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The Estimation of Heritability of Weekly Body Weights in Japanese Quails with MINQUE(Minimum Quadratic Unbiased Estimation) Method

Gökhan Tamer Kayaalp[1*], Mikail Baylan[1], Sibel Canoğulları[2]

[1]*Department of Animal Science, Agriculture Faculty, Çukurova University, 01330 Adana, Turkey*
[2]*Department of Animal Production and Technologies, Agricultural Science and Technologies Faculty, Niğde University, 51240 Niğde, Turkey*

A R T I C L E I N F O

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* Corresponding Author:
E-mail: tkayaalp@cu.edu.tr

A B S T R A C T

In this study the heritability of body weights of Japanese quails (*Coturnix coturnix Japanica*) were estimated by using MINQUE (Minimum Quadratic Unbiased Estimation) methods. Firstly the variance components were estimated by using MINQUE method which were later estimated the heritability for weekly body weights. The estimation of heritability of body weights are following: for third week : 0.302±0.018; for fourth week: 0.70±0.15; for fifth week : 0.30±0.067

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 (Falconer,1989).

In order 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 (Kawahara and Saito, 1976; Minvielle et al., 2000). Kawahara and Saito (1976) reported the genetic parameters of different organs and body weights in the Japanese quails.

Minvielle et al. (1999), reported the carcass characteristics of heavy Japanese quail line under introgression with the roux gene.

Toelle et al. (1991), 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 (Minvielle, 2004).

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 $\sigma^2_{\alpha} / \sigma^2_{e}$ value of this method was found greater than the other methods (Kayaalp and Bek, 1994).

Kayaalp et al. (1992), illustrated estimation of variance components with Henderson's 1, Henderson's 2 and Henderson's 3 method. Kayaalp and Bek (1991), estimated of heritability from estimating components of variance by using three different techniques.

Material and Methods

Material

Eighty male and female quails which were developed previously by selection for body weight were used in this study (Baylan et al, 2009). 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 ad libitum and light provided 24 hour. The quails were fed containing 22% crude protein and 3000 kcal ME/kg. Body weights of the quails were determined weekly. Heritability of the 3rd , 4th and 5th body weights were determined according to MINQUE methods.

Method

Firstly the variance components was estimated by using MINQUE methods which was later the heritability (Rao, 1971; Searle, et al. 1992).

Following model was used in this study.

$$Y = X\,b + Z\,u + e$$

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 ~ 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 (Henderson, 1953). The mixed models are following.

$$\begin{bmatrix} b \\ u_1 \\ \\ u_s \end{bmatrix} = \begin{bmatrix} X'X & XZ_1 & \cdots & XZ_S \\ Z'_1X & Z'_1Z_1 + I_{\propto 1} & \cdots & Z'_1Z_s \\ & & & \\ Z'_sX & Z'_sZ_1 & \cdots & Z'_sZ_sI_{\propto s} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'_1Y \\ \\ Z'_sY \end{bmatrix}$$

$$Cr = \begin{bmatrix} c_{00} & c_{01} \cdots c_{0s} \\ c_{01} & c_{11} \cdots c_{1s} \\ & \\ c'_{0s} & c'_{1s} \cdots c_{ss} \end{bmatrix} \begin{bmatrix} Z'Y \\ Z'_1Y \\ \\ Z'_SY \end{bmatrix}$$

For $\alpha_i = \sigma_e^2 / \sigma_i^2$

The required quadratic forms while these forms are following

$u_i' u_i$ 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

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

Then $u_i = (C_{0i}' \;\; C_{i1} \;\; ... \;\; C_{ii} \;\; C_{is})\, r = C_{ir}$

and

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

and

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

The variance components were estimated by using SPSS package program.

The heritability and standard error of heritability were calculated from following equations (Falconer, 1989; Düzgüneş et al, 1987)

$$h^2 = 4\frac{\propto \text{sire}^2}{\propto^2 \text{TOTAL}}$$

$$\propto^2 \text{TOTAL} = \propto \text{sire}^2 + \propto^2 \text{error}$$

$$S_{h^2} = \frac{4(1-r)(1+(n-1)r)}{\sqrt{\left(\frac{1}{2}\right) n(n-1)(b-1)}}$$

$$r = \frac{\propto \text{sire}^2}{\propto^2 \text{TOTAL}}$$

Where,

h^2 : The heritability

$S_h^{\ 2}$: The standard error of heritability

r : The repeatability measurement

n : Total observation value

$\sigma_{\text{sire}}^{\ 2}$: The variance component of sires.

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

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

Results and Discussion

The estimation of the Sire Variance ($\sigma_{\text{sire}}^{\ 2}$) and Error Variance (σ^2_{error}) were 41.730, 11.080,74.264 and 511.612, 520.993 and 922.654 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 MINQUE method which were later estimated the heritability for weekly body weights. The estimation of heritability of body weights are following:

For third week : 0.302±0.018

For fourth week : 0.70±0.15

For fifth week : 0.30±0.067

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}	$h^2 \pm S_h^2$
3rd	41.730	511.612	0.302±0.018
4th	111.080	520.993	0.700±0.150
5th	74.264	922.654	0.300±0.067

These studies normally used body weights at different ages and often used different methods to estimate the heritability. Minvielle et al (1999) 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. (1991) 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 (1998)'s and Toelle et al. (1991) '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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