

Heritability and Variance Component Estimates of Meat Quality in Japanese Quail (*Coturnix coturnix japonica*)

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Received: 30.03.2006

Abstract: A comparison of 3 methods for variance component estimation to compute the heritability of meat quality characteristics (body weight, breast meat weight, breast yield, l, a, b, c, h, and ph) was performed using the methods of maximum likelihood (ML), restricted maximum likelihood (REML), and minimum variance quadratic unbiased estimator (MIVQUE).

The parent population was set up at random from a closed population of Japanese quail (*Coturnix coturnix japonica*). Selection was not applied for any productive characteristics and no special care was taken to avoid inbreeding.

After 12-h feed withdrawal, the birds were weighed and slaughtered at 35 days of age. Their carcasses were dissected. Then 24-h postmortem and breast meat (*pectoralis major* and *pectoralis minor*) weights (BRW) were measured. Ultimate pH values (pHu) of the left breast meat were measured with a pH meter (Hanna Instrument Model 8314) using a penetration electrode (FC-200) after 24 h post-mortem.

Color measurements (brightness "l", redness "a", yellowness "b", chroma "c", and hue "h") of the left breast meat were carried out using a Minolta CM508d spectrophotometer connected to a computer.

Heritabilities of meat quality characteristics estimated by maximum likelihood (ML), restricted maximum likelihood (REML) and minimum variance quadratic unbiased estimation (MIVQUE) ranged from moderate to high.

Key Words: Heritability, ML, REML, MIVQUE

Japon Bildircinlarında (*Coturnix coturnix japonica*) Et Kalitesi için Kalıtım Derecesi ve Varyans Komponent Tahminleri

Özet: Çalışmada, et kalite özelliklerinde (canlı ağırlık, göğüs et ağırlığı, göğüs randımanı, l, a, b, c, h ve ph) maksimum olabilirlik (ML), kısıtlanmış maksimum olabilirlik (REML) ve en küçük varyanslı ikinci dereceden sapmasız tahminleyici (MIVQUE) metodlarıyla elde edilen varyans unsurları ve kalıtım derecelerinin karşılaştırması yapılmıştır.

Et kalite özellikleri (canlı ağırlık, göğüs et ağırlığı, göğüs randımanı, l, a, b, c, h ve ph) için maksimum olabilirlik (ML), kısıtlanmış maksimum olabilirlik (REML) ve en küçük varyanslı ikinci dereceden sapmasız tahminleyici (MIVQUE) metodları ile tahmin edilen kalıtım dereceleri karşılaştırılmıştır.

Ebeveyn popülasyonu, kapalı bir Japon bildircini (*Coturnix coturnix japonica*) popülasyonundan şansa bağlı olarak oluşturulmuş ve herhangi bir verim özelliği için seleksiyon uygulanmamıştır.

Bildircinlar, 35 günlük yaşta, 12 saat aç bırakıldıktan sonra tartıldı ve kesildi. Karkaslar parçalandı. Kesimden 24 saat sonra göğüs eti (*pectoralis major* ve *pectoralis minor*) ağırlıkları alındı. Sol göğüs etine ait son pH değeri (pHu), kesimden 24 saat sonra penetre bir elektrot (FC-200) kullanılarak pH metre ile (Hanna Instrument Model 8314) ölçüldü.

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Renk ölçümleri (parlaklık "l", kırmızılık "a", sarılık "b", kroma "c", ton "h") sol göğüs eti üzerinden bilgisayar bağlantılı Minolta CMS08d marka bir spektrofotometre ile gerçekleştirildi.

Et kalite özelliklerinin maksimum olabilirlik (ML), kısıtlanmış maksimum olabilirlik (REML) ve en küçük varyanslı ikinci dereceden sapmasız tahminleyici (MIVQUE) ile elde edilen kalıtım derecesi tahminleri orta düzeyden yüksek düzeye değişim göstermektedir.

Anahtar Sözcükler: Kalıtım derecesi, ML, REML, MIVQUE

Introduction

Estimation of variance components from mixed and random effect models is of great interest in a variety of fields of statistics such as quality control, determining an appropriate sampling design, and most recently genetic engineering (1). It has a very important role in quantitative genetics. Several co(variance) component estimation methods for animal breeding are available. The choice of a method for estimation of variance components is influenced more by simplicity than by reliability (2). Rao (3) and LaMotte (4) have independently developed methods called MIVQUE and MINQUE (5). These methods, including likelihood and minimum variance quadratic unbiased estimation (MIVQUE), with less restriction on experimental design and a non-negativity constraint, have been suggested (6). Likelihood based methods, namely ML by Hartley and Rao (7) and REML by Patterson and Thompson (8), are becoming more popular.

The ML estimation procedure for a mixed model was derived by Hartley and Rao (7). ML produces estimates that would be most consistent with the data actually observed using iterations. The ML estimates of variance components maximize the likelihood functions over the parameter's space (range from 0 to 1 and variance components are positive).

A modified ML procedure, the so-called Restricted Maximum Likelihood (REML) as described by Patterson and Thompson (8), overcomes this problem by maximizing only the part of the likelihood that is independent of the fixed effects (9).

One criticism of the ML approach is that it does not take into account the loss of degrees of freedom due to the regression coefficients in estimating the variance components. As an alternative to ML estimation, Patterson and Thompson (8) suggested an REML estimation method. This method is based on a transformation that partitions the likelihood function into 2 parts, 1 being free of the fixed regression coefficients.

Meat pH is one of the major contributing factors to poultry meat color. Muscle pH has been shown to be primarily related to the biochemical state of the muscle at time of slaughter and following rigor mortis development (10). In Oğuz et al. (11), the animal model heritability estimate for pHu in Japanese quail was high (0.48). Meat quality is a complex trait, referring to the compositional, visual, and sensory characteristics of a carcass, or its retail cuts (12). Appearance is the most critical trait for the selection of many food commodities, including poultry products. One of the major components contributing to appearance is color. Color has long been known to be a major selection criterion for fresh poultry meat and meat products as well as for final product satisfaction (13). In Oğuz et al. (11), the heritabilities of color characteristics in Japanese quail, namely l, a, b, c and h, estimated from an animal model were 0.23, 0.45, 0.22, 0.38, and 0.23, respectively. These results suggest a predominant role of genetics in the control of color. To our knowledge, no study has examined the inheritance of meat quality characteristics such as pHu and color in Japanese quail.

The aim of this study was to compare the heritabilities of meat quality traits in Japanese quail obtained by the variance components from ML, REML, and MIVQUE.

Materials and Methods

The parent population was set up at random from an unselected closed population of Japanese quail (*Coturnix coturnix japonica*), in which selection was not applied for any productive characteristics and no special care was taken to avoid inbreeding. Data used to estimate genetic and phenotypic parameters of body weight (BW), performance characteristic (breast weight (BRW)), and meat quality characteristics (pHu and color characteristics) were collected from a total of 450 birds of both sexes (approximately equal number) originating from 22 single-sire mating pens, each with 3 dams. After examining the outliers, 42 records were omitted. All chicks were pedigree hatched and wing banded on the day

of hatching. They were reared in battery cages. From hatching to the end of 35 days, light was provided continuously. During the experiment, the birds consumed a 23% CP and 11.51 MJ ME/kg diet ad libitum. The detailed composition of the experimental diet is given in Table 1.

Table 1. Composition of the experimental diet.

Ingredient, %	
Corn	60.00
Soybean meal	24.00
Fish meal	4.00
Dicalcium phosphate	1.20
Limestone	1.37
Salt	0.25
Vitamin/mineral premix*	0.35
Methionine	0.02
Lysin	0.01
<hr/>	
Chemical analyses, %	
Dry matter	90.63
Crude protein	23.06
Crude fat	2.64
Crude fiber	3.80
Crude ash	3.78
Calcium	1.17
Methionine	0.41
Lysin	1.37
Metabolizable energy, MJ/kg**	11.51

*For each kg of the diet: vitamin A 12,000 IU, vitamin E 35.0 mg, vitamin

K₃ 5.0 mg, vitamin B₁ 3.0 mg, vitamin B₂ 7.0 mg, vitamin B₆ 5.0 mg, vitamin B₁₂ 0.015 mg, calcium D-pantothenate 10.0 mg, folic acid 1.0 mg,

D-biotin 0.045 mg, choline chloride 125.0 mg, vitamin C 50.0 mg, Mn 80 mg, Fe 60.0 mg, Cu 5 mg, Co 0.2 mg, Se 0.15 mg.

**The metabolizable energy was found by calculation (14).

After 12-h feed withdrawal, the birds were weighed and slaughtered at 35 days of age. Their carcasses were dissected 24-h postmortem and breast meat (*pectoralis major* and *pectoralis minor*) weights (BRW) were measured. Breast yield (BRY) was calculated in relation to live body weight.

Ultimate pH values (pHu) of the left breast meat were measured with a pH meter (Hanna Instrument Model 8314) using a penetration electrode (FC-200) after 24 h post-mortem. Color measurements of the left breast meat were carried out using a Minolta CM508d spectrophotometer connected to a computer. After placing the measuring lens on the meat surface, it was rotated 0°, 45°, and 90° (clockwise) to obtain 3 different

reflectance measurements that were later averaged. A piece of glass was placed between the sample and the instrument to flatten the meat surface as much as possible (15). Using these spectra, the D65 Illuminant and the CIE 1964 (10°) standard observer, the following colorimetric parameters were calculated: l (brightness), a (red color co-ordinate), b (yellow color co-ordinate). hue (h), defined as $\tan^{-1}(b/a)$, describes the fundamental color of a substance, and chroma (c), defined as the square root of $a^{*2} + b^{*2}$, describes the vividness (16).

All traits were tested for normality using the Shapiro-Wilk test and by examining the residuals in the histogram. Body weight (BW), breast yield (BRY), redness (a), yellowness (b), chroma (c), and pHu showed deviation from normality. For these traits, Box-Cox transformation was applied and resulted in distributions closer to normality. To achieve normality, the omission of outliers or transformation of data into a new scale is suggested to satisfy more closely the normality assumptions (17). There are many transformation methods such as logarithmic, square root, arc-sin, and Box-Cox. Application of the Box-Cox transformation reduced the heterogeneity of error variance and permitted the assumption of equal variance as well as increasing the linearity of genetic regression (18). Transformation was carried out according to Sokal and Rohlf (19).

Meat quality traits were transformed by Box-Cox transformation as follows (20):

$$Z^t = \frac{y(t)_{ijkl}}{J(t)^{\frac{1}{n}}} = \frac{y^t - 1}{tGy^{t-1}} \quad (1)$$

where Z^t is the standardized transformed variate, $y(t)_{ijkl}$ is an original untransformed record, $J(t)^{\frac{1}{n}}$ is the n^{th} root of the Jacobian of the transformation to remove the t-dependent scale effect, and G_y is the geometric mean of the n original observations. These variables are then used to calculate the log-likelihood $L_{\max}(t)$ for trial values of t.

$$L_{\max}(t) = -\frac{n}{2} \log_e \left[\frac{S_e(t)}{n} \right] \quad (2)$$

where $S_e(t)$ is the residual sum of squares of the standardized observations. The optimal t value can be chosen to give the maximum $L_{\max}(t)$ and minimum $S_e(t)/n$ (18).

Actual mean values are presented in Table 2 and heritability estimates obtained from transformed data are shown in Table 3. The data were analyzed using the following models:

$$Y_{ijkl} = \mu + f_i + s_j + d_{j(i)} + e_{ijkl} \tag{3}$$

$$Y_{ijk} = \mu + f_i + s_j + e_{ijk} \tag{4}$$

$$Y_{ijk} = \mu + f_i + d_{ij} + e_{ijk} \tag{5}$$

where Y_{ijkl} is meat quality trait, μ is the overall mean, f_i is hatch weight, s_j and $d_{j(i)}$ are random effects of the sire and dam within the sire, respectively, and e_{ijk} is the residual effect.

The above models are called parent models (sire + dam, sire, and dam model, respectively). Heritabilities were estimated from the sire (σ_s^2), dam within sire ($\sigma_{D:S}^2$), and combined sire and dam ($\sigma_s^2 + \sigma_{D:S}^2$) components separately. To estimate the heritabilities of performance characteristics and meat quality characteristics, the SAS MIXED procedure was used (21).

Results

Results from analysis of normality for meat quality traits using skewness, kurtosis, and probability of the Shapiro-Wilk test are given in Table 2.

Since the normal distribution is symmetric, the expected values for skewness and kurtosis for a normal distribution are zero, but 6 traits (BW, BRY, a, b, c, and pHu) showed non-normality. All traits have positive kurtosis, some of them have negative skewness (BW and BRY), and the others have (a, b, c and pHu) positive

skewness. After applying the Box-Cox transformation to these 6 traits, the distribution of the transformed data became closer to normality ($P < 0.05$).

The means of BW, BRW, BRY, l, a, b, c, h, and pHu were 132.42, 47.25, 51.49, 54.87, 9.68, 3.23, 5.06, 72.06, and 5.92, respectively (Table 3).

Heritability values and variance components are given in Table 4 for performance and meat quality characteristics from REML, ML, and MIVQUE.

It was shown (Table 4) that heritabilities based on dam components are higher than those based on sire components. Some characteristics do not have variance component estimations. Because of the unbalanced data set some of the sire variance component (σ_s^2) estimations are obtained as 0 for BW and b by ML and a by MIVQUE procedures. In addition, the dam variance component (σ_d^2) estimation for h is obtained as 0 by MIVQUE as well. As a result, heritability estimates of characteristics for these components are non-estimated (NE). For other characteristics heritability estimates ranged from moderate to high.

Table 3. Means and standard deviations (SD) of performance characteristics and meat quality characteristics (n = 450).

	Mean	SD
Body Weight, g	132.42	0.68
Breast Meat Weight, g	47.25	0.31
Breast Yield (BRY), %	51.49	0.12
Brightness, l	54.87	0.11
Redness, a*	9.68	0.09
Yellowness, b*	3.23	0.09
Chroma, c*	5.06	0.03
Hue, h*	72.06	0.39
pHu	5.92	0.005

Table 2. Statistics related to normality for untransformed (UT) and transformed data (T) for performance characteristics and meat quality characteristics.

	Skewness		Kurtosis		P(S-W)	
	UT	T	UT	T	UT	T
Body Weight (BW), g	-0.41	-0.24	2.36	0.96	0.0323	0.8244
Breast Yield (BRY), %	-1.25	0.08	8.10	2.62	0.0000	0.1923
Redness, a*	0.54	0.35	1.66	0.89	0.0188	0.1219
Yellowness, b*	0.88	0.10	2.15	0.52	<.0001	0.7821
Chroma, c*	0.47	-0.10	1.41	0.85	0.0016	0.7956
pHu	1.29	0.14	18.73	0.58	0.0000	0.7615

Table 4. Variance components and heritabilities of meat quality traits.

Traits	Methods	σ_s^2	σ_d^2	σ_e^2	h_s^2	h_d^2	h_{s+d}^2
BW	REML	2.74	33.11	179.49	0.05	0.62	0.33
	ML	0	57.55	78.35	NE	NE	NE
	MIVQUE	3.85	18.02	190.05	0.07	0.34	0.21
BRW	REML	1.54	4.80	36.04	0.15	0.45	0.30
	ML	1.21	10.46	15.52	0.18	1.54	0.86
	MIVQUE	1.55	1.89	38.29	0.15	0.18	0.16
BRY	REML	0.30	0.38	4.86	0.22	0.27	0.25
	ML	0.34	0.44	2.28	0.44	0.58	0.51
	MIVQUE	0.24	0.40	4.89	0.17	0.29	0.23
l	REML	0.13	0.58	5.12	0.09	0.40	0.24
	ML	0.07	0.69	2.41	0.09	0.87	0.48
	MIVQUE	0.12	0.59	5.12	0.08	0.40	0.24
a	REML	0.05	0.56	2.85	0.06	0.65	0.35
	ML	0.07	0.65	1.30	0.14	1.29	0.71
	MIVQUE	0	0.63	2.86	NE	NE	NE
b	REML	0.07	0.13	2.39	0.11	0.20	0.15
	ML	0	0.26	1.13	NE	NE	NE
	MIVQUE	0.10	0.15	2.35	0.15	0.23	0.19
c	REML	0.004	0.041	0.25	0.05	0.56	0.31
	ML	0.002	0.051	0.116	0.05	1.21	0.63
	MIVQUE	0.004	0.041	0.252	0.05	0.55	0.30
h	REML	2.45	2.37	60.59	0.15	0.14	0.15
	ML	4.98	0	30.2	NE	NE	NE
	MIVQUE	2.03	3.82	59.66	0.12	0.23	0.18
pHu	REML	0.012	0.001	0.091	0.46	0.04	0.25
	ML	0.011	0.001	0.043	0.80	0.07	0.44
	MIVQUE	0.0013	0.0015	0.0087	0.45	0.52	0.49

Discussion

The ML estimates of variance components maximize the likelihood functions over the parameter's space (heritabilities range from 0 to 1). Furthermore, ML estimates can be biased since ML does not take into account the degrees of freedom used to estimate the fixed effects. REML is another method for variance component estimation, a modification of the ML procedure. REML has some advantage over the methods to avoid the small sample bias associated with fixed effects and selection bias (22).

Rao (3) proposed a general procedure for variance components estimation that requires no distributional assumptions other than the existence of the first 4

moments. This procedure yields MINQUE estimators of the variance components. Under normality of the disturbances, MINQUE is also the MIVQUE estimator. Since we assume normality, we will focus on MIVQUE.

A difficulty in obtaining the MIVQUE and the REML estimators is that the variance matrix of the observation vector of order N (number of observations) is required to be inverted. In practice a large number of observations might be considered, leading to a serious problem in obtaining this inverse. Another aspect of MIVQUE and REML that needs to be noted here is that the estimators obtained by these methods are also functions of the true variance components. Therefore, it is required to supply some a priori estimates for them (1).

Recently many studies have been performed on the application of Gibbs sampling on different data and models used in animal breeding such as response to selection, maternal effect model, multivariate model, threshold model, survival model, segregation, and linkage analysis.

In our study, heritabilities of meat quality characteristics were from moderate to high. ML, REML, and MIVQUE methods of variance component estimation can be used. These 3 methods are commonly used for estimating variance components. All of them could be used in animal science.

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