (cm)	0.09±0.00	0.10±0.01	0.09±0.00
	Wing length (cm)	0.03±0.00	0.27±0.11	0.19±0.07

Table 3: Heritability estimates for body weight and linear body measurements from sire, dam and sire plus dam variance components of IBxNa genotype at different ages

Age (weeks)	Trait	h_s^2	h_d^2	h_{s+d}^2
2	Body weight (g)	0.31±0.13	0.19±0.06	0.25±0.09
	Drumstick length	0.14±0.03		0.40±0.23
	Body width (cm)	0.20±0.07		0.10±0.00
	Keel length (cm)	0.05±0.00		
10	Body Length (cm)	0.13±0.03		0.06±0.00
	Wing length (cm)	0.02±0.00		
	Body weight (g)	0.38±0.17	0.07±0.00	0.23±0.08
	Shank length (cm)	0.08±0.00	0.07±0.00	0.08±0.00
	Drumstick length (cm)	0.02±0.00	0.05±0.00	0.04±0.00
20	Body girth (cm)		0.05±0.00	0.00
	Wing length (cm)	0.12±0.03	0.03±0.00	0.07±0.00
	Body weight (g)	0.11±0.02	0.33±0.14	0.22±0.08
	Shank length (cm)	0.40±0.11	0.12±0.02	0.08±0.00
	Drumstick length (cm)	0.11±0.01	0.12±0.03	0.11±0.03

Body girth (cm)		0.11±0.02	0.02±0.00
Body width (cm)	0.05±0.00	0.13±0.04	0.09±0.00
Keel length (cm)	0.25±0.09	0.46±0.28	0.33±0.14
Body length (cm)		0.17±0.05	0.06±0.00
Wing length (cm)	0.08±0.00	0.36±0.20	0.21±0.08

Table 4: Heritability estimates for body weight and linear body measurements from sire, dam and sire plus dam variance components of IBxN genotype at different ages

Age (weeks)	Trait	h_s^2	h_d^2	h_{s+d}^2
2	Body weight (g)	0.04±0.00		
	Shank length (cm)	2.00±1.41	0.06±0.00	1.00±0.72
	Drumstick length	0.40±0.23	0.19±0.06	0.16±0.04
10	Body weight (g)	0.48±0.27		0.21±0.07
	Shank length (cm)	0.71±0.52		0.33±0.14
	Drumstick length	0.32±0.14	0.14±0.04	0.13±0.03
	Body girth (cm)	0.62±0.44	0.05±0.00	0.34±0.17
	Body width (cm)	0.35±0.19	0.01±0.00	0.18±0.05
	Keel length (cm)	0.51±0.30	0.01±0.00	0.26±0.09
	Wing length (cm)	0.18±0.06	0.01±0.00	0.09±0.00
20	Body weight (g)	0.45±0.24	0.54±0.31	0.44±0.23
	Shank length (cm)	0.53±0.30	0.08±0.00	0.29±0.11
	Drumstick length(cm)	0.36±0.19	0.14±0.3	0.24±0.09
	Body girth (cm)	0.54±0.39	0.31±0.12	0.39±0.21
	Body width (cm)	0.38±0.20	0.10±0.01	0.23±0.08
	Keel length (cm)		1.50±1.03	0.72±0.49
	Body length (cm)	0.50±0.31	0.04±0.00	0.26±0.09
	Wing length (cm)	0.23±0.08	0.26±0.09	0.15±0.04

Table 5: Heritability estimates for body weight and linear body measurements from sire, dam and sire plus dam variance components of FxIB genotype at different ages

Age (weeks)	Trait	h_s^2	h_d^2	h_{s+d}^2
2	Body weight (g)	0.11±0.02	0.22±0.07	0.16±0.04
	Shank length (cm)	0.27±0.12	0.10±0.01	0.19±0.06
	Drumstick length (cm)	0.05±0.00	0.03±0.00	0.04±0.00
	Body girth (cm)	0.04±0.00		
	Body width (cm)	0.08±0.00		0.04±0.00
	Keel length (cm)	0.06±0.00		0.01±0.00
	Body length (cm)	0.02±0.00	0.04±0.00	0.03±0.00
	Wing length (cm)	0.29±0.10		0.14±0.03
10	Body weight (g)	0.46±0.25		0.21±0.07
	Shank length (cm)	0.24±0.09		0.08±0.00

20	Drumstick length (cm)	0.07±0.00		
	Body girth (cm)	0.01±0.00		
	Body width (cm)	0.01±0.00	0.01±0.00	0.01±0.00
	Keel length (cm)	0.19±0.07	0.03±0.00	0.11±0.01
	Body length (cm)	0.01±0.00	0.05±0.00	0.03±0.00
	Wing length (cm)	0.22±0.07		0.01±0.00
	Body weight (g)	0.36±0.17		0.17±0.05
	Shank length (cm)	0.35±0.14	0.01±0.00	0.18±0.06
	Drumstick Length (cm)	0.30±0.12		0.12±0.03
	Body girth (cm)	0.19±0.06	0.02±0.00	0.10±0.01
	Body width (cm)	0.52±0.34	0.01±0.00	0.27±0.11
	Keel length (cm)	0.18±0.05		0.06±0.00
	Body length (cm)	0.32±0.13	0.02±0.00	0.17±0.06
	Wing length (cm)	0.01±0.00		

Table 6: Heritability estimates for body weight and linear body measurements from sire, dam and sire plus dam variance components of NaxIB genotype at different ages

Age (weeks)	Trait	h_s^2	h_d^2	h_{s+d}^2
2	Body weight (g)	0.11±0.02		
	Shank length (cm)	0.45±0.27	0.01±0.00	0.23±0.09
	Drumstick length (cm)	0.06±0.00	0.03±0.00	0.05±0.00
	Body girth (cm)	0.28±0.11		0.12±0.01
	Body width (cm)	0.34±0.16		0.16±0.04
	Keel length (cm)	0.29±0.11		0.13±0.03
	Body length (cm)	0.19±0.07		0.08±0.00
10	Wing length (cm)	0.33±0.12		0.14±0.03
	Body weight (g)	0.02±0.00	0.03±0.00	0.03±0.00
	Shank length (cm)	0.53±0.41		0.24±0.10
	Drumstick length (cm)	0.46±0.25		0.22±0.10
	Body girth (cm)	0.23±0.08	0.02±0.00	0.13±0.025
	Body width (cm)	0.96±0.73	0.05±0.00	0.01±0.00
	Keel length (cm)	0.29±0.10		0.12±0.01
20	Wing length (cm)	0.22±0.05		0.08±0.00
	Body weight (g)	0.20±0.06	0.17±0.05	0.18±0.06
	Shank length (cm)	0.14±0.04	0.37±0.17	0.24±0.08
	Drumstick length (cm)	0.15±0.04	0.21±0.08	0.13±0.03
	Body girth (cm)	0.11±0.01	0.13±0.03	0.12±0.01
	Body width (cm)	0.10±0.01	0.11±0.01	
	Keel length (cm)	0.01±0.00	0.28±0.11	0.14±0.03
	Body length (cm)	0.01±0.00		
	Wing length (cm)	0.03±0.00		

Table 7: Heritability estimates for body weight and linear body measurements from sire, dam and sire plus dam variance components of NxIB genotype at different ages

Age (weeks)	Trait	h_s^2	h_d^2	h_{s+d}^2
2	Body weight (g)		0.13±0.03	0.04±0.00
	Shank length (cm)		0.01±0.00	
	Drumstick length (cm)		0.03±0.00	0.03±0.00
	Body length (cm)		0.01±0.00	
10	Body weight (g)		0.05±0.00	
	Shank length (cm)			
	Drumstick length (cm)	0.05±0.00	0.01±0.00	0.03±0.00
	Body length (cm)	0.03±0.00	0.04±0.00	0.04±0.00
20	Body weight (g)	0.66±0.46	0.27±0.10	0.43±0.21
	Shank length (cm)	0.07±0.00		0.01±0.00
	Drumstick length (cm)	0.13±0.03	0.02±0.00	0.07±0.00
	Body width (cm)	0.80±0.61		
	Keel length (cm)	0.04±0.00		0.28±0.10
	Body length (cm)		0.10±0.01	

4. DISCUSSION

The low to moderate range of heritability estimates obtained for body weight in the different genotypes at various ages (Tables 2-7) were similar to the heritability estimates of body weight reported by Kabir *et al.* (2006) in Rhode Island Red and White chickens. This implied that additive genetic variance for body weight of these crossbred chickens were comparable to that of pure exotic ones, suggesting that the chickens could be used for breeding purposes in the absence of the exotic ones. The low to high heritability estimates for body weight obtained at 20 weeks from the three variance components in IBxF (Table 2), moderate to high estimates at 10 weeks in IBxN and 20 weeks in FxIB, NaxIB and NxIB (Tables 4- 7), high estimates in IBxN at 20 weeks (Table 4), high estimates of shank length, drumstick length, body width, body girth and keel length at 2, 10 and 20 weeks and the low to moderate heritability estimates for the other linear body measurements in IBxNa, FxIB, NaxIB and NxIB especially at 2 weeks are in agreement with the previous studies (Oni *et al.*, 1991; Argentaõ *et al.*, 2002; Momoh and Nwosu, 2008; Adeleke *et al.*, 2011; Osei-Amponsah *et al.*, 2013; Sanda *et al.*, 2014). These different estimates suggested that heritability was dependent on many factors such as genotype and age of estimation in addition to source of variation. This accounts for why heritability estimate of a trait varies greatly in literature (Wray and Visscher, 2008).

The low to moderate heritability estimates obtained for body weight and linear body measurements mostly at 2 weeks indicated existence of low additive genetic relative to non-additive and environmental variances for these traits. This suggested that environmental and non-additive deviations including maternal, dominance and epistasis effects had more influence on body weight of these genotypes at their early stage of growth (Prado-Gonzalez *et al.*, 2003). This implied that less genetic improvement could be achieved if these chickens were selected as early as two weeks of age since environmental and maternal effects had been reported to have more influence on the phenotype at early life of chickens (Barbato and Vasilalos-Younken, 1991; Jasouri *et al.*, 2017). The moderately high heritability estimates obtained for body weight and the

high estimates for shank length, drumstick length, body width, body girth and keel length at 10 and 20 weeks suggested that greater proportion of additive genetic variance relative to non-additive genes and environmental deviations existed with increase in age (Kramer *et al.*, 1998), and that individual selection should be employed for improvement of such traits (Rath *et al.*, 2015; Mebratie *et al.*, 2019). This suggested that as the chickens advanced in age, maternal and environmental effects gradually disappeared, giving way to true genetic effect which resulted in moderate to high heritability estimates at 10 and 20 weeks compared to 2 weeks of age (Prado-Gonzalez *et al.*, 2003; Ndungù *et al.*, 2020). Hence, greater response to selection will be achieved at 10 weeks and above based on the heritability of the traits.

The increasing trend of heritability estimates with age observed for the traits among the genotypes was similar to the previous investigations (Kumararaj *et al.*, 1991; Chambers, 1990; Chaudhary *et al.*, 1996; Adeleke *et al.*, 2011). Prado-Gonzalez *et al.* (2003), however, reported decreasing heritability values with increasing ages in chicken and explained that this might be due to environmental and genetic differences.

The numerically larger estimates of heritability obtained from dam variance components compared to that of the sire at 20 weeks in IBxF and IBxNa chickens support the opinion that heritability estimates from sire variance component is less biased and usually smaller in value than that of dam and sire plus dam variances components using the same data (Kearsey and Pooni, 1996; Astles *et al.*, 2006; Ibe, 2019;). Ibe (2019) explained that the smaller and less biased heritability estimate from sire variance component is due to the fact that sire variance includes proportions of additive genes and various interactions of additive genes only, whereas dam and combined sire and dam variance components in addition may contain additive x dominance interaction and even maternal effects. Kabir *et al.* (2006) reported that maternal effect from pre-oviposition such as egg size contributes to the high heritability estimates obtained from dam variance components in chickens. The inestimable heritabilities obtained for some traits at different ages indicated negative variances which is one of the drawbacks of analysis of variance procedure for estimating heritability (Ibe, 2019).

5. CONCLUSION

Shank length was the most highly heritable trait, followed by body width, body weight, keel length, body girth, drumstick length and body length. Wing length was lowly to moderately heritable. IBxN genotype recorded more traits with high heritability estimates, followed by NaxIB, IBxF, NxIB and FxIB. No trait with high heritability was recorded in IBxNa. Traits with high heritability estimates occurred more from sire variance component at 20 weeks, followed by 10 weeks. The magnitude of high estimates obtained at 10 weeks was larger than those at 20 weeks. It was concluded that growth should best be improved by individual selection of IBxN sire lines using shank length as the most heritable trait between 10 and 20 weeks of age in these crossbred chickens.

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