

Response to selection and genetic parameters of body and carcass weights in Japanese quail selected for 4-week body weight

M. Khaldari,* A. Pakdel,* H. Mehrabani Yegane,* A. Nejati Javaremi,* and P. Berg†¹

*Department of Animal Science, Faculty of Agriculture, University of Tehran, PO Box 4111, 31587-77871 Karaj, Iran; and †Department of Genetics and Biotechnology, Faculty of Agricultural Sciences, Aarhus University, Research Center Foulum, 7739 Tjele, Denmark

ABSTRACT The current study was conducted to investigate the effect of short-term selection in Japanese quail for 4-wk BW and estimate genetic parameters of BW, carcass traits, and egg weight. A selected line and control line were randomly selected from a base population. In each generation, 39 sires and 78 dams were used as parents for the next generation. Data were collected over 2 consecutive hatches for 4 generations, and 1,554 records from 151 sires and 285 dams were used to estimate the genetic parameters. The genetic improvement of 4-wk BW was 9.6, 8.8, and 8.2 g in generations 2, 3, and 4, respectively. There was a significant effect of sex, generation, and line ($P < 0.001$). There was a significant difference for BW and carcass weights but not for carcass percentage components between sexes ($P < 0.01$). Females showed higher figures than males.

The realized heritability for 4-wk BW was 0.55, reflecting the accuracy of selection. However the estimated heritability by using pedigree information was 0.26 ± 0.05 . The genetic correlation among BW and carcass traits was relatively high (ranging from 0.85 to 0.91). Inbreeding caused a decline in the mean for all of the traits, but its effect was only significant for 4-wk BW and carcass weight ($P < 0.05$). Selection for 4-wk BW improved feed conversion ratio 0.16 units over the selection period. Results showed there was a strong genetic correlation between 4-wk BW and carcass traits that suggests that early 4-wk BW can be used as a selection criterion to improve carcass traits. Also, intense selection resulting in high rates of inbreeding might result in decreased response to selection due to inbreeding depression.

Key words: selection, body weight, carcass trait, Japanese quail, inbreeding depression

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INTRODUCTION

Selection experiments provide the framework for the study of the inheritance of complex traits and allow the evaluation of theoretical predictions by testing observations against expectations. Depending on the time scale, the objectives of selection experiments may differ. Short-term experiments for example, can be used to estimate genetic variances and covariances, test their consistency from different sources of information, and estimate the magnitude of the initial rates of response to selection (Martinez et al., 2000). Long-term experiments are useful for measurement of changes in the rates of response or variances caused by the selection itself (Hill and Caballero, 1992; Falconer and Mackay, 1996).

Experimental research indicated that Japanese quail respond quickly to selection for BW (Nestor and Ba-

con, 1982; Caron and Minvielle, 1990; Marks, 1993). Anatomical responses to selection under varying diets (Ricklefs and Marks, 1985); the relationships between egg weight, hatch weight, and growth rates (Marks, 1975, 1993); and survival rates (Aggrey and Marks, 2002) of the different lines have all been documented.

Estimation of genetic parameters for several traits in Japanese quail has been reported (Kawahara and Saito, 1976; Toelle et al., 1991; Minvielle et al., 1999, 2000; Akbas et al., 2004; Vali et al., 2005; Dionello et al., 2006; Mielenz et al., 2006; Saatci et al., 2006; Shokoohmand et al., 2007). Genetic parameters describe genetic and environmental variation and might vary among populations and environments and should thus be estimated in different populations and environments. Accordingly, 3 topics were investigated here using a selection experiment including a randombred control. First, we calculated response to selection for 4-wk BW and correlated responses in carcass traits. Second, we estimated genetic parameters for BW and carcass traits. Third, we assessed the effect of inbreeding depression on these traits.

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¹Corresponding author: Peer.Berg@agrsci.dk

MATERIALS AND METHODS

Birds

The experimental Japanese quail population (*Coturnix coturnix*) originated from a commercial farming center in Yazd, Iran. Around 1,000 birds were transported to the animal research station of the University of Tehran. Before the start of the experiment, the population was not selected for any traits. To establish a selection (S) line and a control (C) line, a total of 234 birds were randomly selected from the population and then distributed equally into 2 lines and allowed to reproduce. The number of parents and progeny at 4 wk of age is presented in Table 1 by line, sex, hatch, and generation.

Birds in the S line were individually leg-tagged. Two females were placed in 2-floor cages and 1 male mated them every second day (1:2 male:female). One male and 2 females from the C line were placed in one cage (25 × 25 × 30 cm). Birds were kept under circumstances that closely resemble commercial practice (i.e., a standard commercial feed containing 20% CP and 2,650 kcal of ME/kg, artificially lighted housing for 16 h per day). Food and water were available ad libitum. Although some of the quail breeders started to lay eggs at 45 d of age, egg collection started at 56 d of age. Eggs were collected daily and labeled by dam number to constitute pedigree. Then they were stored up to 7 d at a temperature of 15°C and humidity of 70%. Eggs were set in the setter for 14 d and then the eggs of each dam were transferred to separate cells in hatcher trays and were set in the hatcher for 3 d. At the time of hatching, the quails from the S line were leg-tagged with a numbered plastic plate that was pitched by nip and quails from each line were placed into separate pens. Two hatches were performed. Quails were raised in group housing with 60 birds/m². Quails had access to artificially lighted housing for 24 h per day and a standard commercial feed containing 26% CP and 2,900 kcal of ME/kg. Food and water were available ad libitum.

Body weights at 4 wk were analyzed by an animal model to predict the breeding values of birds using AS-REML software (Gilmour et al., 2000). The superior birds (78 females and 39 males) were selected as the parents of the next generation and were mated ran-

domly with a 1:2 (sires:dams) mating ratio. A constant ratio was used in generation replacement; therefore, selection intensity was a function of number of birds alive at selection. Birds of the C line (n = 117) were randomly selected.

Traits

The BW was measured at 4 wk of age. At 4 wk of age (early 29 d of age) after 2 h without food, approximately 80 birds of each 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 yield was calculated as the ratio of empty BW relative to 4-wk BW. Breast and leg were separated and residual was calculated as back.

Statistical Analysis

Comparison of means was done by SAS Institute (2000) software 9.2 and the following generalized linear model:

$$Y_{ijklm} = \mu + L_i + H_j + S_k + G_l + L_i \times S_k + e_{ijklm},$$

where Y_{ijklm} was an individual observation for the trait Y , μ was the overall mean, L_i was the fixed effect of the i th line ($i = 1, 2$), H_j was the fixed effect of the j th hatch ($j = 1, 2$), S_k was the fixed effect of the k th sex, G_l was the fixed effect of the l th generation ($l = 0, 1, \dots, 4$), $L_i \times S_k$ was the fixed interaction of L_i and S_k , and e_{ijklm} was residual random effect.

Genetic analyses were carried out with the records of 1,554 offspring (from 151 males and 285 females) fully pedigreed quail. For all traits, the initial models included the additive direct genetic effect, a maternal permanent environment 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 maternal and permanent environmental effects were nonsignificant (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.,

Table 1. Number of parents¹ and progeny in each line by hatch and generation

Generation	Selected 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	39	78	—	—	—	—	39	78	—	—	—	—
1	39	74	102	84	108	94	36	75	90	81	92	87
2	37	68	138	112	84	89	34	74	97	91	68	74
3	36	65	101	107	103	106	35	72	79	74	81	86
4	—	—	83	75	86	82	—	—	76	65	68	71

¹Actual reproducing.

2000). The mathematical model used in bivariate analyses was:

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

where y_1 and y_2 represent different traits and b_1 and b_2 are vectors of fixed effects (including hatch, sex, and generation) for traits 1 and 2, respectively. Vectors a_1 and a_2 are random additive genetic effects, pe_1 is maternal permanent environmental effect for trait 1 (BW), and e_1 and e_2 are the residual effects for traits 1 and 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 , and W_1 associates elements of pe_1 with records in y_1 . The expectation of y_1 is X_1b_1 , and the expectation of y_2 is X_2b_2 . The variance-covariance structure of random effects of the bivariate animal model was as follows:

$$V \begin{bmatrix} a_1 \\ a_2 \\ pe_1 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} A\sigma_{a1}^2 & A\sigma_{a1a2} & 0 & 0 & 0 \\ A\sigma_{a1a2} & A\sigma_{a2}^2 & 0 & 0 & 0 \\ 0 & 0 & pe_1 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{e1}^2 & I\sigma_{e1e2} \\ 0 & 0 & 0 & I\sigma_{e1e2} & I\sigma_{e2}^2 \end{bmatrix},$$

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

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, particularly for 4-wk BW. Selection response for 4-wk BW is presented in Table 3. Genetic improvement was 9.6, 8.8, and 8.2 g for generations 2, 3, and 4, respectively (Table 3). Selection for 4-wk BW improved feed conversion ratio (**FCR**) 0.16 units over the selection period.

Least squares means and SE by sex and generation for different traits are shown in Table 4. The quails from the second hatch generally were heavier ($P < 0.01$) but not different for other traits. There was a significant difference for all traits considered (except yields for breast, leg, and back) between the 2 lines ($P < 0.001$) from generation 2 and onward. Females

Table 2. Descriptive statistics for BW, carcass traits, and egg weight of selected and control lines

Trait	Number of observations		Mean		SE		Minimum		Maximum		CV	
	Selected	Control	Selected	Control	Selected	Control	Selected	Control	Selected	Control	Selected	Control
4-wk BW (g)	1,554	1,295	183.9	168.6	0.57	0.49	117	110	243	224	12.3	9.8
Carcass weight (g)	320	242	110.0	102.1	0.88	0.89	70.1	60.4	151.8	141.1	14.4	13.6
Breast weight (g)	320	242	42.3	38.6	0.41	0.4	26.4	20.0	65.7	57.9	17.5	16.3
Leg weight (g)	320	242	28.1	25.8	0.27	0.25	16.1	13.5	40.6	36.2	17.0	14.9
Back weight (g)	320	242	37.6	35.5	0.45	0.43	18.1	14.1	59.8	58.0	21.3	19.2
Carcass yield	320	242	0.60	0.60	0.002	0.002	0.49	0.49	0.71	0.69	6.0	6.3
Breast yield	320	242	0.39	0.38	0.002	0.002	0.3	0.3	0.47	0.46	7.8	7.2
Leg yield	320	242	0.26	0.25	0.001	0.001	0.2	0.2	0.33	0.33	10.3	6.8
Back yield	320	242	0.35	0.36	0.002	0.002	0.23	0.23	0.46	0.47	12.8	10.3
Egg weight (g)	256	243	13.4	12.8	0.06	0.04	10.9	10.5	15.8	15.2	7.2	5.3

showed higher BW and carcass weight than males ($P < 0.001$). Egg weight was larger in the selected line from generation 1 and onward.

Heritability and variance components are presented in Table 5 based on bivariate models. Heritabilities were intermediate, ranging from 0.13 to 0.32. Genetic and phenotypic correlations between traits were estimated in bivariate analyses and the results are shown in Table 6. There were high genetic and phenotypic correlations between BW and carcass traits. Selection intensity was 1.04 and 0.62 for males and females, respectively.

The mean inbreeding for population and inbred birds is presented in Table 7. The mean percentage of inbreeding of the population and inbred birds was 0.95 and 7.75, respectively. Estimates of inbreeding depression are shown in Table 8. Inbreeding caused a decline in the mean for all traits (except for leg and back yields) but was only significant for 4-wk BW and carcass weight ($P < 0.05$). Figure 1 shows the genetic trend for 4-wk BW in the S line. The response was approximately constant over generations.

DISCUSSION

Genetic Improvement and Correlated Responses

The mean 4-wk BW in the S line and C line in the last generation were 200.5 and 170.9 g, respectively. This is a 17.3% cumulative genetic improvement, or 5.8% improvement per generation. Genetic improvement was 9.6, 8.8, and 8.2 g for generations 2, 3, and 4, respectively (Table 3). The same relative responses have been reported previously (Nestor and Bacon, 1982; Tozluca, 1993; Syed Hussein et al., 1995; Baylan et al., 2009). The different responses to selection in different experiments can be due to selection intensity, accuracy of selection, and genetic variance in their population.

The results showed that selection for 4-wk BW resulted in correlated responses especially in carcass weight components and egg weight and less so in carcass yield components. Mean carcass weights in the S line and C line in the last generation were 124.6 and 105.1 g, respectively (Table 4). This represents 18.6% total increase, or 6.2% per generation. Correlated responses for

breast, leg, and egg weights were 21.8, 17.5, and 6.9% total response or 7.3, 5.8, and 2.3% per generation, respectively (Table 4). These results indicate that BW and carcass traits are favorably correlated.

Mean FCR for the S line and C line in the first generation was 2.62 and 2.59 and in the last generation was 2.44 and 2.57, respectively, and this indicates 0.16-unit improvements for FCR. Improved FCR to a certain BW 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 (G:F). Generally, there is a favorable correlation between growth and FCR because of enhanced pulsative growth hormone release (Leclercq et al., 1989; Buyse et al., 1999).

Results of this experiment are comparable to the study of Turkmut et al. (1999) that considered the effect of selection for 4-wk BW on carcass and reported a significant effect for traits by sex and generation. Carcass yield seemed to be somewhat higher in the S line than in the C line ($P < 0.001$), in agreement with Caron and Minvielle (1990) and Minvielle et al. (2000). There was a significant difference ($P < 0.001$) for BW and carcass weights but not for carcass yield components for sexes between and within lines (Table 4). Females showed higher weights than males ($P < 0.001$), which are supported by other reports (Toelle et al., 1991; Minvielle et al., 1999; Vali et al., 2005).

Genetic Parameters

Realized heritability for 4-wk BW after selection for 3 generations was 0.55 (Table 3). The heritability estimated (0.26 ± 0.05 ; Table 5) from pedigree data was less than the realized heritability. The same situation has been reported by Collins et al. (1968), who calculated heritability by progeny-sire regression and realized heritability. We calculated the mean of reliability for males and females in generation 4 as 0.313 and 0.314, respectively. This equals a correlation between true and estimated breeding values of 0.56, in agreement with the realized heritability. The assumption of phenotypic selection for estimation of realized heritability is not fulfilled in this study, and the estimate obtained rather reflects the realized accuracy of selection.

Table 3. Selection response for 4-wk BW and selection differential¹

Generation	Population mean		Selected mean	Selection differential	Response		Corrected response	Selection differential	
	Selected	Control			Selected	Control		Male	Female
0	164	164	—	—	—	—	—	—	—
1	167.5	164.5	182	14.5	—	—	—	17.3	13.2
2	180.4	167.8	196.7	16.3	12.9	3.3	9.6	16.8	14.2
3	193.2	171.8	210	17.2	12.8	4	8.8	17.5	16.1
4	200.5	170.9	—	—	7.3	-0.9	8.2	—	—
Sum				48			26.6		

¹Realized heritability = $26.6:48 = 0.55$.

Table 4. Least squares means and SE for BW, carcass traits, and egg weight in selected and control lines

Variation source	4-wk BW (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	162.3 ± 1.9	162.2 ± 1.9	98.1 ± 1.2	97.9 ± 1.7	37.0 ± 0.6	36.2 ± 0.8	25.0 ± 0.4	24.3 ± 0.5	32.2 ± 0.7	33.3 ± 0.9
1	166.1 ± 1.0	163.6 ± 1.1	105.5 ± 1.8	98.5 ± 2.0	40.4 ± 0.8	37.1 ± 0.9	27.2 ± 0.5	25.1 ± 0.6	35.9 ± 1.0	34.5 ± 1.0
2	180.5 ± 0.9	168.3 ± 1.5	117.4 ± 1.4	103.1 ± 1.6	44.7 ± 0.7	39.3 ± 0.7	29.8 ± 0.4	26.1 ± 0.5	40.9 ± 0.8	36.1 ± 0.8
3	193.5 ± 0.9	171.7 ± 1.2	124.6 ± 1.4	105.1 ± 1.5	49.1 ± 0.7	40.3 ± 0.7	31.6 ± 0.4	26.9 ± 0.4	43.8 ± 0.8	36.9 ± 0.8
4	201.3 ± 0.9	169.5 ± 0.9								
Sex										
Male	176.6 ± 0.7	165.0 ± 0.8	109.8 ± 1.0	98.3 ± 1.2	42.2 ± 0.4	37.4 ± 0.5	27.9 ± 0.3	24.8 ± 0.4	37.7 ± 0.5	34.0 ± 0.6
Female	184.8 ± 0.7	169.1 ± 0.8	113.0 ± 1.1	104.0 ± 1.2	43.4 ± 0.5	39.0 ± 0.5	28.9 ± 0.3	26.4 ± 0.3	38.7 ± 0.6	36.5 ± 0.6
Overall mean	180.7 ± 0.5	167.0 ± 0.06	111.4 ± 0.08	101.1 ± 0.9	42.8 ± 0.3	38.2 ± 0.3	28.4 ± 0.2	25.6 ± 0.3	38.2 ± 0.4	35.2 ± 0.4
		Carcass yield		Breast yield		Leg yield		Back yield		Egg weight (g)
Generation										
0	0.60 ± 0.004	0.59 ± 0.005	0.39 ± 0.003	0.39 ± 0.004	0.27 ± 0.002	0.26 ± 0.003	0.34 ± 0.004	0.35 ± 0.006	12.9 ± 0.10	12.6 ± 0.10
1	0.61 ± 0.005	0.59 ± 0.006	0.39 ± 0.004	0.38 ± 0.005	0.26 ± 0.002	0.26 ± 0.004	0.35 ± 0.006	0.36 ± 0.007	13.5 ± 0.11	12.8 ± 0.10
2	0.64 ± 0.004	0.61 ± 0.005	0.4 ± 0.004	0.38 ± 0.004	0.26 ± 0.003	0.25 ± 0.003	0.34 ± 0.004	0.36 ± 0.005	13.8 ± 0.10	12.9 ± 0.10
3	0.62 ± 0.004	0.59 ± 0.005	0.4 ± 0.004	0.38 ± 0.004	0.25 ± 0.003	0.26 ± 0.003	0.35 ± 0.005	0.35 ± 0.005	13.9 ± 0.11	13.0 ± 0.11
4										
Sex										
Male	0.62 ± 0.003	0.59 ± 0.004	0.40 ± 0.002	0.39 ± 0.003	0.26 ± 0.002	0.26 ± 0.002	0.35 ± 0.003	0.35 ± 0.004		
Female	0.62 ± 0.003	0.60 ± 0.004	0.40 ± 0.003	0.38 ± 0.003	0.26 ± 0.002	0.26 ± 0.002	0.34 ± 0.004	0.36 ± 0.004		
Overall mean	0.62 ± 0.002	0.60 ± 0.003	0.40 ± 0.002	0.39 ± 0.002	0.26 ± 0.002	0.26 ± 0.002	0.35 ± 0.002	0.36 ± 0.003		

Table 5. Heritability and variance component for BW, carcass traits, and egg weight from bivariate animal models (with BW as 1 trait)¹

Trait	σ_a^2	σ_e^2	σ_{pe}^2	Heritability
4-wk BW	65.5	263.2	25.6	0.26 ± 0.05
Carcass weight	40.7	142.1	—	0.22 ± 0.07
Breast weight	10.1	34.2	—	0.23 ± 0.05
Leg weight	2.3	14.5	—	0.13 ± 0.04
Back weight	6.7	45.6	—	0.15 ± 0.04
Egg weight ²	0.42	0.9	—	0.32 ± 0.06

¹ σ_a^2 = additive variance; σ_e^2 = environmental variance; σ_{pe}^2 = maternal permanent environmental variance.

²From univariate model.

Table 6. Genetic (above diagonal) and phenotypic (below diagonal) correlations of BW and carcass traits

Trait	4-wk BW	Carcass weight	Breast weight	Leg weight	Back weight
4-wk BW (g)	—	0.95 ± 0.07	0.90 ± 0.12	0.85 ± 0.15	0.90 ± 0.12
Carcass weight (g)	0.86 ± 0.02	—	0.88 ± 0.13	0.90 ± 0.11	0.89 ± 0.16
Breast weight (g)	0.73 ± 0.06	0.43 ± 0.05	—	0.73 ± 0.10	0.70 ± 0.07
Leg weight (g)	0.69 ± 0.03	0.71 ± 0.08	0.37 ± 0.07	—	0.66 ± 0.11
Back weight (g)	0.57 ± 0.04	0.71 ± 0.03	0.29 ± 0.09	0.30 ± 0.08	—

Table 7. Mean (±SE) percentage inbreeding in population and inbred birds

Generation	Population		Inbred birds	
	Number	Mean ± SE	Number	Mean ± SE
2				
Male	222	0.79 ± 0.29	7	25 ± 0
Female	184	0.95 ± 0.35	7	25 ± 0
Mixed	406	0.86 ± 0.23	14	25 ± 0
3				
Male	204	0.90 ± 0.24	24	7.68 ± 1.40
Female	205	2.15 ± 0.41	43	10.35 ± 1.34
Mixed	409	1.53 ± 0.24	67	9.33 ± 1.0
4				
Male	169	1.82 ± 0.35	61	5.0 ± 0.81
Female	155	1.52 ± 0.31	54	4.40 ± 0.74
Mixed	324	1.68 ± 0.29	115	7.75 ± 0.55
Mean		0.95 ± 0.10		7.75 ± 0.60

Table 8. Inbreeding depression for BW, carcass traits, and egg weight per 1% change in inbreeding (±SE)

Trait	4-wk BW (g)	Carcass weight (g)	Breast weight (g)	Leg weight (g)	Back weight (g)	Breast yield	Leg yield	Back yield	Carcass yield	Egg weight (g)
Inbreeding depression	-0.521 ± 0.13	-0.48 ± 0.23	-0.26 ± 0.11	-0.11 ± 0.08	-0.09 ± 0.08	-0.0006 ± 0.0005	0.0006 ± 0.0005	0.0005 ± 0.0006	-0.01 ± 0.0008	-0.02 ± 0.01

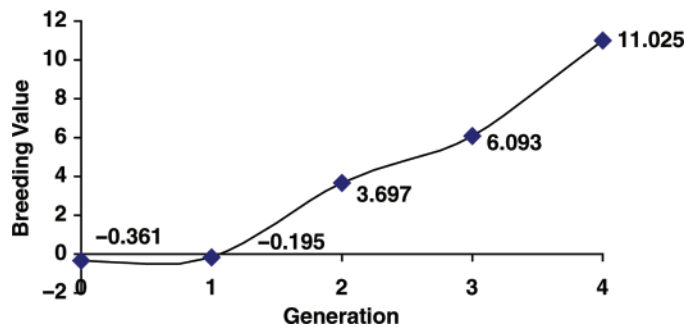


Figure 1. Genetic trend. Average estimated breeding values by generation of hatch.

The predicted value for heritability is in agreement with Baylan and Uluocak (1999; 0.27), Dionello et al. (2006; 0.25), and Saatci et al. (2006; 0.29) and differs with results from Marks (1996; 0.32 to 0.49), Narayan et al. (1996; 0.74), and Schuler et al. (1998; 0.44 to 0.47). Falconer (1960) reported that heritability for a particular trait can take different values according to the population, the environmental condition, 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. We found that correlated responses are due to high genetic correlation between BW and carcass traits (Table 6), which is in agreement with Vali et al. (2005) and Gaya et al. (2006).

Inbreeding and Inbreeding Depression

Inbreeding caused a decline in the mean for all traits (Table 8). Values had a range of -0.521 to -0.0006 for 4-wk BW and leg yield, respectively, but were only significant for 4-wk BW and carcass weight ($P < 0.05$). Abplanalp (1967) reported that in quail populations, 3 times more inbreeding depression for their entire reproductive cycle relative to domestic fowls can be observed; therefore, 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 with chicken). Generally, short-term selections is unilaterally focused on response to selection, whereas for a sustainable development in long-term selection, it should be focused on both genetic gain and average relationship in the next generation because inbreeding is inversely related to the rate of decay of genetic diversity and inbreeding depression in the population (Falconer and Mackay, 1996).

Thus, it can be concluded that there is a strong genetic correlation between 4-wk BW and carcass traits that suggests that early 4-wk BW can be used as a selection criterion to improve carcass traits. Also, intense selection resulting in high rates of inbreeding might result in decreased response to selection due to inbreeding depression.

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