Genetic Evaluation and Trends of Japanese quail Data Selected for 4-wk Body Weight

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Abstract: The present study aimed to estimate the genetic parameters and evaluate the genetics trend of body weight traits and right shank length of Japanese quail data selected two generation for 4-wk body weight. Body weights heritability (h²) estimates ranged from moderate to high and revealed that selection in 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 between 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 wks of age, whilst for the other body weight (non-selected for traits) trend to be negative. Estimated genetic trend also found to be higher in the second generation from the 4th 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, 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 considerable 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 follow the results so that it is possible to evaluate their development, as well as to make effective adjustments, aimed at the optimization of 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 of as a result of short-term divergent selection for 4 wks body weight.

MATERIALS AND METHODS

Experimental Birds were produced and raised at the experimental farm of Faculty of Agriculture, Suez Canal University, Al-Ismailia. 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 (G₁ and G₂). 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 (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 wks 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 (U-17) was for those chicks hatched up to the end of the 17 days from the beginning of incubation process while the second one (M-17) was for those hatched later (till 19 days form the beginning of incubation process).

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). Significant between hatches and generations means were applied by Duncan’s multiple rang test (Duncan, 1955) using SAS (1998). The following general model was used with few modifications according to the application:

\[ Y_{ijkl} = \mu + L_i + S_j(L_j) + F_k + e_{ijkl} \]

Where:
- \( Y_{ijkl} \) = The observation on ijkl\textsuperscript{th} bird.
- \( \mu \) = 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\textsuperscript{th} sire within the fixed effect L.
- \( e_{ijkl} \) = The random error of observations.

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

\( H_k \) = The fixed effect of hatch.
\( S_t \) = The fixed effect of sex.
\( I_m \) = The fixed effect of incubation period.

There are two different studied incubation periods: (U-17) = Incubation period up to 17 days, and (M-17) = Incubation period for more than 17 days.

Genetic parameters:

Heritability (h\textsuperscript{2}):

Heritability (h\textsuperscript{2}) of the selected traits was obtained by dividing the cumulative response (R) by the cumulative selection differentials (S) across the generations. Genetic (r\textsubscript{xy}) correlation coefficients between studied traits were calculated according to Falconer (1996).

\[ r_A = \frac{Cov(x,y)}{\sqrt{Var(x) \cdot Var(y)}} \]

Where:
- \( r_A \) = The Additive genetic correlation coefficient between x and y.
- \( Cov(x,y) \) = 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 regression 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\textsuperscript{2}):

Table (1) represents heritability estimates (h\textsuperscript{2}±SE) of body weight traits for the high (HL), low line (LL), first generation (1\textsuperscript{st} G.) and Second one (2\textsuperscript{nd} G.) from hatch up to 8 wk of age. However, heritability estimates of hatch weight seemed to be inflated (more than 1.0) out the expected range. However, there is a trend of the values of heritability 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, Twefuek 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. 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 (un-absorbed yolk sac). Adeogun and Adeoye (2004) reported that heritability estimate during early life stages in quail were greater than unity and account it to uncontrolled effects of lines, sex, and generation. Such a conclusion has not been reached at by Michaska, 1992, Bahie El-Deen 1994, Bahie El-Deen and El-Sayed 1999, El-Fiky 1991, Samuel and Cheng 1994, Shalan 1998, and Twefuek 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 (untrait) 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 weight probably influence the resultant outputs. Values of h\textsuperscript{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. Heritability estimates (h\textsuperscript{2}±SE) of right shank length for the HL, LL, 1\textsuperscript{st} G., and 2\textsuperscript{nd} G. at 6 and 8 wk of age are presented in Table (1). Aside from being age and other effects studied, these results show that heritability values of shank length (SL) are relatively high, same conclusions can also apply in case low body weight selected line.

Genetic correlation coefficients (r\textsubscript{xy}):

Genetic correlation values for both HL and LL were found to be high (ranged from 0.48 to 0.94) for HL, and ranged from moderate to high level values for LL, and it seemed that they diminish as the time difference of the evaluated ages increases, in the same time the lowest values of r\textsubscript{xy} were between BW\textsubscript{0} and body weight at later ages drive our explanation of BW\textsubscript{0} being affected mainly by egg weight (Table 2).

Genetic correlation values for both first and second generations ranged from intermediate to high value and reduced by the advance of age. The most deprived values of r\textsubscript{xy} were between BW\textsubscript{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) but with those reported by El-Full et al. (2001a&b); Sharaf (1992); Sefton and siegel (1974); and shalan (1998).

Tables (3) representing genetic correlation coefficient between body weights and right shank length. Results made clear that correlation coefficients between body weights and shank length ranged from moderate to high value level. 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 ($h^2$±SE) of body weight and right shank length traits for the studied population (high and low selected line; first and second generation) of Japanese quail from hatch to 8 wk of age.

<table>
<thead>
<tr>
<th>Traits</th>
<th>HL</th>
<th>LL</th>
<th>1st G.</th>
<th>2nd G.</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW&lt;sub&gt;0&lt;/sub&gt;</td>
<td>1.30±0.04</td>
<td>1.34±0.06</td>
<td>1.19±0.07</td>
<td>1.45±0.07</td>
</tr>
<tr>
<td>BW&lt;sub&gt;2&lt;/sub&gt;</td>
<td>0.46±0.05</td>
<td>0.39±0.07</td>
<td>0.44±0.08</td>
<td>0.53±0.10</td>
</tr>
<tr>
<td>BW&lt;sub&gt;6&lt;/sub&gt;</td>
<td>0.35±0.05</td>
<td>0.33±0.07</td>
<td>0.49±0.08</td>
<td>0.29±0.09</td>
</tr>
<tr>
<td>BW&lt;sub&gt;8&lt;/sub&gt;</td>
<td>0.38±0.05</td>
<td>0.35±0.07</td>
<td>0.49±0.08</td>
<td>0.42±0.09</td>
</tr>
<tr>
<td>RSL&lt;sub&gt;6&lt;/sub&gt;</td>
<td>0.44±0.05</td>
<td>0.39±0.07</td>
<td>0.47±0.08</td>
<td>0.56±0.10</td>
</tr>
<tr>
<td>RSL&lt;sub&gt;8&lt;/sub&gt;</td>
<td>0.73±0.05</td>
<td>0.79±0.07</td>
<td>0.61±0.09</td>
<td>0.58±0.10</td>
</tr>
</tbody>
</table>

Table (2): Genetic correlation ($r$±SE) between body weight traits for the studied population (high and low selected line; first and second generation) of Japanese quail from hatch to 8 wk of age.

<table>
<thead>
<tr>
<th>Traits</th>
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<tr>
<td>BW&lt;sub&gt;0&lt;/sub&gt;</td>
<td>BW&lt;sub&gt;4&lt;/sub&gt;</td>
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<tr>
<td>BW&lt;sub&gt;4&lt;/sub&gt;</td>
<td>0.48±0.07</td>
<td>0.58±0.09</td>
<td>0.54±0.10</td>
<td>0.44±0.14</td>
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<tr>
<td>BW&lt;sub&gt;6&lt;/sub&gt;</td>
<td>0.54±0.06</td>
<td>0.64±0.08</td>
<td>0.56±0.09</td>
<td>0.42±0.13</td>
</tr>
<tr>
<td>BW&lt;sub&gt;8&lt;/sub&gt;</td>
<td>0.54±0.06</td>
<td>0.67±0.08</td>
<td>0.52±0.10</td>
<td>0.44±0.12</td>
</tr>
<tr>
<td>BW&lt;sub&gt;2&lt;/sub&gt;</td>
<td>BW&lt;sub&gt;4&lt;/sub&gt;</td>
<td>0.94±0.02</td>
<td>0.96±0.03</td>
<td>0.94±0.04</td>
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<td>BW&lt;sub&gt;6&lt;/sub&gt;</td>
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<td>0.81±0.07</td>
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<td>BW&lt;sub&gt;8&lt;/sub&gt;</td>
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<td>0.61±0.10</td>
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<td>0.88±0.08</td>
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<tr>
<td>BW&lt;sub&gt;6&lt;/sub&gt;</td>
<td>BW&lt;sub&gt;8&lt;/sub&gt;</td>
<td>0.93±0.03</td>
<td>0.90±0.04</td>
<td>0.95±0.04</td>
</tr>
</tbody>
</table>

Table (3): Genetic correlation ($r$±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.

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<td>RSL&lt;sub&gt;6&lt;/sub&gt;</td>
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<td>0.35±0.10</td>
<td>0.71±0.09</td>
</tr>
<tr>
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<td>0.66±0.05</td>
<td>0.58±0.08</td>
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<td>BW&lt;sub&gt;0&lt;/sub&gt;</td>
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<td>BW&lt;sub&gt;2&lt;/sub&gt;</td>
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<td>0.84±0.07</td>
</tr>
</tbody>
</table>
Epigenetic trends (EGT):

Genetic and epigenetic trends for body weight from hatch through 8 wks of age as affected by generation of selection (G); lines selected (High and Low) within generations and incubation period (U-17 and M-17) within generations were illustrated in Figures (1 through 4). 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, regressed against generations (Figure 1) showed that Body weight of the tested quail population have positive genetic trend only at 4 wks of age (weight selected for or selected trait) whilst for the other body weight (non-selected for traits) they tend to be negative. However, genetic trend estimated tend also to be higher in the second generation from the 4th 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.

As regard to the estimated body weight epigenetic trends, of breeding-values' means, expressed as deviations from its overall BLUP mean, regressed against lines selected (as an example of genotype-environment interaction; Figure 2), data of the heavy line revealed that body weight of the tested quail populations have rarely positive genetic trend with a tendency of the second generation to give higher results and consequently higher response to selection from a genetic point of view. However, estimated genetic trend tend also to be higher in the second generation from the 4th wk of age onwards while the reverse was true in the era before; which may mean that birds tend to get better improvement at later ages of life on the expense of that at earlier ages. However when the selection of the 4th wk body weight was applied in the negative direction (left graph-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 (Figure 2), body weight of the tested quail populations data of the 17 days incubation period revealed tended to be higher in the second generation and accordingly higher response to selection from a genetic point of view. However for those chicks hatched later (Figure 2), when the selection of the 4th wk body weight was applied, results were consistently in the negative directions except that for BW8 in the 2nd generation. This epigenetrical 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.

**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 (BW) of the two Japanese Quail lines as affected by generation of selection (G).
Figure (3): Epigenetic trend for body weight (BW) of the two Japanese quail incubation periods as affected by generation of selection (G).

Figure (4): Epigenetic trend for body weight (BW) of the two Japanese quail incubation periods within lines as affected by generation of selection (G).

REFERENCES


