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FLEXIBLE ALTERNATIVES TO MODELS WIDELY USED FOR DESCRIBING GROWTH IN JAPANESE QUAIL

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ABSTRACT

Mathematical functions for modeling the growth of animals are separated into two groups called fixed and flexible according to their inflection behaviors. The aims of this study were to compare fixed and flexible growth functions and to determine the best fit model for the growth data of Japanese quail. The long term growth patterns of Japanese quail were monitored during 110 days from day-old to slaughtering, and were analyzed. The fixed and flexible models used in the study were Gompertz, Logistic, Von Bertalanffy and Levakovich, Janoschek, Morgan Mercer Flodin, respectively. The differences in weight between growth profiles of female and male birds were tested via profile analysis also known as Repeated MANOVA.The results of Profile Analysis revealed that females' live weights were heavier ($P<0.01$). In order to evaluate growth functions, the R^2 (coefficient of determination), adjusted R^2 (adjusted coefficient of determination), MSE (mean square error), AIC (Akaike's information criterion) and BIC (Bayesian information criterion) goodness of fit criteria were used. In the study, it was determined that the best fit model from female and male quail growth data on the basis of these goodness of fit criteria is Janoschek model which has a flexible structure. The Janoschek model is not only important because it has a higher number of parameters with biological meaning than the other functions (the mature weight and initial weight parameters), but also because it was not previously used in the modeling of the quail growth.

Keywords: Flexible models, Growth curve, Janoschek model, Quail.

INTRODUCTION

In modeling of data related to agriculture, asymptotic models are mostly used and these models are classified into three categories, namely teleonomic, empirical and mechanistic models (Thornley and France, 2007). Because of the limited use of the teleonomic models, the mathematical models of the growth have an empirical or a mechanistic structure. The parameters of a good mechanistic model should represent biochemical processes that control the growth. However, if the details of the mechanisms that manage the process are not known, and if the interpretation of data obtained in the experiment is in question, the mathematical function of the process can be empiric and the goodness of fit the model allowsones to evaluate the ability of compliance to the experimental data (Narinç *et al*., 2014a). Majority of mathematical models have been used for a long time in order to model the growth-time data in poultry, and are asymptotic-mechanistic models. These models include the biological functions that are based on the fact of the animal's growth. The independent variable is at infinite in the models while the dependent variable is a predicted asymptotic value. Many models have been made by including more mechanistic biological meaningful parameters in an empirical infrastructure. In this way, many models are derived from each other. A comprehensive review and history of the growth models used in poultry species is given by DarmaniKuhi *et al*. (2010).

Japanese quail (*Coturnix coturnix Japonica*) is known as the smallest species in livestock animals. Futhermore these birds have high meat and egg yield for commercial production. (Üçkardeş *et al*., 2015).Japanese quail has been used as the model animal in studies of poultry breeding, animal production, health and behavioral fields.(Karabağ *et al*., 2010; Alkan *et al*., 2012). Many studies have been conducted for along time to modelquail growth in obtaining form the production modeland the genetic improvement.However, the growth data is collected until the age ofsexual maturity was analyzed in several previous studies (Akbaş and Oğuz, 1998; Gürcan *et al*., 2012; Beiki *et al*., 2013; Narinç *et al*., 2014b). Even though quail reaches slaughter age (about 35-42 days of age), the growth still goes on. It is known that the sexual maturity age of Japanese quail is between 37-44 days (Minvielle *et al*., 2000; Karabağ *et al*., 2010; Narinç *et al*., 2013). However, as it is known, the sexual maturity in livestock occurs when nearly 2/3 of the mature weight is reached. In this situation, the parameters which were obtained from nonlinear regression analyses used the incomplete growth data may be incorrect.

The Gompertz model was reported to be the best model in the goodness offit criteria in several previous studies conducted for modeling data growth-time data in Japanese quail (Akbaş and Oğuz, 1998; Alkan *et al*.,2009; Narinç *et al*., 2010b; Üçkardeş and Narinç, 2014). However, it was reported that Logistic and VonBertalanffy growth models have been used extensively (Narinç *et al*., 2010b). The common feature of these three growth functions of the model is that these models have fixedinflection point. The weight at the inflection point is defined as 37% of the asymptoticweight in the Gompertz model, as 50% in the Logistic growth function and as 30% inthe Von Bertalanffy model (Akbaş and Oğuz, 1998). This comes along with several problems; for example, inbreeding studies, it can be seen as a loss in terms of breeding since geneticvariations of these parameters are equal to each other. In recent years, someresearchers have focused on flexible alternative models. Ahmadi and Mottaghitalab (2007) applied Hyperbolastic models in order to provide a more flexible data structure forbroiler growth data, and compared with some models, such as the Gompertz andRichards. Similarly, Porter *et al*. (2010) used the flexible structures of Richards, VonBertalanffy and Morgan models in order to model the growth in turkeys as analternative to Gompertz model.

The purpose of this study was to model the growth timedata of Japanese quail by means ofthe growth functions having flexible and fixed structures and to determine the best fitmodel describing the sigmoid relationship between the growth-time data. In the study, the growth in Japanese quail was monitored for a long-term (110days) and the growth was modeled with widely used models, such as Gompertz, Logistic, Von Bertalanffy as well as the flexible functions, such as Levakovich, Janoschek, Morgan Mercer Flodin. The differences between the growth profiles ofmale and female quail were tested by Profile analysis.In the study, it was aimed tocompare the growth of male and female quail with the best fit function that wasdetermined according to the goodness of fit criteria.

MATERIALS AND METHODS

Animal husbandry and data collection: The study was conducted with animals kept in quail unit of Namık Kemal University Department of Animal Science. The live weights of the quail that were used as animal material were weighed in 10-day periods until the age of 110 to 125 days from hatching. As soon as the animals hatched, their identifications were performed by attaching the wing and leg numbers. A total of 120 animals, including 70 females and 50 males were used in the study. The birds obtained from a non-selected and randomly mated flock in a commercial producer. The sex allocation of the animals used in the study was done by looking at the 3 week-old animals' chest feathers. At this age, the ones with dark chest feathers were defined as male and the ones with light chest feathers were defined as female. The newly hatched animals were grown in the host machine for 3 weeks and were grown in group cages after this age. The animals were fed with 28% crude protein and mixed feed containing metabolic energy of 3050 kcal/kg in the initial period, and fed with 20% crude protein and mixed feed containing metabolic energy of 2900 kcal/kg in the growth period as ad-libitum. For the first week 23 hours light, afterwards 16 hours light were supplied for birds up to end of the study (Alkan*et al*., 2012). The birds were weighed regularly using a digital scale (precision of 0.1 g).

Growth functions: In the study, tLevakovich, Janoschek and Morgan Mercer Flodinnon-linear growth models are described as flexible in the inflection point, whereas Gompertz, Logistic and Von Bertalanffy non-linear functions exhibit stable behavior in terms of the inflection point. The expressions, growth rates and inflection point coordinates of these functions are given in Table 1. In all models, the β_0 parameter refers to the asymptotic weight, in addition, the β_3 parameter of Janoschek model presents the initial live weight; all the other parameters are defined as the constants related to the shape and the instant growth rates of the growth curve.

Goodness of fit criteria: The following goodness of fit criteria were used to evaluate performance of the candidate non-linear functions used for describing growth – time data in Japanese quail.(Narinç *et al*., 2010b; Orhan *et al*. 2010; Eyduran and Akbaş, 2015).

The Determination Coefficient, R^2=1-(SSE/SST); where, SSE: Sum of square errors,SST: Total sum of squares.

The Adjusted Determination Coefficient, adj.R^2=R2-((k-1/n-k)(1- R^2)); where, n: thenumber of observations, k: the number of parameters.

The Mean Square Error, MSE=SSE/(n-k); where, n: the number of observations, SSE: Sumsquare of errors, k: the number of parameters.

The Akaike's Information Criterion, AIC=n.ln(SSE/n)+2k; where, n: the number ofobservations, SSE: Sum square of errors, k: the number of parameters.

The Schwarz Bayesian Information Criterion BIC=n.ln (SSE/n)+k.ln(n); where, n: the number of observations, SSE: Sum of square errors, k: the number of parameters

Comparison of male and female growth profiles: The profile analysis method has been used in determining the difference between the female and male quail in terms of the live weights measured at equal time points. The profile analysis is a special form of multivariate analysis of variance (MANOVA) (Narinç *et al*., 2010c; Eyduran *et al*., 2008; Eyduran and Akbaş, 2010). This method has been used in the comparison of the profiles related to the level of independent variable whena quantitativetrait like body weight, and milk yield is taken from the same experimental unit at different time points. Basically, three hypotheses have been tested by profile analysis. These tests included the parallelism (H_{01}), overlapping (H_{02}) and level (H_{03}) tests of profiles. The most emphasized test in profile analysis is the parallelism test and the other tests depend on providing the parallelism condition. If the difference between the successive points of the measurements of the dependent variable is the same at all levels of the independent variable, then the group profiles are parallel. The null hypothesis in the parallelism test can be shown as (Sristava, 1987; Eyduran *et al*., 2008);

$$H_{01} = \begin{pmatrix} \mu_{11} - \mu_{21} \\ : \\ \mu_{p-1,1} - \mu_{p,1} \end{pmatrix} = \cdots = \begin{pmatrix} \mu_{1,k} - \mu_{2,k} \\ : \\ \mu_{p-1,k} - \mu_{p,k} \end{pmatrix}$$

$$g = 1,\ldots,k\ ;\ t = 1,\ldots,p$$

In the equations, "k" refers to the number of groups included in an independent variable, "p" refers to the time points. The Hotelling-Lawley Trace statistic, which is one of the multivariate test statistics, was used in the testing of the parallelism (Narinç *et al*., 2010c). All of statistical analyses and calculations were performed using SAS software (SAS Institute, 2011).

RESULTS AND DISCUSSION

As a result of the analyzes conducted by using different non-linear growth functions, the values estimated for β_0 parameter representing the mature weight in each function (174.0-193.4 g, Table 2), were found to be consistent with the previous values (186.9 g and 174.2 g, respectively) estimated with the Gompertz and Logistic functions reported by Gürcan *et al*. (2012). The β_0 parameter was reported between 215.0-244.7 g by the several previous researchers, who conducted non-linear growth modeling studies of randomly mating quail, such as Akbaş and Yaylak (2000), Hyankova *et al*. (2001), Kızılkaya *et al*. (2005), Alkan*et al*. (2012) and Narinç *et al*. (2014b). On the contrary, Anthony *et al*. (1986) estimated β_0 parameter as 119.9 g with the Gompertz function, and Aggrey (2009) estimated it as 103.5 g for the male quail and 132.4 g for the females with the Logistic function.

It was observed that there were quite considerable differences between the inflection point of ages and of weights estimated with different functions in Japanese quail (Table 2). The inflection point of ages estimated with Levakovich, Janoschek and Morgan Mercer Flodin functions (51.25, 49.21, 56.56 days, respectively) defined as flexible in terms of the inflection point were found higher compared to the values estimated for the Gompertz, Logistic and Von Bertalanffy models point (33.27, 40.25, 29.20 days, respectively). Similar results were also encountered for the inflection point of ages (Table 2).The growth analysis in Japanese quail performed by Beiki *et al*. (2013) was conducted on 7 non-linear functions, and the inflection points of ages were reported to be between 14.34-19.74 days.The values of inflection point (age and weight) reported by Beiki *et al*. (2013) was found significantly lower than the present values recorded in this study. Similarly, Gürcan *et al*. (2012), who performed the analysis with 5 different growth models, reported that quail inflection point of ages of thegrowth curve ranged between 17.60 and 30.97 days. In addition, Akbaş and Oguz (1998), Kızılkaya *et al*. (2006), Narinc *et al*. (2010b) reported lower inflection point of the age and weight values compared to our study. The reason for this inconsistency has been thought to be due to the growth data analyzed by some researchers were obtained from the quail growth occurred from hatching to 35-56 days. However, 110 days of growth data were used in this study. Growth parameters might have been estimated wrongly in previous studies due to the fact that the growth period was incomplete. Indeed, when examining Figure 1, of live weight gain in quail can be observed to take up to about 70 days of age.

The R^2 and adjusted R^2 values of non-linear growth functions in this study were found very close to each other (Table 2), and because they are too close to 1, all of the functions have been determined to be quite successful in explaining the data. In addition, the lowest values in MSE, AIC and BIC goodness of fit criteria, were obtained from the Janoschek function, followed by the Morgan Mercer Flodin function as the second best fit model in terms of MSE, AIC and BIC values (27.82, 41.08, 42.67, respectively) and the Logistic function as the third one (34.64, 45.09, 46.54, respectively). Similar results were reported for residual means and standard deviations (Table 2). In literature, many studies have been conducted to determine the best model that describes the growth in Japanese quail (Tzeng and Becker, 1981; Anthony *et al*., 1991; Akbaş and Oğuz, 1998; Kızılkaya *et al*., 2005; Alkan *et al*., 2009; Narinc *et al*., 2010a; Beiki *et al*., 2013). The functions specified in these studies were listed as follows: Gompertz, Richards, Logistic, Bertalanffy, Brody, Morgan Mercer Flodin, Negative Exponential and Hyperbolastic. Tzeng and Becker, (1981), Akbas and Oguz (1998), Alkan*et al*. (2009), Narinç *et al*. (2010a) reported that Gompertz function was the best fit growth curve function describing the growth-time relationship for the quail in their studies, whereas Kızılkaya *et al*. (2005) and Gürcan *et al*. (2012) reported that the Logistic function describes the data better, and Beiki *et al*. (2013) reported that the Richards function describes the data better. As far as we know, there are no studies conducted on the analysis of the growth in the Japanese quail by using Levakovich and Janoschek functions in the literature.

As a result of comparison of live weights of male and female quail in the repeated measures structure with the Profile analysis (Table 3), it was determined that the profiles were not parallel to each other ($P<0.05$) and that the female quail live weight was higher than that of males. This result supports the finding reported in many studies (Toelle *et al*., 1991; Oğuz *et al*., 1996; Sezer *et al*., 2006; Karaman *et al*., 2013) where the females of Japanese quail had higher weights than that of males. The growth analysis of male and female quail was performed separately by the Janoschek function selected as the best fit model to describe the growth of quail, and the growth curves, absolute and the relative growth rate values are shown in Figure 2. As seen from Figure 2, the first difference between the live weights of female and male quail emerged between the ages of 24-31 days (Table 3) and continued throughout the experiment ($P<0.05$). These findings were consistent with the findings of many researchers who reported the difference in live weights of male and female quail emerged in 3-4 weeks of age (Toelle*et al*., 1991; Soysal *et al*., 2000.

Table 1.Model expressions and parameters of study growth functions

Model	**Levakovich**	**Janoschek**
Y_T	$\beta_0\left(1+\beta_1 t^{-\beta_2}\right)^{-\beta_3}$	$\beta_0-(\beta_0-\beta_3)e^{-\beta_1 t^{\beta_2}}$
AGR	$\beta_3\beta_1\beta_2\beta_0\left(1+\beta_1 t^{-\beta_2}\right)^{-\beta_3-1} t^{-\beta_2-1}$	$\beta_1\beta_2(\beta_0-\beta_3)t^{\beta_2-1}e^{-\beta_1 t^{\beta_2}}$
RGR	$\beta_3\beta_1\beta_2\, t^{-\beta_2-1}(Y_t/\beta_0)^{1/\beta_3}$	$\beta_1\beta_2 t^{\beta_2-1}\left((\beta_0/\beta_3)-1\right)$
IPT	$(\beta_1(\beta_3\beta_2-1)/\beta_2+1)^{1/\beta_2}$	$(\beta_2-1/\beta_1\beta_2)^{1/\beta_2}$
IPW	$\beta_0((\beta_3\beta_2-1)/(\beta_2(\beta_3+1)))^{\beta_3}$	$\beta_0-(\beta_0-\beta_3)e^{-((\beta_2-1)/\beta_2)}$
Model	Morgan Mercer Flodin	Gompertz
Y_T	$\beta_0-\left((\beta_0-\beta_3)/\left(1+(\beta_1 t)^{\beta_2}\right)\right)$	$\beta_0 e^{-\beta_1 e^{-\beta_2 t}}$
AGR	$(\beta_0-Y_t)\left(\dfrac{\beta_2{\beta_1}^{\beta_2}t^{\beta_2-1}}{1+(\beta_1 t)^{\beta_2}}\right)$	$\beta_1\beta_2 e^{-\beta_2}Y_t$
RGR	$\left(\dfrac{\beta_0}{Y_t}-1\right)\left(\dfrac{\beta_2{\beta_1}^{\beta_2}t^{\beta_2-1}}{1+(\beta_1 t)^{\beta_2}}\right)$	$\beta_2(ln\beta_0-lnY_t)$
IP_T	${\beta_1}^{-1}((\beta_2+1)/(\beta_2-1))^{1/\beta_2}$	$ln(\beta_1)/\beta_2$
IP_W	$\dfrac{(\beta_2-1)\beta_0+(\beta_2-1)\beta_3}{2\beta_2}$	β_0/e
Model	Logistic	Von Bertalanffy
Y_T	$\beta_0/\left(1+\beta_1 e^{-\beta_2 t}\right)$	$\beta_0\left(1-\beta_1 e^{-\beta_2 t}\right)^3$
AGR	$\beta_0\beta_1\beta_2 e^{-\beta_2 t}/\left(1+\beta_1 e^{-\beta_2 t}\right)^2$	$3\beta_2\beta_0\left(1-\beta_1 e^{-\beta_2 t}\right)^2\beta_1 e^{-\beta_2 t}$
RGR	$\beta_2(1-Y_t/\beta_0)$	$3\beta_2\left((\beta_0/Y_t)^{1/3}-1\right)$
IP_T	$(ln\beta_1)/\beta_2$	$(ln3\beta_1)/\beta_2$
IP_W	$\beta_0/2$	$8\beta_0/27$

Y_T: Model Expression, AGR: Absolute Growth Rate (dY_t/dt), RGR: Relative Growth Rate ($(dY_t/dt)/Y_t$), IP_T: Point of inflection time, IP_W: Point of inflection weight

Table 2. Goodness of fit criteria for growth models

Parameters and Criterion	Levakovich	Janoschek	Morgan Mercer Flodin
β_0	174.0	174.5	181.3
β_1	7.78×10^{23}	$4.15\text{x}10^{-6}$	1.406
β_2	13.42	3.08	1.023
β_3	0.123	10.26	74.73
IP_T	51.25	49.21	56.56

IP_W	116.9	90.73	75.93
R^2	0.9971	0.9976	0.9954
adj R^2	0.9957	0.9967	0.9937
MSE	58.15	14.81	27.82
AIC	51.89	34.15	41.08
BIC	53.83	35.74	42.67
Mean RSD	1.74	$8x10^{-7}$	$8x10^{-7}$
SD RSD	6.25	3.28	4.50
	Gompertz	Logistic	Von Bertalanffy
β_0	189.0	180.3	193.3
β_1	5.59	30.62	1.17
β_2	0.052	0.085	0.043
IP_T	33.27	40.25	29.20
IP_W	69.74	90.15	57.27
R^2	0.9942	0.9981	0.9919
adj R^2	0.9923	0.9974	0.9891
MSE	103.60	34.64	145.80
AIC	58.23	45.09	62.33
BIC	59.69	46.54	63.79
Mean RSD	1.95	0.99	2.56
SD RSD	8.98	5.22	11.59

Table 3. Differences among the gender groups for different weeks (Profile analysis results)

Sequential Week Difference	**P Value**
3-10	0.2465
10-17	0.9918
17-24	0.2888
24-31	0.0156
31-38	0.0168
38-45	0.0280
45-52	0.0044
52-68	0.0011
68-72	0.0001
72-85	0.0001
85-110	0.0001
Hotelling-Lawley Trace	0.0001

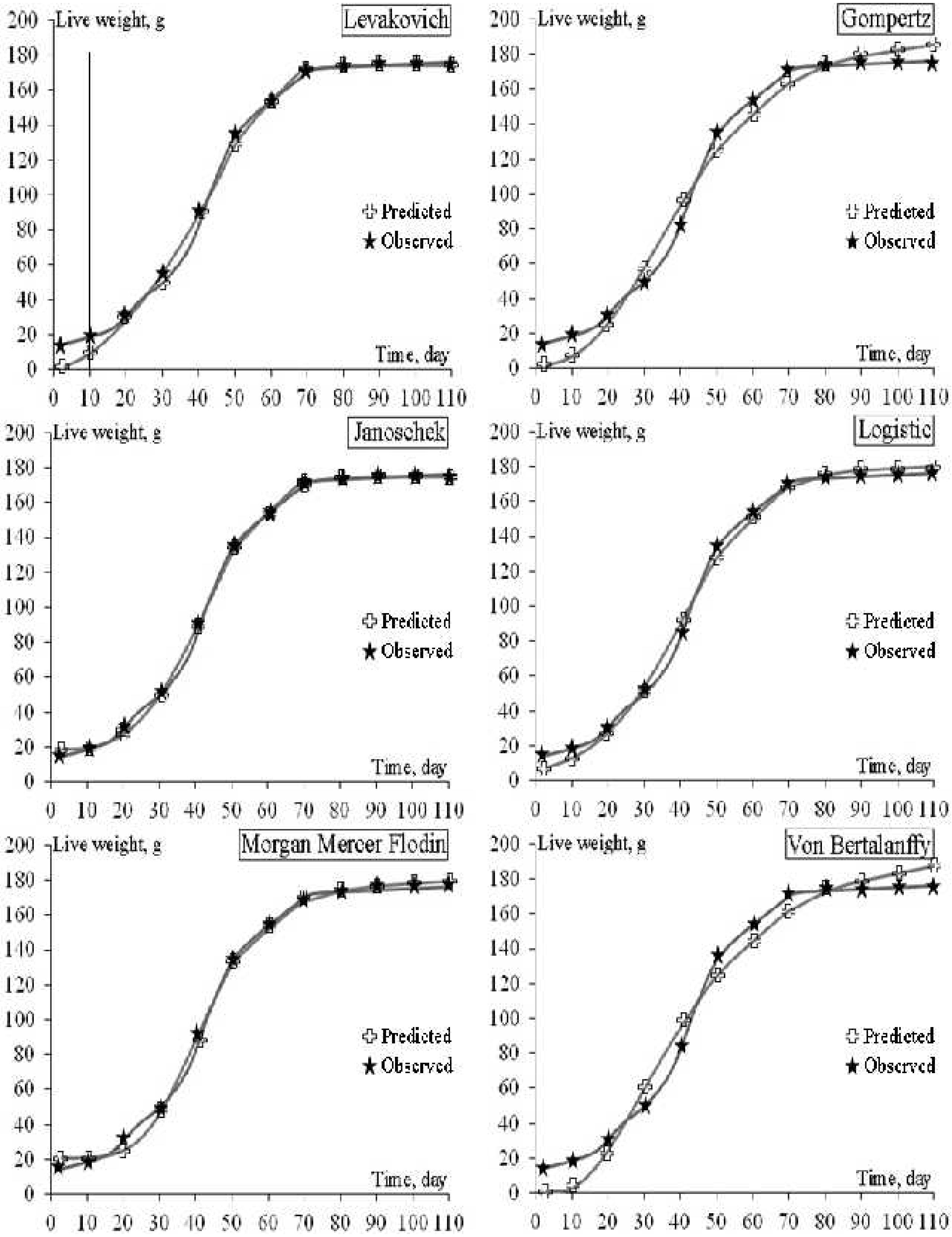

Figure 1. Shapes of growth curve

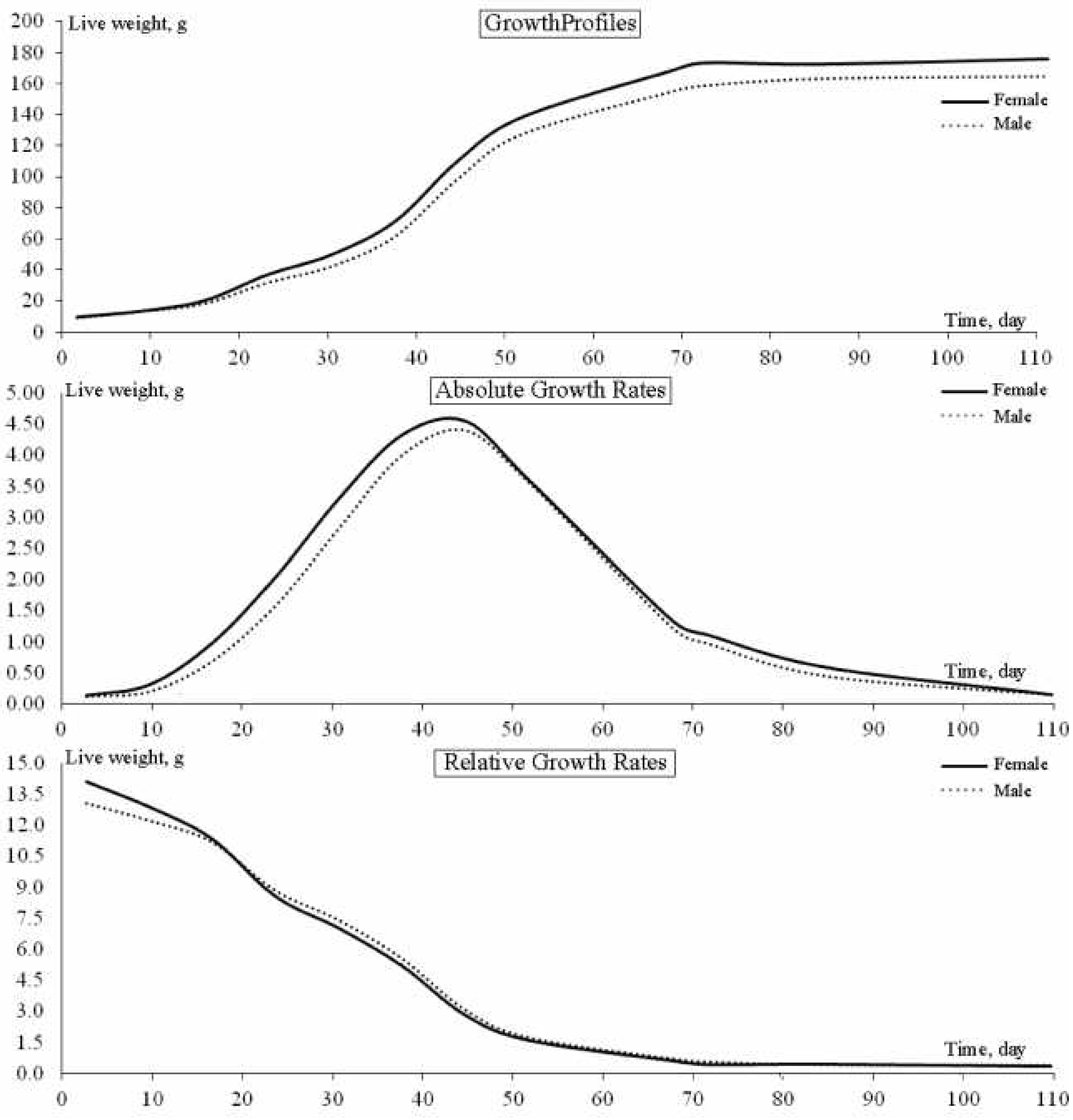

Figure 2. Growth curves and growth rates of female and male quails

Conclusion: In this study, the Janoschek function, which is the best fit model in terms of quail growth data, has a flexible structure in terms of inflection point. Recently, it has been recommended to use the functions in flexible structure by various researchers (Porter *et al.*, 2010; Darmani Kuhi *et al.*, 2010; Faridi *et al.*, 2011). The inflection point coordinates of the flexible functions are not constant values, and this is especially important for genetic variation.In breeding studies, the genetic variance of inflection point coordinates estimated from functions with a fixed class, such as the Gompertz and Logistic functions is equal to the genetic variance of the adult weight parameters. And this can lead to some problems in using these characteristics as selection criteria. The Janoschek model is not only important because it has a higher number of parameters with biological meaning than the other functions (the mature weight and initial weight parameters), but also because it was not previously used in the modeling of the quail growth.

Author contributions: E. K. G: was responsible all of the study and statistical analyses. Ö. Ç.: has reviewed the paper. S. K.: was responsible the animal management and preparation of data.

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