HERITABILITIES OF AND GENETIC CORRELATIONS BETWEEN SOME GROWTH TRAITS IN NIGERIAN LOCAL CHICKENS

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ABSTRACT

Heritabilities of and genetic correlations between body weight, shank length, keel length and breast width in a population of Nigerian local chickens at 6 weeks of age were estimated, using a total of 170 chicks of both sexes obtained from 5 sires each mated to 4 dams by artifical insemination in a nested fashion. Average body weight, shank length, keel length and breast width at this age were 114.97g, 3.48cm, 3.35cm and 3.22cm, respectively. Heritability estimates from the sire, dam and combined components of variance for body weight, shank length and breast width were 0.41 0.66 and 0.36; 0.58, 0.14 and 0.36; and 0.58, 0.36 and 0.48, respectively. The heritability of keel length from sire and combined variance components were 0.34 and 0.17, respectively. Genetic correlations between the traits were positive and high, ranging from 0.99 to 1.51. The moderate to high heritabilities (h_s^2) of these growth traits at 6 weeks point to the existence of an appreciable amount of additive genetic variance in the local chicken population and indicate that improvement in these traits can be brought about by intrapopulation selection. The high genetic correlations indicate the pleiotropic action of genes controlling these traits and that, by direct selection for any one of them, genetic improvement in the others will be realized as correlated responses.

Keywords: Heritability, genetic correlation growth traits, local chickens

INTRODUCTION

The local chicken of Nigeria constitutes 75 to 80% of the total population of chickens in the country (Trait, 1980). It is, however, characterised by poor growth, small body size and small egg size, which are not desirable in a competitive economic situation. Considering the huge foreign exchange implication of importation of improved exotic stock (Ibe, 1990) and also genotype-environment interaction (Johanssen and Rendel, 1968; Hill and Modebe, 1960; Oluyemi and Oyenuga, 1971) causing considerable loss of fitness, it is desirable to improve the local chickens in the environment in which they are fairly well adapted. A pre-requisite of an appropriate breeding plan for genetic improvement of stocks is knowledge of genetic parameters (heritabilities and genetic correlations) of relevant traits in that population.

Information on heritabilities and genetic correlations of growth traits in the Nigerian local chicken is comparatively scanty in available literature. Nwosu and Asuquo (1984) obtained heritability estimates for 4, 8, 12, 16 and 20 week body weight from sire, dam and combined variance components as 0.36, 0.38 and 0.37; 0.32, 0.36 and 0.34; 0.36, 0.38 and 0.37; 0.40, 0.49 and 0.44; and 0.33, 0.43 and 0.38, respectively. Oluyemi and Oyenuga (1971) reported a heritability (h_s^2) of 0.31 for 12-week body weight. There was no report in available literature regarding heritabilities of and genetic correlations between shank length, keel length and breast width in the Nigerian local chicken.

The aim of this study, therefore, is to estimate heritabilities of and genetic correlations between body weight, shank length, keel length and breast width of Nigerian local chickens at 6 weeks of age.

MATERIAL AND METHODS

Material

Experimental chicks were obtained from matings made between sires and dams randomly chosen from a base population of random mating, unselected local fowls maintained at the

University Poultry Teaching and Research Farm. The base population was established following two generations of random mating of local stock procurred from four different locations in Enugu State of Nigeria.

The mating design was hierarchical in which each of 5 sires was mated to 4 dams and each dam produced a number of progeny. Both the breeding cocks and hens were housed individually in single-bird cages and fed layers' mash *ad libitum*. Water was provided continuously. All the matings were by artificial insemination, using undiluted semen collected from the cocks by the massage technique described by Burrows and Quinn (1937) and by Lake (1957). Eggs were collected, pedigreed and stored in an air conditioned room for at most two weeks before they were incubated.

Day-old chicks were produced in 8 hatches, two weeks apart. On hatching, the chicks were wing-banded, pedigreed by sire and dam and vaccinated against Newcastle disease by the intra-ocular route. They were then transferred to the brooding unit of the Farm where they were brooded on deep litter, in pens each measuring 4.5 x 3.0m, providing a floor space ranging from 0.47 to 2.25m^2 per chick, for the varying numbers of chicks per hatch.

Commercial chick mash was provided *ad libitum* up to 6 weeks when the chicks were weighed with a sensitive Avery scale. At this time also , shank length, keel length and breast width of each chick were measured with a graduated ruler. Data from runts and individuals judged to have lost condition were excluded in the analysis.

Statistical Analysis

The following mixed model was used to analyse all traits:

$$Y_{ijkl} = \mu + H_i + S_j + D_{jk} + \epsilon_{ijkl}$$

Where Y_{ijkl} is the observation on the 1-th chick of the K-th dam mated to the J-th sire in the i-th hatch, μ is the overall mean, H_i is the fixed effect of hatch, S_j is the random effect of sire, D_{jk} is the random effect of the k-th dam mated to the j-th sire, and ϵ_{ijkl} is the random error.

The data were analysed using the Mixed Model Least-Squares and Maximum Likelihood Computer Program (Harvey, 1987) which used Henderson's Method 3 (Henderson, 1953) to estimate the observable variance components due to sire (σ_s^2), dam (σ_d^2) and error (σ_e^2) by equating computed mean squares to their expectations and solving for the components. Heritabilities and genetic correlations were then estimated using standard expressions (Becker, 1984). The appropriate standard errors of the estimated heritabilities and genetic correlations were also computed by the programme.

RESULTS AND DISCUSSION

Means and standard errors of the growth traits at 6 weeks of age are presented in Table 1. Although no values for body weight at this age were found in available literature, the values obtained here are considered low and lend support to the fact that local chickens are relatively small in size. However, these experimental birds were unconsciously inbred since their parents are a product of three generations of unrestricted random mating. This could have contributed to the small body size of these birds. There were variations in the mean values of the traits among hatches, with WT, SL, KL and BW ranging from 92.93 to 191.43g, 3.24 to 4.01cm, 2.87 to 4.04cm and 2.75 to 3.75cm, respectively. Significant hatch effects ($P < .05$) were observed for all traits (Analysis of variance tables 2, 3, 4 and 5, for WT, SL, KL and BW, respectively). This justifies the inclusion of the fixed effect of hatch in the mixed model to remove its influence on the traits and hence lead to more reliable estimates of components of variance for the estimation of genetic parameters.

Estimates of heritability from sire, dam and combined components of variance for the various growth traits are given in Table 6. Heritabilities of all traits using sire components of variance (h_s^2) are moderate to high. The implication of heritability of this magnitude is that appreciable additive genetic variance exists for these traits in the local chicken population and hence fast response to mass selection is expected. The amount of additive genetic variance in a given population is largely a function of the level of selection that has been done in that population. Selection depletes additive genetic variance. The local chicken population used in this study had not been subjected to any conscious selection for any trait. Kinney (1969) gave average heritability (h_s^2) of 6-week body weight of different pure lines and crosses as ranging between 0.30 and 0.46. Estimates for breast width, keel length and shank length for different breeds at different ages were also given as 0.17, 0.47 and 0.13, respectively. The relatively lower values reported by this author for these traits are probably due to the fact that the populations considered consisted of improved breeds that had been subjected to selection pressures.

Table 6 also shows that heritablity of body weight from dam component of variance (h_d^2) is higher than its heritablity from the sire component, whereas the reverse is true for SL, KL, and BW. A similar observation was made for body weight by Nwosu and Asuquo (1984) in the Nigerian local chicken and by Amer (1965) in the Egyptian Fayoumi. This shows that, in addition to additive genetic variance, maternal, common environmental and dominance effect variances contribute to variation in body weight. On the other hand, for the linear body measurements, sex linkage rather than maternal and dominance effects is important.

Table 7 gives the genetic correlations between the traits, using sire components of variance, with the exception of the correlation between WT and SL. (0.99), all the other correlations are greater than 1. Although theoretically meaningless, such values can be realized in practical situations, depending, among other things, on the nature and size of data. They are frequently taken simply as indicative of very high correlations. Merritt (1966) reported high genetic correlations of 0.71 and 0.77 between 6-week body weight and 9-week keel length and between same trait and 9-week shank length, respectively. Also, correlations of 0.74 and 0.87 were reported for 12-week body weight and 12-week keel length and between same trait and 12-week shank length, respectively (Lerner *et al.*, 1947; Abplanalp *et al.*, 1960). The very high correlation between each linear body measurement and body weight is not surprising, since the latter is a measure of overall body growth which itself is the sum total of increases in size of different structural body components (Ibe and Nwakalor, 1987). It also indicates the pleiotropic action of genes responsible for these characters. Another obvious practical implication of the high and positive genetic correlations between the traits is that, by direct selection for any one of them, genetic improvement in the others will be realized as correlated responses.

CONCLUSION

Improvement in the body size of the local chicken of Nigeria is desirable from point of view of improving its subsequent egg size. There is fairly good agreement that the best age to select breeders for efficient and rapid growth is at 6 weeks. Data presented indicate that appreciable additive genetic variance exists in the local chicken population for 6-week body growth traits. Consequently, rapid genetic progress can be made through intrapopulation selection either for body weight or for a principal component index of body size (see Ibe, 1989), which would give a more reliable measure of true body composition of animals than scale weight. The benefits of improved body size will subsequently be realized both in increased egg size and in the post-lay value of the chicken.

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Table 1 AVERAGE VALUES OF GROWTH TRAITS, BY HATCH

				Trait[a]	
HATCH NO.	N	WT (g)	SL (cm)	KL (cm)	BW(cm)
1	4	191.43	3.99	4.04	3.60
		(17.40)	(0.22)	(0.30)	(0.24)
2	5	130.79	4.01	3.94	3.00
		(17.00)	0.21	(0.29)	(0.24)
3	3	(21.93)	(0.28)	(0.39)	(0.30)
4	14	103.93	3.35	3.14	3.20
		(10.65)	(0.14)	(0.17)	(0.16)
5	15	92.93	3.29	3.28	3.25
		(11.19)	(0.14)	(0.18)	(0.17)
6	8	108.65	3.37	3.37	3.29
		(13.25)	(0.17)	(0.22)	(0.19)
7	3	135.75	3.67	3.75	3.26
		(18.47)	(0.23)	(0.32)	(0.25)
8	11	100.31	3.24	2.87	2.79
		(16.95)	(0.21)	(0.29)	(0.24)
Mean		114.97	3.48	3.35	3.22

a WT = body weight,
SL = Shank Length KL = keel length

Standard errors in parentheses

Table 2 ANALYSIS OF VARIANCE TABLE FOR BODY WEIGHT

Source	d.f.	M.S.	E(EMS)	F
Hatch	7	4686.031		6.35**
Sire	4	1727.059	$\sigma_e{}^2 + 3.4\sigma_d{}^2 + 8.88\sigma_s{}^2$	
Dam/Sire	12	879.953	$\sigma_e{}^2 + 2.65\sigma_d{}^2$	
Progeny/Dam/Sire	34	737.600	$\sigma_e{}^2$	
Total	57			

** $P < .01$

Table 3 ANALYSIS OF VARIANCE TABLE FOR SHANK LENGTH

Source	d.f.	M.S. E(MS)		F
Hatch	7	.4547		3.96**
Sire	4	.2938	$\sigma_e{}^2 + 3.4\sigma_d{}^2 + 8.89\sigma_s{}^2$	
Dam/Sire	12	.1164	$\sigma_e{}^2 + 2.65\sigma_d{}^2$	
Progeny/Dam/Sire	34	.1147	$\sigma_e 2$	
Total	57			

** $P < .01$

Table 4 ANALYSIS OF VARIANCE TABLE FOR KEEL LENGTH

Source	d.f.	M.S.	E(MS)	F
Hatch	7	.5307		2.20*
Sire	4	.3785	$\sigma_e{}^2 + 3.4_d{}^2 + 8.89\sigma_s{}^2$	
Dam/Sire	12	.1233	$\sigma_e{}^2.65\sigma_d{}^2$	
Progeny/Dam/Sire	34	.2409	$\sigma_e{}^2$	
Total	57			

*$P < .05$

Table 5 ANALYSIS OF VARIANCE TABLE FOR BREAST WIDTH

Source	d.f.	M.S.	E(MS)	F
Hatch	7	.2742		2.19*
Sire	4	.4376	$\sigma_e^2 + 3.4\sigma_d^2 + 8.89\sigma_s^2$	
Dam/Sire	12	.1442	$\sigma_e^2 + 2.65\sigma_d^2$	
Progeny/Dam/Sire	34	.1249	σ_e^2	
Total	57			

** $P < .05$

Table 6 HERITABLITY ESTIMATES[a] OF GROWTH TRAITS

Traits[b]	h_s^2	h_d^2	h^2_{s+d}
WT	0.41(0.59)	0.66(0.59)	0.36(0.30)
SL	0.58(0.62)	0.14(0.55)	0.36(0.30
KL	0.34(0.50	-	0.17(0.26)
BW	0.58(0.62)	0.36(0.57)	0.48(0.31)

[a] Standard errors in parentheses: - means negative heritability

[b] See Table 1 for meanings of trait abbreviations

Table 7 GENETIC CORRELATIONS[a] BETWEEN THE GROWTH TRAITS

Trait[b]	WT	SL	KL	BW
WT	1.00	0.99(0.15)	1.13(0.38)	1.09(0.17)
SL		1.00	1.51(0.88)	1.11(0.13)
KL			1.00	1.01(0.41)
BW				1.00

[a] Standard errors in parentheses

[b] See Table 1 for meanings of trait abbreviations