

Genetic Evaluation and Trends of Japanese Quail Data after Two Generations of Divergent Selection for 4-wk Body Weight

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Abstract: The present study aimed to estimate the genetic parameters and evaluate the genetic trends of body weight traits and right shank length of Japanese quail after two generations of divergent selection for 4-wk body weight. Body weights heritability (h^2) estimates ranged from moderate to high and revealed that selection in high body weight line (HL) individuals is probably more efficient at later ages. For shank length, heritability values found to be relatively high and individual selection may apply early in quails' life. Genetic correlations among body weight traits were high, while the correlation between body weight and shank length was found to be moderate and mostly insignificant. Body weight of the tested quail population have positive genetic trend only at 4 wk of age (selection criteria), whilst for the other body weight (non-selected for traits) tends to be negative. Estimated genetic trend also found to be higher in the second generation from the 4 wk of age onwards while the reverse was true in the era before. This may mean that birds tend to get better improvement at later ages of life on the expense of that at earlier ages.

Keywords: Japanese quail, Divergent selection, Body weight, Shank length, heritability, Genetic correlation, Genetic trend.

INTRODUCTION

Genetic improvement of body weight in chickens and turkeys has been the result of selection at a fixed age. However, the additive nature of genetic variation for growth has resulted in dramatic body weight improvement in chickens (Siegel, 1962; Chambers, 1990) and Japanese quail (Marks, 1978, 1990; Nestor *et al.*, 1982) as a result of individual phenotypic selection.

Initial estimates for the heritability values of body weight and growth in Japanese quail ranged from 0.18 to 0.68 in unselected control and short-term selected population for body weight (Marks, 1990). Though these ranges indicate substantial variation, heritabilities for body weight in Japanese quail appeared to be similar to those for body weight in chickens (Siegel, 1962; Kinney, 1969) and these results supporting the conclusion by (Wilson *et al.*, 1961) that Japanese quail should be an excellent pilot bird for studying the genetics of growth in chickens.

As in any animal breeding program, it is necessary to study the outcome that it is possible to evaluate trait development, as well as to make effective adjustments, for optimizing genetic gain and increase the profitability of production. It is therefore, the study of genetic trend in a population is an important element in the monitoring of selection methods, since it corresponds to observed changes in the average breeding values of animals studied for a specific trait during the selection work. According to Costa *et al.* (2001), the study of genetic trend allows for the visualization of the efficiency of the selection procedures used and the quantification of the genetic changes of the traits under selection over time, besides the possibility of correcting eventual mistakes in the direction of selection (Van Melis *et al.*, 2001). According to Hudson and Kennedy (1985), the follow-up and the interpretation of genetic trend estimates allows monitoring the efficiency of improvement strategies and assures that the selection pressure is directed towards the traits of economic

importance, besides assisting in the definition of the selection objectives.

Therefore, the objective of the present study on Japanese quail was to evaluate the genetic trend for body weights and shank lengths for short-term divergent selection for 4 wk body weight.

MATERIALS AND METHODS

Experimental Birds were produced and raised at the experimental farm of the Faculty of Agriculture, Suez Canal University, Al-Ismailia, Egypt. The Japanese quail (*Coturnix coturnix Japonica*) base population was derived from four hatches of a random mated flock. This flock was used for subsequent divergent selection to produce the next two generations (G_1 and G_2). Marked eggs for their respective pen number were collected daily.

Management of eggs (before and during incubation), hatched chicks and adult birds was carrying out as described by Badawy *et al.* (2010).

Selection and mating methods:

The topmost 2/3 ranked birds for 4-wk body weight was considered the high body weight line while the lowest 1/3 ranked ones was considered the low body weight line. At 5 wk of age, each female was assigned at random to a non-sib male from the same category.

Studied traits:

Individual body weights (BW) were recorded at hatch, 2, 4, 6, 8 wk of age. However, right shank length was measured only at 6 and 8 wk of age. Hatched chicks was assembled into two classes, the first incubation period ($U-17$) was for chicks hatched up to 17 days of incubation while the second one ($M-17$) was for those hatched later (from 17th till 19th days of incubation).

Statistical analysis:

Data were corrected for hatch effect by fitting least squares constants (Harvey, 1979). All factors' effects affecting the studied traits were analyzed using model

(3) of Mixed Model Least Square and Maximum Likelihood procedure (Harvey, 1990). Significance between hatches' and generations' means were applied by Duncan's multiple rang test (Duncan, 1955) using (SAS Institute, 1998). The following general model was used with few modifications according to the application:

$$Y_{ijkl} = \mu + L_i + S_j(L)_{ij} + F_k + e_{ijkl}$$

Where:

- Y_{ijkl} = The observation on $ijkl^{\text{th}}$ bird.
 μ = The overall mean for the trait under consideration.
 L_i = The fixed effect of the lines tested.
 S_j = The random nested effect of j^{th} parent within the fixed effect L_i
 e_{ijkl} = The random error of observations.

For the studied traits of the first and second generations, the fixed effect (L_i) define as the fixed effect of the line of selection, while the fixed effect (F_k) of the other factors included as a HIS combination as follows:

- H = The fixed effect of hatch.
 S = The fixed effect of sex.
 I = The fixed effect of incubation period, two levels of incubation periods: ($U-17$) = Incubation period up to 17 days, and ($M-17$) = Incubation period for more than 17 days till 19 days of incubation.

Genetic parameters:

Heritability (h^2):

Heritability (h^2) of the selected traits was obtained by dividing the cumulative response (R) by the cumulative selection differentials (S) across the generations. Genetic (r_A) correlation coefficients between studied traits were calculated according to Falconer and Mackay (1996).

$$r_A = \frac{Cov_{(xy)}}{\sqrt{Var_{(x)} \cdot Var_{(y)}}}$$

Where:

- r_A = The Additive genetic correlation coefficient between x and y .
 $Cov_{(xy)}$ = The sire covariance between traits x and y .
 $Var_{(x)}$ = The sire variance components of trait x .
 $Var_{(y)}$ = The sire variance components of trait y .

The genetic trend for the body weights was estimated by regressing of average breeding values of birds on generations of selection (G), incubation Period (Inc) and lines selected (L). The average genetic trend was estimated using SAS software (SAS Institute, 1998) to determine genetic development in the population for all traits studied.

RESULTS AND DISCUSSIONS

Heritability (h^2):

Heritability estimates of hatch weight seemed to be inflated, (more than 1.0), out the reasonable range. The confounding revealed by the unusual heritability value of hatch body weight may be arose from the method of analysis or chick being so light and the sensitivity of balances used to measure weight are not fairly appropriate to account for the variances at this age and/or due to the correlated huge maternal effect (unabsorbed yolk sac). Adeogun and Adeoye (2004) reported that heritability estimate during early life stages in quail were greater than unity and accounted it to uncontrolled effects. Such a conclusion has not been reached at by Michalska (1992); Bahie El-Deen (1994); Bahie El-Deen and El-Sayed (1999); El-Fiky (1991); Samuel and Cheng (1994); Shalan (1998); and Tawefeek (1995& 2001), who reported heritability values for hatch weight though high but lower than unity. Resende *et al.*, 2005 avoided the Henderson III methodology. They analyzed the traits one by one (unitrait) but using MTGSAM (Multiple -Trait Gibbs Sampler Animal Model methodology; Van Tassel and Van Vleck, 1995), and they found the heritability of hatch body weight to be 0.33. There is possibly a great correlated influence of the environmental effect on hatch body weight, this effect decreased with advance of age. The fact that hatch's weight is a function and being limited by egg's weight probably influence the resultant outputs.

However, there is a trend of heritability values to be intermediate, if hatch figures are excluded, and show a general curve-linear relationship with age, tends to decrease with age to a given age and restore upward rising thereafter. Comparable heritability ranges has been reported by Baumgartner, 1993, Adeogun and Adeoye 2004, Marks and Lepore 1968, Tawefeek 1995 & 2001, Samuel and Cheng 1994, Bahie El-Deen 1994 and Bahie El-Deen and El-Sayed 1999. However, Shalan (1998) reported lower heritability values for body weight from 2 to 6 wk of age.

Values of h^2 revealed also that individual selection in the HL population would be more efficient either at very early or very late ages. However, selection at early ages might be more advantageous because of its drawback on the generation interval and economic concerns.

Conversely, Heritability estimates ($h^2 \pm SE$) of right shank length as an example of conformation trait for whichever of the HL, LL, G_1 and G_2 at 6 and 8 wk of age are relatively high (Table 1).

Genetic correlation coefficients (r_A):

Genetic correlation values between body weight measurement at different ages for both HL and LL were found to be high (ranged from 0.48 to 0.94) for HL, and vary from moderate to high for LL. It is visible that these figures becoming diminish as the time difference of the evaluated ages increase. Consequently, the lowest values of r_G were between BW_0 and body weight at later ages (Table 2). Genetic correlations arise from the evaluated traits are affected by some shared loci and genes (permanent) and/or carried on same chromosome

with small crossing-over distance (temporary). It is expected that body weights as a composite trait and at different juvenile ages to be influenced by a number of shared loci and these numbers are getting lesser as those birds approach puberty. It appears that the decreasing number of shared loci with the increasing age is responsible for these genetic correlations getting gradually slighter.

Genetic correlation values for both G_1 and G_2 generations ranged from intermediate to high value and reduced yet again by the advance of age. The most deprived values of r_G were between BW_0 and body weight at later ages harmonizing the conclusions arrived at for HL and LL. (Table 2). The current results were

found to be in agreement with those reported by Adeogun and Adeoye (2004); Aref (2002); Abdellatif (1999); and Bahie El-Deen (2002); and Bahie El-Deen and El-Sayed (1999), while in contrast with those reported by El-Full *et al.* (2001a&b); Sharaf (1992); Sefton and siegel (1974); and shalan (1998).

Genetic correlation coefficients between body weights and right shank length made clear that correlation coefficients between body weights and shank length ranged from moderate to high values (Table 3). These results were in harmony with those of Nestor *et al.* (1967), Havenstein *et al.* (1988), and Aref (2002) and even with those obtained on turkey by Zaky and Amin (2007).

Table (1): Heritability estimates ($h^2 \pm SE$) of body weight (BW) and right shank length (RSL) traits for the studied population (high and low selected lines; first and second generations) of Japanese quail from hatch to 8 wk of age.

Traits	HL	LL	G_1	G_2
BW_0	1.30±0.04	1.34±0.06	1.19±0.07	1.45±0.07
BW_2	0.46±0.05	0.39±0.07	0.44±0.08	0.53±0.10
BW_4	0.35±0.05	0.33±0.07	0.49±0.08	0.29±0.09
BW_6	0.38±0.05	0.35±0.07	0.49±0.08	0.42±0.09
BW_8	0.44±0.05	0.39±0.07	0.47±0.08	0.56±0.10
RSL_6	0.73±0.05	0.79±0.07	0.61±0.09	0.58±0.10
RSL_8	0.87±0.05	0.90±0.07	0.70±0.09	0.75±0.10

$BW_0, BW_2, BW_4, BW_6, BW_8$ = Body weight at hatch, 2, 4, 6, 8 wk of age, respectively. RSL_6, RSL_8 = Right shank length at 6, 8 wk of age, respectively. HL and LL = the lines selected for high and low 4 wk of age body weight, respectively. G_1 and G_2 = the first and the second generations, respectively.

Table (2): Genetic correlation ($\pm SE$) among body weight (BW) traits for the studied population (high, HL and low, LL selected line; first, G_1 and second, G_2 generation) of Japanese quail from hatch to 8 wk of age.

Traits		HL	LL	G_1	G_2
BW_0	BW_2	0.50±0.06	0.55±0.08	0.65±0.09	0.51±0.11
	BW_4	0.48±0.07	0.58±0.09	0.54±0.10	0.44±0.14
	BW_6	0.54±0.06	0.64±0.08	0.56±0.09	0.42±0.13
	BW_8	0.54±0.06	0.67±0.08	0.52±0.10	0.44±0.12
BW_2	BW_4	0.94±0.02	0.96±0.03	0.94±0.04	0.97±0.05
	BW_6	0.77±0.05	0.70±0.08	0.84±0.07	0.81±0.07
	BW_8	0.59±0.07	0.48±0.11	0.75±0.10	0.70±0.10
BW_4	BW_6	0.92±0.02	0.88±0.04	0.94±0.03	0.95±0.03
	BW_8	0.74±0.06	0.61±0.10	0.77±0.09	0.88±0.08
BW_6	BW_8	0.93±0.03	0.90±0.04	0.95±0.04	0.95±0.04

$BW_0, BW_2, BW_4, BW_6, BW_8$ = Body weight at hatch, 2, 4, 6, 8 wk of age, respectively. RSL_6, RSL_8 = Right shank length at 6, 8 wk of age, respectively. HL and LL = the lines selected for high and low 4 wk of age body weight, respectively. G_1 and G_2 = the first and the second generations, respectively.

Table (3): Genetic correlation ($\pm SE$) between body weight traits and right shank length for the studied population (high and low selected line; first and second generation) of Japanese quail from hatch to 8 wk of age.

Traits		HL	LL	G_1	G_2
BW_0	RSL_6	0.34±0.06	0.35±0.08	0.46±0.09	0.25±0.13
	RSL_8	0.32±0.06	0.32±0.08	0.43±0.10	0.23±0.12
BW_2	RSL_6	0.45±0.07	0.35±0.10	0.71±0.09	0.60±0.11
	RSL_8	0.42±0.07	0.31±0.11	0.67±0.10	0.55±0.12
BW_4	RSL_6	0.54±0.07	0.43±0.10	0.71±0.08	0.72±0.11
	RSL_8	0.51±0.07	0.39±0.11	0.68±0.10	0.66±0.12
BW_6	RSL_6	0.66±0.05	0.58±0.08	0.80±0.06	0.75±0.08
	RSL_8	0.66±0.06	0.58±0.09	0.84±0.07	0.69±0.10
BW_8	RSL_6	0.69±0.05	0.67±0.07	0.73±0.08	0.76±0.07
	RSL_8	0.70±0.05	0.70±0.07	0.84±0.07	0.72±0.08

$BW_0, BW_2, BW_4, BW_6, BW_8$ = Body weight at hatch, 2, 4, 6, 8 wk of age, respectively. RSL_6, RSL_8 = Right shank length at 6, 8 wk of age, respectively. HL and LL = the lines selected for high and low 4 wk of age body weight, respectively. G_1 and G_2 = the first and the second generations, respectively.

Epigenetic trends (EGT):

Figures 1 through 4 illustrate genetic and epigenetic trends for body weight from hatch through 8 wk of age as affected by generation of selection (G); lines selected (High and Low) within generations incubation period (U-17 and M-17). From the overall-genetic trend of the whole tested quail population, estimated body weight genetic trends, of breeding-values' means, expressed as deviations from its overall BLUP mean, plotted against generations (Figure 1). Results of the body weight of G₁ showed positive genetic trend only at 8 wk of age, whilst they tend to be negative for the other body weight traits. However, estimated tend seemed to be higher in G₂ at the 4 wk, (selected trait), and 6 wk of age.

As regard to body weight epigenetic trends, plotted against the selected lines (as an example of genotype-environment interaction; Figure 2), data of the heavy line revealed that body weight of the tested quail populations followed the same pattern reported for the whole results with a tendency of the second generation to give higher results and consequently higher response to selection from a genetic point of view. However

when the selection of the 4 wk body weight was applied in the negative direction (low line, figure 2), results were inconsistent with a tendency to hinder artificial selection with some sort of natural selection.

However, breeding-values regressed against incubation period within generation (Figure 3), body weight of the tested quail populations' data of the 17 days incubation period tended to be positive and higher in G₂ than that in G₁ and accordingly higher response to selection in the G₂ from a genetic point of view.

However for those chicks hatched later (Figure 2), when the selection of the 4 wk body weight was applied, results were generally in the negative directions. This epigenetic trend of the late hatched chicks revealing adverse response may indicate that birds intended for breeding should be from the early hatched chicks since it appears that they are able to respond better to selection judging from body weight of Japanese quail. Therefore this trait should be considered in selection indices to produce birds capable of better selection response.

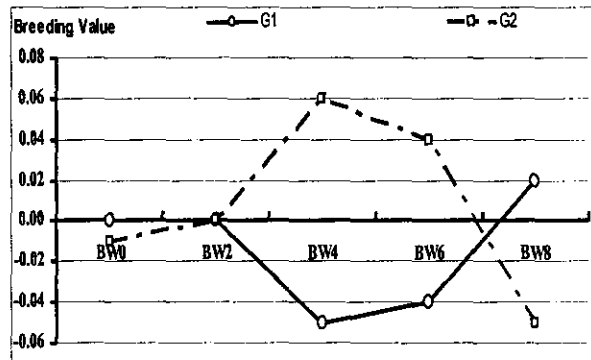


Figure (1): Overall Genetic trend for body weight (BW) of Japanese quail, as affected by generation of selection (G).

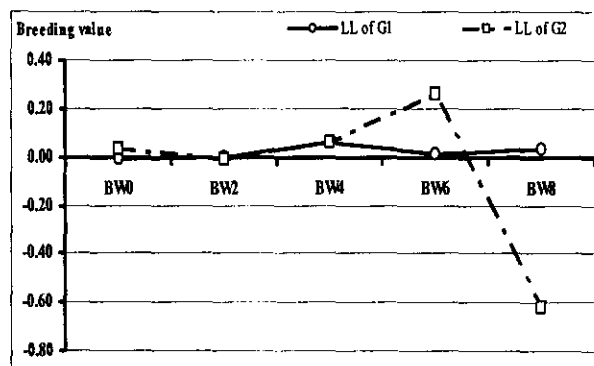
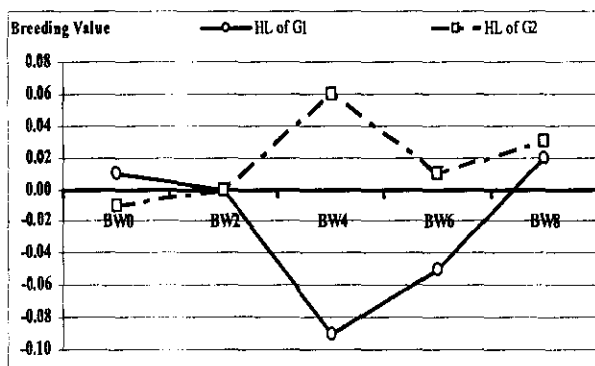


Figure (2): Epigenetic trend for body weight of the two divergent Japanese quail lines as affected by generation (G).

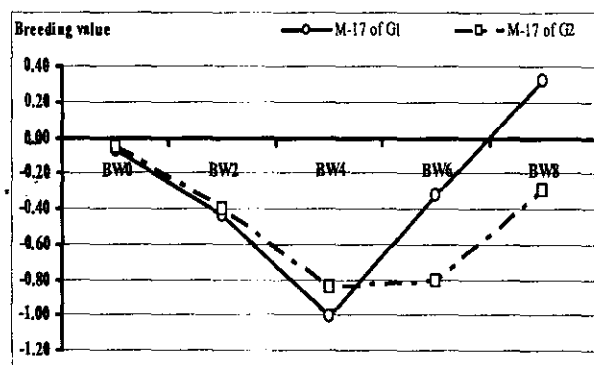
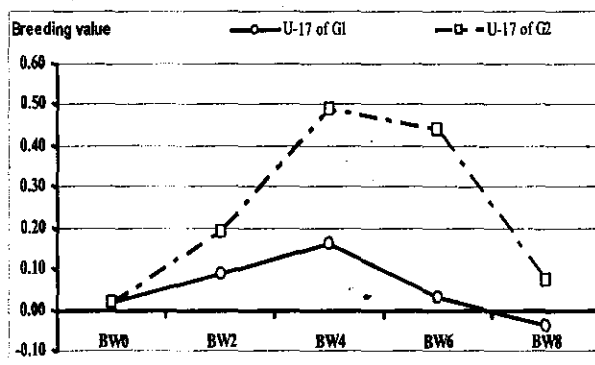


Figure (3): Epigenetic trend for body weight of the two Japanese quail incubation periods as affected by generation.

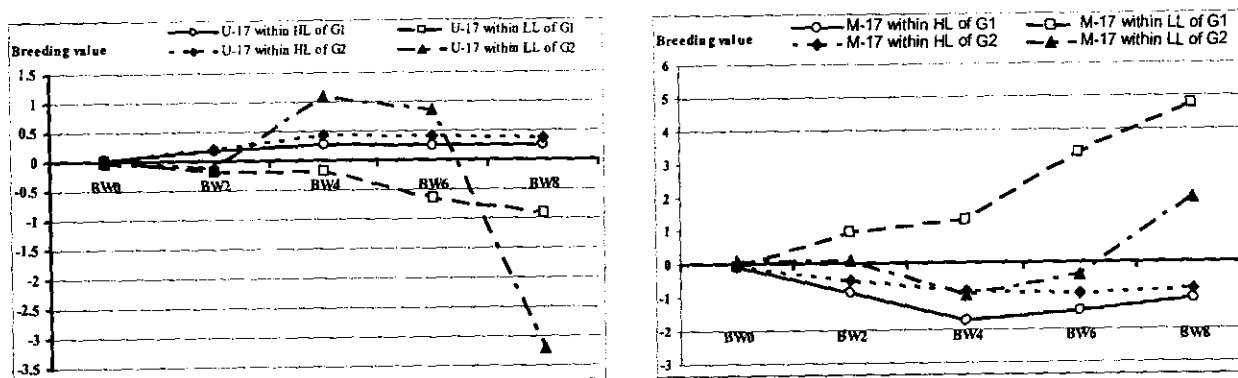


Figure (4): Epigenetic trend for body weight of the two Japanese Quail incubation periods within line as affected by generation (G).

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التقييم الوراثي لبيانات السمان الياباني بعد جيلين من الانتخاب في اتجاهين متضادين لصفة وزن الجسم عند عمر ٤ أسابيع

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قسم الإنتاج الحيواني والثروة السمكية - كلية الزراعة - جامعة قناة السويس - ٤١٥٢٢ الإسماعيلية - مصر

هدفت هذه الدراسة إلى تقييم عشائر السمان الياباني بعد جيلين من الانتخاب في اتجاهين متضادين لصفة وزن الجسم عند عمر ٤ أسابيع وذلك من خلال تقدير المقاييس الوراثية وتقييم الاتجاه الوراثي لصفتي وزن الجسم وطول الساق عند أعمار مختلفة. استخدمت صفة طول الساق لأن الانتخاب في وزن الجسم ربما ينعكس إلى ضعف في الأرجل وما يسببه ذلك من فقد إقتصادي كما هو الحال في معظم الطيور التي تعرضت للانتخاب الصناعي. تراوحت قيم المكافئ الوراثي لصفات وزن الجسم من المتوسطة إلى عالية وأظهرت القيم المتحصل عليها أن الانتخاب لأفراد الخط المنتخب لوزن الجسم العالي ربما يكون أكثر كفاءة في الأعمار المتأخرة عنه في الأعمار المتقدمة وما يعكسه ذلك من طول فترة الجيل وتكلفة الانتخاب والإستبعاد. وهذه النتائج تتفق وبيولوجية الطيور لإحتياجها في حياتها الطبيعية إلى إنخفاض وزن الجسم لتساعده على الطيران والهجرة كما يحدث في السمان البري. كما وجدت قيم المكافئ الوراثي لصفة طول الساق عالية نسبياً مما يعكس أن الانتخاب الفردي يمكن أن يتم تطبيقه في فترة مبكرة من حياة السمان. وجدت قيم الارتباط الوراثي بين صفات وزن الجسم عالية في حين أن قيم معامل الارتباط الوراثي بين صفات وزن الجسم وصفات طول الساق وجدت كانت متوسطة وغالباً غير معنوية. الاتجاه الوراثي لصفة وزن الجسم في عشيرة السمان المنتخبة ظهرت موجبة فقط عند عمر ٤ أسابيع بينما ظهرت سالبة غالباً في باقي الأعمار وأظهر الاتجاه الوراثي أن الكتاكيت الفاقسة مبكراً نسبياً تكون لها استجابة أوضح من تلك الفاقسة متأخراً وأن هذه الصفة يجب الانتخاب لها في قطعان التربية لتحسين العائد من الانتخاب.