Genetic Parameter Estimates of Early Growth Traits of Pure and Crossbred Chicken Progenies in the Humid Environment of Nigeria

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ABSTRACT

Heritabilities, genetic and phenotypic correlations amongst some growth traits in pure and crossbred chickens at day old to 8 weeks of age are estimated using 357 chicken progenies. A total of 23 sires from four different strains (Naked neck, frizzle feather, normal feather and White leghorn) are mated to 45 dams of White leghorn strain through artificial insemination. Data collected on body weight, body length, breast girth and keel length on weekly basis are analysed using Maximum likelihood (ML) computer programme and paternal half-sib analysis. Sire heritabilities for growth traits at day old are generally low, suggesting higher influence of environmental factors. However, estimates for 4 and 8 weeks vary between moderate to high in each sire strain. Also, genetic correlations amongst the traits using combined sire variances were generally high while those of phenotypic correlations vary between low to high. Moderate to high heritability estimates indicate presence of appreciable genetic variabilities in the growth traits studied amongst the sire strains and improvement could be made through mass selection. Similarly, high genetic correlations suggest that the traits are under the same genetic influence (pleiotropism), therefore, selection for one trait would lead to improvement in the other traits as a correlated response. This study therefore concludes that Nigerian local chicken are unimproved and has the potentials of genetic improvement.

Keywords: *Crossbred chickens, pure chickens, heritabilities, genetic and phenotypic correlation*

INTRODUCTION

A prerequisite of an appropriate breeding plan for genetic improvement of chickens is knowledge of genetic parameters (heritabilities, genetic and phenotypic correlations) of relevant traits in that population. These genetic parameters are especially needed when

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applying a combined crossbred and purebred selection method to achieve genetic progress in crossbreeds (Wei and van der Werf, 1994). The genetic characterization of indigenous breeds is of paramount importance, not only for conservation purposes but also for the definition of breeding objectives and the development of breeding programmes. Ndofor-Folong, Uberu and Nwosu (2006) obtain heritability estimates of light and heavy weight chickens ecotypes reared in Nsukka in the derived savanna zone of Nigeria to be 0.40 and 0.37 respectively. Moderate to high heritabilities at early ages in chickens have also been reported (Iraqi, Hanafi, Khalil, EI-Labban and Ell-sissy, 2002; Ebangi and Ibe, 1993; Nwosu and Asuquo, 1984). Sires consideration in poultry farming is very important because they produce many offspring during their lifetime, therefore failure to select good sires will spell genetic doom for the whole flock. Sire heritabilities of 0.36, 0.32, 0.36, 0.40, and 0.33 for body weight at 4, 8, 12, 16 and 20 weeks respectively have been reported (Nwosu and Asuquo, 1984) in the chicken population of Nigeria.

However, Ebangi and Ibe (1993) report 0.41, 0.58, 0.34 and 0.58 representing sire estimates for body weight, shank length, keel length and breast width in the same chicken population. There are various magnitudes of genetic and phenotypic correlations of growth traits in the local chickens; growth traits were under the same gene actions (Ebangi and Ibe, 1993). The genetic correlation between crossbred and purebred performance and crossbred heritability are important genetic parameters for optimizing and evaluating crossbreeding systems (Wei and van der Steen, 1991). Crossbred heritability is related to the amount of genetic variation among purebreds for crossbred performance. While there were some literatures about heritability estimates for body weight and linear body measurements of local chickens of Nigeria, there is little information on the extent to which locally adapted sire chicken can contribute to the overall inheritance of the crossbreeds. Therefore, this study seeks to determine the genetic contributions of some of the locally adapted sire chicken to the overall genetic make-up of the crossbred as well as establishing relationship amongst their growth traits.

MATERIALS AND METHOD

The study was carried out at the Poultry Breeding Unit of the Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Ogun State, Nigeria. The area lies in the southwestern part of Nigeria and has a prevailing tropical climate with a mean annual rainfall of about 1037mm. The mean ambient temperature ranges from 28^0C in December to 36^0C in February with a yearly average of 34^0C. Relative humidity ranges from 60% in January to 94% in August with a yearly average of about 82%. The vegetation represents an interphase between the tropical rainforest and the derived savannah.

Experimental birds and their management: The experimental birds consists of 23 sires belonging to four different sire strains and 115 (one hundred and fifteen) pure bred White leghorn dams randomly selected from a population of birds reared in the institution. The 4 sire strains were three locally adapted chickens (Naked neck, Normal feather and Frizzle feather) and one exotic (White Leghorn). Sires and dams were individually caged in an open sided house with a cage space of $0.4m^2$. The experimental birds were wing tagged individually for identification purpose, adequately fed and water given *ad libitum*. They were exposed to natural daylight for 13 hours per day.

Mating procedure, egg collection and incubation: The sires were trained by abdominal massage (Lake, 1962) for some weeks before semen collection. The semen collection was done twice a week in the evening (1700hrs) and each dam was also inseminated twice a week throughout the investigation period. Eggs laid by the dams were collected twice daily, pedigreed along sire lines. The eggs were stored in a cool room to accumulate at a temperature of between 20^0C and 25^0C and 80% relative humidity for five days before been transferred to the hatchery. Proper cleaning, disinfection and fumigation were done before setting of eggs in the incubator. The mating procedure is as shown below:

Normal feather (sire) *x* White Leghorn (dam)
Naked neck (sire) *x* White Leghorn (dam)
Frizzle feather (sire) *x* White Leghorn (dam)
White Leghorn (sire) *x* White Leghorn (dam)

Management of chicks: The resulting 357 pure and crossbred chicks were properly identified; wing tagged and then transferred to previously disinfected brooder cages in the brooding unit. Each batch was brooded for four weeks. The chicks were fed *ad libitum* on a chick starter mash containing 22 – 24% crude protein and 11.1MJ/Kg metabolizable energy up to 8 weeks. Clean water was supplied *ad-libitum* throughout the experimental period. The birds were reared together regardless of sex and growth parameters of 357 progeny chicks were studied from day old to eight weeks. The parameters measured include: body weight, body length, keel length and breast girth. The body weight was measured with use of a sensitive weighing balance (0.05g sensitivity) with a capacity of three decimal digits (gram), while Body length was measured as the distance between the base of the neck and the cloaca using tailor's tape rule (cm) and keel length was measured as the length of the sternum using tape rule (cm). The breast girth was taken as the circumference of the breast around the deepest region of the breast using a tailor's tape (cm). Data collected on weekly basis and on each of the growth traits were corrected for hatch and sex effects. Maximum likelihood (ML) computer programme (Harvey, 1990) was used to compute variances and covariances for genetic and phenotypic correlation while sire heritabilities were estimated using paternal half-sib analysis (Becker, 1975):

$$h^2 s = \frac{4\sigma^2 s}{\sigma^2 s + \sigma^2 e}$$

Where

$\sigma^2 s$ is the variance component due to sire,

$\sigma^2 e$ is variance component due to environment and

$h^2 s$ is the heritability due to sire.

Standard errors of sire heritabilities were also calculated according to Becker (1975) for unequal number of progenies per sire.

RESULTS AND DISCUSSION

Information regarding heritability estimates is very useful in animal breeding as a means to predict potential response to or progress from selection, and knowledge of genetic parameters is essential for any genetic improvement programme. Estimates of heritability from sire components of variance for the various growth traits and at different ages are shown on table 1. At day old, the heritability estimates was generally low, ranging from 0.01 – 0.08 for body weight, 0.03 – 0.12 for body length, 0.08 – 0.11 for breast girth and 0.02 – 0.08 for keel length. The low heritability estimates obtain in this study at day old falls within the range reported by Adeleke *et al*. (2011) in a crossbreeding experiment involving two ecotypes of Nigerian local chickens. They attribute it to a function of environmental factors. The low heritability estimates observed could be due to non-additive genetic effects such as dominance and epistasis. The implication of this is that selection for trait of interest may not result in any appreciable improvement.

The low heritability at younger ages also indicates less genetic variability relative to phenotypic variability among the chicks. Moderate to high heritabilities (0.32 – 0.88) of body weight and linear body measurements of pure and crossbred in 4 weeks and 8 weeks (table 1) as witnessed in this study implies that there were sufficient genetic variabilities in the traits studied and faster response to mass selection is expected. This agrees with the findings of Iraqi *et al.,* (2002); Ebangi and Ibe (1993). As expected, the amount of additive genetic variance in a given population is largely a function of the level of selection that has taken place in that population, therefore, the results of this study are not surprising. Moderate to high heritability estimate is an indication that variability due to additive gene action is probably higher than the non- additive component and genetic progress can be made through selection. This then implies that a large proportion of the superiority of the parents could be retained in the offspring.

Nwosu and Asuquo (1984) report moderate to high sire heritability estimates for body weight in the Nigerian local chicken while heritabilities of body weight at different age due to sire (4 to 20 weeks) were also reported by Asuquo and Nwosu (1987) in the crosses of Nigerian local chickens with imported Gold-link and Yaffa chickens. Adeyinka, Oni, Nwagu and Adeyinka (2006) report lower heritabilities of growth traits in the population of naked neck broiler. The progenies were F_1 crossbreeds that had not been subjected to any selection pressure and more so, three out of the four sire strain used for mating were unimproved Nigerian local chickens. The exotic dam strain used was not enough to lower the genetic variability since sires have been implicated in the production of much more progenies per unit time than dam (Falconer, 1993). Table 2 shows the genetic and phenotypic correlations amongst growth traits using combined sire components of variance at day-old to 8 weeks. With the exception of low genetic correlation between keel length and breast girth (0.029) at day-old, all other correlations magnitude were high. However, the phenotypic correlations of growth traits were generally low to high (not as high as genetic correlations) and varied with age of the birds.

High and positive genetic correlation between growth traits conform to the findings of Ebangi and Ibe (1993), and Abplanalp, Asmundson and Lerner (1960). The estimates of genetic correlation fall within the value reported by Ibe and Nwakalor (1987); Ezzeldin, Hanafi, Khalil, and Sabra (1994). This is expected because body weight is a measure of overall body growth which is a sum total of different structural component (Ibe and Nwakalor, 1987). Also, positive correlations of the growth traits suggest that the traits are under the same gene action (pleiotropism) and by implication selection for improvement in one trait would result in improvement of the other trait as correlated response. Estimates of phenotypic correlations were in line with the findings of Ezzeldin, Hanafi, Khalil and Sabra (1994) in purebred chickens and their crosses. However, the lower values recorded as against the genetic correlations could be as a result of inclusion of environmental variances.

CONCLUSION

The purpose of this study is to determine the genetic contributions of some of the locally adapted sire chicken to the overall genetic make-up of the crossbred and establishing relationship amongst their growth traits. The study was conducted at the Poultry Breeding Unit of the Department of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Ogun State, Nigeria. The experimental birds consisted of twenty three sires belonging to four different sire strains and one hundred and fifteen pure bred White Leghorn dams randomly selected from a population of birds reared in the institution. Information regarding heritability estimates is very useful in animal breeding as a means to predict potential response to or progress from selection, and knowledge of genetic parameters is essential for any genetic improvement programme. Estimates of heritability from sire components of variance for the various growth traits and at different ages show that the heritability estimate was generally low. Hence, positive correlations of the growth traits suggest that the traits are under the same gene action (pleiotropism) and by implication selection for improvement in one trait would result in improvement of the other trait.

Table 1: Heritabilities (± S.E) of growth traits of pure and crossbred chicken progenies per sire strain

Day-old

Sires	body weight	body length	breast girth	keel length
Naked neck	0.08±0.57	0.08±0.03	0.10±0.03	0.06±0.03
Frizzle feather	0.06±0.03	0.08±0.56	0.09±0.58	0.06±0.25
Normal feather	0.01±0.14	0.03±0.35	0.08±0.29	0.02±0.30
White leghorn	0.06±0.14	0.12±0.27	0.11±0.13	0.08±0.57
4 weeks				
Naked neck	0.64±0.11	0.87±0.41	0.83±0.48	0.79±0.50
Frizzle feather	0.68±0.05	0.54±0.23	0.80±0.32	0.75±0.41
Normal feather	0.71±0.09	0.42±0.35	0.71±0.41	0.86±0.61
White leghorn	0.52±0.08	0.34±0.36	0.64±0.46	0.82±0.42
8 weeks				
Naked neck	0.78±0.19	0.48±0.03	0.85±0.03	0.76±0.03
Frizzle feather	0.61±0.03	0.58±0.50	0.89±0.50	0.86±0.25
Normal feather	0.81±0.14	0.40±0.35	0.68±0.29	0.72±0.30
White leghorn	0.66±0.14	0.32±0.27	0.75±0.13	0.88±0.57

Source: Experimentation, 2014

Table 2: Genetic and phenotypic correlations (sire combined) of growth traits of chicken progenies

	day old			
	body weight	body length	breast girth	keel length
Body weight		0.972	0.124	0.84
Body length	0.998		0.132	0.858
Breast girth	0.531	0.588		0.120
Keel length	0.987	0.975	0.029	
	4 weeks			
	body weight	body length	breast girth	keel length
Body weight		0.050	0.068	0.035
Body length	0.416		0.880	0.625
Breast girth	0.513	0.992		0.664
Keel length	0.391	0.975	0.919	
	8 weeks			
	body weight	body length	breast girth	keel length
Body weight		0.226	0.378	0.416
Body length	0.633		0.499	0.373
Breast girth	0.655	0.932		0.632
Keel length	0.659	0.978	0.889	

Note: Values at the lower diagonal are the genetic correlations and the upper diagonal are the phenotypic correlations

Source: Experimentation, 2014

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