



Original Contribution

COMPARISON OF DIFFERENT MODELS TO DESCRIBE GROWTH OF THE JAPANESE QUAIL (*COTURNIX JAPONICA*)

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ABSTRACT

This study compared seven growth models using body weight measurements from 300 progeny obtained from unselected random bred parents. The study which lasted for 20 weeks was carried out at the University of Maiduguri Livestock Teaching and Research farm. R^2 values for the Asymptote regression, Exponential, Gompertz, Logistic, Monomolecular, Richards and Weibull models were 0.994, 0.935, 0.997, 0.997, 0.998, 0.998, 0.998 and 0.999 respectively. The Weibull model had the highest coefficient of determination (R^2) value (0.999) and Exponential (0.935) least. In contrast, the exponential model had the highest MSE (Mean Square Error), SD (Standard Deviation) and AIC (Akaike Information Criterion) values while Weibull model had the least. The exponential had the poorest fit (higher MSE, SD and AIC values and lower R^2) while the Weibull, Gompertz and Richards models best described the data in that order (lower MSE, SD and AIC values and higher R^2). In order words, the nonlinear models described the data better than linear. Therefore, based on goodness of fit criteria; R^2 , MSE, SD and AIC values, the weibull model best described live weight data of the Japanese quail in Nigeria.

Key words: growth, non linear model, Japanese quail, Nigeria

INTRODUCTION

Growth models summarize information needed to understand the biological phenomenon of growth; an important component in livestock production systems (1). They are used to determine the age-live weight relationship of animals and each has its own characteristics and mathematical limitations. An appropriate growth function conveniently summarizes the information provided on animals into a small set of parameters that can be interpreted biologically and used to derive other relevant growth traits (2). It has been observed that animal growth follows a sigmoid pattern (S-shape) and numerous non linear growth equations have been developed to describe and fit the sigmoid relationship between weight and time in poultry.

The commonly used nonlinear growth models are Brody, Bertalanffy, Gompertz, Richards, Logistic, Morgan Mercer Flodine (MMF) and Weibull (3). These curves start at some fixed point, growth rate then increases up to an inflection point after which it decreases asymptotically to a final value (4). The Richard and Gompertz models have been shown to give good descriptions of growth in species such as cattle, elks, chicken, ostrich, turkey and emus (5). The Gompertz growth model has been cited as the model of choice for chicken data based on its overall fit and biological meaning of model parameters (6, 7, 8, 9). In addition, it has good fitting for weight information whose inflection points occur, when approximately 35 - 40% of growth has been achieved (10).

Ricklefs (6) defined growth trend in Japanese quails using Gompertz model while (11) applied the Richards function. The latter study focused on comparison of Richards, Gompertz and

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Logistic models for describing growth characteristics of three meat-type lines of Japanese quail. Though, the authors observed that Richards function converted to Gompertz and Logistic model when shape parameter equals 0 and 1 respectively, Richards function predicted the weight of quails better than the other two. However, (12) reported that the logistic gave the best fit to male and female, selected and unselected quail populations when compared with the Brody, Exponential, Gompertz and Bertalanffy models.

The report of (13) compared three models (Gompertz, Logistic and linear) and observed that though all the models had similar R^2 values (0.982, 0.981 and 0.939 respectively), the Gompertz described weight of broilers more precisely up to slaughter age. Similarly, (9) compared three non linear models (Richards, Logistic and Gompertz) and spline linear regression models for describing chicken growth and observed that the spline gave the poorest fit compared to the non linear models. Maruyama *et al.* (14) reported the best model for ducks to be the Weibull. The non linear models are able to predict the shape of the growth function more logically than linear (13). Ricklefs (15) stated that growth curves of the same or different species are not necessarily best described by the same equation. Generally, there is conflicting reports on the appropriate model for describing growth in the Japanese quail. Similarly, there is a dearth of information on modeling of Japanese quail growth in Nigeria. Therefore, the aim of this study was to assess different models used to describe growth of the Japanese quail in a semi arid region of Nigeria.

MATERIALS AND METHODS

The study was carried out at the Poultry Unit of the University of Maiduguri Livestock Teaching and Research Farm, Maiduguri, Borno State, Nigeria. Maiduguri, the Borno State capital is

situated on latitude $11^{\circ}5'$ N, longitude $13^{\circ}09'$ E and at an altitude of 354 m above sea level. The area falls within the Sahelian region of West Africa, which is noted for great climatic and seasonal variations. It has very short period (3 – 4 months) of rainfall of 645.9 mm/annum with a long dry season of about 8 – 9 months. Relative humidity is 45% in August which usually lowers to about 5% in December and January. Day length varies from 11 to 12 hours (16).

Three hundred Japanese quails hatched from eggs collected from unselected and random mating parents were used for the study. After hatching, the chicks were individually weighed and labeled before brooding for two weeks. Hatched chicks were fed commercial broiler starter ration containing 23% crude protein and 3000 kcal/kg of Metabolizable Energy to 6 weeks of age. The birds were then housed in cages (30x30x45 cm) fitted with improvised feeders and drinkers and fed breeders diet containing 18% crude protein and 2800 kcal/kg of Metabolizable Energy (17) from 6 weeks of age. Birds were weighed weekly from 1-20 weeks of age using a sensitive balance and they had access to feed and water *ad libitum*.

The models were fitted to each quail growth data using Levenberg-Marquardt nonlinear least-squares algorithm in Statistix 9.0 (18). During the iteration procedure, when any parameter value at a current iteration did not change in the successive iteration, the procedure stopped and it was assumed that the convergence criterion of $1.0E-05$ was attained and curve parameters obtained. Goodness of fit for each model was determined by the following statistics R^2 , Akaike's Information Criterion (AIC), convergence criterion, Standard Deviation (SD) and Mean Square Error (MSE). The following non linear models were fitted to the body weight data:

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|----|----------------------------|--|
| 1. | Asymptote regression model | $Y = a - b \cdot c^X$ |
| 2. | Exponential | $Y = a \cdot \text{Exp}(c \cdot X)$ |
| 3. | Gompertz | $Y = a \cdot \text{Exp}(-\text{Exp}(b - c \cdot X))$ |
| 4. | Logistic | $Y = a / (1 + \text{Exp}(b - c \cdot X))$ |
| 5. | Monomolecular | $Y = a \cdot (1 - \text{Exp}(-b \cdot (X - c)))$ |
| 6. | Richards | $Y = a / (1 + \text{Exp}(b - c \cdot X))^{1/d}$ |
| 7. | Weibull-type | $Y = a - b \cdot \text{Exp}(-c \cdot X^d)$ |

For each model, Y is the body weight at a particular age, X is age in weeks, a is the asymptotic weight or maximum growth response, b is a scale parameter related to initial weight, c is the intrinsic growth rate and d the shape parameter.

RESULTS AND DISCUSSION

Overall means, standard error and deviations for body weights of Japanese quails at different ages are presented on **Table 1**. Generally, standard deviations increased with age. This is expected with time series data. Similar observation was made by (9) and (19). Curve parameters of the seven growth models utilized are presented on **Table 2**. The highest value for ‘a’ parameter (asymptote body weight) was recorded in the monomolecular model (160.227 g) followed by the asymptote regression model (160.093 g) while the least values were recorded by the Logistic (151.227 g) and Exponential (70.517 g). The highest value for b parameter (scale parameter or model constant) was recorded by the Asymptote regression model (162.348 g) while the Richards (-4.728 g) had the least. For

the c parameter (relative growth rate) asymptote regression growth model (0.815) had the highest value and the Monomolecular had the least (0.053). The highest d parameter (shape or curve parameter) value was recorded by the Weibull model (1.246) and the Richards (0.140) had the least. For the model selection criteria, the R² values for the asymptote regression, exponential, Gompertz, Logistic, Monomolecular, Richards and Weibull were 0.994, 0.935, 0.997, 0.997, 0.998, 0.998, 0.998 and 0.999 respectively. The Weibull model had the highest coefficient of determination (R²) value (0.999) and the exponential (0.935) had the least. In contrast, the exponential model had the highest MSE (Mean Square Error), SD (Standard Deviation) and AIC (Akaike's Information Criterion) values while Weibull model had the least. The MSE, SD and AIC values for the exponential and Weibull models were 1001.19 vs 318.54, 31.618 vs 17.755 and 5670.90 vs 4717.067. The Richards had the highest number of iterations (80) and monomolecular (10) the least for the convergence criterion.

Table 1. Means and Standard deviations of body weights (grams) at different ages of the Japanese quail

Age (week)	Mean	Standard Error of Mean	Standard Deviation
hatch	5.87	0.09	0.95
1	15.70	0.22	2.44
2	48.15	0.66	7.28
3	73.32	1.00	11.12
4	80.43	1.11	12.26
5	92.00	1.17	13.02
6	102.63	1.30	14.43
7	117.81	1.47	16.33
8	130.54	1.58	17.55
9	136.18	1.84	20.42
10	138.33	1.92	21.30
12	146.13	1.79	19.82
13	147.31	2.12	23.56
14	150.37	1.90	21.11
15	142.08	1.93	21.40
16	144.48	1.91	21.15
17	145.33	1.95	21.61
18	147.35	1.69	18.73
19	148.50	1.93	21.43
20	128.91	4.37	48.43

Table 2. Model parameters and goodness of fit criteria for different growth models fitted to the live weight data of Japanese quail

Model parameters	Models						
	Asymptote regression	Exponential	Gompertz	Logistics	Monomolecular	Richards	Weibull
A	160.093	70.517	153.111	151.227	160.227	153.21	155.946
B	162.348	-	0.935	1.873	0.205	-4.728	151.325
C	0.815	0.047	0.36	0.496	0.053	0.387	0.140
D	-	-	-	-	-	0.140	1.246
R ²	0.994	0.935	0.997	0.997	0.998	0.998	0.999
MSE	332.633	1001.19	326.876	342.636	332.633	327.30	318.54
SD	18.18	31.618	17.982	18.401	18.18	17.994	17.755
AIC	4759.767	5670.90	4736.233	4772.233	4759.767	4738.30	4717.067
Convergence criterion	11	13	15	12	10	80	37

a =Asymptote weight

b = Scale parameter (constant)

c =Relative growth rate

d = Shape parameter

R²= Coefficient of determination

MSE =Mean Square Error

SD = Standard Deviation

AIC = Akaike's Information Criterion

The report of (20) observed that model goodness of fit is generally evaluated by using Mean Square Error and Coefficient of Determination. Brown *et al.* (21) had earlier reported that the model with the smallest standard error is assumed to have the best fit to the data and 'a' parameter values offer the best opportunity to make direct comparisons among models. Comparisons of asymptotic weight obtained with different growth functions showed as earlier stated that Monomolecular model had the highest value (160.227g) followed by the Weibull (155.946 g), Richards (153.210 g), Gompertz (153.111 g) then Logistic (151.227 g). This is in agreement with the report of (22) that compared Monomolecular, Gompertz and Logistic models and ranked the Monomolecular first and Logistic last in terms of asymptote body weight. Similarly, (9) also ranked the Richards ahead of Gompertz and Logistic. Narinc *et al.* (23) ranked Gompertz first, Richards next and Logistic last. The asymptote weights reported by these authors

for the Richards (222.0 g), Gompertz (222.1 g) and Logistic (201.9 g) are much higher than those obtained in this study. This could be due to the fact that asymptote weight is directly related to genotype and environmental effects; hence different quail genotypes fed in different environment will have different asymptote weight. The growth curves of the Japanese quail as predicted by the growth models are presented in **Figure 1**. Goodness of fit criteria R² was generally high for all the models (0.935-0.999). This is in line with the result of (23), which reported R² values of 0.985 - 0.999. Darmani *et al.* (24) also reported a range of 98.87 - 99.99% in chicken. The high R² values indicate that the models adequately described the observed quail data. The exponential had the poorest fit (higher MSE, SD and AIC values and lower R²) while the Weibull, Richards and monomolecular models best described the data in that order (lower MSE, SD and AIC values and higher R²). Maruyama *et al.* (14) reported the Weibull model as best for

fitting weight-age data in ducks. The poor fit in this study has also been previously reported (9, 24). Therefore, the nonlinear models described the data better than the linear as stated earlier by Hruby *et al.* (13) in chickens. Generally, the four parameter models had better fit than three. In contrast, high convergence

of the exponential; a linear model observed criterion for the four parameter models (Richards; 80 and Weibull; 38) compared to low for those with three parameters (10-15) may indicate fitting difficulty. This agrees with the report of (26) that the four parameter models are difficult to fit.

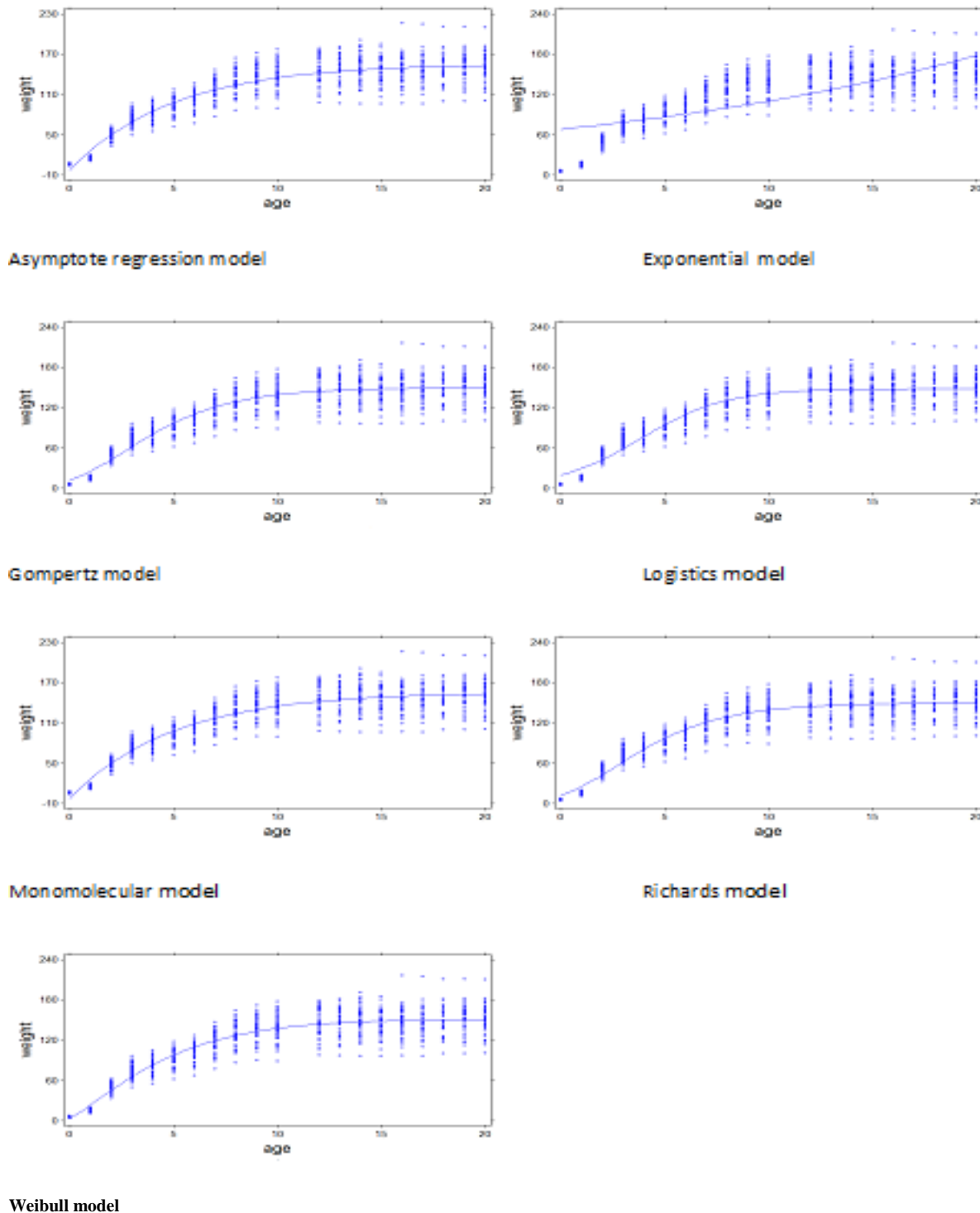


Figure 1. Fitted curves for the different growth models

CONCLUSION

The generally high R^2 for all models indicates that they adequately described Japanese quail live weight changes with age. However, based on goodness of fit criteria; R^2 , MSE, SD and AIC values, the Weibull model best described the live weight data of Japanese quail.

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