

# Response to family selection and genetic parameters in Japanese quail selected for four week breast weight

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## Abstract

An experiment was conducted to investigate the effect of short-term selection for 4 week breast weight (4wk BRW), and to estimate genetic parameters of body weight, and carcass traits. A selection (S) line and control (C) line was randomly selected from a base population. Data were collected over two consecutive hatches for four generations. A total of 1 135 records from 156 sires and 218 dams were used to estimate the genetic parameters. The genetic improvement of 4wk BRW was 3.5, 2.7 and 0.6 g in generation 2, 3 and 4, respectively. The estimated heritability by using pedigree information was  $0.35 \pm 0.06$ . There were a significant difference for BW, and carcass weights but not for carcass percent components between lines ( $P < 0.01$ ). The heritabilities and correlated responses for body weight (BW), carcass and leg weights were 0.46, 0.41 and 0.47, and 13.2, 16.2, 4.4%, respectively. The genetic correlations of BRW with BW, carcass, leg, and back weights were 0.85, 0.88 and 0.72, respectively. Selection for 4 wk BRW improved feed conversion ratio (FCR) about 0.19 units over the selection period. Inbreeding caused an insignificant decline of the mean of some traits. Results from this experiment suggest that BW as a genetically correlated trait can be used to improve BRW.

**Keywords:** family selection, breast weight, carcass traits, Japanese quail, inbreeding

## Zusammenfassung

### Reaktion auf familiäre Selektion und genetische Parameter in Japanwachteln, die gemäß dem 4-Wochen-Brustgewicht ausgewählt wurden

Zur Erforschung der Auswirkung der Kurzzeit-Selektion gemäß dem 4-Wochen-Brustgewicht (4wk BRW) und zur Einschätzung der genetischen Parameter für Körpergewicht und Schlachtkörpermerkmale wurde ein Experiment durchgeführt. Eine Selektionslinie (S) und eine Kontrolllinie (C) wurden statistisch aus einer Basispopulation ausgewählt. Die Messwerte wurden über zwei aufeinanderfolgende Bruten vier Generationen lang gesammelt. Insgesamt wurden zur Bewertung der genetischen Parameter 1 135 Datensätze aus 156 Vätern und 218 Müttern verwendet. Die genetische Verbesserung von 4wk BRW betrug 3,5, 2,7 bzw. 0,6 g in der Generation 2, 3 bzw. 4. Die geschätzte Vererbbarkeit unter Verwendung

der Stammbaum-Informationen betrug  $0,35 \pm 0,06$ . Es bestand ein signifikanter Unterschied für BW (Brustgewicht) und Schlachtkörpergewicht, aber nicht für die in Prozent gemessenen Schlachtkörper-Bestandteile zwischen den Linien ( $P < 0,01$ ). Die Erblichkeit und korrelierten Reaktionen für Körpergewicht (BW), Schlachtkörper- und Beingewicht betragen 0,46, 0,1 und 0,47 bzw. 13,2, 16,2 und 4,4%. Die genetischen Korrelationen von BRW (Brustgewicht) mit BW (Körpergewicht), Schlachtkörper-, Bein- und Rückengewicht waren 0,85, 0,88 bzw. 0,72. Die Selektion gemäß 4 wk BRW (Brustgewicht nach 4 Wochen) verbesserte die Futtermittelverwertung (FCR) um über 0,19 Einheiten über den Selektionszeitraum. Inzucht führte im Mittel zu einem nicht signifikanten Abfall von einigen Merkmalen. Die Ergebnisse aus diesem Experiment legen nahe, dass BW (Körpergewicht) als ein genetisch korreliertes Merkmal zur Verbesserung von BRW (Brustgewicht) verwendet werden kann.

**Schlüsselwörter:** Selektion, Brustgewicht, Schlachtleistung, japanische Wachteln, Inzucht

## Introduction

Family selection refers to a selection method in which family groups are ranked according to the mean performance of each family and whole families are selected or discarded. Often family average contains two different kinds of information. The first is the average breeding value of the family and the second is the environmental condition common to the whole family (Lush 1947). A major advantage with family selection is that, based on phenotypic observations from full or half-sibs, breeding values can be estimated for traits that cannot be measured on the individuals that are to be used as parents (Gjedrem 2005). Anatomical responses to selection under varying diets (Ricklefs & Marks 1985) the relationships between egg weight, hatch weight, and growth rates (Marks 1975) and survival rates (Aggrey 2002) of different lines have all been documented. Some studies show high positive correlations among live body weight and carcass traits. Redish (2004) reported that selection for pectoralis major muscle weight in maternal Japanese quail lines resulted in slight increases in the absolute weight of the pectoralis major muscle. Vali *et al.* (2005) found high correlations between live body weight and carcass weight components but very low correlations with carcass yield components. Breast and leg weights approximately compose 40 and 25 percent of carcass weight in quail, respectively and the remainder is the back which is less favored by consumers. So it seems direct selection for increased breast weight is more useful than indirect selection via increasing live body weight. There is limited data in the literature relative to family selection for carcass traits in quail, and particularly the most effective selection criterion to increase breast weight. Accordingly, three topics were investigated here using a selection experiment including a random-bred control. Firstly, in the present study was calculated response to selection for 4 wk breast weight (BRW) and correlated responses in carcass traits and body weight. Secondly, was estimated genetic parameters for these traits. Thirdly, was assessed the effect of inbreeding depression on the traits.

## Materials and methods

### Animals

The experimental Japanese quail population (*coturnix coturnix*) originated from a commercial farming center in Yazd city, Iran. Around 1 000 birds were transported to the animal research station of Tehran University. Before the start of the experiment, the population was not selected for any traits. To establish a selection line (S-line) and a control line (C-line), a total of 210 birds were randomly selected from the population, then distributed equally and randomly into the two lines, and allowed to reproduce. The number of parents and progeny at 4 wk of age are presented in Table 1 by line, sex, hatch and generation.

Table 1  
Number of parents and progeny in each line by hatch and generation

Generation	Selection Line						Control Line					
	Parents		Hatch 1		Hatch 2		Parents		Hatch 1		Hatch 2	
	Sire	Dam	Male	Female	Male	Female	Sire	Dam	Male	Female	Male	Female
0	35	70	-	-	-	-	39	78	-	-	-	-
1	34	66	86	74	91	82	36	75	90	81	92	87
2	30	52	77	82	81	94	34	74	97	91	68	74
3	26	30	80	72	88	83	35	72	79	74	81	86
4	-	-	26	31	42	46	-	-	76	65	68	71

Birds in the S-line were individually leg-tagged, then two females were individually caged (25×25×30 cm) and mated to a single male every second day, while pairs of C-line females were caged together (25×25×30 cm) and mated to a single male so sex ratio was 1:2 (male:female) in each line. Birds were kept under circumstances that closely resemble commercial practice, i.e. a standard commercial feed containing 20 % CP and 2 650 Kcal Kg/ME, artificially lighted housing for 16 h per day. Food and water were available *ad libitum*. Eggs were collected daily and labeled by dam number to constitute pedigree. Eggs were stored up to 7 days at a temperature of 15 °C and humidity of 70 %. Eggs were set in setter for 14 days, and then, the eggs of each dam transferred to separate cells (S-line) in Hatcher trays for 3 days. At the time of hatching, the quails from the S-line were leg-tagged with a numbered plastic plate and quails from each line placed into separate pens. Quails were raised in group housing with 60 birds per square meter. quails had access to artificially lighted housing for 24 h per day, and a standard commercial feed containing 26 % CP and 2 900 Kcal Kg/ME. Food and water were available *ad libitum*.

Selection was done for three consecutive generations (a total of four generations including the base), and there were two hatches per generation in both lines. To select parents for the S-line, birds of hatch 1 were slaughtered, and then birds from the 50 % of full-sib families with the highest family breast weight (BRW) in hatch 1 were used as parents. Some females didn't lay until 69 days of age, increasing over generations. As, birds from the 50 % superior families, are selected 105, 95 and 80 birds were selected for replacement in generation 1, 2 and 3, respectively but the number of actually reproducing were fewer (Table 1). In the C-line pedigree was not recorded. A total of 105 birds of control line in hatch 2 were randomly selected.

### Traits

Although some of the quail breeders started to lay eggs at 45 d of age, egg collection started at 56 d of age to obtain more eggs and chickens. The body weight (BW) was measured at 4 weeks of age. All quail from the first hatch in the S-line and approximately 80 birds of the C line were slaughtered, plucked, eviscerated and carcasses were kept for 4 h at 4 °C, then each carcass without feet was weighed (empty carcass weight). Carcass percent was calculated as the ratio of empty body weight relative to 4 wk BW. Breast and leg were separated and residual calculated as back.

### Statistical Analysis

Comparison of means was done by SAS software 9.2 (SAS, 2000) using a generalized linear model:

$$Y_{ijklm} = \mu + L_i + H_j + G_k + (LG)_{ik} + fSex_l + e_{ijklm} \quad (1)$$

where  $Y_{ijklm}$  was the observed trait,  $\mu$  was the overall mean,  $L_i$  was the fixed effect of  $i$ -th line ( $i=1,2$ ),  $H_j$  was the fixed effect of  $j$ -th hatch ( $j=1,2$  for BW data),  $G_k$  was the fixed effect of  $k$ -th generation ( $k=0,1,\dots,4$ ),  $(LG)_{ik}$  was the interaction between line and generation,  $fSex_l$  was continuous covariate of average family sex ratio and  $e_{ijklm}$  was the random error.

Genetic analyses were carried out with the records of 1 135 (from 156 males and 218 females) fully pedigreed quail from the selection line. For all traits the initial models included the additive direct genetic effect, a maternal permanent environmental effect, an additive maternal genetic effect, and a covariance between direct and maternal genetic effects. The significance of components was determined using a likelihood ratio test ( $P=0.05$ ) comparing models with and without the component. The models with maternal and permanent environmental effects were non-significant (the only exception was the permanent environmental variance for BW). The variance components, genetic parameters and inbreeding depression were estimated by ASREML software (Gilmour *et al.* 2000). The model used in bivariate analysis was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} pe_1 \\ 0 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \quad (2)$$

where  $y_1$  and  $y_2$  represent different traits,  $b_1$  and  $b_2$  are the vectors of fixed effects (including hatch, sex and generation), for trait 1 and 2, respectively. Vectors  $a_1$  and  $a_2$  are random additive genetic effects,  $pe_1$  is maternal permanent environmental effect when BW is one of the traits, and  $e_1$  and  $e_2$  are the residual effects for trait 1 and trait 2, respectively. The incidence matrices  $X_1$  and  $X_2$  associate elements of  $b_1$  and  $b_2$  with the records in  $y_1$  and  $y_2$ . The incidence matrices  $Z_1$  and  $Z_2$  associate elements of  $a_1$  and  $a_2$  with the records in  $y_1$  and  $y_2$ . Incidence matrix  $W_1$  associates element of  $pe_1$  with records in  $y_1$  (i.e. BW). The expectation of  $y_1$  is  $X_1 b_1$ , and the expectation of  $y_2$  is  $X_2 b_2$ , the variance-covariance structure of random effects of the bivariate animal model was as follows:

$$V \begin{bmatrix} a_1 \\ a_2 \\ pe_1 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a1}^2 & A\sigma_{a1a2} & 0 & 0 & 0 \\ A\sigma_{a1a2} & A\sigma_{a2}^2 & 0 & 0 & 0 \\ 0 & 0 & pe_1 & 0 & 0 \\ 0 & 0 & 0 & 1\sigma_{e1}^2 & 1\sigma_{e1e2} \\ 0 & 0 & 0 & 1\sigma_{e1e2} & 1\sigma_{e2}^2 \end{bmatrix} \quad (3)$$

where  $\sigma_{a1}^2$  and  $\sigma_{a2}^2$  are direct additive genetic variances,  $pe_1$  is the maternal permanent environmental variance,  $\sigma_{e1}^2$  and  $\sigma_{e2}^2$  are the residual variances for trait 1 and 2, respectively;  $\sigma_{a1a2}$  is the direct genetic covariance between traits 1 and 2, and  $\sigma_{e1e2}$  is their residual covariance.  $A$  is an additive relationship matrix and  $I$  is an identity matrix.

## Results

Descriptive statistical parameters of the traits analyzed are presented in Table 2 for both lines. Coefficient of variation was larger in the selected line due to the effect of selection. Genetic improvement was 3.5, 2.7 and 0.6 g for generations 2, 3 and 4 respectively. Selection for 4 wk BRW improved feed conversion ratio (FCR) 0.19 units over the selection period.

Least squares means (family LSM for S-line) and standard errors by hatch and generation for different traits are shown in Table 3. The quails from the second hatch generally were heavier ( $P < 0.01$ ). There were a significant difference for all traits considered (except carcass percent components) between the two lines ( $P < 0.001$ ) from generation 2 and onwards. Egg weight was larger in the selected line from generation 1 and onwards. Heritability and variance component are presented in Table 4 based on bivariate models. Heritabilities ranged from 0.20 for back weight to 0.47 for leg weight. Likewise genetic and phenotypic correlations are shown in Table 5. There were high genetic and phenotypic correlations between BRW and the other traits.

The mean inbreeding for all birds and inbred birds are presented in Table 6 by generation and sex. The mean percentage of inbreeding for all birds and inbred birds was 0.64 and 11.3, respectively. Estimates of inbreeding depression are shown in Table 7. Effects of inbreeding were generally not significant. Figure 1 shows the genetic trend for 4 wk BRW in S-line based on predicted breeding values from the bivariate mixed model. The response was approximately constant over generation.

Table 2  
Descriptive statistics for body weight, carcass traits and egg weight of selected (S) and control (C) lines

Trait	Number of Observations <sup>1</sup>		Mean		Standard Error		Minimum		Maximum		Coefficient of Variation	
	selected	control	selected	control	selected	control	selected	control	selected	control	selected	control
4wk BW, g	260	1 295	179.0	168.6	1.19	0.49	100.2	110	225	224	10.9	10.1
Carcass weight, g	143	242	110.7	102.1	1.31	0.89	66.6	60.4	139.6	141.1	14.1	13.3
Breast weight, g	143	242	42.5	38.6	0.58	0.40	24.1	20.0	58.4	57.9	16.3	16.1
Leg weight, g	143	242	28.1	25.8	0.39	0.25	17.5	13.5	36.2	36.2	16.4	14.9
Back weight, g	143	242	37.7	35.5	0.56	0.39	20.3	14.1	48.7	58.0	17.6	17.0
Carcass yield, %	143	242	63	60	0.33	0.002	52	49	74	69	6.2	5.4
Breast yield, %	143	242	38	38	0.30	0.002	30	30	44	46	9.4	8.0
Leg yield, %	143	242	25	25	0.15	0.001	21	20	31	33	7.1	6.2
Back yield, %	143	242	35	36	0.28	0.002	29	23	46	47	9.5	8.9
Egg weight, g	66	243	13.5	12.8	0.07	0.04	12.2	10.5	13.0	15.2	4.2	4.8

<sup>1</sup>Observations are number of families for selected line and individual for control line.

Table 3  
Family least square means and standard error for body weight, carcass traits and egg weight of selected (S) and control (C) lines

Variation Source	4wk Body Weight, g		Carcass Weight, g		Breast Weight, g		Leg Weight, g		Back Weight, g	
	selected	control	selected	control	selected	control	selected	control	selected	control
Generation										
0	164.5±1.9	164.0±1.9								
1	163.6±1.5	163.6±1.1	99.1±2.0	97.9±1.7	36.9±0.92	36.6±0.8	24.3±0.6	24.3±0.5	34.6±0.8	33.3±0.9
2	177.9±1.8 <sup>A</sup>	168.3±1.5 <sup>B</sup>	109.4±2.7 <sup>A</sup>	98.5±2.0 <sup>B</sup>	42.1±1.2 <sup>A</sup>	38.3±0.9 <sup>B</sup>	27.0±0.8 <sup>A</sup>	25.1±0.6 <sup>B</sup>	38.2±1.1 <sup>A</sup>	34.5±1.0 <sup>B</sup>
3	192.2±1.9 <sup>A</sup>	171.7±1.2 <sup>B</sup>	119.3±2.8 <sup>A</sup>	103.1±1.6 <sup>B</sup>	46.4±1.3 <sup>A</sup>	39.9±0.7 <sup>B</sup>	29.1±0.8 <sup>A</sup>	26.1±0.5 <sup>B</sup>	42.2±1.2 <sup>A</sup>	36.1±0.8 <sup>B</sup>
4	195.2±2.2 <sup>A</sup>	169.5±0.9 <sup>B</sup>	120.8±2.9 <sup>A</sup>	104.6±1.5 <sup>B</sup>	47.1±1.3 <sup>A</sup>	40.0±0.7 <sup>B</sup>	31.7±0.8 <sup>A</sup>	26.9±0.4 <sup>B</sup>	39.5±1.2 <sup>A</sup>	36.9±0.8 <sup>B</sup>
Hatch										
1	176.2±3.5 <sup>A</sup>	165.6±0.8 <sup>B</sup>	112.1±1.2 <sup>A</sup>	101.1±0.9 <sup>B</sup>	43.1±0.6 <sup>A</sup>	38.5±0.8 <sup>B</sup>	28.1±0.3 <sup>A</sup>	25.6±0.3 <sup>B</sup>	38.6±0.5 <sup>A</sup>	35.2±0.4 <sup>B</sup>
2	181.3±3.5 <sup>A</sup>	169.7±0.8 <sup>B</sup>								
Overall Mean	178.7±3.4 <sup>A</sup>	167.0±0.6 <sup>B</sup>	112.1±1.2 <sup>A</sup>	101.1±0.9 <sup>B</sup>	43.1±0.6 <sup>A</sup>	38.5±0.8 <sup>B</sup>	28.1±0.3 <sup>A</sup>	25.6±0.3 <sup>B</sup>	38.6±0.5 <sup>A</sup>	35.2±0.4 <sup>B</sup>

<sup>A/B</sup>Means within each row with different superscript are significantly different ( $P < 0.01$ ).

Table 3  
Continuation

Variation Source	Carcass Percent, %		Breast Percent, %		Leg Percent, %		Back Percent, %		Egg Weight, g	
	selected	control	selected	control	selected	control	selected	control	selected	control
Generation										
0									12.9±0.6	12.8±0.6
1	62±0.6	59±0.5	37±0.4	39±0.4	25±0.3	26±0.3	37±0.5	35±0.6	13.5±0.2	12.9±0.4
2	62±0.8	59±0.6	38±0.5	38±0.5	24±0.4	26±0.4	36±0.6	36±0.7	13.4±0.2	12.8±0.4
3	63±0.8	61±0.5	38±0.5	38±0.4	24±0.4	25±0.3	35±0.6	36±0.5	13.5±0.2	12.9±0.4
4	63±0.8	61±0.5	39±0.6	38±0.4	27±0.4	26±0.3	33±0.7	35±0.5		
Hatch										
1	62±0.3	60±0.3	38±0.2	38±0.4	25±0.2	26±0.6	35±0.3	36±0.6		
Overall Mean	62±0.3	60±0.3	38±0.2	38±0.4	25±0.2	26±0.3	35±0.3	36±0.6	13.3±0.2	12.9±0.2

Table 4  
Heritability and variance component for breast weight, body weight, carcass traits and egg weight of selected (S) lines

Trait	$\sigma_d^2$	$\sigma_e^2$	$\sigma_{pe}^2$	Heritability
Breast Weight, g	14.7	27.8	-	0.35±0.06
4wk Body Weight, g	40.7	124.2	58.4	0.46±0.07
Carcass Weight, g	76.1	108.2	-	0.41±0.08
Leg Weight, g	6.8	7.8	-	0.47±0.09
Back Weight, g	8.1	32.0	-	0.20±0.05
Egg Weight, g <sup>1</sup>	0.42	0.9	-	0.32±0.06

<sup>1</sup>From univariate model.  $\sigma_a^2$ : additive variance,  $\sigma_e^2$ : environmental variance,  $\sigma_{pe}^2$ : maternal permanent environmental variance

Table 5  
Genetic (above diagonal) and phenotypic (below diagonal) correlations of BRW, body weight and carcass weights

Trait	Breast Weight	4wk Body Weight	Carcass Weight	Leg Weight	Back Weight
Breast Weight, g	-				
4wk Body Weight, g	0.82±0.02	0.85±0.06	0.88±0.04	0.72±0.10	0.76±0.11
Carcass Weight, g	0.86±0.04	0.93±0.006	0.90±0.02	0.83±0.005	0.86±0.08
Leg Weight, g	0.69±0.03	0.80±0.02	0.81±0.05	0.73±0.10	0.81±0.06
Back Weight, g	0.43±0.04	0.77±0.03	0.79±0.04	0.46±0.04	0.84±0.20

Table 6  
Mean (± se) inbreeding in population and inbred birds

Generation	Sex		Population		Inbred birds	
	No.	Mean±se	No.	Mean±se	No.	Mean±se
3	Male	1.47±0.12	153	1.47±0.12	16	14.1±3.53
	Female	1.90±0.16	135	1.90±0.16	17	15.1±3.70
	Mixed	1.70±0.10	288	1.70±0.10	33	14.6±2.54
4	Male	2.52±0.31	67	2.52±0.31	17	9.93±2.41
	Female	0.78±0.09	78	0.78±0.09	13	4.69±1.30
	Mixed	1.58±0.13	145	1.58±0.13	30	7.66±1.40
Mean <sup>1</sup>		0.64±0.19				11.3±1.42

<sup>1</sup>Mean is for all populations.

Table 7  
Inbreeding depression for body weight, carcass traits and egg weight per one percent change in inbreeding (±se)

Trait	4wk Body Weight, g	Breast Weight, g	Leg Weight, g	Back Weight, g	Breast Percent, %	Leg Percent, %	Back Percent, %	Carcass Percent, %	Egg Weight, g
Inbreeding Depression	0.06±0.04	-0.05±0.04	0.05±0.03	-0.05±0.04	-0.0003±0.0003	0.0004±0.0003	-0.0003±0.0004	-0.0001±0.0002	-0.02±0.01



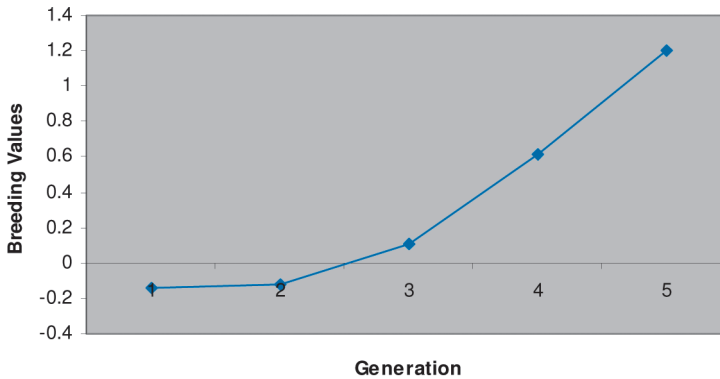


Figure 1  
Genetic trend. Average estimated breeding values by generation of hatch

## Discussion

### *Genetic Improvement and Correlated Responses*

The mean 4 wk BRW in S-line and C-line in the last generation were 47.1 and 40 g, respectively. This is equal to 15.1 % cumulative genetic improvement, or 5.0 % improvement per generation. Genetic improvement was 3.5, 2.7 and 0.6 g for generations 2, 3 and 4, respectively. The responses to short-term selection for body and carcass weights has been reported previously (Nestor & Bacon 1982, Toelle *et al.* 1991, Turkmut *et al.* 1999, Baylan *et al.* 2009).

Brah *et al.* (2001) reported 9 generations of selection for 4 week body weight had increased the superiority of the selected strains over the control line to 44.2 and 35.9 %. Reddish (2004) reported that 6 generations of selection for pectoralis muscle weight resulted in 2.5 and 27 g improvement in pectoralis muscle weight and body weight in Japanese quail, respectively. The different responses to selection in different experiments can be due to selection intensity, accuracy of selection, genetic variance and different environmental conditions.

The results showed that selection for 4 wk BRW resulted in a correlated response especially in BW, carcass weight components and egg weight and less so in carcass percent components. Mean BW in S-line and C-line in the last generation were 195.2 and 169.5 g, respectively (Table 3). This represents 13.2 % total increase, or 4.4 % per generation. Correlated responses for carcass and leg weights were 16.2 and 4.8 % total response or 5.4 and 1.6 per generation, respectively (Table 3). These results indicate that BRW is favorably correlated with BW and carcass weight. Carcass, breast and leg weights in the S-line were higher than in the C-line ( $P < 0.01$ ). Generally differences between trait means in generation 3 and 4 are lower than in previous generations (Table 3). That is likely due to the substantial reduction in actual reproducing females because the progenies were available from fewer families (Table 1). Mennicken *et al.* (2005) reported divergent selection for  $\omega_3:\omega_6$  had no effect on fertility and hatchability. Age at first egg, laying intensity and egg weight were also not different between the selected lines.

The mean of commercial FCR for S and C lines in the first generation was 2.55 and 2.59 and in the last generation, 2.37 and 2.60, respectively (0.19 unit improvement) or equals

8.8% total response. Improved FCR to a certain body weight could be partially due to lower maintenance costs and lower fat deposition of birds with higher growth rate (Pym 1990). Knizetova (1996) concluded that live weight at 4 wk of age affected the relative growth rate and feed efficiency (weight gain/feed). Generally there is a favorable correlation between growth and FCR because of enhanced pulsative growth hormone release (Buyse *et al.* 1999, Leclercq *et al.* 1989).

#### *Genetic Parameters*

Redish (2004) reported 6 generations of selection for pectoralis muscle weight and obtained a realized heritability of 0.25. Vali *et al.* (2005) reported heritability for breast, leg and carcass weights of 0.26, 0.28 and 0.27, respectively. Falconer (1960) reported that heritability for a particular trait can take different values according to the population, the environmental condition surrounding the animal and the calculation method. Prado-Gonzalez *et al.* (2003) reported that differences in heritability may be due to method of estimation, population genetic structure, environmental effects and sampling error from small data set or sample size. As these changes are dependent on the number, effects and frequencies of the genes which influence the quantitative trait, long-term experiments may provide more detailed information about its underlying inheritance (Hill *et al.* 1992). As just pointed out correlated responses are due to high genetic correlation between BRW with BW and carcass traits (Table 5) that are in agreement with Gaya *et al.* (2006) and Vali *et al.* (2005). Shahin *et al.* (2005) reported genetic and phenotypic correlation between body and carcass weight were 0.83 and 0.88, respectively that are in agreement with current study. Redish (2004) reported that selection for pectoralis major muscle in maternal Japanese quail lines resulted in slight increases in absolute BW.

#### *Inbreeding and Inbreeding Depression*

Inbreeding caused a decline in the mean of some traits (Table 7). Values had a range of -0.06 to 0.06 for carcass weight and 4wk BW, respectively but its effect wasn't significant. Inbreeding depression has previously been reported for these traits (Khaldari *et al.* 2010). Brah *et al.* (2001) with the avoidance of mating between relatives reported Inbreeding levels of 0.32 to 0.43% per generation that did not appear to be of any significance in affecting the response. Abplanalp (1967) reported that in quail populations three times more inbreeding depression for their entire reproductive cycle relative to domestic fowls can be observed, so in a closed population of quail a loss of 1% hatchability would be sustained for every increase in the degree of inbreeding (about twice as severe as compared to chicken).

Results from this experiment do not suggest between family selection as the preferred method to increase breast weight because breast weight is highly correlated to BW, and BW is easier to record and can be recorded on selection candidates. Thus selection for BW would efficiently increase BRW, as shown by Khaldari *et al.* (2010).

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