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EFFECT OF POSITIVE ASSORTATIVE MATING ON BETWEEN AND WITHIN LINE VARIATION IN PERFORMANCE TRAITS OF THE NIGERIAN INDIGENOUS CHICKEN (NIC)

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ABSTRACT
Purebred progenies (G_2 generation) derived by positive assortative mating (Like x like) involving 10 parental lines (G_1 generation) of NIC were evaluated for growth performance, feed intake (FI) and feed conversion ratio (FCR) from 4-20 weeks of age and compared to their parental (G_1) generation to ascertain the effect of positive assortative mating on the traits and trait variation within and between body weight (BW) lines. The 10 parental lines were derived from 5 sire families (2 lines per sire family) by separating chicks belonging to each sire family into BW lines (high and low lines) based on mean BW values at 4 weeks. Within each sire family, chicks 20g above the mean were grouped as high line (L_1) while those 20g below were grouped as low lines (L_2). Chicks that did not fall into these BW categories were excluded from the study. Results indicate significant differences ($P \leq 0.05$) between progeny and parental BW lines in BW values. Body weight gain (BWG), feed intake (FI) and feed conversion ratio (FCR) did not differ as much as BW across generations. Lines (high and low lines) belonging to the progeny generation showed greater divergence compared to the parental lines but were less varied within. Generally, progeny high lines (G_2L_1) significantly ($P \leq 0.05$) exceeded the parental high lines (G_1L_1) in BW and FI across the age periods but were mostly similar in BWG and FCR. The parental low lines G_1L_2) were on the other hand superior ($P \leq 0.05$) to their progeny (G_2L_2) in all the traits at most of the age periods. Positive assortative mating improved the body weight value of the high lines, reduced those of the low lines, increased between line variation and reduced within line variation in progeny generation.

KEY WORDS: Purebred Progenies, Parental Lines, Generation, Like to like mating.

INTRODUCTION

Genetic improvement in animal populations is often achieved using two basic tools: selection and selective breeding. Selection deals with the decision as to which animals in a population are allowed to reproduce (contribute progenies to the next generation). Selective breeding deals with the choice of mates. That is, which of the selected males are bred to which of the selected females (Hammack, 2003). Mating animals based on observable or measurable characteristics (phenotypic assortative mating) is often employed to varying ends in animal breeding programmes. Positive assortative mating (like x like) is usually the mating scheme in directional selection (Hammack, 2003; Strandberg and Malmfors, 2006) and leads to greater progeny variation (within the first few generations), fewer intermediates and more extreme phenotypes (genotypes) (Hammack, 2003). Lines hence diverge and differences between lines increase (Tercic *et al.,* 2006).

The growth performance of the Nigerian indigenous chicken can be improved genetically by utilizing the variation existing among individuals of NIC populations (Sonaiya, *et al*., 1998; Ajayi and Agaviezo, 2009; Ajayi, 2010) to select the best to become the parents of future generations.

In the present study, progenies of random breeding NIC populations (5 sire families) were segregated into body weight (BW) lines (high and low lines) using mean BW at 4 weeks of age as the base value. Fourth (4^{th}) week BW was chosen because the period is within the auto accelerating phase of growth for the local chicken (Nwosu, 1990). Individuals of each BW line were then evaluated for performance traits (BW, BWG, FI and FCR) from 4 to 20 weeks of age after which they were mated assortatively to produce progenies from each BW line. The progeny lines were then evaluated for the same performance traits and compared with parental lines to ascertain the effects of within line positive assortative mating on the traits evaluated.

The study aimed to show that using appropriate mating plan (in this case positive assortative mating), the local chicken could be improved in the major growth traits (BW and BWG) and feed conversion ratio.

MATERIALS AND METHODS

Two hundred and fifty (250) day – old chicks (G_1 generation) – purebred progenies of five (5) sire families established from a base population of random breeding NIC (G_0 generation) were the experimental materials. The birds were brooded according to sire groups from hatch to 4 weeks of age. They were then weighed to obtain the mean BW at 4 weeks for each sire group. These values were used as base values for separation into BW lines. Within each sire group, chicks 20g above the 4^{th} week mean BW value were grouped together as high body weight line or high line (L_1) while those 20g below the base mean were grouped together as low body weight line or low line (L_2). Males and females were reared together because of lack of a genetic marker to accurately sex the chicks at this age.

Birds belonging to each body weight line were reared separately and evaluated for growth performance (BW and BWG), feed intake (FI) and feed conversion ratio (FCR) from 4 weeks to 20 weeks of age. At onset of egg production (≡ 24 weeks), two (2) roosters were selected based on mature (20 week) body weight from each BW line and mated to hens of the same line in a mating ratio of 1 cock to ≤ 10 hens. Fertile eggs were collected and hatched to obtain the progenies of each BW line (G_2 generation). The G_2 birds were equally evaluated for growth performance, FI and FCR. All birds were fed on the same standard ration of chicks mash (18% CP, 2800KcalME/kg) from hatch to 8 weeks, growers mash (15%CP, 2670KcalME/kg) from 9 weeks to 20 weeks and layers mash (16.5%CP, 2650KcaME/kg) from onset of egg production (Table 1). All birds shared the same environment and received similar management attention.

TABLE 1: Experimental Ration

(a) Chick Mash		Growers Mash		(c) Layers Mash)	
Feed ingredients (DM Basis)	Composition (%)	Ingredients (DM Basis)	Composition (%)	Ingredients	Composition (%)
Maize	53.0	Maize	43.5	Maize	43.0
Wheat offal	13.0	Wheat offal	30.0	Wheat offal	18.0
Soya bean cake	18.0	Soya bean cake	10.0	Soya bean cake	17.5
Palm kernel cake	9.0	Palm kernel cake	10.0	Palm kernel cake	9.0
Fish meal	3.0	Fish meal	2.5	Fish meal	2.5
Bone meal	3.0	Lysine	0.25	Bone meal	3.0
Lysine	0.25	Methionine	0.25	Lysine	0.25
Methionine	0.25	Vitamin premix	0.25	Methionine	0.25
Vitamin premix	0.25	Salt	0.25	Vitamin premix	0.25
Salt	0.25	Bone meal	3.0	Salt	0.25
Total	100	Total	100	Oyster shell	6.0
				Total	100
Calculated:		**Calculated:**		**Calculated:**	
Crude protein (%)	18%	Crude protein (%)	15%	Crude protein (%)	16.5%
Energy (Kcal ME/kg)	2,800	Energy (Kcal ME/kg)	2,670	Energy (Kcal ME/kg)	2,600

Legend: ME = Metabolizable energy; Kcal = Kilo calories

Data Analysis

Data on body weight (BW), feed intake (FI), body weight gain (BWG) and feed conversion ratio (FCR) for BW lines in the two generations were subjected to independent T-test analysis for equality of line means between generations using the SPSS statistical package (SPSS 2001).

RESULT AND DISCUSSION

Performance Traits

Table 2 presents the mean ± S.E for body weight, feed intake, body weight gain and feed conversion ratio for BW lines (L_1 and L_2) for parent (G_1) and progeny (G_2) generations at different age periods.

TABLE 2. Within line between generation comparative mean ± S.E for performance traits at various age periods (4-20 weeks)

		4		8		12		16		20	
Trait	Gen	L_1	L_2	L_1	L_2	L_1	L_2	L_1	L_2	L_1	L_2
	G_1	178.53±0.95	154.36±1.50	360.67±3.46a	313.89±3.31a	677.01±5.19a	615.92±6.76a	816.96±5.62	743.98±6.81a	958.05±7.75a	869.33±6.77a
BW	G_2	185.02±1.72	154.64±1.59	375.34±3.10b	278.36±3.71b	698.87±5.07b	533.97±5.26b	824.42±6.87	632.33±7.33b	1003.87±6.98b	779.53±8.63b
	G_1	20.78±0.31	19.11±0.27	39.43±0.54a	36.05±0.36a	65.33±0.51a	61.41±0.75a	77.69±0.56a	74.24±0.55	88.50±0.67a	86.89±0.67
FI	G_2	20.42±0.17	18.59±0.22	40.62±0.17b	38.49±0.22b	73.73±0.37b	64.52±0.58b	83.87±0.37b	75.26±0.34	93.47±0.41b	87.26±0.48
	G_1	5.42±0.04	4.53±0.07	6.72±0.13	6.05±0.13	11.55±0.20	10.72±0.26a	5.15±0.10a	4.48±0.10a	5.30±0.15a	4.60±0.18a
BWG	G_2	5.47±0.07	4.70±0.06	7.04±0.11	4.83±0.11	11.40±0.19	8.86±0.19b	4.30±0.19b	3.77±0.14b	6.74±0.20b	5.56±0.19b
FGR	G_1	3.85±0.06	4.31±0.11	6.03±0.16	6.13±0.13a	5.78±0.12a	5.98±0.17a	15.42±0.29a	17.21±0.45a	17.59±0.50a	21.69±1.20a
	G_2	3.77±0.06	4.02±0.08	5.89±0.12	8.16±0.26b	6.60±0.13b	7.53±0.20b	22.03±0.94b	22.23±0.97b	14.80±0.48b	16.87±0.53b

a,b: means in the same column under the same line (L_1or L_2) for the same parameter with different superscripts are significantly different ($P \leq 0.05$).

The table shows highly significant differences ($P \leq 0.01$) in BW values between BW lines across generations (G_1L_1vs. G_2L_1 and G_1L_2 vs G_2L_2). Generally, G_2L_1 significantly ($P \leq 0.01$) surpassed G_1L_1 from the 8th week of age to the 20th week of age. The reverse was, however, the case for the low lines where G_1L_2 consistently surpassed G_2L_2 also from the 8th to the 20th week of age. For instance, at 8, 12, 16 and 20 weeks of age, G_1L_1 averaged 360.67±3.46g; 677.01±5.19g; 816.96±5.62g and 958.05±7.75g, respectively as against the average values of 375.34±3.10g; 698.87±5.07g; 824.42±6.87g and 1003.34±6.98g for G_2L_1 for the same age periods, respectively. For the low lines, the mean BW values for G_1L_2 compared to G_2L_2 (G_1L_2 vs. G_2L_2) for the above age periods were 313.89±3.31g vs. 278.36±3.71g; 615.92±6.76g vs. 533.97±5.26g; 743.98±6.81g vs. 632.33±7.33g and 869.33±6.77g vs. 779.53±8.63g, respectively.

The observed significant differences between progeny and parent BW lines indicate that the mating plan used significantly affected values of the high and low lines of the progeny generation. The significant increases in BW values observed for the G_2L_1 lines and decreases observed for the G_2L_2 lines reflect the effect of positive assortative mating (like x like) which yield progenies that tend towards extreme phenotypes (genotypes) (Hammack, 2003). Reports of studies evaluating body weight lines across generations in the NIC are virtually absent in literature but observations from divergent selection studies involving body weight performances in other poultry species provide collaborative evidence of similar increasing trends for body weight values of the high lines as well as decreasing trends for body weight values of the low lines over generations (Tercic *et al.,* 2006; Tercic and Holcman, 2008). Such increases and decreases in body weight values in high and low lines, respectively, are the direct consequences of changes in gene frequencies as a result of isolation and mating within likes, as genes opposite in effects are concentrated in the different BW lines.

The feed intake values (mean ± S.E) for BW lines in the two generations also showed significant differences ($P \leq 0.05$). Expectedly, the high lines of the progeny generation (G_2L_1) consumed significantly ($P \leq 0.05$) more feed than the parental high lines (G_1L_1) from the 8th to the 20th week of age probably as a result of the increased growth performance. For the low lines, significant differences in FI was observed only at the 8th and 12th week of age, with the low lines of G_2 generation (G_2L_2) surprisingly surpassing those of G_1 generation (G_1L_2).

Table 2 also displays the values (means ± S.E) for body weight gain (BWG) and feed conversion ratio (FCR) for the two generations and component lines. The table shows that BWG was similar for G_1L_1 and G_2L_1 at 4, 8 and 12 weeks of age and for G_1L_2 and G_2L_2 at 4 and 8 weeks of age. At 16 weeks of age, G_1L_1 significantly ($P \leq 0.05$) surpassed G_2L_1 in BWG (5.15± 0.10g vs. 4.30±0.19g) but was significantly inferior at 20 weeks of age (5.30±0.15g vs. 6.74±0.20g). The low lines of G_1 generation (G_1L_2) surpassed ($P \leq 0.05$) those of G_2 generation (G_2L_2) in BWG at 12 and 16 weeks of age but became significantly ($P \leq 0.05$) inferior at the 20th week. The table shows a BWG range of 5.30g to 11.55g for G_1L_1; 4.30g to 11.40g for G_2L_1, 4.48g to 10.72g for G_1L_2 and 3.77g to 8.86g for G_2L_2 from 4 to 20 weeks. The lack of sustained striking differences in BWG between parental and progeny BW lines in the present study suggest that BWG does not increase lineally with age as does BW and are highly influenced by environmental factors (Nordskog and Hardiman, 1982). Again, the truncation based on differences in 4 weeks body weight alone as well as the selection of breeders without recourse to their true breeding values in these traits may have limited not only the response of the progenies in the primary trait (BW), but also the correlated response from associated traits (BWG and FCR).

The values (means ± S .E) for feed conversion ration (FCR) virtually followed the same pattern as BWG in this study. FCR was significantly ($P \leq 0.05$) higher for G_1L_1 compared to G_2L_1 at 12 and 16 weeks of age but became lower at the 20th week of age. For the low lines, G_1L_2 surpassed G_2L_2 in FCR at weeks 8, 12 and 16 but became inferior at the 20th week.

The pattern of differences in the productive traits across generations observed for the various traits (BW, BWG, FI and FCR) indicate that truncation based on body weight differences alone (as was the case in the present study) was not sufficient to bring about substantial improvement in the other components of growth and feed efficiency in the Nigerian indigenous chicken (NIC). Body weight gain and feed conversion ratio are very important economic traits (determine net return on investment) and should be incorporated in selection designs aimed at improving the overall economic worth of the NIC (Smith *et al.,* 1996) and the combined breeding value of selection candidates in these traits should inform the choice of parents.

Within and between line variation

Table 3. presents the within and between line variances in the performance traits.

TABLE 3. Variance components for performance traits for parent (G_1) and progeny (G_2) BW lines in the NIC at various age periods (4-20weeks)

		Within line variance (σ^2_{WL})				Between line variance (σ^2_{BL})			
Age (wk)	Gen	BW	BWG	FI	FCR	BW	BWG	FI	FCR
4	G_1	116.65	0.19	5.37	0.52	209.79	0.27	1.35	0.14
	G_2	253.58	0.29	2.41	0.34	234.49	0.19	1.24	0.03
8	G_1	1095.04	1.18	12.84	1.38	670.34	0.10	4.96	0.12
	G_2	886.23	0.64	2.75	1.41	2866.41	1.56	1.27	2.11
12	G_1	2800.76	3.56	28.19	1.40	1639.19	0.50	4.64	0.04
	G_2	1803.48	2.18	17.41	1.70	8336.85	2.04	22.84	0.46
16	G_1	2675.21	0.54	20.77	8.43	2397.58	0.23	4.14	2.48
	G_2	1996.66	1.18	8.35	45.7	13111.84	0.83	21.07	19.82
20	G_1	2821.54	1.61	25.13	52.22	4557.22	0.49	7.70	12.09
	G_2	3829.58	2.36	13.50	16.10	15787.21	0.70	10.94	3.10

Gen = Generation; BW = Body Weight; BWG = Body weight gain; FI = Feed intake; FCR = Feed conversion ratio.

It is observed from the table that on the average, between line variance (σ^2_{BL}) increased in the G_2 generation for all parameters while the within line variance (σ^2_{WL}) decreased except for FCR. For instance, the between line variance for BW among parental lines (G_1) was 209.79, 670.34, 1639.19, 2397.58 and 4557.22 at 4, 8, 12, 16 and 20 weeks, respectively. The corresponding values for the progeny lines (G_2) were 234.49, 2866.41, 8336.85, 13111.84 and 15787.21, respectively. The within line variance (σ^2_{WL}) for G_1 compared to G_2 for BW (σ^2_{G1WL} vs. σ^2_{G2WL}) were 116.5 vs. 253.58 for week 4, 1095.04 vs. 886.23 for week 8; 2800.76 vs. 1803.48 for week 12, 2676.21 vs. 1996.66 for week 16 and 2821.54 vs. 3829.58 for week 20 body weight. Other traits (except FCR) followed the same trend.

The observed net increase in between line variation and decrease in within line variation in the G_2 (progeny) generation for traits evaluated reflect the effect of segregating NIC population into subpopulations different in growth potentials and gene frequencies. When animal populations are divided into subpopulations, changes in gene frequencies lead to a redistribution of genic variances: a reduction within and an increase between lines (Buis *et al.,* 1994; Kristensen and Sorenson, 2005). The increase in between line variation as a result of within line positive assortative mating progressively isolate lines from each other as individuals within each line become increasingly alike. This between line differentiation and within line homogenization is the basis for the creation of highly specialized but complementary chicken lines used extensively in the development of poultry breeds (Ye *et al.,* 1998; Bacon *et al.,* 2000; deGreef *et al.,* 2001; Mizutani, 2002).

CONCLUSION

I have presented in the foregoing pages the comparison of performance values as well as variance components for body weight lines of parental generation and their progenies produced by intra line positive assortative mating. From the results presented, body weight significantly increased in the high lines but reduced in the low lines as expected. Body weight gain, feed intake and feed conversion ration did not show a definite pattern. Variances increased between progeny lines but reduced within lines. The performance of the NIC in BW can be improved through selection and positive assortative mating.

REFERENCES

Adebambo, O.A. (2005) Indigenous poultry breeds improvement for meat and eggs. Proceedings of the 1st international poultry summit, Feb. 20 – 25, ota, Ogun State, pp. 1 – 8

Ajayi, F.O. (2010) Nigerian indigenous chicken: A valuable genetic resource for meat and egg production. Asian Journal of poultry science,

Ajayi, F.O. and Agaviezor, B.O. (2009) Phenotypic characteristics of indigenous chicken in selected local government areas in Bayelsa State, Nigeria. Proceedings of the 3rd Nigerian international poultry summit. Feb. 22 – 26, Abeokuta, pp: 75 – 78.

Bacon, L. D., Hunt, H.D. and Cheng, H. H. (2000) A Review of the Development of Chicken lines to Resolve Genes Determining Resistance to Disease. Poultry Science (79) 1082 – 1093.

Buis, R.C., Olden-broek, J.K. and Van Der Werf, J.H.J. (1994) Preserving genetic variance resources in commercial and non – commercial populations. Netherland journal of agricultural science 42 (1) 29 – 36.

de-Greef, K.H., Kwakernaak, C., Ducro, B.J., Pit, R. and Gerritsen, C.L.M. (2001) Evaluation of between – line variation for within – line selection against Ascites in Broilers. Poultry Science 80:13 – 31.

Hammack, S. P. (2003) Breeding systems. Aqrilife Extension Texas A and M system. Available online at http://animalscience.tamm.ed/images/pdf/genetics/geneticsE189.pdf.

Kristensen, T.N., and Sorenson, A.C. (2005) Inbreeding – lessons from animal breeding, evolutionary biology and conservation genetics. Animal science 80: 121 – 133 part 2.

Mizutani, M. (2002) Establishment of inbred strains of chicken and Japanese Quail and their potential as Animal models. Exp. Anim. 51(5), 417 – 429.

Nordskog, A.W., and Hardiman, J. (1980) The genetic component of growth. In: Nordskog, A.W.(ed.), Notes on Poultry breeding and genetics. (2nd ed) 123 – 134.

Nwosu, C.C. (1990) Review of Indigenous poultry research in South-Eastern Nigeria. In: Rural Poultry Production in Africa. Ed. Sonaiya E.B. Proceeding of an international workshop on rural poultry in Africa. Ile – Ife, Nigeria. 13 – 16 Nov. 62 – 77.

Smith, C., James, J.W. and Brascamp, E.W. (1996) On the derivation of economic weights in livestock improvement. Anim. Prod. 43: 545.

SPSS (2001) Statistical package for social sciences version (13.0) SPSS Inc. Chicago, U.S.A.

Strandberg, E., and Malmfors, B. (2006) Directional Selection. In: Compendium Selection and Genetic change; version 2006 – 06 – 14. Dept. Anim. Breeding and genetics, Swedish Univ. of Agric. Scs. Uppsala, Sweden.

Tercic, D. and Holcman, A. (2008) Long-term divergent selection for 8 week body weight in chickens – A review of experiments. Acta agricturae Slovenica, 92 (2) 131 – 138.

Tercic, D., Flisar, T., Malovrh, S., Kovac, M. and Holcman, A. (2006) Response to divergent selection for 8 week body weight in chickens. In book of abstracts: supplement of world. Poultry Sci. J. Verona, World poult. Sci. Assoc., 215.

Ye, X., Zhu, J., Velleman, S.G., Bacon, W.L. and Nestor, K.E. (1998) Measurement of Genetic variation within and between Japanese Quail lines using DNA finger printing. Poultry Science 77: 1755 – 1758.