Genetic parameter estimates of growth curve and reproduction traits in Japanese quail

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ABSTRACT The goal of selection studies in broilers is to obtain genetically superior chicks in terms of major economic traits, which are mainly growth rate, meat yield, and feed conversion ratio. Multiple selection schedules for growth and reproduction are used in selection programs within commercial broiler dam lines. Modern genetic improvement methods have not been applied in experimental quail lines. The current research was conducted to estimate heritabilities and genetic correlations for growth and reproduction traits in a Japanese quail flock. The Gompertz equation was used to determine growth curve parameters. The Gibbs sampling under a multi-trait animal model was applied to estimate the heritabilities and genetic correlations for these traits. A total of 948 quail were used with complete pedigree information to estimate the genetic parameters. Heritability estimates of BW, absolute and relative growth rates at 5 wk of age (AGR and RGR), $\beta_0$ and $\beta_2$ parameters, and age at point of inflection (IPT) of Gompertz growth curve, total egg number (EN) from the day of first lay to 24 wk of age were moderate to high, with values ranging from 0.25 to 0.40. A low heritability (0.07) for fertility (FR) and a strong genetic correlation (0.83) between FR and EN were estimated in our study. Body weight exhibited negative genetic correlation with EN, FR, RGR, and IPT. This genetic antagonism among the mentioned traits may be overcome using modern poultry breeding methods such as selection using multi-trait best linear unbiased prediction and crossbreeding.

Key words: genetic parameter, growth curve, reproduction trait, Gibbs sampling

INTRODUCTION

Conversion of small-scale poultry enterprises into the commercial poultry industry began during the mid-twentieth century. This is caused both by improvements in environmental conditions and breeding. Highly selected elite sire and dam purelines form the basis of today’s broiler breeding programs (Pollock, 1999). Commercial broilers are obtained as a 3-way or 4-way cross of specific closed purebreeding lines. The same genetic principles have also been applied to the minor poultry species, particularly to the genetic improvement of turkey and duck populations (Tixier-Boichard et al., 2012).

Despite its small body size, the Japanese quail has an important role in commercial production because of high egg and meat production capacity. Quail are generally reared for egg production in the Far East and Asian countries, and primarily for meat production in European and American countries. Much of the genetic improvement studies on quails have focused on early egg number or BW at fixed ages in which the phenotypic mass selection is considered. Information on quail lines selected for meat or egg production is extensive (Marks, 1990), but the data on heterosis in quail are rare (Chahil et al., 1975; Minvielle et al., 1999). Contrary to commercial broiler production, crossbreeding of highly selected lines have been rather little use in quail production.

Poultry breeding programs are aimed to improve genetic potential of chicks through selection and crossbreeding plans. Initially, realized genetic parameters in selection experiments were used in the estimation of heritabilities and genetic correlations. The estimated genetic parameters for various economic traits of Japanese quail were reported by several researchers. Heritabilities and genetic correlations of weekly BW in Japanese quail were estimated extensively by numerous researchers (Gebhardt-Henrich and Marks, 1993; Aggrey and Cheng, 1994; Marks, 1996; Kumari et al., 2009; Narinc et al., 2010a; Zerehdaran et al., 2012). Genetic parameters for early egg production and some reproductive traits were estimated by Strong et al. (1978) and Mielenz et al. (2006). Only a few studies have presented the genetic parameters for feed efficiency, growth curve parameters, and meat quality traits in

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Japanese quail (Akbas and Yaylak, 2000; Aggrey et al., 2003; Aksit et al., 2003; Narinc et al., 2010a; Narinc et al., 2013).

Genetic improvement of sire and dam lines has given poultry geneticists the opportunity to take advantage of various traits in different parental lines. When selecting females for growth traits, deteriorations in reproductive performances occur as a result of the negative genetic correlation between them (Marks, 1996). Therefore, selection programs in commercial broiler companies are based on multiple selection methods for reproduction and growth traits (Szwaczowski, 2003). This study presents the results of a research carried out in Turkey based on multiple selection methods for reproduction programs in commercial broiler companies are used to obtain the total growth occurs before it and the remainder occurring after (Grimm and Ram, 2009). The coordinates of the point of inflection, IPT and weight at inflection point (IPW), were obtained as follows (Rizzi et al., 2013):

\[
\text{IPT} = \ln\left(\frac{\beta_1}{\beta_2}\right); \quad \text{IPW} = \frac{y_t}{e^{\beta_0}}.
\]

The AGR (equation 4) is obtained from the first derivative of the Gompertz model with respect to time. On the other hand, RGR (equation 5) is defined as the unit increase in BW per unit of time.

\[
\text{AGR} = \beta_0 \beta_1 \frac{e^{\beta_2 t}}{e^{\beta_2 t}} = \beta_0 \beta_1 e^{\beta_2 t},
\]

\[
\text{RGR} = \beta_2 \left(\ln(y_t) - \ln(y_t)\right).
\]

Daily egg production of females was recorded from the day of first lay to the 20 wk of age and the total number of eggs laid (EN) by each female was computed. In total, 20,748 eggs were collected daily during the laying period of the flock, and the total eggs produced at each week were placed in a commercial incubator. At 16 of the incubation period, all eggs were broken and classified as fertile or infertile according to the macroscopic diagnosis. Fertility for each female was determined as the proportion of fertile eggs to the number of eggs set.

The descriptive statistics and Kolmogorov-Smirnov normality tests of the traits were obtained using UNIVARIATE procedure of SAS 9.3 software (SAS Institute Inc., Cary, NC). Because the normality was not held for the traits except for BW, \(\beta_0\), \(\beta_2\), and IPT, they were transformed using Box-Cox transformation (Box and Cox, 1964), which resulted in the AGR having a normal distribution. The nonparametric rank transformation (Aulchenko et al., 2007) was performed in R package (R Development Core Team, 2010) for the traits for which the Box-Cox transformation did not yield normally distributed traits.
The following linear mixed effects model was used in the analysis:

\[ y = X\beta + Zu + e, \]

where \( y \) is the vector of observations, \( \beta \) is a vector of fixed effects, and \( u \) is a vector of random genetic effects. The \( X \) and \( Z \) are known design matrices relating phenotypic records to \( \beta \) and \( u \), respectively. The \( e \) is a vector of random errors. It is assumed that

\[ y | \beta, u, R_0 \sim MVN(X\beta + Zu, R_0 \otimes I); \]
\[ u | G_0 \sim MVN(0, G_0 \otimes A), \]

where \( I \) is the identity matrix, \( A \) is the numerator relationship matrix, \( G_0 \) is the additive genetic variance-covariance matrix, and \( R_0 \) is the error variance-covariance matrix. Total number of animals in the pedigree file was 948 where 302 of them were parents without records.

A noninformative prior was assumed for the fixed effects, so that \( p(\beta) \propto \text{constant} \). The prior distributions assumed for \( G_0 \) and \( R_0 \) were inverted Wishart (IW) distributions given as follows:

\[ G_0 | v_G, V_G \sim IW(v_G, V_G), \]
\[ R_0 | v_R, V_R \sim IW(v_R, V_R), \]

where \( v_G, V_G, v_R, \) and \( V_R \) are the parameters for the prior distributions (Waldmann and Ericsson, 2006). We chose a prior by replacing the diagonal elements with 0 and the off-diagonal elements with the variances of the corresponding traits in the hyperparameters \( V_G \) and \( V_R \), and using \( v_G = v_R = 8 \).

Bayesian analyses were carried out using R package (R Development Core Team, 2010). In the implementation of the Gibbs sampling, a single sampling chain of 200,000 iterations was considered with a 20,000 cycles of burn-in period and a thinning interval of 18 cycles to obtain 10,000 samples of the parameters of interest. Heritabilities, \( h_i^2 \), and genetic correlations, \( r_{g(i'j')} \), were calculated from the posterior means of variance and covariance parameters as follows:

\[ h_i^2 = \frac{\sigma_{a_i}^2}{\sigma_{a_i}^2 + \sigma_{e_i}^2}; \]
\[ r_{g(i'j')} = \frac{\sigma_{a_{i'j'}}}{\sigma_{a_{i'j'}} + \sigma_{e_{i'j'}}}, \]

where \( i \) and \( i' \) represents the trait(s) of interest and \( \sigma_{a_{i'j'}}^2 \) and \( \sigma_{e_{i'j'}}^2 \) are the diagonal elements of \( G_0 \) and \( R_0 \) matrices, respectively. Also, \( \sigma_{a_{i'j'}} \) stands for the additive genetic covariance between the traits \( i \) and \( i' \).

## RESULTS AND DISCUSSION

### Basic Statistics

Descriptive statistics of BW, \( \beta_0 \), \( \beta_2 \), IPT, AGR, RGR, EN, and FR are presented in Table 1. Average BW at 5 wk of age (176.90 g) is in the range of 170.00 to 186.77 g and in agreement with those reported by Narinc et al. (2010a) and Sarı et al. (2010). The average \( \beta_0 \) parameter, the asymptotic limit of the weight when age \( t \) approaches infinity, of the Gompertz growth model was 233.12. Similar results have been reported by Hyankova et al. (2001) and Narinc et al. (2010a). In a selection study aiming to increase BW, Alkan et al. (2009) have reported that the \( \beta_0 \) parameter was in the range of 295 and 306. It was also reported by several researchers that the \( \beta_0 \) parameter for the quail selected for low BW ranged from 151 to 164. As is the case with any genetic improvement study, selection for the BW alters the growth of quails and their growth curve parameters (Akbas and Yaylak, 2000; Narinc et al., 2010a). In the current study, the \( \beta_2 \) parameter representing the instantaneous growth rate was estimated as 0.075. The value concerned is in agreement with the values (0.055–0.084) estimated by Akbas and Oğuz (1998), Akbas and Yaylak (2000), Alkan et al. (2009), and Narinc et al. (2010a). It was stated by various researchers that an increase in the instantaneous growth rate leads to a change in the asymptotic weight parameter, \( \beta_0 \), in the opposite direction (Akbas and Yaylak, 2000; Narinc et al., 2010a).

### Table 1. Descriptive statistics for the studied traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Mean</th>
<th>SD</th>
<th>CV</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW (g)</td>
<td>176.90</td>
<td>18.59</td>
<td>10.51</td>
<td>124.70</td>
<td>241.20</td>
</tr>
<tr>
<td>( \beta_0 )</td>
<td>233.12</td>
<td>33.42</td>
<td>14.33</td>
<td>149.67</td>
<td>331.49</td>
</tr>
<tr>
<td>( \beta_2 )</td>
<td>0.075</td>
<td>0.01</td>
<td>15.47</td>
<td>0.046</td>
<td>0.122</td>
</tr>
<tr>
<td>IPT (d)</td>
<td>17.31</td>
<td>2.50</td>
<td>14.02</td>
<td>12.28</td>
<td>26.73</td>
</tr>
<tr>
<td>AGR (g)</td>
<td>3.56</td>
<td>0.84</td>
<td>23.66</td>
<td>1.40</td>
<td>5.70</td>
</tr>
<tr>
<td>RGR (%)</td>
<td>1.90</td>
<td>0.63</td>
<td>33.15</td>
<td>0.14</td>
<td>3.56</td>
</tr>
<tr>
<td>EN (egg)</td>
<td>78.89</td>
<td>10.71</td>
<td>13.57</td>
<td>17.00</td>
<td>97.00</td>
</tr>
<tr>
<td>FR (%)</td>
<td>84.02</td>
<td>16.56</td>
<td>19.70</td>
<td>16.67</td>
<td>100.00</td>
</tr>
</tbody>
</table>

\(^1\text{BW = BW at 5 wk of age; } \beta_0 = \text{asymptotic BW parameter; } \beta_2 = \text{instantaneous growth rate parameter; AGR = absolute growth rate at 5 wk of age; RGR = relative growth rate at 5 wk of age; EN = total egg number up to 20 wk of age; FR = percentage of fertility; IPT = age at inflection point.}\)
In the present study, the IPT was found to be 17.81 d. The IPT was reported to range between 16.00 and 22.30 d (Akbas and Oguz, 1998; Narinc et al., 2010a). In our study, in agreement with Narinc et al. (2010b), the average values for AGR and RGR at 5 wk of age were 3.56/d and 1.90%, respectively. Body weights of an animal over time have a cumulative structure that prevents to distinguish the weekly variation in growth rate (Aggrey, 2003). The AGR represents the change between sequential weeks, whereas RGR is the ratio of the rate of change in BW to the achieved growth at a given age. Aggrey (2004) and Narinc et al. (2010b) have suggested that RGR is favorable in the assessment of growth under various genetic and environmental conditions.

Studies concerning the egg production of Japanese quail have been focused on the number of eggs produced in a short period of production. In the present study, the mean value of cumulative egg number (EN) up to 20 wk of age was 78.89, which is in agreement with Gildersleeve et al. (1987). The researchers found that the number of eggs produced up to 20 wk of age ranged from 69 to 80 for the control line (randomly mated for 4 generations) in a selection experiment. In another study, Drbohlav and Metodiev (1996) found that the egg production up to 150 d of age was 80.36 eggs per quail. In our study, the percentage of fertility (FR) was found to be 84.02%. Similar to our finding, El-Ibiary et al. (1966) and Marks (1990) have reported that fertility of Japanese quail ranged between 76.56 and 88.40%.

### Heritabilities

Summary statistics for the posterior distributions of heritability estimates for the studied traits are presented in Table 2. Heritability of BW at 5 wk of age was 0.36, which is consistent with the other studies where the estimates ranged from 0.35 to 0.55 (Aksit et al., 2003; Narinc et al., 2010a; Sarı et al., 2011).

The heritability estimates of the $\beta_0$ and $\beta_2$ parameters, and IPT of Gompertz growth curves were moderate (0.38, 0.40, and 0.26, respectively). Limited reports were available on the genetic parameter estimates of growth curve parameters in Japanese quail (Akbas and Oguz, 1998; Akbas and Yaylak, 2000; Narinc et al., 2010a). The heritability estimates for $\beta_0$ and weekly BW are typically similar (moderate to high). Akbas and Yaylak (2000) estimated a higher heritability (0.56) for $\beta_0$ than in the present study. Our finding for $\beta_0$ is in line with that reported by Narinc et al. (2010a) as 0.42, whereas Akbas and Yaylak (2000) estimated a low heritability of 0.18 for $\beta_0$. The heritability estimate for $\beta_2$ was similar to that presented by Akbas and Oguz (1998) and Narinc et al. (2010a), but diverged from that found by Akbas and Yaylak (2000). Akbas and Yaylak (2000) have reported moderate heritability estimates for IPT. Based on the estimated heritabilities for $\beta_0$, $\beta_2$, and IPT, one can conclude that the utilization of direct selection for the traits will provide the desired improvement. The heritability estimates for AGR and RGR (0.29 and 0.25) were moderate (Table 2). Narinc et al. (2010b) reported the heritabilities of AGR and RGR as 0.27 and 0.11 in a random-bred quail line.

In the present study, the heritability estimate for EN from the day of first lay to 20 wk of age was 0.37. Moderate estimates for heritability of the number of eggs produced on different periods of laying quail were reported, with values ranging from 0.26 to 0.36 (Strong et al., 1978; El-Fiky et al., 2000). According to numerous studies, the heritability estimate of fertility in Japanese quail is generally low, ranging from 0.07 to 0.11 (El-Fiky et al., 1994). Our finding is well in line with these reports.

### Genetic and Phenotypic Relationships

Genetic and phenotypic correlations among the traits are given in Table 3. This study revealed a strong genetic association (0.63) between BW at 5 wk of age and asymptotic BW parameter ($\beta_0$). Previous reports showed high genetic and phenotypic correlations between BW at 4, 5, and 6 wk of age and the parameter $\beta_0$ in Japanese quail (Akbas and Oguz, 1998; Narinc et al., 2010a). Akbas and Yaylak (2000) reported negative phenotypic correlations between $\beta_0$ and weights at different ages up to 4 wk of age, followed by the positive and high estimates. Genetic correlations between growth curve parameters and BW at different ages were investigated by Akbas and Yaylak (2000). In our study, genetic and phenotypic correlations among the above-mentioned traits were similar to that presented by Akbas and Yaylak (2000). Akbas and Oguz (1998) reported a high heritability for $\beta_0$ and high genetic and phenotypic correlations between $\beta_0$ and weekly BW, indicating that the parameter $\beta_0$ can be used as selection criterion to increase the BW at slaughtering. The parameter $\beta_0$ is related with mature weight; however, the poultry geneticists’ interest is the genetic improvement of BW at early ages. The current study revealed a low and negative genetic relationship between BW and $\beta_2$ ($-0.11$). In addition, $\beta_0$ and $\beta_2$ were also highly negatively correlated ($r_g(\beta_0\beta_2) = -0.76, r_p(\beta_0\beta_2) = -0.73$).

### Table 2. Posterior summary statistics of heritability estimates

<table>
<thead>
<tr>
<th>Trait</th>
<th>Heritability</th>
<th>SD</th>
<th>95% HPDI</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW</td>
<td>0.36</td>
<td>0.02</td>
<td>0.24 to 0.49</td>
</tr>
<tr>
<td>$\beta_0$</td>
<td>0.38</td>
<td>0.02</td>
<td>0.31 to 0.46</td>
</tr>
<tr>
<td>$\beta_2$</td>
<td>0.40</td>
<td>0.01</td>
<td>0.33 to 0.48</td>
</tr>
<tr>
<td>IPT</td>
<td>0.26</td>
<td>0.02</td>
<td>0.21 to 0.31</td>
</tr>
<tr>
<td>AGR</td>
<td>0.29</td>
<td>0.03</td>
<td>0.23 to 0.35</td>
</tr>
<tr>
<td>RGR</td>
<td>0.25</td>
<td>0.01</td>
<td>0.21 to 0.31</td>
</tr>
<tr>
<td>EN</td>
<td>0.37</td>
<td>0.02</td>
<td>0.29 to 0.46</td>
</tr>
<tr>
<td>FR</td>
<td>0.08</td>
<td>0.03</td>
<td>0.05 to 0.10</td>
</tr>
</tbody>
</table>

1BW = BW at 5 wk of age; $\beta_0$ = asymptotic BW parameter; $\beta_2$ = instantaneous growth rate parameter; IPT = age at inflection point; AGR = absolute growth rate at 5 wk of age; RGR = relative growth rate at 5 wk of age; EN = total egg number up to 20 wk of age; FR = percentage of fertility; HPDI = 95% highest posterior density interval.
These estimates were similar to those reported by Akbas and Oguz (1998) and Akbas and Yaylak (2000). This is the fact that an increase in the asymptotic BW results in a decrease in the $\beta_2$ parameter, which denotes the average rate of maturing.

According to Table 3, there was a negative and moderate genetic correlation between BW and IPT ($-0.38$). This result is in good agreement with the estimates of Mignon-Grasteau et al. (2000) who found a strong negative genetic relationship between IPT and BW at 8 wk of age ($-0.60$) in chicken. In the Gompertz growth model, the IPT is inversely related to the instantaneous growth rate, $\beta_2$. As expected, in the present study, a strong and negative genetic relationship ($-0.81$) between IPT and $\beta_2$ was obtained.

Body weight showed a positive and moderate genetic correlation with AGR, whereas its correlation with RGR was negative and lower. To our knowledge, there are no studies reported on the genetic correlations between the BW and AGR-RGR traits. In a previous study on quail lines selected for high (HG) and low (LG) relative growth rate during the early age, Hyankova and Novotna (2007) reported that the selection caused a decrease in BW for the first 4 wk in the HG line (Hyankova et al., 2001). Aggrey (2004) reported that the long-term selection for high 4-wk BW has resulted in higher relative growth rates for the first 2 wk compared with quail from the low line. These selection studies indicated the possible existence of negative relationships between BW and RGR.

Genetic correlation between BW and EN was $-0.27$ (Table 3). Similarly, Kumari et al. (2009) reported that the genetic correlations between BW at 5 wk of age and egg yields up to 12, 16, and 20 wk of age as $-0.12$, $-0.12$, and $-0.16$, respectively. In a previous study in Japanese quail, Mielzen et al. (2006) reported an estimate of 0.07 for genetic correlation between BW at 6 wk of age and the egg production from 42 to 200 d of age. However, there are studies putting forward that there is a negative genetic correlation between BW and egg yield in major poultry species (Besbes et al., 1992; Nestor et al., 2000). The present study revealed a negative genetic relationship between BW and FR, with an estimated genetic correlation of $-0.13$. To our knowledge, no existing research addresses the genetic correlation between BW and FR traits in Japanese quail. On the other hand, Marks (1990) reported that the long-term selection for high BW resulted in a decrease in fertility of quail, indicating the existence of a negative genetic correlation between the traits. A negative genetic correlation between BW and FR was reported by some researchers in chicken and turkey (Barbato et al., 1998; Nestor et al., 2000).

The EN has a negative genetic correlation with RGR ($-0.41$). Selection for high slaughter weight not only causes a decrease in relative growth rates at early ages but also a decrease in the age at sexual maturity (Camici et al., 2002). In a previous study in Japanese quail, Marks (1990) found that an increase in BW resulted in early sexual maturity. These results together indicate that the earlier the age at sexual maturity, the higher the number of eggs from the day of first lay to 20 wk of age. In the present study, the genetic and phenotypic correlations between FR and RGR were low and negative ($-0.11$ and $-0.07$). To our knowledge, there are no studies reporting the genetic correlation between FR and RGR in Japanese quail. On the other hand, Hyankova and Novotna (2007) reported that the selection for relative growth rate caused a change in growth of gonads. Our study revealed a strong genetic correlation between FR and EN (0.83), which is the only report on the genetic relationship of these traits in Japanese quail. It is well known that the genetic correlation between fertility and egg production is positive and high in galliforms (Barbato et al., 1998).

The main objective of most breeding programs is to improve traits of economic importance. For this purpose, dam lines are selected intensively for higher growth rate and egg production, whereas the sire lines are selected for production traits (Tixier-Boichard et al., 1998).
al., 2012). In our study, slaughter weight (i.e., the BW at 5 wk of age) was considered the main trait to be improved in a meat type dam line. High heritability estimate of EN suggested that the reproduction trait may be effectively used in the multi-trait selection of dam line due to its high correlation with FR. In addition, it can be concluded that utilization of growth curves of quail can improve the success of selection study. The use of $\beta_0$ parameter may have unexpected effects, particularly for quail. Furthermore, RGR may be the choice of selection criterion rather than AGR because of its cumulative nature. The use of RGR as selection criterion will also lead to an improvement in IPT due to their strong genetic relationship.

The negative genetic correlations exhibited between BW and each of EN, FR, RGR, and IPT may be overcome by modern poultry breeding methods such as selection via multi-trait best linear unbiased prediction and crossbreeding. It is also known that, more accurate genetic evaluation can be performed by using multi-trait best linear unbiased prediction, which uses the all available information from several correlated traits as well as records of all relatives.

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