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An application of modified Logistic and Gompertz growth models in Japanese quail

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ABSTRACT

Growth functions describe body weight changes over time, allowing information from longitudinal measurements to be combined into a few parameters with biological interpretation. The Gompertz and Logistic models, which have three parameters (A: asymptotic body weight, b: shape parameter,c: constant of average growth rate), have been used extensively in poultry species to describe the development of body weight. The first aim of this study was to gain new two parameters that are called hatching body weight (λ) and maximum growth rate (μ) these parameters which are important for animal breeding to the Logistic and Gompertz models respectively. Furthermore, the second aim of this study was to reveal similarities and differences of both models in growth data of Japanese quail by using various goodness of fit criteria and residual analysis.The growth data of 64 mixed sex Japanese quail consisted of individual live weights of 3-day intervals from hatching (day 0) to 42 days of age. The parameters λ, A and μ of the Gompertz and Logistic models were estimated as, 8.71, 242.10, 6.00 g and 14.71, 208.44, 6.50 g, respectively. As a result of the goodness of fit criteria and residuals analysis, the Gompertz model indicates a much better fit than the Logistic model to Japanese quail data set. According to the results, transformed Gompertz and Logistic models are not only more profitable for poultry species but also more useful for other livestock species such as goat, sheep and cattle.

Key words: Gompertz, Logistic, Model Modification, Japanese Quail

The mathematical models are used in a wide range of disciplines such as food microbiology, biology, crop science and animal science.These models are widely utilized to describe growth, lactation, in vitro gas production or in situ degradation kinetics particularly in animal science.The growth which is the increase in mass and volume per unit of time in terms of an emphasized trait is very important in animal breeding and flock management.Growth curves are used to compare different strains, lines or flocks (Mignon-Grasteau*et al.* 2001; Rizzi*et al.* 2013) to determine the best fitting model in a specific genotype (Aggrey 2002, Ramos *et al.* 2013) and to obtain the parameter estimates that can be used in genetic parameter estimations for selection studies (Akbas and Yaylak 2000; Narinc *et al.* 2010a).

The Japanese quails which have low body weightare used in commercial production for its meat and egg yields. In addition, quails are used particularly in poultry breeding studies and also in the fields of animal production, health sciences and behavioral sciences as model animals because they have a short generation interval such as 3–4 months and high progeny performance.There are a lot of studies which belong to Japanese quailconducted in order to model the growth data. Anthony *et al.* (1991), Kizilkaya *et al.* (2006), Aggrey (2009), Narinc *et al.* (2010b), Beiki*et al.* (2013) and Karaman *et al.* (2013) conducted studies to determine the most suitable growth model for the growth data ofquail. Anthony *et al.* (1986), Akbasand Oguz (1998), Hyankova *et al.* (2001), Balcioglu *et al.* (2005), Kizilkaya *et al.* (2006) and Alkan *et al.* (2009), discussed the results of selection studies which aim to increase or decrease live weight profiles of line susing growth curves. Akbas and Yaylak (2000) and Narinc*et al.* (2010a) estimated heritabilities and some traits with genetic relations for growth model parameters and suggested that it was possible to benefit from these growth models in genetic improvement studies.

The Gompertz and Logistic growth models werecommonly used in modeling of growth of poultry species.However, these models have mathematical parameters (A, b and c) identifying a general structure of the data set. Zwitering *et al.* (1990) emphasized that it was difficult to calculate the confidence intervals and estimate initial values of parameters in such modelswhich havemathematical parameters. The biological parameter (A, l and μ) model giving more information about the

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functioning of the systemcan be preferred instead of the mathematical parametermodel since it is much easier to estimate the initial values using biological interpretable parameters (Zwitering *et al.* 1990; Korkmaz and Uckardes 2013).

The aim of this study is to develop modified forms which have the biologically meaningful parameters of the Logistic and Gompertz models to identify the model which fits better to Japanese quail and to reveal similarities and differences of these two models in Japanese quail by using various goodness of fit criteria and residual analysis.

MATERIALS AND METHODS

Animal husbandry and data collection

The present experiment was conducted at the Poultry Breeding Unit, Animal Science Department, Faculty of Agriculture, Ordu University. The growth data of 64 mixed sex quailconsisted of individual live weights of 3-day intervals from hatching (day 0) to 42 days of age.

Mathematical considerations

Hatching weight in birds (λ), the maximum increase in live weight (A) and maximum growth rate (μ) which are biologically meaningful parameters are important traits in terms of rearing and genetic improvement that have been subjects of many studies (Akbasand Oguz 1998; Hyankova *et al.* 2001; Balcioglu *et al.* 2005). Especially the point where the growth rate starts to decrease causes regression in benefiting from the feed. After this point, it is thought that mentioning to feed the animal will decrease profitability, therefore it is suggested that cutting age of the animal should be moved to this point (Hyankova *et al.* 2001, 2008). It is thought that estimating traits such as hatching weight, the highest increase in live weight and the highest growth rate and conducting breeding studies for these traits would make a significant contribution to genetic improvement. For this purpose, the Logistic and Gompertz models were rewritten with biologically meaningful parameters (Table 1).

As an example, the modification of the Logistic model is shown below;

$$y= a/(1+b\exp(-ct)) \quad (1)$$

Y is the body weight at age (t); a is the asymptotic value; b is the shape constant; c is the rate constant; (t) is the time. Equation 1 is converted into step by step as follows. Firstly, for the initial live weight of the chick t=0 $y_0=a/(1+b)$, $y_0=\lambda$, $\lambda=a/(1+b)$ is found and from this, $b= (a-\lambda)/\lambda$is obtained. If equation 1 is reorganized:

$$y=a\lambda/(a+(a-\lambda)\exp(-ct)) \quad (2)$$

where, parameter in this equation indicates the hatching weight. Secondly, it is necessary to calculate the inflection point of the curve for maximum growth rate (Zwitering *et al.* 1990). For this, second derivative of equation 2 according to t,

$$dy/dt = \lambda a(a-\lambda)c\exp(-ct)/((\lambda+(a-\lambda)\exp(-ct))^2)$$

$$\frac{d^2y}{dt^2} = \frac{2\lambda a(a-\lambda)^2 c^2 \exp(-ct)^2}{((\lambda+(a-\lambda)\exp(-ct))^3)} - \frac{\lambda a(a-\lambda)c^2 \exp(-ct)}{((\lambda+(a-\lambda)\exp(-ct))^2)} \quad (3)$$

At the inflection point, where $t=t_i$, the second derivative is equal to zero ;

$$d^2y/dt^2 = 0 \rightarrow t_i = -\ln(\lambda/(a-\lambda))/c \quad (4)$$

Now an expression for the maximum specific growth rate can be derived by calculating the first derivative at the inflection point (Zwitering *et al.* 1990).

$$\mu = \left.\frac{dy}{dt}\right|_{ti} = \frac{ac}{4} \quad (5)$$

The parameter c in the Logistic equation 2 can be substituted for by c= 4μ/a

$$y = \lambda a/(\lambda+(a-d\lambda)\exp(-4\mu t/a)) \quad (6)$$

The asymptotic value is reached for t approaching infinity,

$$t \rightarrow \infty; y \rightarrow a \Rightarrow A = a$$

If equation 6 is reorganized, the modified Logistic model is obtained as below.

$$y = \lambda A/(\lambda+(A-\lambda)\exp(-4\mu t/A))$$

Where, λisthe live weight at the moment of hatching (gr); A is the maximum growth (g); μ is the maximum growth rate.In conclusion, three biologically meaningful parameters are obtained from the Logistic model (Fig. 1.).

The similar procedures were followed for Gompertz model, and the all results are presented in Table 1.

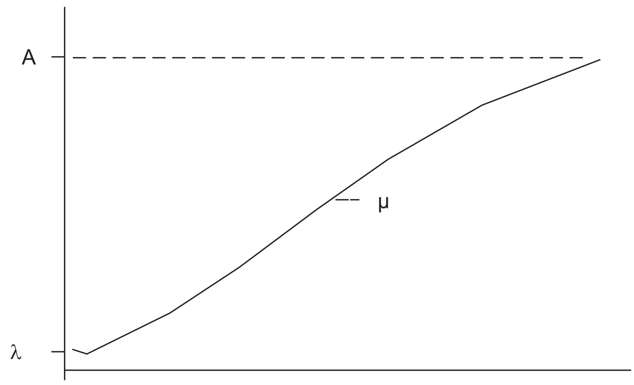

Fig. 1. A growth curve and parameters of modified a model

Table 1. The Logistic and Gompertz models and their modified forms

Model	Equation	Modified Equation	Number of parameters
Logistic	y=A/(1+bexp(-ct))	y=λA/(l+(A-λ)exp(-4μt/A))	3
Gompertz	y=Aexp(-exp(b-ct))	y=A(λ/A)exp(-μexp(t)/A)	3

A is the final body weight, b and c are constants, λ is the initial body weight, and μ is the maximum increase in live weight.

Goodness of fit

Goodness-of-fit of each model was evaluated by using the coefficient of determination (R^2) and Residual Mean Square (RMS) which is appropriate to compare models have the same parameter. For R^2 and RMS the following equations were used,

$$R^2 = 1-(RSS/ SST)$$

$$RMS = RSS/(n-p)$$

Where, RSS is the sum of square errors, SST is total sum of squares, p is the number of parameters of the model and n is thenumber of observations (Korkmaz *et al.* 2011 and Uckardes *et al.* 2013).

The significance of the regression parameters was statistically analyzedfor testing the hypothesis of slope, 1 and intercept, 0 according to Pineiro *et al.* (2008). Nevertheless, Pearson's correlation coefficients were used for determiningthe relationship between predicted and observed values.

Model comparison

Firstly, the F ratio test ($F=(RSS_1)/(RSS_2)\sim F_{((n-p1,n-p2),\alpha)}$) was used for pairwisecomparisonsof the statistical significance of the difference between models (Uckardes *et al.* 2013). Secondly, Akaike Information Criteria (AIC= nln(RSS/n)+2p) was used, based on information theory (Narinc *et al.* 2010b).

Examination of Residuals

The Runs test and Durbin-Watson (DW) test were used to determine the independence and the normality of residuals as described by Uckardes *et al.* (2013).

Curve fitting and statistical analyses were done using the program Graph Pad 5.0 under Windows 7. This program uses a Levenberg-Marquardt algorithm (Graph Pad 2007). Independent two-sample t test was done in order to determine differences between the parameters of each model.

RESULTS AND DISCUSSION

The results of goodness of fit for the Logistic and Gompertz models were given in Table 2 and shown in Fig. 2. The maximumlive weight of the Gompertz model (A=242.10) wasfound bigger than that of the Logistic model (A=208.44). Akbas and Oguz (1998) estimated A parameter as 208.3 g with the Gompertz model, 179.3 g with the Logistic model, Narinc *et al.* (2010a,b) estimated A parameter as 222.1 g with the Gompertz model, 201.9 with the Logistic model, Gurcan*et al.* (2012) estimated the same parameter as 186.9 g with the Gompertz model, 174.2 g with the Logistic model. In all three studies, it has been seen that estimated asymptotic weight parameter with Gompertz model is higher than the estimated value with Logistic model and above-mentioned finding has been determined to be consistent with the results of this study and research of Beiki *et al.* (2013).

The λ of the Logistic model was found bigger than that of Gompertz model.In the study conducted by Balcioglu

Table 2. The best fit values and Goodness-of-fit the between Logistic and Gompertz models ($\bar{x} \pm s_{\bar{x}}$)

		Logistic	Gompertz	Significance
Parameters	A	208.44^b ±1.24	242.10^a ±1.73	***
	λ	14.71^a ±0.14	8.71^b ±0.14	***
	μ	6.50^a ±0.05	6.00^b ±0.04	***
RMS values	Average	17.393	2.799	
	Minimum	7.753	0.403	
	Maximum	56.500	26.900	
R^2 values	Average	0.9966	0.9994	
	Minimum	0.9897	0.9951	
	Maximum	0.9985	0.9999	

A is the final body weight, λ is the initial body weight, and μ is the maximum increase in live weight; ***P< 0.001. [ab] : Means within the same row with various superscripts are significant at P<0.05.

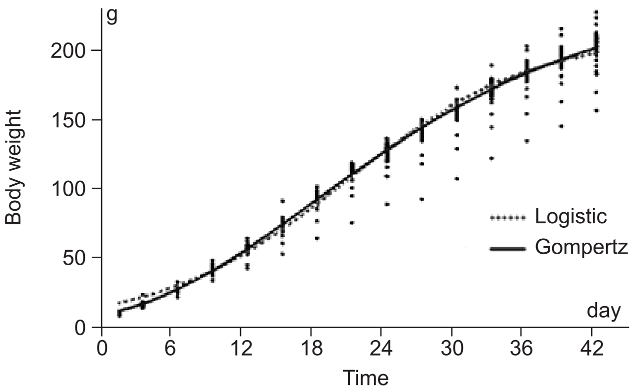

Fig. 2. Logistic and Gompertz growth curves of birds (n=64)

et al. (2005), the quails' growth analyzed by using a line with high body weight and a line with low live body weight obtained by a two-way selection (divergent selection) and also a randomly mated control lineby using the empirical form of the Gompertz model. Similarly, Sekeroglu *et al.* (2013) reported that they compared growth curves of broiler under different stocking densities by the Gompertz model. These researchers misconstrued the shape parameter (b) of the Gompertz model by suggesting that it is the λ. The fact that the shapeparameter gives very close outcomes to the initial weight misleads researchers who study poultry science.

The μ of the Logistic model was found bigger than that of Gompertz model. The Logistic model has a symmetric structure at the inflection point (Fig. 2). Therefore, the growth rate of the Logistic model at the inflection point has been found higher than that of the Gompertz model (Table 2, Fig. 2). Karkach (2006) and Beiki *et al.* (2013) used similar statements for the above-mentioned relationship between the Logistic and Gompertz model in his study.

The proportion of the variation explained was usually high for both of the models. The average R^2 values of models ranged from 0.9966 to 0.9994 (Table 2). The R^2 values were close to unity in most cases.While the Gompertz model had bigger average R^2 (0.9994), the Logistic model had smaller average R^2 (0.9966). A similar tendency occurred to the RMS values. While the Gompertz model had average RMS value (2.799), the Logistic model had average RMS (17.393). According to goodness of fit criteria, the Gompertz model has a better fit than the Logistic model.This result is in good agreement with findings of Anthony *et al.* (1991), Akbas and Oguz (1998), Narinc *et al.* (2010b) who reported that the Gompertz is the best growth model in quail.

The F ratio testand AIC criteria were used for the pairwisecomparison betweenmodels. It was found in data set that the Gompertzmodel was better than the Logistic model in terms of F ratio and AIC criteria (n=64).

The DW test was used to determine whether the errors are scattered randomly around the zero line wherethe significant DW test value indicates serial correlation of residual and a non-significant DW value indicates that serial correlation is small and residuals are distributed randomly around the zero line. The Gompertz model had the largest number of curves with non-significance DW value (total = 54) . While, the Logistic model had the largest number of curves with significant DW values (total = 64).The distribution of the 64 curves for each fitted model was illustrated by dividing them into two groups, which were the number of curves with $\leq$ 4 and $\geq$ 5 runs of sign, respectively. A small number of runs of signwere obtained when the residuals were not randomly distributed, so residuals of the same sign tend to cluster on some parts of the curve. Such clustering indicates that the data points differ systematically from the predictions of the curve. The Logistic model had the smallest number of runs of sign according to Gompertz model (= $\leq 4 = 62$, $P < 0.05$; $\leq 4 = 8$, $p < 0.05$). According to the results,the Gompertz model was more appropriate than the Logistic model.

The results of observed versus predicted regression were shown in Fig. 3. The values of intercept and slope were considered as 0 and 1, respectively. According to the results of the Pearson's correlation analysis, a perfect agreement were found between observed and predicted values of both Gompertz and Logistic models, respectively ($r^2 = 0.9948$, $P<0.001$; $r^2 = 0.9934$, $P<0.001$).

Akbas and Oguz (1998) reported that the various mathematical equations have been found for the Logistic and Gompertz models. These equations are some important parameters such as the maximal growth rate, inflection point age and inflection point of body weight used commonly in poultry breeding.

In conclusion of this study, these parameters which are biologically meaningful have been included in the Logistic and Gompertz models. In selecting the model due to the fact that fewer parameters and usability of parameters of the model are important, the λ and μ parameters were added instead of the growth rate constant and the shape parameter,

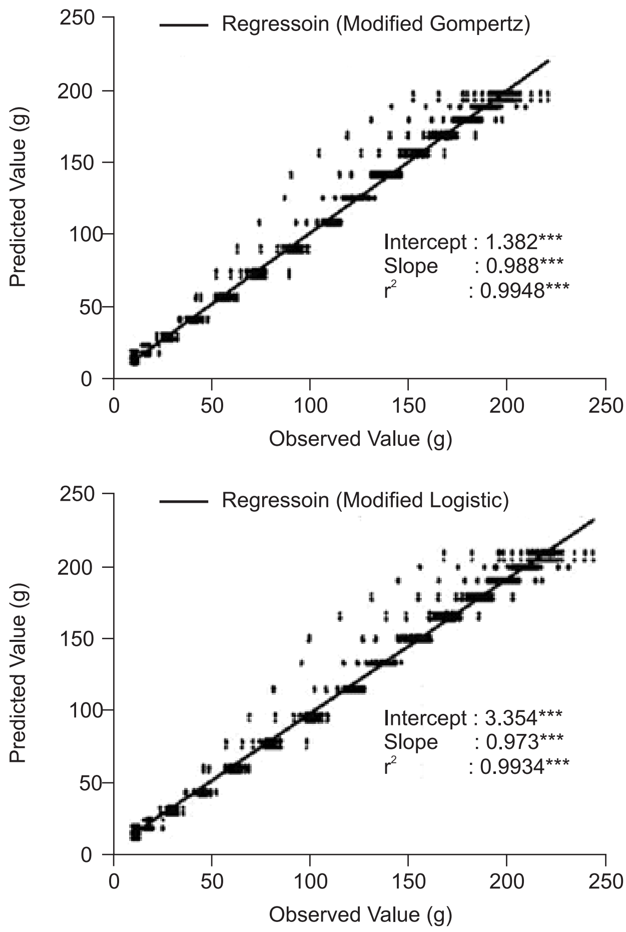

Fig. 3. Scatter plots of observed versus predicted regression (n=64,***: p<0.0001)

which is not very important in terms of animal breedingin the classical Gompertz and Logistic models, and therefore the model has been made more convenient.Thus,the Gompertz and Logistic models transformed into more useful models for not only poultry breeding but also other animal breeding such as goat, sheep and cattle.

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