Model parameters of growth curves of three meat-type lines of Japanese quail

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ABSTRACT: This study was focused on a comparison of the growth characteristics and parameters of three meat-type lines of Japanese quail. The body weight data of wild-type, dotted-white and extended-brown quail lines over time were collected and fitted to Richards equation. The relevant parameters were compared based on the Confidence Interval Test. Confidence Interval Test calculates the percentages of model predictions staying in the confidence intervals of the corresponding experimental data. Both sexes of brown quails showed lower weight gains than the other two lines. Behind the inflection point a decline in the absolute growth rate was slowest for brown females. In general, Richards model parameter values showed deviations of one line from the other lines to a varying extent. Shape parameter for males (0.335–0.618) and maturation index for females (0.067–0.077) tend to be the most critical parameters. When the overall models were used to predict the weight of other lines, the models of white and wild males showed great similarity. Overall model predictions for male brown and white quails, for female brown and wild-type quails showed the largest differences. Like in males, white and wild females were the closest lines but the likeliness percentage was lower than that for males. The proposed method of parameter comparison can be a useful tool for researchers working on biological modelling.

Keywords: quail; growth curve; Richards function; nonlinear model parameter comparison

In biology growth, which is under the control of genetics and environment, can be described by the changes throughout the life accompanied by the utilisation of materials, and leading to an increase in volume, size, or shape of an organism. These changes can be followed by measurements of body weight in regular intervals and summarised by mathematical equations fitted to growth curves. Biologically interpretable growth parameters can smooth the variation caused by the environment and random events (Aggrey, 2002, 2003). Biological meanings of the model parameters provide an opportunity to develop breeding strategies by modifying either management practices or genetic makeup of the shape of growth curves. Additionally, these functions allow for the study of differences between the lines that have diverse genetic background.

In spite of the small body size of Japanese quail, its meat and eggs are widely consumed all over the world. Moreover Japanese quail has recently become a subject of biological research because it is resistant to diseases, easy to manage, and has a short reproductive cycle of only 35 days (Ernst, 2000). The effects of divergent selection (Marks, 1987; Anthony *et al.*, 1996; Hyankova *et al.*, 2002; Aggrey, 2003) and nutritional levels of diet (Hyankova, 1997; Baik and Marks, 1993) on the growth curve of wild type quail have been studied in detail. Feather pigmentation has a potential to effect tissue coloration and consequently affects the sensitivity of consumers to quail meat as an attractive food source (Kerje, 2003). Many Japanese quail strains were established and derived from commercial birds. Some of these strains are closed colonies in which some specific marker genes are fixed such as plumage colour, eggshell colour, or blood typing. It is believed that these marker genes do not affect the growth characteristics of poultry. On the other hand, Minvielle *et al.* (1999) established the effect

of the roux plumage colour mutation on growth. The method of our study does not allow to determine the genetic interaction between plumage colour and growth characteristics. Hence the aim of this study is restricted to establish the usability of determination of the important model parameters using Richards function causing the variations in the growth of three outbred lines selected on the basis of plumage colour.

MATERIAL AND METHODS

Experimentation

The growth data were obtained from an experiment conducted at the Gaziosmanpasa University Quail Breeding Unit. In this study, three outbred lines of Japanese quail were used. All the birds were initially collected among the hatchlings from commercial hatcheries and the Quail Breeding Unit. One of the lines was commercial meat-type Japanese quail (wild-type in colour). The other two lines originated by crossing the wild-type line, then selected as extended brown and dotted-white quails. The dotted-white mutant shows white plumage with a small coloured spot on the head and/or back and an autosomal recessive gene controls this plumage colour (Tsudzuki *et al.*, 1992). Extended brown is incompletely dominant to the wild type. Homozygous brown individuals have uniformly dark brown plumage, with a small area of white feathers around the beak (Truax, 1979; Cheng and Kimura, 1990). The lines hereafter are referred to as wild, white, and brown. The only selection criterion was plumage colour of the lines. Before the study was started, lines were maintained as flocks constituted of 60 females and 20 males and reared at this unit for 6 generations with random-bred mating.

When the chicks hatched, they were weighed and labelled with wing-rings and randomly placed in quail battery brooders. Each battery of the brooders was divided into three parts with stainless steel wire mesh and 10 birds from each line were placed in these parts. Eight groups were formed for each line. Rearing conditions were identical for all the groups. When the birds reached 42 d of age, some of the birds were removed to set a new experiment and afterwards the male:female ratio was 3 : 4 within each group. Therefore the actual death rates over the experiments were 9.7, 10.82, and 7.82

for white, brown, and wild line, respectively. Birds were weighed at 3-day intervals from hatching (day 0) to 48 days of age with a 0.01 g sensitivity electronic balance. Records from quails that died before 48 days of age and removed after 42 days of age were not considered for modelling. A total of 89 females (29–30 quails for each line) and 71 males (23–24 quails for each line) were used for this study. All birds were hatched on the same day. The adjustment of temperature, lighting regime and feeding followed the common practice in the industry. The temperature started at 36°C and it was decreased by 3°C every week and fixed at 24°C after four weeks of age. Birds were housed at 24 hours lighting for the first three weeks, in the following weeks at a 16 : 8 light:dark cycle. Birds had an *ad libitum* access to food and water. They were received 240 g/kg crude protein (CP) and 13.39 MJ ME/kg starter diet for 21 days, 190 g/kg CP and 12.55 MJ ME/kg grower diet between 21 and 35 days of age and thereafter 170 g/kg CP and 11.50 MJ ME/kg breeder diet.

Growth model

Richards function converts to Gompertz and logistic model when shape parameters equal to 0 and 1, respectively. Brisbin *et al.* (1987) suggested that the effect of environmental changes could be masked if the shape parameter was fixed. This problem can arise in comparison with the lines that have diverse genetic makeup. Therefore, Richards function (Richards, 1959) was used to describe the growth pattern of the quail:

$$W_t = \frac{W_0 \times W_f}{[W_0^m + (W_f^m - W_0^m)\, e^{-kt}]^{1/m}} \qquad (1)$$

where: W_t = body weight (BW) of bird at age t
  W_0 = predicted BW at hatching (day 0)
  W_f = predicted final weight or asymptotic weight
  m = shape parameter
  k = maturation index

Absolute growth rate (GR) and relative growth rate (RGR) were calculated as follows:

$$GR = \frac{k \times W_t \times (W_f^m - W_t^m)}{m_t \times W_f^m} \qquad (2)$$

$$RGR = GR/W_t \qquad (3)$$

Weight (W_i) and age (T_i) at the inflection point were calculated as follows:

$$W_t = W_t / \sqrt[m]{m+1} \qquad (4)$$

$$T_i = \frac{1}{k} \times \ln \left| \frac{m}{W_f^m - W_0^m)/W_0^m} \right| \qquad (5)$$

Richards function was fitted to the experimental data using SigmaPlot® software.

Comparison of model parameters

The parameters of a mathematical model can be calibrated for any relevant experimental data set. The comparison of the estimated numerical values of a given parameter can shed light on the fundamental differences between the biological/physical systems being modelled. The comparison of the slope and intercept parameters of a linear model is explained in the literature (Zar, 1996). However, any computer program for calculating the estimates of parameters in a nonlinear regression equation gives an asymptotic standard error for each parameter estimated. It is an approximate standard error. Therefore, the exact confidence interval procedures or exact hypothesis tests are not generally available for parameters in non-linear regression models (Graybill and Iyer, 1994). For this reason, the statistical approach proposed by Mitchell (1997) for empirical validation of models was modified to compare parameter values. The modified approach has three stages. In the first stage, the values of each parameter belonging to two different quail lines were compared. It has the following steps:

1. Line i and Line j were chosen to compare their parameters

2. The 95% confidence intervals of experimental weight data at every sampling points were calculated for both Line i and Line j

3. One of the four model parameters (W_0, W_f, m and k) was chosen for comparison

4. The numerical values of chosen parameter were reciprocally exchanged in the models of Line i and Line j. Then, the models were run

5. The numbers of predictions staying within the confidence intervals of both quail lines were determined. Then, the likeliness percentage was calculated as follows

$$\text{Likeliness percentage } (LP_p) = \frac{k_i + k_j}{n_i + n_j} \times 100 \qquad (6)$$

where: k = the number of predictions staying within the confidence intervals and n is the number of sampling points for each line

In the second stage, the numerical values of all four parameters were reciprocally exchanged at the same time in the models of Line i and Line j. Then, the models were run. The likeliness percentage was calculated as follows:

$$LP_{all} = \left(\frac{k_i + k_j}{n_i + n_j} \right)_{all} \times 100 \qquad (7)$$

In the third stage, the performance of each model for predicting the live weights of its own line was evaluated by calculating the likeness percentage as follows:

$$LP_{own} = \frac{k}{n} \times 100 \qquad (8)$$

When LP_p equals to 100, the parameter values are exactly the same. However, when LP_{own} values are lower than 100, it is more practical to consider LP_{own} values as the upper limit instead of 100. On the other hand, when LP_p equals to 0, the parameter values are totally different from each other. When LP is higher than 0 but lower than the upper limit, the parameter values can be said to show similarity to a varying extent. In addition, the same discussion is valid for LP_{all} values in terms of overall model comparison.

RESULTS AND DISCUSSION

The results of statistical analyses are given together with the number of individuals of each sex within each line in Table 1. Significant interactions between line and sex were found between 12 and 33 d of age. The effect of the line and sex on the hatching weight was not detected ($P > 0.05$). The overall ANOVA results indicated that differences between sexes started at 33 days of age (Table 1). However, the separate ANOVA analysis for each line showed that differences within line between sexes started at 15, 33 and 36 days of age and continued thereafter for wild, white and brown quails, respectively ($P < 0.05$) and became more significant

Table 1. The results of statistical analyses for body weight of Japanese quail lines at different age (means ± standard errors)

Age (d)	ANOVA[1]			Mean comparison[2]					
				male			female		
	Line	Sex	L × S	white (N = 23)	brown (N = 24)	wild (N = 24)	white (N = 30)	brown (N = 30)	wild (N = 29)
0	NS	NS	NS	8.53 ± 0.25 a	8.46 ± 0.20 a	8.71 ± 0.17 a	8.74 ± 0.18 a	8.45 ± 0.21 a	8.97 ± 0.18 a
3	**	NS	NS	13.17 ± 0.49 ab	12.07 + 0.44 a	13.56 ± 0.39 b	12.69 ± 0.32 b	11.48 ± 0.36 a	13.86 ± 0.44 c
6	**	NS	NS	20.82 ± 0.76 a	19.75 ± 0.77 a	20.91 ± 0.71 a	20.61 ± 0.53 b	18.23 ± 0.55 a	22.42 ± 0.77 c
9	**	NS	NS	31.04 ± 1.06 a	29.98 ± 0.95 a	32.61 ± 1.03 a	30.45 ± 0.83 a	28.13 ± 0.82 a	34.87 ± 1.23 b
12	**	NS	*	45.57 ± 1.30 ab	42.17 ± 1.40 a	46.97 ± 1.38 b	44.78 ± 1.14 b	39.94 ± 1.15 a	51.05 ± 1.55 c
15	**	NS	*	61.73 ± 1.23 b	56.17 ± 1.84 a	60.26 ± 1.63 ab	59.75 ± 1.48 b	53.21 ± 1.47 a	66.86 ± 1.89 c
18	**	NS	*	81.12 ± 1.65 b	74.26 ± 2.13 a	79.38 ± 2.0 ab	80.58 ± 1.75 b	72.14 ± 1.65 a	88.06 ± 2.36 c
21	**	NS	*	99.65 ± 1.96 b	92.08 ± 2.31 a	97.10 ± 2.13 ab	99.81 ± 1.88 b	90.07 ± 1.84 a	106.77 ± 2.78 c
24	**	NS	*	113.7 ± 2.20 a	106.8 ± 2.55 a	111.4 ± 2.30 a	114.2 ± 2.14 b	105.8 ± 1.98 a	122.5 ± 3.00 c
27	**	NS	*	127.9 ± 2.40 b	120.5 ± 2.36 a	124.1 ± 2.21 ab	128.0 ± 2.04 b	118.8 ± 1.93 a	135.2 ± 3.11 c
30	**	NS	*	145.2 ± 2.73 b	136.2 ± 3.07 a	140.9 ± 2.47 ab	148.1 ± 2.35 b	134.5 ± 2.23 a	154.8 ± 3.53 b
33	**	**	*	156.0 ± 3.18 a	148.2 ± 3.05 a	153.0 ± 2.72 a	166.6 ± 3.03 b	153.4 ± 1.99 a	174.6 ± 3.98 b
36	**	**	NS	164.2 ± 3.35 a	157.4 ± 2.94 a	160.2 ± 2.71 a	182.7 ± 3.31 b	171.4 ± 2.76 a	189.3 ± 4.14 b
39	*	**	NS	169.9 ± 3.33 a	165.1 ± 2.93 a	168.1 ± 3.17 a	192.7 ± 2.56 a	186.6 ± 2.96 a	202.1 ± 4.19 b
42	*	**	NS	175.0 ± 3.15 a	168.2 ± 3.27 a	172.8 ± 3.06 a	202.1 ± 2.93 a	200.0 ± 3.06 a	211.7 ± 3.64 b
45	*	**	NS	182.6 ± 3.33 b	171.1 ± 3.20 a	177.5 ± 3.19 ab	209.8 ± 2.87ab	205.6 ± 2.91 a	215.7 ± 3.70 b
48	NS	**	NS	185.2 ± 3.15 b	173.9 ± 3.17 a	179.2 ± 3.13 ab	215.2 ± 3.01 a	211.2 ± 2.72 a	219.4 ± 3.90 a

[1]ANOVA analyses consider over sexes and lines: **$P < 0.01$; *$P < 0.05$; NS = non-significant

[2] Means within rows and sex with different letters (a, b, c) are significantly different ($P < 0.05$) based on Duncan's test

with increasing age ($P < 0.01$). Over the growth period, white males were the heaviest line, but different only from brown males ($P < 0.05$). Females were different from each other between 3 and 27 days of age ($P < 0.05$). The white and wild females did not differ from each other between 30 and 36 days of age while white and brown females did not differ from each other between 39 and 45 days ($P > 0.05$). There was no effect of line on final weight (48 days of age) for females ($P > 0.05$). The age of the first egg was 38.13 ± 1.36, 39.38 ± 1.41, and 38.13 ± 1.73 for white, brown, and wild line, respectively.

Figures 1 and 2 illustrate the absolute (GR) and relative (RGR) growth rates of the quail lines for males and females, respectively. The simultaneous consideration of both relative growth rate and absolute growth rate gives better information than examining only one of them to compare the changes

in growth (Aggrey, 2003). Daily gain of the lines showed different behaviour for males and females. Males of the white and females of the wild quail were better than the other lines with respect to growth rate and 48-day body weight.

The differences between the specific growth rates of lines in the early part of developmental period may indicate correlated differences in asymptotic weight. In this study the brown line that has lower relative growth accordingly had lower 48-day weight. On the other hand, the brown line showed lower weight gains than those for the other two lines during the first part of the growth period. Behind the inflection point the expected decrease in the absolute growth rate got slower for brown females. Although males of the white and females of the wild line had higher weight gains than the other lines, there were no clear differences between
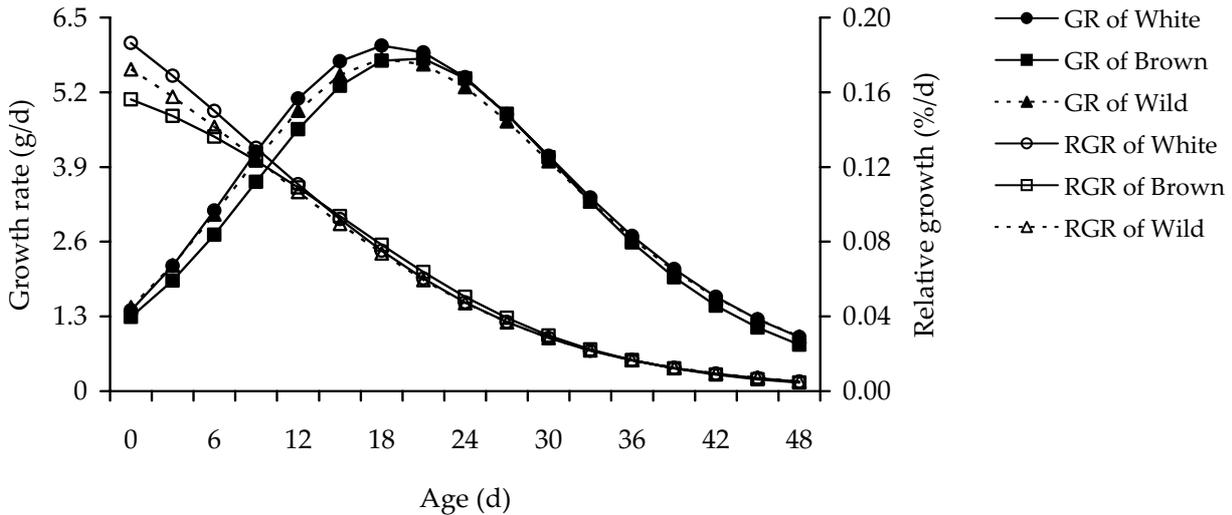
Figure 1. Absolute (GR) and relative growth rate (RGR) of the males of the particular lines

wild and white quails of both sexes in the second part of the growth period.

Although the accumulation of information on the lines and future studies on the genetic makeup of the growth of the lines are necessary, different sets of genes could determine the differences in early and late growth of the lines. This fact was shown in mice (Cheverud *et al.*, 1996) and indications were reported for quail (Aggrey, 2003). In this study different behaviour of the absolute and relative growth rate of brown line from the other lines in the first and the second part of growth supports this conclusion.

The values and standard errors of Richards function parameters are presented in Table 2. Coefficients of determination of the values of models were equal to

or above 99.86%. Likeliness percentages (LP_{own}) of the fitted models for their own data set are presented in Table 2. In general LP_{own} values were higher for males than those for females. This indicates that fitted parameters of Richards model were better in describing the growth of males than that of females. On the other hand, when each point of data was considered (Figure 3), it was found that these differences focused around the first two measurements of BW (0 and 3 d of age). This fact was much clearer when the parameter W_0 and measured hatchling weights, which were between 8.45–8.97 g, were compared especially for white and brown females and white males (Tables 1 and 2). The differences between W_0 and measured hatchling weights appear as a common phenomenon in curve fitting
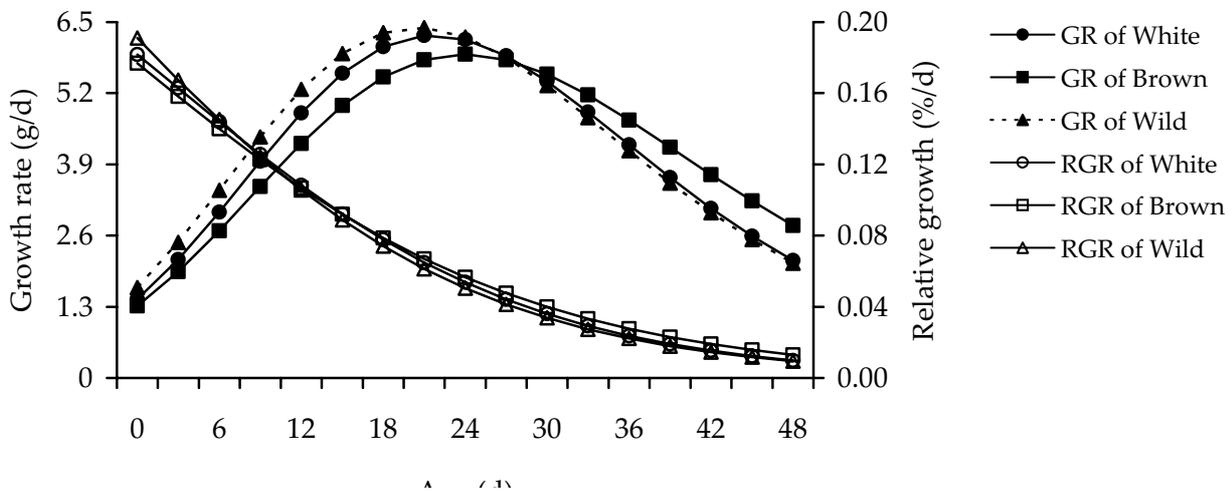

Figure 2. Absolute (GR) and relative growth rate (RGR) of the females of the particular lines

Table 2. Estimated coefficients (± s.e.) of Richards model, age and weight at the inflection point, and LP values for Japanese quail lines

	Male			Female		
	white	brown	wild	white	brown	wild
W_0	7.528 ± 0.748	8.305 ± 0.635	8.461 ± 0.73	7.909 ± 1.27	7.437 ± 1.507	8.630 ± 1.710
W_f	195.040 ± 2.231	182.102 ± 1.731	190.319 ± 2.139	$247\ 387 \pm 7.841$	261.727 ± 14.505	253.835 ± 9.655
m	0.355 ± 0.094	0.618 ± 0.099	0.424 ± 0.097	0.231 ± 0.145	0.175 ± 0.183	0.170 ± 0.176
k	0.098 ± 0.006	0.113 ± 0.006	0.099 ± 0.006	0.077 ± 0.008	0.067 ± 0.010	0.074 ± 0.010
R^2	99.96	99.96	99.97	99.91	99.87	99.86
LP_{own}	94.11	94.11	100	88.24	82.35	94.12
T_i^*	18.48	19.77	18.73	21.68	23.94	20.46
W_i^*	82.89	83.58	82.69	100.62	104.12	100.81

$*P < 0.05$

(Grossman and Bohren, 1982; Mignon-Grasteau *et al.*, 1999; Aggrey, 2002). This could be because of the small standard errors for that part of growth. Therefore the confidence intervals are restricted.

Because of the lower decrease in the growth rate for females of the brown line asymptotic body weight was estimated higher than in the other two lines (Table 2). Additionally, low asymptotic body weight of the males leads to high estimated sexual dimorphism (percentage ratio of female/male body weights) for the brown line (147%). This could be caused by the short duration of the experimental period leading to overestimation of asymptotic weight. Hort *et al.* (1999) compared the curves of sexual dimorphism of low and high gain lines of quail. They reported that the peak of the curve correspond to the fist egg followed by a short period of decrease, caused by the onset of lay of females. Sexual dimorphism at the age of the first egg was

114%, 120% and 113% for white, wild and brown, respectively, and similar to the report of Hort *et al.* (1999).

The maturation index (k) was higher in males than in females. White and wild quails of both sexes have similar k values. Contrary to the asymptotic body weight (W_f) the highest k value was calculated for brown males and the lowest k value for brown females. Such a negative correlation between W_f and k could be expected (Mignon-Grasteau *et al.*, 2000) for the growth curves that have similar shape parameters because the rate of maturation together with the shape parameter determines the speed of the curve to reach the asymptotic body weight.

The analyses of different lines confirmed the results of previous studies stating that the choice of the function was strain-specific (Anthony *et al.*, 1996; Hyankova *et al.*, 1997) and therefore it is best to use four-parameter Richards function with the variable

Table 3. Likeness percentage of estimated growth parameters of Richards model within sex between lines of Japanese quail

	Males			Females		
	white vs brown	white vs wild	brown vs wild	white vs brown	white vs wild	brown vs wild
LP_{W_0}	73.53	61.76	94.12	76.47	76.47	55.88
LP_{W_f}	38.24	94.12	67.65	44.12	85.29	70.59
LP_m	14.71	55.88	23.53	38.24	44.12	91.18
LP_k	17.65	97.06	23.53	02.94	73.53	08.82
LP_{all}	26.47	94.12	58.82	17.65	23.53	5.88

A

B
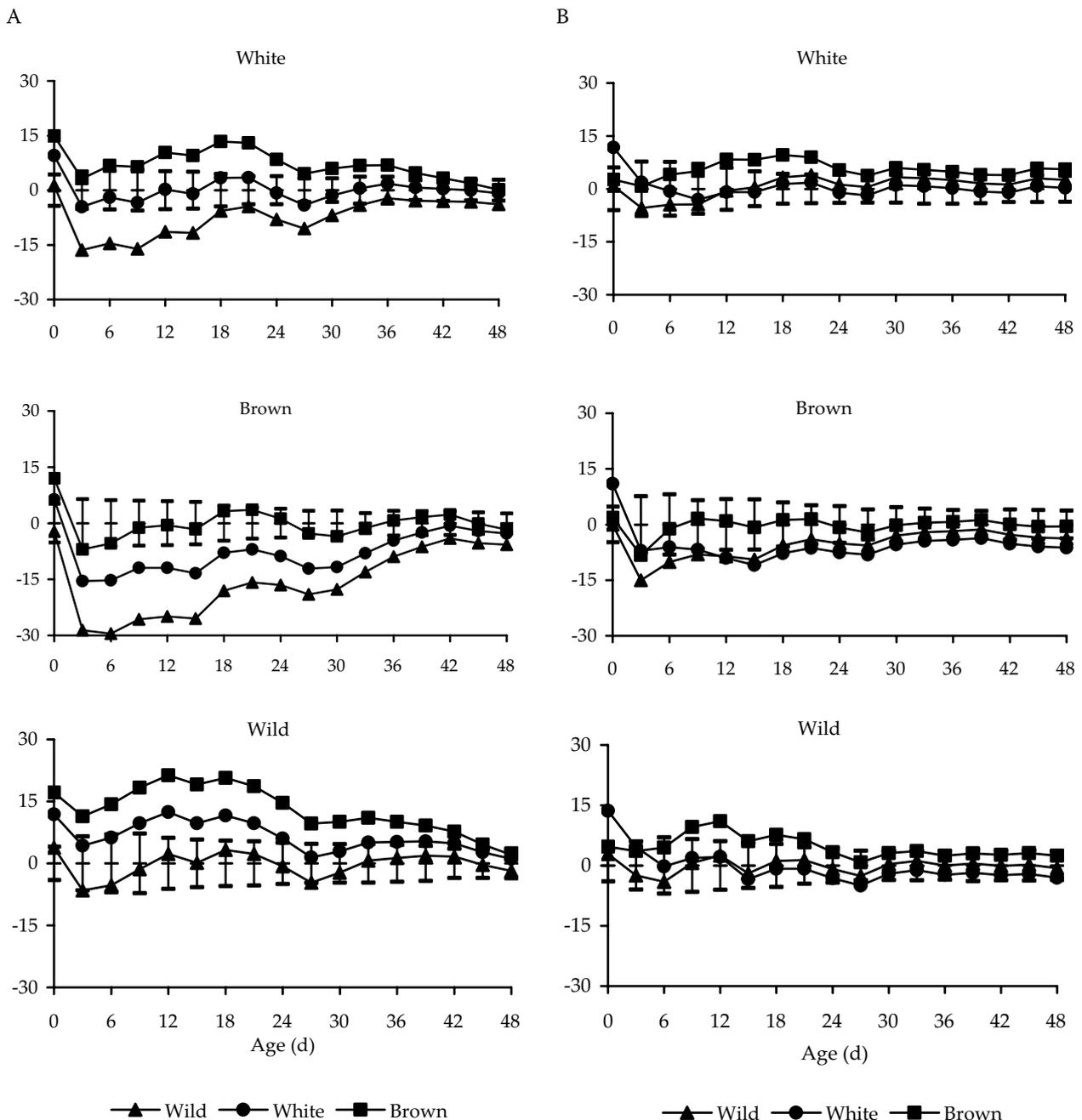

Figure 3. Mean percentage deviations (MPD) between measured and estimated body weight for females (A) and males (B) of each line (*x* ± confidence intervals) and for compared lines after exchanging of all estimated parameters

shape parameter. The shape parameter *"m"* of the fitted curves showed clear differences between the sexes and it was higher in males than in females. Shape parameters estimated for females were close to zero, indicating that their growth curves look like Gompertz model rather than the logistic model. On the other hand, *m* parameters for males were between Gompertz and logistic models.

Males reached the estimated age at maximum growth (T_i) faster than the females. The differences were 3.2, 4.17, and 1.73 for white, brown, and wild quails, respectively. Although the wild males had higher m parameter than the white males, their age and weights at the inflection point (Table 2) were similar. Age and weight at the inflection point were estimated high in this study especially for brown fe-

males. This extension of the acceleration time may also explain the increase in the estimated mature body weight (W_f) of the brown females. The other estimated ages at the inflection point were similar to those reported in the literature (Hyankova *et al.*, 1997). This could be expected when taking into account that the CP% in the diet was at the lower limit of the reports. On the other hand, all the lines were fed with the same diet throughout the experiment; hence, a delay at the inflection point and age of maturation caused by the food randomly affects the differences between the lines and sexes.

Calculated LP_p values for parameters between the lines are summarised in Table 3 for males and females respectively. While the parameter of W_0 of the brown and wild quail (LP_{W_0} = 94.12%) and W_f and k of the white and wild quail (LP_{W_f} = 94.12% and LP_k = 97.06%) are similar for males, the other parameters between lines are clearly different from each other (low LP). On the other hand, m parameter of the brown and wild (LP_m = 91.18%) and W_f of the white and wild (LP_{W_f} = 85.29%) seem similar for females.

To establish the similarities between the lines, the model of one line was compared with the confidence intervals of the other line (Figure 3). The results showed that white and brown males were the most distinct lines and wild males were between the two lines but closer to white rather than brown. Actually the wild line body weight was clearly predicted by using parameters calculated for white line males and vice versa (LP_{all} = 94.12%). For female brown and wild quails showed the largest differences and white and wild females were the closest ones.

CONCLUSION

Richards function adequately described the growth curves of three meat-type quail lines. The brown line had lower growth rate and specific growth rate than the other two lines. On the other hand, the brown line had higher weight and age at the inflection point. The most critical parameter was shape parameter for males (LP_m = 14.71 – 55.88) and maturation index for females (LP_k = 2.94 for brown versus white, LP_{knm} = 8.82 for brown versus wild). The brown line tested in this study had lower growth rate after hatching and entered the second part of the growth with lower body weight. White and wild lines are the closest ones regarding growth parameters and BW. White and

brown lines as commercial lines could be considered with the support of future studies. In addition to the genotypic differences in plumage colour, differences in the shape of growth curves established in this study could be a sign of the genetic dissimilarities of the lines. In the light of this study, it seems also necessary to study the probability of the genetic relationship between plumage colour and growth in detail. Additionally, heterosis in body weight and the other quantitative characters would be assessed. Such studies could not only improve our knowledge of the genetic basis of differences between the lines but also give the chance to choose the best parental lines for practical quail breeding. In addition, the methodology of the comparison of nonlinear model parameters introduced in this study is expected to be a good tool for researchers interested in biological modelling including animal growth models.

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