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A COMPARISON OF FOUR METHODS OF ESTIMATING VARIANCE COMPONENTS AND HERITABILITY FOR GROWTH TRAITS IN CHICKENS

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ABSTRACT

Data of 1137, 916 and 1030 Silver Montazah (SM), Golden Montazah (GM) and Matrouh (MA) chicks respectively, were used in this study. The studied characters were body weight at hatch, 4, 8 and 12 weeks of age, daily gain and relative growth rate during the periods of hatch-4 weeks, 4-8 weeks and 8-12 weeks of age. Variance components and heritability estimates based on sire components were estimated using Henderson's Method 3 (H3), Maximum Likelihood (ML), Restricted Maximum Likelihood (REML) and Minimum Variance Quadratic Unbiased Estimates (MIVQUE). Variance components of sire effect (σ_s^2) for most of growth traits in MA and SM chickens were higher than those obtained in GM. Percentages of σ_s^2 for some of growth traits for all strains determined by REML procedure were high compared to most percentages obtained by the other procedures (e.g. H3, ML and MIVQUE). Results show that biased estimates in variance components of sire and error effects for growth traits in GM chickens were relatively higher than those obtained in SM and MA strains. Biased estimates in variance component of sire effect obtained from REML method for most of growth traits in the three strains were lower than those computed from H3 and MIVQUE methods. Estimates of heritability from sire components (h_s^2) in MA chickens were higher than those estimates of SM and GM chickens. Heritability estimates by REML, ML, H3 and MIVQUE procedures in the three strains for the studied growth traits were variable, while estimates of h_s^2 resulting from REML were unbiased by selection. Commonly, it was concluded that likelihood procedures (ML and REML) were superior for estimating variance components and genetic parameters from unbalanced data. The growth traits in the MA strain could be by individual selection.

Keywords: Growth traits, REML, variance components, heritability

INTRODUCTION

Knowledge of genetic parameters is one of the bases for making decisions in poultry breeding programs. Selection progress is a function of the heritability of the trait involved. The greater the heritability estimate, the less intense the selection

pressure is necessary to achieve significant genetic gain (Falconer and Mackay, 1996). Variance components and heritability can be estimated by different methods. Procedures for estimating variance components differ in their degree of simplicity and their reliability. In general, the choice of a method for estimation of variance components is influenced more by simplicity than by reliability (Falconer and Mackay, 1996).

The prediction of breeding value requires knowledge of the magnitude of the (co)variance of the random effects (including the additive genetic effect or breeding value) in the statistical model. In practical applications these variance components have to be estimated (Hofer, 1998) so that these (co)variances should be estimated without bias (Schaeffer, 1993).

Recently, Schaeffer (1993) pointed out that the variance (or sampling variance) of an estimate of a variance component depends on several factors. These are (1) the true, unknown value of the component, (2) the number of observations, (3) the number of levels for each random factor and the distribution of observations per level, and (4) the method of estimation and choice of quadratic forms.

The objectives of the present study are (1) comparing variance components and heritability estimates calculated by Henderson's Method 3 (H3), Maximum Likelihood (ML), Restricted Maximum Likelihood Estimates (REML) and Minimum Variance Quadratic Unbiased Estimates (MIVQUE) procedures using growth traits data obtained from the Silver Montazah, Golden Montazah and Matrouh chickens, (2) evaluating the genetic parameters for these three strains of chickens, and (3) detecting the bias in estimates of variance components using different methods.

MATERIALS AND METHODS

This study was carried out for one generation started in 1997 at Inshas Poultry Breeding Research Station, Animal Production Research Institute, Ministry of Agriculture, Egypt. Data of one hatch on the three strains named Silver Montazah (SM), Golden Montazah (GM) and Matrouh (MA) were used in this study. The following Table shows the number of sires, dams and chicks produced from each strain.

	SM	GM	MA
No. of sires*	16	15	17
No. of dams	131	114	134
No. of chicks	1137	916	1030

*Each sire was assigned to be the sire of chicks of ten hens located in one breeding pen.

Body weight of each chick was recorded at hatch and each four weeks thereafter up to 12 weeks of age. Traits of daily gain and relative growth rate were calculated at the periods of hatch-4 weeks, 4-8 weeks and 8-12 weeks of age. Relative growth rate (RG) was computed according to Brody (1945) as:

$$RG = \frac{W_j - W_i}{(W_i + W_j) / 2} \times \cdots$$

where W_i = the (first weight) at certain age; W_j = the (second weight) after a certain period.

All chicks were treated and medicated similarly throughout the experimental period under the same managerial climatic conditions.

Model of analysis

To estimate variance components for growth traits of each strain, a mixed linear model was used:

$$y_{ijk} = \mu + x_i + S_j + e_{ijk} \qquad [1]$$

Where y_{ijk} is the observation on the kth chick, x_i is the fixed effect of the ith sex, s_j is the random effect of the jth sire and e_{ijk} is the residual error attributed to the kth chick record. Using matrix notation, this equation, assuming all genetic variation is additive, can be expressed as:

$$y = Xb + Zs + Ie \qquad [2]$$

Where **y** is the vector of observation; X is the design matrix for sex effects; Z and I are design matrices for sire and residual errors, respectively; and b, s and e are vectors with contributions attributed to fixed effect of sex and random effects due to sire and error, respectively. The mixed model equations is then expressed as:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z \end{bmatrix} \begin{bmatrix} b \\ s \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'Y \end{bmatrix} \qquad [3]$$

Henderson's Method 3 (H3)

The ANOVA procedure used to estimate sire (σ_s^2) and error (σ_e^2) variance components was through fitting constants procedure of Henderson commonly referred to as Method 3 (Henderson, 1953). This approach involves substituting sum of squares in the ANOVA procedure with quadratic forms involving least squares solutions for sire plus error effects (Searle, 1971). Briefly, the σ^2 (i.e. $\sigma^2 = \sigma_s^2$ and σ_e^2) are solved by equating reductions in sum of squares, $Y'X(X'X)^{-1}X'Y$, and the differences between these to their expectations under the full model as follows (Searle, 1971):

$$\sigma_s^2 = \frac{[R(s/b) - \sigma_e^2 \{r(X:Z) - R(X)\}]}{tr[Z'Z - Z'X(X'X)^{-1}X'Z]} \qquad [4]$$

$$\sigma_e^2 = \frac{y'y - bX'y - sZ'y}{N_h - r(X:Z)} \qquad [5]$$

where R (s/b) is the additional sire sums of squares after fitting line effects b; r is the number of linearly independent columns of X (rank of X matrix); tr is the sum of diagonal elements of the matrix or trace operator, and N_h is the total number of chick records.

Likelihood Methods

The Maximum Likelihood (ML) estimation procedure for a mixed model was derived by Hartley and Rao (1967). In the present study, Henderson's (Henderson, 1973) mixed model equations are applied to the estimation of sire and error components of variance. Assuming normality, ML variances are obtained as:

$$\sigma_s^2 = \frac{[s's + \sigma_e^2 tr(Z'Z + I\lambda)^{-1}]}{n_s} \qquad [6]$$

$$\sigma_e^2 = \frac{[y'y - b'X'y - s'Z'y]}{N_h} \qquad [7]^*$$

where n_s is the number of sires and λ is σ_e^2 / σ_s^2. In iteration, convergence occurs when computed λ is equal to the variance ratio of the previous cycle; b and s are solutions to the mixed model equations at convergence as in [3].

Restricted maximum likelihood (REML), like ML is an iterative procedure: REML corrects bias in ML that arises from estimating fixed effects. The meaning for REML is that all the information relevant in estimating variance components is combined in any set of $N_h - p$ linearly independent error contrasts, where p is the number of fixed effect and the error contrast is defined as a linear combination of observations whose expectation is zero (Scheffe, 1959). In the present study, variance components were estimated as REML using an analog of Henderson's mixed model equations (Harville, 1977). Applying this analog to the model for growth traits gives

$$\sigma_s^2 = \frac{[s's + \sigma_e^2 tr(\hat{Z}'Z + I\lambda)^{-1}]}{n_s},$$ [8]

$$\sigma_e^2 = \frac{[v'y - b'X'y - s'Z'v]}{[N_h - r(X)]}.$$ [9]

Minimum Variance Quadratic Unbiased Estimator (MIVQUE)

In the VARCOMP procedure of base SAS^N software (SAS, 1996) a priori values are set at 0 and 1, for σ_s^2 and σ_e^2, respectively. With the assumption of normality, the vector of MIVQUE is

$$\sigma^2 = \begin{bmatrix} \sigma_s^2 \\ \sigma_e^2 \end{bmatrix},$$ [10]

where σ_s^2 and σ_e^2 are determined from algebraic equations as in Sorensen and Kennedy (1986).

Estimates of the calculated heritability were computed as:

$$h_s^2 = \frac{4\sigma_s^2}{\sigma_s^2 + \sigma_e^2}$$ [11]

and, based on classical statistic, the biased estimate in variance component of sire and error effects was computed as a difference between the estimated value of variance components and the estimated value averaged over all methods. A separate analysis was made for each growth trait.

RESULTS AND DISCUSSION

1. Variance component

Estimates of variance component due to sire effect (σ_s^2) for most of growth traits in MA and SM chickens are higher than those obtained in GM (Table 1&2&3). This could be due to that MA and SM strains were not subjected to any method of selection (Sorour, 1984). However, percentages of σ_s^2 in MA chickens were higher than those presented in the other two strains at 4 and 12 weeks of age. Estimates of variance components in the present study agree with results of Ayoub (1965), Farrag (1977) and Sorour (1984) with Dandarawi, Dokki-4 and White Baladi chickens. Percentages of sire variance component in the present study were high compared to those previously reported by many Egyptian investigators (Ezzeldin, 1970; Iraqi, 1991&1999) for Fayoumi and Dokki-4 strains of chickens.

Maximum likelihood estimates of σ_s^2 were smaller than those obtained when using H3, REML and MIVQUE procedures. The lower estimate from the ML

Table 1. Variance components of sire and error and their percentages estimated by different methods for body weights in Silver Montazah, Golden Montazah and Matrouh chickens.

Breed and method	BW0				BW4				BW8				BW12			
	Sire		Error		Sire		Error		Error		Sire		Error		Sire	
	σ_s^2	%	σ_e^2	%	σ_s^2	%	σ_e^2	%	σ_e^2	%	σ_s^2	%	σ_c^2	%	σ_s^2	%
Silver Montazah	N=1137				N=1084				N=1037				N=983			
H3	0.793	10.5	6.75	89.5	11.71	3.7	302.9	96.3	3119.7	93.6	213.7	6.4	8885.7	89.7	1019.1	10.3
ML	0.729	9.8	6.733	90.2	10.37	3.3	302.3	96.7	3114.9	94.1	195.6	5.9	8879.24	90.1	976.02	9.9
REML	0.790	10.5	6.744	89.5	11.35	3.6	302.6	96.4	3117.9	93.6	212.0	6.4	8888.22	89.4	1052.5	10.6
MIVQUE	0.802	10.6	6.739	89.4	12.52	4.0	301.8	96.0	3116.2	93.6	214.4	6.4	8929.15	90.2	969.95	9.8
Golden Montazah	N=916				N=892				N=866				N=846			
H3	0.517	8.3	5.74	91.7	21.14	6.4	311.4	93.6	3013.9	97.3	85.0	2.7	8762.82	95.1	446.97	4.9
ML	0.486	7.8	5.731	92.2	18.22	5.5	313.0	94.5	3027.7	98.1	58.1	1.9	8812.72	96.0	365.25	4.0
REML	0.527	8.4	5.738	91.6	20.09	6.0	313.3	94.0	3031.1	97.9	66.24	2.1	8821.98	95.6	407.07	4.4
MIVQUE	0.506	8.1	5.75	91.9	18.65	5.6	313.7	94.4	3028.9	97.8	68.86	2.2	8848.06	96.1	355.64	3.9
Matrouh	N=1030				N=966				N=926				N=897			
H3	0.488	8.2	5.48	91.8	32.76	8.6	346.2	91.4	3112.1	94.0	198.7	6.0	10608.2	83.4	2108.6	16.6
ML	0.457	7.7	5.475	92.3	30.51	8.1	345.8	91.9	3108.9	94.4	185.7	5.6	10596.9	83.8	2046.9	16.2
REML	0.491	8.2	5.48	91.8	32.81	8.7	346.2	91.3	3112.3	93.9	201.1	6.1	10608.9	83.5	2188.9	16.5
MIVQUE	0.483	8.1	5.485	91.9	32.68	8.6	346.2	91.4	3116.3	94.1	194.2	5.9	10702.1	84.2	2008.7	15.8

* H3= Henderson's Method 3; ML= Maximum Likelihood; REML= Restricted Maximum Likelihood Estimates; MIVQUE= Minimum Quadratic Unbiased Estimates.

** BW0= Body weight at hatch; BW4= Body weight at 4 weeks; BW8= Body weight at 8 weeks; BW12= Body weight at 12 weeks.

procedure may arise due to its inherent bias under mixed model (Sorensen and Kennedy. 1986). On the other hand, percentages of σ_s^2 for some of growth traits for all strains determined by REML procedure were slightly high compared to most percentages obtained by the other procedures (Tables 1&2&3). Many authors (i.e. Sorensen and Kennedy. 1983; Searle. 1989; Besbes *et al.*. 1992; Smith and Savage. 1992; Ferraz and Johnson. 1993; Johnson and Thompson. 1995; Van Tassel *et al.*. 1995; Hofer. 1998) reported that REML procedure is preferred in estimation of variance components relative to other methods of estimation because: (1) it is give variance components estimators which are unbiased by the fixed effects and characterized by many valuable features, such as non-negativity and unbiasedness. (2) it is extremely flexible and can be adapted to a wide range of chickens of interest in the analysis of poultry breeding data. (3) it is applied to an animal model, which the inclusion of all data (on which selection was based) as well as the full additive relationship matrix and consequently it avoid most biases in estimates of variance components that are due to selection. and it is preferable computationally in the multivariate models, and (4) REML's estimates of σ^2 are the values in the parameter space (i.e. estimates of h^2 ranged from 0 to 1).

Table 2. Variance components of sire and error and their percentages estimated by different methods for daily gains in Silver Montazah, Golden Montazah and Matrouh chickens.

Breed and method[*]	Variance components[**]											
	DG4				DG8				DG12			
	Sire		Error		Sire		Error		Sire		Error	
	σ_s^2	%	σ_e^2	%	σ_s^2	%	σ_e^2	%	σ_s^2	%	σ_e^2	%
Silver Montazah	N= 1084				N= 1037				N= 983			
H3	0.013	3.0	0.439	97.0	0.190	5.9	3.051	94.1	0.480	7.3	6.07	92.7
ML	0.012	2.6	0.438	97.4	0.175	5.4	3.046	94.6	0.450	6.9	6.06	93.1
REML	0.014	3.1	0.438	96.9	0.190	5.9	3.049	94.1	0.488	7.4	6.07	92.6
MIVQUE	0.014	3.1	0.437	96.9	0.187	5.8	3.05	94.2	0.465	7.1	6.08	92.9
Golden Montazah	N= 892				N= 866				N= 846			
H3	0.024	4.9	0.454	95.1	0.103	3.3	3.058	96.7	0.653	8.6	6.92	91.4
ML	0.021	4.3	0.455	95.7	0.084	2.7	3.065	97.3	0.605	8.0	6.92	92.0
REML	0.023	4.7	0.456	95.3	0.094	3.0	3.068	97.0	0.657	8.7	6.93	91.3
MIVQUE	0.022	4.5	0.456	95.5	0.090	2.8	3.070	97.2	0.636	8.4	6.94	91.6
Matrouh	N= 966				N= 926				N= 897			
H3	0.047	8.3	0.516	91.7	0.162	5.5	2.803	94.5	1.431	15.0	8.13	85.0
ML	0.044	7.8	0.515	92.2	0.151	5.1	2.800	94.9	1.383	14.6	8.12	85.4
REML	0.047	8.3	0.516	91.7	0.164	5.5	2.803	94.5	1.480	15.4	8.13	84.6
MIVQUE	0.046	8.2	0.516	91.8	0.159	5.4	2.806	94.6	1.368	14.3	8.19	85.7

[*] H3= Henderson's Method 3; ML= Maximum Likelihood; REML= Restricted Maximum Likelihood Estimates; MIVQUE= Minimum Quadratic Unbiased Estimates.
[**] DG4= Daily gain during the period of hatch-4 weeks; DG8= Daily gain during the period of 4-8 weeks; DG12= Daily gain during the period of 8-12 weeks.

In general, estimates of σ_s^2 obtained from ML. REML and MIVQUE procedures are preferable to H3 because they have built in optimality properties

(Searle, 1989, Beaumount, 1991; Smith and Savage, 1992; Schaeffer, 1993). On the other hand, some estimates of σ_e^2 estimated by H3 and REML methods for growth traits of all strains are identical. This is could be due to that data are nearly balanced. In this respect, Searle (1989) and Hofer (1998) found, for balanced data from all mixed models, the REML estimator (neglecting the normality assumption and the constraint of REML estimates to the parameter space) is identical to the ANOVA estimators.

Table 3. Variance components of sire and error and their percentages estimated by different methods for relative growth rates in Silver Montazah, Golden Montazah and Matrouh chickens.

Breed and method*	Variance components**											
	RG4				RG8				RG12			
	Sire		Error		Sire		Error		Sire		Error	
	σ_s^2	%	σ_e^2	%	σ_s^2	%	σ_e^2	%	σ_s^2	%	σ_e^2	%
Silver Montazah	N= 1084				N= 1037				N= 983			
H3	3.860	10.3	33.6	89.7	3.23	4.4	70.0	95.6	1.947	2.7	69.5	97.3
ML	3.575	9.64	33.5	90.4	2.99	4.1	69.9	95.9	1.764	2.5	69.4	97.5
REML	3.848	10.3	33.6	89.7	3.27	4.5	69.5	95.5	1.967	2.8	69.5	97.2
MIVQUE	3.871	10.3	33.5	89.7	3.11	4.3	70.1	95.7	1.875	2.6	69.5	97.4
Golden Montazah	N= 892				N= 866				N= 846			
H3	3.127	8.84	32.2	91.2	5.39	7.3	68.5	92.7	7.158	8.6	75.7	91.4
ML	2.941	8.34	32.3	91.7	5.10	6.9	68.3	93.1	6.568	8.0	75.6	92.0
REML	3.211	9.03	32.3	91.0	5.54	7.5	68.4	92.5	7.116	8.6	75.6	91.4
MIVQUE	2.864	8.11	32.4	91.9	5.24	7.1	68.6	92.9	7.365	8.9	75.5	91.1
Matrouh	N= 966				N= 926				N= 897			
H3	5.466	11.1	43.6	88.9	6.58	9.0	66.9	91.0	8.332	7.9	97.1	92.1
ML	5.149	10.6	43.6	89.4	6.0	8.2	66.8	91.8	7.855	7.5	97.0	92.5
REML	5.521	11.2	43.6	88.8	6.45	8.8	66.9	91.2	8.471	8.0	97.1	92.0
MIVQUE	5.394	11.0	43.7	89.0	6.77	9.2	66.7	90.8	8.115	7.7	97.3	92.3

* H3= Henderson's Method 3; ML= Maximum Likelihood; REML= Restricted Maximum Likelihood Estimates; MIVQUE= Minimum Quadratic Unbiased Estimates.
** RG4= Relative growth rate during the period of hatch-4 weeks; RG8= Relative growth rate during the period of 4-8 weeks; RG12= Relative growth rate during the period of 8-12 weeks.

2. Biased estimates in variance components

Results presented in Tables 4&5 show that biased estimates in variance components of sire and error for growth traits in GM chickens were relatively higher than obtained in SM and MA strains. This may be due to a small number of records (1137 records for SM and 1030 records for MA vs 916 records for GM). In this respect, Smith and Savage (1992) and Hofer (1998) pointed out that the bias becomes more severe and significant as the number of levels of fixed effects increases, the number of levels of the random effect decrease and the number of observations per smallest subclass decrease.

As expected biased estimates in variance component of sire effect (Tables 4&5) obtained from REML method for most of growth traits in the three strains were larger

than those computed from H3 and MIVQUE methods (Hofer. 1998). While bias in sire variance component for most of growth traits estimated by ML is larger than estimates resulting when using REML. This is because the ML estimator takes account of the loss in degrees of freedom that results from estimating the fixed effects (Harville. 1977; Foulley. 1993). The REML method combines the desirable properties of ML with accountability for loss in degrees of freedom when fixed effects are first estimated.

Table 4. Bias in estimates of sire and error variance components estimated by different methods for body weight traits in Silver Montazah, Golden Montazah and Matrouh chickens.

Breed and method[*]	Bias in variance components[**]							
	BW0		BW4		BW8		BW12	
	σ_s^2	σ_e^2	σ_s^2	σ_e^2	σ_s^2	σ_e^2	σ_s^2	σ_e^2
Silver Montazah								
H3	0.034	0.012	0.850	0.461	9.878	3.243	4.825	1.9645
ML	-0.030	-0.006	-0.492	-0.142	-8.201	-1.511	-38.22	-4.492
REML	0.031	0.006	0.492	0.142	8.201	1.511	38.22	4.492
MIVQUE	0.043	0.001	1.657	-0.580	10.60	-0.211	-44.29	45.42
Golden Montazah								
H3	0.008	0.000	1.616	-1.439	15.45	-11.54	53.24	-48.58
ML	-0.020	-0.009	-1.304	0.117	-11.45	2.291	-28.48	1.326
REML	0.018	-0.002	0.567	0.432	-3.308	5.713	13.34	10.58
MIVQUE	0.000	0.010	-0.878	0.891	-0.692	3.535	-38.09	36.66
Matrouh								
H3	0.008	0.000	0.569	0.071	3.756	-0.307	45.33	-20.81
ML	-0.020	-0.005	-1.68	-0.289	-9.236	-3.474	-16.39	-32.10
REML	0.011	0.000	0.623	0.073	6.194	-0.114	25.62	-20.17
MIVQUE	0.003	0.005	0.491	0.145	-0.715	3.896	-54.56	73.08

[*] H3= Henderson's Method 3; ML= Maximum Likelihood; REML= Restricted Maximum Likelihood Estimates; MIVQUE= Minimum Quadratic Unbiased Estimates.

[**] BW0= Body weight at hatch; BW4= Body weight at 4 weeks; BW8= Body weight at 8 weeks; BW12= Body weight at 12 weeks.

Spilke and Mielenz (1992) showed, based on comparisons of ANOVA, MIVQUE and REML methods, large differences in bias between ANOVA and the other two methods. One disadvantage of ANOVA-based methods for animal breeding applications is that covariances among effects of genetically related animals, cannot be accounted for. This bias occurs if data are from a population under selection (Sórensen and Kennedy, 1984). Furthermore, covariances between two traits can only be estimated from animals that have both traits measured. This yields biased estimates in cases where only animals that were selected on the first trait have a chance of expressing the second trait. Sorensen and Kennedy (1984) have shown that the MIVQUE estimator is not biased by selection on a translation invariant criterion when an animal model with the complete relationship matrix A and all data back to the unselected base population is used.

3. Heritability

Estimates of heritability (h_s^2) determined by different methods for growth traits in the SM. GM and MA chickens are presented in Table 6. Estimates of h_s^2 in MA

Table 5. Bias in estimates of sire and error variance components estimated by different methods for daily gain and relative growth rate in Silver Montazah, Golden Montazah and Matrouh chickens.

Breed and method[1]	Bias in variance components											
	Daily gain traits[**]						Relative growth rate traits					
	DG4		DG8		DG12		RG4		RG8		RG12	
	σ_s^2	σ_e^2	σ_s^2	σ_e^2	σ_s^2	σ_e^2	σ_s^2	σ_e^2	σ_s^2	σ_e^2	σ_s^2	σ_e^2
Silver Montazah												
H3	-0.00003	0.00095	0.0045	0.00225	0.00917	-0.00228	0.072	0.034	0.077	0.155	0.059	0.036
ML	-0.00150	-0.00035	-0.0107	-0.00315	-0.02043	-0.00727	-0.214	-0.029	-0.160	0.055	-0.120	-0.077
REML	0.00078	0.00005	0.043	-0.00025	0.01707	-0.00117	0.060	0.002	0.122	-0.430	0.078	-0.009
MIVQUE	0.00078	-0.00065	0.0019	0.00115	-0.00582	0.01072	0.083	-0.008	-0.040	0.215	-0.010	0.050
Golden Montazah												
H3	0.0015	-0.00132	0.01045	-0.00718	0.01525	-0.00553	0.091	-0.099	0.070	0.015	0.106	0.108
ML	-0.0016	0.00005	-0.00915	-0.00018	-0.03315	-0.00653	-0.095	-0.023	-0.220	-0.120	-0.480	-0.058
REML	0.0005	0.00057	0.00105	0.00283	0.01965	0.00157	0.175	0.011	0.232	-0.040	0.064	0.034
MIVQUE	-0.0005	0.00067	-0.00235	0.00453	-0.00175	0.01047	-0.172	0.111	-0.070	0.147	0.313	-0.085
Matrouh												
H3	0.0011	0.00035	0.003	0.0000	0.0155	-0.0125	0.083	-0.006	0.131	0.065	0.139	-0.027
ML	-0.0024	-0.00055	-0.008	-0.0030	-0.0325	-0.0215	-0.234	-0.051	-0.450	-0.010	-0.340	-0.129
REML	0.0009	-0.00005	0.005	0.0000	0.0645	-0.0125	0.139	-0.005	0.001	0.060	0.278	-0.021
MIVQUE	0.0004	0.00025	0.000	0.0030	-0.0475	0.0465	0.011	0.062	0.319	-0.110	-0.080	0.177

[1] H3= Henderson's Method 3; ML= Maximum Likelihood; REML= Restricted Maximum Likelihood Estimates; MIVQUE= Minimum Quadratic Unbiased Estimates.

[**] DG4= Daily gain during the period of hatch-4 weeks; DG8= Daily gain during the period of 4-8 weeks; DG12= Daily gain during the period of 8-12 weeks; RG4= Relative growth rate during the period of hatch-4 weeks; RG8= Relative growth rate during the period of 4-8 weeks; RG12= Relative growth rate during the period of 8-12 weeks.

Table 6. Estimates of heritability estimated by different methods for growth traits in Silver Montazah, Golden Montazah and Matrouh chickens.

Breed and method[a]	Body weight traits[b]				Daily gain traits[b]			Relative growth rate traits[b]		
	BW0 h_s^2 ±SE	BW4 h_s^2 ±SE	BW8 h_s^2 ±SE	BW12 h_s^2 ±SE	DG4 h_s^2 ±SE	DG8 h_s^2 ±SE	DG12 h_s^2 ±SE	RG4 h_s^2 ±SE	RG8 h_s^2 ±SE	RG12 h_s^2 ±SE
Silver Montazah										
H3	0.42±.15	0.15±.07	0.26±.10	0.41±.15	0.11±.05	0.22±.09	0.28±.11	0.39±.14	0.16±.07	0.10±.05
ML	0.39±.14	0.13±.06	0.24±.09	0.40±.14	0.13±.06	0.23±.09	0.30±.11	0.41±.14	0.18±.08	0.11±.05
REML	0.42±.15	0.14±.06	0.25±.10	0.42±.15	0.13±.06	0.23±.09	0.28±.11	0.41±.15	0.17±.07	0.11±.05
MIVQUE	0.43±.15	0.16±.07	0.26±.10	0.39±.14	0.12±.06	0.23±.09	0.29±.11	0.41±.14	0.18±.07	0.11±.05
Golden Montazah										
H3	0.33±.17	0.25±.10	0.11±.06	0.19±.09	0.17±.08	0.11±.06	0.32±.13	0.33±.13	0.28±.11	0.32±.13
ML	0.31±.16	0.22±.09	0.08±.05	0.16±.08	0.19±.08	0.12±.06	0.35±.13	0.36±.14	0.30±.12	0.34±.13
REML	0.34±.17	0.24±.10	0.09±.05	0.18±.08	0.18±.08	0.11±.06	0.34±.13	0.32±.12	0.28±.11	0.36±.14
MIVQUE	0.32±.16	0.22±.10	0.09±.05	0.15±.07	0.2±.09	0.13±.07	0.34±.13	0.35±.13	0.29±.12	0.35±.13
Matrouh										
H3	0.33±.13	0.35±.12	0.24±.09	0.66±.21	0.31±.11	0.20±.08	0.58±.19	0.42±.14	0.33±.12	0.30±.11
ML	0.31±.13	0.32±.12	0.23±.09	0.65±.20	0.33±.12	0.22±.09	0.62±.20	0.45±.15	0.35±.13	0.32±.12
REML	0.33±.13	0.35±.12	0.24±.09	0.66±.21	0.33±.12	0.21±.09	0.57±.18	0.44±.15	0.37±.13	0.31±.11
MIVQUE*	0.32±.13	0.34±.12	0.23±.09	0.63±.20	0.33±.12	0.22±.09	0.60±.19	0.45±.14	0.36±.13	0.32±.12

[a] H3= Henderson's Method 3; ML= Maximum Likelihood; REML= Restricted Maximum Likelihood Estimates; MIVQUE= Minimum Quadratic Unbiased Estimates.

[b] BW0= Body weight at hatch; BW4= Body weight at 4 weeks; BW8= Body weight at 8 weeks; BW12= Body weight at 12 weeks; DG4= Daily gain during the period of hatch-4 weeks; DG8= Daily gain at the period of 4-8 weeks; DG12= Daily gain during the period of 8-12 weeks; RG4= Relative growth rate during the period of hatch-4 weeks; RG8= Relative growth rate during the period of 4-8 weeks; RG12= Relative growth rate during the period of 8-12 weeks.

chickens were higher than those of SM and GM chickens. This might be due to this strain was not subjected to any method of selection (Sorour, 1984). Therefore, we can recommend utilizing this strain to improve the growth traits by individual selection. On the other hand, estimates of h_s^2 in SM for weight at hatch was higher (0.42) than at later ages (0.25 at 8-weeks). This might be due to the small maternal effects and variation in egg size of the sires' and dams' daughters (hens), i.e. decreasing the non-additive genetic variance effects. This would encourage poultry breeders in Egypt to select in this strain for body weight at early ages without waiting to later ages, and consequently, the cost of breeding programs is reduced.

In general, estimates of heritability estimated by REML, ML, H3 and MIVQUE procedures in the three strains for the studied growth traits are variable. Where estimates of h_s^2 resulting from REML were unbiased by selection (Tables 4&5) (Besbes *et al.*, 1992; Ferraz and Johnson, 1993; Gebhardt-Henrich and Marks, 1993; Dieters *et al.*, 1995). However, biased estimates were found in MIVQUE procedure when the pre-assigned values deviated from the true values. MIVQUE has not been widely used by animal breeders. Estimates of h_s^2 for growth traits in the present study in the three strains were larger than those presented in the reviewed studies (El-Maghraby and Bakir, 1977; Iraqi, 1991&1999) for Dokki-4 chickens.

Conclusion

Matrouh chickens have high variance components and heritability estimates from sire components for growth traits. Therefore, we can recommend utilizing this strain in Egypt to improve the growth traits by individual selection. Estimates of genetic parameters resulting from REML method were unbiased by selection (Dieters *et al.*, 1995 and Johnson and Thompson, 1995). Also, estimates of bias in variance components determined by REML were low compared to the other three methods (H3, ML and MIVQUE). REML procedure has been widely applied by animal breeders. Commonly, it was concluded that ML and REML are superior for estimating variance components and genetic parameters from unbalanced data.

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مقارنة استخدام أربعة طرق لتقدير مكونات التباين والمكافئ الوراثي لصفات النمو في الدجاج

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استخدم في هذه الدراسة بيانات ١١٣٧، ٩١٦ و ١٠٣٠ كتكوت من دجاج منتزه فضي ، منتزه ذهبي و مطروح– على التوالي لدراسة صفات : وزن الجسم عند عمر الفقس و ٤، ٨ و ١٢ أسبوع و مقدار الزيادة اليومية في وزن الجسم و معدل النمو النسبي خلال الفترات من الفقس ــ ٤ أسابيع ، ٤ ــ ٨ أسابيع و ٨ ــ ١٢ أسبوع . تم تقدير مكونات التباين الأبوي والمكافئ الوراثي من هذا المكون باستخدام طرق Henderson Method₃ & ML & REML & MIVQUE . كما تم تقدير التحيز في مكون التباين الأبوي وتباين الخطأ، وأوضحت النتائج أن :

كانت مكونات التباين الأبوي لمعظم صفات النمو في كل من دجاج مطروح والمنتزه الفضي أعلــى عــن مثيلاتها المقدرة من دجاج المنتزه الذهبي . كانت نسب التباين الأبوي المقدرة بواسطة الـــــ REML لبعض أوزان الجسم ومقدار الزيادة اليومية ومعدل النمو النسبي للسلالات الثلاث أعلى من مثيلاتها المقدرة بالطرق الأخرى.

كان مقدار التحيز في مكونات التباين الأبوي وتباين الخطأ لصفات النمو في المنتزه الذهبي أعلـــى مــن نظائره المقدرة لدجاج المنتزه الفضي ودجاج مطروح وكان مقدار التحيز في المكون الأبوي المقــدر مــن طريقة الـــــ REML اقل لمعظم صفات النمو من تلك الأخرى المقدرة بطرق Henderson Method₃ & ML MIVQUE في الثلاثة سلالات.

كانت قيـــم المكافئ الوراثـــي المقدرة من المكون الأبوي لدجاج مطروح أعلــى مــن مثيلاتها المقدرة لكل من دجاج المنتـــزه الفضـــي والمنتــزه الذهــبي . كما كانت قيم المكافئ الوراثي المقدار بالطرق الأربعة مختلفة فيما بينها .

وبصفــة عامـــة يمكن استنتــــاج انـــه تفضـل طـرق REML & ML لتقدير مكونـــات التبايـــن والمعايير الوراثيـــة عن الطريقتين الأخريين خاصة للبيانات غير المتزنة Unbalanced data. كما يمكن تحسـين صفـات النمـو لدجــاج المطروح بواسطة الانتخاب الفردي.