G.J.A.S.R

GLOBAL JOURNAL OF ANIMAL SCIENTIFIC RESEARCH

Journal homepage: www.gjasr.com

Print ISSN:2345-4377 *Online ISSN:2345-4385*

Original Article

Heritability of semen quality traits of crossbred Isa Brown and Nigerian indigenous cocks

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ABSTRACT

Main and reciprocal crossbred cocks from a population of 531 day-old chicks were used to study heritability of semen volume (SV), sperm motility (SM), sperm concentration (SC) and live sperm (SP) at 36 and 40 weeks of age. Analysis of variance was performed for unbalanced nested design. The analysis yielded variance components of sire (σ_s^2), dam (σ_d^2) and sire plus dam (σ_{s+d}^2), and heritability (h^2) of the traits was estimated therefrom. The estimates ranged from 1.33 to 0.02 and 1.481 to 0.03; 1.48 to 0.10 and 0.96 to 0.08; 0.97 to 0.12 and 0.89 to 0.04 at 36 and 40 weeks for SV, SM, SC and LS, respectively. Estimates from σ_s^2, σ_d^2 and σ_{s+d}^2 ranged from 1.48 to 0.02, 1.04 to 0.03 and 0.85 to 0.06 ; 1.10 to 0.04, 1.21 to 0.18 and 0.90 to 0.05; 0.96 to 0.09, 1.48 to 0.01and 0.76 to 0.10; 0.97 to 0.04, 0.89 to 0.12 and 0.69 to 0.08 for the four traits, respectively. Large additive genetic variances existed for most of the semen quality traits, especially the live sperm from sire and sire plus dam variance

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Cite this Article: Isaac, U. C., Adeolu, A. I., Ukwu, H.O., Nwankwo, C. A., Obike, O. M., and Ibe, S.N. (2021). Heritability of semen quality traits of crossbred Isa Brown and Nigerian indigenous cocks. *Global Journal of Animal Scientific Research,* 9(2), 65-81.
Retrieved from http://www.gjasr.com/index.php/GJASR/article/view/85
Article History: Received: 2021.08.15 Accepted: 2021.10.02

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components of the reciprocal crosses at 40 weeks. These traits were highly heritable and could be improved by individual selection.

Keywords: chickens, crosses, heritability, semen, variance components.

INTRODUCTION

The local chickens of Nigeria are known to have low reproductive potential due to their poor genetic profile combined with unfavorable environmental factors affecting them (Besbe, 2009). Good environment is not hereditary, and therefore cannot bring stable improvement without genetic enablement (Rauw and Gomez-Raya, 2015). Hence, Genetic improvement of semen quality traits remains a veritable option for improvement of the reproductive potential of the local chickens (Biscarini *et al.,* 2015). This can be realized by estimation of heritability of semen quality traits of the cocks (Oleforuh-Okoleh, 2011). Heritability is a genetic parameter which indicates the proportion of total phenotypic variance that is due to additive genetic effect (Getabalew *et al*., 2019). It is essential in predicting the animal's breeding value (Zhang *et al*., 2005; El-Labban *et al*., 2011) and response to selection (Elamin *et al*., 2012). Heritability estimates reveal the amount of additive genetic variance for a trait and enable selection decision to be made (Wray and Visscher, 2008). These estimates are fall into low (0-19 %), moderate (21-39 %) and high (40 % and above) ranges (Falconer, 1989). Estimates close to zero indicate negligible additive genetic variance and high environmental and other genetic variances for a trait (Miranda *et al*., 2019). High estimate indicate existence of substantial additive genetic variance for a trait, implying that individual selection for that trait should be employed for improvement (Sae-Lim *et al*., 2015). Low to moderate or intermediate estimates require family or pedigree selection for trait improvement (Khadiga *et al*., 2016).

Heritability estimates for semen quality traits like other traits in chicken have a wide range in literature. Factors such as population size, breeding method, genotype, environment, method and age of estimation account for differences in heritability estimates for a trait (Yin *et al*., 2019). Estimates of heritability for semen quality traits of cocks have been reported. Bongalhardo *et al*. (2000) reported heritability estimates of 0.27, 0.34 and 0.26 for semen volume, sperm concentration and sperm motility from White Leghorn roosters at 26 weeks of age. Kabir *et al*. (2007) estimated heritability of 0.82 for sperm motility in Rhode Island Red cocks at 18 weeks of age. Barbato (1999) reported that traits related to semen quality of White Leghorn roosters were of moderate to low heritability while Ansah *et al*. (1985) maintained that sperm quality traits are moderately heritable. Kabir (2006) reported medium to high heritability estimates for semen traits in Rhode Island Red and White strains of chickens whereas Gabriel *et al*. (2009) reported that semen volume, semen pH and sperm motility of breeding cocks at 38 weeks of age were highly heritable. Heritability of semen quality traits of main and reciprocal crossbred cocks from full

sib correlation involving sire, dam and sire plus dam variance components is scare in available literature. Nwosu and Asuquo (1984) and Ebangi and Ibe (1994) who reported heritability from the three variance components focused on growth traits of chickens. Kabir *et al*. (2007) reported heritability of semen traits of pure bred strains of chickens using only sire variance components. The present study is quite novel and could bridge the gap in research for genetic information needed for improvement of reproductive traits of crossbred cocks of Nigeria. The general objective of this study was to determine the heritability estimates of semen quality traits of the main and reciprocal crossbred Isa Brown and Nigerian local cocks.

MATERIALS AND METHODS

Experimental location

The experiment was conducted at the Poultry Unit of the Teaching and Research Farm of Michael Okpara University of Agriculture, Umudike. The University is located on Latitude 05^0 29′ North and Longitude 07^0 33′ East. It is approximately 122 m above sea level. The area is characterized by maximum and minimum daily temperature ranges of 27-36 ^oC and 20-26 ^oC, respectively, average annual rainfall of 2177 mm, monthly ambient temperature range of 22-33 °C and relative humidity of 50- 95% (NRCRI, 2008). It is located within the tropical rainforest zone of Nigeria. The crossbred cocks were reared for 40 weeks starting from day-old. Heritability of the semen quality traits was done at 36 and 40 weeks.

Parent stock, F_1 progeny and their management

A total of 69 exotic Isa Brown and Nigerian indigenous chickens consisting of frizzle feathered, naked neck and normal feathered strains were used as parent stock in the experiment. The indigenous chickens composed of 9 sires (3 from each strain) and 24 dams made up of 8 frizzle feathered, 7 naked neck and 9 normal feathered strains. The Isa Brown chickens comprised 9 sires and 27 dams. These were fed layer mash containing 2650 metabolizable energy (ME) per kilogram (kg) weight and 16.5 % crude protein (CP) *ad libitum*. For effective breeding and egg production, the chickens were managed intensively in small cages of 78 x 74 x 66 cm^3dimension constructed with wire gauze on deep litter pens measuring 2.65 x 1.67 m^2. The Isa Brown cocks were used to mate the local hens in main cross while the local cocks were used to mate with the Isa Brown hens in reciprocal cross. One cock mated two to three hens of a particular strain and each hen laid certain number of eggs.

The eggs were identified with permanent markers, set in an incubator and hatched at weekly intervals. A total of 531 first filial generation (F_1) day-old chicks were produced in 12 hatches at weekly intervals. They were reared intensively and fed *ad libitum* with starter mash (0-6 weeks) containing 2800 kcal ME/kg and 20 % CP,

grower mash (6-20 weeks) containing 2550 kcal ME/kg and 15 % CP and breeder mash (20-40 week) containing 2650 kcal ME/kg and 16.5 % CP.

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

Main Cross					Reciprocal Cross				
Genotype	Sire	Dam	DT	ST	Genotype	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				IB_4	9	
		F_5	9			F_2	IB_5	27	
		F_6	15	39			IB_6	11	47
	IB_3	F_7	15				IB_7	16	
		F_8	9	34		F_3	IB_8	19	
	Total			123			IB_9	18	53
IBxNa	IB_4	Na_1	7		NaxIB	Total			137
		Na_2	6			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			IB_{13}	2	
	IB_6	Na_6	6			Na_2	IB_{14}	9	
		Na_7	11	17			IB_{15}	4	15
	Total			49			IB_{16}	2	
IBxN	IB_7	N_1	13			Na_3	IB_{17}	7	
		N_2	11				IB_{18}	7	16
		N_3	15	39		Total			42
		N_4	11				IB_{19}	8	
	IB_8	N_5	14			N_1	IB_{20}	6	
		N_6	14	39			IB_{21}	7	21
		N_7	15				IB_{22}	10	
	IB_9	N_8	15		NxIB	N_2	IB_{23}	5	
		N_9	8	38			IB_{24}	8	23
	Total			116			IB_{25}	1	
						N_3	IB_{26}	8	
							IB_{27}	11	19
						Total			64
	Main cross Total			288		**Reciprocal cross Total**			243
				Grand Total					531

DT= Dam total, ST= Sire total

The genotypes of the chickens produced were Isa Brown x frizzle feathered main cross (IBxF), Isa Brown x naked neck main cross (IBxNa), Isa Brown x normal feathered main cross (IBxN), frizzle feathered x Isa Brown reciprocal cross (FxIB), naked neck x Isa Brown reciprocal cross (NaxIB) and normal feathered x Isa Brown

reciprocal cross (NxIB). Table 1 presents the pedigree and progeny number of the F_1 crossbred chicks (mixed sexes) produced at day-old. The cocks of this population (about 270 at day-old for the different genotypes) that survived till the reproductive age were used for semen traits evaluation and subsequent heritability estimation at 36 and 40 weeks of age. The duration of the experiment was 40 weeks from day-old to the last date of semen collection.

Semen collection and determination of semen quality traits

Semen was collected into a graduated test tube from individual cocks on farm at weekly interval from 36 to 40 weeks of age by abdominal massage technique (Lake, 1962). The collected semen was used to determine the following semen quality traits.

Semen volume: This was read in cubic millimeter (mm^3) directly from the graduated test tube and converted to milliliter (ml).

Sperm motility: This was assessed on farm immediately after collection of semen**.** A drop of semen with the aid of a micro-pipette was placed on a clean microscope slide and covered with a glass cover slip to spread the semen in other to have a uniform thickness and to prevent drying. The semen was viewed under the microscope using a magnification of x 40 objective lens. Two or three fields were examined and the estimated motility was by subjective judgment of the motile sperm. Sperm motility was expressed as the percentage of cells that are motile.

Sperm concentration: Semen concentration was measured using the direct count method. The Neubaeur haemocytometer for counting blood cells was used. It consists of two counting and two dilution pipettes. The counting chambers were 0.1 mm in depth and had a ruled area on the bottom of the chambers that was 1.0 mm^2; the square was sub-divided into 25 smaller squares. Normal saline was mixed with 1 ml of semen at the dilution rate of 1:1000. The diluted semen was then picked up using a micropipette. One drop of the diluted semen was then placed on one end of the haemocytometer and also on the other end and allowed to settle. The loaded Neubaeur haemocytometer was then placed on the microscope at a magnification of x 40. The spermatozoa's head that falls within the sub-divided smaller squares at the four edges and center of the haemocytometer was counted and the average per stain of a cock read. The concentration of the sperm per volume was determined using the expression (1).

$$\text{Concentration}\left(\text{x}\frac{10^9}{\text{ml}}\right) = \frac{\text{Number of spermatozoa counted x Dilution rate}}{\text{Volume of fluid (ml)}} \quad \ldots \quad (1)$$

Live/Dead ratio of sperm: This was determined by mixing freshly collected semen with Eosin/Nigrosin staining dye on the glass slide in order to make the sperm cells visible under the microscope. This is supervital staining (Marini and Goodman, 1969) whereby dead spermatozoa will absorb the staining dye while the live ones will not. The stained semen was smeared on the slide and examined under the microscope

using a magnification of x 40 objective lens. Unit of expression was percentage live sperm, and was estimated based on the rate of movement of the cells.

Experimental design

A mixed model, unbalanced nested design with fixed (hatch) and random (sire and dam) effects was fitted to the data for the analysis. With the design, there was unequal number of progeny per dam within sire, dams per sire and progeny per dam. Twelve (12) hatches, 18 sires and 51 dams were involved in the design. The model is specified in expression (2).

$$\mathbf{Y_{ijkl} = \mu + H_i + S_j + D_{jk} + \epsilon_{ijkl}} \quad \ldots \quad (2)$$

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

Statistical analytical procedures and estimation of heritability

Analysis of variance (ANOVA) was performed on semen data using SAS (1999) software for estimation of variance components. The method of estimation followed the ANOVA table presented in Table 2.

Table 2: Analysis of Variance Table 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, total, sire, dam and error sums of squares in Table 2 were calculated with expressions (3), (4), (5), (6) and (7), respectively according to Becker (1984) and Ibe (2019).

$$CF = \frac{y^2\ldots}{n} \quad \ldots \quad (3)$$

$$SS_t = \sum_{i=1}^{s}\sum_{j=1}^{d}\sum_{k=1}^{n_{ij}} y_{ijk}^{\ 2} - CF \quad \ldots \quad (4)$$

$$SS_s = \sum_i \frac{y_{i..}^2}{n_{i.}} - CF \quad \ldots \quad (5)$$

$$SS_d = \sum_i \sum_j \frac{y_{ij.}^2}{n_{ij}} - \sum_i \frac{y_{i..}^2}{n_{i.}} \quad \ldots \quad (6)$$

$$SS_e = SSt - SSd \quad \ldots \quad (7)$$

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 $k_1 \neq k_2$ so the three coefficients were determined by calculation using expressions (8) – (10), respectively.

$$k_1 = (n.. - \sum_i \frac{\sum n_{ij}^2}{n_{i.}})/\text{d.f. (dams)} \quad \ldots \quad (8)$$

$$k_2 = (\sum_i \frac{\sum n_{ij}^2}{n_{i.}} - \frac{\sum\sum n_{ij}^2}{n..})/\text{d.f. (sires)} \quad \ldots \quad (9)$$

$$k_3 = (n.. - \frac{\sum n_{i.}^2}{n..})/\text{ d.f. (sires)} \quad \ldots \quad (10)$$

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 (11), (12) and (13), respectively (Becker, 1984).

$$\sigma_e^2 = MS_e \quad \ldots \quad (11)$$

$$\sigma_d^2 = (MS_d - MS_e)/k_1 \quad \ldots \quad (12)$$

$$\sigma_s^2 = MS_s - (MS_e + k_2\sigma_d^2)/k_3 \quad \ldots \quad (13)$$

The three variance components were summed to obtain the total phenotypic variance (σ_p^2) for any trait as shown in expression (14).

$$\sigma_p^2 = \sigma_s^2 + \sigma_d^2 + \sigma_e^2 \quad \ldots \quad (14)$$

Heritability was estimated according to Becker (1984) as the ratio of additive genetic variance to total phenotypic variance from sire, dam and combined sire and dam variance components as expressed in (15), (16) and (17).

$$h_s^2 = 4\sigma_s^2/\sigma_p^2 \quad \ldots \quad (15)$$

$$h_d^2 = 4\sigma_d^2/\sigma_p^2 \quad \ldots \quad (16)$$

$$h_{s+d}^2 = 2(\sigma_s^2+\sigma_d^2)/\sigma_p^2 \quad \ldots \quad (17)$$

where h_s^2, h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components. The standard errors of heritability estimates were obtained according to Becker (1984). The variance was computed using expression (18).

$$s^2 = \frac{\Sigma x_i^2 - (\Sigma x_i)^2/n}{n-1} \quad \ldots \quad (18)$$

where $\underline{s^2}$ is variance, Σ, summation, x_i is any semen quality trait with i = 1, 2,…,n and n is number of observations for any genotype.

RESULTS

Heritability estimates for semen volume of main and reciprocal crossbred cocks

Heritability estimates for semen volume from the three variance components at 36 and 40 weeks (Tables 3 and 4) ranged from 0.40 to 1.01 and 0.03 to 0.29, 0.70 to1.33 and 0.54 to 1.48, 0.02 to 0.30 and 0.28 to 0.58, 0.13 to 0.36 and 0.46 to 0.66, 0.26 to 0.63 and 0.06 to 0.69, 0.70 to 1.04 and 0.06 to 0.88 for Isa Brown x frizzle feathered main cross (IBxF), Isa Brown x naked neck main cross (IBxNa), Isa Brown x normal feathered main cross (IBxN), frizzle feathered x Isa Brown reciprocal cross (FxIB), naked neck x Isa Brown reciprocal cross (NaxIB) and normal feathered x Isa Brown reciprocal cross (NxIB) genotypes, respectively. Generally, heritability estimates of main crosses decreased while those of the reciprocal crosses increased with age.

Table 3: Heritability estimates for semen volume of main and reciprocal crossbred cocks at 36 weeks of age

	Main Cross		
Estimate	**IBxF**	**IBxNa**	**IBxN**
h_s^2	0.40±0.21	1.33±1.00	0.02±0.00
h_d^2	1.01±.90	0.70±0.48	0.30±0.12
h_{s+d}^2	0.62±0.42	0.83±0.55	0.16±0.03
		Reciprocal Cross	
	FxIB	NaxIB	NxIB
h_s^2	0.36±0.15	-	0.70±0.48
h_d^2	0.13±0.40	0.63±0.30	1.04±0.88
h_{s+d}^2	0.23±0.10	0.26±0.10	0.72±0.50

Table 4: Heritability estimates for semen volume (ml) of main and reciprocal crossbred chickens at 40 weeks of age

	Main cross		
Estimate	**IBxF**	**IBxNa**	**IBxN**
h_s^2	0.29±0.10	1.48±1.13	0.28±0.11
h_d^2	0.03±0.00	0.54±0.30	0.58±0.30
h_{s+d}^2	0.16±0.5	0.85±0.57	0.40±0.22
		Reciprocal cross	
	FxIB	NaxIB	NxIB
h_s^2	0.66±0.32	0.69±0.31	0.06±0.00
h_d^2	0.46±0.20	0.45±0.22	0.88±0.66
h_{s+d}^2	0.50±0.25	0.06±0.00	0.46±0.22

h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components, respectively, - = Not inestimable

Heritability estimates for sperm motility of main and reciprocal crossbred cocks

Heritability estimates for sperm motility of the crossbred chickens are presented in Tables 5 and 6. The estimates in IBxF generally increased with age. They fell within moderate range (0.26-0.37) at 36 weeks but ranged from moderate (0.30) to high (0.99) level at 40 weeks from the three variance components. In IBxNa, the heritability estimates for sperm motility ranged from 0.66 to 0.52, 0.38 to 35 and 0.47 to 0.40 for the three variance components, respectively at 36 to 40 weeks. Low to moderate estimates for sperm motility were observed at both 36 and 40 weeks from the variance components in IBxN. The heritability estimates for sperm motility in FxIB were high from the three variance components at both ages except for that of sire which was moderate (0.37). In NaxIB, the estimates decreased from high to moderate level from the three variance components at both ages. It was not estimable from sire variance component at 36 weeks and dam variance component at 40 weeks. In NxIB, only sire plus dam variance components had estimates at both 36 and 40 weeks ages, and these were within moderate ranges.

Table 5: Heritability estimates for sperm motility (%) of main and reciprocal crossbred cocks at 36 weeks of age

Estimate	Main cross		
	IBxF	IBxNa	IBxN
h_s^2	0.37±0.19	0.66±0.39	0.15±0.03
h_d^2	0.26±0.09	0.38±0.13	-
h_{s+d}^2	0.29±0.12	0.47±0.22	0.05±0.00
		Reciprocal cross	
	FxIB	NaxIB	NxIB
h_s^2	0.37±0.14	0.48±0.21	-
h_d^2	0.83±0.38	0.44±0.19	0.50±35
h_{s+d}^2	0.53±0.23	0.41±0.18	0.22±0.12

h_s^2, h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components, respectively, - = Not inestimable

Table 6: Heritability estimates for sperm motility (%) of main and reciprocal crossbred cocks at 40 weeks of age

Estimate	Main cross		
	IBxF	**IBxNa**	**IBxN**
h_s^2	0.99±0.75	0.52±0.29	0.04±0.00
h_d^2	0.30±0.12	0.35±0.15	0.18±.08
h_{s+d}^2	0.59±0.37	0.40±0.18	0.11±0.00
		Reciprocal cross	
	FxIB	NaxIB	NxIB
h_s^2	1.10±0.89	0.24±0.10	0.44±0.21
h_d^2	1.21±0.97	0.37±0.14	-
h_{s+d}^2	0.90±0.80	0.28±13	0.20±0.12

h_s^2, h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components, respectively, - = Not inestimable

Heritability estimates for sperm concentration of main and reciprocal crossbred cocks

Heritability estimates for sperm concentration for the crossbred cocks are presented in Tables 7 and 8. Heritability estimates for sperm concentration were moderate from the three variance components (0.21 to 0.22) at 36 weeks, high from sire (0.76) and sire plus dam (0.41) and low from dam variance components (0.08) at 40 weeks in IBxF cocks. The heritability estimates for sperm concentration from sire, dam and sire plus dam variance components in IBxNa cocks were 0.26, 0.18 and 0.21 at 36 weeks and 0.96, 0.47 and 0.62 at 40 weeks, respectively. The estimates increased with age from the three variance components. Low heritability estimates for sperm concentration were observed from sire (0.17) and sire plus dam (0.19) variance components while moderate estimates were observed from dam variance component (0.23) at 36 weeks in IBxN cocks. At 40 weeks in the same genotype, the estimates were high (0.40) from sire and low (0.10) from sire plus dam variance components whereas from dam variance components heritability could not be estimated for sperm concentration. In FxIB, most of the estimates from the variance components ranged from low (0.01) to medium (0.24) at 36 and 40 weeks of age except for that of sire plus dam variance component which was high (0.71). Heritability estimates for sperm concentration in NaxIB from the three variance components were high at both ages, ranging from 0.60 to 0.50 at 36 and 0.80-0.47 at 40 weeks of age. In NxIB, estimates from the three variance components were high at both ages, except that of sire which was low at 36 weeks.

Table 7: Heritability estimates for sperm concentration (x10^9/ml) of main and reciprocal crossbred cocks at 36 weeks of age

Estimate	Main cross		
	IBxF	**IBxNa**	**IBxN**
h_s^2	0.22±0.10	0.26±0.10	0.17±0.04
h_d^2	0.21±0.06	0.18±0.05	0.23±0.09
h_{s+d}^2	0.21±0.06	0.21±0.08	0.19±0.05
		Reciprocal cross	
	FxIB	NaxIB	NxIB
h_s^2	-	0.60±0.31	0.09±0.00
h_d^2	0.01±0.00	0.54±0.28	1.48±1.05
h_{s+d}^2	0.71±0.36	0.50±0.24	0.76±0.45

h_s^2, h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components, respectively, - = Not inestimable

Table 8: Heritability estimates for sperm concentration (x10^9/ml) of main and

reciprocal crossbred cocks at 40 weeks of age

Estimate	Main cross		
	IBxF	**IBxNa**	**IBxN**
h_s^2	0.76±50	0.96±0.69	0.40±0.17
h_d^2	0.08±0.00	0.47±0.24	-
h_{s+d}^2	0.41±0.18	0.62±0.40	0.10±0.00
		Reciprocal cross	
	FxIB	NaxIB	NxIB
h_s^2	0.24±0.10	0.47±0.23	0.68±0.41
h_d^2	0.12±0.04	0.80±0.49	0.41±0.20
h_{s+d}^2	0.17±0.06	0.55±0.27	0.48±0.24

h_s^2, h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components, respectively, - = Not inestimable

Heritability estimates for live sperm of main and reciprocal crossbred cocks

Heritability estimates for live sperm of main and reciprocal crossbred cocks at 36 and 40 are presented in Tables 9 and 10, respectively. In IBxF, estimates from the three variance components ranged from 0.38 to 0.97 at 36 and 0.54 to 0.62 at 40 weeks of age. In IBxNa, high (0.60), moderate (0.34) and low (0.12) estimates were obtained from sire, dam and sire plus dam variance components, respectively at 36 weeks while high range of estimates (0.45 -0.62) were obtained from the three variance components at 40 weeks of age. Estimates in IBxN were all high from the three variance components at both ages except that the heritability from sire variance component at 36 weeks could not be estimated. The heritability estimates for live sperm decreased with age from the variance components in FxIB. These estimates ranged from 0.32 to 0.50 at 36 weeks and 0.04 to 0.12 at 40 weeks of age. In both NaxIB and NxIB, the estimates for live sperm fell within high range from the three variance components at both ages. However, in NaxIB, estimates were higher at 40 weeks, while in NxIB, they were higher at 36 weeks.

Table 9: Heritability estimates for live sperm (%) of main and reciprocal crossbred cocks at 36 weeks of age

Estimate	Main cross		
	IBxF	**IBxNa**	**IBxN**
h_s^2	0.97±0.71	0.60±0.31	-
h_d^2	0.38±0.14	0.12±0.01	0.82±0.60
h_{s+d}^2	0.60±0.40	0.34±0.13	0.40±0.17
		Reciprocal cross	
	FxIB	NaxIB	NxIB
h_s^2	0.32±0.15	0.88±0.53	0.65±0.34
h_d^2	0.50±0.27	0.80±0.48	0.57±0.30
h_{s+d}^2	0.37±0.16	0.69±0.36	0.53±0.25

h_s^2, h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components, respectively, - = Not inestimable

Table 10: Heritability estimates for live sperm (%) of main and reciprocal crossbred cocks at 40 weeks of age

Estimate	Main cross		
	IBxF	**IBxNa**	**IBxN**
h_s^2	0.62±0.36	0.62±0.40	0.63±0.35
h_d^2	0.62±0.36	0.45±0.20	0.89±0.50
h_{s+d}^2	0.54±0.30	0.47±0.26	0.64±0.32
		Reciprocal cross	
	FxIB	NaxIB	NxIB
h_s^2	0.04±0.00	0.87±0.51	0.46±0.20
h_d^2	0.12±0.03	0.49±0.31	0.53±0.24
h_{s+d}^2	0.08±0.00	0.59±0.38	0.44±0.20

h_s^2, h_d^2 and h_{s+d}^2 are heritability estimates from sire, dam and sire plus dam variance components, respectively, - = Not inestimable

DISCUSSION

The high heritability estimates observed for semen volume (Tables 3 and 4) were similar to the estimates reported by Hales *et al*. (1989) for same trait in turkeys but higher than the moderate estimates reported by Bongalhardo *et al*. (2000) for semen volume of White Leghorn roosters at 26 weeks of age. The differences in reported estimates are probably due to age, strain and breeding methods (Niknafs *et al*., 2012). Kabir (2006) also reported that differences in heritability estimates of semen quality traits could be attributed to method of estimation, breed, environmental effects and sampling error due to small data or sample size. The high heritability estimates for semen volume obtained in the present study indicated appreciable additive genetic variance relative to non-additive (dominance and epistasis) and environmental variances for the trait (Prado-Gonzalez *et al.* 2003; Kealey *et al*., 2006). This suggests that the cocks could be improved for semen quality traits, especially semen volume by individual selection (Hu *et al*., 2013). The low heritability estimates of semen volume from sire variance component compared to the other components in IBxF, IBxN and NxIB at 36 weeks and in IBxN at 40 weeks are consistent with the normal expectation. Heritability estimate from sire variance component is less biased and usually smaller in value than those from dam and combined sire and dam variance components using the same data (Ibe, 2019). This is because heritability from sire variance component contains different fractions of epistasis consisting of additive effects of gene only unlike the other two components which in addition to these contain dominance, epistasis, maternal and environmental deviations (Kearsey and Pooni, 1996; Ibe, 2019). The decrease in heritability estimates of semen volume observed in IBxF and NxIB cocks is in agreement with the report of Kabir *et al*. (2007). For these genotypes, their genetic potential for reproductive efficiency can be

realized at younger ages than 40 weeks. The increase in the heritability estimate for semen volume with age in FxIB and NaxIB indicated that the cocks can exhibit their highest genetic potential for semen volume at 40 weeks of age and should be used for breeding purposes without decline in performance at this age. Since the heritability estimates varied with genotypes and crosses, it reveals that different genotypes have different ages for maximum gene expression of reproductive traits.

The general increase in heritability estimates for sperm motility of IBxF with age from the three variance components (Tables 5 and 6) agrees with the report of Soller *et al.* (1965) in White Rock Roosters. This increase suggests that age is capable of influencing the amount of additive genes, and hence heritability of a trait. This is supported by the report of Yin *et al.* (2019) and Réale (1999). Selection at 40 weeks will result in maximum improvement in sperm motility. Individual selection can be employed between 36 and 40 weeks to improve the sperm motility of FxIB cocks since their heritability was high in both ages (Ellen *et al.*, 2007). The inestimable heritability of sperm motility at 36 and 40 weeks from sire and dam variance components, respectively theoretically means negative additive genetic variance (Ibe, 2019) which is attributed to small data size, nature of data and method of estimation (Kabir *et al.*, 2007). The moderate heritability estimates for sperm motility in NxIB cocks suggested that the trait can be improved by pedigree or family selection (Wolc *et al.*, 2019)

The increase with age in heritability estimates for sperm concentration in IBxF and IBxNa cocks (Tables 7 and 8) is similarly reported in chicken (Kabir *et al.*, 2007) and bull (Burren *et al.*, 2019; Gredler-Grandl *et al.*, 2007). This increase is an indication that greatest improvement for sperm concentration can be achieved by individual selection at 40 weeks. The heritability estimates for sperm concentration of IBxN and FxIB which ranged from low to moderate is consistent with the report of Hu *et al.* (2013). The result indicates that sperm concentration of IBxN and FxIB was mostly influenced by non-additive genetic and environmental variation. The sperm concentration of these genotypes may be improved by pedigree or family selection and by improving their environmental conditions (Zhao *et al.*, 2019). The high heritability estimates for sperm concentration observed in NaxIB and NxIB at both ages from almost all the three variance components implies that response to selection can be achieved between 36 and 40 weeks in these genotypes.

The results of Tables 8 and 9 indicated that there were large additive genetic variances existing for live sperm in IBxF, IBxNa, IBxN, NaxIB and NxIB cocks from different variance components and at both ages. However, small additive genetic variance was observed in FxIB. The results suggest that live sperm can be improved by individual selection in genotypes where large additive genetic variances existed. For the genotype with low heritability, information must be provided from its relatives

together with good environment to enable selection for improvement to be made (Hill, 2014).

CONCLUSION

The heritability estimates for the semen quality traits of the crossbred cocks varied with age, variance component, type of cross (main or reciprocal) and genotype of the cocks. The estimates generally increased with age. Most of the estimates fell within high range at 40 weeks from sire and sire plus dam variances components in reciprocal crosses. Live sperm was the most highly heritable while sperm motility was the least.

RECOMMENDATION

Reciprocal crossbreeding of Nigerian local cock with Isa Brown hens is recommended for increased additive genetic variance for improved semen quality traits.

CONFLICT OF INTEREST

The authors declare unequivocally that there is no conflict of interest in this research.

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