SELECTION FOR INCREASING FOUR WEEKS BODY WEIGHT IN JAPANESE QUAILS

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ABSTRACT

Effect of selection for increasing four weeks body weight and estimation of genetic parameters of body weight in Japanese quails was investigated. Data from selected and control lines were collected three generations. The genetic gain of four weeks body weight was 21.68 and 19.84 g for first and second generation; respectively with overall genetic improvement was 41.52 g in selected line. The corresponding values in control line, was 16.50, 13.30, and 29.80 g; respectively. There was significant effect of sex, generation, and lines (P < 0.05). Realized heritability was 0.97, 0.94 in first, and second generations. However, the expected heritability using pedigree information was 0.45 and 0.41. The genetic and phenotypic correlations of body weight at different ages were variable and ranged from 0.09 to 0.68. Selection for four weeks body weights improved body weight.

INTRODUCTION

Due to shortage of animal protein sources, it is essential to produce large sized birds on genetic basis to compensate this shortage. This would occur by applying genetic selection for high body weight of birds. Selection experiments provide the framework for the study of the inheritance of complex traits and allow the evaluation of theoretical prediction by testing observations against expectations and depending on the time scale. The objectives of selection experiments may differ, longterm experiments are useful for measurement of changes in the rates of response or variances caused by selection itself (Khaldari et al., 2010). Experimental research indicated that Japanese quails respond quickly to selection for body weight (Nestor and Bacon, 1982; Caron and Minvielle, 1990; Marks, 1993). Estimation of genetic parameters for several traits in Japanese quails has been reported (Toelle et al., 1991; Vali et al., 2005; Mielenz et al., 2006; Saatci et al., 2006; Shokoohmand et al., 2007) where genetic parameters describe the genetic and environmental variations and might vary among populations and environments and so, should be measured in different population and environments. In addition, genetic parameters estimation is necessary for prediction of response to selection and determination of selection procedure. So, According to the previous points this study was done to investigate the following points; first calculation of direct response to selection for four-week body weight. Second, assessing the genetic parameters for body weight at different ages.

MATERIAL AND METHODS

This experiment was conducted on Japanese quail [Coturnix coturnix japonica] at the research farm belonging to the Department of Animal Wealth Development, Faculty of Veterinary Medicine, Kafrelsheikh University through the period from July 2010 to March 2011.

Management of Experimental Flock:

Source of Experimental Birds:

A total of 650 four weeks old Japanese quails (males and females) were taken from the experimental station belonging to the Department of Animal Husbandry and Animal Wealth Development, Faculty of Veterinary Medicine, Alexandria University and transferred to the Faculty of Veterinary Medicine, Kafrelsheikh University farm where they were reared till sexual maturity. Four hundreds birds (200 males and 200 females) were randomly selected to form 200 sire families from which birds of the base population were obtained.

Birds of the base population:

A total of 1620-day-old Japanese quail chicks were obtained from two successive hatches; wing banded according their hatch and family number and transferred to the brooding room (floor rearing). Weekly body weights were recorded for all birds from hatch till the fourth week of age and the sex was determined at the 4th week of age. Birds were fed ad libitum on ration containing 24% crude protein and 2975.8 Kcal ME/kg ad libitum. At the fourth week of age, 400 birds (200 males and 200 females) were selected for higher body weights from total 1300 birds

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according to their average of body weight (grams) plus half standard deviation ($\overline{x} \pm 1/2 \, 5D$), these birds forming 200 sire families (one male and one female) as parents population to birds of the first generation of selection. The selected birds were cage housed as one male to one female in one room forming a sire family. Egg production started at the 7th week of age (about 50 day of age). Eggs were collected after two weeks when all birds laid standard egg size. The eggs were collected for about two successive weeks and incubated weekly to obtain birds of the first generation.

Birds of first generation:

A total of 1345 hatched quail chicks were obtained from two successive hatches; The same managemental selection procedures applied in base generation were followed in the first generation. At the 4th week of age 280 birds (140 males and 140 females) were selected from total 1245 birds according to their body weight average plus half standard deviation (SD) ($\overline{X} \pm 1/2$ SD). These birds forming 140 sire families used as parents to birds of the second generation of selection.

Birds of second generation:

About one thousand hatched quail chicks were obtained at hatching age reached to about 765 birds at the fourth week of age. The same managemental selection procedures were followed in the second generation, where weekly body weights were recorded for all birds from hatch to four week of age. Selection intensities were estimated depending on the proportion of selection. If the proportion of selection less than 50 percent, the intensity was calculated directly from the intensity table but, if more than 50 percent the intensity calculated as:

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 $P > 50\% = i \times (1-P)/P$ (Falconer, 1965).

P > 50% = any proportion more than 50 percent of the population.

i = intensity of (1 - P).

P = Proportion of selection.

Traits and estimations:

Body weight was recorded to the nearest gram at hatch, 1^{st} , 2^{nd} , 3^{rd} and 4^{th} week of age for all birds.

Statistical analysis:

Data were normally and independently distributed where analysis of hatches effect by using ANOVA between hatches revealed none significant differences so data of hatches were pooled. Testing for normality revealed normal distribution of data. Testing for homogeneity of variance revealed equal variances.

Statistical model:

Statistical analysis was done by the aid of *SAS software*, 2004 according to the model:

 $X_{ijk} = \mu + S_i + D_j + e_{ijk}$

Where:

Xijk =body weight observations.

 μ = overall mean.

Si = sire effect.

Dj = dame effect.

eijk = random error.

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Selection procedures and genetic parameters

Selection differential "S"

Actual selection differential calculated according to Becker (1985).

Standardized selection differential: $S = i \sigma p$ (*Falconer, 1960*).

Where:

i = Selection intensity and σ_p = Phenotypic standard deviation of the population.

Overall selection differential could be calculated by subtracting the population mean of base generation from the mean of selected parents in the last generation.

Response to selection "R"

Response to selection is equal to the difference between mean of the progenies of the selected parents and the mean of the population from which the parents were selected (*Becker*, 1985). Overall response calculated by subtracting the population mean of base generation from the mean of offspring in the last generation.

<u>Heritability</u>

Expected heritability estimates

Heritability estimated in each generation from sire variance components (*Becker, 1985*) as follow:

$$h^{2} = \frac{2 \sigma_{s}^{2}}{\sigma_{s}^{2} + \sigma_{w}^{2}}$$

Where:

 \mathbf{h}^2 = Heritability. $\mathbf{\sigma}^2 \mathbf{s}$ = sire variance components. $\mathbf{\sigma}^2 \mathbf{w}$ = within sire family variance components.

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Realized heritability

Realized heritability calculated according to *Falconer*, 1989 as follow:

Correlations

Genetic and phenotypic correlations: Calculated according to *Becker*, *1985*:

RESULTS AND DISCUSSION

Body weight:

The statistical description of body weight at different ages along two generations of selection of selected and control lines summarized in Table 1 and figure 1. There was significant effect of selection on body weight at different ages in the selected line. Quails selected for body weight exhibited continuous improvement of body weight at different ages along the two generations of selection. The mean values of body weights were 8.30, 8.64, and 8.74 grams for hatch weight. At first week of age, they were 23.66, 26.11 and 27.77 grams. Second week weights were 44.67, 57.17, and 66.07 g. At the third week of age the mean values of body weights were 81.45, 101.71, 103.91 g. Fourth week weights were 128.36, 150.04, and 169.88 grams at the base, first and second generations of selection; respectively. Averages of body weight in the control line (random mating without selection) were 8, 8.30, and 8.50 g for hatch weight, 21.50, 24.30 and 25.2 g for first week, 43.18, 55.13, and 62.85 grams for second week, for the third week, were 75.45, 95.72, and 98.55 grams but at the fourth week of age, the body weight averages

were 111.90, 139.37, and 152.26 grams for the base, first and second generations; respectively. These results of both line (Selected and Control) showed the marked increase of body weight at different ages indicating significant genetic improvement. Table (3) represented the response of selection across the two generations of selection. The selection response was 21.68 grams after the first generation of selection and 19.84 grams after the second generation where the overall response was 42.76 grams and this for the selected line but in the control line the rate of body weight increase per generation were 16.50 grams and 13.30 g for the first and second generations; respectively, but the overall increase was 29.80 grams. These results differed with Baylan et al. 2009 and Khaldari et al. 2010 who reported only 9.6, 8.8, 8.2 g increases in body weight at generation 2, 3, and 4; respectively. These differences in the selection response were due to differences in selection intensity, accuracy of selection and genetic variance in the populations studied. Also, these results differed with Mona, 2008 who reported slight increase in body weight of Japanese quails that selected against the abdominal fat indicating that there was slight correlated response of body weight and selection for or against the abdominal fat.

Genetic parameters

<u>Heritability</u>

Heritability of body weight.

The results in Table (3) show the estimated heritability of hatch weight and weights at first, second, third, and fourth week of age in the selected and control lines. The estimated values of heritability of body weight at hatch declined from 0.43 to 0.32 for the selected line. For the control line values declined from 0.82 to 0.74 from the base to the second generation of selection. These results agreed with *El-Fiky*, *1991*, *El-Full*, *2001*, *and Mona*, *2008*. And disagreed with *Taha*, *2009* who reported an increase in the heritability values for hatch weight from 0.21 to 0.48. Second week body weight had heritability estimates ranged from 0.41 to 0.35 for the selected line but in the control line ranged from 0.77, 0.90, and 0.24 for the base, first, and second generation; respectively. At the fourth week of age, the heritability values ranged from 0.48, 0.45, and 0.41 for the selected line at base, first, and second generation; respectively. These results disagreed with *Khaldari et al.*, *2010* who reported that heritability of fourth week body weight was 0.26 and *Mona*, *2008* who reported that heritability values were 0.34 to 0.35. But these results agreed with *Khaldari et al.*, *2011* who reported an increase in the heritability values by 0.46. Also, disagreed with

Realized heritability

The realized heritability estimates Table 2 were 0.97 and 0.94 for first and second generation with over all realized heritability 0.97 in the selected line but in the control line it was 0.91 for the first and 0.86 for the second generation of selection. These results agreed with *Taha, 2009* who reported decline of the realized heritability of body weight by selection and disagreed with *Khaldari et al., 2010* that reported that the realized heritability was 0.55. The realized heritability estimates were higher than the estimated one reflecting the effect of selection for increasing body weight.

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Genetic and phenotypic correlations.

Tales 4, and 5 represent the estimated correlation coefficient between body weight and measured traits during this study. Body weights (at hatch, 1st, 2nd, 3rd, and 4th weeks) according to sire components of variance and covariance.

Correlation of body weight at different ages.

Tables 4 and 5 represent the genetic and phenotypic correlations of body weight at different ages. Hatch weight showed high genetic correlations with the first week weight ranged from 0.48 for base generation, 0.42 for the first generation but for the second generation became 0.39. At the second week also there were high genetic correlation coefficients ranged from 0.37 to 0.44. Genetic correlation coefficients remained high with third and fourth week weight and ranged from 0.34 to 0.54 for the third and 0.30 to 0.58 for the fourth week weight. On the other hand, the phenotypic correlation coefficient showed variation and ranged from 0.38 to 0.58 for different ages. On the other hand, phenotypic correlations between the first week and second, third and fourth week body weights were moderate to high ranged from 0.20 to 0.63 but the corresponding genetic correlations were low to high and ranged from 0.09 to 0.48. Also, the second week weight was highly genetically correlated with 3rd and 4th week weight with correlation coefficient ranged from 0.41 to 0.47 and overestimated with 3rd week weight in the first generation. The phenotypic correlation was high to very high and ranged from 0.37 to 0.80 and over estimated at the fourth

week during the base generation. The third week weight was highly genetically and phenotypically correlated with fourth week weight where the phenotypic correlation ranged from 0.60 to 0.87 while the genetic ranged from 0.41 to 0.44 and over estimated at the first generation of selection. These results agreed with *Magda, 2010* who reported high genetic and phenotypic correlations among body weight at different ages. Also, agreed with *Sharaf, 1992; Bahie El-Dean, 1994; Saatci et al., 2002. Megeed and Younis 2006, and Shokoohmand et al., 2007.*

Results of two generations of selection:

Results of selection are summarized in Table 6. Selection differentials for selected line were 22.26 and 21.08 for the first and the second generation. Overall selection differential was 42.76 grams. In the control line the selection differentials were 18.05 and 15.50 grams, with overall selection differential was 33.55 grams. Genetic gain to selection was 21.68 grams and 19.84 gm for the first and second generation of selected line. For the control line the same results were 16.50, 13.30, 29.80 gm; respectively. This genetic gain to selection obtained in this study agreed with the results reported by *Deyab*, 2008; and *Baylan et al.*, 2009, and Khaldari et al., 2010 who reported that the genetic selection is efficient to improve body weight and correlated traits. So, it could be concluded from this study that genetic selection is efficient in improving body weight and correlated traits(carcass and body conformation traits) and this will lead to compensate the shortage of animal protein.

Table (1): Means ± standard deviations of body weight (grams) at hatch, 1-wk, 2-wk, 3-wk, and 4-wk of selected and control lines of Japanese quails across two generations of selection for increasing four-week body weight.

Lines	Number	generations	Hatch wt	1-wk wt	2-wk wt	3-wk wt	4-wk wt
			$\overline{x} \pm SD$				
р	1028	Base	8.30 <u>+</u> 0.73	23.66 <u>+</u> 2.67	44.67 <u>+</u> 4.73	81.45 <u>+</u> 9.08	128.36 <u>+</u> 15.48
Selected	1242	First	8.64 <u>+</u> 0.93	26.11 <u>+</u> 3.75	57.17 <u>+</u> 7.50	101.71 <u>+</u> 14.56	150.04 <u>+</u> 14.14
	746	Second	8.74 <u>+</u> 1.27	27.77 <u>+</u> 2.73	66.07 <u>+</u> 11.19	103.91 <u>+</u> 10.26	169.88 <u>+</u> 13.88
-	482	Base	8 <u>+</u> 0.81	21.50 <u>+</u> 2.30	43.18 <u>+</u> 8.72	75.45 <u>+</u> 7.08	111.90 <u>+</u> 14.85
Contro	1022	First	8.30 <u>+</u> 0.88	24.30 <u>+</u> 3.30	55.13 <u>+</u> 8.27	95.72 <u>+</u> 13.45	139.37 <u>+</u> 22.92
	983	Second	8.50 <u>+</u> 0.88	25.20 <u>+</u> 2.50	62.85 <u>+</u> 7.37	98.55 <u>+</u> 12.30	152.26 <u>+</u> 14.81

Fig.(1): Body weight (grams) at hatch, 1-wk, 2-wk, 3-wk, and 4-wk of selected and control lines of Japanese quails across two generations of selection for increasing four-weeks body weight.



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Table (2): Realized heritability estimates of body weight across twogenerations of selection for increasing 4wks- body weight inJapanese quails.

Generation	Realized heritability			
Otheradon	Selected line	Control line		
First	0.97	0.91		
Second	0.94	0.86		
Overall	0.97	0.89		

Table (3): Heritability estimates of body weight at hatch, 1-wk, 2-wk, 3-wk and 4-weeks of ages in selected and control lines of Japanese quails across two generations of selection for increasing fourweeks body weight.

True it	Gamanatian	Expected h ²		
Irait	Generation	Selected	Control	
	Base	0.43	0.82	
hatch wt	First	0.42	0.82	
	Second	0.32	0.74	
	Base	0.42		
1- wk wt	First	0.40		
	Second	0.39		
	Base	0.41	0.77	
2- wk wt	First	0.40	0.90	
	Second	0.35	0.24	
	Base	0.38		
3- wk wt	First	0.34		
	Second	0.32		
	Base	0.48	0.16	
4- wk wt	First	0.45	O.E	
	Second	0.41	0.30	

O.E = Over estimated

Table (4): Genetic correlations of body weight measurements at hatch, 1-wk, 2-wk, 3-wk, and 4-weeks of age across two generations of selection for increasing four-weeks body weight in Japanese quails.

Trait	Generation	Trait				
	Generation	Hatch wt	1-wk wt	2-wk wt	3-wk wt	4-wk wt
	Base	0.48				
1-wk wt	First	0.42				
	Second	0.39				
	Base	0.40	0.42			
2- wk wt	First	0.37	O.E			
	Second	0.44	0.13			
	Base	0.54	0.45	0.42		
3-wk wt	First	0.34	O.E	O.E		
	Second	0.40	0.09	0.43		
4-wk wt	Base	0.58	0.41	0.47	0.41	
	First	0.30	0.48	0.41	O.E	
	Second	0.43	0.09	0.47	0.44	

O.E = Over estimated

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Table (5): Phenotypic correlations among body weight measurements at hatch, 1-wk, 2-wk, 3-wk, and 4-weeks of age across two generations of selection for increasing four-weeks body weight in Japanese quails.

Troit	Generation	Trait					
ITan		Hatch wt	1-wk wt	2-wk wt	3-wk wt	4-wk wt	
1-wk wt	Base	0.58					
	First	0.46					
	Second	0.44					
	Base	0.55	0.63				
2- wk wt	First	0.45	0.30				
	Second	0.48	0.20				
3-wk wt	Base	0.53	0.61	0.61			
	First	0.45	0.24	0.37			
	Second	0.43	0.22	0.65			
4-wk wt	Base	0.53	0.63	O.E	0.60		
	First	0.38	0.63	0.69	0.66		
	Second	0.48	0.25	0.80	0.87		

O.E = Over estimated

Table (6): Selection differential and selection response across two generations of selection for increasing four-weeks body weight in Japanese quails.

	Lines of selection					
Generation	Sele	cted	Control			
	(Actual) selection differential (g)	Selection response (g)	(Actual) selection differential (g)	Selection response (g)		
First	22.26	21.68	18.05	16.50		
Second	21.08	19.84	15.50	13.30		
Overall	42.76	41.52	33.55	29.80		

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الانتخاب لزيادة وزن الجسم عند أربعة أسابيع في السمان الياباني

أجريت التجربة بمزرعة البحوث التابعة لقسم نتمية الثروة الحيوانية بكلية الطب البيطري، جامعة كفر الشيخ في الفترة من يوليو 2010 وحتى مارس 2011.

استهدفت الدراسة اختبار نتائج الانتخاب الوراثي لتحسين وزن الجسم عند أربع أسابيع في السمان الياباني.

وقد اشتملت الدراسة على جيلين من الانتخاب بعد العشيرة الأساسية وقد تم تكوين خطين أحدهما منتخب والأخر غير منتخب يستخدم كاكنترول حتى يسهل المقارنة. كانت الصفات الرئيسية المنتخبة في هذه التجربة هي وزن الجسم عند أربع اسابيع.

أهم النتائج كالتالى:

- إ. زيادة وزن الجسم عند أربع أسابيع من 128.36 جرام إلى 169.88 جرام بعد جيلين من الانتخاب وذلك في الخط المنتخب واختلافهم المعنوي عن خط المقارنة.
- تراوحت معدلات الزيادة المكتسبة في الخط المنتخب من 21.68 جرام في الجيل الأول، 19.84
 جرام في الجيل الثاني من الانتخاب بواقع زيادة كلية كانت تساوى 42.76 جرام.
- 3. كانت المكافئات الوراثية لوزن الجسم عند سن الفقس نتراوح بين 0.43، 0.42، 0.32، أما بالنسبة لوزن الجسم عند عمر أسبوع واحد فكانت تتراوح بين 0.42، 0.40، 0.39 وكانت تتراوح بين لوزن الجسم عند عمر أسبوع واحد فكانت تتراوح بين 0.42، 0.40، 0.30، 0.30، 0.41، 0.34, 0.34
- 4. كما جاءت قيم المكافئ الوراثي المقدر نتراوح بين 0.97 للجيل الأول و 0.94 بالنسبة للجيل الثاني من الانتخاب وذلك في الخط المنتخاب أما بالنسبة للخط المقارنة فكانت 0.91، و 0.86 على التوالي.

وتخلص هذه الدراسة إلى أن الانتخاب الوراثي لزيادة وزن الجسم وسيلة مباشرة لتحسين وزن الجسم ومن هنا يتم تعويض النقص في البروتين الحيواني.