

The Estimation of Heritability of Weekly Body Weights in Japanese Quails with ML (Maximum Likelihood) Method

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Abstract. In this study the heritability of body weights of Japanese quails (*Coturnix coturnix Japonica*) was estimated by using ML (Maximum Likelihood) methods. Firstly, the variance components were estimated by using ML method which were later estimated the heritability for weekly body weights. The estimation of heritability of body weights are following: for third week: 0.272 ± 0.066 , for fourth week: 0.60 ± 0.13 , for fifth week: 0.312 ± 0.074

Keywords: Body weight, Heritability, Maximum Likelihood Method, Variance Components

1. Introduction

The heritability of the metric character is one of the most important properties. It expresses, as we have seen, the proportion of the total variance that is attributable to the average effects of genes, and this is what determines the degree of resemblance between relatives. But the most important function of the heritability in the genetic study of metric characters has not yet been mentioned, namely its predictive role, expressing the reliability of the phenotypic value as a guide to the breeding value. Only the phenotypic values of individuals can be directly measured, but it is the breeding value that determines their influence on the next generation (3).

To establish a breeding program, it is essential to estimate genetic parameters for improving the traits. The scale of the genetic parameters could show the amount of improvement by selection. Some of the estimated genetic parameters for various traits of domestic Japanese quail were reported by several workers (5; 10). Kawahara and Saito (5) reported the genetic parameters of different organs and body weights in the Japanese quails.

Minvielle et al. (10), reported the carcass characteristics of heavy Japanese quail line under introgression with the roux gene.

Toelle et al. (15), estimated genetic and phenotypic relationships between body weight, carcass and some of the organ parameters.

The essential traits used in breeding programs to increase poultry meat production are for body weight and feed consuming. In evaluations regarding growth, live weights measured in fixed ages, growth curve and live weight- gain are used (11).

The components of variance have been used widely in genetic and animal breeding applications. Therefore, the different estimation methods of variance components and their practical value were discussed in this study. The MINQUE method was arisen as the most suitable method, because σ^2_a / σ^2_e value of this method was found greater than the other methods (8).

Kayaalp et al. (7), illustrated estimation of variance components with Henderson's 1, Henderson's 2 and Henderson's 3 method. Kayaalp and Bek (6), estimated of heritability from estimating components of variance by using three different techniques.

2. Material and Methods

Material

Eighty male and female quails which were developed previously by selection for body weight were used in this study (1). One male and one female parents were kept together in individual cages (15×25×20 cm). When these parents were 13 weeks old hatchery management started. Eggs were collected separately from individual cages and eggs of each parents were placed separately incubator table and then transferred to incubator. After hatching, each offspring was identified humanely with an aluminium wing-tag. All offspring were raised in battery brooder until 2 weeks of age and then transferred to growing cages until 5 weeks of age. Feed and water were given adlibitum and light provided 24 hour. The quails were fed containing 22% crude protein and 3000 kcal ME/kg. Body weight of the quails was determined weekly. Heritability of the 3rd, 4th and

5th body weights were determined according to ML methods.

Method

Firstly the variance components was estimated by using ML methods which was later the heritability (13,14).

Following model was used in this study.

$$Y = Xb + Zu + e \quad (1)$$

Where,

Y is an N x 1 vector of single observations,

b is a q x 1 vector of unknown fixed effects,

u is a r x 1 vector of random effects $\sim N(0, \sigma^2_i)$,

e is an N x 1 vector of residuals.

X and Z are known incidence matrices that assign the various effects to Y.

Where b and u are solutions to Henderson's mixed model equations (4). The mixed models are following.

$$\begin{bmatrix} b \\ u_1 \\ \vdots \\ u_r \end{bmatrix} = \begin{bmatrix} X'X & X'Z_1 & \dots & X'Z_r \\ Z_1'X & Z_1'Z_1 + I_{a_1} & \dots & Z_1'Z_r \\ \vdots & \vdots & \ddots & \vdots \\ Z_r'X & Z_r'Z_1 & \dots & Z_r'Z_r + I_{a_r} \end{bmatrix} \begin{bmatrix} X'Y \\ Z_1'Y \\ \vdots \\ Z_r'Y \end{bmatrix}$$

$$C_r = \begin{bmatrix} C_{00} & C_{01} & \dots & C_{0r} \\ C_{01} & C_{11} & \dots & C_{1r} \\ \vdots & \vdots & \ddots & \vdots \\ C_{0r} & C_{1r} & \dots & C_{rr} \end{bmatrix} \begin{bmatrix} X'Y \\ Z_1'Y \\ \vdots \\ Z_r'Y \end{bmatrix}$$

The required quadratic forms while these forms are following

$$u_i' u_i \text{ and } Y' Y - b' X' Y - \sum u_i Z_i' Y$$

If we let $r = W' Y$, the right-hand sides of the Least Squares and mixed model equations, then

$$V(r) = V(W' Y) = \sum W' V_i W \sigma_i^2 = \sum M_i \sigma_i^2$$

$$\text{Then } u_i = (C_{0i} \quad C_{1i}; C_{2i}; C_{3i}) r = C_{ir}$$

and

$$u_i' u_i = r' C_i' C_i r$$

and

$$E(u_i' u_i) = \sum \text{tr}(C_i' C_i M_j) \sigma_j^2$$

The variance components were estimated by using SPSS package program.

The heritability and standard error of heritability were calculated from following equations (3;2).

$$h^2 = 4 \cdot \frac{\sigma_{\text{sire}}^2}{\sigma^2_{\text{TOTAL}}} \quad (2)$$

$$\sigma^2_{\text{TOTAL}} = \sigma_{\text{sire}}^2 + \sigma^2_{\text{error}} \quad (3)$$

$$S_h^2 = \frac{4 \cdot (1-r) \cdot (1+(n-1)r)}{2 \sqrt{(1/2)n(n-1)(b-1)}} \quad (4)$$

$$r = \frac{\sigma_{\text{sire}}^2}{\sigma^2_{\text{TOTAL}}} \quad (5)$$

Where,

h^2 : The heritability

S_h^2 : The standard error of heritability

r : The repeatability measurement

n : Total observation value

σ_{sire}^2 : The variance component of sires.

σ^2_{error} : The variance component of error.

σ^2_{TOTAL} : The variance component of total

3. Results and Discussion

The estimation of the Sire Variance (σ_{sire}^2) and Error Variance (σ^2_{error}) were 34.193, 94.547, and 78.147 and 513.118, 523.165 and 921.574 respectively in the 3rd, 4th and 5th weeks. The effect of sire on body weight was significant for all weeks ($P < 0.01$).

Firstly, the variance components were estimated by using ML method which were later estimated the heritability for weekly body weights. The estimation of heritability of body weights are following:

for third week : 0.272±0.066

for fourth week : 0.60±0.13

for fifth week : 0.312±0.074

The estimated values of heritability and variance components are shown in Table 1.

Table 1. The Estimation of Sire Variance (σ_{sire}^2), (σ^2_{error}) and Heritability for 3., 4. and 5. Weeks

| Weeks | σ_{sire}^2 | σ^2_{error} | $h^2 \pm S_h^2$ |
|-----------------|--------------------------|---------------------------|-----------------|
| 3 rd | 34.193 | 511.606 | 0.272±0.066 |
| 4 th | 94.547 | 523.165 | 0.60±0.1300 |
| 5 th | 78.147 | 921.574 | 0.312±0.074 |

These studies normally used body weights at different ages and often used different methods to estimate the heritability. Minvielle et al (9) who reviewed reports from several studies stated that the heritability estimations for body weights at 4 and 8 weeks of ages ranges from 0.47 to 0.74. Toelle et al. (15) reported that heritability estimations from sire, dam and sire plus dam components unadjusted for body weight 0.49±0.13, 0.70±0.14 and 0.59±0.80 respectively. The results of 4th week in this study are similar with Minvielle (12)'s and Toelle et al. (15)'s results.

It seems that differences in heritability estimates might be attributed to method of estimation, strain, environmental effects and sampling error due to small data set or sample size. The definition of the correct model is important, because more complex model, is required larger effort for solution.

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