

Comparison of Direct and Indirect Response to Selection for Breast Weight in Japanese Quail

Research Article

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ABSTRACT

This study was carried out to investigate the direct and indirect responses to selection for four-week body weight (4 week body (wk BW)) and four-week breast weight (4 week breast weight (wk BRW)) and to determine the genetic contribution of reminder founders to the last generation. A total number of 351 birds were equally allocated to three lines, including two selected lines (S_1 and S_2 for BW and breast weight, respectively) along with a control (C) line. Total net genetic improvement for BW and BRW in S_1 and S_2 lines were 31.6, 7.6 and 28.0 and 7.3 g, respectively. Genetic correlations between 4 wk BW and carcass traits (0.85 to 0.95) and phenotypic correlations (0.43 to 0.93) were positively high in S_1 and S_2 lines. The mean percentage of inbreeding for population and inbred birds in S_1 and S_2 lines were 0.95, 7.75 and 0.64 and 11.3, respectively. The number of retained founders to the last generation of S_1 was more than S_2 . However, more balance genetic contribution to the last generation was outlined by the founders in S_2 line. The BW can be used as a selection criterion to improve the carcass traits because there is a strong correlation between BW and carcass traits, selection for BW is easier to record and also its improvement costs are lower than selection for BRW. Meanwhile, long term response to selection is needed to preserve alleles from the lowest contributed founders.

KEY WORDS carcass trait, family selection, founder, inbreeding depression, Japanese quail.

INTRODUCTION

The long term response can be affected by methods of selection. For instance, family selection is only responsible for half of additive genetic variation (between families) while both between and within variation of families are taken into consideration in the individual selection. Therefore, it seems that variation in a trait due to the between-family selection decreases in long term selection (Gjedrem, 2005). The family selection refers to a selection method in which the families are sorted to select or to cull according to the mean performance (Lush, 1947). There are numbers of cited studies on the effect of selection and correlated

responses for some traits in Japanese quail. Long-term selection for small BW (Suda and Okamoto, 2003), genetic parameters of growth curve and weekly BW (Narinc *et al.* 2010), analysis of growth characteristics in short term selection (Balcioglu *et al.* 2007), direct and correlated responses to selection (Brah *et al.* 2001) are approved. The positive correlations between BW and carcass traits (Reddish, 2004; Sari *et al.* 2011). The correlated responses for reproduction performance and egg weight due to selection for increased live weight or meat breast weight have also been reported (Popovic and Pym, 1998). Varkoohi *et al.* (2010) reported 16.4% correlated response for BW when the family selection was directly used for feed conversion

ratio. Breast and leg weights account for 40 and 25% of carcass weight and the remainder is back which isn't in favor of consumers. Therefore, it seems that the direct selection for breast weight through family selection will improve it better than the indirect selection via the individual selection for BW. The results of selection indicated that early responses to selection were high, but a selection program is needed to maintain genetic diversity for ensuring of long term response to selection (Barker, 2001). Because of potential detrimental effects of loss of genetic diversity in small populations pedigree analysis is recommended (Ralls *et al.* 1986).

Pedigree analysis allows designing breeding plans in such a way that minimize the variation in family size and maximize the genetically effective population size relative to the census population size (Lacy, 2005). Accordingly, the objectives of this study were: 1) investigation of the direct and indirect responses to selection for BW and breast weights; 2) estimation of genetic parameters for BW, carcass and breast weights and 3) estimating the effects of inbreeding depression on these traits and determination the genetic contribution of reminding founders to the last generation in two selected Japanese quail (*Coturnix coturnix japonica*) lines as compared to a control line.

MATERIALS AND METHODS

In this experiment 351 Japanese quails (*Coturnix coturnix japonica*) were randomly selected from a base population and divided equally into three lines (117 birds in each line). Two lines were selected for BW (S_1 line) and BRW (S_2 line) and the third line was a control line (C line). No selection program was performed in the base population. Birds in the selected lines were leg-tagged with numbered plastic plates and two female birds were placed in two floor cages and one male mated them every other day.

For control line, two female birds were placed in one cage along with one male (sex ratio was 1male:2 females; Table 1). The mates were randomly after the selected birds for S_1 and S_2 lines. Birds of the C line ($n=117$) were randomly selected.

The data of 4 week BW analyzed using an animal model to predict the breeding values of birds in S_1 line by AS-REML software (Gilmour *et al.* 2009). The superior birds (78 females and 39 males) were selected based on their estimated breeding value from retained birds as the parents of the next generation and were randomly mated with a 1:2 (sires:dams) sex ratio.

A constant ratio was used in generating replacement; therefore, selection intensity was a function of the number of birds alive at the selection. The parents in S_2 line were selected based on the BRW of slaughtered birds in hatch 1.

Then birds from the 50% of full-sib families with the highest family breast weight in hatch 1 were used as parents from hatch 2.

Some females didn't lie down until 69 days of age, increasing over generations. As a result, the selected birds from the 50% superior families were 105, 95 and 80 birds as replacement for 1, 2 and 3th generations, respectively. However, the numbers of actually reproducing quails were fewer.

The family mean of BRW was calculated and sorted to select the superior families using the following model:

$$Y_{ij} = \mu + fsex_i + e_{ij}$$

Where:

Y_{ij} : family mean of breast weight.

μ : overall mean.

f : regression coefficient.

sex_i : continuous covariate of average family sex ratio.

e_{ij} : random error.

Birds were reared under conditions that closely resemble a commercial flock. They were fed with a standard commercial diet contained 200 g/kg crude protein and 2650 kcal ME/kg under a 16 h per day lightening regimen. Feed and water were provided to the birds *ad libitum*. Eggs were collected daily and labeled by dam number to constitute pedigree. Eggs were weighed and stored up to 7 days at 15 °C and 70% relative humidity. Eggs were set in the setter for 14 days and then, the eggs of each dam from the selected lines were transferred to separate cells in Hatcher trays and kept there for 3 days.

At the time of hatching, the chicks in selected lines were leg-tagged with numbered plastic plates and quails from each line placed into the separate pens. Quails were raised in group housing with 60 birds per square meter under a 24 h per day lightening regimen, and fed with a standard commercial diet contained 260 g/kg crude protein and 2900 kcal ME/kg.

There were two hatches per generation. Feed and water were provided to quails *ad libitum*. The selection was performed for three consecutive generations. At the end of day 28, water and feed removed from available birds and they were weighted.

All of birds in S_2 line and 80 birds from each one of S_1 and C lines in hatch 1 were then randomly selected and slaughtered, plucked, eviscerated and their carcasses were kept for 4 h at 4 °C. Each carcass without feet was weighed (empty carcass weight). Carcass yield was calculated as the ratio of empty BW relative to 4 week BW. Breast and leg were separated from the carcass and the residual was considered as back.

Table 1 The number of male and female birds in each generation, for 4 wk body weight (S₁), 4 wk breast weight (S₂) and control lines (C)

Generation	S ₁ line		S ₂ line		C line	
	Male	Female	Male	Female	Male	Female
0	39	78	39	78	39	78
1	196	214	177	156	201	189
2	202	205	158	176	212	194
3	204	206	168	155	193	197
4	169	156	68	77	161	155

Statistical model and genetic analysis

Least squar means

The following linear model was used to estimait least squar means (LSM) of BW, breast weight, carcass weight, in S₁, S₂ and control linesby SAS (2000).

$$Y_{ijklm} = \mu + L_i + H_j + S_k + G_l + (LG)_{il} + e_{ijklm} \quad (1)$$

Where:

Y_{ijklm}: individual observation for the traits of Table 2.

μ: overall mean.

L_i: fixed effect of the ith line (i=1, 2 and 3).

H_j: fixed effect of the jth hatch (j=1 and 2).

S_k: fixed effect of the kth sex (k=1 and 2).

G_l: fixed effect of the lth generation (l=0, ..., and 4).

(LG)_{il}: fixed interaction of L_i and G_l.

e_{ijklm}: residual random effect.

Estimation of genetic parameters and breeding values

A total of 1554 offspring (from 151 males and 285 females in S₁ line) and 1135 offspring (from 156 males and 218 females in S₂ line) record were used to estimate genetic parameters.

The following bivariate animal model was used to estimate genetic parameters using ASREML software (Gilmour *et al.* 2009):

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

Where:

Y₁ and Y₂: represent different traits in Table 3.

b₁ and b₂: vectors of the fixed effects (including hatch, sex, generationand inbreeding coefficientof individual), respectively.

a₁ and a₂: random additive genetic effects.

P^e₁: maternal permanent environmental effect for BW.

e₁ and e₂: residual effects for BW and BRW, respectively.

X₁ and X₂: associate elements of b₁ and b₂ with the records in Y₁ and Y₂.

Z₁ and Z₂: associate elements of a₁ and a₂ with the records in Y₁ and Y₂.

W₁: associates elements of P^e₁ with records in Y₁.

For all traits, the initial models included the additive direct genetic effect, a maternal permanent environmental effect, an additive maternal genetic effect as random effect and a covariance between direct and maternal genetic effects.

The significance of the 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 contribution of the founders genoms to the last generation and inbreeding coefficients (F) for all animals in the pedigree were calculated using the Eva-Inbred software (Berg, 2010).

RESULTS AND DISCUSSION

All of the main effects were significant for BW trait (Table 2). For carcass weight (CW) and BRW, the effect of generation, sex and interaction of line and sex were significant (P<0.001). Selected lines had significant differences with each other (P<0.05) for all of the considered traits (except for breast yield) and both of them were different from control line (P<0.001). Females had higher BW and CW than males (P<0.05). Egg weight was greater for the selected lines from generation 1 and onward. The mean of egg weight in fourth generation was 13.8, 13.7 and 13.0 g for S₁, S₂ and C lines, respectively. There were differences for all of the traits (except for breast yield) between selected and control lines (P<0.001) from the generation 2 and onward. Direct responses to selection for BW and BRW were 31.6 and 7.3 g in S₁ and S₂ lines, respectively. These equaled 18.6% and 18.1% cumulative genetic improvement or 6.2% and 6.0% per generation for BW and BRW, respectively. Indirect responses to selection for BRW and BW were 7.6 g and 28.0 g in S₁ and S₂ lines, respectively. These equaled to 18.6% and 16.5% cumulative genetic improvement or 6.2% and 5.5% per generation for BRW and BW, respectively. There were also similar correlated responses for CW, breast yield and egg weight in two selected lines (Table 2). Since the correlated response and breast yield (0.40 vs. 0.39) were higher in S₁ line (Table 2) than the other lines, the current study does not support family selection to increase breast weight.

Table 2 Least square means \pm SE. for some traits in selected (S_1 =body weight, S_2 =breast weight) and control (C) lines

Variation source	4 wk BW (g)			Carcass weight (g)		
	S_1	S_2	C	S_1	S_2	C
Generation						
0	164.0 \pm 2.0	164.2 \pm 2.0	162.2 \pm 1.9	-	-	-
1	166.7 \pm 1.1	163.2 \pm 1.1	163.6 \pm 1.1	98.0 \pm 1.4	97.4 \pm 1.8	97.9 \pm 1.7
2	180.1 \pm 0.95	178.2 \pm 1.2	168.3 \pm 1.5	105.0 \pm 1.9	108.1 \pm 1.5	98.5 \pm 2.0
3	193.1 \pm 0.95	192.4 \pm 1.1	171.7 \pm 1.2	116.8 \pm 1.4	117.6 \pm 1.39	103.1 \pm 1.6
4	202.9 \pm 1.1	199.5 \pm 1.6	169.5 \pm 0.9	123.5 \pm 1.7	123.2 \pm 1.66	105.1 \pm 1.5
Sex						
Male	176.9 \pm 0.75	175.0 \pm 0.90	165.0 \pm 0.8	109.7 \pm 0.97	108.0 \pm 1.0	98.3 \pm 1.2
Female	185.0 \pm 0.76	183.2 \pm 0.90	169.1 \pm 0.8	112.7 \pm 1.1	115.7 \pm 1.0	104.0 \pm 1.2
Overall mean	180.9 \pm 0.57	179.1 \pm 0.65	167.0 \pm 0.6	112.2 \pm 0.75	111.8 \pm 0.77	101.1 \pm 0.90
Variation source	4 wk BRW (g)			Breast yield		
	S_1	S_2	C	S_1	S_2	C
Generation						
0	-	-	-	-	-	-
1	37.1 \pm 0.63	36.7 \pm 0.84	36.2 \pm 0.80	0.39 \pm 0.003	0.37 \pm 0.40	0.39 \pm 0.004
2	40.5 \pm 0.88	41.8 \pm 0.70	37.1 \pm 0.9	0.39 \pm 0.003	0.38 \pm 0.50	0.38 \pm 0.005
3	44.4 \pm 0.67	45.7 \pm 0.65	39.3 \pm 0.70	0.40 \pm 0.004	0.38 \pm 0.50	0.38 \pm 0.004
4	48.8 \pm 0.79	48.1 \pm 0.78	40.3 \pm 0.70	0.40 \pm 0.004	0.39 \pm 0.60	0.38 \pm 0.004
Sex						
Male	42.1 \pm 0.47	41.6 \pm 0.47	37.4 \pm 0.50	0.40 \pm 0.002	0.39 \pm 0.002	0.39 \pm 0.003
Female	43.3 \pm 0.52	44.6 \pm 0.47	39.0 \pm 0.50	0.40 \pm 0.003	0.38 \pm 0.002	0.38 \pm 0.003
Overall mean	42.7 \pm 0.35	43.1 \pm 0.36	38.2 \pm 0.3	0.40 \pm 0.002	0.39 \pm 0.002	0.39 \pm 0.002

Similarly relative responses have also been reported by the other researchers (Brah *et al.* 2001; Zhao *et al.* 2007; Varkoohi *et al.* 2010).

Varkoohi *et al.* (2010) reported 16.4% correlated response for BW when the family selection was directly used for feed conversion ratio. Our results were also in agreement with Brah *et al.* (2001) who reported 3.4 g and 0.18 g increase per generation for BW and egg weight, respectively. It has been shown that Japanese quail responds quickly to selection (Caron *et al.* 1990; Marks, 1993). Accordingly, the amount of response can be a function of selection intensity, accuracy of selection, genetic variance and environmental factors (Bourdon, 2000).

The estimated genetic and phenotype correlation of 4 wk BW with CW and BRW were high (0.85 to 0.95) (Table 3). Therefore, direct selection for BW led to considerable correlated responses for breast, carcass and egg weights (Table 2). Similar results have been reported by the others (Shahin *et al.* 2000; Gaya *et al.* 2006). Shahin *et al.* (2000) reported that genetic and phenotypic correlations between BW and CW were 0.83 and 0.88, respectively. Sari *et al.* (2011) found high genetic correlations between slaughter, carcass and breast weights (from 0.87 to 0.97). Such high genetic correlations provide an opportunity to select for breast weight on the basis of BW. The differences in amounts of correlation in different studies are the function of number, effects and frequencies of the genes that influence quantitative traits, long term selection may supply more details about underlying inheritance (Hill and Caballero, 1992).

The mean percentage of inbreeding for population in S_1 line was more than S_2 line. This was due to the covariance between breeding values of selected relatives as an outcome of BLUP. Inbreeding caused a decline in the mean of traits, but its effect was only significant for BW and CW in S_1 line ($P < 0.05$) (Table 4).

Brah *et al.* (2001) showed inbreeding rates in selected lines and control line were 0.32 and 0.34% per generation and assessed to be 2.88% in the selected lines over nine generations without any significant effects on the considered traits. These low levels of inbreeding were due to avoidance of mating relatives (Brah *et al.* 2001). Generally, inbreeding is inversely related to the rate of decay of genetic diversity and inbreeding depression in populations (Falconer and Mackey, 1996).

Genetic contributions of the retained founders to the last generation are presented in Figures 1 and 2 for S_1 and S_2 lines, respectively. The number of retained founders to the last generation of S_1 line was more, but founders in S_2 line presented more balanced genetic contribution to the last generation.

Short term selection unilaterally focuses on response to selection, while for a long term sustainable development of a selection program needs both genetic gain and genetic diversity. The variable contribution of founders to the number of alive descendants showed 62 (49%) and 67 (57%) of founders either didn't breed or left no descendants to the last generation in S_1 and S_2 lines, respectively (Figures 1 and 2).

Table 3 Genetic (above diagonal) and phenotypic (below diagonal) correlation between BW and carcass traits in selected lines

Trait	S ₁ line			S ₂ line		
	4 wk BW (g)	CW (g)	BRW (g)	4 wk BW (g)	CW (g)	BRW (g)
4 wk BW (g)	-	0.95±0.07	0.90±0.12	-	0.90±0.02	0.85±0.06
CW (g)	0.86±0.02	-	0.88±0.13	0.93±0.006	-	0.88±0.04
BRW (g)	0.73±0.06	0.43±0.05	-	0.82±0.02	0.86±0.04	-

BW: body weight; CW: carcass weight and BRW: breast weight.

Table 4 Inbreeding depression for BW, carcass traits and egg weight per one percent change in inbreeding (±SE) in selected lines

Traits	S ₁ line				S ₂ line			
	4 wk BW (g)	CW (g)	BRW (g)	EW (g)	4 wk BW (g)	CW (g)	BRW (g)	EW (g)
Inbreeding depression	-0.52±0.13	-0.48±0.23	-0.26±0.11	-0.02±0.01	0.06±0.04	-0.06±0.05	-0.05±0.04	-0.02±0.01

BW: body weight; CW: carcass weight; EW: egg weight and BRW: breast weight.

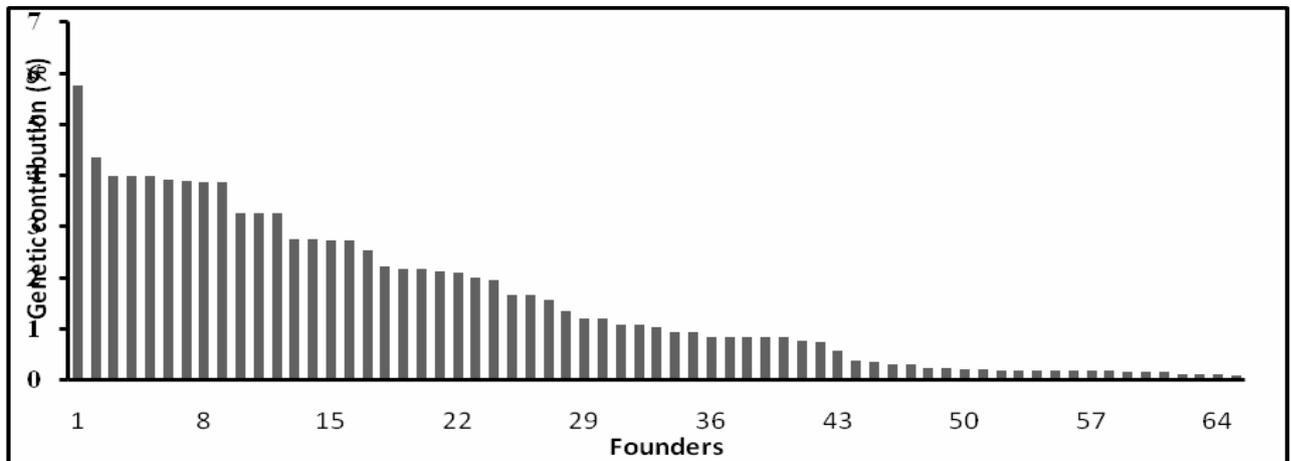


Figure 1 Genetic contributions to the last generation of each of the 64 retained founders in S₁ line

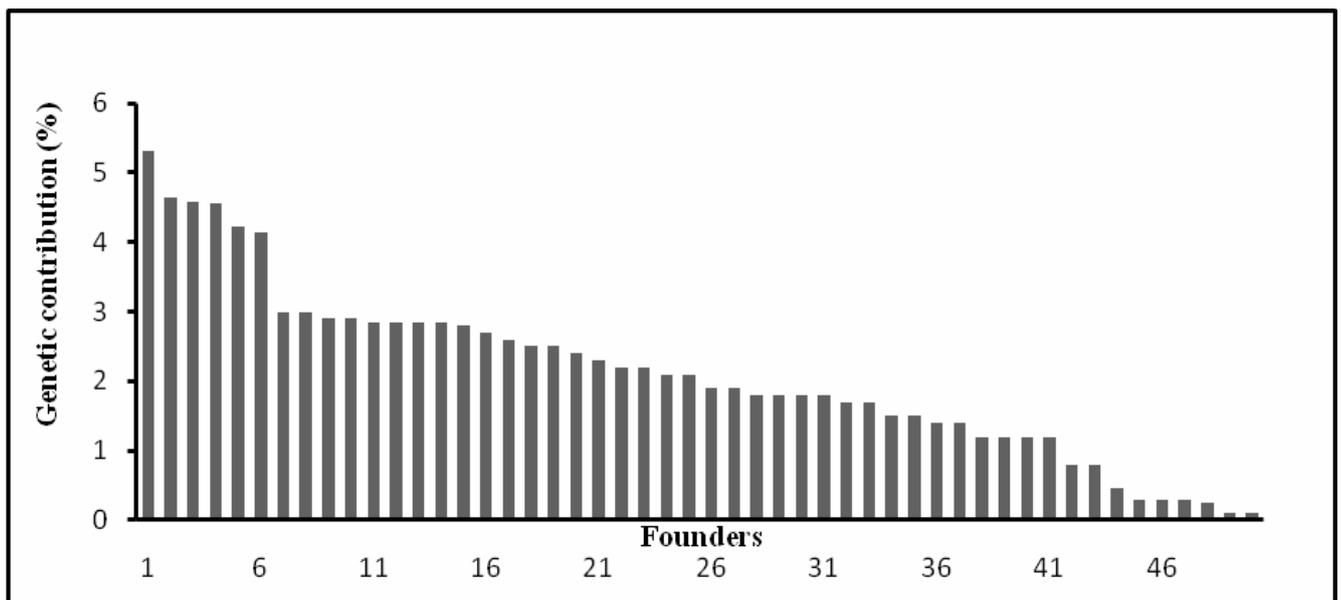


Figure 2 Genetic contributions to the last generation of each of the 50 retained founders in S₂ line

Although about 87% and 95% of genetic contribution to the last generation was composed by only 34 and 42 and 32 and 40 founders in S₁ and S₂ lines, respectively, but 22 and 10 founders were contributed to 5% of genetic contribution in S₁ and S₂ lines, respectively. Therefore, family selection caused founders present more balanced genetic contribution to the last generation. This indicates that family size variance in family selection was less than individual selection which led to less inbreeding in S₂ line (Falconer and Mackey, 1996). The unbalanced contribution of founders to the last generation is one of the factors which increases the inbreeding. The unequal representation of the founders' genetic contribution leads to less genetic variability (Lacy, 2005). This loss of variation can be reflected as loss of heterozygosity and loss of allelic variants. Lower heterozygosity often results in lower average fitness of individual or inbreeding depression (as observed for body and carcass weight in S₁ line), while lack of allelic variants prevents long-term adaptive response to selection (Falconer and Mackey, 1996). The results of the current study showed that BW can be used as a selection criterion to improve the carcass traits due to the strong correlation between BW and carcass traits. Although family selection presented a more equal genetic contribution of founders to the last generation, but this experiment showed that it is not an appropriate method to increase BRW because individual selection for BW is easier to record and also its improvement costs are lower. Genetic diversity is essential to maintain in a population under selection to ensure long term responses. Therefore, a sustainable development of response to the selection, conservation of alleles from the lowest contributed founders should be an urgent task.

CONCLUSION

It can be concluded that BW can be used as a selection criterion to improve the carcass traits because there is a strong correlation between BW and carcass traits, in addition, selection for BW is easier to record and also its improvement costs are lower than selection for BRW. Meanwhile, long term response to selection is needed to preserve alleles from the lowest contributed founders.

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