RESULTS AND DISCUSSION

1- Validity of design assumptions:

The genetic variance components were calculated from Design-I as suggested by Comstock and Robinson (1948). In their derivations several assumptions were considered as follows:

1) Regular diploid behaviour at meiosis;
2) Random distribution of genotypes relatives;
3) Random choice of individuals mated for production of experimental progenies;
4) No maternal effects;
5) No multiple alleles;
6) No linkage effects; and
7) No epistasis.

Failure of the assumptions given above to hold would results in baised estimaties 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 fullfiled in the material under study.

As the synthetic variety "Giza-2" is an open-pollinated variety and it is produced annually, and is in linkage equalibrium or no correlation of genotypes at separate loci may exist.

For random choice of individuals mated for production of experimental progenies was not fullfiled. It is caused negative estimates of the dominance genetic variance consistently have been obtained in all traits under study. This agrees with the previously reported findings (Lindsey et al. 1962; Goodman 1965; Lonnquist et al. 1966; Hallaur and Wright 1967; Marquez-Sanchez 1970 a and b ; Nawar 1971; Galal et al. 1977; Diab 1979 , Nawar 1981; Nawar et al. 1983 and others). There are some of explainations for the negative value as mentioned before, the first one was error sample and the second one was the assortative mating. These two reasons will be discussed in the second part of the discussion of this study.

The effect of multiple alleles, Kempthorne (1957) stated that multiple alleles alone would not change the genetic expectation of covariance full-sib and covariance half-sib.

2- Estimation of Genetic and Environmtal Parameters:

Means, coefficient of variability and environmental error for nine characters under study in each location and for combined analysis are given in Table (4).

In general, for most traits under study means for the two locations were similar.

The environmental variance ($\sigma^2 e$) was higher for the second location (Moshtohor) than the first(Shebin-El-Kom) for most traits under investigation. Consequently, the coefficient of variability was higher in the second location than the first location. For silking and tasseling date the coefficients of variability were relatively smaller in the second location than the first.

The analysis of variance for each character in each of the two locations and their combined analysis are given in Tables (5,6,7 and 8).

For the first location, the mean squares of males was significant for all traits except yield of ears per plant. The female component was also significant for all traits except yield of ears per plant, number of kernels per row, silking date and tasseling date where

Table 4 : Mean ($\bar{X}$), environmental eror (σ^2_e) and coefficient of variation (C.V. %) for all characters studied.

Characters	$\bar{X}$ (cm)			σ^2_e			C.V. %		
	Shebin	Moshtohor	Combined	Shebin	Moshtohor	Combined	Shebin	Moshtohor	Combined
Yield of ears/ plant (gm)	275.33	278.83	277.08	2293.70	2807.95	2550.82	17.39	19.00	18.23
Ear length(cm)	20.67	18.64	19.66	2.03	5.60	3.81	6.89	12.7	9.93
Ear diam. (cm)	5.23	4.68	4.96	0.05	0.32	0.16	4.28	12.09	8.06
No. of row / ear	14.00	14.00	14.00	1.11	1.32	1.20	7.53	8.21	7.82
No. of kernels / row	42.00	37.00	39.00	9.56	24.82	17.19	7.36	13.46	10.63
Plant height (cm)	311.75	304.01	307.88	317.43	448.87	383.15	5.72	6.97	6.36
Ear height(cm)	166.05	167.56	165.80	170.97	224.03	197.50	7.87	8.93	8.43
Tasseling date (days)	64.00	65.00	65.00	4.41	4.02	4.21	3.28	3.08	3.16
Silking date (days)	66.00	68.00	67.00	3.08	2.62	3.11	2.66	2.38	2.63

the estimates of error variance were higher than expected.

For the second location, the male components were significant for all traits under study except yield of ears per plant and ear length. The female component was non-significant for all traits.

For the combined analysis, it was assumed that the error variance for the two locations was homogenous. This assumption was not valid for all characters under study except for yield of ears per plant, number of rows per ear, silking and tasseling date. The heterogeneity of error would over estimate the variance component calculated from the combined analysis. The male variance component was significant for all characters under study. The female variance components was also significant for all characters with the expection of yield of ears per plant. The interaction between males x locations were significant for all traits except yield of ears per plant and number of rows per ear, it is means that the behaviour of males were differed from one location to another for these traits, while the interaction between females x locations was non-significant for all trats, indicating that the behaviour females of these traits were stable from one location to another. The estimates of variance components for males, females and their interactions with

Table 5 . Mean squares for grain yield / plant and ear length for both two locations and combined analysis.

S. O. V.	d.f		Mean squares					
			Yield per plant			Ear length		
	LOc.	Comb.	Shebin	Moshtohor	Combined	Shebin	Moshtohor	Combined
Location/S	-	1	---	----	80861.43**	---	----	1125.63**
Rep's /S	1	2	22591.86**	51228.28**	36910.07**	46.94**	456.11**	251.53**
Enteries/S	252	252	2208.35	2766.33	2689.80	3.00**	5.52	5.24**
Males/S	60	60	2741.78	3435.65	3553.08*	4.51**	5.91	6.73**
F / M / S	192	192	2041.65	2557.16	2420.03	2.53*	5.40	4.78*
Ent./S x L	-	252	---	----	2284.87	---	----	3.28
M / S x L	-	60	---	----	2624.34	---	----	5.73**
F / M / S x L	-	192	---	----	2178.79	---	----	3.15
Error	252	504	2293.70	2807.95	2550.82	2.03	5.60	3.81

* , ** Significant at 0.05 and 0.01 levels of probability, respectively.

Table 6 . Mean squares for ear diameter, number of rows per ear and number of kernels per row for both two locations and combined analysis.

S.O.V.	d.f.		Mean squares								
			Ear diameter			Number of rows / ear			Number of kernels/row		
	Loc.	Comb.	Shebin	Moshtohor	Combined	Shebin	Moshtohor	Combined	Shebin	Moshtohor	Combined
Location/S	—	1	—	—	78.55**	—	—	18.98**	—	—	8827.64**
Rep's/S	1	2	1.91**	18.77**	16.79**	8.63**	9.59**	9.11**	98.98**	1424.65**	761.82**
Enteries/S	252	252	0.10**	0.40*	0.28**	1.98**	1.88**	2.70**	15.17**	29.41	25.37**
Males/S	60	60	0.81**	0.81**	0.58**	3.17**	2.85**	4.63**	17.99**	48.31**	33.07**
F/M/S	192	192	0.07**	0.27	0.19*	1.61**	1.55	2.09**	11.69	23.50	22.97**
Ent./S x L	—	252	—	—	0.22**	—	—	1.14	—	—	19.21
M/S x L	—	60	—	—	0.40**	—	—	1.38	—	—	33.23**
F/M/S x L	—	192	—	—	0.16	—	—	1.07	—	—	14.92
Error	252	504	0.05	0.32	0.16	1.11	1.32	1.20	9.56	24.82	17.19

* , ** Significant at 0.05 and 0.01 levels of probability, respectively.

Table 7 . Mean squares for plant height and ear height for both two location and combined analysis.

S.O.V	d.f		Mean squares					
			Plant height			Ear height		
	Loc.	Comb.	Shebin	Moshtohor	Combined	Shebin	Moshtohor	Combined
Location/S	—	1	—	—	41484.54**	—	—	6225.26**
Rep's/S	1	2	56823.03**	35391.00**	46107.02**	33887.41**	8385.08**	21136.25**
Enteries/S	252	252	623.84**	880.75**	1055.10**	393.67**	406.45**	583.11**
Males/S	60	60	980.64**	2324.64**	2428.11**	835.95**	1074.03**	1475.73**
F/M/S	192	192	512.34**	429.54	626.03**	255.45**	197.82	233.62*
Ent./S x L	—	252	—	—	449.50*	—	—	217.00
M/S x L	—	60	—	—	877.17**	—	—	434.29**
F/M/S x L	—	192	—	—	315.85	—	—	149.12
Error	252	504	317.43	448.87	383.15	170.97	224.03	197.50

* , ** Significant at 0.05 and 0.01 levels of probability, respectively.

Table 8 . **Mean** squares for tasseling date and silking date for both two locations and combined analysis.

S.O.V	d.f		Mean squares					
			Tasseling date			Silking date		
	Loc.	Comb.	Shebin	Moshtohor	Combined	Shebin	Moshtohor	Combined
Location/S	—	1	—	—	645.77**	—	—	819.79**
Rep's/S	1	2	177.74**	215.88**	196.81**	257.66**	155.19**	273.26**
Enteries/S	252	252	5.14	6.58**	7.13**	4.90**	3.77**	5.81**
Males/S	60	60	10.39**	12.17**	57.07**	10.92**	6.79**	12.62**
F/M/S	192	192	3.50	4.83	5.14*	3.02	2.82	3.68*
Ent./M/S x L	—	252	—	—	4.41	—	—	2.86
M/S x L	—	60	—	—	33.20**	—	—	5.09**
F/M/S x L	—	192	—	—	2.98	—	—	2.16
Error	252	504	4.41	4.02	4.21	3.08	2.62	3.11

***, ** Significant at 0.05 and 0.01 levels of probability, respectively.**

locations were used to calculate additive and dominance variance and their interactions with locations for different characters.

Estimates of additive and dominance variances are presented in Table (9). For the yield of ears per plant, the additive genetic variance was non-significant in both locations and the combined analysis. At the same time, the amount of additive genetic variance in the second location (Moshtohor) was higher than in the first location (Shebin-El-Kom). On the other hand, the dominance variance was negligible in both of the two locations, where the amount of the dominance variance deduced to zero because they had negative values. In the combined analysis the dominance genetic variance was highly significant. The additive genetic variance for ear length was only significant at Shebin El-Kom location. Its estimate was not consistent among the different locations, however, the magnitude of additive genetic variance was higher in Shebin El-Kom than in Moshtohor location. Also the two estimates of dominance were not important in each of the two locations, but it is highly significant in the combined analysis.

For ear diameter, the additive genetic variance was significant at the two locations, but not significant in combined analysis. The magnitude of additive genetic variance was higher in Moshtohor than at Shebin-El-Kom. On the other hand, the three values of dominance genetic variance deduced to zero.

The additive genetic variance was consistent for the number of rows per ear. The three estimates of additive genetic variance were significant, while the dominance variance was only significant in the combined analysis.

For number of kernels per row, the additive genetic variance was significant only at Moshtohor location, while it was not significant at Shebin-El-Kom and showed negative value in the combined analysis. The dominance genetic variance exhibited negative value at Moshtohor and non-significant value at Shebin El-Kom but showed significant value in combined analysis. The magnitude of genetic variance in this trait may be due to additive genetic variance, where this component only predominant and contributed the major role in the expression of this trait.

For plant height, ear height, silking and tasseling date , the additive genetic variance was consistent among the two locations. The three estimates of additive genetic were significant. At the same time, the magnitude of the dominance values were not important except plant height at Shebin-El-Kom location, where the most estimates had negative values. Consequently, the additive genetic variance was the predominant parameter in the inheritance of these traits. Dominance value for plant height trait at Shebin-El-Kom only was highly significant.

From the previous results it could be concluded that the additive genetic variance was the major component of genetic variation for all traits. These results are in general agreement with those reported by Gardner (1963) who summarized the various estimates of genetic parameters in open-pollinated varieties. He stated that, "additive genetic variance has been shown to exist at least in moderate amounts even in adapted open-pollinated variety". At the same time, our results exhibited bias estimates of dominance genetic variance, where the most values of dominance were negative. It might be due to the non-randomness of pollination caused by difference within the population in pollen shedding and silking date. No attempet was taken to avoid that bias. Lindsey <u>et al</u>. (1962) showed that the non-randomness of pollination would result in crossing the early male parents to the early female plants and the late males to the late females. The positive phenotypic assortative mating would increase the variance among females. Consequently, it would under-estimate dominance variance and it might result in negative estimates of dominance variance. The bias due to the non-random mating would affect silking dates and its correlated characters. Lindsey _et_ _al_. (1962), in an attempt to reduce the positive assortative mating, planted the male plants one week later than the female plants. The estimates of the dominance variance increased after minimizing the effects of positive assortative mating while the estimates of additive genetic variance decreased.

Another source of bias in the deviation of the variance components is the epistatic components. Cockerham (1963) demonstrated for a random mating population with no linkage, the covariance among half-sib and full-sib families will be function of the following geneti parameters:

$$\text{Cov. half-sib} = \tfrac{1}{4}\sigma^2_A + \frac{1}{16}\sigma^2_{AA} + \frac{1}{64}\sigma^2_{AAA} + \ldots ,$$

$$\text{Cov. full-sib} = \tfrac{1}{2}\sigma^2_A + \tfrac{1}{4}\sigma^2_D + \tfrac{1}{4}\sigma^2_{AA} + \frac{1}{8}\sigma^2_{AD} + \frac{1}{16}\sigma^2_{DD} + \ldots\ldots\ldots\ldots\ldots ,$$

On the assumption of no epistasis, the additive and the dominance variance were calculated as;

$\sigma^2 A = 4$ cov. half-sib,

$\sigma^2 D = 4$(cov. full-sib $-$ 2 cov. half-sib)

If epistasis is not negligible, the amount of bias in the two estimates will be:

for $\sigma^2 A = \frac{1}{4}\sigma^2_{AA} + \frac{1}{16}\sigma^2 AAA + \ldots\ldots\ldots\ldots\ldots\ldots$,

for $\sigma^2 D = \frac{1}{2}\sigma^2 AA + \frac{1}{2}\sigma^2 AD + \frac{1}{4}\sigma^2 DD + \ldots\ldots\ldots$,

The amount of bias in the case $\sigma^2 A$ is a function of the additive type of epistasis, while the bias in the dominance variance is a function of all types of epistasis. Moreover, the amount of bias in the estimator of $\sigma^2 D$ is greater than twice the bias in the estimator of $\sigma^2 A$. Also, most of reported results indicated that the epistatic gentic variance in the open-pollinated variety of maize were either negligible or had little contributions to the amount of genetic variations (Chi, 1965; Eberhart et al.,1966;Stuber,1966; El-Rouby, and Penny, 1967; Nawar, 1971; Diab, 1979; Galal et al., 1979, a and b; Nawar et al., 1983 and other). Therefore, the estimates reported from this study should be considered with reservation due to the bias introduced of assortative mating and epistatic effects.

The ratio of the dominance variance to the additive variance is an indication of the degree of dominance (Table 9). It varied from zero where no dominance was estimated to ∞ where the additive genetic variance was an estimate of zero. This ratio was highly affected by location and the character under study. The ratios of degree of dominance in our results ranged from zero in most cases to ∞ in few cases. It is expected where the additive genetic variance inthe composite variety "Giza-2" is the predominant source of the genetic variation for all characters under study in the two locations and in the combined analysis in most cases. Robinson et al. (1955) calculated the average degree of dominance upon hypothesizing different gene frequencies taking their calculation into consideration. It might be concluded that no to partial dominance was the major type of gene action previaling for the loci controlling the traits under study.

Estimation of the interaction between the additive and dominance genetic variance x Locations are presented in Table (10).

In general, all estimates of the interaction between additive genetic variance were highly significant for all traits except yield of ears per plant and number of rows

Table 9 . Estimates of additive $\sigma^2 A$, dominance ($\sigma^2 D$) genetic variance and degree of dominance ($\sigma^2 D/ \sigma^2 A$) for all characters studied.

Characters		$\sigma^2 A$	$\sigma^2 D$	$\sigma^2 D / \sigma^2 A$
Yield of ears/plant	Shebin El-Kom	350.06 ± 267.15	-854.15 ± 15.19	0.00
	Moshtohor	439.24 ± 334.73	-940.82 ± 17.2	0.00
	Combined	171.88 ± 214.87	69.37** ± 12.48	0.40
Ear length	Shebin El-Kom	0.99* ± 0.43	0.01 ± 0.62	0.01
	Moshtohor	0.26 ± 0.60	- 0.65 ± 0.71	0.00
	Combined	- 0.16 ± 0.42	1.78** ± 0.11	0.00
Ear diameter	Shebin El-Kom	0.05** ± 0.02	- 0.01 ± 0.12	0.00
	Moshtohor	0.27** ± 0.001	- 0.37 ± 0.26	0.00
	Combined	0.04 ± 0.04	- 0.01 ± 0.08	0.00
No. of rows/ear	Shebin El-Kom	0.78** ± 0.30	0.22 ± 0.52	0.28
	Moshtohor	0.65* ± 0.27	- 0.20 ± 0.49	0.00
	Combined	0.56** ± 0.22	0.47** ± 0.14	0.84
No. of kernels/ear	Shebin El-Kom	3.15 ± 1.72	1.10 ± 1.24	0.35
	Moshtohor	12.40** ± 4.50	- 15.04 ± 2.02	0.00
	Combined	- 2.08 ± 2.22	10.12** ± 0.75	0.00
Plant height	Shebin El-Kom	234.16** ± 91.82	155.66** ± 9.19	0.66
	Moshtohor	947.55** ± 209.89	-986.22 ± 14.23	0.00
	Combined	310.19** ± 117.28	- 0.01 ± 6.79	0.00
Ear height	Shebin El-Kom	290.25** ± 76.18	-121.28 ± 8.52	0.00
	Moshtohor	438.10** ± 96.97	-490.51 ± 9.67	0.00
	Combined	239.24** ± 69.43	-154.74 ± 15.80	0.00
Tasseling date	Shebin El-Kom	3.45** ± 0.95	- 5.26 ± 0.89	0.00
	Moshtohor	3.67** ± 1.12	- 2.05 ± 1.01	0.00
	Combined	5.43 ± 2.99	- 3.99 ± 1.55	0.00
Silking date	Shebin El-Kom	3.95** ± 0.99	- 4.07 ± 2.02	0.00
	Moshtohor	1.99** ± 0.63	- 1.60 ± 0.69	0.00
	Combined	1.50* ± 0.62	0.02 ± 0.43	0.01

*, ** Significant at 0.05 and 0.01 levels of probability, respectively.

per ear. All estimates of the interaction between dominance genetic variance x locations had negative values and deduced to zero. In other words, the interaction between genetic variance components x locations may be mainly due to additive genetic variance x locations. Rojas and Sprague (1952), Matzinger _et al_. (1959), Robinson and Moll (1959), Goodman(1965), Nawar (1971), Diab (1979), and others showed that the amounts of the interactions of dominance x location or dominance x years were higher than did in additive genetic variance. Also, Cerrate (1968), using Design-II for the estimation of genetic variability within two open-pollinated varieties indicated that the non-additive x environment interaction was greater than additive x environment interaction. On contrary to these findings Moll and Robinson (1967) reached the conclusion that the interaction variances are propartional to the genetic components themselves. Consequantly, the additive x environment interaction was greater than the dominance x environment interaction. It seems that the magnitude of interaction would depend on the environmental conditions under which the experiment is conducted.

Estimation of the additive genetic variance , dominance variance and error variance were used to

Table 10 . Estimates of additive x location (A x L) and dominance x location (D x L) for all characters studied.

Characters	σ^2 A x L	σ^2 D x L
Yield of ears per plant	222.78 ± 260.34	- 966.83 ± 16.92
Ear length	1.29^{**} ± 0.54	- 2.61 ± 0.51
Ear diameter	0.12^{**} ± 0.04	- 0.14 ± 0.03
No. of rows per ear	0.16 ± 0.14	- 0.43 ± 0.36
No. of kernels per row	9.15^{**} ± 3.08	- 13.70 ± 0.80
Plant height	280.66^{**} ± 80.39	- 415.25 ± 1.82
Ear height	142.57^{**} ± 39.73	- 239.34 ± 0.75
Tasseling date	15.11^{**} ± 2.99	- 17.57 ± 1.48
Silking date	1.47^{**} ± 0.47	- 3.37 ± 0.34

*, ** Significant at 0.05 and 0.01 levels of probability, respectively.

calculate the heritability in the narrow sense for full-sib families. Heritability values for the different characters are given in Table (11). The estimates of heritability were similar in the two locations and combined analysis. The stabilizing trend of the heritability values for yield of ears per plant over two locations may be attributed to favourable growing conditions characterizing these locations. The heritability value of ear length dropped drastically in Moshtohor location. For this trait the error variance in Moshtohor was higher than in Shebin-El-Kom by two times and their interaction between additive x location was highly significant, also, the amount of this interaction in Moshtohor was more than the same interaction in Shebin-El-Kom. In general, the heritability values based on the combined analysis ranged from zero for ear length and number of kernels per row to 80.75% for ear height. The zero value of heritability for the two previous traits may be attributed to the negative values of additive genetic variance in each case.

3- Phenotypic and Genotypic correlations:

The genotypic and phenotypic covariances between yield of ears per plant and each of the other characters were calculated for the two locations. These covariances

Table 11 . Estimates of heritability % (h^2) in the narrow sense for all characters studied from F.S families.

Characters	Shebin El-Kom	Moshtohor	Combined
Yield per plant	14.18	14.51	11.77
Ear length	32.83	4.46	0.00
Ear diameter	51.55	34.89	25.41
No. of rows per ear	38.92	34.95	38.79
No. of kernels per row	23.75	39.97	0.00
Plant height	37.20	65.51	54.24
Ear height	72.46	98.88	80.75
Tasseling date	56.16	55.06	56.11
Silking date	78.14	43.77	50.80

were used to estimate the additive genetic and phenotypic correlations and they are presented in Table (12). The phenotypic correlations were tested for the significanse from zero, while the additive genetic correlations were not. For the first location (Shebin-El-Kom), the yield of ears per plant was highly significant positive correlated with ear length,number of kernels per row, while it was only significant negative correlated with silking date. There was no correlation between yield and ear diameter, number of rows per ear, plant and ear heights and tasseling date. The magnitude of the genetic correlation was almost similar to the phenotypic correlation. For the second location (Moshtohor), the yield of ears per plant was phenotipically highly positive correlated with number of kernels per row and ear height,while it was only significantly negative correlated with silking date. There was no correlation between yield per plant and all traits except the three previous characters. Also, the magnitude of genetic correlation in this location in most cases were similar with phenotypic correlations. In general, the most correlation values in the second location were lower than in (Shebin-El-Kom), it is due to the higher value of error variance in the second location than in the first as mentioned before. The most

Table 12 . Estimates of the phenotypic (rph) and the additive genetic correlations (rA) between yield per plant and other characters studied.

Characters	Shebin El-Kom		Moshtohor	
	rph	rA	rph	rA
Ear length	0.44^{**}	0.81	0.14	-0.09
Ear diameter	0.16	0.21	0.10	0.40
<u>No</u>. of rows / ear	0.07	0.23	0.04	0.72
<u>No</u>. of kernels / row	0.36^{**}	0.29	0.25^{**}	0.27
Plant height	0.07	-0.02	-0.07	-0.66
Ear height	0.02	-0.01	0.41^{**}	-0.73
Tasseling date	-0.13	-0.73	0.10	-0.36
Silking date	-0.22^{*}	-0.81	-0.21^{*}	-0.02

*, ** Significant at 0.05 and 0.01 levels of probability, respectively.

correlation values in the two locations were similar such as silking date, tasseling date, plant height, number of kernels per row, number of rows per ear and ear diameter. The correlation values were contradicted for yield of ears per plant and ear length among the two locations, it is due to the error variances with both locations as mentioned before. Most correlation coefficient had no predictive value to utilize these coefficients in indirect selection programmes. The main causes of genetic correlation are peliotropic effects or linkage. As the variety under study was assumed to be in linkage equalibrium, peliotropic effects would be the main causes of the genetic correlation reported in this study. Eberhart et al. (1966) pointed out that linkage cannot be eliminated as a source of some of the correlations, but it is apparently not the source of some of the larger and more consistent ones, which must have arisen from that the characters are affected by some of the same underlying processes in the plant.

Finally, it can be emphasized from the previous results, that number of kernels per row is the important character which had high influence on yield per plant. A simultaneous selection of this character should bring an improvement in yield.

4- Predicted Genetic Advance From Selection:

Several alternative selection procedures have been developed and studied in some detail. These include (1) mass selection, (2) modified ear-to-row selection, (3) half-sib selection, (4) full-sib selection, (5) S_1 selection , and (6) test cross selection with a broad-base tester or with an inbred-line tester.

The theoretical and specific gain for six methods of intra-population improvement are given in Tables(3) and (13).

In mass selection, half-sib selection, and modified ear-to-row selection, 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 ($C = ½$). If the trait is expressed before pollination, undesirable plants can be eliminated to give parental control of both sexes ($C = 1$). Alternatively, pollen can be collected from selected plants, bulked and used to pollination other selected plants, or the selected plants can be selfed and this seed can be planted in isolation the following season for recombinations. Obviously selecting both sexes will give twice as much gain as selection for one sex only and will often justify the extra expense involved (Table 3). For characters such as yield with large genotype x environmental interactions the phenotypic variance will be normally very large for mass selection in comparison with any method of family selection where trials have been grown in different environments. But expense also will be much less for mass selection than for family selection. Our expected improvement value per cycle for mass selection was 1.98g.based on selecting one sex and 3.95g.based on the two sexes. Lonnquist (1967) reported even greater yield improvement from mass selection for prolificacy. Adapted mass selection in two adapted and eight semi-exotic populations in Nebraska was effective in increasing yield and prolificacy, especially in the semi-exotic populations where yield was increased by an average of 5% per year. Gardner (1963) has reported a good rate of progress (2.7g.per year) for grain yield in"Hays Golden" . Kamis (1970) in egypt obtained an average gain per cycle of 7.97% from mass selection for the variety American Early and 10% for "Weakly variety" with respect to the original populations.

(1970) in Egypt reported an average increase of 8.9% in yield per cycle in "American Early" variety of modified ear-to-row. El-Rouby and Salem (1979) obtained an average increase of 14.1, 8.9 and 2.6% for actual, fitted and predicted gain per cycle of the base population "Alexandria synthetic No.1" in the first cycle of improvement, but they obtained 3.8, 8.9 and 2.6 for actual, fitted and predicted, respectively in the second cycle of improvement.

The expected improvement in yield from half-sib family selection was 2.84 g.per cycle. El-Rouby and Salem (1979) obtained an expected average increase of 3.6% with "Alexandria Synthetic Variety No.1" relative the original population. However, Shehata _et_ _al_.(1981) obtained an expected average increase of 3.0% with ""American Early" variety.

Full-sib-family selection requires only two generations per cycle if plant-to-plant crosses are made between plants from different selected families because recombination and family formation will be accomplished simultaneously, i.e., season 1 (recombination-family formation) and season 2 performance trails. Although gain will be proportional to ($\frac{1}{2}\sigma^2A$), the phenotypic variance will be larger than half-sib selection. If plants within each full sib family are selfed in the nursery the same season as the performance trails are conducted and a bulk of seed from several elite selfed plants are used to represent each selected line for recombination, gain from selection will be increased because the parents of the full-sib families will be inbred for the subsequent cycle, $\sigma^2 g' = (1 + F)\sigma^2 A$. Our expected gain value per cycle was 6.38 g. Moll and Stuber (1971) reported 2.5% to 4.0% gain per cycle in five varieties in North Carolina. Nawar (1971) obtained a predicted average increase of 16.7 % per year from full-sib family selection for "American Early" variety. El-Rouby and Salem (1979) obtained an average increase 8.5%, 8.9% and 3.9% for actual, fitted and predicted gain per cycle, respectivelly of Co of the first cycle of improvement, while they obtained 5.9, 8.9 and 6.0 for actual, fitted and predicted gain per cycle, respectivelly of Co for the second cycle of improvement. Nawar _et_ _al_. (1983) obtained an expected average increase of 13.19% per year from full-sib family selection for "Alexandria Synthetic No.1".

When the population improvement is obtained through S_1 selection, the improvement in the population _per_ _se_ cannot be predicted exactly unless dominance effects are negligible because the defination of $\sigma^2 A$ changes slightly with inbreeding (Cockerham, 1963; and Empig et al.,1972). The formula presented in Table (3) will give a good estimation of expected gain for the population is approximately proportional to the gain in the mean S_1 line performance. El-Rouby et al. (1978) showed that the expected genetic variance among half-sib families equals $\frac{1}{4}\sigma^2 A$ whereas between S_1 lines approaches $\sigma^2 A$. Therefore, the precision of H.S families will be less than S_1 line design is easier than half-sib design. Random S_1 line could be isolated from any maize population with sufficient seed for testing over a number of locations. The data showed an expectation average increase of 8.42 of S_1 selection. Burton, et al. (1971) obtained an average of increase 16.3% by four cycles of S_1 selection for the yield of BSK (S).

Test cross selection is a form of half-sib selection. Three seasons were required per cycle because each phase requires a separate season. In test cross selection , a plant is selfed and crossed to several random plants from the population as tester. Alternatively, plants can be selfed one season, and the S_1 lines can be interplanted with the tester in the next season and detasseled to obtai the test-cross seed. But for rather than three seasons pe cycle are required with the latter procedure. After test for a non-related line versus the population tester. The inbred line tester should be changed periodically, however, because no selection pressure can be applied at loci with a frequency 1.0 for the favourabl allele in the tester line.

Most interapopulation programs involving family performance testing have been restirected in effective population size. Consequently, inbreeding has increased rapidly and many alleles have reached fixation because of random drift, or possibly linkage rather than as a response to selection (Burton et al., 1971 ; Eber-hart et al., 1971; and Horner et al., 1973). Our results showed an average predicted increase from the test cross selection of 4.52% through one cycle. El-Rouby and Salem (1979) obtained an expected gain in grain yield / plant from progeny test as Δg / year % of Co by 3.6% with "Alexanderia Synthetic No.1". Meanwhile, Shehata et al. (1981) with "American Early" variety obtained an average increase of 4.1%.

From the previous result it could be concluded that the S_1 family and 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.

Table 13. Expected genetic advance for yield per plant from six methods of selections.

Methods of selection		Selection intensity %	Crop season per cycle	Expected gain per cycle(gm.).
Mass- selection	One sex	10	1	1.98
	Both sexes	10	1 or 2	3.95
Modified-Ear-to-row		20	1	1.13
Half-sib (H)		10	2	2.84
Full-sib (F)		10	2	6.38
Test cross population as a tester		20	3 cr 4	4.52
S_1 selection		20	3	8.42