

Effects of Multi-Trait Selection on Phenotypic and Genetic Changes in Japanese Quail (*Coturnix coturnix japonica*)

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The present study in Japanese quail was aimed to develop multi-trait genetic selection program for a meat type sire line utilizing the mixed-model methodology. In total, 2000 pedigreed quail were formed the basis of the research where a multi-trait animal model was performed. A flock consisting of a total of 160 families (1 male: 3 female) was developed from the initial flock (base population of sire line), so as to obtain a selection flock sire line. Body weight at 5 weeks of age was chosen as a primary selection criterion in flock. The age at point of inflection derived from Gompertz growth curve, feed conversion ratio between 3 to 5 weeks of age, and carcass yield at 5 week of age were determined as selection criteria. Multi-trait BLUP methodology was carried out for genetic improvement of birds. In flock, 25 percent of males and females with highest breeding value were selected to produce next generation. Genetic parameter estimates, realized genetic parameters, selection responses, and genetic trends were obtained. Significant ($P < 0.01$) selection responses for body weight, age at point of inflection, feed conversion ratio, and carcass yield traits on generations were observed. The results of the study revealed that the negative genetic relationships exhibited between some studied traits had overcome by modern poultry breeding methods such as selection via multi-trait BLUP.

Key words: BLUP, Multi-trait selection, negatively correlated traits, selection response

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Introduction

The advantages of Japanese quail, which have been widely reared for meat and egg production because they have small body size (large number of birds can be kept in a limited space), fast growth, early sexual maturity, high yield and reproductive capacity, short generation interval (3 to 4 generations per year). Quail are generally reared for egg production in the Far East and Asian countries, and primarily for meat production in European and American countries (Minvielle, 2004). Body weights at fixed ages or short term egg productions were accentuated and short term selection was applied on performed limited genetic improvement studies in Japanese quail (Marks, 1996; Minvielle, 1998; Hyánková *et al.*, 2001). In the most of mentioned studies, modern genetics improvement tools were not utilized and mass selection based on phenotype characters was carried out. Also researchers performing short term selection studies ensured notably results through early partial egg production

and weekly body weight are highly heritable traits (Minvielle, 1998). On the other hand some characters such as fertility or egg quality of which are negatively related mentioned traits had deteriorated and the studies have become unsustainable (Marks, 1996).

Results of genetic improvement studies in Japanese quail could not be converted into an important trading item for poultry industry. In today's Japanese quail used in production are generally randombred birds and becoming flocks which have lower yield capacity than the existing production potential (Nariñç *et al.*, 2014). Information on quail lines selected for meat or egg production is extensive but the data on heterosis in quail are rare. Contrary to commercial broiler production, crossbreeding of highly selected lines has been rather little utilized in quail production. Although some researchers (Mielenz *et al.*, 2006; Nariñç *et al.*, 2011) using mixed model methodology had estimated genetic parameters, to our knowledge the only research (Nariñç and Aksoy, 2014) conducted on selection experiment using multi-trait BLUP framework in Japanese quail. This study presents the results of a research carried out in Turkey in which a multi-trait genetic improvement program was performed for parental meat type quail lines. This paper reports the genetic and phenotypic changes in a sire line after short term

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selection.

Material and Methods

Genetic Stocks and Management

This research was carried out in the Poultry Research Unit of Akdeniz University, Turkey. The care and use of animals were in accordance with laws and regulations of Turkey and approved by The Ethical Committee of Akdeniz University (Decision number 09/69-02.14.2011). About 2000 hatching eggs for establish a base population were collected from non selected and randombred flocks located in different research centers of Turkey. 80 males and 240 females were randomly selected from the initial flock as parents of the experimental population. About 1,500 pedigreed eggs of the selected birds were collected from 10 to 12 wk of age, incubated and hatched. One day old chicks were wing banded and brooded in cages for 3 wk before being feather-sexed. 160 males and 480 females were randomly selected to form an experimental population. The female birds of experimental population were reared in individual breeder cages (275 cm²/bird). Families consisted of 3 females and 1 male avoid full and half-sib mating, and males were shifted through the 3 female cages daily. About 1200 hatching eggs from the experimental population were collected from 10 to 12 wk of age in order to make up a new flock. All of birds belonging to the flock were slaughtered at 5 weeks of age and their measured carcass traits used to estimate breeding values of their parents by the mixed model methodology. After determining the breeding values, selection was performed, and the second generation was created by the same procedure. Total of 3541 pedigreed birds were used during the research. All birds had *ad libitum* access to water and feed during the study. A starter diet containing 11.8 MJ of DM/kg of ME and 209 g of CP/kg was given between 0 and 35 d, followed by a breeder diet 12.3 MJ of DM/kg of ME and 180 g of CP/kg from d 36 to the end of the experiment. All adult birds were kept under constant artificial lighting for 18 h/d.

Measurements of Traits, Selection Procedures, and Statistics

This study was part of a breeding program using multi-trait BLUP methodology where the prime interest was to achieve a line that has a slaughtering age at 5 week of age. Age at point of inflection (IPA) derived from Gompertz growth curve, cumulative feed conversion ratio (FCR) between 3 to 5 weeks of age, and carcass yield (CY) at 5 weeks of age were the traits of interest, as well as body weight (BW) at 5 week of age. To obtain the estimates of individual growth curve parameters, all birds were weighed weekly from hatching to 8 wk of age. The Gompertz non-linear regression model (1) was used to estimate the growth curve of each.

$$y_t = \beta_0 e^{(-\beta_1 e^{-\beta_2 t})} \quad (1)$$

where y_t is the weight at age t , β_0 is the asymptotic (mature) weight parameter, β_1 is the scaling parameter (constant of integration) and β_2 is the instantaneous growth rate (per day) parameter (Narinc *et al.*, 2014). The age at inflection point

(IPA) was obtained as follows (2):

$$IPA = \ln(\beta_1) / \beta_2 \quad (2)$$

To record cumulative feed intake between 3 to 5 weeks of age, the given feed for each bird was weighed and then reweighed after 14 days of *ad libitum* consumption. The cumulative feed conversion ratios were individually defined, relating cumulative feed intake to body weight gain. The birds that have been produced to determine carcass yields for their parents in each generation were fasted for 4 hr, weighed, and slaughtered at 5 week of age. Hot carcasses were eviscerated manually, chilled in an ice-water tank, drained for 15 min at 4°C temperature, and cold carcasses were weighed. The multi-trait animal model was utilized to estimate breeding values of birds. The following linear mixed effects model was used in the analysis:

$$y = X\beta + Zu + e$$

where y is the vector of observations, β is a vector of fixed effects, and u is a vector of random genetic effects. The X and Z are known design matrices relating phenotypic records to β and u , respectively. The e is a vector of random errors. Total number of animals in the pedigree file was 1836 where 452 of them were parents without records. Within each generation, 25 percent of males and females with highest breeding value were selected to produce next generations. Realized genetic parameters (heritabilities and genetic correlations), selection responses, and genetic trends were obtained.

Results

The descriptive statistics for BW, FCR, IPA and CY traits according to BHBS (base population of the line), BHSS-1 (generation 1) and BHSS-2 (generation 2) flocks were presented in Table 1. In the present study, carcass yield (CY) was not gained due to there was not slaughter flock BHBS population.

The results of hypothesis tests and Duncan multiple comparison tests which were performed for the determination of differences between the generations in terms of 4 traits were given the Table 1. The least square means of BW, FCR, IPA and CY traits in BHSS-2 flock have been found statistically significant than means in BHBS and BHSS-1 flocks ($P < 0.01$). There were only significant phenotypic correlations between BW and IPA traits. The correlation coefficients in BHBS, BHSS-1 and BHSS-2 generations were -0.33 , -0.36 and -0.65 , respectively.

The selection differentials, selection responses and realized heritabilities for all traits were demonstrated in Table 2. The genetic changes matrix which is consisting of changes in heritabilities and genetic correlations via multi-trait selection was given in Fig. 1. The estimated BLUP values for individuals for each trait and genetic trends according to generations were presented in Fig. 2. The estimated of genetic trend was necessary for following and assessment of the ongoing breeding programme. Increasing animal breeding values were expected in the populations

Table 1. Descriptive statistics for studied traits and results of hypothesis tests

Trait	Generation	n	Mean	SE	CV (%)	Min.	Max.
BW, g	Base	157	174.25 ^b	1.65	12.06	84.10	227.30
	1	625	177.79 ^b	0.80	11.23	89.00	236.80
	2	602	182.82 ^a	0.72	9.60	132.61	233.25
P Value				0.008			
FCR	Base	157	4.63 ^c	0.04	18.74	1.90	8.53
	1	625	4.24 ^b	0.04	24.93	1.91	10.72
	2	602	4.08 ^a	0.03	19.45	2.24	8.33
P Value				0.002			
IPA, day	Base	157	17.42 ^b	0.17	12.53	13.02	23.66
	1	625	17.59 ^b	0.10	14.62	12.02	28.32
	2	602	19.35 ^a	0.12	15.69	13.14	35.60
P Value				0.000			
CY, %	Base			not available			
	1	625	69.77 ^b	0.12	4.20	55.36	85.61
	2	602	70.78 ^a	0.02	3.75	62.03	77.57
P Value				0.009			

BW: 5 week body weight g; FCR: cumulative feed conversion ratio between 3 to 5 weeks of age; IPA: Age at point of inflection, day; CY: carcass yield at 5 weeks of age, %; ^{a-c}: Means within each column with different superscript are significantly different ($P < 0.01$).

Table 2. Selection differentials, selection responses and realized heritabilities

	Selection Differentials	Selection Response	Realized Heritability
BW	16.7633	5.0300	0.3001
FCR	-0.2345	-0.1600	0.6822
IPA	3.1411	1.9300	0.6144
CY	1.9827	1.0100	0.5094

BW: 5 week body weight g; FCR: cumulative feed conversion ratio between 3 to 5 weeks of age; IPA: Age at point of inflection, day; CY: carcass yield at 5 weeks of age, %.

which has ongoing breeding programme. Mean of estimated BLUP values for BW in BHBS, BHSS-1 and BHSS-2 flocks were found 0.1332, 0.2075, and 0.3484, respectively. Mean of estimated BLUP values in BHBS, BHSS-1, BHSS-2 populations were found for IPA trait -0.0147, -0.0530, -0.0002, for FCR trait 0.0035, -0.0022, -0.0037, and for CY trait 0.0331, -0.0121, -0.0531, respectively.

Discussion

As shown in Table 1, mean values of body weight at 5 weeks of age (BW) in BHBS, BHSS-1 and BHSS-2 flocks were found as 174.25, 177.79, and 182.82 g, respectively. These findings for BW in Japanese quail were in agreement with results reported by Narinç *et al.* (2010) (180.97 g), Sari *et al.* (2010) (175.73 g) Narinç and Aksoy (2014) (174.40 g). However, some researchers (Aggrey *et al.*, 2003; Adeogun and Adeoye 2004; Saatci *et al.*, 2006; Aggrey 2009; Narinç

et al., 2009, 2013) reported lower values (91.63–168.12 g) than our study. By the way, Baylan *et al.* (2009) determined considerable high BW at 5 weeks of age in quail range from 188.2 to 302.2 g. As shown in Table 1, mean value of BW at 5 weeks of age in BHSS-2 was found significantly higher than means of other flocks ($P < 0.01$), 2.75% increase in BW trait occurred as a result of multi-trait selection. Baylan *et al.* (2009) worked with three different lines and stated that there was a 3.32–9.12% increase in BW at 5 weeks of age with single trait selection. It was thought that high phenotypic variation resulted from making selection only for single trait (body weight at 5 weeks of age).

Mean values of feed conversion ratio (FCR) between 3 to 5 weeks of age in BHBS, BHSS-1 and BHSS-2 flocks which was one of the selection criterion in sire line were calculated 4.63, 4.24, and 4.08, respectively. In some researches which were involved feed efficiency in Japanese quail, FCR was determined by Akşit *et al.* (2003) 3.64, Chumpawadee *et al.* (2009) 3.47, and Bonos *et al.* (2010) 2.95. These reports were lower than our results. However, FCR was found by Kul *et al.* (2006) 4.52–4.78, Baylan *et al.* (2009) 3.89–4.36, and Şeker *et al.* (2009) 4.15–5.07 in the same period. Thus, these reports were close to our results. In the current study, the best FCR was determined in BHBS flock, the worst FCR determined in BHSS-2 flock ($P < 0.01$). With multi-trait BLUP selection in birds of BHSS-2, 3.92% progress occurred in FCR ($P < 0.01$). There was a study encountered in literature (Varkoohi *et al.*, 2010) which was about breeding of FCR in Japanese quail. Varkoohi *et al.* (2010) reported that FCR value in base population (2.68) became (2.13) at the end of 4 generation by means of selection for 4 week

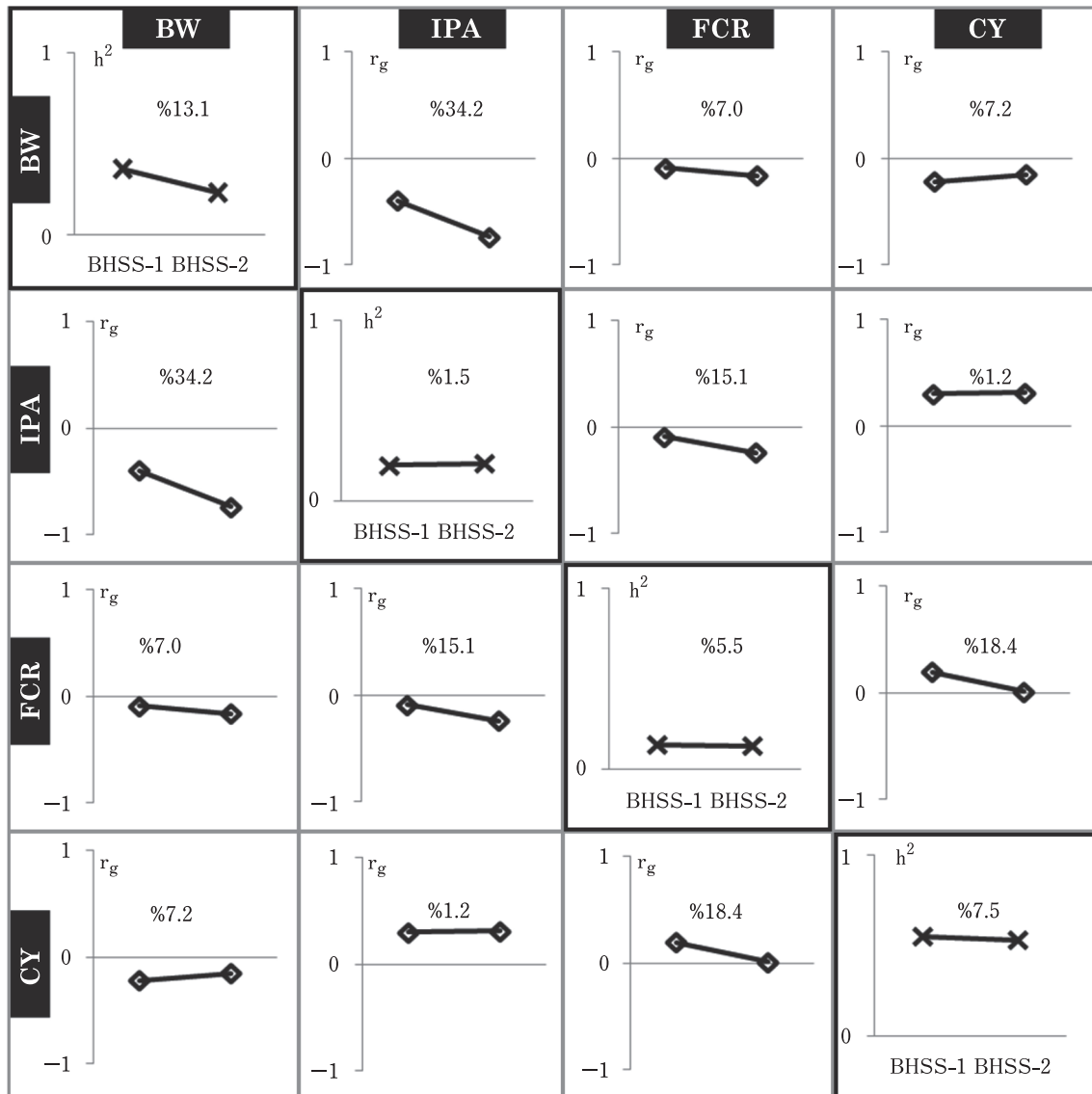


Fig. 1. Change (%) matrix of additive variance-covariance (heritabilities on diagonal, genetic correlations above and below the diagonal, % values on each element represent absolute changes in the variance-covariance).

cumulative feed efficiency. Because difficulty of determining individual feed intake especially in first three weeks, researchers were calculated FCR in family level. It was stated that progress in FCR also increased body weight. Next, 16.4% increase in body weight at 4 weeks of age reported by researchers (Varkoohi *et al.*, 2010). Similar results were also stated for relative growth rate by Hyánková *et al.* (2001) and those findings are in agreement with our study.

Age at point of inflection (IPA) of Gompertz growth curve for BHBS, BHSS-1 and BHSS-2 populations were estimated 17.42, 17.59 and 19.35 respectively. The results of numerous studies about IPA in Japanese quail reported by Anthony

et al. (1986), Akbaş and Oğuz (1998), Hyánková *et al.* (2001), Aggrey *et al.* (2003), Balcıoğlu *et al.* (2005), Aggrey (2009), Alkan *et al.* (2009) were 17.0, 18.74, 16.85, 18.11, 19.67, 19.88, and 18.13 days, respectively, are in agreement with the current study. However, the higher IPA values (22.7 and 24.5 day) were reported by Akbaş and Yaylak (2000) and Kızılkaya *et al.* (2006), respectively, and Kızılkaya *et al.* (2005) and Nariç *et al.* (2009) determined the lower IPA values (16.19 and 15.8 day, respectively). As a result of selection in the present study, It was found that BHSS-2 quail reached late IPA about 1.76 day ($P < 0.01$). Similarly, Hyankova *et al.* (2001) have reported that making selection for relative growth rate effected IPA value and this

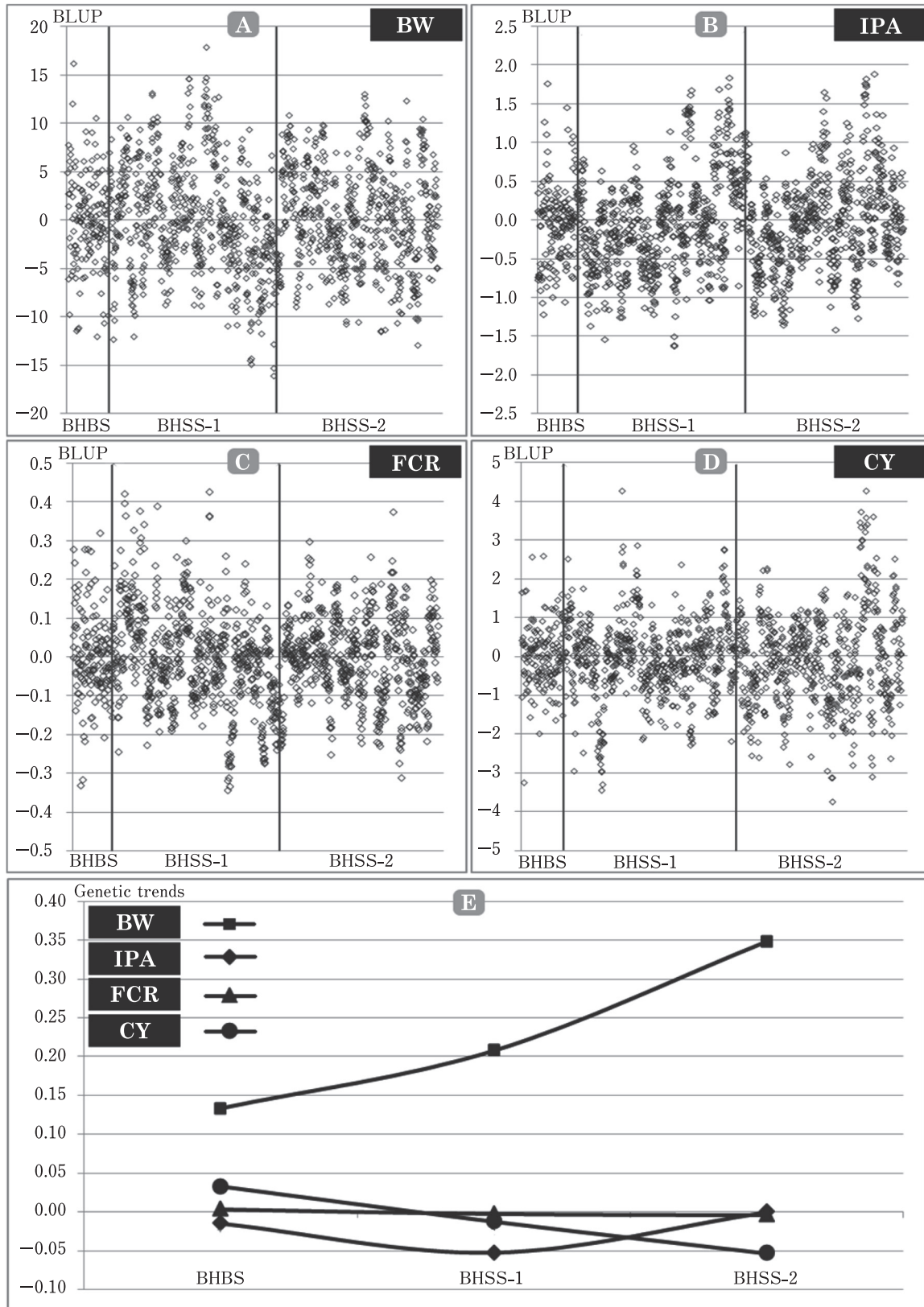


Fig. 2. Estimated individual BLUP values in A, B, C, D according to BW, IPA, FCR, CY, respectively and genetic trends for traits in E (by generations).

also increased mean of IPA in birds which have high growth rate. Kızılkaya *et al.* (2006) have reported that short term selection effected IPA trait in quail. It was also reduced 1.7 day IPA value in short-term selected flock for low body weight than randombred quail. However, there were different studies reported that there was no change in IPA trait with short term selection (Akbaş and Oğuz, 1998; Nariñç *et al.*, 2009). Akbaş and Oğuz (1998) was also stated that there was no significant difference related to IPA values between increased body weight quail via selection and randombred control group. But, the researchers pointed out that females which has higher average body weight than males was also higher IPA (male 18.74 day; female 21.22 day). Similarly, Aggrey (2009) was found mean values of IPA for males and females 17.5 and 22.26 day, respectively.

Since, there was not slaughter flock of BHBS, carcass yield (CY) was not obtained in this study (Table 1). As shown Table 1, mean values of CY in BHSS-1 and BHSS-2 flocks were found 69.77 and 70.78%, respectively, and the difference between populations was statistically significant ($P < 0.01$). Determined CY values in the current study were in agreement with those reported by Kırkpınar and Oğuz (1995), Kırmızıbayrak and Altınel (2001), Akşit *et al.* (2003), Móri *et al.* (2005), Kul *et al.* (2006) as 69.78, 69.69, 70.58, 71.10, 69.66%, respectively. There was no study in literature, which was about using carcass yield as a selection criterion in Japanese quail. On the other hand, the effect of selection for different traits on carcass yield was studied previously (Türkmüt *et al.*, 1999; Yolcu *et al.*, 2006; Hyánková *et al.*, 2008; Alkan *et al.*, 2010; Khaldari *et al.*, 2010, 2011). Türkmüt *et al.* (1999) and Alkan *et al.* (2010) have stated that the selection for increase body weight at 4 and 5 weeks of age were not affected carcass yield. However, Yolcu *et al.* (2006) suggested that the selection for increase or decrease body weight at 5 week of age effected carcass yield in the same direction. But, many of study in broiler chicken (Le Bihan-Duval *et al.*, 1998; Zerehdaran *et al.*, 2004) have reported that increasing body weight can also increased abdominal fat. Negative correlation occurred between abdominal fat content and carcass yield. As a result of increasing body weight can lead to decreased carcass yield indirectly. In this study, similar results were determined. But, genetic improvements were provided in both negatively related traits using multi-trait BLUP selection.

To our knowledge, there was no study reported on selection for IPA of growth curves of Japanese quail in literature. Anthony *et al.* (1986, 1991) reported that the IPA trait decreased through increased body weight via selection. They reported that there was a substantial negative genetic correlation between both traits. Similarly, the negative phenotypic and genetic correlations (Fig. 1) were estimated between BW and IPA traits in our study. However, the genetic improvements occurred with multi-trait BLUP selection. Varkoohi *et al.* (2010) performed selection in order to amend FCR character and reported selection differential in the first generation 10.22%, selection response 8.21%, heritability as a 0.80. Varkoohi *et al.* (2010) have reported that as a result

of selection through the 4 generations, FCR value (2.68) was improved to 2.13. However, selection response and cumulative heritability for mentioned trait decreased. Researchers suggested that there was a 20.52% improvement in FCR, 16.40% increase of BW. Negative genetic correlation was detected between BW and FCR at the end of the 4 generations. The findings of Varkoohi *et al.* (2010) were in agreement with our results. There has been 1.45% increase in CY trait with multi-trait selection in the current study ($P < 0.01$). There was not any selection study for CY. However, the studies which aimed to increase BW reported that CY did not change (Caron *et al.*, 1990; Oğuz *et al.*, 1996; Alkan *et al.*, 2010; Varkoohi *et al.*, 2010).

During the selection experiment, genetic improvement of first generation was higher than next generations (Caron *et al.*, 1990; Marks, 1996; Nestor *et al.*, 2000; Khaldari *et al.*, 2011). It's well known that decrease of genetic variation gave rise to this situation. Oğuz and Türkmüt (1999) asserted that it was not possible to increase selection response via increasing selection intensity. Next, decrease of selected individual number in each generation gave rise to reduce the allele. This allele has small but useful effects and increase of selected individual number can conserve and increase genetic variation. As a result of selection in this study, genetic variations of BW and CY traits were decreased 6% and 1% respectively, there were no differences of IPA and FCR traits additive genetic variations. Similarly, there appeared to 6% decrease additive genetic variation of BW trait in the study of Nariñç and Aksoy (2014).

In the present study, heritabilities of BW trait in BHSS-1 and BHSS-2 flocks 0.36 and 0.23, respectively. Heritability estimates of IPA, FCR and CY traits were not significantly changed through the generations. In BHSS-1 population, genetic correlations between BW with IPA and BW with FCR were found -0.40 and -0.09 , respectively. After selection, negatively increasing genetic correlations were determined in BHSS-2 population. Genetic correlations between BW with IPA, and BW with FCR were estimated -0.74 and -0.24 , respectively. Genetic correlations of BW-CY, IPA-CY, IPA-FCR, FCR-CY were not significantly changed in BHSS-1 and BHSS-2 populations.

By using the method in this study, Nariñç and Aksoy (2014) have been used BW, total egg number, relative growth rate and fertility rate traits as a selection criterion. Researchers reported that there was % 1.92 selection response occurred while using the same method. Although heritability estimates of BW was lower, 2.83% selection response occurred in the current study. It was thought that this difference was occurred due to selection response of FCR trait. In the present study, negative genetic correlations between BW with IPA was determined. On the other hand, it was put forward a possible multi-trait genetic selection program to increase BW. Similarly, negative genetic correlations between BW with CY were determined. By the conclusion of using multi-trait BLUP methodology, important selection responses revealed for all the traits.

It is expected that due to the decrease of additive genetic

variance in selection experiments, the selection response decreases eventually under the same selection intensity. Decreasing of additive genetic variance by multi-trait selection is lower. This situation is important for sustainability of breeding programs. While the additive genetic variation is decreasing via the multi-trait selection method, it is possible to increase negative covariance between some traits. In that case, it has a limiting affect on sustainability of breeding program. In current study, additive genetic variances of BW and CY traits were decreased (6% and 1%, respectively) as a result of multi-trait selection. It was not observed any important difference additive genetic variations of IPA and FCR traits. Besides, it was determined important increase related to negative genetic correlations between BW with IPA traits. It is predicted that negative genetic correlations between the traits will going to increase in next generations.

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