SELECTION RESPONSES FOR AUGMENTING EARLY GROWTH RATE IN JAPANESE QUAIL

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ABSTRACT: Throughout a selection experiment, which extended over five generations: the base and four generations of selection for augmenting early growth rate (GR) during the period from hatch to 21 days of age in Japanese quail, a total number of 8724 birds were used: 1726 in the base population, 5176 for the selected line (HGR_{1-21}) and 1822 for the control line. The most important results obtained as follows: Genetically, heritability (h^2) for all body weights (BW) showed moderate h^2 ranged from 0.19 to 0.29. The GR_{1-21} positively correlated with all body weights weekly measured except BW at hatch ($BW_{1)}$ with genetic correlations (r_g) ranged from 0.06 to 0.47, and a wide range of phenotypic correlation (r_p) ranged from 0.18 to 0.52.

The GR during different periods of growth had medium h^2 ranged from 0.17 to 0.28 and showed a wide range of moderate to high r_g with the selection criterion (0.15 to 0.70) and had a broader range of r_p ranged from 0.03 to 0.67.

The HGR_{1-21} line in the 4th generation had the best growth performance for each of BW_7, BW_{21}, BW_{28}, GR during the periods 1-7, 1-14, 1-28 and 1-35 days of age with significant differences. The realized cumulative response after four generations of selection was 0.063 (6.30%) for GR_{1-21}, the cumulative correlated responses for BW s and GR s ranged from 1.19,g to 23.94,g and from 3.10% to 17.00%, respectively. So, the current study aimed to evaluate the effectiveness of the selection program through estimation of direct and correlated responses to selection for fast GR_{1-21}, and determination of correlations between selection criterion and either body weights at different ages or GRs during different growth periods for Japanese quail.

INTRODUCTION

Selection programs not only provide the useful information and knowledge needed for studying the inheritance of metric traits but also improving the performance of selected populations where the short term selection experiments aimed to estimate genetic variances and covariances and examine their dependability from different sources of information and estimate the value of selection response (Martinez *et al*., 2000). Moreover, Japanese quail showed quick response to selection because of the short generation interval, rapid growth rate, early sexual maturity and high egg production (Alkan *et al.,* 2010). Most selection programs indicated that selection based on genetic parameters of growth traits at different ages lead to improve selection responses in body weight and body weight gain at different ages of Japanese quail (Hussain *et al.,* 2014, Hussen *et al.,* 2016 and El-Attrouny *et al.,* 2020). Most of selection studies in Japanese quail have been conducted on body weight at different ages, however, few studies examined early growth rate. In selection experiments, the magnitude of selection response depends on the genetic correlation between selection criterion and other traits under selection, the response to selection will change according to the heritability of tested traits, and either sign or strength of the genetic covariance among them (Jensen *et al.,* 2003). Abdel Fattah (2006) found that there were positive genetic correlations among GR and both BWs at different ages and GR during different periods of growth. Thus, selection for highly heritable characters such as growth traits may be accompanied by correlated genetic improvement in the other growth traits in the selected lines. The efficiency of selection experiments appear through increased genetic trend in the selected generations, hence the estimation of selection response either direct or correlated was essential for the assessment of the breeding programs.

So, the current study aimed to evaluate the efficiency of the selection breeding programs through estimation of direct and correlated responses for high GR during the period from hatch to 21 days of age and determination of correlations between selection criterion and either BWs at different ages and GRs during different growth periods for Japanese quail.

MATERIALS AND METHODS

This study was conducted at the poultry farm of the Agricultural Experiments and Research Center, Faculty of Agriculture, Fayoum University which extended over five generations: the base and four generations of selection for augmenting early growth rate (during the period from hatch to 21 days of age, HGR_{1-21}) in Japanese quail (*Coturnix coturnix japonica*). Throughout a selection experiment, a total number of 8724 birds: 1726 in the base population, 5176 for the HGR_{1-21} line and 1822 for the control line (CL) were used during the five generations as shown in Table 1.

The selected breeders were housed (two females were randomly assigned to each male) in breeding cages. Matings of close relatives were avoided to decrease the rate of inbreeding depression. Eggs were daily collected in a pedigree system for each family depending on the shell color and patterns of each female when ages of females were 11−14 weeks of age. The newly hatched chicks were wing banded using small size plastic bands and brooded on the floor until 35 days of age. According to NRC (1994), all quail were

fed *ad libitum* on a starter diet containing 24% crude protein and 2900 K Cal ME (from hatch to 35 days of age). All chicks were individually weighed to calculate growth rates. From 42 days of age to the end of egg laying period, a breeder diet containing 20% crude protein, 2900 K Cal ME, 2.25% calcium and 0.43% available phosphorous was supplied. The clean fresh water was available for quails all over the experimental period. Birds were kept in continuous light during the first 35 days of age and then reduced to 16 hours of light per day thereafter. Birds were kept under the same managerial hygienic and environmental conditions.

Selection Program:

Aggregated breeding values of a criterion of selection were estimated in two lines of Japanese quail that were simultaneously bred. The HGR_{1-21} (a line selected for high growth rate during the period from one to 21 days of age) was selected according to the estimated aggregated breeding values for four successive generations, while the CL was kept under random mating without selection.

Studied traits:

Selection criterion:

Growth rate during the period from 1-21 days of age (GR_{1-21}) was calculated according to Brody (1945) as the following formula:

$$GR = [BW_2 - BW_1 / {}^{1}/{}_{2} (BW_2 + BW_1)]$$

where: BW_1: the weight at the beginning and BW_2: is the weight at the end of the period.

Body weights at different ages:

Body weights at hatch, seven, 14, 21, 28 and 35 days of age (BW_1, BW_7, BW_{14}, BW_{21}, BW_{28} and BW_{35}, respectively) were individually recorded to the nearest 0.01g.

Growth rates during different periods of growth:

Also, growth rates per chick during the periods: 1-7, 1-14, 1-28 and 1-35 (GR_{1-7}, GR_{1-14}, GR_{1-28} and GR_{1-35}) were calculated according to Brody (1945).

Statistical analyses:

The recorded data of the growth traits (BWs and GRs) were analyzed by PROC MIXED (SAS, 2011) to calculate the generation, line and sex specific means using the following model:

$$Y_{ijklm} = \mu + a_i + G_j + L_k + S_l + G_j x L_k + G_i x S_l + L_k x S_l + G_j x L_k x S_l + e_{ijklm}$$

where: Y_{ijkim}: is the observation for a trait μ: is the overall mean, a: is the random additive genetic effect of the ith animal, G: the effect of jth generation, L: the effect of kth line, S: the effect of lth sex, $G_j x L_k$: the effect of interaction of the jth generation with the kth line, $G_j x S_l$: the effect of interaction of the jth generation with the lth sex, $L_k x S_l$: : the effect of kth line with the lth sex, $G_j x L_k x S_l$: the effect of interaction of the jth generation with the kth line with the lth sex and e_{ijklm}: is the random error term; the random variable was the birds within line. Means of generation were compared using multiple range test (Duncan, 1955).

The generation by line interactions were presented to be used in the estimation of the selection response (direct and correlated) for the studied traits.

Genetic parameters:

Both univariate and bivariate linear animal models used to estimate heritabilities (h^2) of studied traits and correlations. (REML procedures by WOMBAT program software, Meyer, 2007) as follows:

The univariate model to estimate direct h^2 was:

$$y = Xb + Za + e$$

The bivariate model to estimate correlations between selection criterion trait and other studied traits was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 & 0 \\ 0 & x_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} z_1 & 0 \\ 0 & z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where: for trait i (i=1, 2), y_i=vector of observations, b_i= vector of fixed effects (i.e., generation and line, a_i=vector of random direct genetic effects, e_i=vector of random residual effects, and X_i and Z_i are incidence matrices relating the observations to the respective fixed and direct genetic effects.

Selection intensity (i):

Proportion of selected animals for breeding (Selected proportion = the number of selected birds / number of all population) used to acquire the expected theoretical values of selection intensity for varying extents of coefficients according to Falconer and Mackay (1996).

Direct response (ΔG) at the first generation of selection :

The direct selection response calculated according to Falconer and Mackay (1996). as follows: $\Delta G = h^2 i \delta_p$

where: ΔG: Direct genetic response, h^2: the heritability of the trait under selection, i: the selection intensity and δ_p: the phenotypic standard deviation of the trait.

Correlated response (CR_y) at the first generation of selection:

The CR_y is the change in one trait as a result of selection for another trait, correlated response calculated according to Falconer and Mackay (1996) as follows:

$$CR_y = i\, h_x\, h_y\, r_{gxy}\, \delta_{p(Y)}$$

where: h_X, $h_{Y:}$ the square root of heritabilities of X and Y traits, r_g :the genetic correlation between X and Y traits, $\delta p_{(y)}$: the phenotypic standard deviation of Y trait and i : the selection intensity for trait X.

Direct and correlated responses from second to fourth selection generations:

The realized genetic gain at specific generation (t) was done according to the equation of Guill and Washburn (1974) as follows:

$$SR_t = (S_t - S_{t-1}) - (C_t - C_{t-1})$$

where: SR_t realized gain due to selection in the tth generation, S_t and S_{t-1} were least square means for selection criterion and studied traits at generation t and the first generation for the selected line and C_t and C_{t-1}: were least square means for selection criterion and other studied traits at generation t and the first generation for the CL.

RESULTS AND DISCUSSION

Descriptive statistics of BWs and GRs during the selection experiment presented in Table 2. Estimates of variation coefficient (CV%) ranged from 5.23% to 11.25% for body weights and from 1.09% to 8.55% for GRs which showed wider range of CV% than BWs .The CV% estimates for body weights in this work had lower than those reported by Barbieri *et al.* (2015) and El-Attrouny *et al.* (2020). Average of GR_{1-21} in this study was 1.74 which was in agreement with those reported by Rezvannejad *et al.* (2013). The average of selection criterion (GR_{1-21}) had higher values than those calculated by many investigators (Abdel Fattah, 2006, Abou Khadiga *et al.*, 2014 and Mahmoud *et al.*, 2014) whereas, Aggrey *et al.* (2003) recorded higher GR's during the previously mentioned periods estimates than those calculated in the present study. The BWs at seven, 14, 21,28 and 35 days of age averaged 8.48, 33.36, 70.54, 115.44, 161.90 and 192.80 g, respectively. The present results of the averages of BW traits were in the range

of reviewed studies for each of BW_1 (Aggrey *et al.,* 2003*,* Balcıoğlu *et al.,* 2005 and Abdel Fattah, 2006), both BW_7 and BW_{14} (Aggrey *et al.,* 2003), BW_{21}(Balcıoğlu *et al.,* 2005 , Abou Khadiga *et al.*, 2014 and Mahmoud *et al.*, 2014), BW_{28}(Rezvannejad *et al.*, 2013) and BW_{35} (Balcıoğlu *et al.,* 2005) compared to the selected lines for high body weight in these studies.

Genetically, h^2 for BWs at different ages showed moderate h^2 ranged from 0.19 to 0.29. The BW_1 had higher h^2 of 0.29 whereas, BW_7 showed lower h^2 of 0.19 than other BW's (Table 3). In the current study, h^2 estimates of BWs were in agreement with the reports of other studies concerning BW_1 (Sezer *et al.*, 2006), BW_7 (Saatci *et al.*, 2006 and Barbieri *et al.*, 2015), both BW_{14} and BW_{21} (Silva *et al.*, 2013), BW_{28} (Khaldari *et al*., 2010) and BW_{35} (Barbieri *et al.*, 2015). Whereas, h^2 values of the this work were lower than those literatured by several investigators for BW_1 (Silva *et al.*, 2013), both BW_7 and BW_{21} (Sezer *et al.*, 2006 and Silva *et al.*, 2013), BW_{14} (Sezer *et al.*, 2006), BW_{28} (Sezer *et al.*, 2006 and Silva *et al.*, 2013) and BW_{35} (Sezer *et al.*,2006). On the other hand, h^2 for both BW_1 and BW_{35} were low (0.07 and 0.03) as found by Saatci *et al.* (2006) and Barbieri *et al.* (2015) and h^2 BW_{35} being 0.13 (Saatci *et al.*, 2006). These differences in h^2 estimates could be due to the variations of populations structure, selection criteria, method of estimation and statistical models.

The GR_{1-21} found to be positively correlated with all body weights weekly measured from 7 to 35 days of age with r_gs ranged from 0.06 to 0.47, and r_p ranged from 0.18 to 0.52 as shown in (Table 3). Conversely, either genetic or phenotypic correlation between GR_{1-21}

and BW_1 was negative being -0.15 and -0.50, respectively. Similarly, genetic and phenotypic correlations between GR_{1-21} and BW_1 were negative ranged from -0.41 to -0.47 (Abdel Fattah, 2006). Genetic correlations can arise in several ways, they can be caused by pleiotropic gene effect which occurs when one locus affects multiple traits and linkage (Falconer and Mackay, 1996). Selection for high growth rate, body weights and skeletal measurement traits could improve growth traits of quail (Abdel Fattah, 2006 and Emam, 2015) due to the expected positive r_gs among these traits. Estimates of r_g and r_p between GR_{1-21} and body weights from seven up to 35 days of age were positive except r_g between GR_{1-21} and BW_7 based on sire variance component was negative as well as r_g estimates that ranged from low to high (0.11 to 0.71) whereas r_p ranged from moderate to high (0.33 to 0.75, Abdel Fattah, 2006) as regards of r_g of the combined sex between GR_{1-21} and body weights at various ages ranged from 0.11 to 0.61 (Abdel Fattah 2006).

The GR's during different periods of growth had medium h^2 ranged from 0.17 to 0.28 and showed a wide range of moderate to high r_g (0.15 to 0.70) and had a broader range of r_p ranged from 0.03 to 0.67 (Table 4). Similarly, heritability estimate of GR_{1-35} being 0.29 as reported by Narinç *et al.* (2014).

Both line and generation of selection significantly influenced BWs and GRs from one up to 35 days of age, similarly sex significantly affected all studied BWs and GRs except each of BW_1, GR_{1-7} and GR_{1-21} (Tables 5 and 6). Regardless of generations, the HGR_{1-21} line showed heavier BW at all ages studied than the control from seven up to 35 days of age except for BW_1. Similarly, selected lines

in the literature for BW at different ages had significantly heavier BW's than the CL (Khaldari *et al*., 2010, Abou Khadiga *et al.* , 2014 and Taskin *et al.,* 2017).

Generation by line interaction significantly affected each of BW at hatch, seven, 21, 28 days of age and GR during the periods 1-7, 1-14, 1-28 and 1-35 days of age, whereas all other 2nd and 3rd order interactions had insignificant effects on GR during different periods studied as well as all studied BW's, except (Generation by Sex for Bw_{14}) as shown in Table 5 and 6. The HGR_{1-21} line in the 4th generation had the heaviest BW_7, BW_{21} and BW_{28}, similarly the HGR_{1-21} line of the 3rd generation had the heaviest BW_1 (Table 5). The HGR_{1-21} line in the 4th generation had the fastest GR during the periods 1-7, 1-14, 1-28 and 1-35 days of age however, the CL of both the 3rd and 2nd generations showed slower GR_{1-7},GR_{1-14} and GR_{1-35} than other generation by line groups, also the CL of the 2nd and the 3rd generations had the lowest GR_{1-28} (Table 6). Similarly, significant generation by line interaction affected BW_1, BW_{21} (Abdel Fattah, 2006), BW from hatch up to 35 days of age (Mahmoud *et al.,* 2014), BW from seven up to 35 days of age (Emam, 2015) and GR_{1-21}(Abdel Fattah, 2006) were reported. Although, generation by line interaction had insignificant effects on BW at all ages except, BW at hatch (Farrag, 2011).

There were fluctuations across generations in direct selection responses being 0.013 (1.30%), 0.03 (3.0%), 0.01 (1.0%), 0.01 (1.0%) in the 1st ,2nd ,3rd and 4th selection generations, respectively, the realized cumulative response after four generations of selection was 0.063 (6.30%) for GR_{1-21}, these estimates revealed the importance of selection for

GR_{1-21}in Japanese quail. (Table 7). The results of this study were higher than those reported by Abdel Fattah (2006) who found the genetic gain for GR_{1-21} was 0.003 in the selected line for high GR_{1-42}. Also, Abdel Fattah (2006) found fluctuations ranged from -0.04 to +0.03% and from -0.01 to +0.03% in GR_{1-21} due to selection for high BW_{42} and high GR_{1-42}. Varkoohi and Kaviani (2014) reported that selection for high BW_{28} was effective in its genetic improvement with a high degree of correspondence between the expected and realized genetic changes. Genetic response in the first generation of selection for a metric trait is solely a tool of selection precision (breeding values of individuals and the correlation between the selection criterion), additive genetic variance in the population and intensity of selection (Falconer and Mackay, 1996).

Correlated responses for BWs at different ages and GRs during different periods through four selection generations are presented in Tables 8 and 9. Although, there were positive inconsistent changes across generations in correlated responses for BWs and GRs, selection for high growth rate during the period from 1-21 days of age had improved all BWs and GRs over selection generations as shown in Tables 8 and 9. There were positive correlated responses for BWs at different ages over the selection generations, expect BW_1 in the 1st generation (-0.041). A similar trend was found for all GRs during the different periods, the cumulative correlated responses for BWs and GRs ranged from 1.19g to 23.94 g and from 3.10% to 17.00%, respectively. These findings displayed that selection for early and fast GR_{1-21} would bring an associated enhancement in BWs and GRs at later ages as a correlated response to the

selection. The results of this work agreed with the findings of previous studies (Ayatollahi Mehrgardi, 2013, Varkoohi, 2014, Hussen *et al.*, 2016 and El-Attrouny *et al.*, 2020). The cumulative selection responses of this study were higher than those reported by El-Attrouny *et al.* (2020) who found cumulative selection responses for BW_1 and BW_{14} of 0.83 and 10.88 g, respectively after four selected generations. Finally, responses to selection differed which may be due to different selection accuracy, selection intensity, number of selected generations, environmental conditions, genetic correlation between selection criterion and other traits and genetic variance of population under study.

CONCLUSION

Japanese quail showed quick response to selection for high and early growth rate during 1-21 days of age. The generations of selection indicated that selection for GR_{1-21} was accompanied by an improvement in BWs and GRs traits so, improving growth performance genetically could be achieved through applying selection for growth rate during 1-21 days, furthermore, enhancement could be attained through selection for more generations.

Table (1): Sires, dams and progeny numbers in the selection experiment.

Generations	line	Number of sires	Number of dams	Number of progeny
Base	-	132	264	1726
1	CL	70	139	454
	HGR_{1-21}	89	178	1359
2	CL	48	96	456
	HGR_{1-21}	86	172	1138
3	CL	40	80	472
	HGR_{1-21}	90	180	1296
4	CL	68	136	440
	HGR_{1-21}	88	176	1383

HGR_{1-21}: the selected line for high growth rate during 1-21 days of age and CL: the control

Table (2): Descriptive statistics of body weights (BW) and growth rates (GR) during the selection experiment.

Trait	Abbreviation	Mean	SD	CV%
Body weight at hatch (g)	BW_1	8.48	0.63	7.43
Body weight at seven days of age (g)	BW_7	33.36	2.69	8.06
Body weight at 14 days of age (g)	BW_{14}	70.54	7.89	11.19
Body weight at 21 days of age (g)	BW_{21}	115.44	12.99	11.25
Body weight at 28 days of age (g)	BW_{28}	161.90	12.52	7.73
Body weight at 35 days of age (g)	BW_{35}	192.80	10.09	5.23
Growth rate during the period from 1-7 days of age	GR_{1-7}	1.17	0.10	8.55
Growth rate during the period from 1-14 days of age	GR_{1-14}	1.56	0.07	4.49
Growth rate during the period from 1-21 days of age	GR_{1-21}	1.74	0.03	1.72
Growth rate during the period from 1-28 days of age	GR_{1-28}	1.80	0.02	1.11
Growth rate during the period from 1-35 days of age	GR_{1-35}	1.83	0.02	1.09

Table (3): Heritability, genetic and phenotypic correlations ±SE between GR_{1-21} and body weights at different ages.

Trait	$h^2 \pm SE$	$r_g \pm SE$	$r_p \pm SE$
BW_1	0.29±0.030	-0.15±.04	-0.50±0.02
BW_7	0.19±0.029	0.06±0.03	0.26±0.03
BW_{14}	0.28±0.030	0.17±0.03	0.18±0.03
BW_{21}	0.25±0.031	0.47±0.02	0.41±0.03
BW_{28}	0.26±0.005	0.44±0.02	0.52±0.02
BW_{35}	0.26±0.006	0.33±0.10	0.24±0.03

h^2: heritability, SE: stander error, r_g: genetic correlation, r_p: phenotypic correlation, BW_1, BW_{21} and BW_{35}: body weights at hatch, 21and 35 days of age, respectively.

Table (4): Heritability, genetic and phenotypic correlations ±SE between GR_{1-21} and growth rate traits during different periods of growth.

Trait	$h^2 \pm SE$	$r_g \pm SE$	$r_p \pm SE$
GR_{1-7}	0.18±0.005	0.48±0.04	0.26±0.03
GR_{1-14}	0.17±0.005	0.42±0.03	0.17±0.03
GR_{1-21}	0.28±0.005		
GR_{1-28}	0.19±0.004	0.15±0.04	0.67±0.02
GR_{1-35}	0.20±0.004	0.70±0.05	0.03±0.01

h^2: heritability, SE: stander error, r_g: genetic correlation, r_p: phenotypic correlation, GR_{1-7}, GR_{1-14} GR_{1-21}, GR_{1-28} and GR_{1-35}: growth rates during the periods from 1-7, 1-14,1-21, 1-28 and 1-35 days of age, respectively.

Table (5): Least square means ± SE for body weights at different ages in the selection experiment as affected by Generation x Line interaction

Generation by Line interaction							
Item		**BW_1,g**	**BW_7,g**	**BW_{14},g**	**BW_{21},g**	**BW_{28},g**	**BW_{35},g**
Generation	Line						
1	CL	8.38 ± 0.07^d	32.20 ± 0.50^c	66.05 ± 1.57	115.04 ± 1.23^c	150.86 ± 1.58^e	188.78 ± 1.32
	HGR_{1-21}	7.64 ± 0.04^f	34.16 ± 0.29^b	70.79 ± 0.98	125.79 ± 0.87^b	154.07 ± 0.84^f	190.84 ± 1.41
2	CL	8.80 ± 0.07^c	30.46 ± 0.37^d	60.35 ± 1.16	103.41 ± 1.22^d	155.13 ± 1.66^f	181.46 ± 1.61
	HGR_{1-21}	8.89 ± 0.04^c	33.95 ± 0.19^b	72.21 ± 0.59	117.70 ± 0.63^c	167.37 ± 0.86^c	187.84 ± 0.84
3	CL	9.31 ± 0.10^b	30.28 ± 0.52^d	62.73 ± 1.15	100.30 ± 1.55^e	161.93 ± 1.70^d	180.57 ± 1.59
	HGR_{1-21}	9.37 ± 0.06^a	35.97 ± 0.32^b	79.12 ± 0.65	128.47 ± 0.89^b	175.05 ± 1.02^b	190.48 ± 0.91
4	CL	7.62 ± 0.06^f	31.16 ± 0.29^{cd}	67.56 ± 1.48	107.82 ± 1.43^d	166.39 ± 1.51^c	188.42 ± 2.07
	HGR_{1-21}	8.04 ± 0.03^e	38.07 ± 0.21^a	84.59 ± 0.73	140.00 ± 0.64^a	183.08 ± 0.72^a	209.58 ± 1.03
Significance							
Generation		***	***	***	***	***	***
Line		**	***	***	***	***	***
Sex		NS	**	***	***	***	***
Generation*Line		***	**	NS	**	***	NS
Generation*Sex		NS	NS	**	NS	NS	NS
Line*Sex		NS	NS	NS	NS	NS	NS
Generation*Line*Sex		NS	NS	NS	NS	NS	NS

Means having different superscripts within each effect in the same column are significantly differed at specified probability, SE: stander error, BW_1, BW_7, BW_{14}, BW_{21}, BW_{28} and BW_{35}: body weights at hatch, 7, 14, 21, 28 and 35 days of age respectively, HGR_{1-21}: the selected line for high growth rate during 1-21 days of age, CL: the control line, NS: Not significant. ** and***: significance at 0.01 and 0.001.

Table (6): Least square means ± SE for growth rate (GR) traits during different periods of growth as affected by Generation x Line interaction.

Item		Generation by Line interaction				
Generation	Line	GR_{1-7}	GR_{1-14}	GR_{1-21}	GR_{1-28}	GR_{1-35}
1	CL	1.19 ± 0.01^c	1.53 ± 0.01^d	1.69 ± 0.002	1.79 ± 1.23^d	1.79 ± 0.002^e
	HGR_{1-21}	1.26 ± 0.01^b	1.60 ± 0.01^b	1.72 ± 0.001	1.80 ± 0.87^c	1.٨٠ ± 0.001^d
2	CL	1.07 ± 0.01^e	1.51 ± 0.01^e	1.67 ± 0.005	1.78 ± 1.22^e	1.80 ± 0.003^d
	HGR_{1-21}	1.15 ± 0.01^d	1.59 ± 0.003^c	1.73 ± 0.002	1.80 ± 0.63^c	1.٨٢ ± 0.001^b
3	CL	1.05 ± 0.01^e	1.51 ± 0.01^e	1.68 ± 0.004	1.78 ± 1.55^e	1.80 ± 0.003^d
	HGR_{1-21}	1.14 ± 0.01^d	1.61 ± 0.004^b	1.75 ± 0.003	1.81 ± 0.89^b	1.٨٣ ± 0.002^b
4	CL	1.25 ± 0.01^b	1.54 ± 0.01^d	1.69 ± 0.005	1.79 ± 1.43^d	1.81 ± 0.002^c
	HGR_{1-21}	1.35 ± 0.01^a	1.68 ± 0.004^a	1.77 ± 0.004	1.83 ± 0.64^a	1.٨٥ ± 0.003^a
Significance						
Generation			***	***	***	***
Line		***	***	**	***	***
Sex		NS	***	NS	***	***
Generation* Line		**	**	NS	***	***
Generation* Sex		NS	NS	NS	NS	NS
Line*Sex		NS	NS	NS	NS	NS
Generation* Line*Sex		NS	NS	NS	NS	NS

Means having different superscripts within each effect in the same column are significantly differed at specified probability, SE: stander error, GR_{1-7}, GR_{1-14}, GR_{1-21}, GR_{1-28} and GR_{1-35}: growth rates during the periods from 1-7, 1-14, 1-21, 1-28 and 1-35 days of age, respectively, HGR_{1-21}: the selected line for high growth rate during 1-21 days of age, CL: the control line, NS: Not significant, ** and***: significance at 0.01 and 0.001.

Table (7): Direct response to selection for high growth rate during the period from hatch to 21 days of age (GR_{1-21}) of combined sex in Japanese quail.

Direct response for the first generation $= h^2 i \delta$		G_2	G_3	G_4	Cumulative
Absolute	0.28*1.554*0.03= +0.013	+0.03	+0.01	+0.01	+0.063
Percentages	+1.30	+3.0	+1.0	+1.0	+6.30

G_2, G_3 and G_4 are the 2nd, 3rd and 4th generation, respectively.

Selection, early growth rate, direct and correlated response, Japanese quail.

Table (8): Correlated response for body weight at different ages through four selection generation of combined sex in Japanese quail.

Trait	correlated response, for the first generation $i\,h_x\,h_y\,r_g\,\delta_{p(Y)}$	G2 $(S_t\text{-}S_{t\text{-}1})\text{-}(C_t\text{-}C_{t\text{-}1})$	G3	G4	Cumulative
BW_1,g	-0.041	+0.83	-0.03	+0.36	+1.119
BW_7,g	+0.061	+1.53	+2.2	+1.22	+5.011
BW_{14},g	+0.58	+7.12	+4.54	+0.65	+12.89
BW_{21},g	+2.51	+3.54	+13.88	+4.01	+23.94
BW_{28}.g	+2.31	+9.03	+0.88	+3.57	+15.79
BW_{35}.g	+1.39	+4.32	+3.54	+11.25	+20.50

BW_1, BW_7, BW_{14}, BW_{21}, BW_{28} and BW_{35}: body weights at hatch, seven, 14, 21, 28and 35 days of age, respectively.

Table (9): correlated response for growth rates during different periods through four selection generations of combined sex in Japanese quail.

Trait	correlated response, for the first generation $i\,h_x\,h_y\,r_g\,\delta_{p(Y)}$		G2-G1 $(S_t\text{-}S_{t\text{-}1})\text{-}(C_t\text{-}C_{t\text{-}1})$	G3-G2	G4-G3	Cumulative
$GR_{1\text{-}7}$	Absolute	+0.016	+0.01	+0.01	+0.01	+0.046
	Percentages	+1.6	+1.0	+1.0	+1.0	+4.60
$GR_{1\text{-}14}$	Absolute	+0.01	+0.10	+0.02	+0.04	+0.17
	Percentages	+1.0	+10.00	+2.0	+4.0	+17.00
$GR_{1\text{-}28}$	Absolute	+0.001	+0.01	+0.01	+0.01	+0.031
	Percentages	0.10	+1.0	+1.0	+1.0	+3.10
$GR_{1\text{-}35}$	Absolute	+0.005	+0.01	+0.01	+0.01	+0.035
	Percentages	+0.50	+1.0	+1.0	+1.0	+3.50

$GR_{1\text{-}7}$, $GR_{1\text{-}14}$, $GR_{1\text{-}28}$ and $GR_{1\text{-}35}$: growth rates during the periods from 1-7, 1-14, 1-28 and 1-35 days of age, respectively, $BWG_{1\text{-}35}$: body weight gain during the periods from 1-35 days of age, Sig.: significance, * : significance at 0.05 and NS: insignificant .

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الملخص العربى

الاستجابات للانتخاب لزيادة معدل النمو المبكر فى السمان اليابانى

إنصاف أحمد الفل، بثينة يوسف فؤاد محمود، دعاء عبد الحميد محمود صميدة و أحمد محمد إمام

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خلال تجربة الانتخاب والتي امتدت لخمسة أجيال: العشيرة القاعدية وأربعة أجيال من الانتخاب لزيادة معدل النمو المبكر (خلال الفترة من الفقس إلى ٢١ يوم من العمر) في السمان الياباني تم استخدام إجمالي عدد ٨٧٢٤ طائر: ١٧٢٦ في العشيرة القاعدية، ٥١٧٦ للخط المنتخب (HGR$_{1-21}$) و ١٨٢٢ لخط الكنترول. أهم النتائج المتحصل عليها كالتالي: وراثيا، كان المكافئ الوراثي لجميع أوزان الجسم متوسط وتراوح بين ٠.١٩ إلى ٠.٢٩. ارتبط معدل النمو في الفترة من الفقس حتى ٢١ يوم من العمر بشكل إيجابي مع جميع أوزان الجسم الاسبوعية التي تم قياسها باستثناء وزن الجسم في عمر يوم حيث تراوحت قيم معامل الارتباط الوراثي من ٠.٠٦ إلى ٠.٤٧، وكان لقيم الارتباط المظهري مدى واسع حيث تراوحت من ٠.١٨ إلى ٠.٥٢.

أظهرت معدلات النمو خلال فترات النمو المختلفة قيم متوسطة للمكافئ الوراثي تراوحت من ٠.١٧ إلى ٠.٢٨ وأظهرت مدى واسع من الارتباط الوراثي مع الصفة المنتخبة من المتوسط إلى العالي (٠.١٥ إلى ٠.٧٠) ومدى أوسع من الارتباط المظهري يتراوح من ٠.٠٣ إلى ٠.٦٧.

حقق الخط المنتخب في الجيل الرابع أفضل أداء للنمو بفروق معنوية في وزن الجسم عند عمر ٧، ٢١، ٢٨ يوم من العمر ومعدلات النمو في الفترات ١ـ ٧، ١ـ ١٤، ١ـ ٢٨ و ١ـ ٣٥ يوم من العمر. كانت الاستجابة المباشرة التراكمية المحققة بعد أربعة أجيال من الانتخاب ٠.٠٦٣ (٦.٣٠٪) لمعدل النمو في الفترة من ١ـ ٢١ يوم من العمر، وتراوحت الاستجابات المرتبطة التراكمية لأوزان الجسم ومعدلات النمو من ١.١٩ جرام إلى ٢٣.٩٤ جرام ومن ٣.١٠٪ إلى ١٧.٠٠٪ للصفات على التوالي. لذلك ، هدفت الدراسة الحالية إلى تقييم فاعلية برنامج الانتخاب من خلال تقدير الاستجابات المباشرة والمصاحبة للانتخاب لمعدل النمو المرتفع خلال الفترة من الفقس إلى ٢١ يومًا من العمر، وتحديد الارتباط بين معيار الانتخاب وكلا من أوزان الجسم في مختلف الأعمار ومعدلات النمو خلال فترات النمو المختلفة للسمان الياباني.

الكلمات الدالة: الانتخاب ، معدل النمو المبكر، الاستجابات المباشرة والمصاحبة، السمان الياباني.