



Comparative evaluation of first derivatives of growth models among indigenous and locally adapted exotic chickens

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Abstract

Weekly body weight of 993 offspring generated from direct crossing of indigenous chickens (Naked Neck-NN, Frizzle Feather-FF and Normal Feather-NF), locally adapted exotic (Nera Black-NB, White Leghorn-WL and Giriraja-GR) and crossbred chickens (FUNAAB Alpha-BA) were used to compute the absolute growth rate (AGR), absolute maturing rate (AMR) and relative growth rate (RGR) on the Logistic (L), the Gompertz (G), the Richards (R) and the Bertalanffy (B) growth function. The growth parameters A , B , k and m obtained from the growth function were used on their first derivatives to compute the AGR, AMR and RGR for the genotypes. In all the growth functions, GR was significantly better than other genotypes with respect to AGR. However, FF was significantly higher in AMR and RGR. The study showed that the indigenous genotypes were able to record better RGR than other genotypes through optimal protein deposition relative to initial weight, though the curve may not be as steep as that of tropically adapted exotic genotypes.

INTRODUCTION

Efficiency of body-weight growth in poultry depends on the understanding of how genetic and environmental elements can be used to manipulate attributes, such as average lifetime instantaneous growth rate, relative growth rate and maturing independently of mature weight thereby altering the shape of the growth curve because growth performance in poultry production is a blend of both the genetic and environmental elements. Perotto *et al.* (1992) and Demunar *et al.* (2017) reported

that among the statistical procedures available for analyzing growth data, is the fitting of nonlinear functions which offers an opportunity to summarize the information contained in the entire sequence of weight-age points into a small set of parameters that can be interpreted biologically and used to derive other relevant growth traits. Furthermore, nonlinear functions have been used extensively to represent changes in sizes with age, so that the genetic potentials of animals for growth can be evaluated (Ozoje

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et al., 2007). This shows that the growth performances of any animals recorded repeatedly during their lifetime are typical longitudinal data where the traits of interest are changing gradually but continually, overtime. This come to say that an appropriate growth function therefore, summarizes the information provided by observation on an animal and mathematically expresses its lifetime growth course (Kratochvilova et al., 2002).

The knowledge of average lifetime absolute growth rate (AGR), absolute maturing rate (AMR) and relative growth rate (RGR) in poultry production facilitates decision making on management practices with respect to feeding regime, nutritional requirement and environmental modification for optimal performance. Given the AGR, the RGR is larger in magnitude if the initial value is at a lower level than if it is higher because AGR is the measurement and comparison of total growth per unit time while the RGR is the growth of the animal per unit time expressed on a common basis. Absolute growth rate represents a linear body-weight difference given in quantity ($W_2 - W_1$) between predetermined two inferential points (t_1 and t_2) on a time scale while RGR is a measure of percentage growth which gives an insight into the exponential pattern of the growth rate. Absolute maturing rate gives the variance in growth potential of the animal at different stages of the growing phase. The differences between functions, with respects to AGR and AMR, reflect differences in rate of growth and maturing throughout the growing and maturing interval (Perotto et al., 1992). These parameters complement each other in helping the farmers understand the extent to which a growth indicator has changed over

time in achieving optimal profit.

Thus the present study was aimed at comparing chicken genotypes on AGR, AMR and RGR calculated from growth parameters obtained from four nonlinear functions.

MATERIALS AND METHODS

Experimental animals

The body weight records for this study came from the progeny of seven genotypes of chickens reared at the Poultry Breeding Unit of the University Farms, Federal University of Agriculture, Abeokuta, Nigeria. The composite chicken population comprises of Giriraja (GR) - 105, Bovan Nera (NB) - 133, White Leghorn (WL) - 93, Naked Neck (NN) - 197, Normal Feathered (NF) - 186, Frizzle feathered (FF) - 164 and FUNAAB Alpha (an improved indigenous chicken) (BA) - 115. The population was divided into locally adapted exotic genotypes (GR, NB and WL), indigenous genotypes (NN, NF and FF) and crossbred genotype (BA).

Feeding and management

All the birds had access to chick mash diet that supplied 21.49% crude protein and 2816.45kcal/kg metabolizable energy from 0-8 weeks of age and thereafter with grower's mash that supplied 16.90% crude protein and 2715.35kcal/kg metabolizable energy *ad libitum*. The birds also had free access to water. Drugs and vaccines were administered according to the prevailing regime.

Data collection

Growth data were collected individually on a weekly basis from day-old till 20 weeks of age with the aid of sensitive scale of 0.05g sensitivity with the capacity of two decimal

digits (Camry sensitive computer).

Statistical analysis

The four nonlinear functions compared in this present study for animal *i* is expressed as:

$$BW_{ij} = f(\theta_p, t_{ij}) + e_{ij} \dots \dots \dots i = 1, \dots, N \text{ and } j = 1, \dots, n_i \quad (\text{Kizilkaya et al., 2006})$$

Where *f* is the nonlinear function relating the response variable (*BW_{ij}*) to time (*t_{ij}*), *θ_i* is a vector including the parameters of the non-linear function, *N* is the number of animals and *n_i* is the number of measurements taken from animal *i*, *e* is the residuals with the assumption of *e_i* ~ *N*(*θ*, *σ²I_i*) where *σ²I_i* is the residual variance structure for all subjects, assuming that no covariance structure exists between the residuals of the model. The resulting chicken growth data were fitted to the fixed effect function of Logistic, Gompertz, Richards and Bertalanffy model and some of their important properties as shown in Table 1. Where *A* is the final (asymptotic) weight or an estimation of mature weight as age approaches infinity (*t_i* = ∞); *B* is the integration constant defining the degree of maturity at *t_i* = 0; *k* is the constant that expresses the rate at which a logarithmic function of *W* specific for each of the nonlinear equations, changes linearly with time; *t* = age of the bird; *m* = shape parameter determining the position of the inflection point at which the auto acceleration growth phase passes into the

auto retardation phase. The first derivative of each function with respect to age expresses the absolute (instantaneous) growth rate (AGR) at time *t* (*dW/dt*). Relative growth rate (RGR) ((1/*W*)(*dW/dt*)) is AGR relative to current weight while absolute (instantaneous) maturing rate (AMR) ((1/*A*)(*dW/dt*)) is AMR relative to final weight (Perotto et al., 1992). Mathematically, AGR is the average height of the curve resulting from plotting *dW/dt* against *W* for the entire growing interval. Absolute maturing rate is the average height of (1/*A*)(*dW/dt*) plotted against *W/A* for the entire maturing interval. RGR is the growth rate relative to the size of the population. It is also called the exponential growth rate, or the continuous growth rate. Relative growth rate is a measure used to quantify the speed of growth.

Mathematically, AGR is the average height of the curve resulting from plotting *dW/dt* against *W* for the entire growing interval; AMR is the average height of (1/*A*)(*dW/dt*) plotted against *W/A* for the entire maturing interval; and RGR is the ratio of *dW/dt* at inflection to the weight at inflection (*W_i*).

The nonlinear procedure of SAS (2000) was used to fit the functions to the actual growth curves. The initial values of the functions were run by using PROC NLIN in SAS. The average lifetime AGR, AMR and RGR values of each animal were computed using

Table 1. First derivatives of the nonlinear functions for describing the growth curve of chicken genotypes

Function	AGR (<i>dW/dt</i>)	(AMR) ((1/ <i>A</i>)(<i>dW/dt</i>))	(RGR) ((1/ <i>W</i>)(<i>dW/dt</i>))
First derivative	(<i>dW/dt</i>)	((1/ <i>A</i>)(<i>dW/dt</i>))	((1/ <i>W</i>)(<i>dW/dt</i>))
Logistic	ABk*exp{- <i>kt</i> }	(1/ <i>A</i>)(AGR)	(<i>W_{inf}</i>) ⁻¹ *(AGR)
Gompertz	ABk*[(exp-B{exp- <i>kt</i> })- <i>kt</i>]	(1/ <i>A</i>)(AGR)	(<i>W_{inf}</i>) ⁻¹ *(AGR)
Richard	[(LOG)(B*{exp{- <i>kt</i> }}+1) ^{-(1/<i>m</i>)-1}] <i>m</i> -1	(1/ <i>A</i>)*(AGR)	(<i>W_{inf}</i>) ⁻¹ *(AGR)
Bertalanffy	(3ABk*exp{- <i>kt</i> })(1-B*exp{- <i>kt</i> }) ²	(1/ <i>A</i>)*(AGR)	(<i>W_{inf}</i>) ⁻¹ *(AGR)

LOG = Logistic function, GMP = Gompertz function, RCD = Richards function, BER = Bertalanffy function.

the corresponding estimates of A , B , k and m and then subjected to analysis of variance using a fixed effect model where growth model is the only independent variables.

RESULTS

Table 2 presented the computed first derivatives of growth traits estimated by fitting Logistic function to the observed growth curves of the chicken genotypes. The result as presented in Table 2 showed

value of 127.70 g. In AMR, FF was significantly ($P < 0.05$) different from other indigenous genotypes (NN and NF) while NB was least significant though not far from BA. Similar significant pattern in AMR was observed in RGR where estimated value in FF (0.1294) was most significant while NB (0.1082) was least significant.

Computed growth traits estimated by fitting Gompertz function to the observed growth

Table 2. Computed first derivatives of growth traits using Logistic growth function

Factors	AGR	AMR	RGR
Genotype			
<i>Indigenous chickens</i>			
NN	75.3490 ^b	0.0612 ^{ab}	0.1225 ^{ab}
FF	77.5410 ^b	0.0647 ^a	0.1294 ^a
NF	68.8850 ^b	0.0612 ^{ab}	0.1225 ^{ab}
<i>FUNAAB Alpha chicken</i>			
BA	77.3050 ^b	0.0566 ^{bc}	0.1131 ^{bc}
<i>Locally adapted exotic chickens</i>			
NB	84.1940 ^b	0.0541 ^c	0.1082 ^c
WL	72.5770 ^b	0.0587 ^{abc}	0.1175 ^{abc}
GR	127.7070 ^a	0.0618 ^{ab}	0.1236 ^{ab}

^{abc} = Means with same letters along the column are not significantly different ($P > 0.05$)
 AGR=Absolute Growth Rate; AMR=Absolute Maturing Rate; RGR=Relative Growth Rate,
 NN=Naked Neck, FF=Frizzle Feathered, NF=Normal Feathered, BA=FUNAAB Alpha,
 NB=Nera Black, WL=White Leghorn and GR=Giriraja

that there was no significant ($P > 0.05$) differences in AGR between the genotypes except for GR which produced the highest

curves of the chicken genotypes is presented in Table 3. The computed AGR, AMR and RGR in Gompertz growth model

Table 3. Computed first derivatives of growth traits using Gompertz growth function

Factors	AGR	AMR	RGR
Genotype			
<i>Indigenous chickens</i>			
NN	69.7499 ^{bc}	0.0429 ^{ab}	0.1166 ^{ab}
FF	72.6691 ^{bc}	0.0466 ^a	0.1267 ^a
NF	64.1700 ^c	0.0445 ^{ab}	0.1210 ^{ab}
<i>FUNAAB Alpha chicken</i>			
BA	72.9180 ^{bc}	0.0374 ^{bc}	0.1019 ^{bc}
<i>Locally adapted exotic chickens</i>			
NB	83.2880 ^b	0.0346 ^c	0.0941 ^c
WL	68.9839 ^{bc}	0.0409 ^{abc}	0.1113 ^{abc}
GR	119.3850 ^a	0.0440 ^{ab}	0.1197 ^{ab}

^{abc} = Means with same letters along the column are not significantly different ($P > 0.05$)
 AGR=Absolute Growth Rate; AMR=Absolute Maturing Rate; RGR=Relative Growth Rate,
 NN=Naked Neck, FF=Frizzle Feathered, NF=Normal Feathered, BA=FUNAAB Alpha,
 NB=Nera Black, WL=White Leghorn and GR=Giriraja.

showed significant ($P < 0.05$) difference between genotypes. The GR had the highest significant value in AGR while FF was most significant in AMR and RGR. The least significant value in AGR was recorded in NF while the least AMR and RGR was recorded in NB. Values obtained for the indigenous chickens (NN and FF), BA and WL were not significantly ($P > 0.05$) different from one another but differ significantly from other genotypes.

Presented in Table 4 is the computed growth traits estimated by fitting Richards function to the observed growth curves of the chicken genotypes. There was significant ($P < 0.05$) difference between the AGR obtained in GR (112.59) and other genotypes. Similar significant different pattern was observed in both the AMR and RGR. There was no significant ($P > 0.05$) difference between GR and WL and the indigenous chickens (NF and FF) but differ significantly from NB.

Table 4. Computed first derivatives of growth traits using Richards growth function

Factors	AGR	AMR	RGR
Genotype			
<i>Indigenous chickens</i>			
NN	63.24 ^b	0.0389 ^{ab}	0.1050 ^{ab}
FF	64.00 ^b	0.0415 ^a	0.1103 ^a
NF	59.18 ^b	0.0414 ^a	0.1118 ^a
<i>FUNAAB Alpha chicken</i>			
BA	67.05 ^b	0.0338 ^{ab}	0.0338 ^{ab}
<i>Locally adapted exotic chickens</i>			
NB	67.80 ^b	0.0269 ^b	0.0269 ^b
WL	68.91 ^b	0.0411 ^a	0.1110 ^a
GR	112.59 ^a	0.0418 ^a	0.1132 ^a

^{abc} = Means with same letters along the column are not significantly different ($P > 0.05$)

AGR=Absolute Growth Rate; AMR=Absolute Maturing Rate; RGR=Relative Growth Rate, NN=Naked Neck, FF=Frizzle Feathered, NF=Normal Feathered, BA=FUNAAB Alpha, NB=Nera Black, WL=White Leghorn and GR=Giriraja

Table 5. Computed first derivatives of growth traits using Bertalanffy growth function

Factors	AGR	AMR	RGR
Genotype			
<i>Indigenous chickens</i>			
NN	69.534 ^b	0.0321 ^{ab}	0.1083 ^{ab}
FF	74.358 ^b	0.0360 ^a	0.1216 ^a
NF	64.636 ^b	0.0347 ^{ab}	0.1171 ^{ab}
<i>FUNAAB Alpha chicken</i>			
BA	75.757 ^b	0.0261 ^{bc}	0.0879 ^{bc}
<i>Locally adapted exotic chickens</i>			
NB	103.259 ^a	0.0226 ^c	0.0764 ^c
WL	73.059 ^b	0.0303 ^{abc}	0.1023 ^{abc}
GR	120.411 ^a	0.0337 ^{ab}	0.1137 ^{ab}

^{abc} = Means with same letters along the column are not significantly different ($P > 0.05$)

AGR=Absolute Growth Rate; AMR=Absolute Maturing Rate; RGR=Relative Growth Rate, NN=Naked Neck, FF=Frizzle Feathered, NF=Normal Feathered, BA=FUNAAB Alpha, NB=Nera Black, WL=White Leghorn and GR=Giriraja

Table 5 showed the computed AGR, AMR and RGR estimated for the genotypes in Bertalanffy growth model. The values obtained for AGR showed that GR (120.411) and NB (103.259) were significantly ($P < 0.05$) different from other genotypes. Similar significant different pattern was observed in AMR and RGR for all the genotypes. Frizzle Feathered had the highest means in AMR (0.0360) and RGR (0.1216) which differ significantly ($P < 0.05$) from BA (AMR=0.0261 and RGR=0.0879) and NB (AMR=0.0266 and RGR=0.0764) which is least significant.

DISCUSSION

Growth models show the specific and predictable pattern of growth of an animal based on feeding and other management factors. Generating the first derivative of these model articulates more about the model in terms of the direction of the growth curve. Absolute growth rate (AGR) which is the net growth per unit time was better in GR than other genotypes. However, the performance of FF, though not significantly different, was better when numerically compared to other indigenous genotypes. Giriraja being a dual purpose breed was superior to other breeds based on the fact that they thrive well under varying climate (Rao, 2005).

Oke (2011) reported that the FF homozygous main cross manifested the greatest growth characteristics in terms of body weight changes and growth rates. Furthermore, BA, despite not being significantly different from the indigenous genotypes, had relatively higher computed AGR values, which may be due to the heterotic advantage of crossbreeding. Absolute maturing rate (AMR) defines in relative terms the weight increase per unit of

time as the animal grows and determines the degree of the steepness of the growth curve. The weight increase of FF chicken per unit time was superior to NB but closely related to other genotypes across the models which translate to the fact that AMR is a function of AGR relative to the final weight (Perotto *et al.*, 1992). The AMR of the BA chickens was more closely related to the exotic genotypes than the indigenous genotypes.

The computed values obtained in this study for RGR was similar to AMR with respect to their pattern of significance. However, RGR relates the growth increase to the initial value as a measure of percentage growth giving an insight into the exponential pattern of the growth rate in which case it shows superiority of FF and is closely followed by other indigenous genotypes and GR for all the models considered except Richards model. In Richards model, the RGR of BA was in between the indigenous and the exotic genotypes inferring the expression of hybrid vigour. Perotto *et al.* (1992), in their work, referred to RGR as the instantaneous growth rate relative to current weight. The authors further stated that RGR is the ratio of dW/dt at inflection to the weight at inflection (W).

CONCLUSION

Despite the high AGR recorded in this study for the tropically adapted exotic genotypes, the indigenous genotypes were able to record better RGR. This is an indication of optimal protein deposition relative to initial weight for the indigenous genotypes though the curve may not be as steep as that of tropically adapted exotic genotypes.

Conflict of interest

The authors declared none.

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