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# Effects of Genetic and Non-genetic Factors on Body Weight and Carcass Related Traits in Two Strains of Japanese Quails

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### Abstract

The current study was conducted to investigate the effects of genetic and non-genetic factors on body weight and carcass traits of Japanese quails. Two strains of Japanese quail (150 wild quails and 150 white quails) were used as base population. Four mating groups were used to produce progenies: wild male × wild female, white male × wild female, wild male × white female and white male × white female. Quails were weighed then slaughtered at 35 days of age. The carcass traits consisting carcass weight, breast meat weight, thigh meat weight, skin weight, and abdominal fat weight were recorded after slaughter and after removing feathers, internal organs, and digestive system. Based on these weights, the percentages of carcass, breast, thigh, skin, and abdominal fat were estimated. The effects of sex, hatch, and mating group on body and carcass composition traits were investigated. Sex had a significant effect on all traits (P < 0.01), with the exception of the thigh percentage. Moreover, female birds showed higher values for all traits. There were significant differences between hatches and mating groups and wild male × wild female offspring showed highest values of carcass weight, breast weight, thigh weight, skin weight and abdominal fat weight (P < 0.01). The heritability estimates for body and carcass related traits were moderate to high (0.22 to 0.66). The carcass percentage traits showed lower heritability, ranged from 0.22 to 0.33. Genetic correlations between body weight and carcass weight, skin weight, breast weight, thigh weight, and abdominal fat weight were moderate to high (0.37 to 0.94). These results showed that selection for increasing body weight and decreasing abdominal fat will improve carcass related traits.

# Introduction

In the poultry world, quail meat production is negligible compared to broilers, but occupies a relevant place in poultry breeding and contributes to the variety in poultry meat production (Maiorano *et al.*, 2011). As an agricultural species, quails produce eggs and meat that have unique flavor. These birds are also low cost maintenance, have small body size (80-300 g) and short generation interval (3-4 generation per year), and are resistant to diseases. Further, quails have high egg production that makes it an excellent laboratory animal (Vali, 2008). Quails are bred for egg and meat production, and the relative importance of its two products varies between countries (Minvielle, 1998).

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Several researchers have reported genetic differences in body weight and carcass traits among various strains of Japanese quail. Heritability of body weight was reported to range from 0.23 to 0.77 (Vali et al., 2005; Shokoohmand et al., 2007; Khaldari et al., 2010; Lotfi et al., 2011; Silva et al., 2013; Akbarnejad et al., 2015). Genetic improvement of body weight in Japanese quail occurs in a few generations and a positive genetic trend is reported for this trait (Varkoohi and Kaviani, 2014). Indirect selection could be used to improve carcass traits since there are positive genetic correlations between body weight and carcass traits (Daikwo et al., 2013). For example, a positive genetic correlation between body weight and abdominal fat has been reported (Narinc et al., 2013), showing that selection based on live body weight will increase abdominal fat.

Many factors affect carcass quantity and quality in Japanese quail, such as strain (Vali et al., 2005; Shokoohmand et al., 2007; Kumari et al., 2008; Charati and Esmailizadeh, 2013), sex (Vali et al., 2005; Saatci et al., 2006; Shokoohmand et al., 2007; Beiki et al., 2011; Marefat et al., 2014), quail body weight, age (Lotfi et al., 2011; Raji et al., 2015), and hatching time (Vali et al., 2005; Khaldari et al., 2010; Lotfi et al., 2011; Daikwo et al., 2013). There are many studies that investigate the effects of strain and genotype on carcass traits in broilers, but only few reports exist for Japanese quails. The aim of the current study was to demonstrate the effect of strain and mating system on body weight, carcass composition, and fat deposition in two strains of wild and white Japanese quails.

## Materials and Methods Collecting data

Two strains of Japanese quail consisting of 150 wild quails (50 male and 100 female birds) and 150 white quails (50 male and 100 female birds) were used as base population at Aghghala quail station (Golestan province, Iran). Four mating groups were used to produce progenies: wild male × wild female (group 1), white male × wild female (group 2), wild male × white female (group 3), and white male × white female (group 4). One male quail with two female quails were placed in each cage. During the laying periods, quails were fed a diet containing 20% crude protein (CP) and 3000 Kcal/kg metabolizable energy (ME). Eggs were collected, numbered, and placed in the setter and were transferred to

identified according to each dam based on patterns on the egg surface. Most quails hatched at 17 days old. Three hatches were used in total.
To recognize the chicks of each dam and sire,

the hatcher trays after 14 days. Eggs were

hatcher trays were partitioned by cartoon plat and each box was numbered according to the pedigree information. Hatched chicks were numbered by using leg bands and transferred to a rearing room of 35°C. The temperature was reduced weekly until 24°C at five weeks of age. Quails were fed a diet containing 24% CP and 2900 Kcal/kg ME. Chicks received 24 hrs of light/day and fed ad libitum during the growth period. Quails were weighed and then slaughtered at 35 days of age. Carcass traits including carcass weight (CW), breast meat weight (BRW), thigh meat weight (TW), skin weight (SW), and abdominal fat weight (AFW) were recorded after slaughter and after removing feathers, and internal organs. Based on these traits, we calculated the percentage of carcass, breast, thigh, skin and abdominal fat relative to live body weight at five weeks of age (BW5).

# **Statistical Analysis**

To investigate the effects of sex, hatch, and mating group, general linear model of SAS procedure was used as following model:

$$y_{ijkl} = \mu + S_i + H_j + G_k + e_{ijkl}$$

where  $y_{ijkl}$  is the observation of each quail,  $\mu$  is the grand mean,  $S_i$  is the fixed effect of sex (*i* = 1, 2),  $H_j$  is the fixed effect of hatching time (*j* = 1, 2, 3),  $G_k$  is fixed effect of mating group (*k* = 1, 2, 3, 4) and  $e_{ijkl}$  is random residual effect. The means of traits were compared using Duncan test.

Univariate and bivariate analysis with restricted maximum likelihood procedure and ASREML software (Gilmour *et al.*, 1999) were used to estimate (co)variance components and genetic parameters. The following simple animal model was used:

$$y_{ijkl} = \mu + S_i + H_j + G_k + a_l + e_{ijklm}$$

where  $y_{ijkl}$  is the observation of each quail,  $\mu$  is the grand mean,  $S_i$  is the fixed effect of sex (*i* = 1, 2),  $H_j$  is the fixed effect of hatching time (*j* = 1, 2, 3),  $G_k$  is fixed effect of mating group (*k* = 1, 2, 3, 4),  $a_l$  is the random additive genetic of the quail and  $e_{ijklm}$  is random residual effect.

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#### **Results and Discussion**

Descriptive statistics of the data are shown in Table 1. The mean values of BW, CW, SW and TW were higher than those previously reported (Vali *et al.*, 2005; Vali, 2008; Alkan *et al.*, 2010; Khaldari *et al.*, 2010; Narinc *et al.*, 2010; Sari *et al.*, 2011; Lotfi *et al.*, 2011). Estimates of carcass percentage, breast percentage, and thigh percentage means were 67.24, 27.3 and 16.40, respectively, which were higher than those previously reported by Raji *et al.* (2015) for wild and light brown Japanese quails and by Narinc *et al.* (2010) and Lotfi *et al.* (2011) for pure bred Japanese quails. The mean values of abdominal

<b>Table 1.</b> Descriptive statistics of the tra
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fat weight and abdominal fat percentage were 2.06 g and 0.96%, respectively, and were similar to the results of Lotfi et al. (2011) and Narinc et al. (2010). Skin percentage (SP) obtained 5.96%, which was higher than a previously reported value (5.2%) by Lotfi et al. (2011) for Japanese quail at 42 days of age. These results were in contrast with another study (Wilkanowska and Kokoszynski, 2011) that reported greater breast muscles, muscles, leg and skin with subcutaneous fat in Pharaoh quails (Coturnix Coturnix pharaoh) at 42 days of age rather than at 33 days of age.

Trait	n <sup>2</sup>	Mean	SD	CV (%)
Body weight <sup>1</sup> (g)	721	210.60	24.97	12
Carcass weight (g)	722	141.42	18.54	13
Carcass percentage (%)	722	67.24	5.37	8
Skin weight (g)	724	12.55	2.69	21
Skin percentage (%)	721	5.96	1.07	18
Breast weight (g)	724	57.36	8.34	15
Breast percentage (%)	722	27.30	2.68	10
Thigh weight (g)	724	34.46	4.57	13
Thigh percentage (%)	722	16.40	1.34	8
Abdominal fat weight (g)	711	2.06	0.51	25
Abdominal fat percentage (%)	710	0.96	0.20	21

<sup>1</sup> BW at 5 weeks of age

<sup>2</sup> Variation the number of observations is due to missing data.

The effects of sex and hatch on body and carcass traits are presented in Table 2. Sex had a significant effect on all traits (P < 0.01), with the exception of thigh percentage, as female birds exhibited greater values for all traits. These results were similar to findings of Vali et al. (2005) who also reported that females showed greater carcass weight, breast weight, breast percent, and thigh weight, but not thigh percent, compared to males. In disagreement with these results, Lotfi et al. (2011) found higher percentages of carcass traits (carcass percentage, breast percentage, thigh percentage, skin and breast intramuscular percentage, fat percentage), except abdominal fat percentage, in males. Similarly, Daikwo et al. (2013) found that sex had a significant effect (P < 0.01) on preslaughter, carcass, breast and thigh weights. In a study on three commercial strains of Japanese quail, Shokoohmand et al. (2007) found that body weights between male and female birds were similar from hatch to 28 days of age, but females were heavier than males at 42 days of age, suggesting that it could be due to lower sexual maturity age in males than females (five

weeks *vs.* six weeks) and releasing testosterone hormone at this age which may decrease growth rate. The larger body weights of female quails may be the results of their higher reproductive system (Marks, 1993).

There were significant differences between hatches (P < 0.01) but not in BW (Table 2). The first hatch showed greater values in all carcass related traits compared to the third hatch, but the sample size of the third hatch was small. The first and second hatches were similar in carcass weight, carcass percentage, skin weight, skin breast percentage, breast weight, and percentage. A similar conclusion has been drawn by Charati and Esmailizadeh (2013), who reported reductions in slaughter and carcass weights in the second and third hatches compared to the first hatch. In disagreement with these results, Khaldari et al. (2010) showed that the quails from the second hatch generally were heavier (P < 0.01), but were similar in carcass traits. Vali et al. (2005) found significant differences across hatches (P < 0.01) in body weight at 35 days of age, but not similar patterns for consecutive hatches. Daikwo et al. (2013) reported no significant effect of hatch on carcass traits in Japanese quails. Lotfi *et al.* (2011) found significant effects of hatch in all carcass traits at 42 and 91 days of age in Japanese quails and

showed that the progeny of older mothers had greater mean values of carcass traits than the progeny of younger mothers.

**Table 2.** Comparison of least squares means (± standard errors) of sex and hatch for body and carcass traits

Troit	Se	x		Hatch	
11all <sup>1</sup>	Male	Female	1	2	3
BW (g)	$206.73 \pm 1.23^{a}$	215.03± 1.39 <sup>b</sup>	210.60 ±	1.75 210.67 ± 1.30	$210.35 \pm 2.05$
CW (g)	137.01 ± 0.09 ª	146.46 ± 1.05 <sup>b</sup>	$144.19 \pm 1$	1.24 × 142.14 ± 0.96 ×	133.53 ± 1.56 y
CP (%)	$66.36 \pm 0.26$ a	68.24 ± 0.30 b	$68.63 \pm 0$	$.37 \times 67.63 \pm 0.25 \times$	63.20 ± 0.51 y
SW(g)	11.90 ± 0.13 a	13.29 ± 0.16 <sup>b</sup>	$12.86 \pm 0$	.21 × 12.57 ± 0.13 ×	11.89 ± 0.26 y
SP (%)	5.76 ± 0.05 ª	$6.18 \pm 0.06$ b	$6.08 \pm 0.$	$08 \times 5.98 \pm 0.05 \times$	$5.63 \pm 0.10$ y
BRW(g)	55.23 ± 0.39 ª	$59.82 \pm 0.46$ b	57.73 ± 0	$.54 \times 58.1 \pm 0.43 \times$	53.91 ± 0.73 y
BRP (%)	$26.80 \pm 0.14$ a	27.87 ± 0.15 <sup>b</sup>	$27.48 \pm 0$	$.18 \times 27.66 \pm 0.13 \times$	25.66 ± 0.25 y
TW(g)	33.58 ± 0.22 ª	35.46 ± 0.25 <sup>b</sup>	$35.73 \pm 0$	$.30 \times 34.42 \pm 0.23 \text{ y}$	$32.24 \pm 0.41$ y
TP (%)	$16.29 \pm 0.07$	$16.53 \pm 0.08$	$17.02 \pm 0$	$10 \times 16.37 \pm 0.06 \mathrm{y}$	$15.34 \pm 0.13$ z
AFW(g)	$1.76 \pm 0.06$ a	2.39 ± 0.07 b	$2.32 \pm 0.$	$08 \times 2.03 \pm 0.06 \text{ y}$	$1.67 \pm 0.11$ z
AFP (%)	0.84± 0.03 ª	1.11 ± 0.03 b	$1.10 \pm 0.$	$04 \times 0.94 \pm 0.03 \text{ y}$	$0.77 \pm 0.05 ^{z}$

 $^{1}BW = BW$  at five weeks of age; CW = carcass weight; CP = carcass percentage; SW = skin weight; SP = skin percentage; BRW = breast weight; BRP = breast percentage; TW = thigh weight; TP = thigh percentage; AFW = abdominal fat weight; AFP = abdominal fat percentage.

\*Values within a row and classification (sex and hatch) with no common superscript are significantly different (P < 0.01).

**Table 3.** Least squares means and standard errors by different mating groups for body weight and carcass related traits

$\frac{1}{1} \qquad 2 \qquad 3 \qquad 4$	
BW (g) 218.24 ± 1.30 <sup>a</sup> 205.88 ± 1.71 <sup>b</sup> 201.73 ± 2.44 <sup>bc</sup> 196.79 ± 2	.27 c
CW (g) $147.39 \pm 0.93$ a $138.53 \pm 1.24$ b $133.90 \pm 1.97$ c $129.20 \pm 1$	.77 d
CP $\binom{\%}{}$ 67.73 ± 0.28 a 67.44 ± 0.39 a 66.46 ± 0.65 ab 65.46 ± 0.	59 <sup>b</sup>
SW (g) $13.23 \pm 0.15^{a}$ $12.00 \pm 0.19^{b}$ $12.00 \pm 0.28^{b}$ $11.37 \pm 0.53^{b}$	26 <sup>b</sup>
SP (%) $6.07 \pm 0.06^{a}$ $5.83 \pm 0.08^{ab}$ $5.97 \pm 0.13^{ab}$ $5.76 \pm 0.13^{ab}$	1 <sup>b</sup>
BRW (g) $59.46 \pm 0.42$ a $56.52 \pm 0.57$ b $54.12 \pm 0.90$ c $52.56 \pm 0.52$	83 c
BRP ( $\sqrt[6]{}$ ) 27.41 ± 0.14 <sup>ab</sup> 27.57 ± 0.20 <sup>a</sup> 26.84 ± 0.32 <sup>bc</sup> 26.70 ± 0.	28 c
TW (g) $35.97 \pm 0.23$ a $33.66 \pm 0.31$ b $32.46 \pm 0.47$ b $31.46 \pm 0.$	43 c
TP (%) $16.54 \pm 0.07 \text{ a}$ $16.41 \pm 0.10 \text{ a}$ $16.20 \pm 0.16 \text{ab}$ $16.00 \pm 0.$	15 <sup>b</sup>
AFW (g) $2.30 \pm 0.07 \text{ a}$ $1.82 \pm 0.08 \text{ b}$ $1.92 \pm 0.13 \text{ b}$ $1.65 \pm 0.13 \text{ c}$	1 <sup>b</sup>
AFP (%) $1.05 \pm 0.03 a$ $0.88 \pm 0.04 b$ $0.95 \pm 0.05 ab$ $0.82 \pm 0.05 ab$	)5 <sup>ь</sup>

<sup>1</sup> BW = BW at five weeks of age; CW = carcass weight; CP = carcass percentage; SW = skin weight; SP = skin percentage; BRW = breast weight; BRP = breast percentage; TW = thigh weight; TP = thigh percentage; AFW = abdominal fat weight; AFP = abdominal fat percentage.

<sup>2</sup> Group 1 = wild male × wild female; group 2 = white male × wild female; group 3 = wild male × white female; group 4 = white male × white female.

Least squares means of different mating groups for body weight and carcass related traits are shown in Table 3. Group 1 (wild male×wild female) showed the highest values for BW5, CW, SW, BRW, TW and AFW traits (P < 0.01). Although group 1 had the highest estimates of carcass component percentages (with the exception of BRP), these differences were not significant (P > 0.05). Shokoohmand *et al.* (2007) reported greater body weights at 14, 28 and 42 days of ages in wild Japanese quails compared to white Japanese quails. The effects of white and wild genotypes of Japanese quail on carcass

traits were investigated by Charati and Esmailizadeh (2013) who reported a positive heterosis (+10.09%) for pre slaughter and carcass weights in crossed progenies of white and wild Japanese quails. These results were in contrast to our results, which founded offspring of crosses showed lower body and carcass weights compared to the progenies of wild parents. Vali et al. (2005) found that carcass percentage, breast carcass weight, weight, and thigh percentage were significantly affected by variations in quail strain (*P* < 0.01).

Table 4: approxima	Estimates of ate SE for boo	f heritability dy weight ar	v (diagonal, nd carcass rel	in bold), ge lated traits	enetic (abov	e diagonal),	, and phenc	otypic (belov	v diagonal)	correlations	with their
Trait <sup>1</sup>	BW	CW	CP	SW	$\operatorname{SP}$	BRW	BRP	ΤW	ТР	AFW	AFP
BW	$0.44 \pm 0.08$	$0.94 \pm 0.03$	$0.42 \pm 0.09$	$0.52 \pm 0.10$	$-0.15 \pm 0.13$	$0.93 \pm 0.03$	$0.59 \pm 0.09$	$0.84 \pm 0.04$	$0.18 \pm 0.05$	$0.37 \pm 0.12$	$0.13 \pm 0.11$
CW	$0.78 \pm 0.01$	$0.61 \pm 0.08$	$0.72 \pm 0.12$	$0.65 \pm 0.09$	$0.02 \pm 0.09$	$0.98 \pm 0.07$	$0.79 \pm 0.11$	$0.76 \pm 0.08$	$0.38 \pm 0.11$	$0.23 \pm 0.11$	$0.03 \pm 0.11$
C	$-0.24 \pm 0.03$	$0.39 \pm 0.03$	$0.23 \pm 0.06$	$0.61 \pm 0.10$	$0.36 \pm 0.12$	$0.67 \pm 0.12$	$0.89 \pm 0.08$	$0.87 \pm 0.12$	$0.92 \pm 0.04$	$-0.10 \pm 0.22$	$-0.24 \pm 0.13$
SW	$0.47 \pm 0.03$	$0.47 \pm 0.03$	$0.05 \pm 0.03$	0.27±0.07	$0.75 \pm 0.08$	$0.65 \pm 0.09$	$0.57 \pm 0.18$	$0.63 \pm 0.11$	$0.45 \pm 0.14$	$0.44 \pm 0.16$	$0.32 \pm 0.19$
SP	$-0.06 \pm 0.04$	$0.06 \pm 0.03$	$0.22 \pm 0.03$	$0.83\pm0.01$	$0.24\pm 0.07$	$0.04 \pm 0.09$	$0.26 \pm 0.14$	$0.05 \pm 0.09$	$0.40 \pm 0.11$	$0.26 \pm 0.11$	$0.29 \pm 0.21$
BRW	$0.70 \pm 0.02$	$0.93 \pm 0.03$	$0.41 \pm 0.03$	$0.42 \pm 0.03$	$0.05 \pm 0.03$	$0.66 \pm 0.08$	$0.83 \pm 0.09$	$0.92 \pm 0.02$	$0.30 \pm 0.11$	$0.22 \pm 0.10$	$-0.01 \pm 0.11$
BRP	$-0.20 \pm 0.04$	$0.35 \pm 0.03$	$0.88 \pm 0.08$	$0.03 \pm 0.02$	$0.17\pm0.03$	$0.54 \pm 0.02$	$0.25 \pm 0.07$	$0.78 \pm 0.11$	$0.65 \pm 0.10$	$-0.08 \pm 0.11$	$-0.25 \pm 0.12$
TW	$0.76 \pm 0.01$	0.26 ±0.01	$0.29 \pm 0.03$	$0.47\pm0.03$	$0.06 \pm 0.02$	$0.81 \pm 0.01$	$0.21 \pm 0.03$	$0.54 \pm 0.08$	$0.58 \pm 012$	$0.14 \pm 0.11$	$-0.04 \pm 0.10$
TP	$-0.25 \pm 0.03$	$0.26 \pm 0.03$	$0.80 \pm 0.01$	$0.04 \pm 0.02$	$0.21 \pm 0.03$	$0.23 \pm 0.04$	$0.63 \pm 0.02$	$0.42 \pm 0.03$	$0.33 \pm 0.07$	$-0.23 \pm 0.12$	$-0.29 \pm 0.11$
AFW	$0.33\pm0.03$	$0.27 \pm 0.03$	$-0.07 \pm 0.03$	$0.35\pm0.03$	$0.19\pm0.03$	$0.16\pm0.04$	$-0.16 \pm 0.03$	$0.23 \pm 0.03$	$-0.12 \pm 0.03$	0.22±0.06	$0.96 \pm 0.01$
AFP	$0.15\pm0.03$	$0.13 \pm 0.04$	$-0.03 \pm 0.02$	$0.27 \pm 0.03$	$0.21 \pm 0.03$	$0.04 \pm 0.04$	$-0.13 \pm 0.03$	$0.09 \pm 0.04$	$-0.08 \pm 0.03$	$0.97 \pm 0.02$	$0.22 \pm 0.06$
<sup>1</sup> BW = BW i weight; TP =	at five weeks of thigh percentag	age; CW = carc șe; AFW = abdc	cass weight; CP minal fat weigh	= carcass perce tt; AFP = abdom	ntage; SW = ski iinal fat percents	in weight; SP = age.	skin percentage	e; BRW = breast	: weight; BRP =	· breast percenta	ge; TW= thigh

Estimates of heritability and other genetic parameters for body weight and carcass related traits are presented in Table 4. The heritability estimates of carcass related traits were moderate to high (0.22 to 0.66) but when these traits were expressed as percentages of body weight at five weeks of age, heritability was lower, ranging from 0.22 to 0.33. Similar results were obtained by Akbarnejad *et al.* (2015). Heritability of body weight at five weeks of age was 0.43 which was lower than that obtained by Vali *et al.* (2005) and Shokoohmand *et al.* (2007) (the latter of which reported a heritability range of 0.48 to 0.72 for body weight at 42 days of age in three strains of Japanese quails).

The estimates of heritability for carcass weight, breast weight, and thigh weight were 0.61, 0.66, and 0.54, respectively, which are higher than those values reported by Sari et al. (2011) and Akbarnejad et al. (2015), though the heritability of BW were similar. Narinc et al. (2010) and Lotfi et al. (2011) also found similar results for carcass weight, breast weight, and thigh weight. The pattern of heritability for carcass component percentages (0.22 to 0.33) was similar to the results of Vali et al. (2005), Narinc et al. (2013) and Lotfi et al. (2011) but higher than values reported by Khaldari et al. (2010). The reason of lower heritabilities for carcass component percentages in comparison with carcass component weights may be originated of adjusting the measurements to live body weight. The differences between reported estimates for heritability may depend on the population, environmental conditions, the method of estimation (Falconer and MacKay, 1996), statistical model, and sampling error due to small data set or sample size (Prado-Gonzalez et al., 2003).

Heritability for skin weight, skin percentage, abdominal fat weight, and abdominal fat percentage ranged from 0.22 to 0.27, which is similar to values obtained by Lotfi *et al.* (2011). Narinc *et al.* (2013) found heritabilities of the abdominal fat weight and abdominal fat percentage to be 0.4 and 0.29, respectively. Heritability estimates of abdominal fat in broilers range from 0.08 to 0.71 (Griffin, 1996; Rance *et al.*, 2002; Zerehdaran *et al.*, 2004).

Genetic correlations between body weight and carcass weight, skin weight, breast weight, thigh weight, and abdominal fat weight were moderate to high (0.37 to 0.94). Correlations between percentages of these traits were lower (0.13 to 0.59) and even negative for skin percentage (-0.15). These results showed that selecting for body weight can increase skin weight, breast weight, thigh weight, and consequently abdominal fat weight. Therefore, selection for increasing body weight and decreasing abdominal fat increases skin weight, breast weight, and thigh weight and decreases abdominal fat weight. Genetic correlations among body weight and carcass weight traits were obtained previously and ranged from 0.28 to 0.95 (Vali et al., 2005; Khaldari et al., 2010; Lotfi et al., 2011; Narinc et al., 2013; Akbarnejad et al., 2015). Carcass weight showed greater genetic correlations with breast percentage and thigh weight and lower genetic correlation with abdominal fat percentage, compared to body weight. Genetic correlations between breast and thigh percentages and abdominal fat percentage were negative (-0.25 and -0.29, respectively), which is in agreement with results of Narinc et al. (2013) who reported a negative genetic correlation (-0.24) between breast yield and abdominal fat in Japanese quails using a multiple animal model. Similarly, Narinc et al. (2010) reported a negative genetic correlation (-0.34) between these traits using Bayesian methods. These results indicate that selecting for breast percentage and thigh percentage, not only increase these traits but also reduce abdominal fat percentage.

Positive genetic correlations were found between skin weight, skin percentage, abdominal fat weight, and abdominal fat percentage, and ranged from 0.26 to 0.44, which was lower than those reported by Lotfi et al. (2011) (0.35 to 0.96). No comparable estimates of genetic correlations for these traits were found in quails. Zerehdaran et al. (2004) reported a high genetic correlation between abdominal fat weight and skin weight (0.54) in broilers, whereas the genetic correlation between abdominal fat weight and intramuscular fat percentage was almost zero (0.02). Abdominal and subcutaneous fat are regarded as the main sources of waste in the slaughterhouse. Subcutaneous fat mainly determines the weight of skin. Therefore, as observed in the current study, skin weight and skin percentage were considered as indicator traits of subcutaneous fat weight and subcutaneous fat percentage (Zerehdaran et al., 2004).

#### Conclusion

The greatest body weight and carcass composition traits were found in the progenies of wild parents. Crossed progenies had lower values in comparison. The findings of this study show that using a wild strain of the Japanese quail is more profitable for meat production. Also, moderate to high genetic correlations were found between BW and carcass related traits.

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