

A Growth Performance and Nonlinear Growth Curve Functions of Large- and Normal-Sized Japanese Quail (*Coturnix japonica*)

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This study aimed to evaluate the differences between the growth patterns of large- and normal-sized Japanese quail strains and their F₁ progeny, by fitting their growth parameter values to five nonlinear regression growth models (Weibull, Logistic, Gompertz, Richards, and Brody). The Richards model presented the best fit for both sexes of the large-sized quail strain, whereas the Gompertz model presented the best fit for both sexes of the normal-sized quail strain, based on goodness-of-fit criteria (higher adjusted R² and lower Akaike and Bayesian information criteria). Both sexes of F₁ birds derived from the cross between normal-sized females and large-sized males were best fitted by the Richards model. In contrast, growth parameters of the F₁ birds derived from the cross between large-sized females and normal-sized males were best fitted to the Gompertz model. The data could be fitted nearly as well to the Weibull and Logistic models as to the Richards and Gompertz models. The Brody model presented the poorest fit for the growth parameter values. The results indicated that the Richards and Gompertz models could best describe the growth characteristics of both large- and normal-sized quails. Moreover, the observed growth pattern of the F₁ birds was likely inherited from the male parental strain. To the best of our knowledge, this is the first study comparing the growth curves of the reciprocal F₁ generations with their parental strains in quails.

Key words: body weight, growth curve, Japanese quail, large-sized quail strain, normal-sized quail strain

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Introduction

Bird growth is a vital quality criterion for industrial poultry producers. It involves changes in the size, shape, weight, and volume of the animals, and is influenced by genetic and environmental factors (Sezer and Tarhan, 2005a). Growth variation is evaluated by fitting growth curve models to the body weight measurements. In poultry science, growth curve

models provide useful information on animal management and health, age at sexual maturity, appropriate slaughter age, and effects of genetic improvements (Kaplan and Gürçan, 2018).

The Japanese quail (*Coturnix japonica*) is a model bird species for biological research (Minvielle, 2004; Jeke *et al.*, 2018) and meat/egg production studies (Tsudzuki, 2008), due to its small size, high production efficiency, rapid generational turnover, and sexual maturity at an early age of ~6 wk (Padgett and Ivey, 1959; Woodard *et al.*, 1973; Cain and Cawley, 1974; Ernst, 1978). Several nonlinear growth models, such as Gompertz (Gompertz, 1825), Logistic (Blumberg, 1968), Richards (Richards, 1959), Weibull (Weibull, 1951), Brody (Saeid Bathaei and Leroy, 1998), von Bertalanffy (von Bertalanffy, 1957), and Hyperbolic (Tabatabai *et al.*, 2005), have been developed to describe Japanese quail growth patterns. The Gompertz, Logistic, and von Bertalanffy models have fixed inflection points and present sigmoidal curves. The Brody model has a diminishing return behavior. The Richards model has a flexible

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inflection point and four parameters. There are conflicting results regarding the most suitable model for describing Japanese quail growth, in terms of the strain, line, and sex (Akbaş and Yaylak, 2000). Several studies have reported that the Gompertz model is the best suited, based on its goodness-of-fit criteria (Narinc *et al.*, 2010; Santos *et al.*, 2018). However, the Richards, Logistic, Weibull, and Brody models have also been successfully fitted to Japanese quail growth data (Karaman *et al.*, 2013; Raji *et al.*, 2014a; Abdallah, 2017).

Large-sized (LS) Japanese quail are characterized by their relatively high body weight (~200 g for females and ~170 g for males at maturity) and are used primarily for meat production. Normal-sized (NS) Japanese quail are distinguished by their normal body weight range (~130 g for females and ~100 g for males at maturity) and are used mainly for egg production (Kirkwood and Hubrecht, 2010). Reciprocal matings between these two strains yield quails with heterozygous characteristics and good growth rates. Several previous studies have focused on the growth rate of Japanese quail (Telekan *et al.*, 2017; Faraji-Arough *et al.*, 2018); however, to the best of our knowledge, no studies have compared the growth curves of the reciprocal F₁ generation with those of their parents, which differ genetically in terms of the trait of interest. The aim of the present study was to evaluate the differences between the growth patterns of LS and NS quails, by fitting the growth metrics of these two quail strains and their reciprocal F₁ progeny to five different nonlinear regression growth models (Weibull, Logistic, Gompertz, Richards, and Brody).

Materials and Methods

Experimental Birds

LS and NS quails were reared at the research farm of Hiroshima University, Higashi-Hiroshima, Japan. One hundred quails from each of the two strains and 50 birds from each of their reciprocal F₁ generations were used in this study. The F₁ birds were obtained by reciprocal matings between one male and three females. The body weights of all birds were measured weekly, from hatching up to the age of 16 wk. Newly hatched chicks were leg-banded and weighed before being transferred to heated brooders, where they were reared until the age of 4 wk. Thereafter, they were housed in individual cages (depth 15 cm, width 18 cm, height 18 cm). Chicks were fed a standard chick diet (22% crude

protein (CP); 2,900 kcal metabolizable energy (ME) kg⁻¹), available *ad libitum*, from 0 to 4 wk of age, and then with a grower diet (17% CP; 2,850 kcal ME kg⁻¹) from 4 to 16 wk of age. The birds were maintained under a 24-h photoperiod for 4 wk, and then under a 14h:10h light:dark cycle. The birds were reared following the protocol described in the Guidelines for Proper Conduct of Animal Experiments (Science Council of Japan, 2006).

Statistical Analysis and Model Comparison

The mathematical expressions for growth rate and age and weight at inflection points of the Weibull, Logistic, Gompertz, Richards, and Brody growth models are presented in Table 1. For all equations, *y* is the body weight at a given age, *x* is the time duration, *a* is the asymptotic weight, *b* and *c* are constants for the initial body weight and instantaneous growth rate, respectively, and *d* is the shape parameter in the Weibull and Richards models.

The coefficient of determination (R²), adjusted coefficient of determination (adj. R²), Akaike information criterion (Akaike, 1974), Bayesian information criterion (Schwarz, 1978), and root mean square error (RMSE) were used to evaluate the accuracy of the growth curve model predictions. The comparison parameters were calculated as follows:

Coefficient of determination: R²=1-(SSE/SST)
 Adjusted coefficient of determination: Adj. R²=R²-((p-1/n-p)(1-R²))
 Akaike’s information criterion: AIC=n.ln(SSE/n)+2p
 Bayesian information criterion: BIC=n.ln(SSE/n)+p.ln(n)
 Root mean square error: RMSE=(SSE/n)^(1/2)
 where *SSE* is the sum of square errors, *SST* is the total sum of squares, *p* is the number of parameters, and *n* is the number of observations.

The nonlinear regression models of the growth curves were computed using the nonlinear least squares (nls) function in R v. 3.6.1. (R Core Team, 2019). The body weights of the two sexes were compared between the parental and F₁ generations and within the Gompertz and Richards models by Tukey’s HSD test, in JMP v. 11.0.2 (SAS Institute Inc., Tokyo, Japan).

Results

The body weights of the LS and NS Japanese quail strains and their F₁ progeny were measured from hatching up to 16 wk (Tables 2 and 3). The body weight of LS quails was significantly higher than that of NS quails at hatching (8.19 g

Table 1. Equations for age and weight at inflection points of the growth curve models used in the present study

Model	Equation	Age at inflection point (IP _T)	Weight at inflection point (IP _w)
Weibull	$y = a - (a - b) \cdot \exp(-c \cdot x^d)$	$(1/c)^{1/d} \cdot ((d - 1)/d)^{(1/d)}$	$a - (a - b) \cdot \exp(-(d - 1)/d)$
Logistic	$y = (b \cdot a) / (b + (a - b) \cdot \exp(-c \cdot x))$	$1/c \cdot \ln((a - b)/b)$	$a/2$
Gompertz	$y = a \cdot \exp(-b \cdot \exp(-c \cdot x))$	$\ln(b)/c$	a/e
Richards	$y = (b \cdot a) / ((b^d + (a^d - b^d) \cdot \exp(-c \cdot x))^{1/d})$	$-(1/c) \cdot \ln(d / ((a^d - b^d)/b^d))$	$a / ((d + 1)^{1/d})$
Brody	$y = a \cdot (1 - b \cdot \exp(-c \cdot x))$	—	—

y: body weight at given age; *x*: time duration; *a*: asymptotic weight; *b*: constant for the initial body weight; *c*: constant for the instantaneous growth rate; *d*: shape parameter.

Table 2. Body weights of female LS and NS quails and their F₁ hybrids from ages 0 to 16 wk

Age (wks)	LS ♀ (n=50)	NS ♀ (n=50)	F ₁ ♀ (NS ♀ × LS ♂) (n=25)	F ₁ ♀ (LS ♀ × NS ♂) (n=25)
0	8.19±0.1081 ^a	6.09±0.0701 ^c	6.89±0.1948 ^b	8.54±0.1156 ^a
1	27.21±0.4147 ^{ab}	21.29±0.3610 ^c	25.62±0.4885 ^b	28.52±0.4235 ^a
2	56.72±0.9537 ^a	44.02±0.5758 ^c	52.27±1.0695 ^b	57.66±0.7144 ^a
3	95.96±1.4451 ^a	71.77±0.7218 ^c	88.51±1.6145 ^b	94.27±0.9892 ^a
4	136.58±1.6558 ^a	93.41±0.9440 ^c	119.44±1.4137 ^b	120.94±1.3883 ^b
5	156.48±1.7929 ^a	110.25±1.2636 ^c	140.06±1.9374 ^b	144.68±1.8153 ^b
6	190.49±2.1768 ^a	127.26±1.6862 ^c	160.82±2.4042 ^b	161.33±2.4006 ^b
7	206.44±2.2449 ^a	133.40±1.8839 ^c	165.45±2.3364 ^b	164.41±1.5985 ^b
8	211.60±2.4029 ^a	133.69±1.9436 ^c	165.55±2.5531 ^b	169.41±2.0241 ^b
9	214.86±2.6711 ^a	138.86±1.8348 ^c	166.14±2.5730 ^b	170.96±1.8260 ^b
10	219.96±2.4104 ^a	141.96±1.8178 ^c	173.47±2.5533 ^b	175.55±1.9170 ^b
11	222.21±2.6928 ^a	141.79±1.7043 ^c	172.07±2.4935 ^b	178.06±2.1360 ^b
12	221.88±2.7306 ^a	142.78±1.9305 ^c	171.43±2.8522 ^b	175.87±2.4514 ^b
13	222.30±2.8112 ^a	142.90±1.7938 ^c	173.98±2.7404 ^b	179.90±2.5148 ^b
14	224.78±2.8199 ^a	145.01±1.8112 ^c	173.89±3.0529 ^b	179.63±2.4565 ^b
15	226.11±3.0813 ^a	143.52±1.8351 ^c	173.80±2.7708 ^b	178.86±2.3888 ^b
16	225.76±3.1284 ^a	145.02±1.8940 ^c	174.82±2.8449 ^b	178.51±2.4085 ^b

Values are indicated as mean±SE. ^{a-c} Values with different superscript letters within a row are significantly different (Tukey's HSD test, $P<0.05$).

Table 3. Body weights of male LS and NS quails and their F₁ hybrids from ages 0 to 16 wk

Age (wks)	LS ♂ (n=50)	NS ♂ (n=50)	F ₁ ♂ (NS ♀ × LS ♂) (n=25)	F ₁ ♂ (LS ♀ × NS ♂) (n=25)
0	7.94±0.1085 ^a	5.91±0.1004 ^c	7.00±0.2084 ^b	8.41±0.1381 ^a
1	24.93±0.4269 ^a	19.74±0.4369 ^b	25.02±0.5041 ^a	26.70±0.4850 ^a
2	51.52±0.8122 ^a	40.58±0.8742 ^b	52.32±0.6438 ^a	53.79±1.1689 ^a
3	88.18±1.2760 ^a	67.12±1.0250 ^b	86.82±1.0810 ^a	86.50±1.4508 ^a
4	126.25±1.5340 ^a	86.71±1.2028 ^c	112.91±1.2347 ^b	111.81±1.6727 ^b
5	144.04±1.7180 ^a	99.12±1.1275 ^c	127.80±1.4059 ^b	126.50±2.1312 ^b
6	161.08±1.7221 ^a	105.18±1.0584 ^c	139.47±1.6887 ^b	135.30±2.3824 ^b
7	172.50±1.8566 ^a	108.53±1.1249 ^c	143.10±1.6768 ^b	138.07±2.4159 ^b
8	175.12±1.7995 ^a	110.47±1.1934 ^c	141.75±1.9866 ^b	139.26±2.3179 ^b
9	177.95±1.8264 ^a	112.97±1.2029 ^c	143.71±1.9388 ^b	141.55±2.3285 ^b
10	180.54±1.9801 ^a	114.14±1.2882 ^c	144.36±2.0119 ^b	143.79±2.4521 ^b
11	183.77±1.9132 ^a	115.66±1.3473 ^c	146.21±2.0676 ^b	144.66±2.5081 ^b
12	182.17±1.8441 ^a	116.80±1.3508 ^c	147.54±2.0810 ^b	146.55±2.5609 ^b
13	183.26±1.8740 ^a	117.57±1.3788 ^c	148.61±2.2061 ^b	146.98±2.5887 ^b
14	185.29±1.8339 ^a	120.02±1.3672 ^c	149.14±2.0725 ^b	147.31±2.7661 ^b
15	186.94±1.8485 ^a	120.38±1.4489 ^c	150.30±2.1422 ^b	148.31±3.1589 ^b
16	188.01±1.9008 ^a	121.13±1.5092 ^c	150.31±1.8934 ^b	146.58±3.1935 ^b

Values are indicated as mean±SE. ^{a-c} Values with different superscript letters within a row are significantly different (Tukey's HSD test, $P<0.05$).

vs. 6.09 g for females and 7.94 g vs. 5.91 g for males of LS and NS strains, respectively). No significant differences could be detected between the body weights of LS and F₁ (LS ♀ × NS ♂) females from hatching up to 3 wk. The NS females exhibited the lowest body weights from hatching up to 16 wk. No significant differences were observed in the body weights of F₁ females from 4 wk of age onwards. The NS males presented the lowest body weights among all the quail generations from 0 to 16 wk of age. No significant differences were recorded between the body weights of LS

and the F₁ males from the age of 1 to 3 wk. Significant differences were observed between the body weights of parental and F₁ males from the age of 4 to 16 wk. The LS and NS males presented with the highest and lowest body weights, respectively. No significant differences were detected in the body weights of F₁ males from the age of 4 wk.

Goodness-of-fit criteria for the Weibull, Logistic, Gompertz, Richards, and Brody models are shown in Table 4. The Richards model presented the best fit for both female and male LS quails (adj. $R^2=0.999$, 0.999; AIC=92.007, 81.742;

Table 4. Goodness-of-fit criteria for the five growth models

Model	R ²	Adj. R ²	AIC	BIC	RMSE
LS Female					
Weibull	0.999	0.998	92.983	97.149	2.778
Logistic	0.997	0.997	103.852	107.184	4.056
Gompertz	0.998	0.998	93.538	96.871	2.995
Richards	0.999	0.999	92.007	96.173	2.699
Brody	0.975	0.973	139.634	142.967	11.619
LS Male					
Weibull	0.998	0.998	93.050	97.216	2.784
Logistic	0.997	0.997	98.180	101.513	3.433
Gompertz	0.999	0.999	82.108	85.441	2.140
Richards	0.999	0.999	81.742	85.908	1.996
Brody	0.976	0.974	131.710	135.043	9.203
NS Female					
Weibull	0.999	0.999	74.936	79.102	1.634
Logistic	0.997	0.996	90.584	93.917	2.746
Gompertz	0.999	0.999	67.341	70.674	1.386
Richards	0.999	0.999	68.734	72.900	1.361
Brody	0.981	0.979	118.688	122.021	6.275
NS Male					
Weibull	0.995	0.995	90.169	94.335	2.557
Logistic	0.993	0.993	94.328	97.661	3.065
Gompertz	0.994	0.993	79.516	82.849	1.983
Richards	0.997	0.997	81.215	85.381	1.965
Brody	0.982	0.981	109.324	112.657	4.764
F ₁ Female (NS ♀ × LS ♂)					
Weibull	0.998	0.998	85.889	90.055	2.255
Logistic	0.998	0.997	90.811	94.144	2.764
Gompertz	0.998	0.998	86.568	89.901	2.440
Richards	0.999	0.999	82.531	86.697	2.043
Brody	0.973	0.971	131.062	134.395	9.030
F ₁ Male (NS ♀ × LS ♂)					
Weibull	0.000	0.998	84.290	88.456	2.151
Logistic	0.997	0.997	87.197	90.530	2.485
Gompertz	0.998	0.998	78.948	82.281	1.950
Richards	0.999	0.998	77.291	81.457	1.751
Brody	0.976	0.974	122.884	126.217	7.099
F ₁ Female (LS ♀ × NS ♂)					
Weibull	0.998	0.998	85.731	89.897	2.244
Logistic	0.997	0.997	96.221	99.553	3.241
Gompertz	0.999	0.999	75.623	78.956	1.768
Richards	0.999	0.999	76.338	80.504	1.703
Brody	0.980	0.979	126.051	129.383	7.792
F ₁ Male (LS ♀ × NS ♂)					
Weibull	0.997	0.997	85.215	89.381	2.211
Logistic	0.997	0.997	87.965	91.298	2.542
Gompertz	0.999	0.998	74.466	77.799	1.709
Richards	0.999	0.999	74.397	78.563	1.608
Brody	0.979	0.978	119.025	122.357	6.338

R²: coefficient of determination; Adj. R²: adjusted coefficient of determination; AIC: Akaike information criterion; BIC: Bayesian information criterion; RMSE: root mean square error.

and BIC=96.173, 85.908 for females and males, respectively). The Gompertz model exhibited the best fit for both sexes of the NS strain (adj. R²=0.999, 0.993; AIC=67.341, 79.516; and BIC=70.674, 82.849 for females and males, respectively). Data for the F₁ (NS ♀ × LS ♂) birds was the best fitted with the Richards model (adj. R²=0.999, 0.998;

AIC=82.531, 77.291; and BIC=86.697, 81.457 for females and males, respectively). In contrast, the Gompertz model presented the best fit for the F₁ (LS ♀ × NS ♂) birds (adj. R²=0.999, 0.998; AIC=75.623, 74.466; and BIC=78.956, 77.799 for females and males, respectively). All quail generations were best fitted using the Richards or Gompertz

Table 5. Values of the equation parameters and age and weight at inflection points for female quails estimated by the Gompertz and Richards models

Model	Parameter	LS ♀ (n=50)	NS ♀ (n=50)	F ₁ ♀ (NS ♀ × LS ♂) (n=25)	F ₁ ♀ (LS ♀ × NS ♂) (n=25)
Gompertz	a	226.53 ± 2.7194 ^a	144.51 ± 1.7641 ^c	174.27 ± 2.5580 ^b	178.88 ± 2.0100 ^b
	b	6.0278 ± 0.1056 ^{ab}	5.5716 ± 0.1555 ^b	6.5714 ± 0.1860 ^a	5.5596 ± 0.1366 ^b
	c	0.4917 ± 0.0071 ^c	0.5133 ± 0.0086 ^{bc}	0.5753 ± 0.0121 ^a	0.5382 ± 0.0104 ^{ab}
	IP _T	3.6550 ± 0.0314 ^a	3.3187 ± 0.0246 ^b	3.2694 ± 0.0368 ^{bc}	3.1816 ± 0.0262 ^c
	IP _W	83.337 ± 1.0004 ^a	53.164 ± 0.6490 ^c	64.110 ± 0.9410 ^b	65.807 ± 0.7394 ^b
Richards	a	221.20 ± 2.7369 ^a	143.73 ± 2.0426 ^c	172.37 ± 2.9994 ^b	175.46 ± 2.5181 ^b
	b	3.3941 ± 0.2910 ^a	2.0483 ± 0.2041 ^b	2.7962 ± 0.2680 ^{ab}	2.7560 ± 0.3090 ^{ab}
	c	0.6037 ± 0.0170 ^b	0.6184 ± 0.0252 ^b	0.7298 ± 0.0340 ^a	0.6427 ± 0.0240 ^{ab}
	d	0.4327 ± 0.0519 ^a	0.3301 ± 0.0664 ^a	0.5393 ± 0.0743 ^a	0.3525 ± 0.0572 ^a
	IP _T	4.0563 ± 0.0585 ^a	3.5654 ± 0.0792 ^b	3.7126 ± 0.0605 ^b	3.4893 ± 0.0613 ^b
IP _W	95.134 ± 1.6155 ^a	59.448 ± 1.4616 ^c	76.589 ± 1.8191 ^b	73.942 ± 1.6121 ^b	

Values are indicated as mean ± SE. ^{a-c} Values with different superscript letters within a row are significantly different (Tukey's HSD test; $P < 0.05$).

a: asymptotic weight; *b*: constant for the initial body weight; *c*: constant for the instantaneous growth rate; *d*: shape parameter; IP_T: age at inflection point (wk); IP_W: weight at inflection point (g).

Table 6. Values of the equation parameters and age and weight at inflection points for male quails estimated by the Gompertz and Richards models

Model	Parameter	LS ♂ (n=50)	NS ♂ (n=50)	F ₁ ♂ (NS ♀ × LS ♂) (n=25)	F ₁ ♂ (LS ♀ × NS ♂) (n=25)
Gompertz	a	185.46 ± 1.8273 ^a	117.85 ± 1.3514 ^c	148.32 ± 1.9648 ^b	146.46 ± 2.6416 ^b
	b	6.3288 ± 0.1296 ^a	5.7744 ± 0.1606 ^b	6.5512 ± 0.1765 ^a	5.9672 ± 0.2398 ^{ab}
	c	0.5434 ± 0.0073 ^c	0.5723 ± 0.0104 ^{bc}	0.6288 ± 0.0116 ^a	0.6075 ± 0.0172 ^{ab}
	IP _T	3.3896 ± 0.0302 ^a	3.0418 ± 0.0288 ^b	2.9843 ± 0.0265 ^b	2.9249 ± 0.0331 ^b
	IP _W	68.227 ± 0.6722 ^a	43.355 ± 0.4972 ^c	54.565 ± 0.7228 ^b	53.880 ± 0.9718 ^b
Richards	a	183.98 ± 2.0043 ^a	112.02 ± 1.9159 ^c	147.36 ± 2.8801 ^b	145.16 ± 3.1394 ^b
	b	2.1132 ± 0.1896 ^a	1.7851 ± 0.1905 ^a	2.4984 ± 0.3666 ^a	2.1772 ± 0.2777 ^a
	c	0.6437 ± 0.0199 ^b	0.7633 ± 0.0232 ^a	0.8103 ± 0.043 ^a	0.7783 ± 0.0495 ^a
	d	0.3592 ± 0.0501 ^a	0.4570 ± 0.0548 ^a	0.5621 ± 0.0956 ^a	0.4635 ± 0.102 ^a
	IP _T	3.7204 ± 0.0564 ^a	3.3767 ± 0.1553 ^b	3.3846 ± 0.0518 ^b	3.2205 ± 0.0602 ^b
IP _W	77.522 ± 1.4486 ^a	49.007 ± 1.3727 ^c	65.654 ± 1.5298 ^b	62.188 ± 1.4512 ^b	

Values are indicated as mean ± SE. ^{a-c} Values with different superscript letters within a row are significantly different (Tukey's HSD test; $P < 0.05$).

a: asymptotic weight; *b*: constant for the initial body weight; *c*: constant for the instantaneous growth rate; *d*: shape parameter; IP_T: age at inflection point (wk); IP_W: weight at inflection point (g).

models, with the Weibull and Logistic models presenting a comparable fit to these models.

The estimated equation parameters and age and weight at inflection points of the Gompertz and Richards models for female and male quails are shown in Tables 5 and 6. In case of female quails, significant differences were observed in the asymptotic weights (*a*) and age (IP_T) and weight (IP_W) at inflection points of the parental generations in the Gompertz model. The LS and NS females presented the highest and lowest *a*, respectively. No significant differences were observed between the reciprocal F₁ generations for any of the parameters estimated by both models, except the initial body weight (*b*) in the Gompertz model. No significant differences were observed between the instantaneous growth rates (*c*) of the parental generations in the Gompertz and Richards models. The shape parameter (*d*) did not differ between

generations. In case of males, no significant differences could be detected between the parameter values of the reciprocal F₁ generations in the Gompertz and Richards models (Table 6). The *c* value was the lowest for LS males in the Richards model. The estimated values for *a*, IP_T, and IP_W in both models were the highest for LS males. The *b* and *d* values in the Richards model did not differ between generations.

The Gompertz and Richards models for the LS, NS, and reciprocal F₁ generations are shown in Fig. 1. The Gompertz and Richards IP_T for both LS sexes was observed to be higher than that for the NS and F₁ quails (3.6550 wk vs. 4.0563 wk for the Gompertz and Richards models, respectively, in females, and 3.3896 wk vs. 3.7204 wk for the Gompertz and Richards models, respectively, in males). No significant differences were observed between the Gompertz and Richards IP_T values of both NS and F₁ quail sexes,

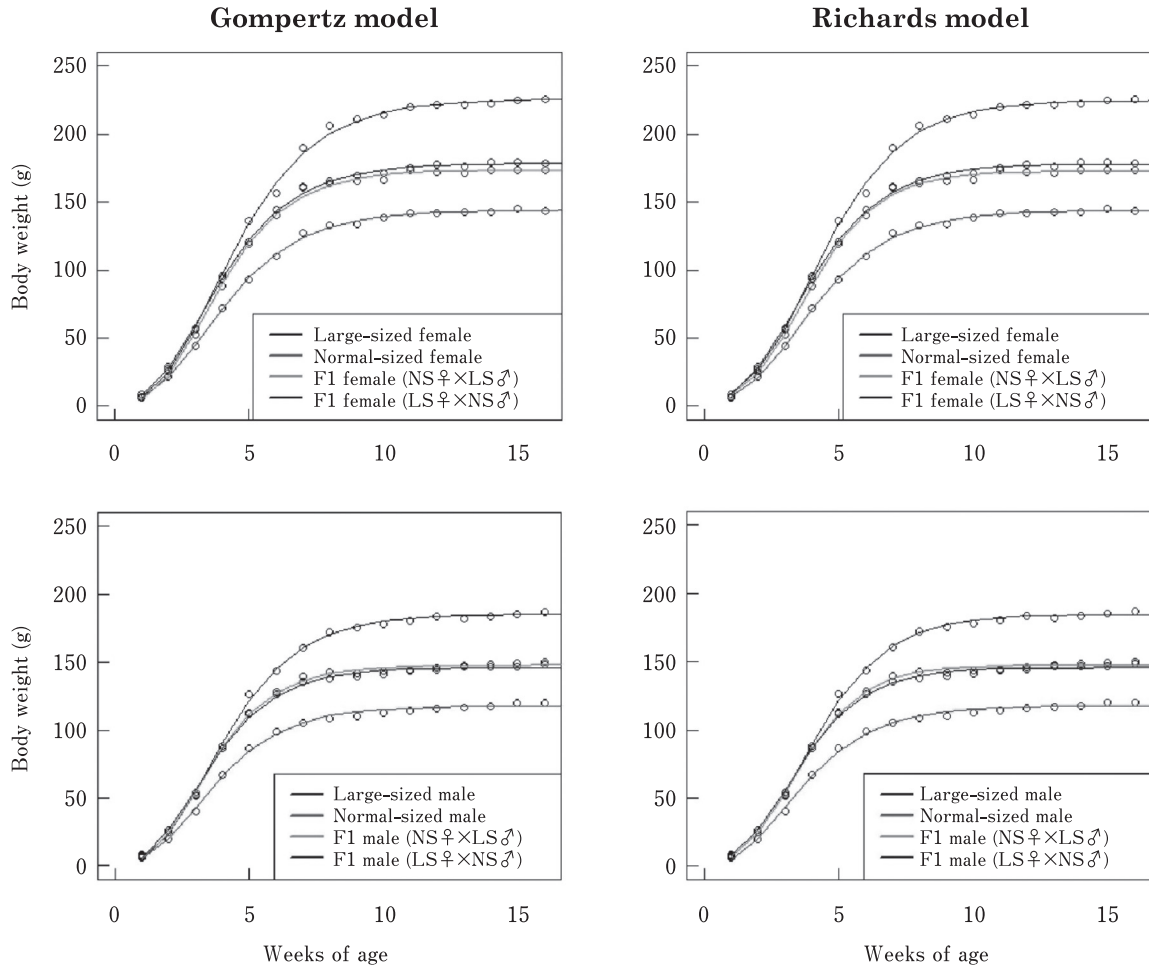


Fig. 1. Gompertz and Richards models for the two sexes of the LS and NS quails and their reciprocal F₁ progeny. LS and NS indicate large- and normal-sized quail strains, respectively.

except for the NS and F₁ (LS ♀ × NS ♂) females in the Gompertz model. Both sexes of the LS and NS quails exhibited the highest and lowest IP_W values, respectively, in the Gompertz and Richards models. The F₁ birds presented intermediate body weights when compared with those of their LS and NS parents from ages 4 to 16 wk.

Discussion

Our results demonstrated that the Gompertz model presented the best fit for NS and F₁ (LS ♀ × NS ♂) birds among all the five models examined. Faraji-Arough *et al.* (2018) and Santos *et al.* (2018) have previously reported that the Gompertz model is the most suited for plotting Japanese quail growth curves. However, the Richards model includes more parameters and possesses greater flexibility than the other growth models (Yin *et al.*, 2003), and presented the best fit for LS and F₁ (NS ♀ × LS ♂) quails in the present study. These results were consistent with those of previous studies evaluating Japanese quail growth (Sezer and Tarhan, 2005b; Beiki *et al.*, 2013; Teleken *et al.*, 2017; Kaplan and

Gürçan, 2018). Goto *et al.* (2011), Norris *et al.* (2007), and Raji *et al.* (2014b) further reported that the Gompertz model is the best for describing Galliformes and Japanese quail growth. However, some studies support that both the Gompertz and Richards models can effectively illustrate Japanese quail growth patterns (Akbaş and Oğuz, 1998; Sezer and Tarhan, 2005a; Alkan *et al.*, 2009; Narinc *et al.*, 2010; Firat *et al.*, 2016). In the present study, the Weibull and Logistic growth models fit nearly as well as the Gompertz and Richards models. Abdallah (2017) reported that the Logistic model best described the growth in LS and control Japanese quail lines. The Brody model yielded the poorest results in the present study. It has previously been reported that the Brody model is the most suited for ruminants (Marinho *et al.*, 2013; Simanca *et al.*, 2017; Kheirabadi and Rashidi, 2019), which require a longer time period to reach their mature body weight, when compared with Galliformes. These observations corroborate the results of studies on mathematical models used to describe Japanese quail growth (Teleken *et al.*, 2017). Data for the F₁ (LS ♀ × NS ♂ and NS ♀ × LS

♂) birds could be best fitted by the Gompertz and Richards models, respectively, in the present study. Our results suggest that male birds may be primarily responsible for inheritance of traits from parental lines.

The Gompertz and Richards models include three and four parameters, respectively, and were employed to describe the differences between the growth patterns of the NS and LS birds and their F₁ hybrids. The *a* values were higher for females than for males for both parental strains and their F₁ progeny. Unlike other Galliformes, this finding was expected for quails, and was consistent with a previous report modeling Japanese quail growth (Karaman *et al.*, 2013). The *a* values in the Richards and Gompertz models for the Japanese quails under study were lower than those previously reported (Kaplan and Gürcan, 2018). Several studies have reported *a* values between 174.0 g and 244.7 g obtained using nonlinear growth models for Japanese quail (Kizilkaya *et al.*, 2006; Alkan *et al.*, 2012; Gürcan *et al.*, 2017), which are consistent with those obtained in the present investigation. The *a* value is contingent upon genetic and environmental factors (Raji *et al.*, 2014b), and thus, it is expected to vary for quails with distinct genotypes and those reared under diverse environmental conditions. The estimated values of *b* in the Gompertz and Richards models were higher than those previously reported (Narinc *et al.*, 2010; Kaplan and Gürcan, 2018), and those in the Gompertz model were not consistent with the values reported for quail lines selected for high and low body weight at 6 wk of age (Abdallah, 2017). It is evident from Fig. 1 that the *c* curve was S-shaped, as the parameter value changed as the quails approached their mature weight. This parameter value was higher for males than for females across all generations. Males attained their mature weight at inflection point and asymptotic weight earlier than females. These findings are consistent with those obtained by a growth curve analysis of divergently selected Japanese quail (Kizilkaya *et al.*, 2006). Aggrey (2003) studied the effect of sex on growth rate parameters. The estimated values for parameter *c* in the present study were not consistent with those obtained in a previous study on nonlinear growth models for Japanese quails (Sezer and Tarhan, 2005a). In quail, the growth period and *a* value increase as the *c* value decreases. Similar results for *a* and *c* have been previously reported (Karaman *et al.*, 2013), whereas Aggrey (2009) estimated relatively higher *c* values for male and female quails using mixed-effects Logistic models. The *d* values in the Richards model were higher for males than for females across all generations, except for LS quails. Similar results were reported by Sezer and Tarhan (2005a) in their study on meat-producing quail growth curves.

The age and weight at inflection points of LS quails in the Gompertz and Richards models were 3.6550 vs. 4.0563 wk and 83.337 vs. 95.134 g, respectively, for females, and 3.3896 vs. 3.7204 wk and 68.227 vs. 77.522 g for males, respectively. Kaplan and Gürcan (2018) reported comparatively higher weight at inflection points of Gompertz and Richards models (105.84 vs. 107.44 g, respectively, for females, and 81.96 vs. 82.88 g, respectively, for males). They

also reported similar or relatively lower values for age at inflection points of the Gompertz and Richards models (25.05 vs. 25.29 d, respectively, for females, and 21.20 vs. 21.30 d, respectively, for males). The age and body weight at inflection points of the Gompertz model for a control Japanese quail line have previously been reported as 2.8193 wk and 72.51 g (Abdallah, 2017). These findings are inconsistent with those of the present study. The age at inflection point estimated for Japanese quail using the Gompertz model by Gürcan *et al.* (2017) was higher than that determined in the present study. These discrepancies may be attributed to the differences in the growth period included in the previous studies; in the present study, quails were reared until 16 wk of age.

The two sexes exhibit different growth characteristics across generations, which is known as sexual dimorphism. Hyánková *et al.* (2001), Aggrey (2003), and Kizilkaya *et al.* (2006) have previously reported sexual dimorphism in Japanese quail. The present study did not indicate any influence of sex on hatching weight across all generations. Sex differences were observed at 1 wk of age in all generations, except for the F₁ (NS ♀ × LS ♂) generation. The distinct sexual phenotype of this generation had manifested by the age of 4 wk. These observations were different from those reported by Ashok and Prabakaran (2012). They observed a significant effect of sex on body weight between ages 1 and 6 wk. In contrast, Sezer and Tarhan (2005a) did not report any sex differences in quails raised for meat; however, they observed sex differences at 15 d of age in the wild type quails.

Our findings provide a holistic idea of age at sexual maturity and appropriate slaughter age for Japanese quail. The results indicated that the male parental strain played a key role in the inheritance of characteristics in the F₁ offspring. This is the first report on the effect of male parents on the mode of inheritance of growth traits. Further studies on growth performance traits are required prior to their application in developing poultry breeding strategies. The quantitative trait loci (QTL) for growth curve parameters of Japanese quail have not yet been studied. Hence, our results provide the basis for future QTL analyses to understand the genetic basis of variation in growth curve parameters.

Here, we demonstrated that the Richards model is the most suitable for describing growth patterns of the LS and F₁ (NS ♀ × LS ♂) quails, whereas the growth measurements of the NS and F₁ (LS ♀ × NS ♂) quails can be best fitted with the Gompertz model. The growth patterns observed in the F₁ birds were likely inherited from the male parental strain.

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Conflicts of Interest

The authors declare no conflict of interest.

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