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Response to Selection for Body Weight in Japanese Quail (*Coturnix coturnix japonica*)

Research Article

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ABSTRACT

The present study investigated the impact of selection for body weight (BW) on productive performance, predicted BW and genetic improvement of related traits in Japanese quail. Base population, selected parent and F1 progeny were tested. Pens and cages were used for rearing and breeding. A total of 240 birds in two successive generations, 27 sires and 54 dams (as selected parents) were used. Body weight from multiple regression equation, covariance analysis and combining models were estimated, response to selection, realized heritability and genetic correlation were computed for BW, weight gain (WG), feed intake (FI) and feed conversion ratio (FCR). The results showed that the response to selection for BW, WG, FI and FCR were 11.48 g, 27.04 g, 37 g and -0.2, respectively. The estimated heritabilities for the same traits were 0.78, 0.67, 0.52 and 0.77, respectively. Predicted equation (DUHOK equation) for BW as dependent variable on the initial body weight and sex ratio was derived. The final response for the body weight was determined as 5.84 % of live BW.

KEY WORDS body weight, genetic parameters, Japanese quail, predicted equation, selection response.

INTRODUCTION

In many European and Asian countries, Japanese quail is considered one of the main sources for meat production (Minvielle, 1998; Kayang *et al.* 2004; Ayasan, 2013). Thus body weight (BW) is a very important trait beside feed conversion ratio (FCR) to be improved from economical point of view (Kayang *et al.* 2004; Kaur *et al.* 2008; Baylan *et al.* 2009). It was indicated that selection for BW and FCR in Japanese quail improved the weight gain for the next generation (Kayang *et al.* 2004; Kaur *et al.* 2008; Baylan *et al.* 2009). Moreover, the accumulative response to selection for FCR was estimated to be 0.52 (Varkoohi *et al.* 2010), and the mass selection together with the differences in initial body weight resulted in an increase of body weight (Caron and Minvielle, 1990; Darden and Marks, 1989).

Marks (1993a) concluded that the body weight differences ranged from (15 to 24%) at 4 weeks of age. Karaman *et al.* (2013) found that the live body weight of quail males at 1, 21 and 42 days old were 8.75, 111.42 and 178.13 gm., respectively and for females at the same previous ages were 9.07, 118.97 and 219.07 gm., respectively. The same authors derived 3 different fitted models for growth by nonlinear mixed effects modeling and they concluded that the best model has reduced variance by about 37%. In an experiment conducted by Muir *et al.* (2013) who compares multilevel selection for 43 days weight and survival with Japanese quail birds housed either in kin (*K*) or random (*R*) groups. They observed that multilevel selection has significantly increased weight and response in *K* more than *R*. In another study conducted by Vali (2009) to compare two strains of Japanese quail and their reciprocal crosses, it was found that the body weight at different ages (from 1 up to 63 days old) were highly significant between males and females for all studied groups. Also feed intake of just one hybrid significantly surpassed other groups, while feed efficiency did not differ significantly.

Estimated heritability for body weight at 28 days of age and weight gain between 7 to 28 days of age were 0.22 and 0.28, respectively and the genetic correlation between FCR and each of WG and FI were -0.45 and 0.24, respectively (Varkoohi *et al*. 2011).

The aim of the present work was to investigate the impact of selection for body weight on productive performance, predicted BW and genetic improvement of related traits in Japanese quail.

MATERIALS AND METHODS

The present work was conducted at poultry production farm of the Department of Animal Production, Faculty of Agriculture and Forestry, University of Duhok, Kurdistan Region, Iraq during 2014.

Rearing both generations and selection

A total of 240 Japanese quail birds that resulted from hatching fertile eggs obtained from commercial flock in Mosul city (Nineveh Province), Iraq were used as a base population (*F0*). The hatched one-day-old unsexed chicks were divided equally into 8 pens up to 21 days (30 birds/pen and was considered as a family). From 22 days old up to 42 days, the birds were re-divided into 30 replicates (8 birds each).

Selected parent on the basis of their live body weight for both sexes were chosen, and the intensity of selection was determined as the percentage of individuals that had more than the average live body weight of each sex within the flock. Male to female ratio was 58 and 42 %, respectively, and the ratio of the selected males to females was 46 and 54%, respectively. Selection intensity was determined as 0.8 for females and 0.9 for males (0.85 as average for both sexes). After sexual maturity (42 days of age as average for females), sires and dams were identified, separated and redivided randomly (54 females were housed individually in a cages of 30×50×30 cm) for egg laying, while 58 males maintained in the pens and 27 of them were selected randomly to mate females twice a week intervals by putting each male with each female in a cage for reproduction. A total of 280 chicks were hatched as first generation (*F1*), 240 of them was randomly divided as same as the previous generation. Water and feed were submitted *ad libitum*. Light was provided 23 hours/day, vitamins (AD3K) was provided twice, ventilation was provided by using water coolers for both generations, and eggs were collected daily.

Rations (combined from yellow corn, soya bean meal, wheat, barley, wheat bran, protein concentrate, vegetable oil, limestone, di-calcium phosphate, DL-methionine, L-lysine, phytase, salt and vit. Premix) fed to both flocks contained 2904 kcal. ME/kg diet with 26% CP; 2937 kcal. ME/kg diet with 21% CP and 2793 kcal. ME/kg diet with 18.3% crude protein (CP) for starter (1-21 d), grower (22-42 d) and layer or breeder (43-end of trial), respectively according to Lesson and Summers (2005).

Traits under consideration

Body weights (g) were individually recorded at 1, 21 and 42 days old for both generations. Weight gain (g) was computed as the difference between next and previous body weight. Feed conversion was calculated as the ratio of feed intake (g) to weight gain (g), at the same studied periods for both generations. The main estimated parameters for the studied traits were selection differentials, which were computed as the difference between selected parent mean and the base population mean; response to selection, was calculated as the difference between offspring *F1*- mean and the base population *F0*- mean; the response percentage was calculated as the ratio between response to selection value and *F0* live body weight × 100; realized heritability was estimated from dividing response to selection on the selection differential for each trait and genetic correlation, was estimated from the covariance between two traits according to the equation of geometric method (Falconer and Mackay, 1996):

$$r_g = \sqrt{(\text{cov } Z2X1 \times \text{cov } Z1X2)} \,/\, \sqrt{(\text{cov } Z1X1 \times \text{cov } Z2X2)}$$

Where:
1 and 2: characters.
Z: observations of selected parents.
X: observations of progeny.

Statistical analysis

The experiment was designed according to completely randomized design (CRD); the raw data were analyzed using SAS software (SAS, 2010). For all studied quantitative traits at different ages, general linear model (GLM) procedure was used as multivariate model to analyze the effect of selection, as following:

$$Y1_{ij}\ Y2_{ij}\ Y3_{ij}\ Y4_{ij} = \mu + G_i + e_{ij} \qquad \text{(Model 1)}$$

Where:
$Y1_{ij}$: observations of the BW.
$Y2_{ij}$: observations of the WG.
$Y3_{ij}$: observations of the FI.
$Y4_{ij}$: observations of the FCR.

μ: overall mean.
G_i: effect of generation.
e_{ij}: experimental error.

For body weight trait only at 42 days old, the following three models (two way-analyses and multiple regression equation within GLM procedure and covariance analysis within MIXED procedure, respectively) were used in order to illustrate the interaction between the generation and sex (Model 2), to predict the final BW via initial BW and sex ratio (Model 3) and to eliminate the sex effect, as following:

$$Y42_{ijk} = \mu + G_i + S_j + (G\times S)_{ij} + e_{ijk} \quad \text{(Model 2)}$$

Where:
$Y42_{ij}$: observations of the BW.
μ: overall mean.
G_i: effect of generation.
S_j: effect of sex.
$(G\times S)_{ij}$: interaction between generation and sex.
e_{ij}: experimental error.

$$Y42_{ijk} = \mu + W1_i + SR_j + e_{ijk} \quad \text{(Model 3)}$$

Where:
$Y42_{ijk}$: observations of the BW.
μ: overall mean.
$W1_i$: observations of BW at 1 day old for males of both generations.
SR_j: observations of sex ratio for each family (pen).
e_{ij}: experimental error.

The multiple prediction equation obtained from the previous analysis called male model and it was as following: $Y_{42} = b_1 X_1 + b_2 X_2 + a$

Where:
Y_{42}: predicted body weight at 42 days old.
b_1 and b_2: partial regression coefficients.
X_1: average body weight at 1 day old.
X_2: average male sex ratio % in the flock.
a: intercept.

$$Y42_{ijk} = \mu + G_i + fSex_j + (Cov\ G\times Sex)_{ij} + e_{ijk} \quad \text{(Model 4)}$$

Where:
$Y42_{ijk}$: observations of the BW.
μ: overall mean.
G_i: effect of generation.
$fSex_j$: continuous fixed regression factor of generation on female sex ratio.
$(Cov\ G\times Sex)_{ij}$: covariance between generation and female sex ratio.
e_{ij}: experimental error.

The analysis of covariance $(Cov\ G\times Sex)_{ij}$ was used to derive predicted body weight at 42 days old, in order to eliminate the sex effect, it is called female model. After applying the last model, regression analysis was used to estimate the predicted final BW from one-day old BW (modifying Model 3 for both sexes) via the following model:

$$Y42_{ijk} = \mu + W1_i + e_{ij} \quad \text{(Model 5)}$$

Where:
$Y42_{ijk}$: predicted live body weight at 42 days old.
$W1_i$: observed one-day old live body weight for both sexes and both generations.

Duncan's multiple range test was used to compare means that resulted from GLM procedure (Duncan, 1955).

RESULTS AND DISCUSSION

Body weight

Live body weights as affected by selection at different ages are given in Table 1. It can be noticed from the table that *F1* surpassed significantly (P<0.01) the *F0* generation and the difference between them amounted to average of 29.2%. Such result encourages applying selection for successive generations. This finding agreed with those obtained by Varkoohi *et al.* (2011), who concluded that the difference between base population (culled line) and selected line for 4 generations was (27 g) at 28 days of age. Similar results had been found by (Marks, 1993b; Grasteau and Minvielle, 2003).

Response to selection

The responses to selection for body weight of both males and females at 42 days of age are shown in Table 2. It appears from the table that the body weight of females are significantly (P<0.01) higher than the body weight of males for base population, selected parents and their progeny. The interaction between generation and sex was significant (P<0.05), where *F1* females recorded the highest value.

The response to selection in males was higher than females (7.06 *vs.* 4.87%). Such values reflect the important of selection for body weight in quail. Thus, the overall response to selection for body weight at 42 days of age was estimated to be 11.48 gm., which is equivalent to 5.84%.

The selection differential for males was higher than females by 3.8 gm., which was due to the wide range in the body weights within selected female individuals.

Table 1 The effect of selection on live body weight (g) of Japanese quail at major ages (LSM±SE)

Age (day)	*F0*	*F1*	Superiority %	Sig. (P)
1	7.52±0.06^b	10.56 0.04^a	40.4	< 0.0001
21	86.02±0.85^b	113.12±0.6^a	31.5	< 0.0001
42	191.37±2.92^b	221.44±2.17^a	15.7	< 0.0001

The means within the same row with at least one common letter, do not have significant difference (P>0.01).
F0: base population and *F1*: first generation.
LSM: least square mean and SE: standard error.

Table 2 Response to selection (*R*) for live body weight trait (g) of Japanese quail at 42 days old, for both sexes (LSM±SE)

Sex	Base population (*F0*)	Selected parent	Selection differential	Progeny (*F1*)	*R* (g)	*R* (%)
Male	169.6±2.48^b	188.1±1.06^b	18.5	181.58±1.51^b	11.98	7.06
Female	223.6±2.29^a	238.3±2.35^a	14.7	234.49±1.87^a	10.89	4.87
Overall	196.53±1.70	213.2±1.05	16.6	208.01±1.27	11.48	5.84

The means within the same column with at least one common letter, do not have significant difference (P>0.01).
The interaction between generation and sex was significant (P<0.05).
LSM: least square mean and SE: standard error.

However, the overall selection differential was estimated as 16.6 gm. at 42 days of age. Response to selection for males was higher than that of females (11.98 *vs*. 10.89 gm.). Such values reflect the importance of selection in studied birds, because both previous values shared as increasing in live body weight by 7.06 and 4.87% for males and females, respectively. However, the overall response to selection was determined as genetic improvement by 11.48 g of the live body weight, which equal 5.84% increasing in overall live body weight of Japanese quail at 42 days of age (irrespective of the sex). This result disagree with that of Vali (2009), who indicated that the difference between males and females in the live body weight of Japanese quail recorded only 4.22 gm. at 42 days of age. On the other hand, the present result is in agreement with the results obtained by (Minvielle *et al.* 2000) for the significant difference between both sexes. Marks (1993b) concluded that the response to selection for body weight of J. quail for 40 generations achieved 110 g.

Body weight prediction

The prediction of the final live body weight (BW at 42 days of age) was computed depending on one day old and sex ratio. The following prediction equations were derived:

$$BW_{42(M)}= 5.86\ BW_1 - 0.63\ M_{SR} + 176.18 \qquad \text{(Male model)}$$
$$BW_{42(F)}= 1.06\ F_{SR} + 176.18 \qquad \text{(Female model)}$$

Where:
$BW_{42(M)}$ and $BW_{42(F)}$: *BW* at 42 days old for males and females, respectively.
BW_1: initial body weight (one day old BW).
M_{SR} and F_{SR}: sex ratio for males and females, respectively in families.
176.18: intercept.

It can be noticed that both equations have the same intercept (176.18) in spite that each was analyzed separately and in different methods; but both have a different regression coefficients for sex ratio % (-0.63 for males and 1.06 for females) and body weight at one day old variable was included for the male model only. So, both models have been joined (combined), to derive a new model called DUHOK equation (coming from DUHOK university and Determining Unsexed Homogeneity Offspring Kids), which could be used in Japanese quail. The final model used to eliminates the effect of sex (considering a sex ratio equal 50%) and predicting with average final live body weight at 42 days old was as follows:

$$BW_{42}= 5.86 \times BW_1 + 154.68 \qquad \text{(DUHOK equation)}$$

The final equation was applied, and its result (predicted values) are shown with the observed values (Figure 1).

It could be noticed from the figure, that there is a high variation in the observed values. Predicted values tended to reduce such variation. So, it could be applying the selection program in the future on the basis of predicted values for body weight at hatching, by determining either the selection intensity or culling individuals depending on the special variation range. The statistical parameters for the three models are given above the curves, where the PW42 represent DUHOK equation. Karaman *et al.* (2013) found that the relationship between predicted and actual observations of Japanese quail's body weight was linear for all models. The growth as affected by some parameters was studied successfully via different functions to illustrate the optimum fit (Davis, 2002; Hall and Clutter, 2004; Sengul and Kiraz, 2005; Narinc *et al.* 2010).

Genetic parameters

The estimated realized heritabilities for BW, WG, FI and FCR at 42 days of age were 0.78, 0.67, 0.52 and 0.77, respectively (Table 3). Such high values encourage the use of selection for improving the body weight and FCR in Japanese quail.

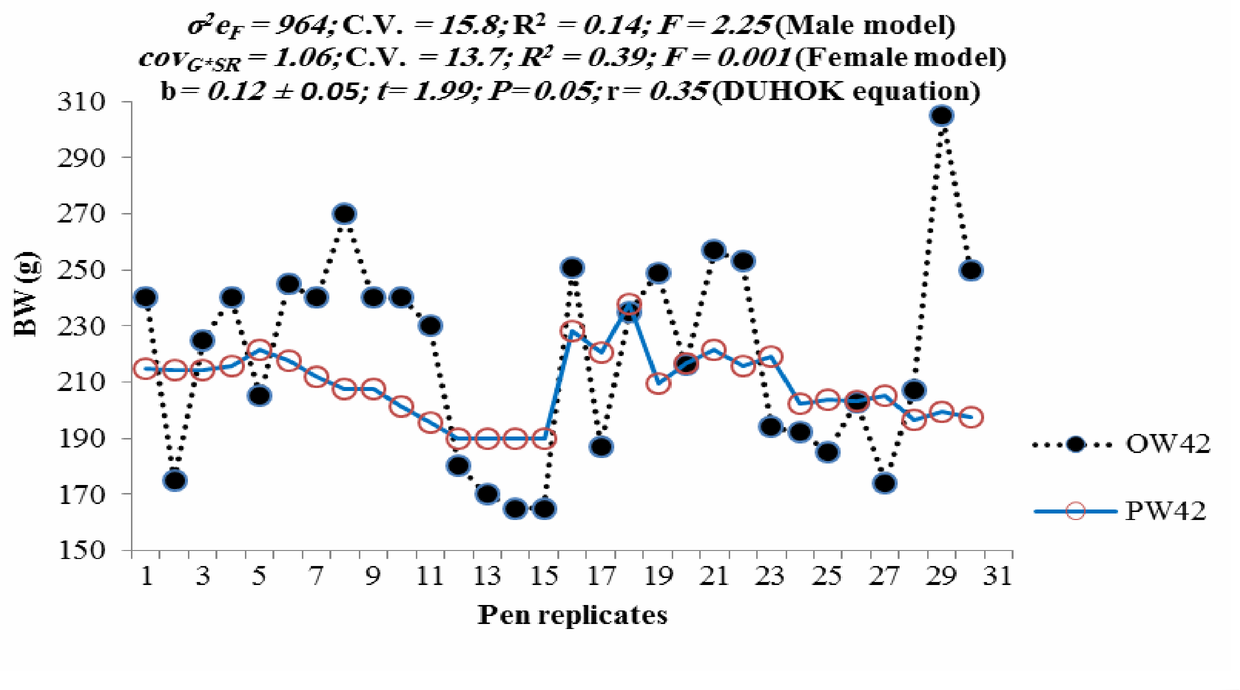

Figure 1 Observed *vs*. Predicted live body weight at 42 days old

Table 3 Phenotypic correlation coefficients (above the diameter), genetic correlation (under the diameter) and realized heritability (on the diameter) for some productive traits in Japanese quail at 42 days old

	BW	WG	FI	F CR
BW	0.78±0.02**	0.99±0.009**	0.94±0.015**	-0.28±0.053
WG	0.99±0.008**	0.67±0.035*	0.91±0.018**	-0.29±0. 055
FI	0.92±0.017**	0.94±0.014**	0.52±0.042*	0.02±0.009
FCR	0.45±0.06	-0.41±0.061	0.08±0.003	0.77±0.022*

BW: body weight; WG: weight gain; FI: feed intake and FCR: feed conversion ratio.
* (0.05) and ** (0.01).

Several authors have indicated that the heritability of FCR ranged between 0.2-0.8 (Chambers *et al.* 1984; Leenstra *et al.* 1986; Mielenz *et al.* 1994; N'Dri *et al.* 2006; Aggrey *et al.* 2010). Moreover, the genetic correlations between BW and each of WG and FI were high (0.99 and 0.92, respectively). A low values were found between WG and FI (0.45) and between FI and FCR (0.08). However, a negative genetic correlation exists between WG and FCR (-0.41). Similarly, Varkoohi *et al.* (2011) noticed that the genetic correlation between FCR and WG was negative.

The phenotypic correlation coefficients between BW and WG; BW and FI; FI and WG were high (0.91-0.99), while FCR was correlated negatively with both BW and WG (-0.28 and -0.29), but it was correlated positively with FI. These results suggest that increased BW resulted in increase of both WG and FI. Similar findings were obtained by Varkoohi *et al.* (2011), for productive traits of Japanese quail at 28 days of age, these research workers concluded that a low FCR is genetically related to a high WG and low FI.

Weight gain

Weight gain comparison, between both generations and its linear curves at different periods, showed that *F1* individuals surpassed *F0* one, especially at initial and final periods (Figure 2).

As it is shown from Figure 2, the accumulative response to selection for WG from 1-42 days old was estimated to be 27.04 gm. Also it could be noticed that both generations have a linear parallel curves, except the midpoint was almost the same for both generations. Two equations were described to predict WG as linear curve within each generation for the studied periods (1, 2 and 3). Varkoohi *et al.* (2010) stated that WG has a linear curve when selection was applied, during different periods of age for all generations.

Feed intake

Feed intake for *F1* at initial and final periods was higher than *F0* birds, except at the mid period where approximatly equal to *F0* intake (Figure 3).

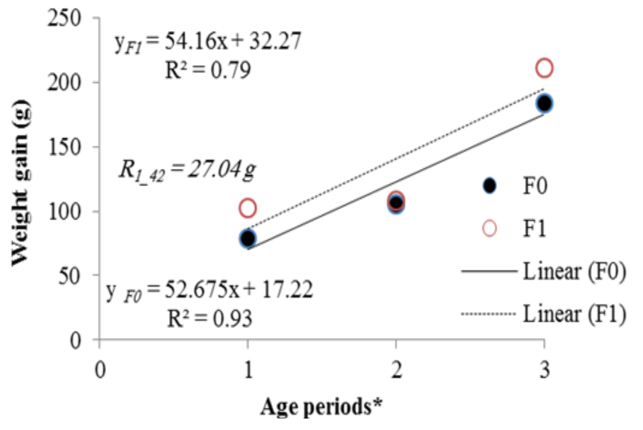

Figure 2 Weight gain and its linear curves for both generations of Japanese quail as affected by selection
* 1= WG during the period from 1-21 d; 2= WG from 22- 42 d and 3= WG from 1- 42 d

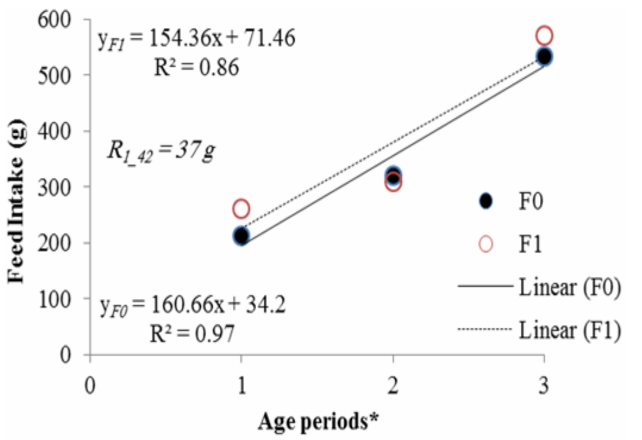

Figure 3 Feed Intake and its linear curves for both generations of Japanese quail as affected by selection
* 1= FI during the period from 1-21 d; 2= FI from 22-42 d and 3= FI from 1-42 d

Accumulative response to selction for FI trait was estimated to be 37 gm., this amount of feed was considered little than expected, which may be due to the sudden rise in environmental temperature (36 ˚C) for 3 days at period from 24 to 27 days old (June month). Both R^2 for both linear curves are high (0.86 and 0.97), which indicate that the studied periods strongly affecting FI. This result is in agreement with the finding of Knizetova (1996) who found that selection for the live body weight in quail leads to a lower FI associated with higher WG and improved feed efficiency (WG:FI).

Feed conversion ratio

Feed conversion ratio (FCR) in *F1* individuals was less and better than *F0* flock during the study periods and the pooled response to selection for FCR is -0.2 (Figure 4). This response is considered valuable for one generation. But both R^2 of equations for both linear curves are relatively small (0.25 and 0.32).

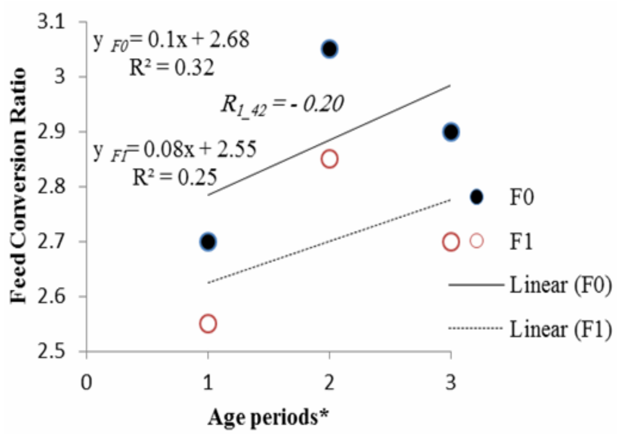

Figure 4 Feed conversion ratio and its linear curves for both generations of Japanese quail as affected by selection
* 1= FCR during the period from 1-21 d; 2= FCR from 22-42 d and 3= FCR from 1-42 d

This finding is in accordance with that obtained by Varkoohi *et al.* (2010), who concluded that response to selection for FCR at 28 days old was (-0.22) in the first generation.

CONCLUSION

From the results obtained in the current work, it can be concluded that selection for BW in Japanese quail resulted in an improvement in FCR.

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