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Heritabilities and Correlations Between Body Weights and Growth Curve Parameters of Indigenous Chicken Populations Reared Intensively in Kenya

[1, 5, 6]K. Ngeno, [1, 2]T.M. Magothe, [1, 3]T.O. Okeno, [4]B.O. Bebe and [1]A.K. Kahi
[1]Animal Breeding and Genetics Group, Department of Animal Sciences,
Egerton University, P.O. Box 536, 20115 Egerton, Kenya
[2]Livestock Recording Centre, Ministry of Livestock Development,
P.O. Box 257, 20117 Naivasha, Kenya
[3]Department of Molecular Biology and Genetics,
Centre for Quantitative Genetics and Genomics, Aarhus University, 8830 Tjele, Denmark
[4]Livestock Production Systems Group, Department of Animal Science,
Egerton University, P.O. Box 536, 20115 Egerton, Kenya
[5]Animal Breeding and Genomics Centre, Wageningen University, P.O. Box 338, 6700 AH,
Wageningen, The Netherlands
[6]Animal Breeding and Genetics Group, Department of Animal Sciences,
Pwani University, P.O. Box 195-80108, Kilifi, Kenya

Abstract: The objective of this study was to estimate heritabilities and genetic and phenotypic correlations among and between Body Weights (BW) to 20 weeks of age and growth curve parameters (asymptotic weight, A, scaling parameter, b and maturity index, k of Indigenous Chicken (IC) populations in Kenya. The growth parameters was estimated using the Gompertz Model and a sire model was used to estimate (co) variance components for BW at specific ages and growth curve parameters (A, b and k). The heritability estimates were low for the BW at hatch (BW_0, 0.170), moderate for BW in week 20 (BW_{20}, 0.280) and high for the BW in week 8 (BW_8, 0.560). The high heritability estimate for BW_8 indicates that genetic variability for BW seems to be high enough for selection. Thus, the use of BW_8 as selection criterion would seem more efficient than the use of bodyweight at other ages. The heritability estimates were low for b (0.050) and moderate for A (0.260) and k (0.290). The moderate heritability estimates for A and k indicate the growth curve parameters could be applied to change the shape of the growth curve through selection. The correlations between mature weight and maturation rate were negative indicating that if selection is used to increase asymptotic weight then there will be negative indirect selection on maturation rate.

Key words: Growth curve parameters, Gompertz Model, indigenous chicken, heritability, Kenya

INTRODUCTION

The unimproved Indigenous Chicken (IC) remains predominant in African villages despite the introduction of commercial hybrids and crossbreeding of these with IC (Adetayo and Babafunso, 2001). The objective for introduction of crossbreeding was to improve genetic potential of IC for meat and egg production through growth traits such as live weights, sexual maturity (Gueye, 1998), daily weight gains and feed use efficiency (Merritt, 1974). Although, crossbreeding programmes with specialized meat type or egg type chicken have shown to improve IC productivity significantly (Pedersen, 2002; Segura-Correa *et al*., 2004), it has been unsuccessful due to considerable adaptation problems with resulting mortalities of 50% or more (FAO, 2004). The use of exotic birds led to loss in hatching ability in the flock and therefore a breakdown of the self-sustaining system of production at the scavenging production systems level (Tadelle *et al*., 1999). Crossbreeding is also threatened by the current global move on conservation of indigenous genetic resources (Kosgey, 2004). This has necessitated a need to look for an alternative approach for genetic improvement of IC. One of the approaches for genetic improvement is to involve quantitative knowledge through selection within the IC ecotypes (Lwelamira *et al*., 2008).

The knowledge on growth processes measured in body mass change overtime is important to improve meat production of IC. Growth curve models provide a visual

Corresponding Author: K. Ngeno, Department of Animal Sciences, Pwani University, P.O. Box 195-80108, Kilifi, Kenya

assessment of growth as a function of time and prediction of Body Weight (BW) at a specific age. There are several growth models for estimating growth curve parameters in chicken by fitting longitudinal experimental data. Of these models, the most often used which yields mathematical growth parameters that have biological meaning are nonlinear functions including Logistic, Gompertz, Brody and Von-Bertalanffy Models (Fitzhugh, 1976; Karkach, 2006). The growth parameters such as the initial BW, the mature BW, the rate of maturing and daily gain are important fragmentary aspects of each growing point and can describe the shape of a growth curve correlations among them (Fitzhugh, 1976; Tsukahara *et al*., 2008). Estimation of growth parameters of IC provides biological information useful for predicting growth rates, feed requirements and responses to selection.

Selection as a basic tool in animal breeding requires that measurable characters be used to improve targeted traits. However, traits targeted for improvement must be heritable, variable and phenotypically or genetically correlated with the chosen characters (Rewe, 2004). The IC have lived and produced for several years in diverse environments but without directional selection, so largely under natural selection which has enhanced their adoption to local environments and may be carrying genes valuable for future poultry industry (Momoh and Nwosu, 2008). Lwelamira (2007) revealed that local chicken ecotypes have significant additive genetic variation in traits which can be a good starting genetic material for improving meat and egg production.

Estimation of heritabilities of and genetic and phenotypic correlations between growth curve parameters will provide sound biological basis for designing genetic interventions targeted at improving productivity, efficiency and capability of whole growth process (Lambe *et al*., 2006). These estimates are of paramount importance for the definition of breeding objectives and the development of breeding programmes. Lack of information on genetic variance components and genetic parameters limits genetic improvement since knowledge of these is crucial for accurate estimation of breeding values, optimum combination of traits in a selection programme, optimization of breeding schemes and enhanced prediction of response to selection (Prado-Gonzalez *et al*., 2003; Adeogun and Adeoye, 2004; Norris *et al*., 2004).

Indigenous chickens have not been subjected to intensive artificial selection programmes and therefore the foundation flocks established through collection of eggs from unselected, random mating population of IC from the rural farmers should exhibit high genetic variation (Iraqi *et al*., 2002). This offers great potential for genetic improvement of this population (Norris and Ngambi, 2006). Such differences among IC populations give the chance to choose the best parental lines for practical IC breeding, develop breeding strategies by modifying either management practices or genetic make-up of the shape of growth curves and developing a commercial stock through selection and/or crossing programs within the IC populations. Information on genetic and phenotypic parameters of growth curve variable is scarce. Even in cases of limited information, attempts at estimating genetic and phenotypic parameters are better than no attempt at all.

The objective of this study was to estimate heritabilities of and genetic and phenotypic correlations among and between BW to 20 weeks of age and growth curve parameters (asymptotic weight, A, scaling parameter, b and maturity index, k) estimated using the Gompertz Model. Earlier analyses of data from the parental generation showed that the Gompertz Model fitted the data well (Ngeno, 2011).

MATERIALS AND METHODS

Data source: Growth data were obtained from an experimental flock of IC population kept for breeding and nutrition research purposes at Naivasha National Animal Husbandry Research Centre of the Kenya Agricultural Research Institute. Initially the flocks were established through collection of eggs from unselected, random mating population of IC from the rural farmers. Eggs were collected from Kakamega, Bondo, Narok and Bomet regions which were chosen because there has been minimum indigenous chicken genes dilution in the regions. Five hundred eggs were collected from each area and each of the area represents an ecotype sample. Therefore, in this study, four ecotypes were included namely Kakamega (KE), Bondo (OE), Narok (NE) and Bomet (BE) ecotypes. Data from the parent generation have already been analyzed to compare live BW of IC ecotypes at different ages from 0-34 weeks of age and model the growth curves using four growth models (Ngeno, 2011).

Management of experimental birds: Twenty six cocks were randomly sampled from the progeny generation and each allocated between 5 and 10 unrelated hens and housed together in deep litter pens to produce the study population. Eggs were collected daily, labelled to identify an individual egg and its cock family and stored at room temperature for at most 14 days before incubation. The eggs were first-candled on the 7th day of incubation. After the 2nd candling on the 18th day of incubation, each egg was placed into an individual compartment for hatching. Eggs were simultaneously incubated but separated according to ecotype within incubator. At hatching, each chick was weighed (hatching weight-BW_0) and wing tagged with an identification number. Brooding was from hatching (day old) to 6 weeks. Brooding of chicks from each ecotype was separated in deep litter brooders using infra-red electric bulbs. The population density was 12 birds/m^2. At the beginning of the 7th week, chicks were transferred to randomly selected deep litter rearing pens within the same house. Sex was determined by phenotypic appearance. The birds were fed *ad libitum* commercial formulated feeds for hybrids on a starter diet from 0-6 weeks of age, a growing diet from 7-20th weeks and a laying diet thereafter. These were commercial formulated feeds for hybrids. Clean water was provided daily *ad libitum*. Disinfection of brooding and rearing pens were done procedurally. All birds were vaccinated against marek's, gumboro, fowl typhoid, newcastle and infectious bronchitis as per recommendations of the veterinarian. Any other incidence of disease condition was treated promptly by resident veterinarian.

Data collection and analyses: Age-weight data was collected bi-weekly for each bird until 20 weeks of age. A total of 9,292 body weight records from 404 birds (160 BE, 166 KE, 41 OE and 37 NE) produced from 3 hatchings were available. These were progeny of 26 sires and 178 dams. The PROC GLM of SAS (1998) was used for the analysis of the biweekly BW from hatch (BW_0) to 20 weeks of age (BW_{20}). The model fitted was:

$$Y_{ijkl} = \mu + H_i + E_j + S_k + ES_{jk} + e_{ijkl} \qquad (1)$$

Where:

Y_{ijkl} = BW of the lth bird at a particular age

μ = Overall mean

H_i = Fixed effect of ith hatch (i = 1, 2, 3 batches)

E_j = Fixed effect of jth ecotype (KE, OE, NE and BE)

S_k = Fixed effect of kth sex (k = male, female)

Es_{jk} = Interaction between ecotype and sex

e_{ijkl} = Error term associated with each BW at a particular age

In the analysis of BW at hatch, egg weight was fitted as a covariate while in all other ages; BW_0 was fitted as a covariate. The least squares means were separated using the probability differences option. Gompertz Growth Curve Model was fitted to the longitudinal growth data set for each individual birdusing PROC NLIN of SAS (1998) to obtain growth curve parameters (A, b and k) using a nonlinear procedure by the Gauss-Newton Method. The equations for the Gompertz Model (Fitzhugh, 1976) fitted was:

$$\text{Gompertz}: yt = Ae^{-be^{-kt}} \qquad (2)$$

Where:

yt = Size y, at age t

t = Age in weeks

A = Asymptotic size

b = Scaling parameter

k = Maturing index

The PROC GLM of SAS (1998) was used for the analysis of growth curve parameters using Eq. 1. A sire model was used to estimate (co) variance components for BW at specific ages and growth curve parameters (A, b and k) from the Gompertz Growth Curve Model using the DFREML program (Meyer, 1997). In matrix notation the sire model was written as:

$$y = Xb + Zg + e \qquad (3)$$

Where:

y = Observation vector

X = Incidence-matrix indicating for each observation, the fixed effects

b = A vector with fixed effects

Z = Incidence-matrix indicating for each observation the random effects of sire

g = Vector with random effects

e = Vector with error terms

The (co) variance components were estimated assuming that the data were from a single population but adjusting for the effect of ecotype. This was necessary because of the limited data size for each ecotype. Therefore, the fixed effects and covariate were similar to those fitted in Eq. 1 for each biweekly BW and growth curve parameters.

Both univariate and bivariate analyses were performed to estimate heritabilities and genetic and phenotypic correlations among and between the growth curve parameters and weight at hatch (BW_0), 8 weeks (BW_8) and 20 weeks (BW_{20}) of age. Heritability, genetic or phenotypic correlations were calculated from variance and covariance components. Heritability estimates (h^2) were derived from:

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

where, σ^2_s and σ^2_e were the sire and residual variances, respectively. The genetic correlations (r_g) were estimated as:

$$r_{g\,(A,\,B)} = \frac{\sigma_{s\,(A,\,B)}}{\sqrt{\sigma^2_{y(A)} \times \sigma^2_{y(B)}}}$$

Where:

$r_{g(A, B)})$ = The genetic correlation between trait A and B
$\sigma_{s(A, B)}$ = The sire covariance between trait A and B
$\sigma_{y(A)}^2$ = The sire variances of trait A and B, respectively

The phenotypic correlations (r_p) were estimated as:

$$r_{p\,(A,\,B)} = \frac{\sigma_{s\,(A,\,B)}}{\sqrt{\sigma^2_{y(A)} \times \sigma^2_{y(B)}}}$$

Where:

$r_{p(A, B)}$ = The phenotypic correlation between trait A and B
$\sigma_{s(A, B)}$ = The sire covariance between trait A and B
$\sigma_{y(A)}^2$ and $\sigma_{y(B)}^2$ = The phenotypic variances of trait A and B, respectively

This study adjusted for the effect of ecotype in the estimation of genetic and phenotypic parameters. Magothe *et al.* (2010) estimated genetic parameter for egg and BW of IC in Kenya using data from a mixed population of IC collected from different regions of Kenya. In that study, the effect of ecotype was not adjusted for. Significant different between ecotypes has been reported in Tanzania (Msoffe *et al.*, 2001), Ethiopia (Dessie and Ogle, 2001), Zimbabwe (Mcainsh *et al.*, 2004), Bangladesh (Bhuiyan *et al.*, 2005), Botswana (Badubi *et al.*, 2006) and Kenya (Ngeno, 2011). These literatures have demonstrated presence of several ecotypes, breeds and strains of IC that are well adapted to specific environmental conditions.

The sire model was used in this study. In this model, only the genetic effect of the sire was taken into account. Genetic evaluation methods have moved to the use of animal models to account for genetic effects of sires and dams. The sire model assumes that all sires are mated to an average group of dams and that all dams are unrelated. In this study, the dams were average dams and were all unrelated. However, this will change as the programme progresses since animals may have more genetic covariances than only through their sires. This will require the use of an animal model to include the genetic relationships between all animals and account for selection.

Although, the data in this study was longitudinal, random regression models based on covariance functions methodology were not used in the analysis of BW because of the high imbalance in the data structure arising from the small population size. However, random regression models should be exploited as recording infrastructures improves and more records on IC ecotype become available.

RESULTS AND DISCUSSION

Performance of ecotypes and parameter estimation: The least squares means and standard errors of Body Weight (BW) for the different ecotypes are presented in Table 1. The mean hatching weights were significantly different ($p<0.05$), KE and OE chicks being heavier compared to BE and NE chicks. These differences were maintained to week 18 which is consistent with findings in Ethiopia of Tadelle *et al.* (2003). There are usually a large number of genes involved in growth which results in differences in BW. Le-Rouzic *et al.* (2008) demonstrated that avian growth involves large numbers of genes with some being activated or deactivated at different stages of development depending on the genetic background of the birds. The observed average BW at 20 weeks was heaviest for OE though not different ($p\geq 0.05$) from KE, NE and BE. The growth of all species after age at the inflection point is generally found to be comparable (Knizetova *et al.*, 1995) which was consistent with results of the study.

Table 1: Least square means for observed live body weights of IC ecotypes at different ages from 0-20 weeks

	Ecotypes^b				
Bw_t^a traits	BE	KE	OE	NE	Overall
BW_0	0.032±0.000^a	0.033±0.000^a	0.033±0.0000^a	0.032±0.000^a	0.034±0.000
BW_2	0.089±0.001^a	0.093±0.001^b	0.093±0.0020^b	0.091±0.002^a	0.092±0.002
BW_4	0.268±0.004^a	0.243±0.004^b	0.250 ±0.008^b	0.221±0.009^c	0.246±0.006
BW_6	0.362±0.005^a	0.373±0.005^b	0.379±0.0100^b	0.345±0.011^c	0.368±0.007
BW_8	0.489±0.007^a	0.591±0.007^b	0.524±0.0150^b	0.460±0.016^d	0.516±0.011
BW_{10}	0.606±0.010^a	0.828±0.010^b	0.872±0.0210^b	0.554±0.023^d	0.673±0.016
BW_{12}	0.751±0.013^a	0.941±0.013^b	0.979±0.0260^b	0.738±0.028^a	0.835±0.020
BW_{14}	0.885±0.015^a	1.07±0.0150^b	1.04±0.03000^b	0.863±0.032^a	0.963±0.023
BW_{16}	1.02±0.0170^a	1.15±0.0170^b	1.15±0.03400^b	1.01±0.0370^a	1.108±0.026
BW_{18}	1.13±0.0170^a	1.26±0.0170^b	1.29±0.03500^b	1.17±0.0380^a	1.236±0.027
BW_{20}	1.26±0.0190^a	1.39±0.0190^a	1.39±0.03800^a	1.23±0.0410^a	1.365±0.029

^{a}BW_t = Live Body Weight (kg) at age t in weeks; ^{b}BE = Bomet Ecotype; KE = Kakamega Ecotype; OE = Bondo Ecotype; NE = Narok Ecotype; ^{a}Means in a row with one or more letter superscripts in common are not significantly different ($p\geq 0.05$)

The overall mean BW at all ages for example BW_0 (0.034 kg), BW_8 (0.516 kg) and BW_{20} (1.37 kg) were lower than reported for the parental generation in an earlier study (Ngeno, 2011). The depressed BW may be due to diurnal ambient temperature variations and changes in the management regime which shifted to a rather low input system. Fluctuations in growth performance as a result of temperature variations with limited management interventions are common (Al-Atiyat, 2009; Tadelle *et al*., 2003). The growth performances of ecotypes studied underlined the differences between ecotypes with some remarkably higher growth performance levels (KE and OE) than other ecotypes (BE and NE) which is in agreement with Ngeno (2011). The difference in performance may be attributed to difference in Feed Conversion Efficiency (FCE) with heavier ecotypes having higher FCE and perhaps due to smaller maintenance requirements (Tadelle *et al*., 2003).

Table 2 presents the least squares means of growth curve parameters and R^2 by ecotype. The R^2 were high (R^2>0.89) demonstrating the adequacy of the model in fitting and describing the growth data well. The BE was significantly different from the other ecotypes for A. The k and b were similar for all ecotypes. The BW estimated in this study was lower than estimated using data from the parental population (Ngeno, 2011). The underestimation observed may be a result of the fact that only one part of the growth curve is being observed (Lambe *et al*., 2006) and there are no measurements in the data set reflecting growth after 20 weeks of age. An earlier study on growth of mice up to full maturity and throughout their lifetime showed that if the growth curves were based on data from early growth periods they underestimated considerably the mature BW (Bunger and Schonfelder, 1984). Therefore, the estimated A values should not be considered as predictors of true mature BW but as final BW value (Lambe *et al*., 2006). The Gompertz curve inflection point occurs at 0.370A (Fitzhugh, 1976; Karkach, 2006).

Table 2: The least squares means of growth curve parameters and R^2 by ecotype Compertz Model

		Parameters^b			
Ecotype^a	Observed BW_{20}	A	b	k	R^2
BE	1.26±0.019	1.72±0.047^a	1.16±0.020^a	0.11±0.004^a	0.908
KE	1.39±0.019	1.75±0.036^b	1.27±0.050^a	0.14±0.010^a	0.897
OE	1.39±0.038	1.74±0.042^b	1.27±0.050^a	0.14±0.010^a	0.893
NE	1.23±0.041	2.19±0.053^c	1.24±0.030^a	0.09±0.009^a	0.899

^{a}BE = Bomet Ecotype; KE = Kakamega Ecotype; OE = Bondo Ecotype; NE = Narok Ecotype; ^{b}A = Asymptotic size body weight (kg); b = Scaling parameter; k = Maturity index; $^{a-c}$Means in a column with one or more letter superscripts in common are not significantly different ($p \geq 0.05$)

The differences between breeds and lines in the shape of the growth curve suggest that selection for BW may alter the growth pattern (Marks, 1978; Tzeng and Becker, 1981; Zelenka *et al*., 1986). Age at selection may contribute to the timing and magnitude of the growth response observed and this should be done between hatch and 18th week of age for the IC ecotype. Most differences in the shape of the growth curve among chickens occurred between hatching and the point of inflection (Anthony *et al*., 1991). Barbato (1992) reported that selection for high growth rate immediately after hatching (0-14 days of age) did not change the BW at maturity while selection for high BW, at or near the age of the inflection point of the growth curve resulted in increased adult BW.

The modeling of growth curves is a useful tool for the derivation of space and food requirements at different ages (Kohn *et al*., 2007). Forni *et al*. (2007) revealed that the knowledge of the growth curve in poultry science is very useful for setting commercial strains bases, defining ages and/or weights for selection and setting management procedures. Additionally, the functions allow for the study of differences between the lines that have diverse genetic background (Sezer and Tarhan (2005). Early predictors of adult BW are of particular interest in designing breeding programs (Meyer, 1995). The growth curve parameters in this study will provide an opportunity to develop breeding strategies by modifying either management practices or genetic makeup of the shape of growth curves. Mature BW, predicted by parameter A of the growth curves could be included in selection programmes.

Estimates of heritability: Table 3 presents the heritability estimates of and genetic and phenotypic correlations between and among BW and growth curve parameters

Table 3: Heritability estimates of (along diagonal) and genetic (above diagonal) and phenotypic (below diagonal) correlations between and among body weights and growth curve parameters^a

Parameters	A	b	k	BW_0	BW_8	BW_{20}
A	0.260±0.15	0.336±0.27	-0.833±0.290	0.927±0.330	0.920±0.560	0.927±0.42
b	0.080	0.050±0.15	0.924±0.240	-0.137±0.110	0.571±0.280	0.672±0.30
k	-0.399	0.382	0.290±0.16	-0.104±0.170	0.963±0.360	-0.241±0.39
BW_0	0.472	-0.046	-0.034	0.170±0.23	0.540±0.410	0.927±0.39
BW_8	0.290	0.188	0.313	0.160	0.560±0.23	0.940±0.38
BW_{20}	0.578	0.296	-0.060	0.414	0.520	0.280±0.18

^{a}A = Asymptotic size body weight (kg); b = Scaling parameter; k = Maturity index; BW_0 = Hatch weight; BW_8 = Body Weight in the 8th week; BW_{20} = Body Weight in the 20th week

(A, b and k). The heritability estimates were low for BW_0 (0.170), moderate for BW_{20} (0.280) and high for BW_8 (0.560). The low heritability estimate at hatch could mean that dominance, epistatic and environmental effects are more important than the genetic additive effects on BW at hatch (Adeyinka *et al.*, 2006). The high heritability estimate for BW_8 indicates that genetic variability for BW seems to be high enough for selection. The high heritability indicates that response to selection at the 8th week could be rapid and will improve BW in the subsequent generations. The high heritability estimate at 8 weeks of age also indicated a potential to select for a meat type bird in IC population in Kenya because the 8th week is the broiler marketing age. Mignon-Grasteau *et al.* (2000) established that selection on BW_8 modified the whole growth curve as all the parameters describing the growth curve evolved with selection. The moderate heritability estimate for BW_{20} was in harmony with the value reported by Udeh and Omeje (2004) for the Nigerian heavy ecotype. This could mean that there is potential to select for egg production because the 20th week is the layer age (Momoh and Nwosu, 2008).

Chambers (1990) and Norris and Ngambi (2006) reported that heritability for BW of chicken tends to increase with age. However, Adeyinka *et al.* (2006) and Saatci *et al.* (2006) established decreasing heritability of BW with age. In this study, the heritability estimates consistently increased to 8 weeks of age and then decreased. A similar trend was reported by Magothe *et al.* (2010). The age to age variations in the heritability estimates of BW are indicative of differences in genetic background and changes in the contributions of environmental deviation components of total variation in BW (Momoh and Nwosu, 2008).

The heritability estimates were low for b (0.050±0.15) and moderate for A (0.260±0.15) and k (0.290±0.16) (Table 3). The heritability estimates for A, b and k were lower than reported by Mignon-Grasteau *et al.* (1999, 2000). Heritability estimate for A was lower than the value of 0.325 reported for the Scottish blackface sheep (Lambe *et al.*, 2006). The moderate heritability estimate for A indicated that some genetic gain through selection could be achieved, consistent with the findings for partridges (Tholon *et al.*, 2006). Parameter A can be used as a selection criterion to fix adult weight when selecting for growth rate (Forni *et al.*, 2007). Selection modifies the growth curve, as all the parameters describing the growth curve evolved with selection (Mignon-Grasteau *et al.*, 2000).

The heritability estimate for k was similar to that reported for Rhode Island Red (0.250) and lower than for White Leghorn birds (0.620) (Grossman *et al.*, 1985). Parameter k is a function of the ratio of maximum growth rate to mature size (Fitzhugh, 1976) and could be used in selection programmes as a selection criterion indicating the rate of approach to mature BW (Forni *et al.*, 2007). Taylor and Young (1966) have related k to intrinsic efficiency of growth. The moderate additive genetic variance of k in the study proved that its inclusion in selection programs would be effective. The low heritability estimate for b is inconsequential. Parameter b is related to the initial conditions of the growth curve but since BW_0 is usually available, BW_0 can be used in selection programmes without the need for estimates of parameter b and hence has no biological meaning (Tholon *et al.*, 2006; Forni *et al.*, 2007). Brody (1945) employed the scaling parameter to adjust the age scale.

Genetic and phenotypic correlations: The genetic correlations estimates presented in Table 3 for BW were highly positive (0.540-0.940). Correlations among different measures of size for the same individual at the same or different ages tend to be quite high (Taylor and Craig 1965; Brown *et al.*, 1973; Lobo *et al.*, 2000; Albuquerque and Meyer, 2001). Therefore, the size parameter may be taken as generally indicative of body size. Body size is an exceedingly important trait given the reported relationships with a diverse range of traits including growth rate, maintenance requirements, optimal slaughter weights and economic efficiency (Long *et al.*, 1975). Lobo *et al.* (2000) and Albuquerque and Meyer (2001) disclosed that the BW at different ages are highly and positively genetically correlated and an increase in mature BW can be expected increasing the costs of maintaining a parent population.

The genetic correlation between A and k was high (-0.830) whereas their phenotypic correlation was low (-0.020). Comparisons between species (Brody, 1945) and within species (Taylor and Fitzhugh, 1971; Brown *et al.*, 1972) confirm the general negative genetic relationship between mature size and earliness of maturing. Negative correlation between A and k has been reported from analyses of data from Australian beef cows (Meyer, 1995) and sheep (Lewis and Brotherstone, 2002). The genetic correlation estimates between A and k (-0.830) was higher than reported for layer chickens (-0.590) (Lopez and Quaas, 1997) and partridges (-0.600) (Tholon *et al.*, 2006).

The negative correlations between mature weight and maturation rate observed in this study indicated that if selection is used to increase asymptotic weight then there will be negative indirect selection on maturation rate and k will be slowing down. The high negative correlation also indicated that IC that grow faster do not attain a large mature weight compared to those that mature more slowly in early life. Mignon-Grasteau *et al.* (2000) has explained the negative correlation between A and k to be related to a rapid decrease in growth rate after inflection resulting in a lower asymptotic BW. On the other hand, faster-maturing animals, probably associated with a lighter mature weight would be more efficient and producing more offspring during their productive lives (Lopez de Torre *et al.*, 1992).

Generally, a high k is associated with fast early growth, low age and size at maturity (Karkach, 2006). Koivula *et al.* (2008) noted that the components of growth are likely innately in balance and it is biologically impossible that maturation rate would increase infinitely in relation to mature weight. Therefore, these values indicated that selection could be applied to change the shape of the growth curve and improved growth rate would result in lighter adult birds. Selection for growth has a correlated response on adult BW in different species (Archer *et al.*, 1998; Mignon-Gasteau *et al.*, 2000; Piles *et al.*, 2003). Selection for size or closely correlated traits will increase the time taken to maturity. It is this negative relationship between the size and earliness of maturing which largely determines shape of the curve (Taylor and Fitzhugh, 1971). The genetic correlation between b and k was positive and high (0.920). The genetic correlation between parameters b and k was too large. Regardless of that the relationship between the initial conditions and subsequent growth is explained well by the large and positive genetic correlations between early BW (Forni *et al.*, 2007). The genetic correlation between A and b was moderate (-0.340). Usually, lighter preweaning and weaning weight tend to result in lighter weight at maturity. Thus, IC ecotypes with a higher asymptotic weight have a higher birth weight.

Genetic correlation between the A and BW were positive and high while phenotypic correlation were positively moderate to high demonstrating that birds with high A had high BW_0. Akbas and Yaylak (2000) and Narinc *et al.* (2010) reported the highest correlation between parameter A and final weight. These highest correlations show that the parameter A is a reflector of the final weight (Akbas and Oguz, 1998; Akbas and Yaylak, 2000; Narinc *et al.*, 2010). Genetic correlations between k and BW_0 and BW_{20} were -0.100 and -0.240, respectively (Table 3). These negative genetic correlations indicated that selection for improved BW will result in indirect selection for growth rate. Selection for k in IC would be expected to decrease BW at various ages.

Genetic correlations were negative between b and BW_0 and positive between b and BW_8 and BW_{20} (Table 3). The negative genetic correlations between b and BW_0 found in IC ecotypes population could be attributed to the great influence of the maternal effect. The phenotypic correlation between b and BW_0 was negative and low, low and positive for BW_8 and moderate for BW_{20}. Both the genetic and phenotypic correlation between k and BW_8 were positive demonstrating that birds which had high maturing rate were also heavier at week 8. The correlations between b and live weights at younger ages show that the parameter b is a reflection of initial weight (Akbas and Oguz, 1998; Akbas and Yaylak, 2000).

CONCLUSION

The study revealed that body weight of indigenous chicken can be improved through selection. High heritability estimate for body weight in week 8 indicated that the use of this trait as selection criterion would seem more efficient than the use of body weight at other ages. The heritability estimates of the asymptotic weight and the maturity index are of sufficient magnitude to be applied to change the shape of the growth curve through selection. These parameters will provide an opportunity to develop breeding strategies by modifying either management practices or genetic makeup of the shape of growth curves. The negative correlations between mature weight and maturation rate observed indicated that if selection is used to increase asymptotic weight then there will be negative indirect selection on maturation rate. The estimates of heritabilities of and correlation (genetic and phenotypic) among and between body weight to 20 weeks of age and growth curve parameters presented in this study are important as initial estimates but would later be updated as more data are collected and analysed once the breeding programme is in place.

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