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GENETIC PARAMETERS FOR SOME GROWTH TRAITS OF NIGERIAN LOCAL CHICKENS

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Abstract: Genetic parameters were estimated for bodyweight (BWT), shank length (SHL), and wing length (WL) of Nigerian local chicken (NLC) from 4 to 20 weeks of age by fitting dyadic mixed model (dmm) equations which yield estimates of variance components equivalent to minimum norm quadratic unbiased estimator (MINQUE). Data obtained from 600 chicks, progenies of 300 hens and 30 cocks were used for the analysis. The heritability estimates range from 0.08 to 0.80 for BWT, 0.03 to 0.69 for SHL and 0.22 to 0.47 for WL. The genetic correlations among BWT, SHL and WL at different ages were high and positive and range from 0.18 to 0.96 with the exemption of SHL and WL at 16 weeks (-0.06). The phenotypic correlations were positive and range from 0.10 to 0.91. The results imply that NLC could be improved on any of the studied traits through mass selection and that improvement in one trait will result to correlated improvement in the others.

Keywords: Correlations, dyadic mix model, heritability, Nigerian local chickens.

Introduction

The population of chicken in Nigeria has been estimated at approximately 166 million (*FAOSTAT, 2007*). The local chicken constitutes about 80% of this number (*Dana et al., 2011*). The Nigerian local chicken is characterized by poor growth, small body size, small egg size and egg number which is not desirable in a competitive economy (*Ebangi and Ibe, 1994*). Despite these undesirable characteristics, the NLC still plays important role in the rural economy of Nigeria by providing meat, egg and house hold income to the rural people. Studies have shown that the local chicken in Africa exhibit high genetic variability within their populations indicating their potential for genetic improvement through selective breeding (*Osei-Amponsah et al., 2010, Dana et al., 2011*). Knowledge of genetic parameters is necessary for designing an appropriate breeding plan for genetic

improvement of NLC. Estimates of genetic parameters for growth traits in NLC have been reported by many workers. *Asuquo and Nwosu (1987)* reported average h^2 estimates of 0.35 to 0.74, 0.31 to 0.89 and 0.27 to 0.49 for bodyweight of two 3 way crosses (YA x LC x GL, YA x GL x LC) and the local crosses (LC2 x LC1 x LC1) respectively. *Ndofor-Foleng et al. (2006)* reported h^2 estimates of 0.40 and 0.37 for bodyweight of light and heavy ecotypes of NLC. *Udeh and Isikwenu (2013)* reported h^2 estimates of 0.25-0.51 and 0.24-0.40 from sire-son and dam-daughter regressions respectively for bodyweight of NLC from 8 to 20 weeks of age. *Osei-Amponsah et al. (2013)* reported average h^2 estimates of 0.54 and 0.42 for bodyweight and shank length of local chicken of Ghana. The objective of this study was to estimate heritabilities, genetic and phenotypic correlations of bodyweight, shank length and wing length of NLC using dyadic mix model analysis.

Materials and Methods

The experiment was conducted at the poultry breeding unit of the Department of Animal Science, Enugu State University of Technology Enugu, Nigeria. The foundation stock comprised 300 hens and 50 cocks of NLC. These birds were the surviving population of NLC chicks housed intensively at day old and raised to sexual maturity. At sexual maturity, the 300 hens were grouped into 30 mating groups of 1 cock to 10 hens. Each group was randomly assigned into deep litter floor pens partitioned to hold 10 hens and 1 cock. Eggs collected from each mating group were sire and dam identified. Eggs were incubated and hatched according to pedigree (sire and its group of hens) using very efficient locally made incubators. A total of 600 chicks were produced at 2 hatches. The chicks from each mating group were tagged according to sires and reared on deep litter pens. The chicks were brooded for six weeks during which they were fed with chick mash diet with 20 % cp and 2685 kcal ME/kg. They were provided with growers mash with 16 % cp and 2642 kcal ME/kg from 8-18 weeks and layer mash containing 2676 kcal ME/kg, 17 % cp and 3 % calcium from 18 weeks to end of lay. Feed and water were provided *ad libitum*. The chicks were separated into sexes at 7 weeks of age. All necessary vaccinations were administered. The bodyweight of the birds were recorded at 4 weekly interval starting from week 4. Shank length and wing length were taken using a tape as described by *Adeleke et al. (2013).* Estimates of variance components, heritability and correlations as well as their standard error were obtained by fitting dyadic mixed model (dmm) equations. DMM is an r package used for modelling pairs of observations or dyads and yields estimates that are equivalent to minimum norm quadratic unbiased estimator (MINQUE) if the fixed effect is adjusted using ordinary least square (OLS) or biased corrected maximum likelihood estimates if the fixed effect was adjusted using generalized least square (GLS). In this case the fixed effect of sex and hatch were adjusted

using OLS. Prior to the analysis, the data frame which include pedigree and parameter files was converted into a suitable format using modify data frame function (MDF) in the dmm package (*Jackson, 2016*).

Results and Discussion

The correlation between variance environmental individual (VarE(I)) and variance genetic individual additive (VarG(Ia)) was used to check if the dyadic equations have collinearity problem. As shown in Table 1, the correlation between VarE(I) and VarG(Ia) were 0.56. This shows that collinearity was not a serious problem in this analysis and that the two components of interest were well separated. It also implies that the data used for the analysis was adequate (*Jackson, 2016*).

Table 1. Correlation between VarE(I) and VarG(Ia)

	VarE(I)	VarG(Ia)
VarE(I)	1.00	0.56
VarG(Ia)	0.56	1.00

Note: VarE(I)= Variance environmental individual, VarG(Ia)= Variance genetic individual additive.

The heritability of bodyweight, shank length and wing length are presented in Table 2. The h^2 estimates were high and range from 0.50 to 0.80 for BWT and 0.52 to 0.69 for SHL. The only exemption was BWT and SHL at 4 weeks of age which had very low h^2 estimates of 0.08 and 0.03 respectively. The h^2 estimates of WL were moderate to high in magnitude and range from 0.22 to 0.47. The high h^2 estimates for BWT and SHL as well as the moderate to high h^2 estimates of WL imply that additive genetic variance made a greater contribution to the total phenotypic variance compared to environmental and gene combination variance. This implies that mass selection for any of the aforementioned trait could result to rapid improvement. Generally fitness traits such as BWT and SHL tend to have higher h^2 estimates compared to traits that are not connected to reproductive efficiency of animals. *Kinney* (*1969*) summarized the h^2 estimates of BWT, SHL and other body parameters of chicken published in literature and concluded that BWT of chicken was a highly heritable trait with h^2 range of 0.25 to 0.75. Similar observation was reported by *Adeyinka et al. (2006)*. The h^2 estimates of BWT and SHL observed in this study were in line with estimates of 0.41 (BWT) and 0.58 (SHL) reported for the local chicken at 12 weeks by *Ebangi and Ibe (1994)*. *Adeleke et al. (2011)* reported h^2 range of 0.15 to 0.29 for WL of pure and crossbred progenies of NIC which was less than the range of 0.22 to 0.47 observed in this study. In a recent study, *Rotimi et al. (2016)* estimated h^2 of BWT of three genotypes of NLC at 0-16 weeks from sire component of variance that range from 0.17 to 0.65 which was within the range reported in this study. *Osei-Amponsah et*

al. (2013) reported an average h^2 estimate of 0.54 for bodyweight of Ghanaian local chicken from 0 to 40 weeks which fall within the range reported in this study. Differences in h^2 estimates reported by different researchers could be attributed to method of estimation, breed, environmental effects and sampling error due to sample size (*Prado-Gonzalez et al., 2003*). The genetic correlations among BWT, SHL and WL were high and positive and range from 0.18 to 0.96. The only exemption was SHL and WL at 16 weeks of age with a genetic correlation of -0.06. This indicates pleiotrophic action of genes governing the three traits and implies that selection of any of the three traits will give positive correlated response to the other traits. *Ebangi and Ibe (1994)* reported genetic correlation between growth traits that range from 0.99 to 1.51 which is higher than the range observed in this study. Similarly, *Adeleke et al. (2011)* reported genetic correlation among growth traits in pure and crossbred progenies of NIC that range from 0.43 to 0.99 which was slightly higher than the range reported in this study. The phenotypic correlations among BWT, SHL and WL were positive and range from 0.10 to 0.91 implying high predictability among the three variables. Similar results were reported by *Momoh and Kershima (2008)* and *Ukwu et al. (2014)* in Nigerian local chickens.

Table 2. Heritabilities and genetic and phenotypic correlations of bodyweight, shank length and wing length of Nigerian local chickens at 4, 8, 12, 16 and 20 weeks of age.

Weeks	Bodyweight	Shank length	Wing length
4			
Bodyweight	**0.08(0.11)**	0.57(0.09)	0.10(0.09)
Shank length	0.36(0.35)	**0.03(0.11)**	0.42(0.07
Wing length	0.37(0.40)	0.56(0.34)	**0.31(0.08)**
8			
Bodyweight	**0.67(0.15)**	0.91(0.03)	0.86(0.03)
Shank length	0.94(0.05)	**0.69(0.15)**	0.80(0.04)
Wing length	0.96(0.05)	0.91(0.07)	**0.31(0.09)**
12			
Bodyweight	**0.80(0.17)**	0.79(0.05)	0.75(0.06)
Shank length	0.93(0.07)	**0.52(0.13)**	0.43(0.08)
Wing length	0.92(0.09)	0.74(0.13)	**0.47(0.11)**
16			
Bodyweight	**0.52(0.15)**	0.39(0.09)	0.41(0.10)
Shank length	0.56(0.15)	**0.59(0.10)**	0.21(0.10)
Wing length	0.18(0.24)	-0.06(0.07)	**0.22(0.10)**
20			
Bodyweight	**0.50(0.17)**	0.72(0.07)	0.59(0.08)
Shank length	0.83(0.11)	**0.57(0.13)**	0.73(0.05)
Wing length	0.53(0.16)	0.31(0.08)	**0.45(0.12)**

Heritabilities in bold, genetic correlations on lower diagonal and phenotypic correlations on upper diagonal. Standard errors are in parentheses.

Conclusion

From the high h^2 estimates for BWT and SHL at 8-20 weeks of age and the moderate to high h^2 estimates for WL from 4 to 20 weeks of age, it is inferred that these traits could be improved through mass selection. The high genetic correlations among the traits suggest that improvement in one trait will give correlated improvement in the others.

Genetski parametri za neke osobine porasta nigerijskih lokalnih rasa pilića

I. Udeh

Rezime

Genetski parametri su određivani za osobine telesne mase (BWT), dužinu tarzusa (SHL), kao i dužinu krila (WL) Nigerijskih lokalnih pilića (NLC) od 4 do 20 nedelje starosti postavljanjem jednačine diadičnog mešovitog modela (dmm) koji daju procenu varijanse komponenti ekvivalentne jednačini mešovitog modela MINQUE (Minimum Norm Quadratic Unbiased Estimator - MINQUE). Podaci dobijeni za 600 pilića, potomaka 300 kokošaka i 30 petlića, su korišćeni u analizi. Procene heritabilnosti su u rasponu od 0,08 do 0,80 za BWT, od 0,03 do 0,69 za SHL i 0,22 do 0,47 za WL. Genetske korelacije između BWT, SHL i WL u različitim uzrastima su bile visoke i pozitivne, i kreću se od 0,18 do 0,96 izuzimajući SHL i WL u 16. nedelji (-0,06). Fenotipske korelacije su bile pozitivne i kretale su se u rasponu od 0,10 do 0,91. Rezultati ukazuju da bi NLC mogle da budu poboljšane u pogledu bilo kojeg od ispitivanih svojstava, kroz selekciju i da će poboljšanje u jednoj osobini dovesti do korelativnog poboljšanja ostalih.

Ključne reči: korelacije, dijadički mešoviti model, heritabilitet, nigerijske lokalne rase pilića

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