



Comparison of Variance Components Methods for One Way Random Effects Model in Cotton

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Author's contribution

The sole author designed, analyzed and interpreted and prepared the manuscript.

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ABSTRACT

In this study, emphasis is placed on comparing the variance components for one way model in cotton by ten methods: analysis of variance (ANOVA), Quasi-maximum-likelihood method (QML), Maximum-likelihood method (ML), Full maximum likelihood Procedure (FML), Restricted maximum-likelihood method (REML), Modified maximum-likelihood method (MML), Federer's estimator (FE), Moment (MOM), Klotz-Milton-Zacks (KMZ) and Stein estimator (SE) methods. The results showed that the estimation of variance components in some methods were found equal to each other and some other methods gives different values. The environmental variance for ANOVA, QML, ML, FML, REML, MML, FE and MOM methods by equating mean square of error to its expected value in analysis of variance. The MOM method was registered the highest values of genetic variance, followed by ANOVA, REML and FE methods and followed by QML, ML and FML methods for all studied traits in cotton. While, the lowest values of genetic variance were found with MML, KMZ and SE methods. The cluster analysis for the methods of genetic variance estimates based on studied traits contained into four clusters i.e., the cluster I (MOM), the cluster II (ANOVA, REML and FE), the cluster III (QML, ML and FML) and the cluster IV (MML, KMZ and SE). These results indicate a similarity of the methods in the same each cluster and differences between the four clusters. The differences of these methods due to differed in calculated the genetic variance. The ten studied methods for BSH and σ_G^2/σ_E^2 ratio estimations were showed the same results for genetic variance for all studied traits, and quite the opposite for σ_E^2/σ_P^2 ratio.

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1. INTRODUCTION

In experimental design, all elements which may vary during the experiment and may affect the response are called factors. The categories of each factor are called levels of the factor. In classifying data in terms of factors and their levels, the interest is in the effect of a level of a factor on the response variable of the experiment, that is how much the level affects the response [1]. If levels of factor in study are used to represent only a sample of a larger set of levels, the effect is called random [2]. If every factor of the model has random effect on the response variable, the model is called random effects model.

The one-way random effects model is a one-way linear model where the main effects are random variables. This model is used in breeding, biology, environmental experiments and other areas of statistics where the levels for the effects have been selected at random from a population of levels and the experimenter wishes to obtain some information about parameters of the distribution of those levels in the population. The main reasons for the analysis would be: (1) Estimating parameters of the one-way random effects model or functions of these parameters (2) testing hypotheses about the mean, and the variance components of the model or functions of these parameters [3].

The random effects analysis of variance model, or variance component model, can be traced as far back as to the works of the astronomer Airy [4] and Chauvenet [5]. After Fisher [6] had defined variance analysis method, it has been using widely in order to test the significance of the effects of treatments. If the effects of several factors are examined on one dependent variable, the rate of each factor in total variance can be calculated. In other words, variance components can be calculated. According to Crump [7], another use of analysis of variance enables to estimate variance components.

In recent years evaluations of methods related to estimating variance components are very important for some of the researchers who are engaged in scientific work about statistics. Researchers in the field of applied statistics, science and especially health sciences tend to emphasize on the importance of this issue because of the need for the estimation of

variance components. The models which are used in plant breeding for determination of the genetic variance and error variance in the total variation are of great importance. Because in determining the heritability which is the key parameter at genetic improving, in addition to the error, the components of other fixed and random effects should also be estimated.

Traditionally, the estimators used most often have been the analysis of variance (ANOVA) estimators, which are obtained by equating observed and expected mean squares from an analysis of variance and solving the resulting equations [8]. Variance components estimation originated with estimating error variance in analysis of variance by equating error mean square to its expected value. This equating procedure was then extended to random effects models, first for balanced data (for which minimum variance properties were subsequently established) and later for unbalanced data. Unfortunately, this ANOVA methodology yields no optimum properties (other than unbiasedness) for estimation from unbalanced data. Today it is being replaced by maximum likelihood (ML) and restricted maximum likelihood (REML) based on normality assumptions and involving nonlinear equations that have to be solved numerically [9].

This study aims to compare of variance components methods existing in the simplest case of a one-way random effects model for some quantitative traits in cotton.

2. MATERIALS AND METHODS

2.1 Genetic Material and Field Procedure

Eight cotton (*Gossypium barbadense*, L.) cultivars were evaluated for yield, yield components and fiber traits during one year (2016). The four genotypes (Giza 45, Giza 85, Giza 88 and Giza 93), the two genotypes (Pima S6 and Pima S7), one genotypes (Asturaly), one genotype (Karashanky) used in the present investigation belong to Egyptian, American Egyptian, Australian and Russian cultivars, respectively. The Experiment was conducted at Sakha Agricultural Research Station at Kafr El-Shiekh Governorate. A randomized complete block design with four replications was used. Each replicate consisted of 24 rows, 3 rows for each genotype. Each row 4 meters long and 0.60 m in a wide and comprised 10 hills. Hills were

spaced at 40 cm apart and thinned to one plant per hill. All the recommended cultural practices of cotton production in the area were done as usually.

2.2 Traits Measurement

The data on an individual plant basis of the eight cotton genotypes recorded for number of bolls/plant (No. of B/P), boll weight in grams (BW, g), seed index (SI, g), lint percentage (L%), seed cotton yield/plant in grams (SCY/P, g), 2.5% Span length (2.5% SL, mm), fiber fineness (FF) and fiber strength (FS, gm/tex) traits. All guarded plants were harvested to measure of these traits. All fiber properties were measured in the laboratory of the Cotton Technology Research Department, Cotton Research Institute at Giza.

2.3 Statistical and Genetic Procedures

In one way classification random model, the variance components can be estimated by various several methods. The variance components were estimated with analysis of variance (ANOVA) by Fisher [6], Quasi-maximum-likelihood (QML) by Sahai and Ojeda [10], Maximum-likelihood (ML) by Herbach [11], Full maximum likelihood (FML) by Searle et al. [1], Restricted maximum-likelihood (REML) by Anderson and Bancroft [12], Modified maximum-likelihood (MML) by Stein [13] and Klotz et al. [14], Federer's estimator (FE) by Federer [15], Moment (MOM) by Sahai and Ojeda [10], Klotz-Milton-Zacks (KMZ) by Klotz et al. [14] and Stein estimator (SE) by Stein [13]. Results of these methods could be obtained via the SPSS and the statistical methods by Sahai and Ojeda [10]. Cluster analysis was performed using K-means clustering and tree diagrams based on Euclidian distances was developed by Ward's method using StatistiXL 1.11 software for the eight genotypes of the eight traits in cotton. Broad sense heritability and standard errors were calculated according to Singh et al. [16]. The

heritability estimates categorized as suggested by Robinson et al. [17] (0-30% = low; 31-60% = moderate; above 60% = high).

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

In Table 1, the mean squares of genotypes showed highly significant for yield, yield components and fiber traits in cotton. These results indicated existence of genetic variability in the material studied, this provides for selection from these genotypes and the genetic improvement of cotton for all studied traits. The mean squares from analysis of variance revealed highly significant ($p < 0.01$) differences among 20 Egyptian cotton genotypes for yield and yield components traits [18]. Nizamani et al. [19] mentioned that the analysis of variance revealed that genotypes differed significantly at 5% probability level for all the traits except that seed index and staple length were non-significant.

3.2 Descriptive Statistics

The mean, range and coefficient of variation (CV%) for studied traits in eight cotton varieties are presented in Table 2. The mean performances of some genotypes were higher than grand mean for studied traits. The variety Giza 45 for seed index and fiber traits, the variety Asturaly for lint percentage and seed cotton yield/plant traits, the variety Pima S6 for boll weight and the variety Pima S7 for number of bolls/plant were recorded the highest and best values of mean performances. On the other hand, the lowest or undesirable values of mean performances were found for Giza 88 (number of bolls/plant, seed index and seed cotton yield/plant traits), for Karashanky (2.5% span length and fiber strength traits), for Giza 45 (lint percentage), for Giza 93 (boll weight) and for Asturaly (fiber fineness). Generally, the genotypes Asturaly and Giza 45 were exhibited

Table 1. Estimates of mean squares among eight genotypes for yield, yield components and fiber traits in cotton

SOV	df	No.B./P	B.W. (g)	S.I. (g)	L. %	S.C.Y./P (g)	2.5% S.L.	F.S.	F.F.
Replications	3	1.42	0.01	0.06	0.54	15.16	0.47	0.04	0.02
Genotypes	7	24.84**	0.09**	1.28**	21.10**	196.80**	20.35**	3.29**	0.82**
Error	21	2.16	0.01	0.04	0.49	8.44	0.61	0.13	0.03

Significance levels: $p < 0.01$ ***,

Table 2. Descriptive Statistics of eight genotypes for yield, yield components and fiber traits in cotton

Traits genotypes	No.B./P	B.W.(g)	S.I.(g)	L. %	S.C.Y./P (g)	2.5% S.L.	F.S.	F.F.
Pima S ₆	21.57	3.15	9.27	40.01	67.63	29.80	10.07	4.16
Pima S ₇	27.00	2.94	9.69	37.56	73.64	33.53	8.55	4.33
Asturaly	26.70	3.01	8.81	40.90	79.97	31.97	10.23	4.46
Karashanky	22.44	2.80	9.12	40.30	62.68	29.70	9.90	4.14
Giza 45	26.08	2.85	10.05	33.75	74.23	35.59	11.85	3.32
Giza 85	23.44	2.84	8.66	38.28	66.20	32.60	9.93	4.16
Giza 88	21.16	2.75	8.31	38.39	57.91	34.03	10.57	4.05
Giza 93	26.72	2.71	8.84	36.90	67.16	35.34	10.15	3.24
Grand mean	24.39	2.88	9.09	38.26	68.68	32.82	10.16	3.98
Range	5.84	0.44	1.74	7.16	22.06	5.89	3.31	1.22
CV%	6.03	3.51	2.30	1.82	4.23	2.39	3.58	4.23

the best mean performances for yield and fiber traits, respectively. The differences between the studied genotypes indicated the presence of genetic variability for the studied traits in the studied materials. The coefficient of variation (CV %) is a good base for comparing the extent of variation. In addition, the CV% is a parameter which is not related to unit of measured traits and will be effective in comparing of the studied traits. The values of CV% were lowest for studied traits and which varied from 1.82% for lint percentage to 6.03% for number of bolls/plant, which displayed the least influence of environment on these traits. These results of CV% indicate to degree of precision and a good index of the reliability or validity of the experiment. The magnitude of CV% indicated that the genotypes had exploitable genetic variability for all studied traits. Abd El-Mohsen and Amein [18] reported that the CV% of the traits varied from 0.85% for lint percentage % to 8.38% for seed index.

3.3 Variance Components

The variance components estimates for yield, yield components and fiber traits were calculated by ten methods and are presented in Table 3. By all studied methods the variance component between the genotypes is a little bit overestimated while the residual variance component is a bit underestimated. The estimates of genetic and environmental variances by ten methods were recorded the highest values for seed cotton yield/ plant followed by number of bolls/plant, lint percentage and 2.5% span length traits. While, the lowest values of genetic and environmental variances were found for boll weight trait.

The ten studied methods based on values of error variance were divided into two groups for all

studied traits. These methods in each group were found equal values of error variance. The first group consisted of eight methods i.e., ANOVA, QML, ML, FML, REML, MML, FE and MOM estimators. The second group comprised of KMZ and SE methods. The values of error variances by methods in the first group were greater than the methods in the second group for all studied traits. Variance components estimation originated with estimating error variance in analysis of variance by equating error mean square to its expected value for ANOVA, QML, ML, FML, REML, MML, FE and MOM methods.

In respect to values of genetic variance, the studied methods were divided into five groups for all studied traits. The five groups were recorded different values of genetic variances by the methods in these groups. The first and second groups comprised of three methods i.e., (ANOVA, REML and FE) and (QML, ML and FML), respectively. The third group consisted of two methods (KMZ and SE). However, the fourth and fifth groups were included MML and MOM methods, respectively. The methods in each group were exhibited similar values of genetic variance.

The comparison of genetic variance using the studied methods, the highest values of genetic variance were recorded by MOM method, followed by ANOVA, REML and FE methods and followed by QML, ML and FML methods for all studied traits in cotton balanced data. On the other hand, the MML method had registered the lowest values of genetic variance for all studied traits. The values of MML, KMZ and SE methods were close for all studied traits.

Table 3. Estimates of genetic variance (σ_G^2) and environmental variance (σ_E^2) from the data set by different studied methods

Traits	Variances	Methods									
		ANOVA	REML	FE	QML	ML	FML	MML	MOM	KMZ	SE
No. B./P		5.668	5.668	5.668	4.892	4.892	4.892	4.289	6.613	4.356	4.356
		2.163	2.163	2.163	2.163	2.163	2.163	2.163	2.163	1.747	1.747
B.W. (g)		0.019	0.019	0.019	0.016	0.016	0.016	0.014	0.022	0.014	0.014
		0.010	0.010	0.010	0.010	0.010	0.010	0.010	0.010	0.008	0.008
S.I. (g)		0.310	0.310	0.310	0.270	0.270	0.270	0.238	0.361	0.240	0.240
		0.044	0.044	0.044	0.044	0.044	0.044	0.044	0.044	0.035	0.035
L. %		5.152	5.152	5.152	4.493	4.493	4.493	3.980	6.011	3.996	3.996
		0.487	0.487	0.487	0.487	0.487	0.487	0.487	0.487	0.394	0.394
S.C.Y./		47.089	47.089	47.089	40.939	40.939	40.939	36.156	54.938	36.420	36.420
P (g)		8.443	8.443	8.443	8.443	8.443	8.443	8.443	8.443	6.820	6.820
2.5%		4.935	4.935	4.935	4.299	4.299	4.299	3.804	5.757	3.823	3.823
S.L.		0.614	0.614	0.614	0.614	0.614	0.614	0.614	0.614	0.496	0.496
F.S.		0.790	0.790	0.790	0.687	0.687	0.687	0.607	0.922	0.611	0.611
		0.132	0.132	0.132	0.132	0.132	0.132	0.132	0.132	0.107	0.107
F.F.		0.198	0.198	0.198	0.173	0.173	0.173	0.153	0.231	0.154	0.154
		0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.028	0.023	0.023

In Fig. 1, the cluster analysis for the methods of genetic variance estimates based on studied traits resulted into groups (A and B). The group A divided into two clusters i.e., the cluster I (MOM method) and the cluster II (ANOVA, REML and FE methods). However, the group B comprised of two clusters i.e., the cluster III (QML, ML and FML methods) and the cluster IV (MML, KMZ and SE methods). The tree diagram detected minimum distance or dissimilarity between the methods of the clusters inside each group. While, the highest distance were found of the methods among the clusters in two groups. The methods were grouped in the same cluster, indicating a similarity between them. However, the results indicating differences existing between the four clusters. The obtained result can be explained with the data collected from population that had a balanced design.

Explicit solutions are given for the ML and REML equations under normality for four common variance components models with balanced (equal subclass numbers) data. Solutions of the REML equations are identical to ANOVA estimators. The ratio of mean squared errors of REML and ML solutions are also given [20]. There is little evidence that ML estimation is inferior to REML except for the appealing result that REML produces the same estimators as ANOVA methods with balanced data [21,22], and ANOVA estimators have well known optimal properties in these circumstances.

According to the results, the reason of finding higher for both balanced data of error variance

ratios obtained by most studied methods can be explained with the inhomogeneity of variances and not having normal distribution at sub levels of each factor related to studied traits data. Because, for the data which is consist of continuous variables, these methods estimation of variance components are based on generally normality distribution [1,8]. It is an expected result that these methods, except from ML, QML and FML methods, give the same estimation related to variance components. Because an ML, QML and FML method doesn't take into account the degree of freedom related to effects in model [1].

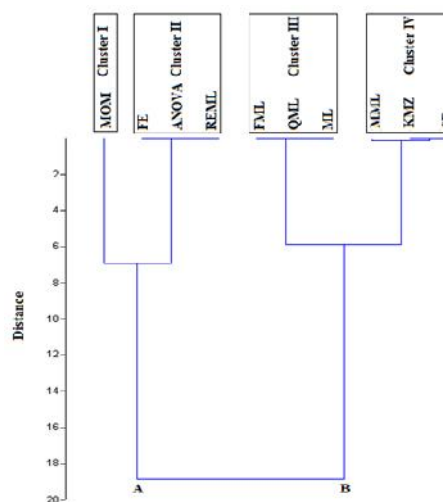


Fig. 1. Tree diagram for ten methods of estimates genetic variance using ward's method

Patterson and Thompson [23] stated that one of the important features of REML method gives the equal estimation to ANOVA method for the balanced data. Khatree and Gill [24] made some comparisons for different experimental design and ANOVA was emphasized as the most favourite method to estimate. In contrast with REML was emphasized as the most favourite method to estimate. Patterson and Thompson [23] mentioned that REML method gives the best result. Henderson [25] reported that if the degrees of freedom belonging to effects of factors are no more; REML and ML for balanced data give the best results.

Holland [26] reported that the REML method generally performed better, resulting in higher power of detection of correlations and more accurate 95% confidence intervals. Except for ML, the REML gave reasonable good estimates even if the full biomedel is complicated. This suggests that variance components can be estimated without bias using REML regardless of whether the design is balanced or not, whereas estimated variances obtained through the ML method tend to be influenced by the fixed effects. The mixed model approach-based estimators, such as REML have superior accuracy and precision compared to ANOVA estimators [27]. In study of comparative for variance components estimation methods on the balanced data, Doğan and Kilic [28] stated that the effect of studied traits are calculated equal by using ANOVA and REML methods and the lowest estimation is given by ML method.

Estimates of σ_G^2/σ_E^2 and σ_E^2/σ_P^2 ratios for studied traits based on variance components estimation methods are illustrated in Table 4. The highest values of σ_G^2/σ_E^2 ratio were observed for lint percentage using variance components estimation methods, followed by 2.5% span length, seed index and fiber fineness traits. However, the lowest values of σ_G^2/σ_E^2 ratio for boll weight trait were found. As for the comparison of σ_G^2/σ_E^2 ratio estimated by ten methods, the MOM method was recorded the maximum values, but the method of MML had small for all studied traits. The values of σ_G^2/σ_E^2 ratio according to methods of (ANOVA, REML and FE), (QML, ML and FML) and (KMZ and SE) were equal for all studied traits.

The ratio of error variance of phenotypic variance (σ_E^2/σ_P^2 ratio) by all studied methods exhibited that; the greatest values were registered for boll weight followed by number of bolls/plant, whilst, the lowest values were noticed for lint percentage. From compare among estimates of the variance components methods during σ_E^2/σ_P^2 ratio, the MML method was recorded the highest values for all studied traits, followed by the methods of QML, ML and FML, followed by KMZ and SE methods and followed by ANOVA, REML and FE methods and finally MOM method. Doğan and Kilic [28] made some comparison of error variance ratios according to variance components estimation methods, the error variance ratio for ANOVA and REML methods is found about 0.27, but it is found 0.42 by ML. As in balanced data the error ratio was calculated higher than the others.

Table 4. Estimates of σ_G^2/σ_E^2 and σ_E^2/σ_P^2 ratios among genotypes for studied traits based on studied methods

Traits	Variances	Methods									
		ANOVA	REML	FE	QML	ML	FML	MML	MOM	KMZ	SE
No. B./P		2.621	2.621	2.621	2.262	2.262	2.262	1.983	3.058	2.494	2.494
		0.276	0.276	0.276	0.307	0.307	0.307	0.335	0.246	0.286	0.286
B.W. (g)		1.845	1.845	1.845	1.583	1.583	1.583	1.379	2.152	1.746	1.746
		0.352	0.352	0.352	0.387	0.387	0.387	0.420	0.317	0.364	0.364
S.I. (g)		7.095	7.095	7.095	6.177	6.177	6.177	5.463	8.278	6.803	6.803
		0.124	0.124	0.124	0.139	0.139	0.139	0.155	0.108	0.128	0.128
L. %		10.573	10.573	10.573	9.221	9.221	9.221	8.168	12.336	10.152	10.152
		0.086	0.086	0.086	0.098	0.098	0.098	0.109	0.075	0.090	0.090
S.C.Y./P (g)		5.577	5.577	5.577	4.849	4.849	4.849	4.282	6.507	5.341	5.341
		0.152	0.152	0.152	0.171	0.171	0.171	0.189	0.133	0.158	0.158
2.5% S.L.		8.041	8.041	8.041	7.005	7.005	7.005	6.198	9.381	7.713	7.713
		0.111	0.111	0.111	0.125	0.125	0.125	0.139	0.096	0.115	0.115
F.S.		5.966	5.966	5.966	5.189	5.189	5.189	4.585	6.960	5.715	5.715
		0.144	0.144	0.144	0.162	0.162	0.162	0.179	0.126	0.149	0.149
F.F.		6.991	6.991	6.991	6.085	6.085	6.085	5.382	8.156	6.702	6.702
		0.125	0.125	0.125	0.141	0.141	0.141	0.157	0.109	0.130	0.130

3.4 Broad Sense Heritability

The broad sense heritability (BSH) estimates by the studied methods were displayed significant for all studied traits (Table 5). Because the values of BSH with studied methods were exceeded the values of standard errors for all studied traits. The values of BSH by different studied methods were ranged from 0.66 to 0.75, from 0.58 to 0.68, from 0.85 to 0.89, from 0.89 to 0.93, from 0.81 to 0.87, from 0.86 to 0.90, from 0.82 to 0.87 and from 0.84 to 0.89 for number of bolls/plant, boll weight, seed index, lint percentage, seed cotton yield/plant, 2.5% span length, fiber strength and fiber fineness traits, respectively. The ten studied methods of BSH estimates exhibited the greatest values (BSH > 0.60) for all studied traits according to Robinson et al. [17], except MML method for boll weight.

The highest and lowest values of BSH by MOM and MML methods were recorded for all studied traits, respectively. The estimates of BSH with studied methods were showed the same direction and results in genetic variance for all studied traits. The studied methods were exhibited various values of BSH, but their were close and showed same direction for all studied traits except boll weight. Because, the range values were low among these methods and varied from 0.04 to 0.10 for all studied traits.

A high value of BSH (>60%) indicate that the preponderance of dominance variance in governing the studied traits. Also, the genetic variance more than the environmental variance and plays a major part in total variance and will make the selection process effective for genetic improvement of these traits. While, low values of BSH indicate that environmental variance is of importance or environmental factors strongly influence trait and breeding for such trait is difficult. Individual plant selection may be practiced in early generations to make genetic gain when high values of BSH, but, the selection for yield should be based on replicated plot trials at multiple locations in more advanced generations when low values of BSH. The low values for Estimates of broad and narrow sense heritability indicate that effects by the environmental error were larger than those of genetic components [29]. El-Hashash [30] noticed that the values of BSH were highly for yield, yield components and fiber traits in single and double-cross hybrids. The higher BSH estimates were recorded for almost all the studied traits except seed index. Such results revealed that improvement in those traits can be made through direct phenotypic selection [19]. Eswari et al. [31] reported that the traits number of bolls/plant, ginning percentage, boll weight, 2.5% span length, seed cotton yield/plant exhibited high estimates of heritability.

Table 5. Estimates of broad sense heritability (h_b^2) along with their respective standard errors among genotypes for traits based on studied methods

Traits	Variances	Methods									
		ANOVA	REML	FE	QML	ML	FML	MML	MOM	KMZ	SE
No. B./P	h_b^2	0.724	0.724	0.724	0.693	0.693	0.693	0.665	0.754	0.714	0.714
	SE	0.135	0.135	0.135	0.146	0.146	0.146	0.155	0.124	0.139	0.139
B.W. (g)	h_b^2	0.648	0.648	0.648	0.613	0.613	0.613	0.580	0.683	0.636	0.636
	SE	0.160	0.160	0.160	0.170	0.170	0.170	0.178	0.149	0.163	0.163
S.I. (g)	h_b^2	0.876	0.876	0.876	0.861	0.861	0.861	0.845	0.892	0.872	0.872
	SE	0.069	0.069	0.069	0.077	0.077	0.077	0.084	0.061	0.072	0.072
L. %	h_b^2	0.914	0.914	0.914	0.902	0.902	0.902	0.891	0.925	0.910	0.910
	SE	0.050	0.050	0.050	0.056	0.056	0.056	0.062	0.044	0.052	0.052
S.C.Y./I	h_b^2	0.848	0.848	0.848	0.829	0.829	0.829	0.811	0.867	0.842	0.842
	SE	0.083	0.083	0.083	0.092	0.092	0.092	0.100	0.074	0.086	0.086
P (g)	h_b^2	0.889	0.889	0.889	0.875	0.875	0.875	0.861	0.904	0.885	0.885
	SE	0.063	0.063	0.063	0.070	0.070	0.070	0.077	0.055	0.065	0.065
F.S.	h_b^2	0.856	0.856	0.856	0.838	0.838	0.838	0.821	0.874	0.851	0.851
	SE	0.079	0.079	0.079	0.088	0.088	0.088	0.096	0.070	0.082	0.082
F.F.	h_b^2	0.875	0.875	0.875	0.859	0.859	0.859	0.843	0.891	0.870	0.870
	SE	0.070	0.070	0.070	0.078	0.078	0.078	0.085	0.062	0.072	0.072

4. CONCLUSIONS

Variance components methods of one way random effects model for studied traits in cotton balanced data exhibited that some studied methods were found equal to each other, while the some methods differ only slightly from each other. The genetic variance comparison according to ten methods were highest by MOM method, followed by ANOVA, REML and FE methods and followed by QML, ML and FML methods, while, the MML method was gave the lowest values for all studied traits. The ten studied methods for BSH and σ_G^2/σ_E^2 ratio estimations were showed the same results for genetic variance for all studied traits, and quite the opposite for σ_E^2/σ_P^2 ratio.

COMPETING INTERESTS

Author has declared that no competing interests exist.

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