

Heritability and Genetic Correlations of Growth Traits Among Inbred Population of Nigerian Chickens

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Abstract

This study was carried out to estimate heritability for body weight, as well as the genetic correlations between these traits of the Nigerian inbred Local Chicken (NILC) reared at the University of Nigeria, Nsukka (UNN). The study lasted for 2 months, and the heritability and genetic correlations of the traits were estimated using Animal Model Design of the SAS 2004 statistical procedure. The direct heritability for body weights of NILC were 0.51, 0.76, 0.89, 0.22 and 0.20 at weeks 1, 2, 4, 6 and 8. In the present study, high heritability estimates (0.51, 0.76 and 0.89) were recorded for weeks 1, 2 and 4, respectively, but medium for weeks 6 and 8. Genetic correlations between 1BW and 4BW, 8BW, 4BL, 8BL, 4SL, 8SL, 4CG, 8CG were 0.984, 0.763, 0.953, 0.735, 0.72, -0.952, 0.989 and -0.481, respectively. Estimates for genetic correlations ranged from -0.481 to 0.989 among the traits considered in this study. High and positive genetic correlations were recorded for 1BW and other traits except for 8SL and 8CG, which had negative genetic correlations. High estimates of heritability found in the present study indicate that additive genetic variances exist for these traits. Selection for body weight at 1 or 2 weeks of age, therefore, is likely to result in a genetic gain in the NILC. Furthermore, the high and positive genetic correlations observed indicate that selection for one trait will result in a correlated response on the other traits compared in the study.

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Introduction

The Nigerian native chicken constitutes 80% of the 120 million poultry birds in Nigeria (Adedokun SA, Sonaiya EB 2001).

Native chicken constitutes about 45.8-83.2% of the total meat consumed in Africa. This meat is characterized by high resistance to diseases, hardiness, excellent taste, flavor, juiciness and tenderness. It is nutritious and appetizing with low fat and cholesterol (Adejoh, 2006). Such fitness traits are the outcome of several generations of natural selection. Although the indigenous chicken outputs (egg and meat) are readily available and it serves as good sources of protein and income to villagers and people in urban semi-urban areas, its meat yield remains grossly inadequate to address the alarming protein deficiency and hunger facing Africa.

The population of the Nigerian indigenous chicken represents an essential gene pool for the development of diverse chicken breeds for global chicken. Unfortunately, these benefits are yet to make a positive economic impact in Nigeria, because Nigerian local chicken (NLC) is yet to attain a standard chicken breed. As a consequence, growth and reproductive traits like body weight (live and carcass), weight gain, egg size and the number of eggs/hens, for example, are likewise generally low (Ohagenyi *et al.*, 2022). The contribution of the Nigeria chicken to its economy to date still lingers far way behind its exotic counterpart (broiler and Layer). The low frequency of the quantitative genes controlling meat and egg laying performance of the indigenous is chiefly the reason for its minimal performance. The frequency of genes responsible for these endowed desirable traits needs to be concentrated through selection and mating systems for their full exploitation.

The local Animal breeders at the University of Nigeria Nsukka have keyed into the global plan of food security and reduction in food loss through genetic improvement of its indigenous local chicken. Ndofor- Foleng *et al.* (2006) estimated the genetic parameters of traits of the Nigerian heavy local chicken ecotypes (NHLCE) that were gathered from rural communities. Genetics estimates were determined for growth and reproductive traits of inbred populations of the Nigerian heavy local chicken ecotypes by Ohagenyi *et al.*, (2012), and Agu *et al.*, (2016). In addition, the NHLCE was lightly bred under controlled breeding for three generations of selection Ogbu *et al.*, (2012), Agbo *et al.*, (2018) further selected the NHLCE till the 8th generation, Udeh, (2019). Eze. (2020) and Ohagenyi *et al.*, (2020) evaluated the genetic parameters of growth traits of four strains, while Ohagenyi *et al.*, (2021) did a comparative study of the NHLCE, broiler and nondescript Nigerian unimproved chicken. These studies showed some genetic progress in the meat trait and egg traits of the NHLCE and revealed that while meat genes have been fixed in broiler it is yet to be fixed in NHLCE and recommends mass selection and index selection. Consequently, the present study has employed inbreeding as a veritable way to expedite the creation of indigenous meat and egg-type chicken breed.

Accurate estimation of the individual breeding value (BV) particularly heritability (h^2) and performance records combined with proper mating methods for generations have been adopted by breeders to produce exotic breeds, as well as, expedite the genetic progress among the meat and egg type chickens. As a result, the exotic chickens have consistently maintained highly improved meat and egg performance with amazing trade that has grown to a macro economy in America and many civilized countries. For instance, USDA (2022) reports showed that the American total chicken production in 2021 was 518,271,000 chickens, 59.4 billion pounds of broiler meat and American poultry (broiler, turkey, eggs and chickens) generated US\$35.547 billion dollars in 2020 in American. The broiler sales and broiler meat of the leading 20 states in US broiler production in 2020 ranged from 82 million to 2.95 billion dollars and 225 million to 8.1 billion pounds in Wisconsin and Georgia, respectively. The report also showed that over 40 states of America have

substantial input in poultry production and sales. Thus, consolidating breeding as a science, an art and a macroeconomic business (Khan and Ashok 2000).

Improving the access of the vulnerable population to food and ensuring food security in low- and middle-income countries in Asia, Africa, Latin America and the Caribbean will be key to eradicating hunger over the next 15 years. Agriculture and food systems will need to meet the food and nutritional demands of people with high income and changing diets, as well as the demands of a growing number of poor and hungry (FAO 2017). The Nigerian indigenous chicken gene pool, therefore, represents a highly valuable resource for global livestock development and food security because the ongoing non-systemic selection process (natural selection) confers fitness and extensive genetic diversity to the indigenous chicken generation after generation. Thus, the exploitation of the superfluous genetic resources embedded in the Nigerian indigenous poultry will provide a basis for genetic improvement and diversification necessary for the production of numerous poultry breeds that are adapted to diverse global conditions for the benefit of farmers in both developed and developing countries and the world populace in future (FAO 2020).

Food losses in Low-income countries occur throughout the whole value chain owing to managerial and technical limitations in production, harvesting, storage and processing are partly responsible for 800 million that are critically hungry (2017). Great losses of the Nigerian poultry will be maximally curtailed, if efforts are geared towards increasing the accuracy of breeding values of superior chickens across diverse locations and climates, through estimation of heritability for the purpose of genetic improvement of its indigenous chicken, which was reported to constitute 80 percent of the 120 million national chicken populations. Without additional efforts to promote pro-poor development, which ensures that the weakest participate in the benefit of market integration and investment in agriculture, some 653 million people would still be undernourished by 2030 (FAO 2017). The indigenous chicken of Nigeria is a valuable asset for the attainment of this goal.

Materials And Methods

Location And Duration of Study

This study which lasted for two months was carried out at the poultry unit of the Department of Animal Science Teaching and Research farm, University of Nigeria, Nsukka. Nsukka is located on latitude 050 22 north and longitude 070 24' east with annual rainfall ranging from 986-2098mm (Asadu 2002). Nsukka's climate is typically humid tropical with relative humidity ranging from 34%-78%. The average diurnal minimum temperature ranges from 22C-24.7C. The rainy season is between April- October and the dry season is between November-March.

Management Of Experimental Population

The experimental birds comprised a population of 100-day-old Nigerian inbred local chickens generated from related selected parents of Nigerian local chickens. The 24 weeks records of the related individual of the local chickens were

used to score superior parents for breeding value. Selection of parents for each strain was based on high breeding value for body weight, body length, egg weight, feather colour and egg colour. The brooding house was partitioned into four compartments measuring 4m x 6m for the rearing of the four strains. The experimental birds were fed ad-libitum with broiler starter from day 1 to 4 weeks and broiler finisher from 5-8 weeks of age. Water was provided at all times, and the birds were vaccinated routinely. Routine medications were administered in addition to proper management practices.

Statistical Analysis

Data obtained from body weight, body length, shank length and chest girth were subjected to analysis of variance (ANOVA) in an animal model design, all data generated were analysed using SAS (2004) statistical procedure and were used to derive the variance and covariance components of all traits under study. Heritability estimates were further calculated using the formula:

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

Where h^2 is the heritability estimate of a trait; σ_s^2 is variance due to sire and σ_e^2 is variance due to error. Genetic correlation estimates were also further calculated using the formula:

$$r_g = \frac{\sigma_{xy}}{\sqrt{\sigma_x^2 * \sigma_y^2}}$$

Where r_g is Genetic correlation; σ_{xy} is Covariance of trait x and trait y; σ_x^2 is Variance of trait x and σ_y^2 is Variance of trait y.

Results And Discussion

Heritability

The heritability estimates for body weight are presented in Table 2 below. The direct heritability for body weights of NILC were 0.51, 0.76, 0.89, 0.22 and 0.20 at weeks 1, 2, 4, 6 and 8. Estimates of heritability ranged from 0.20 at week 8 to 0.89 at week 4. In the present study, high heritability estimates (0.51, 0.76 and 0.89) were recorded for weeks 1, 2 and 4, respectively, but medium for weeks 6 and 8. The present findings are higher than the values reported by Ohagenyi et al. (2012) and Ndofor-Foleng et al. (2014) and are in contrast with the reports of Eze (2019), who reported low heritability estimates for body weight at weeks 1 and 4 (0.00 and 0.20, respectively). The disparity in values observed in this study could be attributed to differences in the genetic composition of the population and environment. Corroborating the fact that heritability is an attribute of a population hence it varies with the population (Ashok and Khan 2002).

Table 1. Statistical description of body weight and allometric traits of four genetic groups of Nigerian Inbred Local Chicken (NILC)

| Weeks | Strains | Body weight (Kg) | | | | Body length (cm) | | | | Chest girth (cm) | | | | Shank length (cm) | | | |
|-------|---------|------------------|-----|----|------|------------------|------|-----|------|------------------|------|-----|-----|-------------------|-----|-----|------|
| | | Mean | TM | SE | CV | Mean | TM | SE | CV | Mean | TM | SE | CV | Mean | TM | SE | CV |
| 1 | White | 0.1 | | | | 8.68 | | | | 8.23 | | | | 3.25 | | | |
| | Barred | 0.11 | | | | 9.04 | | | | 8.3 | | | | 3.02 | | | |
| | Brown | 0.11 | | | | 9 | | | | 9.1 | | | | 3 | | | |
| | Black | 0.11 | 0.1 | 0 | 10.2 | 8.38 | 8.83 | 0 | 8.67 | 8.4 | 8.39 | 0.1 | 6.3 | 3.2 | 3.1 | 0 | 11.5 |
| 4 | White | 0.26 | | | | 0.26 | | | | 11.75 | | | | 6.08 | | | |
| | Barred | 0.31 | | | | 0.31 | | | | 12.43 | | | | 6.32 | | | |
| | Brown | 0.33 | | | | 0.33 | | | | 12.03 | | | | 6 | | | |
| | Black | 0.28 | 0.3 | 0 | 19.8 | 0.28 | 0.3 | 0.2 | 14.7 | 11.78 | 12.1 | 0.1 | 8.3 | 5.63 | 6.1 | 0.1 | 9.62 |
| 8 | White | 0.65 | | | | 19.03 | | | | 14.9 | | | | 8.34 | | | |
| | Barred | 0.61 | | | | 21 | | | | 14.2 | | | | 8.15 | | | |
| | Brown | 0.58 | | | | 17.63 | | | | 14.25 | | | | 8.8 | | | |
| | Black | 0.59 | 0.6 | 0 | 16.7 | 20.13 | 19.7 | 0.4 | 21.6 | 13.72 | 14.4 | 0.1 | 6.7 | 8.21 | 8.3 | 0.1 | 12.4 |

TM = Total mean; SE = Standard Error; CV = Coefficient of variation.

Table 2. Variance components and heritability estimates of body weight traits of NILC at different weeks

| | Body weight | | |
|--------|--------------|--------------|--------------|
| | σ_s^2 | σ_e^2 | $h^2 \pm SE$ |
| Week 1 | 0.000016 | 0.000110 | 0.51±0.51 |
| Week 2 | 0.000014 | 0.000576 | 0.76±0.77 |
| Week 4 | 0.000780 | 0.002737 | 0.89±0.83 |
| Week 6 | 0.000511 | 0.008755 | 0.22±0.38 |
| Week 8 | 0.000525 | 0.010150 | 0.20±0.27 |

σ_s^2 = variance due to sire; σ_e^2 = variance due error; h^2 = heritability estimate; SE = Standard error

Table 3. Genetic and environmental and phenotypic correlation between the different traits of the NILC (body weight, body length, shank length and chest girth)

| Traits and Week | r_g | r_e | r_p | | | r_g | r_e | r_p |
|-----------------|--------|--------|-------|--|----------------|--------|--------|--------|
| BW1*BW4 | 0.984 | 0.072 | 0.25 | | BW1*SL8 | -0.952 | 0.069 | -0.001 |
| BW1*BW8 | -0.763 | 0.217 | 0.137 | | BW1*CG4 | 0.989 | -0.164 | -0.043 |
| BW1*BL4 | 0.953 | 0.103 | 0.185 | | BW1*CG8 | -0.481 | 0.053 | -0.023 |
| BW1*BL8 | 0.735 | 0.168 | 0.223 | | BW2*CG8 | -0.937 | 0 | -0.089 |
| BW1*SL4 | 0.72 | -0.001 | 0.11 | | BW2*BW4 | 0.931 | 0 | 0.369 |

r_g = genetic correlation; r_e = environmental correlation; r_p = phenotypic correlation

Genetic Correlation

Table 3 shows genetic, environmental and phenotypic correlations for the traits observed in this study. Genetic correlations between 1BW and 4BW, 8BW, 4BL, 8BL, 4SL, 8SL, 4CG, 8CG were 0.984, 0.763, 0.953, 0.735, 0.72, -0.952, 0.989 and -0.481, respectively. Estimates for genetic correlations ranged from -0.481 to 0.989 among the traits considered in this study. High and positive genetic correlations were recorded for 1BW and other traits except for 8SL and 8CG, which had negative genetic correlations. The coefficient of genetic correlations found in the present study between body weight and 4BW and 8BW is in conformity with the reports of Eze. (2019) and Ohagenyi et al. (2012), however, the value recorded for 1BW and chest girth at week 8 (-0.481), is comparable with Eze. (2019) who reported negative correlations at this age (-0.718) whilst comparing. The negative correlations recorded for body length and shank length at week 4 (-0.237) are in contrast with the value reported by Ohagenyi *et al.* (2012) which was 0 at week 4. The genetic correlation between 1BW and 8SL was -0.952 and does not agree with Ohagenyi *et al.* (2012), who reported (0) for these traits.

Conclusion

High estimates of heritability were found for body weights of NILC at 1,2 and 4 weeks of age, but medium heritability estimates were obtained at 6 and 8 weeks of age.

The study further revealed high genetics correlations between week 1 body weight and other traits.

High estimates of heritability indicate that additive genetic variances exist for these traits. Selection for these traits at weeks, therefore, is likely to result in a genetic gain in the NILC.

The positive genetic correlations observed indicate that selection for one trait will result in a correlated response on the other trait compared in the study.

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