

ORIGINAL ARTICLES

Estimation of Genetic Variance and its Components in New Synthetic "Moshtohor₂" of White Maize

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ABSTRACT

This study was undertaken at Experimental and Research Center, Faculty of Agriculture, at Moshtohor to estimate genetic variance components as well as the expected gain from different methods of selection in maize. A design 1 mating system consisting of 36 males crossed to four females was developed in new synthetic "Moshtohor₂" in 17th May 2008 season. These entries were evaluated in 30th May 2009 season. The studied traits were: tasseling and silking dates, ear length, ear diameter, no. of rows/ear, no. of kernels/row, 100-kernel weight and grain yield/plant. Genetic components were calculated according to Comstock and Robison, (1948). The estimates of genetic and environmental variances were used to calculate the expected genetic gain in intra-population according to Hallaur and Miranda, (1981). The male and female variance components were significant for all traits. The additive genetic variance was significant for all traits except ear diameters. However, the dominance genetic variances were significant for all traits except ear length and no. of kernels/row. Ratio of σ^2D/σ^2A was over dominance for all traits except ear length and no. of kernels/row where partial dominance was detected. In general, the dominant genetic variance was more important than additive variance for all traits. Low to moderate heritability values in narrow sense were obtained for all traits. The heritability values ranged from 0.68 for no. of kernels/row to 0.10 for ear diameter. The expected genetic improvement gain% from selection for grain yield/plant was 7.54, 15.08, 3.61, 7.22, 9.02, 12.57, 24.1 and 18.94% $\Delta g\%/cycle$ by mass selection one sex and two sexes, modified ear-to-row one sex and two sexes, half-sib selection, full sib selection, test cross and s1 selection, respectively. The most efficient scheme would be test cross population followed by S₁ selection.

Key words: Maize, Genetic Variance, Additive, Dominance, Heritability, Selection Methods.

Introduction

Estimation of genetic variance components in maize population is of prime importance for breeder to select the best breeding programs. The choice of the most efficient breeding scheme for improving maize population is dependent upon the relative amount and type of genetic variability involved. Predominance of additive genetic effects suggests the effectiveness of selection within population. While, hybrid program may be the appropriate choice if non-additive variance is the major component.

Design 1 mating scheme which was suggested by Comstock and Robinson 1948, has been extensively used for estimating genetic variations for quantitative characters in maize populations. Several workers reported that additive genetic variance constituted the major portion of total genetic variance in maize varieties and composites. Among those are: El-Hosary (1987), Sedhom, (1993), Mani *et al.*, (2000) and Raposo and Ramalho (2004). On the other hand, Malvar *et al.*, (1996), Shehata, (1998) and Soliman *et al.*, (2005) revealed that non-additive gene effects were played an important role in the inheritance of most traits.

The main objectives of this investigation were: to estimate the amount of genetic variance and its components in new synthetic "Moshtohor₂", to estimate heritability values for all the studied characters, and to estimate the expected genetic advance for grain yield from six selection methods.

Materials and Methods

The field work dealing with the present study was conducted during the two seasons 2008 and 2009 at Moshtohor Agricultural Research Station. New synthetic "Moshtohor₂" was used as base population in this study which was composed by Prof. Dr. A.A.M. El-Hosary. In 17th May of season 2008, 100 ridges new synthetic "Moshtohor₂" were grown to produce the material seeds of design mating as outlined by Comstock and Robinson, (1948). One plant was chosen at random to be used as male pollen parent and was crossed with seven random plants used as female plants. At harvest, ear were taken from the first four females per each male

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which had sufficient seeds for evaluation. Only 36 males groups (half-sib) families were obtained each had four full-sib families. Therefore, the total numbers of full-sib families were 144. The thirty six male groups (half-sib) were divided at random into four sets each of 9 half-sib families. In 30th May of season 2009, the full-sib families (144) were grown in a randomized complete block design with three replications. Each full-sib family was represented by one ridge (plot) 6 m long and 70 cm apart. Spacing between hills was 25 cm in one side of the ridge. Maize was grown under irrigation and was fertilized at a rate of 90 kg N/fad.

Data were collected from guarded plants within each plot and were averaged over the number of harvested plants. The studied traits were, grain yield per plant (g) adjusted to 15.5% moisture, days to 50% silking and tasseling, ear length, ear diameter no. of rows/ear, no. of kernels/row and 100-kernel weight (g).

Estimates of genetic components were calculated according to Comstock and Robinson (1948). The estimates of genetic and environmental variances were used to calculate the expected genetic advance from the six methods of intra-population according to Hallaur and Miranda (1981).

Results and Discussion

The genetic variance components were calculated from Design-1 as suggested by Comstock and Robinson (1948). Assumptions of this type of analysis are; regular diploid, random distribution of genotypes relatives, random choice of individuals mated for production of experimental progenies, no maternal effects, no multiple alleles and no epistasis. Failure of the assumptions given above to hold would result in biased estimates of the genetic variances and the parameters associated with them. The assumption of diploid inheritance, no environmental correlations among relatives and no maternal effects were fulfilled in the material under study. New synthetic "Moshtohor₂" as an open-pollinated population and it is produced annually, and is in linkage equilibrium or no correlation of genotypes at separate loci may exist. The random choice of individuals mated for production of experimental progenies was not fulfilled. It is caused negative estimates of the dominance genetic variance. Also, the assumption of no epistasis may not be fulfilled. Its epistasis is operating, both additive and dominance variances would be overestimated. The effect of multiple alleles, alone would not change the genetic expectation of covariance full-sib and covariance half-sib.

The analysis of variance for each trait is given in Table (1). The male and female variance components were significant for all traits. Male variance gave the importance part of total genetic variances for all studied traits (Table, 1). The estimates of variance components for males and females were used to calculate additive and dominance variance.

Table 1: Mean square, mean (X) and coefficient of variability (C.V. %) for all studied traits in new synthetic "Moshtohor₂" H.S. families.

S.O.V	d.f	Days to 50% tasseling	Days to 50% silking	Ear length	Ear diameter	No of rows / ear	No of kernels / row	100- kernel weight	Grain yield / plant
Sets (S)	3	3.10**	4.03**	1.78	0.47	7.43**	40.48**	13.39	3138.97**
Rep. (R)/S	8	1.89**	1.41**	1.86	0.21	1.53	28.13**	16.04	703.64*
Males (M)/S	32	9.78**	12.67**	10.72**	0.71**	4.44**	73.67**	20.54**	2442.11**
Females (F)/M/S	108	5.68**	6.67**	4.37**	0.58**	2.16**	24.82**	13.52**	1061.76**
Error	280	0.16	0.18	1.88	0.36	1.00	9.01	9.13	337.49
X	3	64.63	67.78	15.23	4.63	13.49	30.24	33.14	147.95
C.V. (%)		0.62	0.64	9.01	12.99	7.40	9.93	9.12	12.42

*and** Significant at 5% and 1% level of probability, respectively.

Estimates of additive and dominance variance are presented in Table (2). The additive genetic was significant for all traits except ear diameters. However, the dominance variance was significant for all traits except ear length and no. of kernels/row. Therefore, it could be concluded that the dominance variance was the major and the significant source of the genetic variations within new synthetic "Moshtohor₂". These results are in general agreement with those reported by El-Hosary (1987) and Sedhom (1993).

The additive genetic variance was less important than the non-additive one. Ratio of σ^2D/σ^2A was over dominance for all traits except ear length and no. of kernels/row where partial dominance was detected. In general, the dominant genetic variance was more important than additive variance for all traits.

In this respect, suggested the important role of dominant genetic variance than additive variance. For instance, Malvar *et al.* (1996) showed the dominance was larger than additive genetic variance in the inheritance of grain yield/plant, ear and plant heights as well as ear length. The obtained results are in good agreement with those reported by Malvar *et al.* (1996) and Soliman *et al.* (2005) revealed that non-additive gene effects were played an important role in the inheritance of most traits.

On the other hand, Pal *et al.* (1986), Mani *et al.* (2000), Alves *et al.* (2002), Raposo and Ramalho (2004) and Revilla *et al.* (2004) where they found that the additive genetic variance was predominant in the inheritance of yield and most of its component in maize.

Table 2: Genotypic (σ^2G) variance, additive (σ^2A), dominance (σ^2D) variance, degree of dominance (σ^2D/σ^2A), heritability narrow sense (h_n^2) of all studied traits in new synthetic "Moshthor₂".

Characters	σ^2G	σ^2A	σ^2D	σ^2D/σ^2A	h_n^2
Days to 50 tasseling	7.36	1.37	5.99	4.38	0.18
Days to 50% silking	8.65	2.00	6.65	3.32	0.23
Ear length (cm)	3.31	2.12	1.20	0.56	0.54
Ear diameter (cm)	0.29	0.04	0.25	5.74	0.10
No. of rows/ear	1.55	0.76	0.79	1.04	0.40
No. of kernels/raw	21.08	16.28	4.80	0.29	0.68
100-kernel weight (g)	5.86	2.34	3.52	1.51	0.26
Grain yield/plant (g)	965.70	460.12	505.59	1.10	0.43

Generally, Hallauer and Miranda (1981) summarized the estimates of σ^2A and σ^2D from many scientific reports (99 reports) for 19 different traits. They showed that most estimates were obtained by using mating designs I, II and III. Also, few estimates for F_2 population were obtained by Mather's models (1949) and estimates from diallel analysis were included. Also, they concluded for yield that the ratio of dominance to additive variance was quite large and dominance variance seemed to be important in the expression of yield. But, they added that, assuming, no epistasis and linkage effects, σ^2A on the average accounted for 61.2% and σ^2D accounted for 38.87% of the total genetic variations. The ratios of σ^2D/σ^2A were considerably higher for other traits than for yield.

From the previous representation, our results were not completely agreed with those presented in the review of literature. It is expected and logic that the obtained results herein may be due to genetic back grounds of the population and mating system designs used for estimating the genetic variance components in each case.

Estimates of the additive, dominance and error variances were used to estimate the heritability in narrow sense for full-sib families. The heritability values ranged from 0.68 for no. of kernels/row to 0.10 for ear diameter. Low heritability values were detected for all traits except ear length and no. kernels/row indicating that dominance genetic variance played the major role in the inheritance of these traits. These results confirmed the previous results which indicated the majority of dominance genetic variance in the total genetic variances in this respect. Moderate heritability values were obtained for the exceptional two traits, suggested the important role of additive genetic variance obtained for both traits.

In this respect, many authors reported estimates of heritability in narrow sense. For instance Nawar *et al.* (1983) found that heritability values in narrow-sense were (63.9%) for ear height, (57.4%) for days to tasseling (50.5%) for ear length and 44.4% for grain yield and (32.9%) for ear diameter. Nawar (1985) showed that heritability in narrow-sense were high for plant height (3%), ear diameter (64%), no. of grains/row (91%) and it was for grain yield (34%) in the composite variety "Shedwan 3".

El-Hosary (1986) showed that heritability in narrow sense were high for plant height (84.04%), ear diameter (85.92%), no. of rows/ear (77.08) and it moderate for ear husk 47.51, ear length 52.22%, no. of kernels/row and grain yield/plant 62.11% in open pollinated variety "American Early".

El-Hosary (1987) estimated heritability in narrow sense in the composite variety "Cairo 1" maize. Low to high heritability values ranged from 67.09 for number of kernels/row to 23.53 for number of rows/ear.

Clavdio-Jobet and Borriga (1988) showed that heritability in narrow-sense was high for plant height (51%) and ear length 54% but low for grain yield 22% and 14% for number of ears/plant. Nawar *et al.* (1995) estimated heritability values in Giza₂ maize population. They found that estimates of heritability were (46%) for number of rows/ear, (5%) for no. of kernels/row (13%) for 100-kernel weight, (37%) for ear length, (11%) for ear diameter, (21%) for plant height, (43%) for ear height, (96%) for days to tasseling, (46%) for days to silking. Barakat (2003) studied genetic variance for grain yield and other valuable traits in Gemmeiza yellow maize population. He found that estimates of heritability for all the studied traits were high.

In general, Hallauer and Miranda (1981) summarized the heritability estimates either in broad and narrow sense for different traits. Their presentations were collected from 99 published reports as shown in the following Table after few modifications.

Yield	Ear length	Ear diameter	No. of rows/ear	100-kernel weight	Ear height	Plant height	Days to tasseling
18.7	38.1	36.1	57.0	41.8	66.2	56.9	57.9
(99) [@]	(36)	(35)	(18)	(11)	(52)	(15)	(48)

@ Digits between brackets refer to the number of reports.

Moreover, Falconar and Mackay (1996) stated that genetic gain of selection for a given traits depend on the heritability estimates. Heritability is going to determine the breeding strategy. Trait with high heritability can be selected on individual plant basis. On the other hand, single-plant selection would be inefficient or less efficient for low heritability traits and a type of family selection will be required. Also, the extensions of replicated testing (reps. and environments) depend on the heritability. More testing is required for low heritability traits. Lastly, Hallauer and Miranda (1988) demonstrated that different traits showed different heritability estimates.

They summarized the ranges and average estimates of heritability for maize traits on a per plot basis in maize as follows:

Heritability estimates (%)	Trait
H>70	Percent of oil
50<H>70	Plant and ear heights, kernel row number, days to flower and grain moisture
30<H<50	Number of ears, ear length, ear diameter, kernel weight, husk extension and diameter
H<30	Grain yield and kernel depth

The six methods of intra-population selection used to estimate the predicted genetic advance were; mass selection, modified-ear-to-row selection, half-sib selection, full-sib selection, S₁ selection and test cross selection with a broad-base tester or with an inbred-line tester.

It is well known that in the first three methods of selection, no controlled pollination is necessary, but they require adequate isolation during the selection program. Moreover, in mass selection, if selection is practiced on the maternal plant only (one sex) genetic gain will be reduced as a result of lacking control for the pollen source. However, the genetic advance from selection will be doubled if mass selection is practiced in both sexes.

The six methods of intra-population selection used to estimate the predicted genetic advance were; mass selection, modified ear-to-row selection, half-sib selection, full-sib selection, S₁ selection and test cross selection with a broad-base tester or with an inbred-line tester. The expected and predicted genetic gains for all traits from six methods of selection are presented in Table (3).

The first three methods, no controlled pollinations are necessary, but adequate isolation is essential. With mass selection, when it is practiced on the maternal plants only (one sex), gain will be reduced because of the lack of parental control for the pollen source ($C=1/2$). Full-sib family selection requires only two generations per cycle if plant crosses are made between plants from different selected families because recombination and family formation will be accomplished simultaneously, i.e., season₁, (recombination family formation) and season₂ performance traits.

The expected improvement from six methods were: 0.67 and 1.35; 0.59 and 1.18; 1.47; 1.24; 3.14 and 1.76 for tasseling date, 0.87 and 1.74 ; 0.69 and 1.38 ; 1.75, 1.56, 3.63 and 2.23% for silking date, 5.34 and 10.67; 2.26, and 4.52; 5.65; 8.63; 15.72 and 13.31% for ear length, 1.0 and 2.0; 0.45 and 0.89; 1.11; 1.79; 5.2 and 3.02% for ear diameter, 3.09 and 6.19; 1.37 and 2.73; 3.42; 5.18; 10.36 and 8.09% for no. of rows/ear, 8.59 and 17.18; 3.54 and 7.08; 8.86; 13.41; 22.45 and 20.23 for no. of kernels/row, 1.59 and 3.19; 0.65 and 1.30; 1.62; 2.74; 6.43 and 4.62 for 100-kernel weight, 7.54 and 15.08; 3.61 and 7.22; 9.02; 12.57; 24.10; and 18.94% for grain yield/plant by mass selection (one sex and both sexes), modified ear two row (one sex and both sexes), half-sib, full-sib, test cross population as a tester and S₁ selection, respectively.

Table 3: Genetic gain for all studied traits from six methods of selection in new synthetic "Moshtohor₂".

Method	Grop season/ cycle	Tasselingdate		Silking date		Ear length		Ear diameter	
		Δg	Δg%	Δg	Δg%	Δg	Δg%	Δg	Δg%
Mass selection	1								
a) One sex		0.44	0.67	0.59	0.87	0.81	5.34	0.05	1.00
b) Both sexes		0.87	1.35	1.18	1.74	1.63	10.67	0.09	2.00
Modified ear to row	1								
a) One sex		0.38	0.59	0.47	0.69	0.34	2.26	0.02	0.45
b) Both sexes		0.76	1.18	0.94	1.38	0.69	4.52	0.04	0.89
Half - Sib	2	0.95	1.47	1.17	1.75	0.86	5.65	0.05	1.11
Full- sib	2	0.80	1.24	1.06	1.56	1.31	8.63	0.08	1.79
Test cross population as a tester (HT)	3 or 4	2.03	3.14	2.46	3.63	2.39	15.72	0.24	5.20
S1 selection	3	1.14	1.76	1.51	2.23	2.03	13.31	0.14	3.02
G. C. V. %		0.00		4.40		11.95		11.59	
ph. C.V.%		0.04		4.42		13.03		13.80	
Method	Grop season/ cycle	No of rows/ ear		No of kernels/ row		100 - kernel weight		Grain yield/plant	
		Δg	Δg%	Δg	Δg%	Δg	Δg%	Δg	Δg%
Mass selection	1								
a) One sex		0.42	3.09	2.60	8.59	0.53	1.59	11.15	7.54
b) Both sexes		0.83	6.19	5.19	17.18	1.06	3.19	22.30	15.08
Modified ear to row	1								
a) One sex		0.18	1.37	1.07	3.54	0.21	0.65	5.34	3.61
b) Both sexes		0.37	2.73	2.14	7.08	0.43	1.30	10.68	7.22
Half - Sib	2	0.46	3.42	2.68	8.86	0.54	1.62	13.35	9.02
Full- sib	2	0.70	5.18	4.05	13.41	0.91	2.74	18.59	12.57
Test cross population as a tester (HT)	3 or 4	1.40	10.36	6.79	22.45	2.13	6.43	35.65	24.10
S1 selection	3	1.09	8.09	6.12	20.23	1.53	4.62	28.03	18.94
G. C. V. %		9.24		15.18		7.31		21.00	
ph. C.V.%		10.18		16.23		9.01		22.19	

Horner *et al.*, (1973) reported greater improvement in the test-cross yields for the Flureda 767 sub-strain improved with the population *per se* as tester. With the assumption of complete dominance at all loci and negligible epistasis, statistical theory would predict superiority for the use of an inbred line from the population as tester. The genetic variance among test cross would be greater, because an inbred line would have a gene frequency of 0.0 or 1.0 at all loci for the favourable allele. Our results showed an average predicted increase from the test cross selection of 24.10% through one cycle. Abd El-Sattar (2003) obtained the expected and predicted gain per cycle by test cross selection where the value was 36.5 g ($\Delta g = 21.64\%$) in Giza 2. EL- Seidy *et al.*, (2010) obtained an expected gain in grain yield/plant by test cross selection as $\Delta g/\text{cycle}$ was 25.20 and 18.81% with Nobaria and Gemmeza yellow populations, respectively. The expected and predicted genetic advance from S_1 selection in the present investigation was 28.03 g ($\Delta g\% = 18.94\%$) in grain yield/plant. Also El-Hosary (1987) with American Early variety obtained an average increase 43.34 $\Delta g/\text{cycle}$ ($\Delta g\% = 16.6\%$). EL- Seidy *et al.*, (2010) obtained expected gain a $\Delta g\% = 20\%$ and 11.14% per cycle by S_1 selection for Nubaria and Gemmeza yellow populations, respectively.

From the previous result it could be concluded that test cross and selection followed by full-sib Family selection may be taken into consideration to improve this population under study where they showed the highest expected values of gain from selection.

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