JOURNAL OF APPLIED ANIMAL RESEARCH, 2018
VOL. 46, NO. 1, 112–117
https://doi.org/10.1080/09712119.2016.1268965

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Comparison of growth curves using non-linear regression function in Japanese quail

Selçuk Kaplan[a] and Eser Kemal Gürcan[b]

[a]Faculty of Veterinary Medicine, Department of Genetics, Namık Kemal University, Tekirdağ, Turkey; [b]Faculty of Agriculture, Department of Animal Science, Namık Kemal University, Tekirdağ, Turkey

ABSTRACT
This study was conducted to determine the goodness of fit of Gompertz, Logistic, Von Bertalanffy, Richards, Levakovich and Janoschek growth models in Japanese quail. Therefore, weekly live-weight data obtained from 372 females and 339 males were fitted. Females' live weights were found to be higher than that of males, and the first divergence in the growth of female and male birds occurred in 21–28 days, and it survived until the experiment ($P < .001$). The coefficient of determination (R^2), adjusted coefficient of determination (adj. R^2), mean square error (MSE), Akaike's information criteria (AIC) and Bayesian information criterion (BIC) were used to determine the best growth model. R^2 and adjusted R^2 values of the growth models were similar and close to 1, indicating that all models perform well in describing age-related changes in live weight in quail. Based on the MSE, AIC and BIC values, Richards model was determined to be the best fitting model to the growth data of both sexes. Consequently, it has been demonstrated that Richards function which has a flexible structure in terms of inflection point is the most appropriate growth function for both female and male birds.

ARTICLE HISTORY
Received 20 May 2016
Accepted 30 November 2016

KEYWORDS
Growth curve; flexible function; profile analysis; Richards; quail

1. Introduction

Growth in an animal is a whole of complex physiological and morphological processes from hatching to maturity which is defined as the increases in the weight and volume measurements of the organs or body for a given time (Topal et al. 2003; 2004; Topal & Bölükbaşı 2008). Numerous growth models have been used considering the growth of poultry species. There are differences between species, lines or individuals in terms of growth (Akbaş & Yaylak 2000; Narinç, Karaman et al. 2010). Live weights of birds at certain time points are related to both genetic factors and environmental conditions. Growth modelling in poultry species gives information on suitable slaughter age, general management and health conditions, age of sexual maturity and the effects of genetic improvement studies. Determining the deviation on the standard growth curve of the production flock in the feeding period is carried out to eliminate the negative effects (Akbaş & Oğuz 1998; Narinç, Üçkardeş et al. 2014). Scientists have been working on the expression of growth with different mathematical functions for a long time. In the case of birds, the observed growth curve is a sigmoidal (S-shape) structure (Akbaş & Oğuz 1998). Generally, semi-empirical non-linear regression functions have been used to model growth. These functions have a varying number of parameters, among which at least one has a biological meaning (Akbaş & Oğuz 1998; Tzeng & Becker 1981). The most common growth models used in poultry animals are Gompertz, Richards, Von Bertalanffy, Brody, Logistic, Negative Exponential, Morgan–Mercer–Flodin and recently the Hyperbolastic models (Ahmadi & Mottaghitalab 2007; Narinç, Aksoy, Karaman 2010).

Japanese quail (*Coturnix coturnix japonica*) have high meat and egg production capability. Having a short generation interval of three to four months, Japanese quail is used in genetic improvement studies, animal production treatments, and health and behavioural sciences as a model for poultry species (Akbaş & Oğuz 1998; Karabağ et al. 2010; Alkan et al. 2012). Recently, quail commercial production has increased, especially in South America, the Middle East and some African countries. In many studies conducted for the modelling of Japanese quail growth data, it has been reported that Gompertz model is the best model in terms of goodness-of-fit criteria (Tzeng & Becker 1981; Akbaş & Oğuz 1998; Narinç, Aksoy, Karaman 2010, Alkan et al. 2009; Alkan et al. 2012). In addition, Logistic and Von Bertalanffy growth models were used extensively in many studies (Narinç, Aksoy, et al. 2010). A common characteristic of these functions is the fixed model inflection point. Inflection point weight is identified as 37% of the asymptotic weight in the Gompertz model, 50% of the Logistic growth function and 37% of the Von Bertalanffy. This situation comes with some drawbacks. In fixed growth models, the genetic variations of asymptotic weight and point of inflection weight are equal and this situation is a problem for genetic improvement studies (Porter et al. 2010).

Recently, some researchers emphasized the use of flexible alternative models. Ahmadi and Mottaghitalab (2007) applied a flexible hyperplastic model in evaluating broiler growth data and compared it with Gompertz and Richards models. Similarly, Porter et al. (2010) used flexible structures of Richards, Von Bertalanffy and Morgan models alternatively to the Gompertz model in order to model the growth in turkeys. The aim of

CONTACT Selçuk Kaplan skaplan@nku.edu.tr Faculty of Veterinary Medicine, Department of Genetics, Namık Kemal University, Tekirdağ 59100, Turkey

this study was to compare non-linear models for best fitting which are used to determine the age-related changes in the live weight of female and male quails. The growth was followed and modelled with commonly used models such as Gompertz, Logistic and Von Bertalanffy. Moreover, flexible functions such as Richards, Levakovich and Janoschek were used to model the growth. Differences between the female and male quails were tested with profile analysis. This study aimed to compare male and female quail growth with the most appropriate function according to the goodness-of-fit criteria.

2. Material and methods

2.1. Animal material and husbandry

This study was performed in the Poultry Research Unit of Namık Kemal University, Turkey. Japanese quail (*Coturnix coturnix japonica*) were used as animal material. Approximately 1200 eggs were obtained from non-selected 40 males and 120 females. A total of 711 birds, including 372 females and 339 males were used in the study. All chicks were wing-banded and then weighted from hatching to six weeks of age. The chicks were housed in heated brooding cages (82.56 cm^2/quail) for the first three weeks. Then, they were transferred to grower cages (150 cm^2/quail). The diet supplied contained 24% CP (crude protein) and 2900 kcal of ME (metabolizable energy)/kg, and ad libitum feeding and a 23-h lighting programme were applied from hatching to the end of the experiment (Narinç et al. 2016). The study was approved by the Animal Experimentation Ethics Committee of Namık Kemal University (Protocol 2014/06).

2.2. Profile analysis

In determination of the difference between female and male quails in terms of body weight measurements at a time point, profile analysis method was utilized. Profile analysis is a special case of multivariate analysis of variance (MANOVA) (Alkan et al. 2012; Narinç, Aksoy, Karaman, Çürek İlaslan 2010). The method can be utilized to compare profiles of the levels of an independent variable either when different traits from the same experimental unit were considered, or when a single trait of the same unit was measured at several time points. Basically three hypotheses are tested by profile analysis. These tests are parallelism (H_{01}), overlap (H_{02}) and levels (H_{03}) of profiles. The most emphasized test in profile analysis is the parallelism test, and other tests depend on the provision of parallelism condition. Profiles of the groups are parallel if the differences between successive measurements of the dependent variable are the same at all levels of the independent variable. Null hypothesis is related to the parallelism test.

$$H_{01} = \begin{pmatrix} \mu_{11} - \mu_{21} \\ \vdots \\ \mu_{p-1,1} - \mu_{p,1} \end{pmatrix} = \cdots = \begin{pmatrix} \mu_{1,k} - \mu_{2,k} \\ \vdots \\ \mu_{p-1,k} - \mu_{p,k} \end{pmatrix}$$
$$g = 1, \ldots, k;\ t = 1, \ldots, p.$$

Here, '*k*' and '*p*' represent the number of groups in the independent variable and time points, respectively. The multivariate test statistics of the Hotelling–Lawley trace was used for testing parallelism (Srivastava 1987).

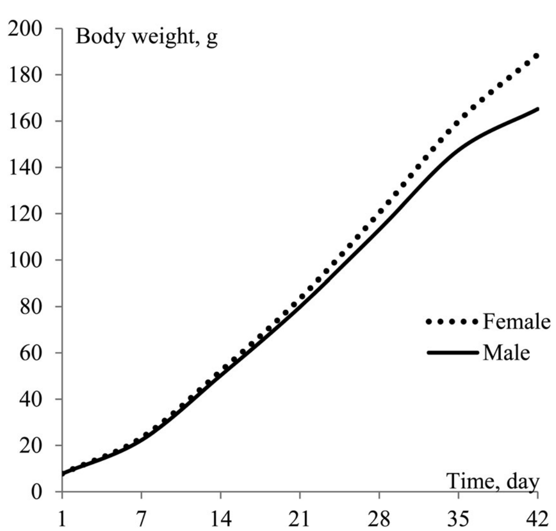

Figure 1. Average values of weekly body weights of female and male quail.

2.3. Non-linear regression

In this study, Richards, Janoschek and Levakovich that are known as flexible inflection point models and Gompertz, Logistic and Von Bertalanffy functions which exhibit fixed behaviour in terms of inflection point were used to determine the most consistent growth model for quails (Aggrey 2002; Korkmaz & Uckardeş 2013; Üçkardeş et al. 2013). Expression, growth rate and inflection point coordinates of these functions are presented in Table 1. β_0 parameter is the asymptotic (mature) weight, β_1 and β_2 are constants, β_3 is the hatching weight in the Janoschek model and β_3 is the age at the point of inflection in the Richards function. Model parameters were analysed utilizing the SAS 9.3 software NLIN (non-linear) procedure using the Levenberg–Marquardt iteration method (Karaman et al. 2013).

2.4. Goodness-of-fit criteria

The goodness-of-fit criteria to compare the studied functions that explain the growth of Japanese quail are as follows:

- Determination Coefficient, $R^2 = 1-(SSE/SST)$, where SSE is the sum of square errors and SST the total sum of squares.
- Adjusted Determination Coefficient, adj. $R^2 = R^2-((k-1/n-k)(1-R^2))$, where *n* is the number of observations and *k* the number of parameters.
- Mean Square Error, $MSE = SSE/(n-k)$, where *n* is the number of observations, SSE sum square of errors and *k* the number of parameters.
- Akaike's Information Criteria, $AIC = n.\ln(SSE/n) + 2k$, where *n* is the number of observations, SSE sum square of errors and *k* the number of parameters.
- Schwarz Bayesian Information Criterion, $BIC = n.\ln(SSE/n) + k.\ln(n)$, where *n* is the number of observations, SSE sum of square errors and *k* the number of parameters (Narinç, Üçkardeş et al. 2014).

Table 1. Model expressions and parameters of studied growth functions.

Model	Richards	Janoschek
Y_T	$\beta_0[1-(1-\beta_1)e^{[-\beta_2(t-\beta_3)/\beta_1^{\beta_1/(1-\beta_1)}]}]^{1/(1-\beta_1)}$	$\beta_0-(\beta_0-\beta_3)e^{-\beta_1 t^{\beta_2}}$
IP_T	β_3	$(\beta_2-1/\beta_1\beta_2)^{1/\beta_2}$
IP_W	$\beta_1^{1/(1-\beta_1)}$	$\beta_0-(\beta_0-\beta_3)e^{-((\beta_2-1)/\beta_2)}$
Model	Levakovich	Gompertz
Y_T	$\beta_0(1+\beta_1 t^{-\beta_2})^{-\beta_3}$	$\beta_0 e^{-\beta_1 e^{-\beta_2 t}}$
IP_T	$(\beta_1(\beta_3\beta_2-1)/\beta_2+1)^{1/\beta_2}$	$ln(\beta_1)/\beta_2$
IP_W	$\beta_0((\beta_3\beta_2-1)/(\beta_2(\beta_3+1)))^{\beta_3}$	β_0/e
Model	Logistic	Von Bertalanffy
Y_T	$\beta_0/(1+\beta_1 e^{-\beta_2 t})$	$\beta_0(1-\beta_1 e^{-\beta_2 t})^3$
IP_T	$(\ln \beta_1)/\beta_2$	$(\ln 3\beta_1)/\beta_2$
IP_W	$\beta_0/2$	$8\beta_0/27$

Y_T: Model Expression, IP_T: Point of inflection time, IP_W: Point of inflection weight.

3. Results

The results of the profile analyses, which were performed to determine the difference between consecutive time points for female and male quails' growth, are presented in Table 2. Actual growth curves of female and male birds are presented in Figure 1. The test statistic is significant ($P < .001$) and it was determined that there was no parallelism in the growth of female and male birds. Moreover, there was no difference between the sexes in terms of the first three weeks weight ($P < .001$).

The goodness-of-fit criteria (R^2, MSE, adj. R^2, AIC and BIC) computed using Richards, Janoschek, Levakovich, Gompertz, Logistic and Von Bertalanffy growth models are shown in Table 3 for both sexes. R^2 and adj. R^2 values of the growth models were similar and close to 1, indicating that all models perform well in describing age-related changes in live weight in quails. The values of MSE, AIC and BIC ranged between 3.62 and 23.02, −1044.97 and −499.76, and −488.37 and 1029.19, respectively. According to the lowest values of MSE, AIC, BIC, and high *R*2 and adj. *R*2, the Richards growth curve was determined to be the best fitting model to the growth data of both female and male quails.

Non-linear regression parameters of Richards, Janoschek, Levakovich, Gompertz, Logistic and Von Bertalanffy functions are presented in Table 4. The actual and estimated growth curves of the different models are shown in Figures 2 and 3.

4. Discussion

According to the results of the profile analyses, the first divergence in the growth of female and male birds occurred in 21–28 days ($P < .001$), and it remained until the end of the experiment ($P < .001$ for all successive time intervals). Similar findings were reported by many researchers (Alkan et al. 2012; Karaman et al. 2013). However, some researchers reported that the sexual dimorphism was not observed in quail (Oğuz et al. 1996; Beiki et al. 2013). This may be caused by environmental factors or empirical analysis. The comparison of the models according to the goodness-of-fit criteria was carried out seperately, as the growth samples of male and female birds were not parallel.

As seen in Table 3, R^2 and adjusted R^2 values of all models were found to be between 0.9987–0.9998 and 0.9901–0.9944, respectively. Many researchers (Balcıoğlu et al. 2005; Alkan et al. 2009; Narinç, Aksoy, Karaman 2010) have reported quite high values of the determination coefficients for growth models such as Richards, Logistic and Von Bertalanffy. In the current study, the best fitting growth model for female quail was determined to be the Richards growth function according to the lowest values of MSE, AIC and BIC (3.62, −1034.12 and −1018.94, respectively). Also, a similar result was found for male quail. MSE, AIC and BIC values of the Richards model were the smallest (6.01, −1044.97 and −1029.19, respectively). The Richards model, which also assesses the shape of a growth curve, has had limited use in quail (Hyankova et al. 2001; Aggrey et al. 2003; Beiki et al. 2013). Beiki et al. (2013) investigated the growth patterns of quail using seven non-linear regression models (Hyperbolastic 1, Hyperbolastic 2, Hyperbolastic 3, Richards, Logistic, Gompertz and Von Bertalanffy). They reported that the Richards growth curve was the best fitting model for quail growth data, which is in agreement with the results of the current study. The Richards model is important not only due to having a flexible structure with

Table 2. Differences between the gender groups for sequential weeks (Profile analysis results).

Sequential week difference	*P* value
Week 1	.2465
Week 2	.0918
Week 3	.0588
Week 4	.0006
Week 5	.0000
Week 6	.0000
Hotelling–Lawley Trace	.0001

Table 3. Goodness-of-fit criteria for the studied growth functions (female, $n = 372$; male, $n = 339$).

Functions	R^2	MSE	Adj. R^2	AIC	BIC
Female					
Richards	99.98	3.62	99.07	−1034.12	−1018.94
Janoschek	99.94	5.78	99.03	−960.51	−945.33
Levakovich	99.92	23.01	99.01	−505.80	−490.61
Gompertz	99.98	4.00	99.37	−988.87	−977.49
Logistic	99.92	17.68	99.31	−499.76	−488.37
Von Bertalanffy	99.98	4.90	99.37	−996.72	−985.33
Male					
Richards	99.97	6.01	99.18	−1044.97	−1029.19
Janoschek	99.87	9.46	99.09	−981.68	−965.91
Levakovich	99.91	21.55	99.12	−667.84	−652.07
Gompertz	99.97	6.10	99.44	−1040.83	−1029.00
Logistic	99.93	13.17	99.40	−747.84	−736.01
Von Bertalanffy	99.95	8.86	99.43	−899.00	−887.17

Y_T: model expression; β_0: asymptotic weight; β_1, β_2: constants; β_3: hatching weight in Janoschek; β_3: age at the point of inflection in Richards; IP_T: point of inflection time; IP_W: point of inflection weight.

Table 4. Estimates of parameters for the studied growth functions.

Functions	β_0	β_1	β_2	β_3	IP_T	IP_W
	Female					
Richards	324.0	0.818	0.040	25.29	25.29	107.44
Janoschek	354.9	0.002	1.552	7.27	28.18	111.31
Levakovich	251.7	836,145	3.846	0.39	23.20	134.36
Gompertz	287.7	3.588	0.051	–	25.05	105.84
Logistic	219.4	16.679	0.109	–	25.82	109.70
Von Bertalanffy	374.8	0.751	0.031	–	26.20	111.05
	Male					
Richards	216.4	1.085	0.064	21.30	21.30	82.88
Janoschek	215.6	0.002	1.718	8.07	22.41	78.96
Levakovich	231.7	957,861	3.569	0.35	20.98	107.27
Gompertz	222.8	3.494	0.059	–	21.20	81.96
Logistic	183.3	15.492	0.118	–	23.22	91.65
Von Bertalanffy	265.6	0.740	0.039	–	20.45	78.69

Y_T: model expression; β_0: the asymptotic weight; β_1, β_2: constants; β_3: hatching weight in Janoschek; β_3: age at the point of inflection in Richards; IP_T: point of inflection time; IP_W: point of inflection weight.

respect to the point of inflection, but also due to having more interpretable parameters than others.

Our results are in disagreement with the previous reports putting forward that the Gompertz model was the best-fitting model for galliforms (Tzeng & Becker 1981; Akbaş & Oğuz 1998; Narinç, Aksoy, Karaman 2010). Growth is a phenomenon affected by both genetics and environmental conditions, and thus, it does not depend on species, strain, line or family (Narinç & Aksoy 2012; Üçkardeş & Narinç 2014). Therefore, it is necessary to determine the best-fitting model for every studied flock. Moreover, the Gompertz model was defined the second best fitting function in the current study. According to our knowledge, there is no study about the analyses of quail growth data using Janoschek and Levakovich functions. Both functions showed good fit to the quail growth data as indicated by the R^2 and adj. R^2 values. Especially the Janoschek function is the prominent one due to having more interpretable parameters (parameters of mature weight and hatching weight).

Asymptotic weight parameter values of the Richards model for female and male quail (324.0 and 216.4 g) are in agreement with the value reported by Beiki et al. (2013) for their control group involving both sexes. In another study (Akbaş & Oğuz 1998), the estimated mature weight parameter (β_0) of the Gompertz model for the selection line (239.5 g) was higher than that of the control line (208.3 g), and that of female quail (244.4 g) were higher than male ones (203.5 g). In most of the studies in which the growth of Japanese quail was examined by the Gompertz model, the mature weight parameter was found to be from 204 to 281 g (Akbaş & Oğuz 1998; Kızılkaya et al. 2005; Narinç et al. 2009; Alkan et al. 2009; Narinç, Aksoy, Karaman 2010). Alkan et al. (2009) applied selection to increase the live weight in Japanese quail. They estimated β_0 parameter values to be 295–306 g and 151–164 g for a selected and a non-selected line, respectively. In the other study, Alkan et al. (2009) performed thermal manipulation in the embryonic period of quail, and they reported that the mature weight parameters

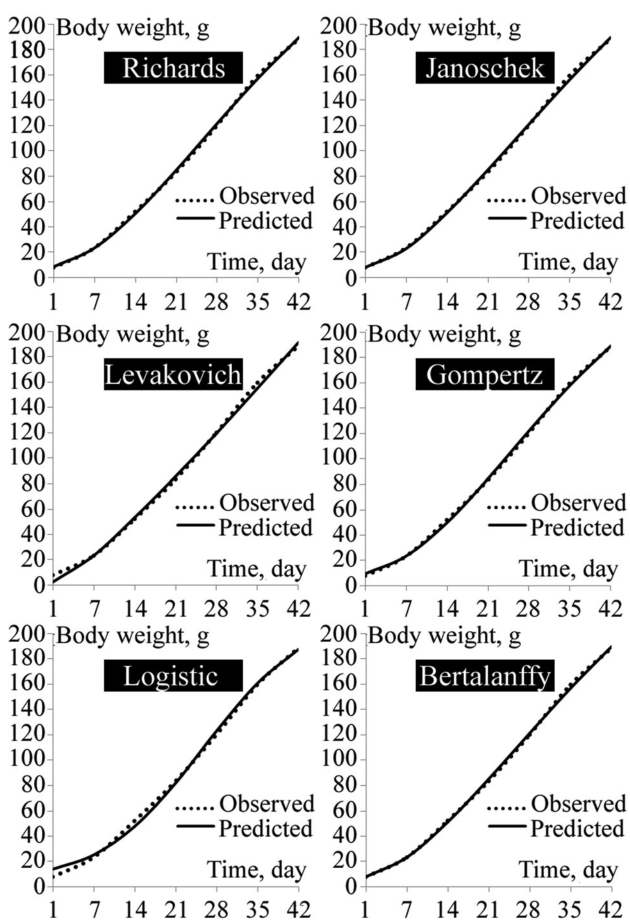

Figure 2. Growth curves of female quail by different growth functions.

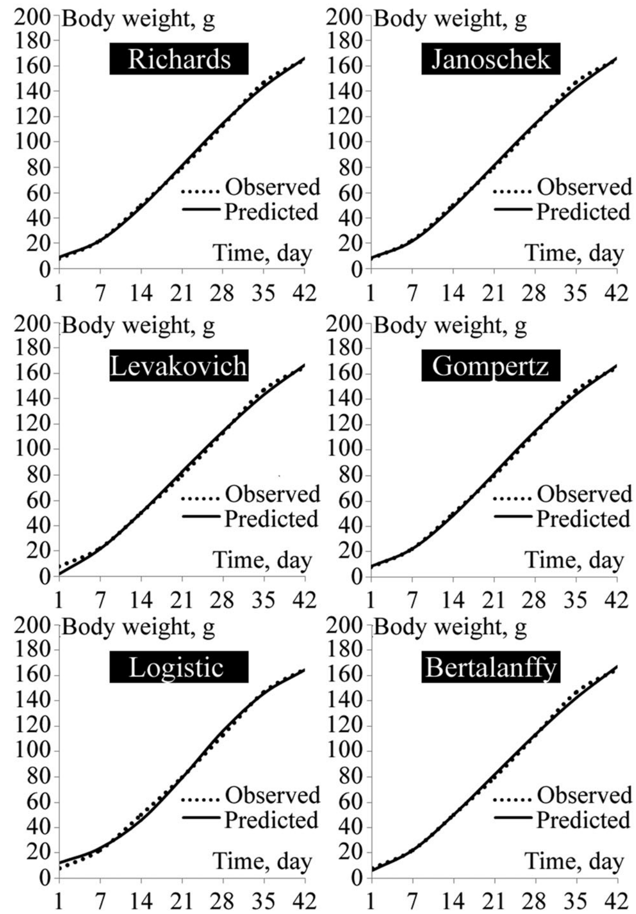

Figure 3. Growth curves of male quail by different growth functions.

were found to be between 203 and 241 g. It is expected that quail growth and growth curve parameters can be changed via breeding studies or environmental practices (Narinç & Aksoy 2014; Narinç, Aksoy et al. 2014).

In all models, β_1 and β_2 are constants related to the shape of the growth curves, and are not intended to be biological meaningful. β_1 and β_2 parameter values for both male and female quail were in the range of 0.002–957786 and 0.039–3.846, respectively. In the current study, β_3 parameter of the Richards model representing age at the point of inflection was estimated to be 25.29 and 21.30 days for female and male quail, respectively. Age at the point of inflection of the Richards function for a non-selected control quail line was determined as 17.08 and 16.38 days for female and male quail, respectively (Aggrey et al. 2003). It is thought that these values are lower than that of the current study due to using lower weight quail. Similarly, Aggrey et al. (2003) reported that the mature weight parameters (β_0) of the Richards function were found to be 144.01 g and 104.42 g for female and male quail.

In the current study, age and weight at the point of inflection of the Gompertz model were determined to be 25.05 days and 105.84 g for female quail, 21.20 days and 81.96 g for male quail. However, Akbaş & Oğuz (1998) reported lower values (19.75 days – 88.13 g and 20.20 days – 76.62 g, respectively) for age and weight at inflection point using the Gompertz model in a selected quail line and a randomly mated line. In other study, Kızılkaya et al. (2005) reported that age and weight at the point of inflection of the Gompertz model were found to be between 16.19 and 17.05 days, and from 81.57 to 82.96 g, respectively. Alkan et al. (2009) estimated age and weight at the point of inflection using the Gompertz model for selected and control lines. They reported that the mentioned parameters in the selection line were found to be 15.68 days and 113 g for female, and 17.64 days and 108 g for male quail. Also, 18.27 days and 82.3 g for female quail, and 17.99 days and 75 g for male quail were found for the control line. As shown here, growth curve parameters of quail can be affected by both the selection and environmental conditions.

As a result, it has been demonstrated that the Richards function, which has a flexible structure in terms of inflection point, is the most appropriate growth function for both female and male birds. In addition, β_3 parameter which was estimated with the Janoschek function represents the hatching weight. This parameter was estimated to be 7.27 g and 8.07 g for female and male birds, respectively. Potential use of the β_3 parameter of the Janoschek model in breeding programmes can be examined by revealing its genetic relationship with weekly body weights, adult weight parameter and point of inflection coordinates. In order to include the parameters of Richards and Janoschek models in breeding programmes, heritabilities of the parameters and their genetic relationships with production traits should be estimated.

Funding

This study was supported by Namık Kemal University, Scientific Research Project Unit, NKUBAP.00.23.AR.14.06.

Disclosure statement

No potential conflict of interest was reported by the authors.

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