# GENETIC VARIANCE, ITS COMPONENTS AND NATURE OF GENE ACTION IN MAIZE UNDER TWO NITROGEN RATES EI-Badawy, M. EI. M.

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# ABSTRACT

A half diallel cross between 8 inbred lines of maize (Zea mays L.) was evaluated under two different nitrogen rates for five quantitative characters i.e. days to 50% silking, no. of rows/ear, no. of kernels/row, 100-kernel weight and grain yield/plant in RCBD with three replications. Nitrogen rates, genotypes, parents, hybrids and parent vs crosses mean squares were significant for all traits under study. Significant parent's x nitrogen rates mean squares were obtained for all traits except, no. of rows/ear and 100-kernel weight. However, insignificant interaction mean squares between hybrid and nitrogen rates were detected for all traits, except days to 50% silking and no. of rows/ear. The mean square associated with general and specific combining ability was significant for all traits except no. of rows/ear in high nitrogen rate (120 Kg n/f). The mean squares of interaction between nitrogen rates and GCA were significant for no. kernels/row. As for days to 50% siliking and for no. of rows/ear, significant SCA x nitrogen rate were obtained. High GCA/SCA ratios which largely exceeded the unity were obtained for 100-kernel weight at low rate of nitrogen fertilization and no. of rows /ear in both nitrogen rates and the combined analysis. The ratio for GCAxN/GCA was higher that ratio of SCAxN/SCA for all traits except for no. of rows/ear. The parental inbred lines no. 3 and 4 were a good combiners for days to 50% siliking and no. of rows/ ear and grain yield/plant. The parental inbred line no. 6 was a good combiner effects for no. of kernels/row, 100kernel weight and grain vield/plant. For grain vield/ plant, 18 crosses had the highest values for SCA. Also, the cross P1xP3 have significantly out yielded the check hybrid S.C. 162 on both nitrogen rates and the combined analysis. The additive component "D" reached the significant level of probability for all traits except silking date and grain yield/plant at both nitrogen rates. Moreover, the component  $t^2$  was significant for both exceptional traits. In addition, the regression coefficients of parental offspring covariance (Wr) on the parental array variance (vr) were significant in both traits to less than unity. Significant values for the dominance component H<sub>1</sub> were obtained for all traits. Moreover, values of  $H_1$  were significantly larger in magnitude than the respective D values in most cases. Significant "h<sup>2</sup>" values were obtained in all traits in both nitrogen rates. Values of  $(H_1/4 H_2)$  was that largely deviated from 0.25 were obtained for most traits at both nitrogen rates. The same trend was detected by "F" values. With the exception of no. of rows/ ear, low heritability values were detected for all traits. For no. of rows/ ear moderate heritability values were detected. Overdominances were obtained by (H/D)<sup>0.5</sup> for all traits . Also, the same trend was obtained by wr/vr graph. The array points were widly scattered for all the characters. The parental inbred line no. 1 for silking date, no. 3 and 6 for no. of rows/ ear, no.6 for no. of kernels/row, no. 7 for grain yield/plant in both nitrogen rates and no.6 and 3 for 100kernel weight at low and high nitrogen rates, respectively seemed to be carry the most dominant genes responsible for the expression of these traits.

# INTRODUCTION

Maize (Zea mays L.) is considered of the most important cereal crops in the world. This crop is used human consumption as well as animal feeding. It also used in industrial purposes such as manufacturing starch and coking oils. The estimation of the genetic variance and its components are of great importance as for the improvement of maize breeding program. The diallel analysis has been used by many investigators to assist in the investigations of partitioning the genetic variance into its components by using Griffing's (1956) and Hyman,s (1954) methods to obtain and test various genetic estimates (Nawar et al., 1979, Sedhom 1994, Nawar et al. 2002, Balci and Turgut 2006, El-Hosary et al., 2006 and Sedhom et al., 2007). The objectives of the present study were (1) To estimate general combining ability GCA and specific combining ability SCA effects and their interaction with the two nitrogen rates. (2) To determine hybrid mean performance and heterosis for the eight selected inbred lines. (3) To estimate the heritability and the genetic components of the total variability and to provide sufficient information of the genetic nature for genes controlling the inheritance of the studied traits.

# MATERIALS AND METHODS

#### **Field experiment**

Eight yellow inbred lines (Zea mays L.) were used as parents in this study. P<sub>1</sub> (101), P<sub>2</sub> (304-2), P<sub>3</sub> (302-f), P<sub>4</sub> (210-B), P<sub>5</sub> (103), P<sub>6</sub> (120-A-4),  $P_7$  (220-c) and  $P_8$  (202-A) were developed at the Department of Agronomy, Fac. of Agric at Moshtohor, Benha Univ. by Prof. Dr. A.A.M. El-Hosary. In the 2007 season the eight inbred lines were split planted in 1<sup>st</sup>, 10<sup>th</sup> and 20<sup>th</sup> May to avoid differences in flowering time and to secure enough hybrid seed. A half diallel set of crosses was carried out among the eight inbred lines by hand method giving a total of 28 crosses. In 17th May 2008 season, two experiments were undertaken in two fertilizer rates (60 kg N/fed. and 120 kgN/fed.) at the Agricultural Research and Experimental Station of the Fac. of Agric., Moshtohor. Each experiment included the eight inbred lines and 28 crosses along with S.C. 162 (check variety). A randomized complete block design with three replications was used. Each plot consisted of two ridges of six m length and 70 cm width. Hills were spaced by 25 cm with three kernels per hill on one side of the ridge. The seedlings were thinned to one plant per hill. The cultural practices were followed as usual for ordinary maize field in the area. Random sample of 10 guarded plants in each plot were taken to evaluate no. of rows/ear, no. of kernels/row, 100-kernel weight and grain vield/plant which was adjusted for 15.5% moisture moreover days to 50% silking dates (days) in 50% of the plant silked.

#### Data analysis

The obtained data were statistically analyzed for analysis of variance by using computer statistical program MSTAT-C. General and specific combining ability estimates were estimated according to Griffing's (1956) diallel cross analysis designated as method 2 model I for each experiment. The genetic components of the total variability and to provide sufficient

information of the genetic nature of the studied traits were estimated by Hyman,s (1954) method. The combined analysis of the two experiments was carried out whenever homogeneity of variance was detected (Gomez and Gomez, 1984). Heterosis expressed as the percentage deviation of the  $F_1$  mean performance from S.C. 162 was determined.

### **RESULTS AND DISCUSSION**

The analysis of variance for ordinary analysis of the two nitrogen rates as well as the combined analysis for all traits is given in Table (1). Nitrogen rates mean squares were found to be significant for all traits, with mean values in high rate being higher than those in low rate of nitrogen for all traits. The increase in these traits at high rate of nitrogen might be due to the simulating effect of nitrogen on metabolic process in maize plant. These results are in agreement with those obtained by (Hassan, 1999 and Medici *et al.*, 2004).

Mean squares for genotypes, parental inbred lines,  $F_1$  hybrids and parent vs crosses were found to be significant for all traits in both nitrogen rates as well as the combined analysis. This indicated the wide diversity between the parental lines used in the present study. Significant genotypes x nitrogen rates interaction mean squares were obtained for days to 50% silking, no. of rows/ear and no. of kernels/row, revealing that the performance of genotypes were differed from rate of nitrogen to another.

Significant parent's x nitrogen rates mean squares were obtained for all traits except, no. of rows/ear and 100-kernel weight. This result might reveal higher repeatability of performance of the parental inbred lines under different nitrogen rates. However, insignificant interaction mean squares between hybrid and nitrogen rates were detected for all traits except days to 50% silking and no. of rows/ear, revealing that the performances of hybrids were responded similar to environmental changes.

Insignificant interaction between mean squares due to parent vs crosses and nitrogen rate were obtained for all traits. This result indicates that the heterotic effects were not affected by the nitrogen changes.

#### Mean performances

The mean performances of the tested eight inbred lines, their 28 hybrids and S.C. 162 at each nitrogen rate as well as the combined analysis for grain yield and at the combined analysis for other traits are presented in table (2).

For days to 50% silking, the inbred line  $P_1$  at the combined analysis gave significant lowest value of this trait. However, inbred line P5 and  $P_7$  had significantly the latest one.

The inbred line no. 4 and 7 had significantly the highest mean values for no. of rows/ ear followed by inbred lines no. 3, 2 and 5. However, the inbred line no. 1 showed the lowest one for this trait. The inbred lines no. 6 and 7 showed significant higher number of kernels/ row. However, the parental inbred line no. 2 gave the lowest one for this trait. The inbred line no. 6 had significantly mean value for 100-kernel weight. However, the inbred lines no. 3, 5 and 7 showed the lowest ones for this trait.

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The parental inbred line no. 6 in the first nitrogen rate, 7 followed by 6 at high nitrogen rate and in the combined analysis had the highest mean values of grain yield/ plant. These inbred lines exhibited high mean values for one or more of the traits contributing to grain yield. However, the parental inbred line no. 1 gave the lowest one for this trait in both nitrogen rates and the combined analysis.

With the exceptional of the all hybrids, the cross  $P_2xP_6$  surpassed the earlier or the lowest performing than S.C. 162 for days to 50% silking revealing that all hybrids were shifted towards the earliness direction. The earliness of silking date was detected by crosses  $P_3xP_5$ ,  $P_4xP_5$  and  $P_5xP_7$ .

Earliness in maize is favourable for escaping destructive injuries caused by *Sesamia cretica* ledi *chilo simplex* But and *Pyrausta nubilialis*.

As for number of rows/ ear, the cross  $P_2xP_7$  had the highest number of rows/ ear followed by crosses  $P_1xP_3$ ,  $P_1xP_4$ ,  $P_2xP_4$ ,  $P_3xP_7$  and  $P_3xP_8$ .

For number of kernels/ row, the hybrid  $P_1xP_3$ ,  $P_1xP_4$ ,  $P_1xP_6$ ,  $P_2xP_6$ ,  $P_3xP_4$ ,  $P_4xP_6$ ,  $P_5xP_7$  and  $P_5xP_8$  had the highest values in the combined analysis. The crosses i.e.  $P_1xP_3$ ,  $P_1xP_5$ ,  $P_1xP_8$ ,  $P_2xP_3$ ,  $P_2xP_8$ ,  $P_3xP_6$ ,  $P_3xP_8$  and  $P_4xP_6$  gave the highest mean values for 100-kernel weight. However, the crossP\_1xP\_7 gave the lowest one for this trait.

Concerning grain yield/ plant the crosses  $P_1xP_3$  and  $P_1xP_4$  in low nitrogen rate and  $P_1xP_3$  in high nitrogen rate and in the combined analysis had significant superiority over the best check hybrid (S.C. 162). These hybrids exhibited significant increase in one or more of traits contributing to grain yield (Table 2). The fluctuation of hybrids from nitrogen rate to another was detected for most traits. These results would be due to significant interaction between hybrids and nitrogen rates. **Heterosis:** 

Heterosis expressed as the percentage deviation of  $F_1$  mean performance from S.C. 162 value for grain yield/plant is presented in Table (2). With the exception of four crosses  $P_1xP_2$ ,  $P_1xP_7$ ,  $P_2xP_8$  and  $P_7xP_8$ , all hybrids gave significant positive or insignificant heterotic effects relative to S.C. 162. Also, the eight hybrids  $P_1xP_3$ ,  $P_1xP_4$ ,  $P_2xP_3$ ,  $P_2xP_5$ ,  $P_3xP_4$ ,  $P_3xP_5$ ,  $P_3xP_6$ ,  $P_3xP_8$  and  $P_5xP_7$ , one cross  $P_1xP_3$  and one cross  $P_1xP_3$  out yielded significantly the check hybrid S.C. 162 for low, high nitrogen rates and the combined analysis, respectively. Hence it could be concluded that these crosses offer possibility for improving grain yield of maize. These hybrids and material may be useful for testing under different investigations, other locations and years. Many investigators reported high heterosis for yield of maize; i.e. (Nawar *et al.*, 2002, Shafey *et al.*, 2003, Singh *et al.*, 2004, El-Hosary *et al.*, 2006 and Sedhom *et al.*, 2007).

Table (2): Mean performance of all genotypes at each nitrogen rates and the combined analysis for grain yield/ plant as well as heterosis relative to SC 162 and at the combined analysis for other traits.

other traits.														
	Dayes	No. of	No. of	100-		Grain								
	to		kernels			ield/ pla	nt							
Genotype (G)	50% silking	10.07		weight	60 kgn/f	120 kgn/f	Comb.							
P1	69.83	9.17	17.80	25.75	32.27	39.00	35.63	Heterosis for						
P2	69.67	12.08	16.90	27.25	45.58	45.87	45.72	grain yield/ plant relative to						
P3	71.67	13.42	17.71	21.75	29.67	45.50	37.58		SĊ. 162					
P4	70.50	14.80	17.80	23.75	37.50	72.83	55.17							
P5	73.83	11.15	22.85	21.33	40.00	41.67	40.83							
P6		10.18	26.76	32.00	72.80	84.93	78.86							
P7	73.83	15.15	28.71	21.75	52.13	114.25	83.19							
P8	70.50	10.83	17.23	24.50	50.00	61.67	55.83	60 kgn/f	120kgn/f	comb.				
P1xP2	66.50	13.00	28.39	26.00	64.96	107.18	86.07	-43.12**	-29.86**	-35.53**				
P1xP3	64.00	15.17	37.02	35.00	166.63	204.95	185.79	45.91**	34.13**	39.17**				
P1xP4	64.50	15.40	38.95			159.60	156.45	34.24**	4.45	17.19				
P1xP5	64.67	11.93	34.23	35.83	128.20	140.17	134.18	12.26	-8.27	0.51				
P1xP6	65.67	13.03	36.01			125.90	119.95	-0.18	-17.60	-10.15				
P1xP7	64.83	14.60	31.05	23.50	89.20	117.60	103.40	-21.89*	-23.04*	-22.55*				
P1xP8	64.50	12.10	32.51	36.25	130.90	142.90	136.90	14.62	-6.48	2.55				
P2xP3		14.08	32.85			164.70	151.50	21.10*	7.79	13.48				
P2xP4	66.50	15.28	32.93	34.25	123.00	149.30	136.15	7.71	-2.29	1.99				
P2xP5	64.17	12.90	34.29	34.25	143.78	153.90	148.84	25.90*	0.72	11.49				
P2xP6	70.17	13.30	36.20			147.40	139.90	15.94	-3.53	4.79				
P2xP7	64.00	16.70	34.23	33.00	114.40	140.00	127.20	0.18	-8.38	-4.72				
P2xP8	64.50	13.63	31.85	35.00	89.18	117.85	103.51	-21.91*	-22.87*	-22.46*				
P3xP4	64.50	14.72	36.50	28.00	139.87	172.40	156.13	22.48*	12.83	16.95				
P3xP5	61.67	14.20	34.98			151.70	148.75	27.67**	-0.72	11.42				
P3xP6	64.33	14.13	33.60	36.50	143.80	153.35	148.58	25.92*	0.36	11.29				
P3xP7	67.33	15.63	32.23	29.50	105.20	138.73	121.97	-7.88	-9.21	-8.64				
P3xP8	64.33	15.33	35.18	39.58	137.67	144.65	141.16	20.55*	-5.33	5.74				
P4xP5	61.33	13.20	35.50	31.50	129.50	141.60	135.55	13.40	-7.33	1.54				
P4xP6	65.33	14.86	36.26	35.75	133.50	171.42	152.46	16.90	12.18	14.20				
P4xP7	65.67	14.98	30.51	32.75	130.17	131.27	130.72	13.98	-14.09	-2.08				
P4xP8	67.00	13.00	31.34	32.50	121.20	130.60	125.90	6.13	-14.53	-5.69				
P5xP6	66.17	12.50	31.40	34.25	115.50	123.30	119.40	1.14	-19.31	-10.56				
P5xP7	62.17	13.73	41.34		146.33	172.67	159.50	28.14**	13.00	19.48				
P5xP8	64.17	11.11	36.53	33.50	121.50	125.67	123.58	6.39	-17.76	-7.43				
P6xP7	66.00	13.90	31.18	32.50	101.10	123.43	112.26	-11.47	-19.22	-15.91				
P6xP8	66.33	12.60	36.10		130.10	138.60	134.35	13.92	-9.29	0.64				
P7xP8	68.00	14.45	28.65	33.25	92.80	102.60	97.70	-18.74	-32.85**	-26.82*				
SC 162	75.33	13.80	34.20	31.17	114.2	152.8	133.50							
mean of (p)		12.10	20.72	24.76	44.99	63.21	54.10							
mean of (cr)	65.10	13.91	33.99	33.02		142.62	133.49	1						
mean of (G)	66.73	13.51	31.13		106.73		116.33	1						
L.S.D 5%	2.04	1.44	4.32	4.72	22.76	32.94	27.90							
L.S.D 1%	2.67	1.89	5.66	6.19	30.19	43.69	36.58	1						
						hability		1						

\*and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

#### Combining ability

The analysis of variance for combining ability at the combined analysis for all the studied traits is presented in Table (1). The mean square of general combining ability includes the additive and additive x additive genetic portion while specific combining ability represents the non additive genetic portion of the total variance arising largely from dominance and epistatic deviations. The mean square associated with general and specific combining ability was significant for all traits except no. of rows/ear in high nitrogen rate (120 Kg n/f), revealing that both additive and non-additive types of gene action were involved in determining the performance of single-cross progeny.

If both general and specific combining ability mean squares are significant, one may ask which type and or types of gene action are important in determining the performance of single- cross progeny. To overcome such situation the size of mean squares can be used to assume the relative importance of general and specific combing ability mean squares which were highly significant. Hence, GCA/SCA ratio was used as measure to reveal the nature of genetic variance involved.

High ratios for GCA/SCA which largely exceeded the unity were obtained for 100-kernel weight at low rate of nitrogen fertilization and no. of rows /ear in both nitrogen rates and combined analysis. Indicating that large part of the total genetic variability associated with these traits was additive and additive by additive gene action.

For the other remain cases, GCA/SCA ratios, were less than unity. Therefore, it could be concluded that the large portion of the total genetic variability associated with these traits is due to non-additive gene action. (Amer, 2005, El-Hosary and El-Badawy, 2005, El-Hosary *et al.*, 2006 and Sedhom *et al.*, 2007)

Significant interaction mean squares between nitrogen rates and GCA were detected for no. kernels/row. Such result indicated that additive and additive by additive effects were more influenced by nitrogen rates than non-additive genetic effects of this trait. Whereas, significant interaction mean squares between nitrogen rates and SCA were obtained for days to 50% siliking and for no. of rows/ear, revealing that non additive effects was more changed with nitrogen rates than additive genetic effects for both traits.

On the other hand, insignificant mean squares of interaction between nitrogen rates and both combining ability was obtained for on. 100-kernel weight and grain yield/plant, revealing that all types of gene action did not appreciably fluctuate in magnitude from nitrogen rate to another. These finding confirm those obtained above from the ordinary analysis of variance. The interaction between both types of combining abilities and seasonal changes were reported to be significant for earliness and grain yield/plant (Mosa, 2003, EI-Hosary and EI-Badawy, 2005, Mosa and Motawei, 2005 and Sedhom *et al.*, 2007).

It is fairly evident that ratio for GCAxN/GCA was higher than ratio of SCAxN/SCA for all traits except for no. of rows/ear. This result indicated that additive effects were more influenced by nitrogen rates than non additive

genetic effects of these traits. This conclusion is in well agreement with those reported by Gilbert (1958).

#### General combining ability effects:

Estimations of GCA effects ( $\hat{g}_i$ ) for individual parental inbred lines for each trait in the combined analysis are presented in Table (3) General combining ability effects estimated herein differ significantly from zero. High positive values would be of interest under all traits in question except days to 50% siliking where high negative effects would be useful from the breeder's point of view.

The parental inbred line no. 2 showed significant positive effects  $(\hat{g}_i)$  for no. of rows/ ear and 100-kernel weight. The parental inbred lines no.

3 and 4 showed significant negative ( $\hat{g}_i$ ) effects for days to 50% siliking.

Also, they showed significant positive (  $\hat{g}_{i}$  ) effects for no. of rows/ear and

grain yield/plant. The parental inbred line no. 5 was a good combiner for days to 50% siliking and no. of kernels/row. The parental inbred lines no. 1 and 8 seemed to be a poor combiner for most traits. The parental inbred line no. 6 exhibited significant positive ( $\hat{g}_i$ ) effects for no. of kernels/row, 100-kernel weight and grain yield/plant. The parental inbred line no. 7 expressed the good combiner for no. of rows/ ear and no. of kernels/ row.

These results indicated that these parental inbred lines possess favorable genes and that improvement in yield may be attained if they are used in hybridization program.

Table (3): General combining ability effects for all studied traits in the combined analysis.

Trait	Dayes to 50% silking	No. of rows /ear	No. of kernels/row	100-kernel weight	Grain yield/ plant
Parent					
P1	-0.40**	-0.80**	-0.56**	-0.99**	-4.87**
P2	0.13	0.15*	-1.49**	0.81**	-5.81**
P3	-0.44**	0.85**	-0.16	0.14	8.64**
P4	-0.25**	0.95**	-0.18	-0.74**	6.10**
P5	-0.64**	-0.97**	1.46**	-0.67**	0.88
P6	0.73**	-0.69**	1.49**	2.26**	4.20**
P7	0.73**	1.27**	0.72**	-2.19**	-2.35*
P8	0.15	-0.77**	-1.28**	1.39**	-6.79**
L.S.D(0.05) gi	0.17	0.12	0.36	0.39	2.32
L.S.D(0.01) gi	0.22	0.16	0.47	0.52	3.05
L.S.D(0.05) gi-gj	0.32	0.23	0.68	0.75	4.41
L.S.D(0.01) gi-gj		0.30	0.90	0.98	5.78

\*and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

#### Specific combining ability:

Specific combining ability effects  $S_{ij}$  for the studied 36 hybrids were computed for all the studied traits (Table 4). The most desirable inter and

intra allelic interactions were presented by combinations:  $P_1xP_3$ ,  $P_1xP_4$ ,  $P_1xP_6$ ,  $P_1xP_7$ ,  $P_1xP_8$ ,  $P_2xP_3$ ,  $P_2xP_5$ ,  $P_2xP_7$ ,  $P_2xP_8$ ,  $P_3xP_4$ ,  $P_3xP_5$ ,  $P_3xP_6$ ,  $P_3xP_8$ ,  $P_4xP_5$ ,  $P_4xP_6$ ,  $P_4xP_7$ ,  $P_5xP_7$ ,  $P_5xP_8$ ,  $P_6xP_7$  and  $P_7xP_8$  for days to 50% siliking,  $P_1xP_3$ ,  $P_1xP_4$ ,  $P_1xP_6$ ,  $P_2xP_4$ ,  $P_2xP_7$ ,  $P_2xP_8$ ,  $P_3xP_5$ ,  $P_3xP_8$  and  $P_4xP_6$  for number of rows/ear,  $P_1xP_3$ ,  $P_1xP_5$ ,  $P_1xP_8$ ,  $P_2xP_3$ ,  $P_2xP_4$ ,  $P_2xP_5$ ,  $P_2xP_7$ ,  $P_3xP_6$ ,  $P_3xP_6$ ,  $P_3xP_8$ ,  $P_4xP_6$ ,  $P_4xP_7$ ,  $P_5xP_7$ , and  $P_7xP_8$  for no. of kernels/row,  $P_1xP_7$ ,  $P_2xP_6$ ,  $P_3xP_4$ ,  $P_3xP_8$  and  $P_4xP_6$  for 100-kernel weight and  $P_1xP_3$ ,  $P_1xP_4$ ,  $P_1xP_5$ ,  $P_1xP_3$ ,  $P_2xP_4$ ,  $P_2xP_5$ ,  $P_2xP_6$ ,  $P_2xP_7$ ,  $P_3xP_6$ ,  $P_3xP_8$ ,  $P_4xP_6$ ,  $P_5xP_7$ ,  $P_4xP_6$ ,  $P_5xP_8$  and  $P_6xP_8$  for grain yield/ plant.

analys	analysis.											
Trait Cross	Dayes to 50% silking	No. of rows /ear	No. of kernels/row	100-kernel weight	Grain yield/ plant							
P1xP2	0.29	0.15	-0.61	-5.01**	-19.11**							
P1xP3	-1.64**	1.61**	6.70**	4.66**	66.17**							
P1xP4	-1.33**	1.75**	8.65**	1.54	39.36**							
P1xP5	-0.78	0.19	2.29*	6.30**	22.32**							
P1xP6	-1.14*	1.01**	4.04**	-0.71	4.77							
P1xP7	-1.98**	0.62	-0.15	-4.51**	-5.23							
P1xP8	-1.73**	0.16	3.31**	4.66**	32.70**							
P2xP3	-1.68**	-0.43	3.45**	6.62**	32.82**							
P2xP4	0.14	0.67*	3.55**	3.00**	20.00**							
P2xP5	-1.81**	0.22	3.27**	2.93**	37.91**							
P2xP6	2.82**	0.34	5.15**	-1.25	25.66**							
P2xP7	-3.34**	1.77**	3.95**	3.20**	19.51**							
P2xP8	-2.26**	0.74*	3.57**	1.62	0.26							
P3xP4	-1.29**	-0.59	5.80**	-2.58*	25.54**							
P3xP5	-3.74**	0.81*	2.64**	0.59	23.38**							
P3xP6	-2.44**	0.46	1.23	2.92**	19.89**							
P3xP7	0.56	0.00	0.63	0.37	-0.17							
P3xP8	-1.86**	1.74**	5.58**	6.87**	23.46**							
P4xP5	-4.26**	-0.29	3.18**	1.73	12.72*							
P4xP6	-1.63**	1.09**	3.91**	3.05**	26.31**							
P4xP7	-1.29**	-0.75*	-1.07	4.50**	11.12							
P4xP8	0.62	-0.69*	1.75	0.67	10.74							
P5xP6	-0.41	0.65	-2.59**	1.48	-1.53							
P5xP7	-4.41**	-0.08	8.12**	2.43*	45.12**							
P5xP8	-1.83**	-0.66*	5.31**	1.59	13.64*							
P6xP7	-1.94**	-0.19	-2.08*	1.25	-5.43							
P6xP8	-1.03*	0.55	4.85**	0.67	21.09**							
P7xP8	0.64	0.44	-1.84	2.87**	-9.01							
LSD5% (sij)	0.92	0.65	1.96	2.14	12.65							
LSD1% (sij)	1.21	0.86	2.57	2.81	16.59							
LSD5%(sij-sik)	1.37	0.96	2.90	3.17	18.71							
LSD1%(sij-sik)	1.79	1.27	3.80	4.15	24.54							
LSD5%(sij-skl)	0.46	0.32	0.97	1.06	6.24							
LSD1%(sij-skl)	0.60	0.42	1.27	1.38	8.18							

 Table (4): Specific combining ability effects for all studied traits in the combined analysis.

\*and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

These crosses may be prime importance in breeding programmes either towards hybrid maize production or synthetic varieties composed of hybrids which involved the good combiners for the traits in view. **Hayman analysis:** 

# Genetic behavior:

Data were also subjected to the diallel analysis proposed by Hayman (1954) to obtain more information about the genetic behavior for the traits under study. The computed parameters for all traits are presented in Table (5). The additive component "D" reached the significant level of probability for all traits except silking date and grain yield / plant at both fertilizer rates. For the exceptional both traits (Silking date and grain yield/ plant, insignificant D value inspite of a significant GCA mean squares were obtained. Dominance may be has a role in GCA estimate as emphasized by (Jinks 1954). Moreover, the component t<sup>2</sup> was significant (Table 5 ). In addition, the regression coefficients of parental offspring covariance (Wr) on the parental array variance (vr) were significant in both traits to less than unity, revealing the presence of complementary type of epistasis. Therefore, the contradiction in magnitude detected herein between D and GCA estimate for both traits could be attributed to the great role of both allelic and non allelic genetic types on the expression of these traits. Significant values for the dominance component  $H_1$  were obtained for all traits. Moreover, values of  $H_1$  were significantly larger in magnitude than the respective D values in most cases, revealing that non-additive genetic type was the most prevalent in these traits. Therefore, it could be concluded that both allelic and non allelic genetic types had roles in the expression of these traits., (Saeed et al., 2000, Nawar et al., 2002, Saleem et al., 2002, Balci and Turgut 2006, El-Hosary et al., 2006 and Sedhom et al., 2007)

The relative size of D and  $H_1$  were estimated as a weighted measure of the average of dominance at each locus. The results revealed the presence of over dominance for all traits except no. of rows/ear at 120 kgN rates. For the exceptional case complete dominance was detected. Significat "  $h^{2"}$  values were obtained in all traits in both fertilizer rates, indicating that dominance was unidirectional. This finding confirms the results reached above for parent vs. crosses. (Nawar *et al.*, 1979, Saeed *et al.*, 2000, Saleem *et al.*, 2002, Shafey *et al.*, 2003, Singh *et al.*,2004, Balci *and Turgut* 2006).

The average frequency of negative vs. positive alleles in the parental population, it could be detected by computing the ratio  $(H_1/4 H_2)$ . Values that largely deviated from 0.25 were obtained for all cases except 100-kernel weight in both nitrogen rates, no. of kernels/ row and grain yield/ plant at low nitrogen rate and silking date at high nitrogen rate, revealing that negative and positive alleles were unequally distributed among the parents. Moreover, significantly positive "F" values were detected for the same cases, indicating asymmetry with dominance alleles being more frequent. With the exception of no. of rows/ ear, low heritability values were detected. This result indicates

that the bulk method could be more efficient for obtaining desirable improvement.

El-Badawy, M. El. M.

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#### Graphical analysis:

Graphical presentation (vr, wr) of different traits are given in figures 1 to 10. With the exception of 100-kernel weight under 120 kgN/fed, the regression coefficient "b" of (wr, vr) is different from unity, indicating that a complementary type of epistasis was involved. For the exceptional case, regression coefficients of "wr" on "vr" is not different from unity, suggesting that the genetic system can be deduced to be additive without complication of non-allelic interaction. With the exception of no. of row/ear at 120 kgN/fed a significant negative intercept was obtained, suggesting over-dominance. However, the exceptional case (no.of rows/ear at (120 kgN/ fed), the regression line was passed through the origin, indicating the presence of complete dominance. The same results were obtained by (H/D)<sup>0.5</sup> in (Table 5). The array points were widly scattered for all the characters, indicating genetic diversity among the parents.

The appreciable correlation coefficient between (yr) and (wr+vr) detected for silking date might revealed that earliness behaved as dominant trait. On the contrary the appreciable negative correlation values between (yr) and (wr+vr) obtained for other traits indicated that increase genes were dominant over decreases.

The parental inbred line no. 1 for silking date, no. 3 and 6 for no. of rows/ ear, no.6 for no. of kernels/row, no. 7 for grain yield/ plant in both fertilizer rates and no.6 and 3 for 100-kernel weight at low and high nitrogen rates, respectively seemed to be carry the most dominant genes responsible for the expression of these traits. However, the parental inbred lines no. 5 for silking date, no. 1 for no. of rows/ ear in both nitrogen rates, no.4 and 1 in low nitrogen rate and no. 2 and 1 at high nitrogen rate for no. of kernels/ row, no. 3 in low and 6 in high nitrogen rates had high concentration of recessive genes for these traits.

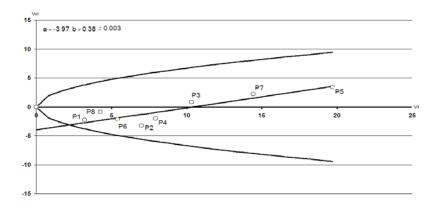


Fig (1): Wr/Vr graph for days to 50% silking, 60 Kg N/ fed.

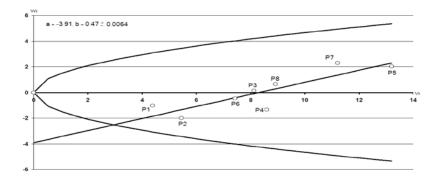


Fig (2): Wr/Vr graph for days to 50% silking, 120 Kg N/ fed.

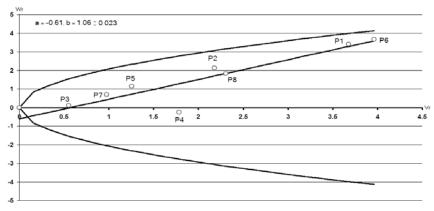


Fig (3): Wr/Vr graph for no. of rows/ear, 60 Kg N/ fed

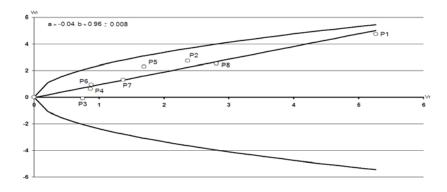
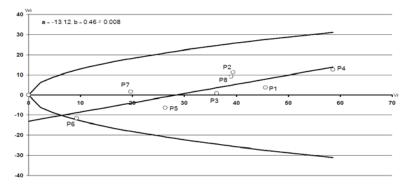
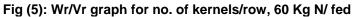


Fig (4): Wr/Vr graph for no. of rows/ear, 120 Kg N/ fed.

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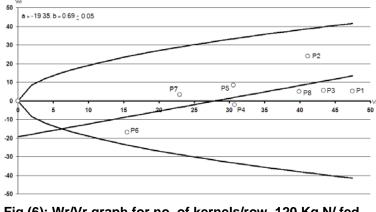


Fig (6): Wr/Vr graph for no. of kernels/row, 120 Kg N/ fed.  $\ensuremath{\mathbb{W}}\xspacer$ 

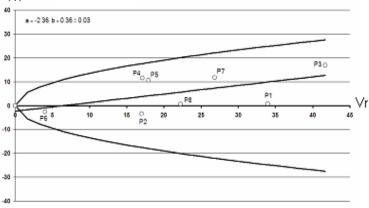


Fig (7): Wr/Vr graph for 100 kernel weight, 60 Kg N/ fed.

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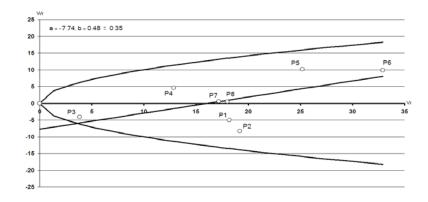


Fig (8): Wr/Vr graph for 100 kernel weight, 120 Kg N/ fed.

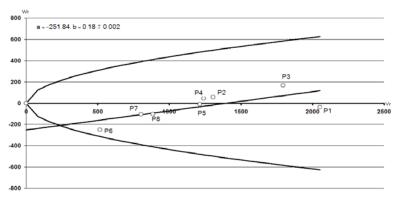


Fig (9): Wr/Vr graph for grain yield/plant, 60 Kg N/ fed.

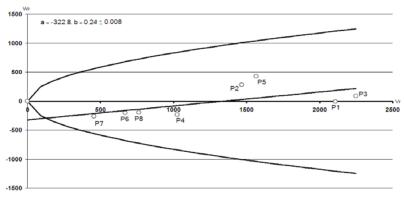


Fig (10): Wr/Vr graph for grain yield/plant, 120 Kg N/ fed.

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# التباين الوراثي و مكوناتة وطبيعة فعل الجين في الذرة الشامية تحت مستويين من التسميد الاروتي

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تم تقييم الهجن الناتجة من التهجين النصف دائرى لثمانية سلالات من الذرة وذلك تحت مستويين من التسميد الازوتى (60 و 120 كجم نيتروجين/ فدان ) لخمس صفات كمية فى تصميم قطاعات كاملة العشوائية. كانت متوسطات التباين لكل من مستويان التسميد والتر اكيب الوراثية والآباء والهجن معنوية فى كل الصفات تحت الدراسة لكلا المستويين من التسميد و التحليل المشترك . كما كان متوسط التباين للتفاعل بين الأباء ومستويى التسميد معنوي فى كل الصفات تحت الدراسة لكلا المستويين الصفوف/ كوز و وزن المائة حبة. كما أظهر متوسط التباين للتفاعل بين الهجن ومستوى فى كل الصفات تحت الدراسة ما طرد 50% من النورة المنكرة وعد الصفوف / كوز . و كانت التباين للقدرة العامة والخاصة على التألف معنويا لكل الصفات تحت الدراسة ما عدا صدق متوسط التباين التفاعل بين الهجن ومستوى التسميد معنوي فى كل الصفات تحت الدراسة ما عدا تحت الدراسة ما عدا التفاعل بين الأباء ومستويي التفاعل بين الهجن ومستوى التسميد معنوية لصفات تحت الدراسة ما عدا تحت الدراسة ما عدا معنوسط التباين التفاعل بين الهجن ومستوى التسميد معنوي فى كل الصفات تحت الدراسة ما عدا عدد

وكان متوسط التباين للتفاعل بين مستويى التسميد والقدرة العامة معنوى لعدد الحبوب/ صف ومتوسط التباين للتفاعل بين مستويى التسميد والقدرة الخاصة معنويا لكل من عدد الايام حتى طرد 🛛 50% من النورة المذكرة و عدد الصفوف \ كوز . وكانت النسبة بين القدرة العامة والقدرة الخاصة أكبر من الوحدة لكل من صفة وزن المائة حبة في مستوى التسميد المنخفض، عدد الصفوف/كوز في كل من مُستويى التسميد و التحليل المشترك . وكانت النسبة للتفاعل بين القدرة العامة والتسميد/ للقدرة العامة عالية عن النسبة بين التفاعل للقدرة الخاصة والتسميد / للقدرة الخاصة لكل الصفات تحت الدراسة ما عدا عدد الصفوف / كوز. أظهرت السلالة الأبوية رقم3 و 4 قدرة جيدة عامة على التوافق لصفة عدد الايام حتى طرد 50% من النورة المؤنثة وعدد الصفوف/ كوز ومحصول الحبوب / نبات . كما أظهرت السلالة رقم 6 قدرة جيدة على التألف لصفة عدد الحبوب / صف وزن المائة حبة ومحصول الحبوب / نبات . أعطت الهجن . P1xP8, P1xP5, P1xP4, P1xP3, P6xP8,P5xP8, P5xP7, المائة حبة ومحصول الحبوب / نبات . قدرة خاصة عالية على P4xP6,P4xP6,P4xP5, P3xP8,P3xP6, P3xP4, P2xP7, P2xP6,P2xP5, P2xP4, التآلف لمحصول الحبوب/ نبات. و حقق الهجين P1xP3 تفوقا في قوة الهجين عن الصنف التجاري 162 تحت مستويي التسميد و التحليل المشترك . أظهرت النتائج أن قيمة الفعل الاضافي (D) معنويا لكل الصفات ما عدا عدد الايام حتى طرد 50% من النورة المؤنثة و محصول الحبوب/ نبات تحت مستوبي التسَّميُّد. (وكانت قيمة (t²) معنوية وكذلك قيمة انحدار (wr/vr) معنوية عنَّ الوحدة لكلَّ الصفات تحت الدراسة . وكان تأثير السيادة (H1 ) معنوي لمعظم الصفات وأكبر من الجزء المضيف وكانت قوة الهجين (h<sup>2</sup>) معنوية لكل الصفات . كانت الأليلات المتنحية والساندة غير متساوية في الأباء لمعظم الصفات وذللك باستخدام (H1/4 H2) وقيمة (F) وكانت درجة التوريث منخضة في كل الصفات ما عدا عدد الصفوف \ كوز حيث أظهرت قيمة مُتوسطة وكانتُ السيادةُ الفائَّفة ذات التأثير الأكبر في معظم الصَّفات . أظهرت السلالة رقم 🛛 الصفة التزهير ورقم 3و 6 لعدد الصفوف/كوز و رقم 6 لصفة عددالحبوب / صفَّو 7 لمحصول الحبوب / نبات و 6 و 3 لصفة وزن المائة حبَّة أنها تحمل معظم الأليلات السائدة لهذة الصفات.

قام بتحكيم البحث

أد / محمود سليمان سلطان أد / على عبد المقصود الحصري

كلية الزراعة – جامعة المنصورة كلية الزراعة – جامعة بنها

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well as the combined analysis.																	
		d.f.	dayes	s to 50%	silking		no. of	rows/ea	r	no. c	of kernels	/row	100	)-kernel w	eight	Grain yield/ plant	
S.O.V.	S.	Comb	60 kgn/f	120kgn/f	comb.	60 kgn/f	120kgn/f	comb.	60 kgn/f	120kgn/f	comb.	60 kgn/f	120kgn/f	comb.	60 kgn/f	120kgn/f	comb.
nitrogen		1			238.56**			27.68**			424.06**			524.22**			17980.36**
Rep/L	2	4	2.29	0.15	1.22	1.72	0.70	1.21	2.73	0.43	1.58	12.26	13.72	12.99	10.96	65.09	38.03
Genotypes	35	35	33.48**	30.92****	60.63**	9.12**	9.18**	16.95**	136.18**	131.83**	255.93**	83.43**	67.18**	144.42**	4626.32**	4926.24**	9257.24**
parent	7	7	13.47**	6.52**	16.52**	12.96**	16.93**	28.41**	49.76**	109.05**	135.33**	54.38**	30.15**	77.61**	568.95*	2072.69**	1991.73**
Cross	27	27	12.02**	12.56**	20.61**	5.77**	5.63**	10.06**	30.03**	32.06**	53.06**	49.34**	29.50**	72.68**	1493.84**	1489.00**	2768.50**
Par.vs.cr.	1	1	752.97**	697.57**	1450.01**	72.72**	50.91**	122.66**	3606.97**	2985.26**	6577.54**	1207.14**	1343.95**	2549.26**	117605.09**	117706.53**	235311.61**
G/N		35			3.77**			1.35*			12.08*			6.19			295.33
par./N		7			3.46*			1.48			23.47**			6.92			649.92*
Cr./N		27			3.97**			1.34*			9.03			6.16			214.33
Par.vs.cr.Vs.N		1			0.53			0.97			14.69			1.84			0.01
Error	70	140	1.14	2.09	1.62	0.70	0.92	0.81	5.33	9.25	7.29	7.73	9.66	8.70	196.43	411.39	303.91
GCA	7	7	2.39*	3.90**	5.51**	8.07**	9.02**	16.90**	16.12**	15.80**	25.94**	34.04**	11.11**	41.36**	387.38**	470.05**	683.56**
SCA	28	28	13.35**	11.91**	23.89**	1.78*	1.57	2.84**	52.71**	50.98**	100.15**	26.25**	25.21**	49.84**	1830.79**	1935.09**	3686.29**
GenotypexN		35			3.77**			1.35**			12.08**			6.19**			295.33**
GCAxN		7			0.78			0.19			5.98*			3.80			173.87
SCAxN		28			1.38**			0.52*			3.54			1.63			79.59
Error	70	140	0.38	0.70	0.54	0.23	0.31	0.27	1.78	3.08	2.43	2.58	3.22	2.90	65.48	137.13	101.30
GCA/SCA			0.18	0.33	0.23	4.52		5.96	0.31	0.31	0.26	1.30	0.44	0.83	0.21	0.24	0.19
GCA x N/GCA					0.14			0.01			0.23			0.09			0.25
SCA x N/SCA					0.06			0.18			0.04			0.03			0.02

Table (1): Observed mean squares from ordinary analysis for all traits at both nitrogen rates as well as the combined analysis.

\* and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

	dayes to5	0% silking	no. of ro	ws /ear	no. of kei	rnels/row	100-kern	el weight	Grain yie	eld/ plant	
Gentetic		120 kg	60 kg	120 kg		120 kg		120 kg			
component	60 kg N/fed	N/fed	N/fed	N/fed	60 kg N/fed	N/fed	60 kg N/fed	N/fed	60 kg N/fed	120 kg N/fed	
D	4.10	1.49	4.08 **	5.34 **	14.83 *	33.35 **	15.51 *	6.79 *	125.89	556.97	
F	10.44 *	3.19	1.91 *	3.33 **	20.21	52.10 *	9.46	11.02	404.41	1232.19 *	
H1	41.61 **	33.81 **	5.63 **	5.31 **	138.50 **	147.78 **	78.47 **	70.57 **	5040.22 **	5523.20 **	
H2	33.64 **	30.02 **	4.69 **	3.98 **	127.11 **	126.20 **	70.74 **	61.89 **	4517.20 **	4618.04 **	
h <sup>2</sup>	123.36 **	114.15 **	11.83 **	8.22 **	591.00 **	488.46 **	196.90 **	219.07 **	19266.69 **	19252.64 **	
E	0.39	0.68	0.24	0.30	1.75	3.00	2.62	3.26	63.76	133.92	
(H1/D)^0.5	3.19	4.76	1.18	1.00	3.06	2.11	2.25	3.22	6.33	3.15	
(H2 /4H1)	0.20	0.22	0.21	0.19	0.23	0.21	0.23	0.22	0.22	0.21	
KD/Kr	2.33	1.58	1.50	1.91	1.57	2.18	1.31	1.67	1.68	2.08	
h(n.s)	0.08	0.11	0.52	0.56	0.08	0.04	0.25	0.11	0.09	0.08	
YD	67.19	69.15	7.30	8.74	1.72	-9.76	11.69	16.45	-89.58	-250.06	
Yr	77.79	77.40	18.32	20.04	46.41	93.94	39.85	43.43	269.95	721.56	
r	0.97	0.90	-0.87	-0.71	-0.97	-0.70	-0.85	-0.90	-0.93	-0.89	
ť	33.67**	12.89**	1.10	0.00	10.65**	0.01	1.84	0.59	61.32**	15.46**	
b	0.38	0.47	1.06	0.96	0.46	0.69	0.36	0.48	0.18	0.24	

Table (5) : Genetic component for all studied traits in both nitrogen rates.

\*and \*\* significant at 0.05 and 0.01 levels of probability, respectively.

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