# Single-Trait Bayesian Analysis of Some Growth Traits in Japanese Quail

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## ABSTRACT

The aim of this study was to estimate the heritability for some growth traits of Japanese quail through the estimation of variance components by Bayesian methodology. For this purpose, 340 progenies of 34 sires were used. Live weight (LW42) and absolute and relative growth rates at 42 days of age (AGR42 and RGR42, respectively) were submitted to single-trait analysis under a sire model. A software (package MCMCglmm) was used for the estimations, and a single chain with 65,000 rounds was run for each trait with a thinning interval of 50. Burn-in was set at 15,000 and inferences were built on posterior samples of 1,000 draws for each trait. All marginal posterior densities were unimodal and marginal posterior distributions of sire variance are slightly skewed to the right. The results of the analyses showed high, moderate, and low heritability of LW42, AGR42, and RGR42, respectively.

## INTRODUCTION

The main contributions on genetic improvement of Japanese quail have been made in the last decades, particularly during the last 30 years. However, most of these studies have concentrated on live-weight at fixed ages, especially 35 and 42 days of age, or on the number of eggs produced. On the other hand, in modern poultry breeding, new traits related to meat yield are of interest. Meat quality traits (pH, color, tenderness, etc.) and body conformation, which are not yet considered in quail breeding, are used in meat-type chicken breeding (Remignon & Le Bihan-Duval, 2003). Recently, alternative selection criteria have been investigated to increase the efficiency of meat production, such as direct selection for low body fat content or feed conversion ratio or, accompanying these two criteria, selection on the shape of growth curve (Akbas & Yaylak, 2000; Hyankova *et al.*, 2001). There are some studies proposing that the use of absolute and relative growth rates (AGR and RGR, respectively) derived from fitted growth curves, may affect the achievement of the selection goal (Hyankova *et al.*, 2001; Aggrey, 2004). AGR is the change in live weight per unit of time, whereas RGR is the ratio of the rate of change in body weight required to achieve growth goal at a given age (Aggrey, 2004).

Geneticists have mostly been focused on exposing the underlying genetic structure of the traits which are quantitative in nature and show a great variability. Heritability, as a measure of the response rate of the trait under selection, is one of the most important genetic parameters that measures the genetic variability caused by genetic differences among individuals out of the total variability (Kumar *et al.*, 2004). There are two main approaches to estimate heritability: one based on intra-sire regression of offspring on dam (parent-offspring regression) and

the other based on variance components of full-sib or half-sib analysis. The accuracy of the estimates of variance components is directly related with the choice of data, method, and model (Misztal, 1990).

Methods used to estimate variance components date back from Fisher's study on the inheritance of continuous traits, after which several methods have been developed (Robinson, 1987; Searle *et al.*, 1992). Henderson's (Henderson, 1953) ANOVA-based methods have been widely used until the study of Hartley and Rao (Hartley & Rao, 1967) on ML method, which became less popular after Petterson and Thompson (Patterson & Thompson, 1971) have proposed REML method of estimation. A problem with ANOVA-based methods is that they may give a negative estimate of variance components. On the other hand, ML and REML estimations are non-negative, but biased, whereas integral estimates based on the asymptotic distribution of REML may include negative values (Lin & McAllister, 1984; Gianola & Foulley, 1990).

The Bayesian method of estimation is an alternative to the above-mentioned methods and its strengths have been advocated by several researchers from various disciplines, including animal science (Wang *et al.*, 1994; Sorensen *et al.*, 1994; Firat, 1996a; Van Tassell & Van Vleck 1996). Firat (1996b) described the application of Gibbs sampling using conjugate and non-conjugate prior specifications under a single-trait sire model. From the Bayesian point of view, prior knowledge about the unknown parameters is formally incorporated into the estimation process by assigning prior distributions to these parameters and inferences are derived on posterior distributions of the parameters (Box & Tiao, 1973; Firat, 1996a). Bayesian methods, as generally referred to Markov Chain Monte Carlo (MCMC) methods, attempt to simulate direct draws from distributions and recently became popular due to the developments in computer technology and flexible software programs.

This study aimed at estimating the heritability of some growth traits of Japanese quail by the estimation of variance components via Bayesian methodology.

## MATERIAL AND METHODS

Birds in this study were managed according to the regulations of the European Convention for the Protection of Animals kept for Farming Purposes.

The present experiment was conducted at the Poultry Breeding Unit, Animal Science Department, Faculty of Agriculture, Akdeniz University, Turkey. Birds were housed in individual cages during the experiment. A sex ratio of 1 male to 3 female was used for mating in the parent stock. In total, 340 progenies of 34 sires were used in the study. The number of chicks per sire was fixed at 10 and experimental birds were randomly selected from 643 fully-pedigreed Japanese quail chicks under this condition. Eggs obtained from individual parent cages were incubated at a temperature of 37.5 °C and 55% relative humidity for the first 14 days. They were then transferred to the hatcher located in the bottom of the same incubator individually, and maintained at 37 °C and 70% relative humidity until hatching. Chicks were wing-banded on the first day before being transferred to growing battery cages. They were reared as straight-run flocks under standard brooding temperatures. Birds were fed with a starter feed containing 240 g protein/kg and 12 MJ/kg metabolizable energy for the first 21 days, and then with a grower feed containing 200 g protein/kg and 11.8 MJ/kg metabolizable energy until 42nd days of age. Feed and water were supplied *ad libitum*.

In this study, live weight (LW42) and absolute and relative growth rates (AGR42, RGR42) at 42 days of age were the traits of interest. Therefore, a preliminary step was necessary to estimate the AGR42 and RGR42 of each animal. First, the following Gompertz non-linear model was fitted to the weekly live weight measurements of each bird from hatching to 42 days of age using SAS 9.2 software NLIN procedure (SAS Institute Inc., 2009):

$$y_j = \beta_0 \times \exp\left(-\beta_1 \times \exp\left(-\beta_2 t_j\right)\right)$$

where, $y_j$ is the live weight at time $t$ (the age of the quail in days), $\beta_0, \beta_1$ and $\beta_2$ are the parameters to be estimated. Then, AGR42s and RGR42s of each animal were estimated from their parameter estimates as follows (Yang *et al.*, 2006),

$$AGR42 = \beta_2\beta_0\beta_1 \times \exp\left(-\beta_1 \times \exp\left(-\beta_2 \times 42\right)\right) \times \exp\left(-\beta_2 \times 42\right)$$

$$RGR42 = \beta_2 \times \left(\ln\left(\beta_0\right) - \ln\left(y_{42}\right)\right)$$

The balanced one-way sire model is considered in representing the each observation and is given by

$$y_{ij} = \mu + s_i + e_{ij} \qquad i = 1,\ldots,s; j = 1,\ldots,n$$

where $y_{ij}$ represents the observation (LW42, AGR42 or RGR42) for $j$th offspring of $i$th sire, $\mu$ is the constant inherent to data, $s_i \sim N\left(0, \sigma_s^2\right)$ is the random effect

associated with $i$th sire and $e_{ij} \sim \left(0, \sigma_e^2\right)$ is the residual error term. $\sigma_s^2$ and $\sigma_e^2$ are the variance components related to sire and environment effects, respectively.

Given the data, model inferences are based on the joint posterior distribution $p(\theta|\mathbf{y})$ where y is the data and $\theta$ is the vector of unknown parameters, in this case $\theta = \left\{\mu, \mathbf{s}, \sigma_s^2, \sigma_e^2\right\}$, where $\mathbf{s} = \left\{s_1, \ldots, s_s\right\}$ is a vector. Bayes theorem states that posterior distribution is a product of prior distribution for the model parameters, $p(\theta)$, and the likelihood function, $p(\mathbf{y}|\theta)$ (Gianola & Fernando, 1986):

$$p(\theta|\mathbf{y}) \propto p(\theta)\, p(\mathbf{y}|\theta)$$

For $\mu$, we assumed a flat-improper prior.

$$f(\mu) \propto \text{constant}$$

The normal distributions assigned to $s_i$'s are viewed as prior distributions as well.

$$f\left(s_i | \sigma_s^2\right) \propto \left(\sigma_s^2\right)^{-\frac{1}{2}s} \exp\left\{-\frac{1}{2\sigma_s^2}\sum_{i=1}^{s} s_i^2\right\}$$

Prior distributions of variance components are assumed to follow inverse gamma distribution, which is common because it is often the conjugate prior for the variance components under the sire model (Bink *et al.*, 1998).

$$f\left(\sigma_s^2 | v_s, s_s^2\right) \propto \left(\sigma_s^2\right)^{-\frac{1}{2}(v_s+2)} \exp\left\{-\frac{v_s s_s^2}{2\sigma_s^2}\right\}$$

$$f\left(\sigma_e^2 | v_e, s_e^2\right) \propto \left(\sigma_e^2\right)^{-\frac{1}{2}(v_e+2)} \exp\left\{-\frac{v_e s_e^2}{2\sigma_e^2}\right\}$$

where $s_s^2$ and $s_e^2$ are prior expectations of variance components $\sigma_s^2$ and $\sigma_e^2$, respectively; $v_s$ and $v_e$ are precision parameters analogous to degrees of freedom, reflecting the degree of belief on the prior values of variance components. The likelihood for the model is given by,

$$f\left(\mathbf{y}|\mu, \mathbf{s}, \sigma_s^2, \sigma_e^2\right) \propto \left(\sigma_e^2\right)^{-\frac{1}{2}sn} \exp\left\{-\frac{1}{2}\left[\frac{\sum_{i=1}^{s}\sum_{j=1}^{n}\left(y_{ij} - \mu - s_i\right)^2}{\sigma_e^2}\right]\right\}$$

From the joint posterior density (not shown here), the full conditional distributions of the parameters can be obtained by treating the others as constants

and having the terms involving the parameter of interest. Hence, the full conditional distributions of the parameters can be summarized as follows,

$$\mu | \mathbf{s}, \sigma_s^2, \sigma_e^2, \mathbf{y} \sim N\left(\frac{\sum_{i=1}^{s}\sum_{j=1}^{n}\left(\bar{y}_{..} - s_i\right)}{ns}, \frac{\sigma_e^2}{ns}\right),$$

$$\mathbf{s} | \mu, \sigma_s^2, \sigma_e^2, \mathbf{y} \sim N\left(\frac{n\sigma_s^2\left(y_{i.} - \mu\right)}{\sigma_e^2 + n\sigma_s^2}, \frac{\sigma_s^2\sigma_e^2}{\sigma_e^2 + n\sigma_s^2}\right),$$

$$\sigma_s^2 | \mu, \mathbf{s}, \sigma_e^2, \mathbf{y} \sim IG\left(\frac{s + v_s}{2}, \frac{\sum_{i=1}^{s} s_i^2 + v_s s_s^2}{2}\right),$$

$$\sigma_e^2 | \mu, \mathbf{s}, \sigma_s^2, \mathbf{y} \sim IG\left(\frac{sn + v_e}{2}, \frac{\sum_{i=1}^{s}\sum_{j=1}^{n}\left(y_{ij} - \mu - s_i\right)^2 + v_e s_e^2}{2}\right)$$

The Bayesian approach is considered and computations were performed using Markov Chain Monte Carlo (MCMC) technique (Robert & Casella, 2004). Analyses were performed using the MCMCglmm package of R software (R Development Core Team, 2010; Hadfield, 2010). Each trait was analyzed separately. A single chain of length 65,000 was run for each trait, and after discarding the first 15,000 iterations and saving the every 50th sample, 1,000 posterior samples were stored for each parameter. Parameters for prior distributions of sire and environment variances were obtained from their corresponding REML estimates.

Posterior estimates of the heritabilities for the traits were calculated from the posterior expectations of sire and environment variance components using the formulae given as,

$$h^2 = \frac{4\sigma_s^2}{\sigma_s^2 + \sigma_e^2}.$$

## RESULTS

Some descriptive statistics of the traits are presented in Table 1. Live weight at 42 days of age was found to be 200.130g in this study. The means of AGR42 and RGR42 were found to be 2.394 and 0.010, respectively.

**Table 1 –** Descriptive statistics of the traits

| Trait | Mean (g) | Std Dev | CV | Minimum | Maximum |
|-------|----------|---------|--------|---------|---------|
| LW42 | 200.130 | 22.286 | 11.136 | 104.700 | 255.600 |
| AGR42 | 2.394 | 0.688 | 28.745 | 0.808 | 4.429 |
| RGR42 | 0.010 | 0.003 | 34.539 | 0.001 | 0.031 |

Autocorrelations among consecutive observations for variance components were low (r < 0.05). Posterior distributions of $\mu$ for each trait were normally distributed. Descriptive statistics for the posterior expectations of variance components and heritabilities are given in Table 2. The most frequently used descriptive statistics for the parameters of interest were the mode, median and the mean of the posterior distribution. However, inferences on parameters may be made by considering their posterior distributions rather than only point estimates. It can be seen that mode, median and mean estimates are similar for environmental variance of AGR42 and RGR42, whereas they are somewhat different for LW42. For sire variance, point estimates tend to differ in all traits considered. Further, the 95% credible intervals for expected sire variances are asymmetric, being long above the mean as below the mean. Monte Carlo Errors (MCE), which measures the error in parameter estimation, are small, indicating that the length of each chain is sufficient (Van Tassell & Van Vleck 1996).

Figure 1 summarizes the marginal posterior distributions of the parameters for each trait. Marginal posterior distributions of the heritabilities appear in the right-most panel of Figure 1 and the first two panels represent the marginal posterior distributions of $\sigma_s^2$ and $\sigma_e^2$, respectively. Close examination of the distributions indicates that all marginal posterior densities are unimodal and, as expected, variance components for all traits do not include negative values. Moreover,

the densities of heritabilities are close to normality and the marginal posterior distribution of $\sigma_s^2$ is slightly skewed toward the right.

The estimate of the heritability coefficients tends to differ depending on which point estimate is considered, mode, median or mean (Table 2). However, each leads to the same conclusion. Heritability of LW42 was found to be high. According to our findings, AGR42 may be considered as a moderate heritable trait, whereas RGR42 is low heritable.

## DISCUSSION

Mean value for LW42 is in good agreement with that reported by Baylan *et al*. (1997) and Narinc *et al*. (2010a), but higher than that of Saatci *et al*. (2003) and Shokoohmand *et al*. (2007). The few studies in Japanese quail have determined absolute and relative growth rates from the growth curve. AGR42 and RGR42 means obtained in the present study were similar to the values (1.90 and 0.0094, respectively) reported by Narinc *et al*. (2010b). Hyankova *et al*. (2001) have also reported similar findings (data were shown in figures) for absolute and relative growth rates.

This LW42 heritability estimate is higher than that obtained by Saatci *et al*. (2006), who reported 0.15. In another study, Shokoohmand *et al*. (2007) reported heritability estimates for different strains as 0.48, 0.50 and 0.72. Sezer *et al*. (2006) reported higher heritability estimate for 42-d-old males (0.60) and a

**Table 2 –** Posterior expectations of variance components and heritabilities, and Monte Carlo Errors (MCE) of the estimates

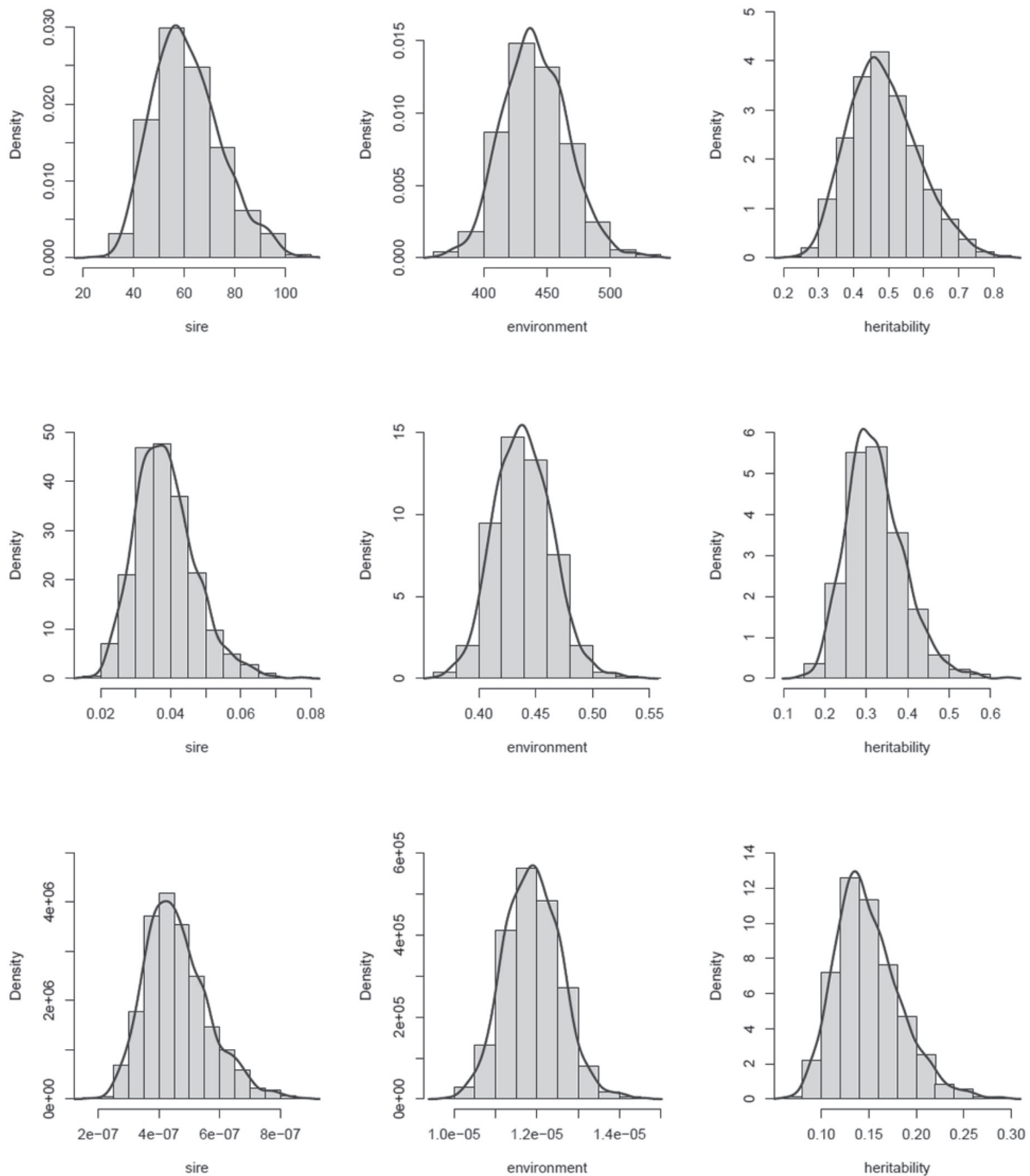| Trait | Parameter | Mode | Median | Mean | SD | MCE | Credible Interval (%) | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | | 2.5 | 97.5 |
| LW42 | $\sigma_s^2$ | 54.665 | 59.508 | 61.187 | 13.365 | 0.415 | 38.949 | 91.569 |
| | $\sigma_e^2$ | 434.103 | 439.064 | 440.609 | 25.473 | 0.845 | 395.188 | 492.851 |
| | $h^2$ | 0.452 | 0.477 | 0.487 | 0.099 | 0.003 | 0.322 | 0.701 |
| AGR42 | $\sigma_s^2$ | 0.035 | 0.038 | 0.039 | 0.009 | 0.000 | 0.024 | 0.058 |
| | $\sigma_e^2$ | 0.438 | 0.438 | 0.439 | 0.025 | 0.001 | 0.393 | 0.490 |
| | $h^2$ | 0.289 | 0.316 | 0.323 | 0.069 | 0.002 | 0.207 | 0.478 |
| RGR42 | $\sigma_s^2$ | $4.42 \times 10^{-7}$ | $4.45 \times 10^{-7}$ | $4.60 \times 10^{-7}$ | $1.05 \times 10^{-7}$ | $2.92 \times 10^{-9}$ | $2.86 \times 10^{-7}$ | $6.99 \times 10^{-7}$ |
| | $\sigma_e^2$ | $1.21 \times 10^{-5}$ | $1.19 \times 10^{-5}$ | $1.19 \times 10^{-5}$ | $6.76 \times 10^{-7}$ | $2.31 \times 10^{-8}$ | $1.07 \times 10^{-5}$ | $1.33 \times 10^{-5}$ |
| | $h^2$ | $1.43 \times 10^{-1}$ | $1.43 \times 10^{-1}$ | $1.49 \times 10^{-1}$ | $3.42 \times 10^{-2}$ | $9.89 \times 10^{-4}$ | $9.13 \times 10^{-2}$ | $2.26 \times 10^{-1}$ |

**Figure 1** – Marginal posterior distributions of variance componets and heritabilities

lower estimate for females (0.41). Narinc *et al.* (2010a) reported higher LW42 heritability (0.60), whereas Vali *et al.* (2005) reported a lower (0.22) value than that found in this study. Narinc *et al.* (2010b) reported AGR42 and RGR42 heritability estimates of 0.29 and 0.08, respectively. The difference between these heritability estimates may be attributed to the method of estimation, the model used in the study, bird strain, environmental effects, or sampling errors (Mielenz *et al.*, 2006).

The amount of heritability of a trait does not affect the decision of including it in a breeding program and even low heritable traits can be improved by selection. However, the knowledge on the amount of heritability is needed to decide which selection strategy should be used. If the trait has high heritability, rapid genetic improvement is expected by using individual breeding values. Particularly in poultry breeding, for low heritable baits such as reproduction traits, family selection may result in an increased efficiency of genetic improvement.

## CONCLUSION

The present study has focused on the Bayesian estimation of variance components and heritabilities of some growth traits that have rarely been considered in breeding studies of Japanese quail. The method of estimation applied in this study includes the prior knowledge on the parameters as well as information based on these data. The method may be used to obtain accurate estimates of parameters, even when data sets are small. Heritability is one of the most important genetic parameters in animal breeding. Single trait analysis may provide general information for breeders to design selection strategies, while multi-trait analyses are preferred as they allow taking into consideration the genetic relationships between traits. On the other hand, the methodology applied in the present study can easily be extended to multi-trait models.

## ACKNOWLEDGEMENTS

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