EVALUATION OF THE PROGENY TEST OF SOME PRODUCTIVE AND REPRODUCTIVE TRAITS OF THE BLACK AUSTRALORP CHICKEN STRAIN UNDER CONDITIONS OF SEMI-INTENSIVE HOUSING

Mahdi Saleh Mohammad[1], Omar Mardenli[2] and Ali Sami Amin Altawash[1]

[1]Department of Animal Production, Faculty of Agriculture, University of Al-Qadisiyah, Iraq
[2]Department of Animal Production, Faculty of Agriculture, University of Aleppo, Syria
Corresponding author: mahdisaleh99@yahoo.com, mahdi.mohammad@qu.edu.iq, 009647809393896

Abstract

The present study was carried out in order to investigate the genetic preference of some sires of black australorp chicken strain and to estimate their breeding values for some of reproductive and productive traits of their daughters by using contemporary comparison method under semi -intensive housing management. The data included records of 100 chicken daughter resulting from the mating of 5 sires (A, B, C, D and E) with 15 dams. breeding values were estimated for traits of fertility of set eggs, hatchability of fertile and set eggs, hatched chick, egg weight, chick weight and chick length. Results showed that daughters of sire C achieved the highest values of least means squares (P<0.05) in the all previous traits studied (92.83, 94.96, 88.15, 86.99%, 64.9 g, 46.80g and 179.90mm respectively). Also, sire C achieved the highest breeding values across its daughters' group in all the previous traits studied (5.09, 2.81, 6, 6.12%, 3.53, 1.38 g and 1.36 mm respectively). A remarkable increase was observed in the estimated heritability coefficient (h^2) values of the sires for traits of fertility of set eggs, hatchability of fertile and set eggs and hatched chick (0.57, 0.53, 0.48 and 0.45 respectively). Genetic correlation coefficients were characterized by high values among most of the traits studied and ranged between 0.49 and 0.99, while the values of phenotypic correlation coefficients among most of the traits decreased and ranged between 0.02 and 0.90. Within the conditions of semi-intensive housing of the black Australorp chicken strain and through the using of the contemporary companions evaluative method, it is concluded that there are differences in the breeding values of the various reproductive and productive traits of parent sires indicating an additive genetic effect that can be exploited in the processes of selection and different breeding purposes.
Keywords: Progeny testing, breeding value, Black Australorp chicken strain, productive traits, reproductive traits.

Introduction

Selection is considered the second way that comes after mating methods which enables a breeder to change the inheritance of his animal herd. There is no doubt that the selection contributed a lot to the creation of many specialized breeds of different animal species such as sheep, cattle and poultry (Hazel *et al.,* 1994). The study of the genetic features of the economic traits in poultry is of great importance in the plans of breeding and improvement, and as is known, the members of the same population or different populations vary in the rate of their productive performance of the characteristics due to their different genetic compositions as well as environmental conditions (Falconer, 1960). In the field of genetic improvement of domestic birds, the selection aims to increase the frequency of genes desired for economic traits, especially the traits that are affected by the accumulation action of genes, which in turn give breeders the possibility to change the genetic characteristics of animals (Bernon and Chambers, 1985). Under the conditions of housing systems (intensive or semi-intensive), the concept of genetic improvement of different reproductive or productive traits in a specific breed or strain has important positive points, where there is certainly need for stock with the capacity to perform well under the less than optimal environments typically encountered in another environments. The link between performance and nutritional and other management inputs means for different productive and reproductive traits that any genetic improvement in performance capability must be matched by increased inputs (Larzul *et al.,* 1997). Genetic improvement through various mattings (cross-breeding, back-crossing and inbreeding) certainly results in improved egg and/or meat production taking in account the management system, nutritional system

and other management inputs (Cahaner, 2008). The method of progeny test is perhaps an important way in selection, where an individual is selected based on his offspring' records. The breeding values in this way can be estimated by an equation of the Robertson and Henderson or contemporary comparison (CC) (Renand, 1985). Black Australorp (BA) is a dual – purpose breed. BA are good looking birds, easygoing, hardy and prolific layers, making them ideal for novice domestic keepers. They were imported to America in the 1920s and recognized as a standard breed by the American Poultry Association in 1929 (John, 2011). This strain has been introduced in many genetic improvement programs related to crossbreeding and mixed mating with local or commercial breeders with the aim of improving the productive and reproductive traits of the resulting hybrid generations, and with the aim of increasing adaptation in new climates. Therefore, the aim of this study was to estimate the genetic superiority of the sires cocks through their daughters by using contemporary companions method on certain reproductive and productive traits such as fertility of set egg, hatching rate of fertile eggs, hatching rate of set eggs, hatched chicks ,egg weight and weight of day-old chick and its length**.**

Material and Methods

Breeding plan and management

This study was conducted on the strain of Black Australorp chicken. The chicken daughters were chosen as a result of the mating of five males' sires with 15 chickens dam (parent stock). The daughters were divided into three main herds depending on their mothers (dams) as shown in the following table (Table 1):

Table 1 : The distribution of daughters in each herd attributed to their sires and dams

Sire	Dam	Herd	Daughters (n)	Total of daughters/ herd
A	1	1	8	20
A	2	2	5	20
A	3	3	7	20
B	4	1	6	20
B	5	2	9	20
B	6	3	5	20
C	7	1	8	20
C	8	2	7	20
C	9	3	5	20
D	10	1	7	20
D	11	2	7	20
D	12	3	6	20
E	13	1	8	20
E	14	2	5	20
E	15	3	7	20

After installing the metal numbers in their legs, the daughters were distributed to three sections 2×20 m dimensions, these sections were equipped with egg nests, each nest of eggs equipped with two egg traps in order to attributing the eggs. AS for mating, three males were subjected to inseminate the daughters, which were periodically released into the rooms, overlapping at a rate every five days. The total eggs of the daughters were kept at 12°C until the required number of eggs per daughter was completed (30 eggs). Egg weighting process was performed with a sensitive scale of 0.1 g accuracy. In order to identify the fertilized eggs, the Brinsea OvaScope device was used on the seventh day of incubation. After hatching, the day-old chick weights (DOHC) were measured by a sensitive scale of 0.1 g. Day- old chick length (DOCL) was taken by measuring the length of stretched chick from the tip of the beak to tip of the middle toe using a ruler and recorded in millimeters (mm) (Willemsen *et al.,* 2008).

a productive ration was provided for the daughters shown in the following table (Table 2):

Table 2 : Chemical analysis and composition of chicken feed used in the experiment

Feed components	%
Yellow corn	62
Soybeans	23
Barley	7
Limestone	7
Vitamin premix*	0.5
Mineral premix**	0.5
Chemical analysis	
Crude protein (%)	16
Energy (kcal/kg)	2708
Phosphorus (%)	1.44
Calcium (%)	3.36

* Each kg of vitamin premix contains6 000 000 IU vit A, 600 000 IU vit D3 20 000 IU vit E, 2 g vit K, 1.2 g vit B1, 2.4 g vit B2, 2 g vit B6, 12 mg vit B12, 10 g niasin, 300 mg folic acid, 4 g calcium pantothenate 50 mg D-Biotin.125 mg; Mn, 80; Fe, 40 mg; Zn, 60 mg; Cu, 5 mg; Co, 0.1 mg; I, 0.4 mg; Se, 0.15 mg.

** Each kg of mineral premix contains 80 g Mn, 30 g Fe, 60 g Zn, 5 g Cu, 0.5 g Co, 2 g I, 235.68 g Ca.

Data and statistical analysis

After collecting the data and arranging by a sophisticated computer, the data were subjected to statistical analysis. Least mean squares of studied traits, variance components, heritability, genetic and phenotypic correlations were calculated according to the statistical method of two-way of balanced design according to the minimum variance quadratic unbiased estimators' method (MIVQUE) based on the following model:

$$Y_{ijk} = \mu + \alpha + \beta_{ij} + e_{ijk}$$

Where:

Y_{ijk}: progeny record k resulting from j dam which was mated with i sire.

μ: overall mean.

α: random effect of i sire.

β_{ij}: random effect of j dam which was inseminated by the i sire.

e_{ijk}: the random genetic and phenotypic deviations that resulting from an individual difference within sires (vector of random error) which is presumably =0.

The heritability coefficient was calculated according to the following equation:

$$h^2 = \frac{4\sigma_S^2}{\sigma_S^2 + \sigma_e^2}$$

Where:

σ_S^2 : genetic variation of the sires.

$\sigma_S^2 + \sigma_e^2$: phenotypic variation of the sires.

The genetic correlation coefficient was calculated according to the following equation:

$$r_G = \frac{Covxy_G}{\sqrt{\sigma^2 Sx_G . \sigma^2 Sy_G}}$$

Where:

$Covxy_G$ = the genetic covariance of traits X and Y between sires.

$\sigma^2 Sx_G$ = the genetic variance of trait X between sires.

$\sigma^2 Sy_G$ = the genetic variance of trait Y between sires.

The phenotypic correlation coefficient was calculated according to the following equation:

$$r_P = \frac{Covxy_P}{\sqrt{\sigma^2 Sxp . \sigma^2 Sy_P}}$$

Where:

$Covxy_P$ = the phenotypic covariance of traits X and Y between sires.

$\sigma^2 Sx_P$ = the phenotypic variance of trait X between sires.

$\sigma^2 Sy_P$ = the phenotypic variance of trait Y between sires.

The breeding value of sires (EBV)was assessed in CC method according to the following general equation:

$$_{cc}EBV = 2\ STA = 2\ (SGD)\ (b)$$

Where:

STA: sire transmitting ability.

SGD: sire genetic deviation.

$$SGD = \frac{\sum (D)(n)}{\sum W} = \frac{\sum (D)\left(\overline{X_C} - \overline{X_h}\right)}{\sum W}$$

$\overline{X_C}$: mean of the trait of daughters of studied sire.

$\overline{X_h}$: mean of the trait of daughters of rest sires.

W : coefficient of weight.

$$W = \frac{n_1 n_2}{n_1 + n_2}$$

n_1 : total number of studied sire's daughters.

n_2 : total number of daughters that belonging to the rest sires.

b: a slope relating to sire and the mean of number (n) of its offspring.

$$b = \frac{\left(h^2\right)\left(\sum W\right)}{4 + \left(\sum W - 1\right)h^2}$$

The data were analyzed using the general linear model (PROC GLM, SAS Institute Inc., 2004). The differences among specific groups were determined by using Duncan's new multiple range test (Duncan 1955).

Results

The contents of Table 3 indicate a significant difference(p<0.05) among the rates of fertility of set eggs trait (FSE) across different groups of daughters, where the daughters of the sire C archived the highest value compared to their counterparts in other groups and reached the value 92.83%, while the lowest value was achieved by the daughters of the sires B and E (88 and 88% respectively). The rates of hatchability of fertile eggs (HFE) and hatchability of set eggs (HSE) traits has also increased to 94.96 and 88.15% respectively at the daughters of sire C(P<0.05). As for hatched chick trait (HC), rates of each other were somewhat closer across the different groups of daughters and the difference did not exceed 9.33%, nevertheless, the differences were significant (p<0.05), where the daughters of the sire C achieved the highest values (86.99%).

Table 3 : least mean squares of some reproductive traits across groups of daughters in Black Australorp chicken strain

Sire (Family)	[1]FSE (%) Mean ± se	[2]HFE (%) Mean ± se	[3]HSE (%) Mean ± se	[4]HC (%) Mean ± se
A	89.00 ± 1.01 [CB]	93.73 ± 0.56 [AB]	83.38 ±1.04 [C]	80.66 ±1.17 [B]
B	88.00±1.01 [C]	91.17 ± 0.56 [C]	80.22 ±1.04 [C]	77.66 ±1.17 [B]
C	92.83 ±1.01 [A]	94.96 ± 0.56 [A]	88.15 ±1.04 [A]	86.99 ±1.17 [A]
D	91.84 ±1.01 [AB]	94.74 ± 0.56 [A]	87.01 ±1.04 [A]	85.00±1.17 [A]
E	88.00±1.01 [C]	92.53 ±0.56 [CB]	81.40C ±1.04 [B]	80.16 ±1.7 [B]

Each subscript letter denotes a subset of variable whose column proportions do not differ significantly from each other at P<0.05
[1]FSE: fertility of set eggs, [2]HFE: hatchability of fertile eggs,[3] HSE: hatchability of set eggs, [4]HC: hatched chick.

Table 4 shows that the value of eggs weight(EW) trait reached to 64.90 g at daughters of sire C while the daughters of sire A achieved the lowest value (60.80 g), despite the slight difference between these two groups (4.1 g), these differences were significant among all groups of daughters(p<0.05). Also, significantly, the chicks derived from the daughters of sire C achieved the highest weight rates (46.80g) compared to other chicks in other groups(p<0.05). In a simulated way, the rates of the day-old length of the chicks (DOCL) obtained from the daughters of the third group (C) increased compared to other groups (p<0.05), followed by the group D (179.90 and 179.20 mm respectively).

Table 4 : Least mean squares of some productive traits across groups of daughters in Black Australorp chicken strain

Sire (Family)	[1]EW (g) Mean ± se	[2]DOCW (g) Mean ± se	[3]DOCL (mm) Mean ± se
A	60.80[B] ±0.98	42.20[B] ±0.50	175.80[B] ±1.09
B	62.25[AB] ±0.98	45.80[AB] ±0.50	176.85[AB] ±1.09
C	64.90[A] ±0.98	46.80[A] ±0.50	179.90[A] ±1.09
D	62.10[AB] ±0.98	46.45[AB] ±0.50	179.20[AB] ±1.09
E	61.20[B] ±0.98	44.70[B] ±0.50	176.65[B] ±1.09

Each subscript letter denotes a subset of variable whose column proportions do not differ significantly from each other at P<0.05
[1]EW: egg weight, [2]DOCW: day-old chick weight,[3] DOCL: day-old chick length.

Remarkably, the values of heritability coefficients (h^2) belonging to sires increased in the traits of FSE, HFE, HSE and HC, the values were 0.57, 0.53, 0.48 and 0.45 respectively (Table 5), the values were moderate in other rest traits. Generally, the heritability coefficients belonging to sires + dams seemed more moderate where the values ranged between 0.075 and 0.44.

Table 5 : Heritability coefficient values (h^2) of different productive and reproductive traits of daughters

Traits *	$h^2 \pm se$		
	Sire	Dam	Sire + Dam
FSE	0.57±0.022	0.30±0.025	0.43±0.026
HFE	0.53±0.024	0.36±0.031	0.44±0.024
HSE	0.48±0.032	0.08±0.011	0.28±0.027
HC	0.45±0.021	0.24±0.012	0.34±0.027
EW	0.29±0.033	0.21±0.010	0.25±0.02
DOCW	0.27±0.035	0.20±0.023	0.23±0.042
DOCL	0.21±0.01	0.18±0.032	0.19±0.015

*: FSE: fertility of set eggs, HFE: hatchability of fertile eggs, HSE: hatchability of set eggs, HC: hatched chick,
EW: egg weight, [2]DOCW: day-old chick weight,[3] DOCL: day-old chick length.

The contents of Table 6. indicate that most of the estimated genetic correlation coefficient values among the different traits studied were positive, very strong and ranged between 0.75 and 0.99, except the correlation between pairs of HC/HSE, EW/HFE and DOCW/HFE traits (0.49, 0.50 and 0.50 respectively). On the contrary, the estimated phenotypic correlation values were positive and weak, with values ranging between 0.02 and 0.40 except for the correlation between the traits FSE and HSE (0.90), FSE and HC (0.83), the correlation between HFE and HSE and between HFE and HC traits was moderate (0.58 and 0.53 respectively).

Table 6 : Values of genetic correlation coefficients (above the diagonal) and phenotypic correlation coefficients (below the diagonal) for various studied traits across the groups of sire's daughters.

Trait*	FSE	HFE	HSE	HC	EW	DOCW	DOCL
FSE		0.97	0.98	0.97	0.92	0.99	0.99
HFE	0.17		0.96	0.98	0.50	0.50	0.75
HSE	0.90	0.58		0.49	0.75	0.96	0.99
HC	0.83	0.53	0.11		0.75	0.96	0.99
EW	0.04	0.09	0.08	0.11		0.96	0.99
DOCW	0.07	0.11	0.13	0.06	0.22		0.88
DOCL	0.02	0.16	0.11	0.11	0.12	0.40	

*: FSE: fertility of set eggs, HFE: hatchability of fertile eggs, HSE: hatchability of set eggs, HC: hatched chick,
EW: egg weight,[2]DOCW: day-old chick weight,[3] DOCL: day-old chick length.

As for breeding values of studied sires, Table 7 shows that SGD values ranged between -5.42 and 6.07 with a clear superiority of the daughters of the sires C and D in most of the studied traits, especially the FSE trait (6.07 and 3.68 respectively). Continuation of the above-mentioned results, the daughters of the sires C achieved the highest values of STA in most traits especially the HC trait (4.06). The values ranged between -3.61 and 4.06. The daughters of sir C showed a clear superiority in breeding values for the entire traits studied FSE, HFE, HSE, HC, EW, DOCW and DOCL, the values were 5.09, 2.81, 6.00, 6.12%,3.53, 1.38 g and 1.36 mm g respectively. followed by the order the daughters of sire D, the values were 3.42, 2.35, 5.13, 4.93%, -0.23, 0.87 g and 1.12 mm for the same traits respectively, While the daughters of sires A, B and E settled down the rankings and achieved negative values.

Table 7 : Values of SGD, STA and ccEBV for tested sires in the experiment

	SGD					STA					ccEBV				
	Sire A	Sire B	Sire C	Sire D	Sire E	Sire A	Sire B	Sire C	Sire D	Sire E	Sire A	Sire B	Sire C	Sire D	Sire E
FSE	**-1.10**	-2.48	3.50	2.39	-2.36	-0.8	-1.75	2.55	1.71	-1.72	-1.60	-3.51	5.09	3.42	-3.43
HFE	**0.28**	-2.75	1.98	1.65	-1.21	0.195	-1.94	1.41	1.18	-0.86	0.39	-3.89	2.81	2.35	-1.71
HSE	-0.83	-4.77	5.11	3.74	-3.33	-0.57	-3.25	3.50	2.57	-2.28	-2.14	-6.51	6.00	5.13	-4.56
HC	-1.90	-5.42	6.07	3.68	-2.53	-1.27	-3.61	4.06	2.47	-1.69	-2.54	-5.22	6.12	4.93	-3.38
EW	-1.73	-0.14	3.29	-0.21	-1.22	-0.95	-0.08	1.77	-0.12	-0.68	-1.91	-0.16	3.53	-0.23	-1.36
DOCW	-0.73	-0.03	1.29	0.81	-1.36	-0.39	-0.01	0.69	0.44	-0.73	-0.78	-0.03	1.38	0.87	-1.45
DOCL	-2.48	-0.89	2.81	1.93	-1.41	-0.71	-0.25	0.68	0.56	-0.41	-1.43	-0.51	1.36	1.12	-0.81

*: *FSE: fertility of set eggs, HFE: hatchability of fertile eggs, HSE: hatchability of set eggs, HC: hatched chick, EW: egg weight, DOCW: day-old chick weight, DOCL: day-old chick length.*

Discussion

Each mathematical method used to estimate the breeding values of different traits has a set of positive points and negative ones. The estimation of breeding values in CC of herd mates takes into account only one trait and also uses the value of the heritability of the trait studied, but it does not take into account the economic importance of the trait studied against other traits and does not allow the excellent trait to compensate for the less errant qualities trait in the animal. In our study within the semi-intensive management, the breeding values have been perfectly matched with the results of least means squares values of traits studied across groups of daughters. Where it was noted that the daughters of sire C excelled(p<0.05) in all the traits studied compared to other contemporary groups as well as in STA and SGD and $_{CC}$EBV (Tables 3,4 and 7). Theoretically, these results can be explained to the concept of inbreeding within a single breeder or strain. Milgior *et al.* (1995) noted that the harmful effects of inbreeding include increase in homozygosity, decrease in performance of traits and the high risk of mortal alleles. On the other hand, mating of relatives has been used widely over the last centuries to produce breeds, varieties and lines Wilson (1948) noted that reproductive performance is the product of egg, fertility, hatchability and viability of offspring. Knowledge of the effect of inbreeding on each of these traits should be taken into account for the poultry breeder to make decisions regarding the number and size of lines to develop and maintain as well as the ultimate level of inbreeding to be attained. The fluctuation of STA and SGD and $_{CC}$EBV values in our current results can be attributed to environmental factors such as season, age, conditions of management, nutrition and diseases. Also, this fluctuation can be due to the effects of genetic factors which ultimately lead to the control of additive genetic variation which is also defined by the genetic susceptibility of the offspring (Mielenz *et al.*, 1994). The degree of genetic improvement plays an important role in highlighting the breeding values of individuals, whether within the breed or the strain or within the different mating breeds (Johnson and Barton, 2005). Where it is noted that sire C was distinguished from the genetic point of view in most of the traits studied where it showed reasonable and encouraging values, sire D comes the second in ranking while the rest of the sires showed negative values in the genetic possession towards the general level of different traits, whereof, in this scope, the importance of the sire index for parents is highlighted. because sire index is one of the most important producer decisions which in turn requires advance preparation and effort to be successful even

selection of superior parent stock from a different breed that excels in a trait is often more effective than selection within a breed (Gregory *et al.,* 1999; Franke *et al.,* 2001). Table .5 shows that the estimates of the heritability values belonging to sires of FSE, HFE, HSE and HC traits were high and perhaps exceeded the optimal limits of those traits (0.57,0.53, 0.48 and 0.45 respectively), while in other traits, the values were moderate. The high values indicate that environmental factors have a small role in these values and the degree of genetic improvement that this strain has reached may be very large. On the other hand, the small size of the data used in this study may be a clear role in influencing these values. h^2 coefficient of HC trait in our study was higher than the value attained by Morris, (1985). As for EW trait the value of heritability value in our study was less than the value attained by Sylvia Alwel *et al.* (2018). As for DOCW trait, Ogbu *et al.* (2015) attained value for heritability that is similar to the value in our study. While heritability value of DOCL trait was 0.12 in a study conducted by Adeleke *et al.* (2011).

The current study pointed out a rise in of both genetic and some of phenotypic correlations values with a diversity in the degree of correlation from moderate to strong on the one hand and on the other hand characterized by positive values (Table 6). This explains the intensity of the traits to share each other in highlighting the contribution of the genes responsible for the capacity and size of the trait (Lynch and Walsh 1998). Therefore, genetic improvement in any of the previous traits studied in our current study will be accompanied by a genetic improvement of the trait associated with it. Also, the environmental effects often act in the same direction and through the same pathways as genetic effects, which ultimately leads to a similarity in effects between phenotypic and genetic correlations (Cheverud, 1984). The values of FSE trait in our study ranged between 88 and 92.83%, these rates are lower than the 97% that Tsarinko, (1988) have obtained while Bondareev. (2005) attained values ranged between 93 and 95%. As for HSE trait, the values attained by Bessarabov *et al.* (2005) and Zeper, (2005) were 95 and 82% respectively. The DOCL values for layer and broiler in a study conducted by Petek *et al.,* (2008) reached 180.53 and 180.72 mm comparing to our results which ranged between 175.80 and 179.90 mm. Also, the results of Petek *et al.* (2008) indicated that there are high weight differences in DOCW trait between layer and broiler (34.20 and 50.71g respectively). Unfortunately, there are no extensive studies about the Australorp strain in relation to different productive and reproductive traits in order to compare our current results with them, where the main

objective of this strain in previous studies was to hybridize it with local breeds in order to improve the production performance of those breeds. However, the values achieved by daughters in this study for the previous studied traits (Tables 3 and 4) within the semi-intensive conditions of keeping were generally in line with different breeds. in general, the kind of housing condition may be one of the reasons for reaching our current results, especially since BA is a dual purpose strain, Puron *et al.* (1995) referred that that the conditions of housing greatly affect the productive performance of different breeds, where these conditions are characterized by many pros and cons, this related to the type of breeding, the purpose of production and the breed used. Since strains are feed and kept in semi intensive systems from birth to weaning, it can be said that the increase of h^2 and breeding values for different traits may be due to maternal effect was not large influence for some traits rather than others. An alternative explanation for the high heritabilities coefficients and breeding values of these traits might be due to luck of a proper mating program. According to these results, it can be expressed that sire selection should be preferred to increase the production and reproduction performance in the herds.

It concluded from the current study that most of the estimates of breeding values attained by contemporary comparison method and the values of heritability coefficients obtained have fallen within the high and encouraging estimates, and it is also concluded that there is a wide range of genetic variations in previous values that can be used in genetic selection programs.

References

Adeleke, M.A.; Peters, S.O.; Ozoje, M.O.; Ikeobi, C.O.N.; Bamgbose, A.M. and Adebambo, O.A. (2011). Genetic parameter estimates for body weight and linear body measurements in pure and crossbred progenies of Nigerian indigenous chickens. Livestock Research for Rural Development, 23(19): 1-4.

Bernon, D. and Chambers, J.R. (1985). Maternal and sex-linken genetic effect in broiler parent stocks. Poultry Sci., 64:29-39.

Bessarabov, E.E.; Pondareev, Y.Y. and Stoliar, T.A. (2005). Madkour, Y.H.; Mahmoud, T.H. and Mohanna, N.Z. (1982). Poultry Growing and technology of meat and egg A comparative study on egg cycle in relation to egg productin, Lan, Sanckt, Peresporg, Moscow, Krasnadar, 48: 59: 68: 69: 78: 79: 80: 87: 90

Bondareev, Y.Y. (2005). The open growing of poultry. ST. genetics and breeding/W.G. Hill, J.M. Manson, D. Astral Proof Izadat, Moscow, 14: 15.

Cahaner, A. (2008). Breeding broilers for hot conditions. Nigerian Poultry Science Journal, 5(4): 156–163.

Cheverud, J.M. (1984). Quantitative genetics and developmental constraints on evolution by selection. J. Theor. Biol., 110: 155–171.

Duncan, D.B. (1955). Multiple range and mulitple Test. Biometrics, 11: 1–42 .

Falconer, D.S. (1960). Introduction to quantitative genetics. Roland press, New York.

Franke, D.E.; Habet, O.; Tawah, L.C.; Williams, A.R. and DeRouen, S.M. (2001). Direct and Maternal Genetic Effects on Birth and Weaning Traits in Multibreed Cattle Data and Predicted Performance of Breed Crosses. J. Anim. Sci., 79: 1713-1722.

Gregory, K.E.; Cundiff, L.V. and Van Vleck, L.D. (1999). Composite Breeds to Use Heterosis and Breed Differences to Improve Efficiency of Beef Production. Technical Bulletin Number 1875. ARS-USDA. Washington, DC.

Hazel, L.N.; Dickerson, G.E. and Freeman, A.E. (1994). The selection index–then, now, and for the future. J Dairy Sci., 77: 3236– 3251.

John, L.S. (2011). Chicken Breeds and Varieties (A2880), University of Wisconsin.

Johnson, T. and Barton, N.H. (2005). Theoretical models of selection and mutation on quantitative traits. Phil. Trans. R. Soc. B, 60: 1411–1425.

Larzul, C.; Manfkedi, E. and Elsen, J.M. (1997). Potential gain from including major gene information in breeding value estimation. Genetics Selection Evolution, 29: 161–184.

Lynch, M. and Walsh, B. (1998). Genetics and Analysis of Quantitative Traits. Sinauer Associates, Sunderland, MA. Madison.

Mielenz, N.; Groeneveld, E.; Muller, J. and Spilke, J. (1994). Simultaneous Estimation of Variance And Covariances Using Reml And Henderson In Selected Population of White Leghorns. Br. Poultry Sci., 35(5): 669-676.

Miglior, F.; Burnside, E.B.; Dekkers, J.C.M. (1995). Inbreeding of Canadian Holstein cattle. Journal of Dairy Science, 78: 1168-1167.

Morris, J.A. (1985). Heritability of Chick Viability for Two Breeds of the Domestic Fowl. Poultry Sci., 27: 375-388.

Ogbu, C.C.; Nwachukwu, E.N. and Nwosu, C.C. (2015). Variance Components and Heritability of Some Growth Parameters In Purebred Nigerian Indigenous Chickens. ARPN Journal of Agricultural and Biological Science, 10(5): 192-199

Petek, M.; Orman, A.; Dđkmen, S. and Alpay, F. (2008). Relations Between Day-old Chick Length and Body Weight in Broiler, Quail and Layer. Uludag Univ. J. Fac. Vet. Med., 1-2: 25-28.

Puron, D.; Santamaria, R.; Segura, J.C. and Alamilla, J.L. (1995). Broiler performance at different stocking densities. The Journal of Applied Poultry Research, 4(1): 55-60.

Renand, G. (1985). Genetic parameters of French beef breeds used in crossbreeding for young bull production. II - Slaughter performance, Genet. Sel. Evol., 17: 265-282.

SAS Institute Inc. (2004). SAS/STAT User's Guide. Version 9.1. SAS Inst. Inc., Cary, NC.

Sylvia Alwel, J.J.; Abdur-Rahman, A.; Chukwujindu, N.S. (2018). Heritability estimates of egg weight and egg shell weight in Ikenne, Nigeria. International Journal of Scientific World, 6(1): 38-42.

Tsarinko, P.P. (1988). Improvement of polutry productsquality, Agroprom Izdat. Liningrad, 76: 85-86.

Willemsen, H.; Everaert, N.; Witters, A.; De Smit, L.; Debonne, M.; Verschuere, F.; Garain, P.; Berckmans, D.; Decuypere, E. and Bruggeman, V. (2008). Critical assessment of chick quality measurements as an indicator of post-hatch performance. Poultry Sci., 87: 2358-2366.

Wilson, W.O. (1948). Egg production rate and fertility in inbred chickens. Poultry Sci., 27: 719-726.

Zeper, A.F. (2005). Taking care of parents flock and egg incubation in growing meat producing chicks. A. S.S. 851. Stalker, Moscow, 5: 11-14.