Tanta University
Faculty of Agriculture
Department of Agronomy

BREEDING STUDIES ON CORN
(*Zea mays* L.)

BY

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THESIS
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ABSTRACT

Title of thesis : **Breeding studies on corn (*Zea mays* L.)**
Name of Student : **Emad Mohamed Ahmed Houssein**
Degree : **Ph.D. in Agronomy from the Faculty o**
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The investigation was carried out during the two summer growing seasons 2004 and 2005 to estimate the genetic variance components and expected advance from selection in the two maize populations i.e. expected advance from selection in the two maize populations i.e. Nobaria and Gemmeiza yellow maize population (NYP and GYP) by using Design-I and S_1 line selection methods. Data were collected on: Days to tasseling and silking, plant and ear heights (cm), leaf area of ear (cm^2), number of ears/plant, ear length (cm), ear diameter (cm), number of rows/ear, number of kernels/row, 100-kernel/weight (g) and grain yield/plant (g). The additive genetic variance were found to be significant for Days to silking, ear height, ear diameter, 100-kernel weight and grain yield/plant in (NYP).

Dominance genetic variance were significant for all the study traits in both populations.

The average degree of dominance (σ^2D/ σ^2A) were higher than unity for all traits in both populations, except 100-kernels weight in NYP.

The predicted genetic gain from selection in S_1-line selection method for grain yield/plant were 65.79 and 64.33% in GYP and NYP, respectively. The predicted genetic advance per cycle for improvement the two populations by using mass selection of one sex, modified ear two row selection full sib family selection, half-sib family selection. Test cross population as a tester and S_1 family selection were 6.56, 6.59, 12.44, 14.47, 25.20 and 20.00%, respectively in NYP and 3.19, 8.70, 9.40, 6.49, 18.81 and 11.14%, respectively in GYP. The S_1 family selection were the best method to improving the two population under study.

Key words: Maize – Design-1 – S_1 line selection – genetic varisnce – selection gain from selection.

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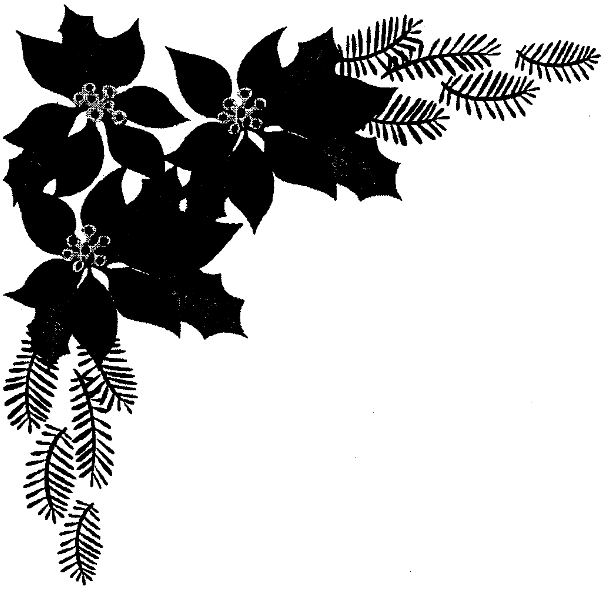
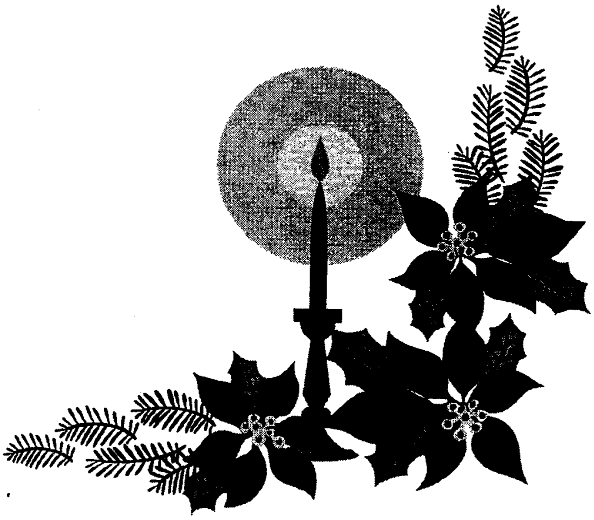


INTRODUCTION



1. INTRODUCTION

Corn or maize (*Zea mays*, L.) is one of the most important cereals crop in Egypt due to its vast acreage, total production and cash value. It had a high yield per both units of labour and area and a short growth period as compared to wheat. Also, it is widely growth in Egypt as compared to certain area such rice and sorghum. It is essential for human consumption and livestock. Moreover, it is, also, used for industrial purposes such as manufacturing starch, cooking, oils and feed animals. Before an efficient breeding methodology can formulated, it is essential that these populations under investigation are subjected to genetic analysis to find out the relative magnitude of additive and non-additive gene action with regard to yield and other metric traits.

Estimation of types of gene action in the breeding populations is very essential for selection among these base population as well as in choosing the most efficient breeding method for improving the populations.

Estimation of heritability, prediction of response to selection and the designed of the most effective breeding schemes are dependent upon the relative proportions of additive and non-additive genetic variances. If the estimates of genetic variance indicate that the additive genetic variance is a major importance. So, narrow-sense heritability would be expected to be relatively high and single plant selection would be initially be effective in improving the traits under consideration. On the other hand, existence of dominance or epitasis justifies the use of hybrid program.

A situation may additive and non-additive genetic variance are of equal magnitude.

Comstock and Robinson (1948) presented the theory and methods for estimating variations for quantitative characters in maize (*Zea mays* L.).

Since then, studies in maize have been reported the relative portion of additive and non-additive genetic variance in populations derived from two inbred lines, open pollinated varieties and synthetic varieties. The methods were reviewed by the same authors.

Lindesey *et al.* (1962) reviewed the efficiency of design-1 and its limiations. **Galal *et al.* (1977)** reported that (4) females with 24 to 30 males is the optimum sample size. **Mohamed (1982)** found that (4) females with 30 to 40 males is the optimum female and male sample size to gain précised information of the genetic variance.

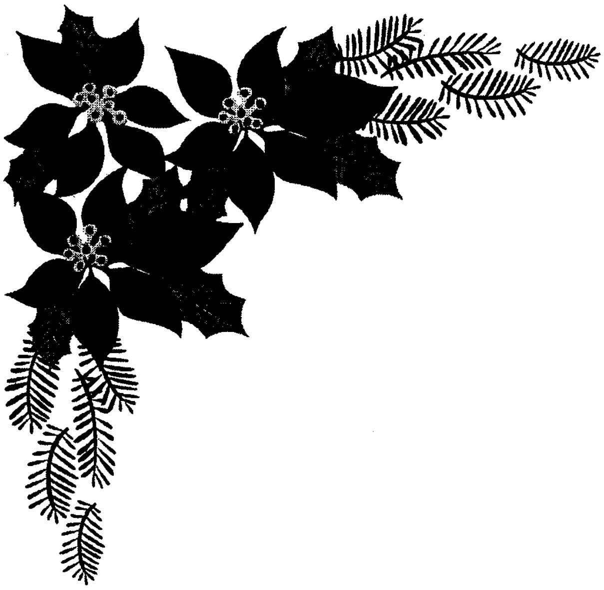
The main objectives of this study were:

1- To estimate the components of genetic variance in two populations i.e., Nobaria and Gemmeiza yellow maize populations.

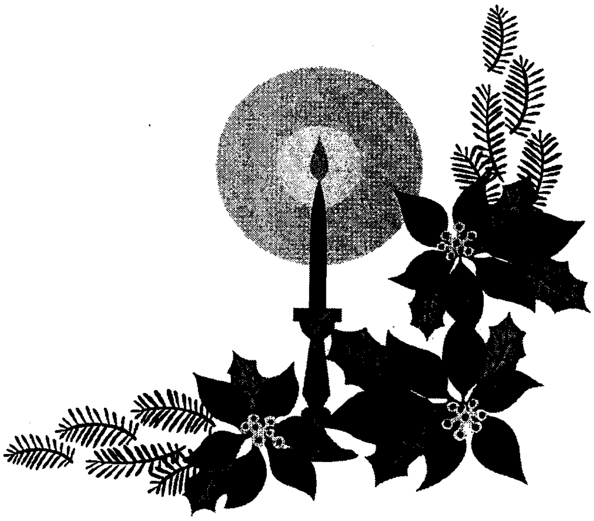
2- To calculate heritability value for all characters under study.

3- To estimate the phenotypic and genotypic coefficient of variability for all characters under study.

4- To detect the most effective selection methods that could be used to improve all characters under study in the two populations.



REVIEW OF LITERATURE



2. REVIEW OF LITERATURE

The available review of literature will be discussed under the following headings.

1- Genetic variance in open-pollinated maize population.

2- Recurrent selection methods and population improvement, heritability and gain from selection.

1- Genetic variance in open-pollinated maize population:

Genetic variance in maize populations is a prime concern of maize breeding. The information is need to determine the most effective breeding methodology.

Nawar *et al.* (1983) executed design I mating within synthetic variety Alexandria-1 to study the genetic variance components of female and male optimum numbers for grain yield/plant, ear height and days to tasseling. Results showed that the additive genetic variance was only the predominant component which played the major role in the inheritance of all traits studied. Also, they found that the optimum estimates of the additive variance were obtained from 30-40 males each mated to at least 4 females.

Nawar *et al.* (1984) estimated genotypic and phenotypic, coefficients of variation and heritability in ten collections of Egyptian maize genotypes. Data of grain yield/plant, ear length, number of rows/ear, ear height and days to silking showed high genetic coefficient of variation. Heritability estimates were high for number of ears/plant, ear length, number of rows/ear, plant and ear heights, days to silking and moisture percentage traits but were moderate for grain yield/plant.

Nawar (1985a) executed design I mating system with 30 males in a maize population. The resulted 120 full-sib families were grown in six sets with six replications. Analysis of data was based on 2, 3, 4, 5 and 6 replications. The results showed that: The additive genetic variance was positive over all numbers of replications and highly significant at 5 replicates. Increasing number of replicates decreased steadily the standard deviation estimates of additive and dominance variances compared with 2 replicates. To obtain maximum and accurate genetic variance estimates and their standard deviation as well as heritability, not less than 4 or 5 replicates must be used. Generally, additive genetic variance components predominated than those of dominance variance in most studied traits including grain yield/plant and some of its components.

Nawar (1985b) estimated additive, dominance variances and their interactions with two levels of nitrogen within the synthetic variety of maize (Corn Belt) using design-I mating system. The additive genetic variance was significant and greater than dominance variance for all traits studied.

Nawar (1985c) calculated additive and dominance variance from design-I in the synthetic variety Shedwan-3. Additive genetic variance was predominated for all the studied traits. Heritability in narrow sense for grain yield/plant, plant height, ear diameter, ear length, number of rows/ear and number of kernels/row were 34, 83, 64, 73, 66 and 91%, respectively.

Nawar (1985d) used design-I mating scheme to study genetic variance components in the maize synthetic variety (C-17). Data showed that the additive and dominance variances were significant at the high nitrogen level for grain yield/plant. The additive genetic variance for yield of ears/plant was only significant under low nitrogen level. While, dominance variance had negative values in most cases.

Shahi and Singh (1985) recorded data on grain yield and five of its components from 192 full-sib families developed, using design-I technique in the early yellow flint population Nevin. The analysis revealed greater importance of non-additive than additive genetic variance for grain yield at both sites and the greater importance of additive than of non-additive variance for all yield related traits, except kernels/row. Heritability for yield was 38% at normal density and 14% at high plant density.

El-Hosary (1986) estimated genetic variance within the adapted Egyptian open pollinated variety of maize (American Early) by using Design I. Data were collected on grain yield per plant, ear height, ear length, ear diameter, no. of rows per ear and no. of kernels per row. σ^2A additive variance was significant and greater than σ^2D dominance variance for all traits. σ^2D was insignificant for all traits under study.

Nawar (1986) presented a study to compare the efficiency of S_1 and design-I mating systems for estimating additive genetic variance in two maize populations (Corn Belt and Tuxpeno c.17) under two levels of nitrogen 60 and 120 kg N/feddan. Results of Corn Belt population showed that (σ^2_g) of S_1 was higher than those of design-I for all studied traits, except ear length, ear diameter and number of days to 50% silking. While, for Tuxpeno c-17 population, the (σ^2_g) from design-I was higher than those obtained from S_1 lines for all studied traits. In general, additive genetic variance component played the major role in inheritance of most studied traits including grain yield/plant and some of its components.

Pal *et al.* (1986) evaluated 256 full-sib families obtained from composite Rattan (a opaque-2 population) using design-I crossing system. The results showed that only additive genetic variance was significant for grain yield, days to silking and number kernels/row. Only dominance variances were significant for plant and ear height. Both additive and dominance variances were significant for plant height, ear height and 500 grain weight. Moreover, they stated that dominance effects being the more important.

El-Hosary (1987) estimated of genetic variance in the composite variety of maize (Cairo 1) by using design I for plant and ear height, ear length, No. of rows per ear, No. of kernels per row and grain yield per plant. The additive genetic variance was the major component than of genetic variation for all traits. Also, the additive genetic variance was significant for all traits. At the same time, exhibited bias estimates of dominance genetic variance, all values of dominance were negative. The dominance was less important than the additive variance. Ratio of $\sigma^2D/\ \sigma^2A$ was zero for all the characters.

Sayed-Ahmed (1987) practiced S_1 and test cross family selection in composite-4 maize population. He found that genotypic variance estimates were greater for S_1 family selection than for test-cross for all traits, except for late wilt percentage, which exhibited greater genetic variance among test-cross families. Estimates of phenotypic and genotypic coefficients of variability for the variance traits tended to assume the same trend in both progenies, but of lesser magnitude for test-cross. The highest coefficient of variability was recorded for wilted plant percentage followed by grain yield.

Clavido-Jobet and Pitrico-Borriga (1988) calculated genetic variance and narrow sense heritability for five quantitative characters in 1986 progenies of half-sib families taken from a sample of maize population. Narrow-sense heritability estimates were high for plant height (0.51) and ear length (0.59), and low for leaves/plant (0.30) and grain yield (0.22). Ears/plant had the lowest heritability value (0.139).

Shahi and Singh (1988) evaluated biparental progenies developed in the composite Nevin at two plant densities (5333 and 9666 plants/ha). They found that estimates of additive genetic variance were higher than those of dominance variance for all the studied traits, except for grain moisture content. The magnitude of additive variance was high at high density.

El-Absawy (1990) compared some experimental mating designs in two maize populations, Corn Belt and Tuxpeno-C17 to estimate genetic variance components. He showed that in design-I, additive genetic variance was significant for grain yield/plant, plant and ear height, days to silking and days to tasseling in Corn Belt population. Only dominance variance was significant for ear diameter in this population. In Tuxpeno-cl7 population, additive genetic variance was significant for ear yield/plant, number of kernels/row, ear length, plant and ear height, and days to silking and days to tasseling.

El-Hosary *et al.* (1990a) found that the mean squares associated with GCA and SCA were highly significant for all growth attributes. High ratios of both which largely exceed the unity were obtained in all traits, except plant height.

El-Hosary *et al.* (1990b) indicated that the variances associated with GCA and SCA were significant for yield and yield components, indicating the presence of that both additive and non-additive types of gene action were detected. With the exception of ear length and ear husk, the large portion of the total genetic variability associated with yield and yield components characters was due to non-additive gene action.

Reddy and Agrawal (1990) evaluated biparental progenies developed following North Carolina design-I in the improved composite D742 at two locations. They found that additive genetic variance was more important than dominance variance for grain yield and its components at both locations. In contrast, dominance variance was the most important for 200-grain weight.

Brenner *et al.* (1991) studied general combining ability (GCA) and specific SCA in a set of diallel crosses among eight maize population. The results indicated that additive effects (GCA) were the most important, with reciprocal and SCA effects important only in specific crosses; the best combinations involved genotypes from 2 population groups i.e. Mexico and Southern Brazil.

Getschman and Hallauer (1991) found variances among progeny variance which were significant and, in all instances larger than the variance estimates within-progeny variance. Additive genetic variance accounted for the genetic variation among progenies of related and unrelated line crosses, and estimates of variability among and within S_1 progeny test crosses were not different from each other and were less among and within S_1 progenies themselves, within the precision of this experiment. On average, 70.7% greater genetic gain would be realized with among S_1 progeny selection.

Moll (1991) used full-sib family selection in open pollinated population (Jarvis Golden Prolific) and the population descended from F_2 generation of the single cross (NC7 x C121) to estimate of accumulated grains through all 6 cycles. Additive genetic variance showed no trend associated with selection in the Jarvis population, but declined with selection in the NC7 x C121 population. Accumulated gains were greater in the NC7 x C121 population, even through genetic variance in that population was smaller initially and has decreased in the later selection cycles.

Guei and Wassome (1992) developed full-sibs within half-sib groups using design-I mating system. Evaluation of these full-sibs groups showed that additive gene action was more important than dominance in controlling the expression of flowering traits. However, more dominance deviation were detected in yield and number of ears/plant. Additive genetic, variance was larger in magnitude under stress than non-stress condition, except for yield in one of the population.

El-Agamy *et al.* (1992) indicated that grain yield was influenced by dominance variance (σ^2D) in population A and by both additive (σ^2A) and dominance variances in Pop-B. Pop-A had higher additive genetic estimates than Pop-13 for most of the studied characters. Realized gains from one cycle by selection in Pop-A and Pop-B were 10.10% and 6.10%, respectively, for grain yield as compared to expected of 10.25% and 6.37% for the two maize populations.

Brigitt and Gallais (1992) studied the effect of assortative mating on male and female variance and components (σ^2 m and σ^2 f, r respectively) in a nested mating design. They found that, under positive assortative mating, additive variance is systematicly over estimated and dominance variance is under estimated.

Guei and Wassome (1993) determined some gene action parameters in two tropical maize populations under drought conditions using the design I mating scheme. Results showed that in both populations, dominance genetic effects were more important than additive gene effects in controlling the expression of this trait. However, very little genetic variability was present in both population for the drought tolerance, although more genetic variation was detected at the flowering stage, when water stress become more severe than at the vegetative stage.

Schnicker and Lamkey (1993) found that genetic variance for all traits (i.e. grain yield, grain moisture, root ledging and lodging) were significant and different from zero, except for root lodging in cycle 11. Genetic variance for grain yield decreased after 11 cycles of selection, although the differences among cycles were not significant. Root lodging, stalk lodging, anthesis and days to silking had significant decreases in genetic variance after 11 cycles of selection change in heritability generally paralleled changes in genetic variance.

Duque-Vargas *et al.* (1994) used design-I mating system to study the inheritance of tolerance to soil acidity in tropical maize population SA-3. They found that additive genetic variance (VA) was similar to dominance variance (VD) for grain yield, greater than (VD) for plant height and ears/plant, less than (VD) for days to silking across acidic soils.

Marquez Sanchez (1994) estimated genetic variances in maize (*Zea mays* L.) up to eight female per male crosses were required to obtain reliable estimate of the dominance variance. Hand pollinations, however, are not always successful in the production of the desired number of female per male crosses. An ear pollinated by several plants is a maternal half-sib (MHS) family. The hand pollination work involved in obtaining (MHS) families is relatively easier than in design 1 mating. If individual plant data are taken within the MHS families, it is shown that the covariances among individuals within MHS families 3/4 sigma A_2 + sigma De. The observable component of variance among families (sigma F_2) is 1/4 sigma A_2. Thus, it is possible to estimate the additive (sigma A_2) and the dominance (sigma D_2) genetic variances. It is suggested that each MHS family could be produced by mixing the pollen of eight or more plants and applying it to a single female plant.

Ochieng and Compton (1994) used generation mean analysis to estimate genetic effects governing grain yield, harvest index and other agronomic traits in the population. Dominance effects were greater than additive effects for change in yield, harvest index, ear length, plant height and number of days to mid-anthesis. However, additive effects were more important than dominance effect for sterial stalks and ears/plant.

Younis *et al.* (1994) estimated genetic variance components in two maize single crosses (S.C.10 and S.C.I 07) using design III mating system. Data showed that additive genetic variance was more important than dominance genetic variance in the two crosses.

Landi and Frscaroli (1995) estimated the genetic variance in maize (*Zea meys* L.). They found that grain yield mean value of cycle C_4 was significantly higher than that of cycle zero C_0 both as S_2 and as Tc, while the two populations did not significantly differ for the genetic variance estimates. The phenotypic correlation coefficients between S_2 and Tc performance for the same trait were significant, but a declining trend was mid from C_0 to C_4 for all investigated traits.

Nawar *et al.* (1995a and b) studied the types of gene action in two maize populations (Giza 2 and composite 5). They found that the additive gene action predominantly controlled the inheritance of days to tassling and days to silkings, while the dominance variance was the predominant genetic components and played the major contribution in the inheritance of most studied traits. For composite 5, the additive genetic variance was more important than dominance variance in the inheritance of 100-kernel weight, ear length, plant height, leaf area and days to silking, while the dominance variance was predominant in the inheritance of grain yield/plant, number of kernels/row, number of rows/ear, ear diameter and days to tasseling. Also, they found that the grain yield/plant had moderate estimate of heritability, while high heritability estimate in broad sense were detected for the most studied traits. Meanwhile, for composite 5, heritability estimates in narrow sense for grain yield/plant, leaf area, stem diameter and days to tasseling were very low, while the number of kernels/row, number of rows/ear, 100-kernel weight, ear length, ear diameter, plant and ear heights and days to silking had high estimates of heritability. Meanwhile, most estimates of heritability in broad sense were very high except for leaf area.

In a study of inheritance of grain yield/plant, ear height and ear length in two maize hybrids in relation to sowing date, **V'Lchinkova (1995)** found that over-dominance and epistatic effects were found for the traits studied. Dominance gene effects were the most important and additive gene effects relatively less important for both traits.

Betran and Hallauer (1996) estimated genetic variance components in three hybrid maize populations using (North Carolina Design II). The additive genetic variance component was the most important component of genetic variability for all traits studied, except for grain yield, additive X environment inter-population variance estimates were smaller than their corresponding of additive variance.

El-Ghonemy (1996) used design-Ill mating system to estimate genetic variance components in maize single cross-10 cultivar. Results indicated that additive and dominance genetic variances were found to be significant for all the studied characters. Moreover, additive genetic variance was more important than dominance genetic variance for all the studied characters. Estimates of heritability varied from low to moderate for most studied traits.

Malvar *et al.* (1996) evaluated full-sib within half-sib groups developed by using design I mating system in two maize populations. The populations showed a similar genetic structure with very small differences. Moreover, the pattern of genetic variability was similar to other germplasm because the greatest proportion of total genetic variance which was attributed to additive effects for most traits. In contrast, estimates of dominance variance were high for yield, ear and plant heights and ear length. The large range of variation and high values of heritability for lodging, ear and kernels traits suggested good potential for improving through inter-population selection programme.

In a study of inheritance of grain yield/plant, ear height, days to silking and grain moisture in a cross of eight parental populations of maize, **Sfakianakis *et al.* (1996)** indicated that the intrapopulation dominance effects had the largest contribution to total variation for yield (37.1%), plant height (61.6%) and ear height (49.6%) for days to silking, additive and dominance effects contributed equally (33.2% and 37.3%, respectively) while for grain moisture, additive effects were the greatest contributing factor (61.2%).

Fountain and Hallaur (1996) estimated genetic variability (σ^2G) of yield within three maize populations in the F_2 (B73 x B84, B90 x M017, and B73 x M017), within three genetically narrow-base synthetic (NBS) (IBSM, M017-Syn., and H73 -Syn] and within three genetically broad base synthetics (BBS) [Bsl 1 (FR) C_9, BSC_1 (R) C_9 and BSSS (R) C_9]. Fifty S_1 progenies for each of the nine populations were evaluated at three locations for two years. Differences among S_1 progenies within each population were significant for most traits. Estimates of σ^2G were determined from the S_1 component of variance, and average estimates of σ^2G for grain yield were similar for F_2 and BBS populations, whereas the average estimate of σ^2G for NBS populations was 40% smaller. Within population types, the related line F_2 cross (B73 x B84) had 50% loss σ^2G for grain yield than the other two F_2 populations. BS 14, H73-syn, and BSCBI (R) C_9 had smaller estimates of σ^2G for grain yield than the other synthetic populations. Estimates of σ^2G suggest selected F_2 and BBS populations have greater potential for improved gains than the NBS populations.

El-Hosary and Abd El-Sattar (1997) estimated additive, dominance variance in the synthetic maize variety (Moshtohor-2). Data showed that additive genetic variance was significant for number of rows/ear, plant height and ear height. Heritability estimates were high for all studied traits, except for 100-kernel weight.

Mani and Dube (1997) evaluated full-sib and half-sib families obtained latter following North Carolina design-I (NCD-I). Results showed a predominant role of additive genetic variance for prolificacy and associated traits i.e., number of ear shoots, first and second ear, days to silking, first and second ear grain yield and total grain yield.

Barakat (1998) practiced two selection procedures, reciprocal recurrent selection and S_1 line selection in Tuxpeno and Tep. 5 in two locations Gemmeiza and Sakha to estimates genetic variance components for eleven traits. Obtained data showed that additive genetic variance were significant for all characters in two population, except for ear diameter and no. of kernels per row of Tep. 5. Dominance variance were not significant for all characters of Tuxpeno, except no. of kernels per row and 100-kernel weight, while for Tep. 5 population, dominance variance was significant for resistance to late wilt desease, ear position, no. of kernel per row and 100-kernel weight, but not significant for all traits. Generaly, dominance genetic variance in Tep. 5 were higher than Tuxpeno, maize population for most of the studies characters. Additive genetic variance for S_1 were high and significant for all characters, except for ear position and no. of kernels per row in Tep. 5 and days to 50% silking, ear position and 100-kernel weight in Tuxpeno.

Shehata (1998) estimated the genetic variance components using design-I mating scheme in Cairo-1 maize population in two growing seasons. Partial and over dominance were dominant and played the major role in the inheritance of most studied traits including yield and some of its components.

Mani *et al.* (2000) evaluated full-sib and half-sib families developed using NCD I under high and normal plant densities. Results revealed that additive genetic variances were significant for ears/plant, prolificacy, ear diameter, kernel rows/ear, 100-kernel weight, ear grain weight and total grain yield.

Alves *et al.* (2002) assessed two hundreds S_1 progenies and corresponding half and full-sib progenies from cycle 0 to cycle 5 in CMS-39 maize population to estimate genetic variance components. The estimates of genetic variance components and heritability suggested the presence of variability in the studied population, indicating that the previous unsuccessful selection could not be attributed to lack of genetic variability. The additive component explained in average more than 75% of the total genetic variance, indicating the predominance of the additive effects of the control of all considered traits.

Barakat (2003) studied genetic variance for grain yield and other valuable traits in Gemmeiza yellow maize population using S_1 lines design. Results showed' that genotypic (σ^2_g) and phenotypic (σ^2_{ph}) variances were significant for all the studied characters. Genotypic variance (σ^2_g) was the major part of phenotypic variance (σ^2_{ph}) for all the studied characters. Estimates of heritability for all studied traits were high in general.

Badu-Apraku *et al.* (2004) evaluated North Carolira Design I (NCD-I) progenies derived from: Pool-16 DT tropical maize population in two dry seasons at two sites for each season. Results showed that the additive genetic variance was much larger than the other components. Narrow sense heritabitity estimate was 73% for grain yield and ranged from 43 to 71 for the other seven traits. In the second season, grain moisture at harvest, ear height, days to anthesis and silking have positive additive genetic variance, but heritability (h^2) estimates were much lower (15-41) than in the first season.

Raposo and Ramalho (2004) found that the magnitude of the additive genetic variance was high and estimates of dominance variance were negative. In addition, estimates of inter-population genetic variance were high.

Revilla *et al.* (2004) developed full-sib and half-sib families in a maize synthetic following the Design-1 mating system. Progenies were evaluated in randomized complete block design with sets within two replications in North Western Spain for two years. Data showed significant additive genetic variance for most studied traits included grain yield. The interaction of different sib-families with environments were not significant in most cases. High heritability values for most studied characters were found.

2- Recurrent selection method and population improvement. [Intra and Inter-population]. Heritability and gain from selection:

Nawar *et al.* (1983) reported that the expected gain for yield for half-sib (H.S) and full-sib (F.S) recurrent selection in the synthetic variety Alexandria-1 were 6.53% and 13.19%, respectively.

Nawar *et al.* (1984) studied the genetic advance under selection in a collection often Egyptian entries of maize. They found that grain yield/plant, number of ears/plant, ear length, number of rows/ear, plant and ear heights and moisture percentage had high genetic gains and some of these traits were important for maize breeders for improving the plant characteristics including grain yield.

Nawar (1985a) found that both recurrent and full-sib family selection were the best methods of selection in increase the grain yield/plant.

Nawar (1985b) used estimates of genetic and environmental parameters to predict the relative genetic advance from mass selection, progeny test, S_1 lines and full-sib family selection. The two later methods gave the highest relative gain for yield, followed by progeny test. Ear to row selection method showed the lowest expected genetic advance for yield.

Nawar (1985c) found that mass selection and ear to row selection methods were effective in increasing grain yield/plant of the synthetic variety Shedwan-3 by 15.6 and 19.5%, respectively. While, recurrent selection and full sib family selection gave the highest expected gains. Their values were 25.6 and 24.3%, respectively.

Nawar (1985d) suggested that the highest values of the expected advance/cycle from selection were obtained from progeny test selection methods. However, taking the number of year into consideration to provide one improvement cycle, the most efficient selection schemes were the S_1 recurrent selection, (R.S) and full-sib-family selection methods.

Nawar (1985e) studied the actual effectiveness of S_1 lines progeny test to improve the composite variety Composite-108. He found that the original population was rapidly improved after one cycle of selection. The increase in grain yield/plant after one cycle was 11% over the basic population.

El-Hosary (1986) found that heritability estimates for Design-1 in (American Early) were the range 84.04, 47.51, 52.22, 85.92, 77.08, 46.61 and 62.11 for plant height, ear height, ear length, ear diameter, No. of rows per ear, No. of kernels per row and grain yield per plant, respectively. The predicted genetic advance per cycle for improvement of the variety under study using mass selection one sex, modified ear to row selection, half-sib family selection, full-sib family selection, progeny test and S_1 family selection were 8.34, 3.52, 5.4, 13.2, 14.09 and 16.6, respectively. The family, full-sib family and test cross were the best methods to improve the variety under study.

El-Hosary (1987) used the design-1 to improving the maize synthetic variety of maize (Cairo 1) for plant and ear height, ear length, number of rows per ear, number of kernels per row and grain yield per plant. The narrow sense heritability values ranged from 67.09 for number of kernels per row to 23.53 for number of rows per ear. The heritability narrow sense were 62.06 for grain yield per plant. The predicted genetic advance per cycle for improvement the variety under study using mass selection one sex, modified ear-to-row selection, half-sib family selection, full-sib family selection, progeny test and S_1 family selection were 10.81, 2.5, 8.01, 15.29, 9.25 and 16.95%, respectively. S_1 family and full-sib family were the best methods to improve the variety under study.

Sayed-Ahmed (1987) practiced S_1 and test-cross family selection methods for improving maize Comp-4 population. He found that actual gain for grain yield w ere 6.32 and 4.34%. While, **Coors (1988)** obtained that broad sense heritability estimates from S_1 lines were higher than those from half-sib recurrent selections.

Coors (1988) indicated that effective recurrent selection for intrapopulation improvement maize (*Zea mays* L.) should be most effective when both inbred and non-inbred progenies are evaluated.

This study was conducted to examine the effectiveness of evaluating both half-sib (H.S.) and selfed (S_1) families during selection to improve population *per se* performance and inbred productivity. Four cycles for combined (H.S.) and (S_1) selection for increased grain yield were completed in a narrow based maize population derived from inbred lines; A 635, W 182E and W 64A. For each cycle both (H.S.) and (S_1) progeness were produced on prolific plant by selfing the bottom ear and exposing the upper ear to random pollen for the population. Increased in yield were not detected in test cross with inbred lines ASS4 and W 117. The yield of bulked composites from random, selfed pollinated plants increased by 20 g/plant over cycle.

Rodriguez and Hallauer (1988) estimated the direct and indirect response to selection in ten populations and their respective S_1 generations for different selection methods. They obtained positive response to selection for greater grain yield for each selection method, except for one population under going reciprocal recurrent selection.

Shehata *et al.* (1989) indicated that S_1 family selection was more effective than half-sib (H.S.)design for improving (Corn Belt C-1) population. The actual gain from selection for grain yield was 39.5% based on the original (C.B.C_1) population in the S_1-line selection relative to 18.0% for half-sib selection method. Expected and actual gain yield using the S_1 family selection were greater than those obtained using half-sib selection method. Expected gain from selection for yield components characters showed that both no. of kernels per row and no. of rows per ear were most effective traits for improving grain yield in S_1-line method. It could be concluded that S_1-line selection method is better than half-sib selection method for improving this population, where the cost-time and efforts will be taken into consiberation for providing one cycle of improvement.

Arha *et al.* (1990) estimated heritability for eight yield related characters in the maize gene pools Be yellow and CD white grown under two environments (different sowing dates). Heritability was highest for days to silking, moderate values were recorded for plant and ear heights, no. of leaves above the ear and ear length.

El-Absawy (1990) estimated the expected genetic advance from selection for yield/plant using sex methods of selection in Corn Belt and Tuxpeno- C17 populations. He found that S_1 family selection and full-sib family selection gave the highest expected gain from selections. The most desirable selection method for improving two maize populations together was the reciprocal recurrent selection to utilize the amounts of additive and dominance genetic variances existing in the two maize populations.

Elsahookie and Wuhaib (1990) studies the heritability among 4 maize population obtained by different mass selection scheme. Heritability of grain yield/plant ranged from 0.18 to 0.45 depending on season and selection scheme used. Heritability tended to be higher in autumn planted than spring planted crops. Selection gain was also higher in autumn than spring. Highest genetic gain (23.5 g/plant/cycle) was achieved by yield efficiency mass selection.

Reddy and Agrawal (1990) indicated that the expected genetic gain from one cycle of full-sib family selections was about three times greater than the expected gain from mass selection. Intra population recurrent selection is suggested for the improvement of the population.

Al-Naggar (1991) used two cycles (C_1 and C_2) of divergent mass selection in cv. Cairo 1 synthetic maize. Selection of prolificacy increased and grain yield per plant were increased by 13.6 and 11.6% per cycle, respectively.

Gouesnard *et al.* (1991) studied the intra and interpopulation selection procedure. Genetic variability of two populations evaluated of cycles C_0 and C_1. Expected response to intra and interpopulation selection were similar in improving both population. Also, the intra and interpopulation selection gave positive expected responses for S_1 performance. However, a selection method combining interpopulation and S_1 progenies was expected to be more effective in improving both populations.

Moll (1991) used full-sib family selection for grain yield in two maize populations; open pollinated population (Jarvis Golden Prolific) and the population descended from F_2 generation of the single cross (NC_7 x C121). Gains due to selection were linear for 16 cycles at a rate of 2.4% per cycle for the Jarvis population and 4.5% per cycle for the NC7 x C121 population. Advanced selection cycles were more responsive to environments than the original populations.

Robert and Moll (1991) studied the responses to full-sib family selection and changes in genetic variances accumulated during 16 cycles in the open pollinated Jams Golden prolific and the population descended F2 generation of the single cross NC7 x C121. Results indicated that gains due to selection were linear for 16 cycles at rate of 2.4% per-cycle for the Jarvis population and 4.5% cycle for NC7 x C121 population.

Soliman (1991) estimated gain from selection using reciprocal half sib and S_1 family selection. He found a good agreement between the expected and actual gain for improved grain yield at both pools through half sib method, while the expected gain was higher than actual gain for S_1 family selection.

Mourad *et al.* (1992) studied improving two maize pools A and B. Only one cycle of half-sib recurrent selection under 20%

selection intensity was completed. Estimated of genetic variance indicated that grain yield was influenced by dominance variances (σ^2D) in pool B and by both additive (σ^2A) and dominance variances in pool A. Pool A had higher additive genetic estimates than pool B for most of the studied characters. Realized gains from one cycle of selection in pool A and pool B were 10.10% and 6.10%, respectively for grain yield as compared to expected of 10.25% and 5.37% for two maize pools.

Nawar *et al.* (1992) used half-sib family selection to improve Cairo-1 maize population and full-sib family selection to improve Alex-II maize population. These methods were effective in improving the yielding ability and other agronomic traits in the two populations. The actual average increasing rate of the first improving cycle for Cairo-1 maize population was 17.5 % ($\Delta g\%$) relative to C_0 population. Meanwhile, the average actual advance of the first improved cycle in Alex-II maize population was 24.6 % relative to its C_0.

Arriel and Ramalho (1993) found that after three cycles of half-sib family selection the observed gains from selection were compared with gains expected based on parameter estimates for each selection cycle. The realized gain per cycle reported as the average for the four cycles was 3.6% which was smaller than the average expected gain per cycle (7.2%).

Carson and Wicks (1993) evaluated selection in maize; the original population (C_0) and two advanced cycles (C_1 and C_2) for each of the three selection schemes were evaluated over two years for grain yield in the absence of disease stress, grain yield under NIB and DSR stress and NIB and DSR resistance *per se*. Grain yield in the absence of disease stress was increased by an average of 6% per cycle. By selection for grain yield in the absence and presence of disease stress, it increased by an average of 3% per cycle with selection for disease resistance *per se*.

Landi and Frascaroli (1993) used full-sib recurrent selection in the Fs population of the single cross A632XMul94. They found positive response for all studied trails. Average response for grain yield reached up to 7.3% per-cycle.

Schnicker and Lamkey (1993) carried out 11 cycles of full-sib reciprocal recurrent selection to improve two maize populations BSSS and BSCB 1. They found that grain yield increased by 0.25 ton/ha (6.4%) per cycle. Genetic variance for grain yield decreased after 11 cycle of selection, although the differences among cycles were not significant.

Ghizan *et al.* (1994) found that simple recurrent selection was effective in increasing grain yield in Bl and MM maize populations. The increasing rates for the tow'populations were 16.7 and 10.2%, respectively. Meanwhile, full-sib reciprocal recurrent selection increased yield by 5.9% in Bl and reduced in MM by 6.4%.

Gritti *et al.* (1994) studied responses to selection and to observe significant changes in yield with six cycles of recurrent selection for seed size in the maize C 103-synthetic variety. They found that the selection was highly effective in producing significant variation among cycles for seed size. Final kernel weight in the cycles increased gradually by 4.01/200 kernels per cycle, while testcross were approximately one half of these cycles. The increase in kernel weight was positively associated with faster rate of grain filling and kernel size. Selection responses for seed size were also moderately effective in increasing grain yield.

Stajsin and Kannenberg (1994) compared the effectiveness of four selection methods (selfed progeny, ear-to-row, half-sib family selection and reciprocal recurrent selection) in five maize populations. They reported that the selfed progeny method was the most effective procedure followed by half-sib family selection. S_1 progeny procedure gave the greatest genetic drift in three out of the five populations.

Moll *et al.* (1994) used recurrent full-sib family and reciprocal recurrent selection to study grain weight of crosses between maize (*Zea mays* L.) varieties (Jarvis Golden Prolific and Indica Chlef). After 14 cycles on sandy soil of the North Carolina Coastal plain, grain yield, dry matter accumulation and (N) nitrogen accumulation in the population hybrid increased by 23, 12 and 4%, respectively, with full-sib family selection and by 27, 21 and 10%, respectively with reciprocal recurrent selection.

Holthaus and Lamkey (1995) estimated the mean performance and genetic variance in BSSS maize population after seven cycles of half-sib progeny selection (HS) and after six cycles of reciprocal recurrent selection (RRS). Half-sib progeny and recurrent selection methods were effective on mean performance responses for grain yield in the population per se. The average increasing rates for the two selection methods were 0.067 and 1.4 t/ha per-cycle, respectively. The S_2 progeny selection procedure in BSSS gave a response of 0.052 t/ha per cycle.

Nawar *et al.* (1995b) estimated the predicted genetic advance from different selection methods (mass selections, ear-to-row, half and full-sib family selection) in maize composite-5. They found that the highest estimates of the expected genetic advance from different selection methods were obtained from full-sib family selection either based on S_1 or S_2 where it gave 66.72 grams (Δg % = 32.93) and 87. grams (Δg % = 42.94%), respectably.

Betran and Hallauar (1996) estimated genetic gains from selection in three hybrid populations , BSSSCO X BSCBICO, BSSS(R) X BSCB 1(R) C9 and Bs13(s) C3 X BSCBl(R) C9 using North Carolina Design-II. Results suggested that reciprocal recurrent selection was an effective for improving the population cross for yield without decreasing genetic variability.

Galal *et al.* (1996) used three selection methods, modified ear to row, half-sib family selection and S_1 lines to improve Giza-2 composite maize variety. They reported that the actual advanced gain from selection after three cycle was 26.96, 15.69 and 20.66'% for modified ear to row, half-sib family arid S_1 lines, respectively.

Holthaus and Lamkey (1996) estimated the mean performance and important genetic parameters in "BSSS" before and after seven cycles of half-sib progeny selection, eleven cycles of reciprocal recurrent selection (RRS) and six cycles of S_1 progeny selection. Progenies from each of the four populations were grown for two years in a randomized incomplete block experiment. The relative effectiveness of the three selection methods for improving the mean performance for grain yield of the BSSS populations *per se* was 0.9% cycles^{-1} for (H.S) selection, 1.1% cycle^{-1} for S-2 progeny selection and 1.4% cycle^{-1} for RRS.

Ferra *et al.* (1996) estimated the efficiency of selection for the trait ear height. Two hundred (H.S.) families, were evaluated in each cycle, using two lattice 10 x10 with two replications per location. The selection rates of 5% among progenies and 12.5% within progenies was used. For the trait ear weight, the analysis of variance, individual and combined, detected significant differences for progenies and for interaction of progenies X location. The additive genetic variance values varied for locations and cycles ranging from 501.4 to 1002.7 (g/plant), the values of those variances at combined analysis were smaller than the values of indivudal analysis 58.0 (g/plant) for the first cycle and 292.7 (g/plant) for the second cycle. Mean expected gains were 1.5% and 8.2% at first and second cycles, respectively.

Abd El-Sattar (1997) estimated the efficiency and expected gain from six selection methods in Moshtohor-1 and Moshtohor-3 maize populations. Obtained results suggested that the inter-population selection programs had good potential for improving grain yield. Test cross and S_1, selection schemes were more effective than mass, modified ear to row, half-sib and full-sib selection schemes.

El-Hosary and Abd El-Sattar (1997) used six selection methods to improve the synthetic maize variety Moshtoher-2. They found that genetic advances per selection cycle were 2.57, 3.01, 7.53, 6.26, 12.04 and 8.79% for mass selection, ear to row selection, half-sib family selection, progeny test and S_1 family selection, full-sib family selection, respectively.

Jeanne *et al.* (1997) studied effects of reciprocal recurrent selection on the molecular genetic variation from C_0 and C_{12}. They substantially diverged. Gene diversity across progenitor populations was very broad and remained at that level to C_{12}. Within both populations, the observed loss of variation was consistent with theoretical expectations resulting from genetic drift of neutral alleles.

Tusuz and Balaban (1997) evaluated 8 hybrid maize in a randomized complete block design with four replications to determine characters (i.e. days to 50% silking, plant height, ear height and moisture percentage at harvest affecting grain yield). Over two years of the experiment, heritability in the broad sense was highest for days to 50% silking (93%) and low for plant height (12%) ear height (31%) and for grain yield (6%). The yield potential of the varieties changed from year to year and significant environmental effect was observed.

Arais and Souza (1998) compared the expected response of reciprocal recurrent selection (RRS), inter-population half-sib family selection (HSS) and modified ear to row selection (MRS) in inter population hybrid. They found that the MRS method was more effective than RRS and HSS methods in producing hybrids from inbred lines.

Roger *et al.* (1998) estimated response to selection for grain moisture, stalk lodging along with other agronomic traits for BS11 maize population. All selection methods were successful in significantly improving the population *per se* performance for grain yield. Furthermore, they found that all selection programs in which index selection was practiced, modified ear to row was successful in improving the population *per se* for all four traits simultaneously.

Shehata (1998) estimated the predicated genetic advance from the most effective selection methods that could be used to improve yielding ability in Cairo-1 maize population. Results showed that the predicated genetic advance values per cycle for improvement the population under investigation using mass selection (one and both sexes), modified ear-to-row selection, half-sib full-sib family selection, test cross population used as a tester and S_1 line selection were 0.47, 2.96, 0.22, 0.65, 0.80, 0.89 and 1.25%, respectively. Generally, the highest estimates of the expected genetic advance from selection were obtained from S_1 considered as the most appropriate methods for improving this population.

Weyhrich *et al.* (1998) compared the response to selection for seven different methods [six intra- and one inter-population] in the BS 11 maize populations. A minimum of four cycles of selection were conducted for each the following methods: mass selection, modified ear-to-row, half-sib with inbred tester, full-sib, s_1 progeny, S_2 progeny and reciprocal full-sib were based on index composed of grain yield.

Response to selection was measured for grain yield. All selection methods were successful insignificantly improving the population *per se* performance for grain yield. S_2 progeny selection had the greatest response for grain yield of 4.5% per cycle. All programs in which selection index was practiced, except for modified ear-to-row, were successful significantly in improving the population *per se* for all traits simulataneously.

El-Sheikh (1999) reported that the recurrent selection on the improvement of grain yield in composite maize cultivar Alex. 4. The average rate of increase in the first improvement cycle (C_1), through recurrent selection for GCA was 28% for grain yield relative to the original population (C_0). Recurrent selection based on progeny test was effective for improving yield and its component in the studied composite maize cultivar Alex. 4.

Guzman and Lamkey (2000) showed that the use of adequate effective population size in maize (*Zea mays* L.) of recurrent selection programs is important because of random genetic drift and inbreeding depression. This research work aimed to (C_1) evaluate the performance of the BS 11 cycle (C_0) and the BS 11 cycle 5 (C_5) population four S_1-progeny selection programs each with a different effective population size [5, 10, 20 or 30] but with a common selection intensity of 20%. Five cycles of selection were conducted by intermating 5, 10, 20 or 30 lines. The four selection programs resulted insignificant increase in grain yield. For yield the 10-S_1 program showed the highest gain per cycle of 0.16 Mg per ha followed by the 30-21 programs with 0.13 Mg per ha per cycle. The 5-S_1 program had a higher gain per cycle the 20-S_1 program.

Mani *et al.* (2000) showed that the highest expected genetic gains were obtained for ear grain weight followed by total grain yield and number of ears/plant. Results also revealed that full-sib selection was more effective than mass selection for improving grain yield in range of 2-4 times.

Vasic *et al.* (2001) found that the largest expected genetic gain from selection for grain yield was obtained from half-sib recurrent selection.

El-Morshidy *et al.* (2002) evaluated 300 S_1 lines from Giza-2 (white) and pop-45 (yellow) maize populations. They found that the expected gain from selection was higher in magnitude than ,actual gain under favorable environment in the two populations. Actual gain from selection was 13.9% for grain yield in Giza-2 population and 6.95% in pop-45 population.

Eraky *et al.* (2003) used two recurrent selection methods, i.e., S_1 family selection and full sib family selection to improve composite-21 yellow maize. Half-sib family selection method was effective in improving and developing earliness characters at 10% selection intensity. S_1 family selection method at 10% selection intensity proved to the best for improving no. of ears per 100 plants, 100-kernels weight and grain yield per plant and plot.

Hadi (2003) evaluated four cycles of S_1 recurrent selection to improve grain yield and other agronomic traits in three maize populations. Data showed that the average increasing rates in grain yield/cycle was 8.2% in MYD, 8.9%/cycle in MV Syn and 4.9%/cycle in Westigua population. The grain moisture at harvest was significantly decreased. Selection didn't change the percentage of stalk lodging.

Lee *et al.* (2003) studied the changes in the genetic structure of phenotypic stability of grain yield grain moisture and broken stalk using reciprocal recurrent selection (RRS) and S_1 recurrent selection in 12 maize populations. They showed that reciprocal recurrent selection was more effective to improved grain yield stability.

Mohamed (2004) used reciprocal recurrent selection to improve two maize populations Results showed that S_1 lines differed significantly for the two populations for all characters under investigation expect for ear diameter in population AA.

Gamea (2005) studied the expected gain from S_1 selection for grain yield/plant in two maize populations. He found that the expected gain from selection for grain yield were 27.1 and 41.1% in pop-A and pop-B, receptively. The actual gain from selection for grain yield/plant was 8.1 and 8.8%, respectively.

Keeratinijakal and Lamky (1993) used reciprocal recurrent selection to improve two populations. Response in grain yield of the BSCB1 (R) x BSSS (R) interpopulation cross was 6.95% (or 0.28 t/ha) per cycle. Grain yield of BSCB1 (R) increased by 1.94% (or 0.06 t/ha) per cycle, but grain yield of BSSS (R) did not significantly change. Mid-parents hetrosis of the interpopulation cross increased from 25.44 to 76.04% for C_0 to C_{11}.

Schnicker and Lamkey (1993) used reciprocal recurrent selection as a breeding procedure designed to improve two populations simultaneously by selection in the interpopulation cross. The objective of this study was to evaluate the effects of 11 cycles of selection on the mean. Genetic variance was evaluated at two locations in 1989 and three locations in 1990. Grain yield increased by 0.25 t/h per cycle (6.46%). After 11 cycles of selection, grain moisture increased by 0.85 g/kg per cycle, root lodging decreased by 0.23% and stalk lodging decreased by 1.64%.

Landi and Frascaroli (1995) studied the full-sib family recurrent selection for grain yield which was conducted for four cycles in an F_2 maize population. They found that the grain yield mean value of C_4 was significantly higher than that of C_0 both as S_2 and as T_c, while the two populations did not significantly differ for the genetic variance estimates and the grain yield mean value of the selected line group was significantly higher than the mean value of the two parents, but selected lines did not significantly exceed the best parent.

Barakat (1998) estimated heritability in narrow sense and genetic gain from Design 1 and S_1 line in Tep. 5 and Tuxpeno populations. Heritability estimates obtained from half-sib in the narrow sense was high for plant height and no. of rows per ear in combined data where the values were 0.63 and 0.78, respectively. While low for 100-kernel weight and no. of kernel per row in combined data where the values were 0.15 and 0.29, respectively in both populations. Generally, heritability estimates in the narrow sense for Tuxpeno were higher than for Tep. 5 in most of the studied characters. Heritability estimates in narrow sense for S_1 were higher than half-sib for grain yield were in combined date where the values 0.34 and 0.62 for Tep. 5 and Tuxpeno, respectively. Generally, heritability estimates were higher for Tuxpeno than for Tep. 5 for most of the study characters Actual grain yield was improved under selection intensity 20% by 3.5% and 8.3% for Tep. 5 and by 12.8% and 11% for Tuxpeno through half-sib and S_1 family selection respectively.

Barakat (2003) estimated the broad sense heritability in the Gemmeiza yellow population, using S_1 family selection method under two locations (Gemmeiza and Sakha) for grain yield (ard/fed), grain yield (g/plant), days to 50% silking, plant and ear heights and late wilt resistance (L.W.R.) which were relatively high for all studied traits at both location and when data were combined over locations with few exceptions. Lower heritability values were obtained for days to silking, ear height and percent of late wilt resistance at Sakha location. Days to silking, plant and ear heights as will as late wilt resistance exhibited moderately low value of heritability. The lowest estimates of heritability in case of the combined data for late wilt resistance (43.90%) from Sakha (74.09%) and Gemmeiza (45.91%) were recorded. Heritability estimates for days to mid silking, plant height and late wilt resistance were relatively close to each other at both locations. For grain yield and ear height, heritability estimates were somewhat high at Gemmeiza and Sakha, respectively. Expected genetic gain (%) from selection of the best 10% of the families for the two characters (grain yield and LWR%). Expected genetic gain was 47.82, 58.67 and 7.97% for grain yield ard/fad and 30.40, 80.80 and 7603% for LWR% at Sakha, Gemmeiza and combined data, respectively. These gains were at higher values than those of the other traits.

MATERIALS & METHODS

3. MATERIALS AND METHODS

This study was carried out during the two summer growing seasons, 2004 and 2005 at the Farm of Etay El-Baroud Agricultural Research Station, Agriculture Research Center (ARC).

Two maize populations were used in this study i.e., Nobaria and Gemmeiza Yellow populations (NYP and GYP) developed by the Egyptian maize research program. The Nobaria population consists of 14 genotypes from different genetic population as follows: population Tuxpeno, ADA, Arifye, AE, Westigua, Antigua, 33, 34, 44, SC.155, SC.161, TWC.351, TWC.352 and line B.73. While, Gemmezia Yellow population consists of 9 genotypes from different genetic populations as follows Gm.1001, Gm.1002, Gm.1003, Gm.1004, Gm.1005, Gm.1006, Dmr, Esr and Y.M.pop. The two maize poulations are a synthetic composed by the Maize Research Section, Agricultural Research Center, from local and exotic genotypes tested for yield and late wilt disease.

The two populations were sown in 2004 during the summer season at the Farm of Etay El-Baroud Agricultural Research Station, hundred ridges from each the two populations were grown to produce the material seeds of Design-1 mating as outlined by **Comstock and Robinson (1948)**. One random plant was chosen from each ridge to use as a male pollen parent and was crossed with seven random plants as female plants. At harvest, ears were taken from the first four females per each male which had sufficient grains for evaluations. Each ear represented a full-sib family, while the ears having a common parent represented a half sib family. Thirty six half-sib families were obtained, each had four full-sib families, therefore, the total number of full-sib families 144 were developed from each population and grouped into 4 sets.

In addition, 100 S_1 lines were chosen within each population (from about 200 randomly selfed plants).

Experimental design for progeny trials:

1. Progeny test trails for yield and the other characters for the design-1 mating were conducted at Etay El-Baroud during the summer season of 2005. Each experiment included 36 males, grouped into 4 sets of 36 progenies full-sib families. These sets were arranged in a randomized complete blocks design with three replications. Within each replication, each set of 9 males were randomly arranged. The females for each male were assigned at random in the plots within each block.
2. A total of 100 S_1 lines *per se* from each of the two populations (Nobaria yellow population) and (Gemmeiza yellow population) were evaluated during the summer season 2005. Each experiment included 100 S1 lines, grouped into 5 sets. These sets were arranged in a randomized complete blocks design (RCBD) with three replications. Within each replication, each set of 20 S1 lines were randomly arranged. The S1 lines were assigned at randomly arranged in the plots within each block. In all experiments, the plot size was one ridge 6 meters long with 70 centimeters between ridge kernels were sown in hills, spaced 25 cm apart within the ridge. Plants were thinned to obtain one plant per hill before the first irrigation (i.e. three weeks after sowing). The nitrogen fertilizer (urea) was added at two times (120 kg N/fed*). The first half was applied before the first irrigation and the second one was applied before the second irrigation. Irrigation intervals were ranged from 12 to 15 days during the growing season. Harvest was carried out 130 days after sowing.

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* **One faddan = 0.42 hectar.**

Data were collected on the following characters:

I. Agronomic characters:

1. **Days to 50% tasseling**, measured as the number of days from sowing to the day on which 50% tasseling had occurred.
2. **Days to 50% silking**, measured as the number of days from sowing to the day on which 50% silking had occurred.
3. **Plant height (cm)**, measured from their soil surface to the upper most node.
4. **Ear height (cm)**, measured from their soil surface to the upper most ear bearing.
5. **Leaf area (cm^2)**, computed according to the formula (Further ear leaf length x further ear leaf width x0.75).

II. Yield and yield components:

1. **Number of ears/plant.**
2. **Ear length**, measured in centimeters for five ears from randomly selected plants. The length were averaged and reported as ear length per plot.
3. **Ear diameter**, reported as average ear diameter per plot for the same five ears used in ear length measurement.
4. **Rows number per ear**, the average rows per ear recorded for the same five ears used in ear length measurement.
5. **Kernel number per row**, the average kernels per row per plot recorded for the same five ears used for ear length and diameter measurements.
6. **Hundred kernel weight**, determined using five hundred kernels taken at random from the shelled grains.
7. **Grain yield (gm)/plant**, the weight of grains adiusted to 15.5% moisture content.

Statistical analysis:

Half-sib family selection (Design I):

1. Analysis of variance

An analysis of variance was made to obtain estimates of the components of variance for all traits. The form of the analysis of variance for each trait is shown in Table (1).

Table (1): The analysis of variance and expected mean square of the half-sib and full-sib families.

S.O.V.	d.f.	M.S.	E.M.S.
Sets (S)	**(S-1)**		
Replications (R)	**S(r-1)**		
Males (M)	**S(m-1)**	**M1**	$\sigma^2e + r\sigma^2f + rf\sigma^2m$
Females/M/S	**Sm(f-1)**	**M2**	$\sigma^2e + r\sigma^2f$
Error	**S(mf-1)(r-1)**	**M3**	σ^2e

Where:

σ^2e = residual error variance.

$\sigma^2 f$ = variance of the female effect.

$\sigma^2 m$ = variance of the male effect.

r = number of replications.

f = number of females within male.

m = number of males, and

s = number of sets.

The previous analysis of variance was used to calculate the variance components in the following mannar:

$$\sigma^2 m = \frac{M_1 - M_2}{rf}$$

$$\sigma^2 f = \frac{M_2 - M_3}{r}$$

$$\sigma^2 e = M_3$$

Within and among the enteries of the experiments, there were some of the relationships, where individual plant within a plot were full-sibs, while the individual plant from a certain family grown in different replications were full-sibs and individual plants in the same of different replications having a common male parent but different females were half-sibs.

Kempthorne (1957) interpreted the variance component in term of covariance among relatives as follows:

$\sigma^2 m$ = Covariance of half-sib,

$\sigma^2 f$ = Covariance of full-sib – covariance of half-sib.

He gave the genetic expection of the covariances of half-sib and full-sib in terms of additive genetic variance, dominance variance and epistatic variance as shown in the following equations:

$$\textbf{Covariance of half-sib } (\sigma^2 m) = \frac{1}{4}\sigma^2 A + \frac{1}{16}\sigma^2 AA + \frac{1}{64}\sigma^2 AAA \ldots,$$

$$\textbf{Covariance of full-sib } (\sigma^2 f) =$$

$$\frac{1}{2}\sigma^2 A + \frac{1}{4}\sigma^2 D + \frac{1}{4}\sigma^2 AA + \frac{1}{8}\sigma^2 AD + \frac{1}{16}\sigma^2 DD \ldots,$$

Only the additive types of variation are included in the covariance of half-sib and both additive and dominance types in the covariance of full-sib. The expected values for the covariance between half-sib and full-sib would be reduced on the assumption of no epistasis as follows:

$$\textbf{Covariance of half-sib } (\sigma^2 m) = \frac{1}{4}\sigma^2 A$$

$$\textbf{Covariance of full-sib } (\sigma^2 m - \sigma^2 f) = \frac{1}{2}\sigma^2 A + \frac{1}{4}\sigma^2 D$$

Hence, the additive and dominance variances were estimated as follows:

$$\sigma^2 A = 4\ \sigma^2 m$$

$$\sigma^2 D = 4\ (\sigma^2 f - \sigma^2 m)$$

In translating the various variance components in terms of additive and dominance variances, these assumption were considered:

1- Regular diploid inheritance,
2- No material effects,
3- No. linkage and epistasis,
4- Random choice of the males and females and
5- No multiple alleles.

The standard deviation of the additive and dominance were calculated as described by **Anderson and Bancroft (1952)** as

$$\text{Var.}\ (\sigma^2 g) = \frac{2}{K^2} \cdot \frac{(Msg)^2}{(fg+2)} \quad \text{and}$$

$$\text{S.D.}\ (\sigma^2 g) = \sqrt{\text{var.}\ (\sigma^2 g)}$$

Msg = The gth mean square used to estimate the variance components
K = The divisor of the function of mean squares.
Fg = The degree of freedom of the gth mean square.

Any variance components exceeding twice its standard deviation was considered different from zero.

Heritability:

From the following equation the heritability (among F.S.) estimates were calculated in the narrow sense.

$$h^2 = \frac{2\sigma^2 M}{(\sigma^2 m + \sigma^2 f) + \dfrac{\sigma^2 e}{r}}$$

Expected genetic gain from selection:

The estimates of the genetic and environmental variances were used to calculate the expected genetic advance from the six methods of intra-population selection as shown in Table (2) according to Hallauer and Miranda (1981).

Table (2): Expected genetic progress per cycle under different intra-population schems with non-inbred parent:

E G
M

Method	Expected gain (G)	Grop season/cycle
Mass selection one sex	$\dfrac{K.(1/2)\,\sigma^2A}{\sqrt{\sigma^2\mu + \sigma^2AE + \sigma^2DE + \sigma^2A + \sigma^2D}}$	1
Modified ear-to-row (E)	$\dfrac{K.(1/8)\,\sigma^2A}{\sqrt{\dfrac{\sigma^2e}{rm} + \dfrac{1/4\,\sigma^2AE}{m} + 1/4\,\sigma^2A}}$	1
Half-sib (H)	$\dfrac{K.(1/4)\,\sigma^2A}{\sqrt{\dfrac{\sigma^2e}{rm} + \dfrac{1/4\,\sigma^2AE}{m} + 1/4\,\sigma^2A}}$	2
Full-sib (F)	$\dfrac{K.(1/2)\,\sigma^2A}{\sqrt{\dfrac{\sigma^2e}{rm} + \dfrac{1/2\,\sigma^2AE + \sigma^2DE}{m} + 1/2\,\sigma^2A + 1/4\,\sigma^2D}}$	2
Test cross population as a tester	$\dfrac{K.(1/2)\,\sigma^2A}{\sqrt{\dfrac{\sigma^2e}{rm} + \dfrac{1/4\,\sigma^2AE}{m} + 1/4\,\sigma^2A}}$	3 or 4
S_1 selection	$\dfrac{K.\,\sigma^2A}{\sqrt{\dfrac{\sigma^2e}{rm} + \dfrac{(\sigma^2AE + 1/4\sigma^2DE)}{m} + (\sigma^2A + 1/2\,\sigma^2D)}}$	3

Where:

$\sigma^2 \mu$ it is the environmental variance within plot.

$\sigma^2 AE$ and $\sigma^2 DE$ are the additive and dominance environmental interaction,

$\sigma^2 A$ and $\sigma^2 D$ are the additive and dominance variance, respectively.

r it the number of replication per environment,

m is the number of environments, and

K is the standardarized selection differential and it is dependent on the intensity of selection as follows:

K = 1.75 with the selection of intensity 10%.

K = 1.40 with the selection of intensity 20%.

2- S_1 lines design:

The analysis of variance for S_1 lines design was calculated for each population. The pertiment part of the analysis of variance is given in Table (3). According to the expected mean squares, the following estimates were calculated:

Table (3): The analysis of variance for genetic parameters for S_1 lines design

S.O.V.	d.f.	M.S.	E.M.S.
Sets (S)	(S-1)		
Blocks	(r-1)		
Line/S	(L-1)	M_1	$\sigma^2 e + r\sigma^2 L$
Error	(r-1)(L-1)	M_2	$\sigma^2 e$

Where:

$\sigma^2 e$ = the residual error variance.

$\sigma^2 L$ = the variance of the S_1 line effects,

r = the number of blocks.

The estimates of variance components were calculated as follows:

$$\sigma^2 L = \frac{M_1 - M_2}{r}$$

$$\sigma^2 e = M_2$$

To obtain the estimates of the genetic variance in the reference populations, it is necessary to translate the variance components to genetic variance components.

Only the additive types of variation are include in the inbred lines, where the dominance effects disappear rapidly within inbreeding **(Hallauer and Miranda, 1981)**. Consequently, the additive genetic variance is calculated as follows:

$$\sigma^2 L = \sigma^2 A$$

The standard deviation of the additive genetic was calculated as described by **Anderson and Bancroft (1952)** as follows:

$$\text{Var. } (\sigma^2 g) = \frac{2}{K^2} \cdot \frac{(Msg)^2}{(d.f. + 2)} \quad \text{and}$$

$$\text{S.D. } (\sigma^2 g) = \sqrt{\text{Var.}(\sigma^2 g)}$$

Where:

Msg = the g^th mean square used to estimate the variance component,

K = the difisor of the function of mean square,

d.f. = the degrees of freedom of the g^th mean squar.

Any variance component exceeding twice its standard deviations was considered to be different from zero.

Heritability:

From the following equation, the heritability estimates were calculated in the narrow sense for the two populations:

$$h^2 = \frac{\sigma^2 L}{\sigma^2 L + \sigma^2 e/r}$$

RESULTS & DISCUSSION

4. RESULTS AND DISCUSSION

The obtained results from this investigation may be classified in two main parts for each population as follows:

A. Estimating some statistical and genetical parameters and genetic variance components for S_1 and design I.

B. Comparing different selection procedures.

A- Estimating some statistical, genetical parameters and genetic variance components for S_1 progenies:

1. Mean squares for S_1 lines/S:

Means (X), error variance σ^2e and coefficient of variability (C.V.%) for all studied traits of both populations are presented in Tables (4 and 5).

Mean squares for sets (S) and S_1 lines/S were significant for all traits in both populations, except mean square for no. of ears/plant and ear length in Nobaria yellow population (NYP) and mean square for S_1 lines/S for number of kernels/row in (NYP).

Mean squares for sets (S) and S_1 lines/S were highly significantlt for all the studied traits in Gemmeiza yellow population (GYP).

For all traits under investigation, NYP gave higher mean values than those obtained from Gemmezia yellow population (GYP), except ear leaf area, ear diameter, no. of kernels/row, 100-kernel weight and grain yield/plant.

Also, the NYP had lower values of error variance (σ^2e) for all traits, except plant height, ear leaf area and ear length. Lower

Table (4): Mean square, mean (X) and coefficient of variability (C.V.%) for all studied traits in Nobaria yellow population (NYP) S_1 progenies.

S.O.V.	Days to silking	Days to tasseling	Plant Height (cm)	Ear Height (cm)	Ear leaf area (cm^2)	No. of ears/plant
Sets (S)	21.78**	16.59**	2523.35**	113.44**	48605.99**	0.33
Rep. (R)/S	7.02**	1.37*	240.16	8.97	256.34*	0.39
S_1 line/S	24.29**	26.02**	2441.95**	619.13**	23389.44**	0.43
Error	1.68	0.64	307.84	7.49	126.39	0.39
X	61.20	67.30	178.80	99.90	562.12	1.03
C.V. (%)	2.12	1.20	9.81	2.74	4.29	60.63

Table (4) Cont.

S.O.V.	Ear Length (cm)	Ear Diameter (cm)	No. of rows/ear	No. of kernels/row	100-kernel Weight (g)	Grain yield/plant (g)
Sets (S)	40.98	0.61**	12.00**	12.00**	21.96**	404.74**
Rep. (R)/S	56.69	0.06*	0.09	0.08	0.69**	31.09**
S_1 line/S	72.88	1.01**	15.49**	15.48	12.47**	5291.20**
Error	54.00	0.03	0.07	0.06	0.11	8.52
X	14.10	4.10	13.10	23.70	13.90	131.90
C.V. (%)	52.12	4.22	2.02	1.03	2.39	2.21

Table (5): Mean square, mean (X) and coefficient of variability (C.V.%) for all studied traits in Gemmezia yellow population (GYP) S_1 progenies.

S.O.V.	Days to silking	Days to tasseling	Plant Height (cm)	Ear Height (cm)	Ear leaf area (cm^2)	No. of ears/plant
Sets (S)	30.91**	12.01**	209.67**	353.58**	37506.03**	0.002**
Rep. (R)/S	1.30	4.82**	9.28	7.14	45.76**	0.0003
S_1 line/S	30.07**	33.22**	1105.34**	686.39**	36057.88**	0.003**
Error	0.87	0.99	10.26	8.26	14.43	0.0001
X	58.20	62.30	169.70	96.40	599.30	1.01
C.V. (%)	1.60	1.60	1.89	2.98	6.34	0.99

Table (5) Cont.

S.O.V.	Ear Length (cm)	Ear Diameter (cm)	No. of Rows/ear	No. of kernels/row	100-kernel Weight (g)	Grain yield/plant (g)
Sets (S)	73.32**	3.49**	26.21**	471.28**	26.21**	11849.78**
Rep. (R)/S	0.12	0.13**	0.48**	2.36	0.48**	15.23
S_1 line/S	27.79**	1.89**	13.15**	183.66**	13.15**	5758.06**
Error	0.09	0.07	0.14	2.41	0.14	70.89
X	12.41	4.14	12.70	25.10	14.71	138.60
C.V. (%)	2.42	6.40	5.04	6.18	2.54	6.07

values of coefficient of variability were obtained for this population in the previous traits, except no. of ears/plant and ear length.

Generally, GYP gave the higher and desirable values for grain yield/plant and some of its components besides relatively earliness. It may be due to many different improvement cycles of selection provided for this population than the second population.

Design I progenies:

The analysis of variances for the two population for all traits under investigations are presented in Tables (6 and 7).

For both maize populations, males and females/male mean squares were significant for all the studied traits, except no. of ears/plant in Nobaria yellow maize population.

In general, for the two maize populations, male variance gave the importance part of total genetic variances for most studied traits (Tables 6 and 7).

2. Genetic parameters:

Phenotypic ($\sigma^2 ph$), genotypic ($\sigma^2 G$) variances, heritability, genetic coefficient (GCA %), phenotypic coefficient (Ph.C.V. %) of variability and genetic gain from selection GS% for all traits in both populations are presented in Tables (8 and 9).

The obtained results from both populations (Tables 8 and 9), showed that genetic variance was highly significant for all studied traits, except no. of ears/plant and 100-kernels weight in GYP. Phenotypic variance was higher for days to silking and days to tasseling, ear height, ear leaf area, ear diameter, no. of kernels/row, 100-kernel weight and grain yield/plant in GYP than those of NYP.

Table (6): Mean square, mean (X) and coefficient of variability (C.V.%) for all studied traits in Nobaria yellow population (NYP) H.S. families.

S.O.V.	Days to silking	Days to tasseling	Plant Height (cm)	Ear Height (cm)	Ear leaf area (cm^2)	No. of ears/plant
Sets (S)	153.25**	213.02**	5140.88**	6107.47**	126298.56	0.05**
Rep. (R)/S	12.40**	14.27**	27.28**	23.52**	854.48*	0.01**
Males (m)/S	23.59**	18.90*	720.94**	530.49**	28996.87**	0.06**
Females (F)/m/S	12.79**	10.44**	435.34**	234.68**	17766.77**	0.06
Error	1.64	1.54	6.87	5.59	428.62	0.00
X	55.46	60.24	214.95	113.29	607.90	1.09
C.V. (%)	2.31	2.06	1.22	2.09	3.41	2.90

Table (6) Cont.

S.O.V.	Ear Length (cm)	Ear Diameter (cm)	No. of Rows/ear	No. of kernels/row	100-kernel Weight (g)	Grain yield/plant (g)
Sets (S)	28.90**	0.41*	2.35**	216.21**	9.39**	17147.58**
Rep. (R)/S	0.86	0.03*	0.18**	7.08**	0.35*	424.45*
Males (m)/S	11.51**	0.57**	8.64**	54.50**	23.44**	4599.56**
Females (F)/m/S	8.21**	0.29**	6.24**	54.44**	7.40**	2280.00**
Error	0.93	0.01	0.06	0.72	0.13	213.28
X	18.11	5.63	16.22	38.64	16.16	189.27
C.V. (%)	5.32	1.78	1.51	2.20	2.23	7.72

Table (7): Mean square, mean (X) and coefficient of variability (C.V.%) for all studied traits in Gemmezia yellow population (GYP) H.S. families.

S.O.V.	Dayes to silking	Dayes to tasseling	Plant height (cm)	Ear height (cm)	Ear leaf area (cm^2)	No. of ears/plant
Sets (S)	400.35**	572.69**	50342.82**	342.15**	77630.43**	0.03**
Rep. (R)/S	1.16	6.62**	61.38*	7.81*	467.30	0.01**
Males (m)/S	27.62**	37.47**	1571.66**	570.96**	28973.08**	0.03**
Females (F)/m/S	20.74**	25.32**	949.76**	273.65**	19506.17**	0.03**
Error	0.98	1.15	30.69	3.90	310.48	0.01
X	56.87	62.23	177.45	101.79	664.53	1.05
C.V. (%)	1.74	1.72	3.12	1.94	2.65	9.52

Table (7) Cont.

S.O.V.	Ear Length (cm)	Ear Diameter (cm)	No. of Rows/ear	No. of kernels/row	100-kernel Weight (g)	Grain yield/plant (g)
Sets (S)	62.69**	1.96**	5.66**	383.72**	35.47**	23175.83**
Rep. (R)/S	0.37**	0.02*	0.37*	1.67**	0.13	95.17
Males (m)/S	14.79**	0.67**	6.19**	82.13**	21.22**	4191.88**
Females (F)/m/S	11.96**	0.41**	4.61**	42.54**	10.19**	2910.67**
Error	0.06	0.01	0.15	0.54	0.08	101.40
X	17.79	5.10	14.17	35.92	19.48	188.98
C.V. (%)	1.38	1.96	2.70	2.05	1.45	5.33

Table (8): Phenotypic (σ^2ph), genotypic (σ^2G) variance, heritability in broad sense (H_b), phenotypic (Ph.C.V. %), genotypic (G.C.V.) coefficient of variability and predected genetic gain (Δg%) for all studied traits in Nobaria yellow population (NYP) S_1 progenies.

Characters	σ^2ph	σ^2G	H_b	Ph.C.V.%	G.C.V.%	Δg%
Dayes to silking	8.10	7.54**	0.93	4.84	4.67	7.88
Dayes to tasseling	8.67	8.46**	0.98	4.56	4.50	7.78
Plant height (cm)	813.98	711.37**	0.87	16.80	15.71	25.70
Ear height (cm)	206.38	203.88**	0.99	16.23	16.13	28.07
Ear leaf area (cm^2)	7796.48	7754.35**	0.99	16.42	16.38	28.59
No. of ears/plant	0.41	0.014**	0.03	62.17	11.48	2.25
Ear length (cm)	24.29	6.29**	0.26	31.30	15.93	14.19
Ear diameter (cm)	0.34	0.32**	0.97	13.07	12.86	22.13
No. of rows/ear	5.16	5.14**	0.99	15.86	15.83	27.64
No. of kernels/raw	5. 61	5. 41**	0.96	10.10	9.82	19.42
100-kernel weight (g)	4.16	4.12**	0.99	14.30	14.23	24.80
Grain yield/plant (g)	1763.73	1760.89**	0.99	36.82	36.79	64.33

Table (9): Phenotypic (σ^2ph), genotypic (σ^2G) variance, heritability broad sense (H_b), phenotypic (Ph.C.V. %), genotypic (G.C.V.) coefficient of variability and predected genetic gain (Δg%) for all studied traits in Gemmeza yellow population (GYP) S_1 progenies.

Characters	σ^2ph	σ^2G	H_b	Ph.C.V.%	G.C.V.%	Δg%
Dayes to silking	10.02	9.73**	0.97	5.46	5.38	9.28
Dayes to tasseling	11.08	10.75**	0.97	5.23	5.15	8.88
Plant height (cm)	368.50	365.03**	0.99	11.68	11.62	20.26
Ear height (cm)	228.80	226.04**	0.99	17.74	17.63	30.67
Ear leaf area (cm^2)	12019.30	12014.50**	0.99	17.69	17.69	30.94
No. of ears/plant	0.001	0.001	0.93	3.14	3.04	5.15
Ear length (cm)	9.26	9.23**	0.99	22.04	22.00	38.45
Ear diameter (cm)	0.63	0.61**	0.96	17.41	17.11	29.04
No. of rows/ear	4.38	4.34**	0.99	12.90	12.72	22.15
No. of kernels/raw	61.22	60.42**	0.99	33.16	32.94	57.27
100-kernel weight (g)	4.38	4.34	0.99	12.80	12.72	22.15
Grain yield/plant (g)	1919.35	1895.72**	0.99	38.06	37.83	65.79

Genotypic and phenotypic variances are differed markedly among populations because of the differences in gene frequency and the relative importance of different types of gene action.

Data in Tables (8 and 9) showed that (Ph.C.V.%) of both NYP and GYP populations were higher than genotypic coefficients of variability (GCV%) coefficient of variability among S_1 progenies. Also, the phenotypic (Ph.C.V.%) and genotypic GCV% coefficient of variability among S_1 progenies of NYP had higher values than those obtained in GYP for plant height, no. of ears/plant, no. of rows/ear and 100-kernel weight. However, the GYP had higher estimates of Ph.C.V.% and GCV% for the other traits.

Half-sib families:

According to the assumption which described by **Comstock and Robinson 1948 and 1952** for design I. The expected mean squares from analysis of variance for data of NYP and GYP were used to determine the components of genetic variances.

Estimates of σ^2**M**, σ^2**F**, σ^2**ph**, σ^2**G**, σ^2**A**, σ^2**D**, σ^2**D**/σ^2**A** ratios, heritability in broad and narrow sense for all studied traits of the two maize populations are presented in Tables (10 and 11).

For NYP, the variance of males was significant for ear height, ear diameter, 100-kernel weight and grain yield/plant. However, female mean squares were significant for all studied traits.

For the GYP, the male variance was significant for plant height, ear height, ear diameter, no. of kernels/row and 100-kernel weight. Also, female variance was significant for all traits, except no. of ears/plant.

The phenotypic variance as well as the genotypic variance were higher for all traits under study in GYP than those of NYP, except no. of ears/plant, no. of rows/ear and no. of kernels/rows whereas the highest estimates were detected in NYP.

For NYP, additive genetic variance estimates were found to be significant for days to silking, ear height, ear diameter, 100-kernels weight and grain yield/plant.

Significant dominance estimates were detected for all traits, except 100-kernel weight. Degree of dominance **(σ^2D/σ^2A ratio)** was higher than unity for all traits, except 100-kernels weight indicating that dominance variance were more important than additive variance in the inheritance of these traits. For the exceptional 100-kernels weight, the **σ^2D/σ^2A** ratio was 0.81 indicating that additive variance was more important than dominance variance in the inheritance of this trait.

For GYP, additive genetic variance estimates were found to be significant for plant height, ear height, no. of kernels/row and 100-kernel weight.

Significant dominance estimates were detected for all traits, except ear height and no. of rows/ear.

Degree of dominance **(σ^2D/σ^2A)** was higher than unity for all traits, indicating that dominance variance were more important than additive variance in the inheritance for all traits under investigation.

In general, in both populations, the dominant genetic variance was more important than additive variance for most traits.

In this respect, many authors suggested the important role of dominant genetic variance than additive variance. For instance, **Malvar *et al.* (1996)** showed that 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 **Nawar *et al.* (1983), Pal *et al.* (1986), Reddy and Agrawal (1990), Mani *et al.* (2000), Alves *et al.* (2002), Raposo and Ramalho (2004), Revilla *et al.* (2004), El-Shenawy *et al.* (2005) and Motawei (2005)** where they found that the additive genetic variance was predomimant in the inheritance of yield and most of its component in maize.

On the other hand, **Malvar *et al.* (1996), Sfakianakis *et al.* (1996), Shehata (1998), El-Shenawy *et al.* (2005), Motawei (2005) and Soliman *et al.* (2005)** revealed that non-additive gene effects were played an important role in the inheritance of most traits.

Generally, **Hallauer and Miranda (1981)** summarized the estimates of $\sigma^2 A$ and $\sigma^2 D$ 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)**, 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, $\sigma^2 A$ on the average accounted for 61.2% and $\sigma^2 D$ accounted for 38.87% of the total genetic variations. The ratio of $\sigma^2 D/\sigma^2 A$ 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 two maize populations and mating system designs used for estimating the genetic variance components in each case.

3- Heritability estimates:

Heritability is considered to be one of the most important parameters to express relative genetic variability whether in a broad and/or narrow sense.

S_1 progenies

Tables (8 and 9) showed that, heritability estimates for both populations (NYP and GYP) S_1 lines were high for all traits, except no. of ears/plant and ear length in NYP.

Estimates of heritability in broad and narrow sense for all the studies traits for the two populations are presented in Tables (10 and 11).

For NYP all broad sense heritability estimates were very high and ranged from 0.80 for ear height to 0.95 for 100-kernel weight in NYP, also it ranged from 0.80 for ear leaf area to 0.95 for no. of kernels/row in GYP. Meanwhile, estimates of heritability in narrow sense ranged from zero for no. of ears/plant to 0.55 for 100-kernel weight in NYP. While, it ranged from 0.03 for no. of ears/plant to 0.27 for 100-kernels weight and ear height in GYP. Low heritability of narrow sense for all traits, indicated that dominance genetic variance played the major role in the inheritance of these traits. These results confirmed the previous results in the previous part which indicated the majority of dominance genetic variance in the total genetic variances in this respect. At the same time, high estimates of broad sense heritability for all traits, suggested the important role of both additive and dominance genetic variances obtained for these traits as shown before.

Table (10): Male (σ^2M), females/male (σ^2F) variance, phenotypic (σ^2ph), genetypic (σ^2G) vaiance, additive (σ^2A), dominance (σ^2D) variance, degree of dominance (σ^2D/σ^2A), heritability broad (H_b) and Narrow (h_n) sense of all studied traits in Nobaria yellow population (NYP) H.S. families.

Characters	σ^2M	σ^2F	σ^2ph	σ^2G	σ^2A	σ^2D	σ^2D/σ^2A	H_b	h_n	Ph.C.V.%	G.C.V.%
Dayes to silking	0.90	3.72**	17.42	14.87	3.60*	11.27**	3.13	0.91**	0.23	7.08	6.95
Dayes to tasseling	0.71	2.97**	14.38	11.87	2.82	9.05**	3.20	0.90**	0.23	5.85	5.73
Plant height (cm)	23.80	142.80**	579.58	571.29	95.20	476.09**	5.00	0.93	0.17	11.14	11.12
Ear height (cm)	24.65*	76.36**	313.32	305.46	98.60*	206.85**	2.09	0.80	0.32	15.47	15.42
Ear leaf area (cm^2)	935.84	5779.38**	23260.40	23117.53	3743.37	19374.16**	5.17	0.81	0.16	24.31	24.24
No. of ears/plant	0.00	0.02**	1.00	0.07	0.00	0.07**	8.09	0.81	0.00	24.45	24.34
Ear length (cm)	0.28	2.43**	13.01	9.70	1.10	8.60**	7.82	0.90**	0.11	0.063	0.002
Ear diameter (cm)	0.02*	0.09**	0.48	0.38	0.09*	0.28**	3.05	0.84	0.24**	12.29	12.25
No. of rows/ear	0.20	2.06**	10.26	8.24	0.80	7.44**	9.28	0.90	0.10	18.36	18.34
No. of kernels/raw	0.01	17.91**	76.87	71.63	0.02	71.61**	3541.90	0.93**	0.03	22.00	21.96
100-kernel weight (g)	1.34*	2.42**	11.73	9.69	5.35**	4.34	0.81	0.95**	0.55*	19.05	19.00
Grain yield/plant (g)	193.26*	689.04**	2827.24	2756.14	773.06*	1983.09**	2.56	0.83	0.27	28.09	27.73

Table (11): Male (σ^2M), females/male (σ^2F) variance, phenotypic (σ^2ph), genetypic (σ^2G) vaiance, additive (σ^2A), dominance (σ^2D) variance, degree of dominance (σ^2D/σ^2A), heritability broad (H_b) and Narrow (h_n) sense of all studied traits in Gemmezia yellow population (GYP) H.S. families.

Characters	σ^2M	σ^2F	σ^2ph	σ^2G	σ^2A	σ^2D	σ^2D/σ^2A	H_b	h_n	Ph.C.V.%	G.C.V.%
Dayes to silking	0.57	6.59**	28.68	26.35	2.29	24.06**	10.49	0.91**	0.09	9.08	9.02
Dayes to tasseling	1.01	8.06**	34.61	32.22	4.05	28.17**	6.95	0.89**	0.12	9.17	9.12
Plant height (cm)	51.82**	306.35**	1236.65	1225.42	207.30**	1018.12**	4.91	0.90**	0.17	19.81	19.73
Ear height (cm)	24.78*	89.92**	364.97	359.68	99.10*	260.57**	2.62	0.81	0.27	18.67	18.64
Ear leaf area (cm^2)	788.91	6398.55**	25697.68	25594.19	3155.65	22439.54**	7.11	0.80	0.12	24.12	24.07
No. of ears/plant	0.00	0.01	0.07	0.04	0.01	0.03**	27.9	0.90	0.03	18.07	17.99
Ear length (cm)	0.24	3.97**	17.88	15.86	0.94	14.92	15.81	0.93**	0.06**	22.02	22.00
Ear diameter (cm)	0.02*	0.13**	0.63	0.53	0.09	0.44**	4.92	0.89	0.17**	13.65	13.61
No. of rows/ear	0.13	1.49**	8.00	5.95	0.53	5.42	10.23	0.88**	0.09*	17.54	17.47
No. of kernels/raw	3.30*	14.00**	58.18	65.00	13.20*	42.80**	3.24	0.95**	0.23	20.80	20.77
100-kernel weight (g)	0.92*	3.37**	16.51	13.48	3.68*	9.81**	2.66	0.94**	0.27	18.87	18.85
Grain yield/plant (g)	106.77	936.42**	3779.49	3754.49	427.07	3318.62**	7.77	0.89	0.11	32.53	32.39

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 *et al.* (1985e)** showed that heritability in narrow-sense were high for plant height (87%), ear height (37%), 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.* (1995a)** estimated heritability values in Giza 2 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 presentation were collected from 99 published reports as shown in the following Table after few modifications

Yield	Ear length	Ear dimater	No. of rows/ear	100-kernels 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 trait 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 extension 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 and number of tillers
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 cab diameter
H < 30	Grain yield and kernel depth

Generally, our obtained results were not completely agreed with these summaries. It may be due to the differences in genetic back growth and mating designs used and environmental conditions predominated in each cases. In S_1 line selection method, the predicted genetic gain from selection ($\Delta g\%$) values ranged from 2.25% for no. of ears/plant to 64.33% for grain yield/plant in Nobaria yellow population and arranged from 5.15% for no. of ears/plant to 65.79% for grain yield/plant in Gemmeiza yellow population (Tables 8 and 9).

The high values for grain yield/plant in both populations refer to high values for some yield components.

4- Expected genetic gain from selection:

Design 1:

The estimates of genetic and environmental variances were used to calculate the expected genetic advance for six methods of intra-population selection. These methods include: 1) mass selection one sex, 2) modified-ear to row, 3) half sib selection, 4) full sib selection, 5) test cross selection with a broad base tester or with an inbred line tester, and 6) S_1 selection.

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 expected and predicted genetic gains from the six methods of selection are presented in Table (12). Concerning mass selection, the expected and predicted genetic gain/cycle was 12.41 g (Δg% = 3.19%) and 6.02 g (Δg% = 3.19%) based on selection of one sex in NYP and GYP, respectively. **Khamis (1970)** obtained an average gain per cycle of 7.97% from mass selection for the variety American early and 10% for "Weekly" variety with respect to the original population. **El-Rouby *et al.* (1973)** obtained a predicted gain from mass selection of the variety American Early by 8.9% per cycle. **El-Absawy (1984)** reported that the expected gain from mass selection in the variety Giza 2 was 1.98% per cycle based on both sexes. **El-Hosary (1986)** obtained an expected gain was 8.34% by mass selection per cycle based one sex in American Early. **El-Hosary (1987)** obtained an expected and predected gain per cycle of 28.46 g (Δg% = 10.81) in the variety Cairo 1 using mass selection one sex. **Mahrous (1990)** obtained an average predicted increases of 3.92% for "Alexanderia" and Cairo 1 composite varieties based on one sex and 8.85% for the two populations based on two sexes. **Sedhom (1993)** using the variety Giza 2 obtained an prodected gain of 10.12% per cycle.

El-Hosary and Abdel-Sattar (1997) obtained an predected gain and Δg% = 6.39% and 2.57%, respectively by using mass selection one sex in Moshtohor "2".

Abd El-Sattar (1997) obtained an average predicted increases of 7.31% and 3.06% for Moshtohor 1 and Moshtohor-3 composite variety using mass selection of one sex.

Abd El-Sattar (2003) obtained an expected improvement value per cycle of mass selection by 35.51(g) (Δg% = 2.11%) for Giza-2 composite variety based on the selection of the two sexes.

Table (12): Genetic gain for all studied traits from six methods of selection in Nobaria (NYP) and Gemmeza (GYP) yellow populations.

Method of selection	Populations	Crop system/ cycle	Selection intensity %	Dayes to silking		Dayes to tasseling		Plant height (cm)		Ear heigh (cm)		Ear leaf area (cm^2)		No. of ears/plant	
				day	Δg%	day	Δg%	cm	Δg%	cm	Δg%	cm^2	Δg%	ear	Δg%
Mass selection of one sex	NYP	1	10	0.78	1.40	0.67	1.11	3.46	1.60	4.89	4.32	21.35	3.51	0.001	0.092
	GYP	1	10	0.38	0.68	0.61	0.98	5.12	2.88	4.55	4.46	17.16	2.58	0.006	0.571
Modified ear to row	NYP	1	20	0.80	1.45	0.71	1.16	4.25	1.97	4.33	3.81	26.54	4.37	0.002	0.183
	GYP	1	20	0.64	1.13	0.86	1.38	6.23	3.51	4.32	4.24	24.40	3.67	0.015	1.439
Half sib	NYP	2	10	1.61	2.90	1.41	2.34	8.49	3.95	8.65	7.64	53.09	8.73	0.004	0.367
	GYP	2	10	1.29	2.26	1.73	2.76	12.46	7.02	8.69	8.53	48.80	7.34	0.029	2.762
Full sib	NYP	2	10	1.64	2.95	1.41	2.32	7.52	3.50	11.66	10.29	45.98	7.56	0.001	0.092
	GYP	2	10	0.78	1.38	1.28	2.06	11.02	6.20	10.58	10.38	36.33	5.47	0.011	1.048
Test cross. pop. as tester	NYP	3-4	20	3.21	5.79	2.83	4.68	16.98	7.90	17.31	15.27	106.17	17.47	0.008	0.734
	GYP	3-4	20	2.57	4.52	3.45	5.54	24.93	14.04	17.37	17.06	97.60	14.69	0.059	5.619
S_1 selection	NYP	1	20	2.47	4.46	2.18	3.06	11.38	5.29	14.07	12.41	70.63	11.62	0.001	0.092
	GYP	1	20	1.39	2.44	2.13	3.41	16.86	9.50	13.53	13.28	58.95	8.80	0.022	2.095

Table (12) Cont.

Method of selection	Populations	Crop system/ cycle	Selection intensity %	Ear length (cm)		Ear diameter (cm)		No. of rows/ear		No. of kernels/row		100-kernel Weight (g)		Grain yield/plant (g)	
				cm	Δg%	cm	Δg%	row	Δg%	kernel	Δg%	gm	Δg%	gm	Δg%
Mass selection of one sex	NYP	1	10	0.30	1.06	0.13	2.31	0.24	1.48	0.01	0.03	1.49	9.22	12.41	6.56
	GYP	1	10	0.21	1.12	0.11	1.96	0.19	1.27	1.54	4.26	0.87	0.23	6.03	3.19
Modified ear to row	NYP	1	20	0.43	2.37	0.26	4.44	0.39	2.40	0.03	0.08	1.01	6.25	11.92	6.59
	GYP	1	20	0.43	2.42	0.13	2.35	0.31	2.19	1.58	4.40	0.84	4.26	8.89	4.70
Half sib	NYP	2	10	0.87	4.75	0.30	5.15	0.78	4.75	0.05	0.13	2.02	12.50	23.85	12.44
	GYP	2	10	0.86	4.83	0.26	4.90	0.62	4.38	3.17	8.83	1.68	8.57	17.77	9.40
Full sib	NYP	2	10	0.59	3.26	0.29	5.15	0.51	3.14	0.01	0.10	4.35	26.92	27.38	14.47
	GYP	2	10	0.43	2.36	0.23	4.31	0.29	1.98	3.48	9.69	2.04	10.42	12.27	6.49
Test cross. pop. as tester	NYP	3-4	20	1.73	9.55	0.53	9.41	1.56	9.56	0.10	0.26	4.04	25.00	47.69	25.20
	GYP	3-4	20	1.69	9.50	0.52	10.00	1.25	8.75	6.34	17.62	3.35	17.20	35.55	18.81
S_1 selection	NYP	1	20	1.06	5.85	0.13	2.31	0.86	5.24	0.01	0.03	3.69	22.77	37.86	20.00
	GYP	1	20	0.76	4.27	0.12	2.16	0.67	4.73	4.72	13.14	2.60	13.30	21.05	11.14

Modified ear-to-row selection **(Lonnquist, 1964)** is a type of half-sib selection in that selection ears are planted ear-to-row in a replicated test in different environments. One trial is grown in isolation and the plant rows are detasseled so that pollen is provided by a bulk sample of all interies. Superior plants are mass selected within the highest yielding ear-rows (based on family means over environments). This method has been extremely effective in improving the mean yield of the population, our prediction gain by this method for improving both populations were 11.92 g (Δg% = 6.59% and 8.89 g (Δg% = 4.70%) for NYP and GYP, respectively. **Paterniani (1967)** obtained an average increase of 13.6% from the ear-to-row selection as an average of three cycles. **Khamis (1970)** reported an average increase of 8.91% in yield per cycle in the variety "American Early". **El-Hosary (1986)** obtained an average increase of 9.2 g (Δg% 3.52%) expected gain per cycle in the variety "American Early". **El-Hosary (1987)** obtained 6.57 g (Δg% = 2.5%) expected and predicted gain per cycle in the variety Cairo 1.

Mahrous (1990) reported an increase of 1.32 g (Δg% = 1.97%) per cycle for "Alexandria 11" and 4.85 g (Δg% = 3.02%) per cycle for "Cairo 1" based on one sex and 2.65 g (Δg% = 3.93%) and 9.17 g (Δg% = 6.03%) for the two maize populations based on the two sexes.

Half-sib selection involves the evaluation of individual through the use of their half-sib progeny. The general procedure for a cycle of selection is to cross the plant being evaluated to common tested evaluate the half-sib progeny from each plant, and intercross the selected individuals to form a new population.

The expected and predicted gain improvements in yield from half-sib family selection were 23.84 g ($\Delta g\%$ = 12.44%) and 17.77 g ($\Delta g\%$ = 9.40%) per cycle for NYP and GYP, respectively. **El-Rouby and Salem (1979)** obtained an predicted average increase of 3.6% with "Alexandria synthetic variety no. 1" relative the original population. **El-Absawy (1984)** obtained an average increase of 2.84 g per cycle in the variety Giza 2. **El-Hosary (1986)** obtained an average increase of 14.11 g ($\Delta g\%$ = 5.4%) with variety "American Early". **El-Hosary (1987)** obtained 21.089 g predicted gain per cycle ($\Delta g\%$ = 8.01%) with variety "Cairo 1".

Abd El-Sattar (1997) obtained the same increasing percent per cycle ($\Delta g\%$ = 5.23%) in "Moshtohor 1" population using modified ear-to-row.

Abdel-Sattar (2003) obtained on the expected and predicted gain by modified ear-two-row for improving Giza-2 was 9.13 g ($\Delta g\%$ = 5.43%).

Amer and Mosa (2004) showed that the predicted genetic advance for selection for grain yield in C-0 were 13.9%, C-1 were 10.01% and C-2 were 3.34% using modified ear-to-row in Sakha-6.

Full-sib family selection requires only two generations per cycle if plant-to-plant crosses are made between plants from different selection families because recombination and family formation will be accomplished simalteneously, i.e., season 1 (recombination-family formation) and season 2 performance traits. Although gain will be proportional to ($\frac{1}{2}\sigma^2A$), the phenotypic variance will be larger than half-sib family are selfed in the nursery the same season as the performance traits are conducted and a bulk of seed from several elite selfed plants are used to represent each selected lines 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 and predicted gain values per cycle were 27.38 g ($\Delta g\%$ = 14.47%) and 12.26 g ($\Delta g\%$ = 6.49%) for NYP and GYP, respectively. **El-Hosary (1986)** obtained an predicted average increase of 13.2% per cycle from full-sib family selection for "American Early". **El-Hosary (1987)** obtained genetic gain per cycle of 40.42 g ($\Delta g\%$ = 15.29%) in the synthetic variety "Cairo 1". **Mahrous (1990)** obtained an increase of 6.96 g ($\Delta g\%$ = 10.33%) and 9.11 g ($\Delta g\%$ = 13.52%) per cycle for "Alexandria 11" and 18.10 g ($\Delta g\%$ = 11.91%) and 25.01 g ($\Delta g\%$ = 16.46%) per cycle for "Cairo 1" based on full sib-family selection (S_1 and S_2), respectively. **Mahrous (1990)** reported that expected genetic improvement in yield from half sib-family selection was 3.33 g/cycle ($\Delta g\%$ = 4.95%) for Alexandria 11 and 11.47 g/cycle ($\Delta g\%$ = 7.57) for "Cairo 1".

Sedhom (1993) reported that the expected gain from this method was 16.95 g/cycle in the variety Giza 2.

Abd El-Sattar (1997) in "Moshtohor 1" obtained expected genetic gain (g) and predicted gain per cycle ($\Delta g\%$) by full-sib family selection were 46.43 and 20.92%, respectively.

Abd El-Sattar (2003) obtained the expected predicted improvement in yield from half-sib family selection in Giza-2 where 22.81 g ($\Delta g\%$ = 13.56%). While in Giza-2 were obtained the expected gain value per cycle was 28.29 g ($\Delta g\%$ = 16.82%) by full-sib family selection.

Test cross selection is a form of half-sib selection. Three seasons were required per cycle because each phase requires a separated season. In this method a plant is selfed and crossed to several random plants from the population as a 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 obtain the test-cross seed. But for rather than three seasons per cycle are required with the latter procedure. After test cross performance is evaluated and the superior families are selected, remnant selfed seed of the corresponding female plant is used for recombination. Progress for test cross selection with the population as tester is proportional to (½ σ^2A) instead of (¼ σ^2A) Table (3), but three or four seasons per cycle are required instead of the two with regular half-sib selection. When the number of tester plants (t) is not infinite, the phenotypic variance, (σ^2ph) is increased by

$$\mathbf{\frac{1}{t}[(1/4\ \sigma^2AE + 1/4\sigma^2DE)/m] + (1/4\sigma^2A + 1/4\sigma^2D)}\ .$$

Our results showed an average expected and predicted increase of 47.69 g (Δg% = 25.20%) and 35.54 g (Δg% = 18.81%) per cycle for NYP and GYP, respectively.

Horner *et al.* (1973) reported greater improvement in the test-cross yields for the Floreda 767 substrain improved with the assumption of complete dominance at all loci and negligible epistasis, Statistical theory would predict a 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 favorable allele. The determination of the theoretical relationship is difficult, but preliminary results from Kenya.

Most intrapopulation 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;**

Eberhart *et al.*, 1971 and Horner *et al.*, 1973). Our results showed an average predicted increase from the test cross selection of Δg% = 47.69% and 35.45% through one cycle from NYP and GYP, respectively. **Shehata *et al.* (1981)** with "American Early" variety obtained an average increase of 4.1%. **El-Hosary (1986)** obtained an expected gain in grain yield/plant from test cross selection were 14.09% per cycle with American Early. **El-Hosary (1987)** reported that the expected gain in the variety "Cairo 1" using this method of selection was 24.36 g/cycle (Δg% = 9.25%).

Abd El-Satter (1997) obtained the expected gain per cycle (g) and (%Δg) in "Moshtohor-1" were 46.73 and 20.92%, respectively by test cross selection.

Abd El-Satter (2003) obtained the expected and predicted gain per cycle by test cross selection where the value was 36.5 g (Δg = 21.69%) in Giza-2.

Regarding S_1 selection method, random S_1 lines could be isolated from any maize population with sufficient seed for testing over a number of locations. The expected and predicted genetic advance from S_1 selection in the present investigation was 37.86 g (Δg% = 20%) and 21.05 g (Δg% = 11.14%) per cycle for NYP and GYP, respectively. **El-Hosary (1986)** with American Early variety obtained an average increase 43.34 g/cycle (Δg% = 16.6%). **Ahmed (1987)** obtained predicted increase of 6.32% per cycle for "Composite 4" by using S_1 lines selection method. **El-Hosary (1987)** with the synthetic variety "Cairo 1" obtained an average increase of 44.639 g/cycle (Δg% = 16.95%). **Mahrous (1990)** obtained a expected and predicated increase of 6.66 g/cycle (Δg% = 9.8%) for Alexandria-11 and 9.30 g/cycle (Ag% = 15.09%) for the variety "Cairo 1". **El-Kilany (1994)** obtained a predicted increase 27.74 g (Δg% = 18.02%) per cycle of "Cairo 1".

Abd El-Sattar (2003) obtained an average increase of S_1 selection of 34.6 g ($\Delta g\% = 20.56\%$) in Giza-2.

In general, in our study, the yield increase would be mainly due to the increase of weight of 100-kernels in NYP followed by no. of rows/ear and then by no. of kernels/row. While, the yield increase of GYP would be mainly due to increase of; no. of kernels/row followed by 100-kernel weight and then by no. of rows/ear.

Also, for most traits, the highest expected gain was detected by test cross method followed by S_1 selection and then by full-sib selection and half-sib selection.

From the previous results, it could be concluded that four selection methods namely, test cross selection, S_1 family selection, full-sib and half-sib selection may be taken into consideration to improve the two synthetic varieties Nobaria and Gemmezia yellow populations, since they expressed the highest values of genetic gain. Also, it is necessary to put in our mined the costs, efforts and the time needed to provide one improvement cycle. S_1 selection method is easier in conducting one improvement cycle and, consequently it needed less costs and efforts.

SUMMARY & CONCLUSION

5. SUMMARY

The main purpose of this investigation was to estimate genetic variance components within two populations i.e. Nobaria yellow maize and Gemmeiza yellow maize populations. Also, to study the mean performances, environmental error variance, genotypic variance components, degree of dominance, heritability and expected genetic advance. Data were taken on the following quantitive characters: tasseling and days to silking, plant and ear heights, ear leaf area, no. of ears/plant, ear length, ear diameter, no. of rows/ear, no. of kernels/row, 100-kernels weight and grain yield/plant. Using the two methods i.e. design 1 mating system and S_1 line selection.

1- In the summer season 2004, 100 ridges from each of the two populations (NYP and GYP) were grow to produce seeds for a design 1 mating. Thirty six plants (S_0) within each population were selected at random (used as male parents and each crossed to four different plants (used as females parents) to produce 36 half-sib or 144 full-sib families.

In the summer season 2005, the 36 half-sib families were assigned at random to 4-sets each of (g) half sib groups or 36 full-sib families.

All sets were grown in three replications in randomized complete blocks design.

Each set was randomly placed in a separate block and the full-sib families were assigned at random to the plots within the block.

2- S_1 line mating: in the summer 2004, one hundered random selected plants, within each population, were selfed to produce 100 S_1 lines in each population.

In the summer 2005, those S_1 lines were evaluated in a randomized complete block design with three replications.

The field work dealing with this study was conducted during the two growing season 2004 and 2005 at Etay El-Baroud Agriculture Research Station. Agriculture Research center.

The results obtained could be summarized as follows:

1- Mean squares for S_1 line were significant for all traits in both populations, except no. of ears/plant and ear length in NYP.

Mean squares for males/S and females/males/S were significant for all the studied traits, except no. of ears/plant in NYP. In both populations, the error variance (σ^2e) had lower value for both selection methods, except plant height and ear leaf area in (GYP). Generally, GYP gave the higher and desirable values for grain yield/plant and the some of its components besides relatively ear lines S_1 line selected method.

2- The genetic variance in S_1 line selection method was highly significant for all traits under study in both populations.

The phenotypic and genotypic variance were higher for all traits under study in GYP than those of NYP, except no. of ears/plant, no. of rows/ear and no. of kernels/row for Design 1 mating system, and the additive genetic variance were found to be significant for days to silking, ear height, ear diameter, 100-kernels weight and grain yield/plant in NYP. However, phenotypic and genotypic were significant for plant and ear height, no. of kernels/row and 100-kernels weight in GYP. Dominance genetic variance estimates were significant for all the studied traits in both populations.

The average degree of dominance (σ^2D/σ^2A) ratio was higher than unity for all traits in both populations, except 100-kernels weight in NYP.

Generally in both populations, the dominance genetic variance was more important than additive one in the inheritance of most traits.

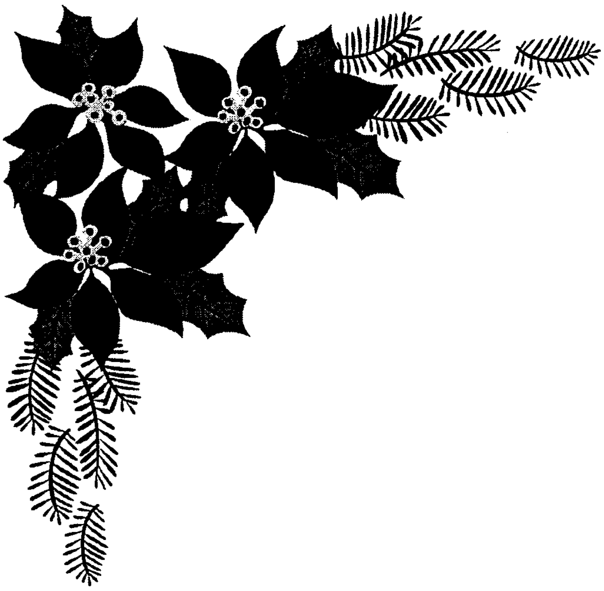
3- The heritability in broad sense in S_1 line selection method ranged from 0.93 for no. of ears/plant to 0.94 for plant and ear height, ear leaf area, ear length, no. of rows/ear, no. of kernels/row, 100-kernels weight and grain yield/plant in GYP and ranged from 0.087 for plant height to 0.99 for ear height, ear leaf area, no. of rows/ear, no. of kernels/row, 100-kernels weight and grain yield/plant in NYP.

The heritability in narrow sense ranged from zero for no. of ears/plant to 0.55 for 100-kernels weight in NYP and ranged from 0.03 for no. of ears/plant to 0.27 for ear height and 100-kernels weight in GYP.

4- The predicted genetic gain from selection in S_1-line selection method for grain yield/plant were 65.79 and 64.33 in GYP and NYP, respectively.

The predicted genetic advance per cycle for improvement the two populations under investigation using mass selection of one sex, modified ear to row selection, full-sib family selection, half-sib family selection, test cross population as a tester and S_1 family selection were 6.56, 6.59, 12.44, 14.47, 25.20 and 20.00%, respectively in NYP, and 3.19, 8.70, 9.40, 6.49, 18.81 and 11.14%, respectively in GYP.

The test cross selection, S_1 family selection, full-sib and half-sib family selection were the best methods for improving the two populations under study when the number of years per cycle, costs and efforts will be taken into consideration.



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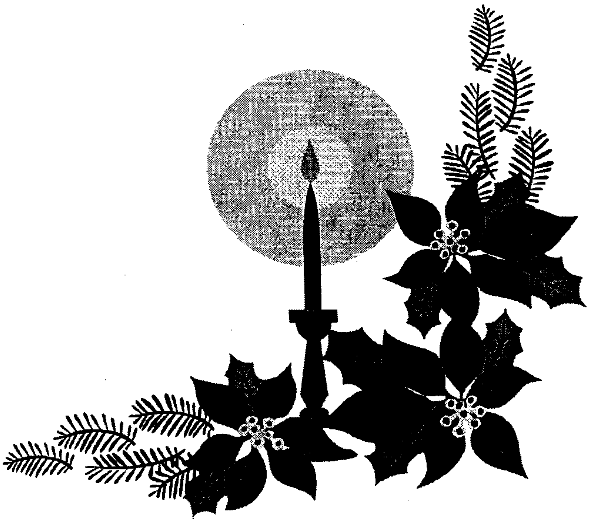
ARABIC SUMMARY



المستخلص العربى

عنوان الرسالة: دراسات على تربية الذرة الشامية.

الأســـم: عماد محمد أحمد حسين

الدرجـــة: دكتوراه الفلسفة فى العلوم الزراعية (محاصيل) – قسم المحاصيل – كلية الزراعة – جامعة طنطا.

أجريت هذه الدراسة خلال موسمين زراعيين هما صيفى ٢٠٠٤، ٢٠٠٥ بهدف حساب مكونات التباين الوراثى والتقدم الوراثى بالانتخاب فى عشيرتين من الذرة وهما عشيرة النوبارية وعشيرة الجميزة للذرة الأصفر باستخدم طريقتى انتخاب هما التصميم الأول وطريقة سلالات الذاتى الأول وأخذت القياسات على الصفات التالية: ميعاد التزهير للنورة المذكرة والمؤنثة – طول النبات – ارتفاع الكوز – مساحة ورقة الكوز – عدد الكيزان/نبات – طول وقطر الكوز – عدد الصفوف/كوز – عدد الحبوب/صف – وزن ١٠٠ حبة – محصول الحبوب/نبات.

كان التباين الوراثى فى طريقة سلالات الجيل الذاتى الأول عالى المعنوية لكل الصفات تحت الدراسة فى العشيرتين والتباين المضيف كان معنوى لصفة ميعاد خروج النورة المذكرة – ارتفاع الكوز – قطر الكوز – وزن ١٠٠ حبة – محصول الحبوب/نبات فى عشيرة النوبارية – التباين السيادى كان معنويا لكل الصفات فى العشيرتين.

درجة السيادة تجاوزت الوحدة فى كل الصفات فى العشيرتين ماعدا وزن ١٠٠ حبة فى عشيرة النوبارية.

كانت درجة التوريث على النطاق العريض فى طريقة انتخاب سلالات الجيل الذاتى الأول تتراوح من ٩٣% لصفة عدد كيزان النبات إلى ٩٤% لصفة طول النبات – ارتفاع الكوز – مساحة ورقة الكوز – طول الكوز – عدد الحبوب/كوز – عدد الحبوب/صف – وزن ١٠٠ حبة محصول الحبوب/نبات فى عشيرة الجميزة وتتراوح بين ٨٧% لصفة طول النبات إلى ٩٩% لصفة ارتفاع الكوز – مساحة ورقة الكوز – عدد الصفوف/كوز – عدد الحبوب/صف – وزن ١٠٠ حبة – محصول الحبوب/نبات فى عشيرة النوبارية وكانت درجة التوريث على النطاق الضيق لطريقة التصميم الول تتراوح بين صفر% لصفة عدد الكيزان/نبات إلى ٥٥% لصفة وزن ١٠٠ حبة فى عشيرة النوبارية وتتراوح من ٠,٠٣% لصفة عدد الكيزان/نبات إلى ٠,٢٧ لصفة ارتفاع الكوز ووزن ١٠٠ حبة فى عشيرة الجميزة.

كان التقدم الوراثى الراجع للانتخاب لتحسين الصفات تحت الدراسة باستخدام طريقة الانتخاب الاجمالى – طريقة الكوز للخط – طريقة العائلات غير الشقيقة – طريقة العائلات الشقيقة – طريقة الانتخاب المبنية على اختيار النسل باستخدام الكشاف وطريقة العائلات الملقحة ذاتيا لمدة جيل واحد بلغت على التوالى ٦,٥٦، ٦,٥٩، ١٢,٤٤، ١٤,٤٧، ٢٥,٢٠، ٢٠,٠٠% فى عشيرة النوبارية ٣,١٩، ٤,٧٠، ٩,٤٠، ٦,٤٩، ١٨,٨١، ١١,١٤% فى عشيرة الجميزة. وكانت أفضل طرق الانتخاب فى هذه الدراسة طريقة انتخاب العائلات الملقحة ذاتيا لمدة جيل واحد.

الكلمات الدالة: الذرة – التصميم الأول – طريقة انتخاب الجيل الذاتى الأول – التباين الوراثى – التقدم الوراثى الراجع للانتخاب.

الملخص العربى

تم إجراء هذه الدراسة فى محطة البحوث الزراعية بإيتاى البارود – مركز البحوث الزراعية فى خلال موسمين زراعيين متتاليين ٢٠٠٤، ٢٠٠٥. وكانت هذه الدراسة بغرض تقدير مكونات التباين الوراثى ودرجة التوريث والتحسين المتوقع الراجع للإنتخاب باستخدام عدة طرق من طرق الانتخاب فى مجتمعين من الذرة الصفراء هى عشيرة النوبارية الصفراء وعشيرة الجميزة الصفراء وذلك باستخدام طريقتين من طرق الانتخاب هما التصميم الأول والذى اقترحه كل من كمستوك وروبنسون ١٩٤٨ وطريقة سلالات الجيل الذاتى الأول (S_1).

فى عام ٢٠٠٤ تم تكوين ١٤٤ عائلة شقيقة ناتجة من تلقيح ٣٦ أب لأربعة أمهات كل على حدة وذلك فى كل عشيرة على حدة. بالإضافة إلى ذلك تم تكوين ١٠٠ عائلة ذاتية التلقيح (S_1) فى كل عشيرة على حدة. وقد اختبرت هذه العائلات بالطريقتين المختلفتين لكل عشيرة على حدة فى عام ٢٠٠٥ فى تصميم قطاعات كاملة العشوائية ذات الثلاثة مكررات.

وقد أخذت القياسات على الصفات التالية.

ميعاد التزهير للنوره المذكرة والمؤنثة – طول النبات – ارتفاع الكوز – مساحة ورقة الكوز – عدد الكيزان/نبات – طول وقطر الكوز – عدد الصفوف/كوز – عدد الحبوب/صف – وزن ١٠٠ حبة – محصول الحبوب/نبات.

وكانت أهم النتائج المتحصل عليها كما يلى:

١- كان تباين S_1 line معنويا لكل الصفات فى العشيرتين ماعدا صفة عدد الكيزان/نبات فى عشيرة النوبارية. وكذلك كان تباين الأباء والأمهات لكل أب معنويا لكل الصفات فى العشيرتين وكان تباين الخطأ (σ^2e) منخفضا فى معظم الصفات فى العشيرتين فى طريقتى الانتخاب.

٢- كان التباين الوراثى لطريقة انتخاب سلالات الجيل الذاتى الأول معنويا لكل الصفات فى العشيرتين وكان التباين الكلى فى عشيرة النوبارية أعلى منه لعشيرة الجميزة لمعظم الصفات تحت الدراسة.

٣- كان التباين الوراثى فى طريقة (Des. I) معنوى لصفة ميعاد خروج النوره المؤنثة – ارتفاع الكوز – قطر الكوز – وزن الـ ١٠٠ حبة – محصول الحبوب/نبات فى عشيرة النوبارية وصفة طول النبات – ارتفاع الكوز – عدد الحبوب/صف – وزن الـ ١٠٠ حبة فى عشيرة الجميزة.

٤- كان التباين الوراثى السيادى عالى المعنوية لكل الصفات فى العشيرتين تحت الدراسة.

٥- كانت درجة السيادة أعلى من الوحدة لكل الصفات فى العشريتين ماعدا وزن الـ ١٠٠ حبة فى عشيرة النوبارية، بما يشير إلى أن التباين الوراثى السيادى هو الجزء المهم فى وراثة معظم الصفات فى العشيرتين.

٦- كانت درجة التوريث بمعناها الواسع فى (S_1) تتراوح من ٠,٩٣ لصفة عدد الكيزان/نبات إلى ٠,٩٩ لصفة طول النبات – ارتفاع الكوز – طول الكوز – عدد الصفوف/كوز – عدد الحبوب/صف – وزن الـ ١٠٠ حبة – محصول الحبوب/نبات فى عشيرة الجميزة. وتتراوح من ٠,٨٧ لصفة طول النبات إلى ٠,٩٩ لصفة ارتفاع الكوز – مساحة ورقة الكوز – عدد الصفوف/كوز – عدد الحبوب/صف – وزن الـ ١٠٠ حبة – محصول الحبوب/نبات فى عشيرة النوبارية.

٧- كانت درجة التوريث بمعناها الضيق فى (Des. I) كانت تتراوح من ٠,٠٣ لصفة عدد الكيزان/نبات إلى ٠,٥٥ لصفة وزن الـ ١٠٠ حبة فى عشيرة النوبارية وتتراوح من ٠,٠٣ لصفة عدد الكيزان/نبات إلى ٠,٢٧ لصفة ارتفاع الكوز وزن الـ ١٠٠ حبة فى عشيرة الجميزة.

٨- كانت قيم التقدم الوراثى الراجع للانتخاب لتحسين الصفات تحت الدراسة باستخدام طريقة الانتخاب الإجمالى، طريقة انتخاب الكوز للخط طريقة انتخاب العائلات غير الشقيقة، طريقة انتخاب العائلات الشقيقة، طريقة الانتخاب المبنية على اختبار النسل باستخدام الكشافات وطريقة انتخاب العائلات الملقحة ذاتيا لمدة جيل واحد (S_1) قد بلغت على التوالى ٦,٥٦،

٦,٥٩، ١٢,٤٤، ١٤,٤٧، ٢٥,٢٠، ٢٠,٠٠% فى عشيرة النوبارية ٣,١٩، ٤,٧٠، ٩,٤٠، ٦,٤٩، ١٨,٨١، ١١,١٤% فى عشيرة الجميزة.

٩- كانت أفضل طرق الانتخاب فى هذه الدراسة هى طريقة انتخاب العائلات غير الشقيقة، طريقة انتخاب العائلات الشقيقة – طريقة الانتخاب المبنية على اختبار النسل باستخدام الكشافات – طريقة انتخاب العائلات الملقحة ذاتيا لمدة جيل واحد (S_1).

جامعة طنطا
كلية الزراعة
قسم المحاصيل

دراسات على تربية الذرة الشامية

رسالة مقدمة من

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بكالوريوس علوم زراعية – جامعة الزقازيق ١٩٩٥
ماجستير علوم زراعية - كلية الزراعة بمشتهر – جامعة الزقازيق (فرع بنها) ٢٠٠٢

للحصول على درجة
دكتوراه الفلسفة فى العلوم الزراعية
(محاصيل)

و قد تمت مناقشة الرسالة و الموافقة عليها

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تاريخ الموافقة: / /٢٠٠٧

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للحصول على درجة
دكتوراه الفلسفة فى العلوم الزراعية
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القاهرة – مصر

٢٠٠٧