4. RESULTS AND DISCUSSION

The present investigation was conducted to asses the genetic basis, to compare genetical analysis basis and to compare genetical analysis methods using half diallel cross. Also, compare the segregating and variation in the three crosses of the F_2 depend on the diversity in the parental inbred lines. Some agronomic characters, i.e. days to 50% tasseling, days to 50% silking, plant and ear heights, ear leangth, ear diameter, number of rows/ ear, number of kernels/ row, 100-kernel weight, ear weight/ plant, grain yield/ plant and shelling percentage of maize for nine parental inbred lines and their 36 F_1 hybrids of all possible combinations excluding reciprocals, were used.

The present investigation included three experiments. The first one the laboratory experiment, the second the half diallel cross experiment and the third the six populations P_1, P_2, F_1, F_2, Bc_1 and Bc_2 of each of the three crosses: P_4xP_9 (I), (close diversity), P_1xP_9 (II) (moderate diversity) and P_1 xP_5 (III) (high diversity) were used.

For good representation and discussion of the results obtained herein, it was preferred to outline these results into three main parts; one part for each of the above mentioned three experiment as follows:

1- Laboratory experiment (experiment I)

Extensive DNA polymorphism can be revealed with the use of random primers and PCR. These random primers were used to determine the polymorphism among the parental inbred lines under investigation that could be associated with genetic diversity among the parental inbred lines.

RAPD experiments were conducted using twenty random primers. Eleven primers gave non-polymorphic fragment. On the other hand, nne primers (A12, A13, A14, A15, A17, A18, A19, A20 and Q11) gave polymorphic amplification products. Therefore, the last nine primers were included in this study and the rest were excluded.

Primer A12:

Data presented in **Table (11)** showed that the pimer A12 produced eleven amplified fragment amplified scorbel fragment (ASF) which ranged between 250b.p. and 2121b.p. The total number of scorable bands were 71 and gave six polymorphic fragments out of eleven, with 54.5% polymorphism as shown in **table (11)**. Also, **Fig. (1)** showed the RAPD pattern of primer A12.

Primer A13:

Among of primers investigated, **Table (12)** showed that the primer A13 gave four fragments which ranged between 319b.p. and 1115b.p.. The total number of scorable bands were 30 bands and the primer gave two polymorphic fragments out of four, with 50% polymorphism. **Fig (2)** showed the RAPD pattern of amplification product of primer A13.

Primer A14:

It is evident from **table (13)** that, the primer A14 gave eight fragments between 543b.p. and 2133b.p. **Table (13)** showed the total number of scorable bands were 44 bands and

the primer gave six polymorphic fragments out of eight, with 75% polymorphism. **Fig (3)** showed the RAPD pattern of amplification product of primer A14.

Primer A15:

Primer A15 produced five amplified fragments (AFS) between 489b.p. and 2251b.p. and produced four polymorphic fragments with 80% polymorphism. The total number of scorable bands were 28 bands **(Table 14). Fig (4)** showed the pattern of amplification product of primer A15.

Primer A17:

With respect to primer A17, six fragments ranged between173b.p. and 1143 b.p. were produced by this primer **Table (15)**. The total number of scorable bands were 37 bands and the primer gave three polymorphism, the estimate of polymorphic for this primer was 50% **Table (15). Fig (5)** showed the pattern of amplification product of primer A17.

Primer A18:

It is evident from **table (16)** that, primer A18 gave 50 bands in nien fragments ranged between 181b.p. and 1535b.p. Also, **Table (16)** showed the primer gave eight polymorphic fragments out of nien, with 88.89% polymorphism. **Fig (6)** showed the RAPD pattern of amplification product of primer A18.

Primer A19:

Table (17) showed that the primer A19 gave eight fragments ranged between 181b.p. and 1763b.p. **Table (17)** showed that the total number of scorable bands was 65 bands

and the primer gave two polymorphic fragments out of eight, with 25% polymorphism. **Fig (7)** showed the RAPD pattern of amplification product of primer A19.

Primer A20:

Table (18) revealed that the total number of AFS developed by using primer A20 was six ranged between 422b.p. and 2020b.p. The total number of scorable bands were 30 bands. The primer gave non-monomorphic fragments out of six, with 100% polymorphism. **Fig (8)** showed the RAPD pattern of amplification product of primer A20.

Primer Q11:

Data presented in **table (19)** showed that the primer Q11 gave 42 scorable bands and produced nine amplified fragments (AFS) ranged between 363b.p. and 2305b.p. and it produced eight polymorphic fragments. The estimate of polymorphic for this primer was 88.89%. **Fig (9)** showed the RAPD pattern of amplification product of primer Q11.

Genetic similarity:

The genetic similarity matrix was produced for the RAPD data using **Nei and Li,s formula (1979)**. Genetic similarity coefficient presented in **Table (20)**. The lowest genetic similarity (0.55) was detected between P_1 and P_5 also, obtaind between P_6 and P_8. While, the highest genetic similarity was (0.90) scorded between the two parental inbred lines P_4 and P_9. The over all mean for genetic similarity between the parental inbred lines was (0.698).

Cluster analysis:

The dendogram constructed from cluster analysis based on RAPD data is presented in **Fig. (10)**. The data collectively distinguished two main clusters. The first main cluster consists of eight inbred lines P_1, P_2, P_3, P_4, P_6, P_9 , P_8 and P_7 and this cluster separated into two sub-clusters: the first sub-cluster contained six inbred lines P_1, P_2, P_3, P_4, P_6 and P_7. Meanwhile, the second sub cluster contained two inbred line P_8 and P_9. In addition, the first sub-cluster divided into two sub-sub clusters the first sub-sub cluster contained P_1 and P_2. While, the inbred lines P_3, P_4, P_6 and P_7 were belonging to the second sub-sub cluster as well as inbred lines P_4 and P_6 being closely. The second main cluster contains the inbred lines only P_5. In this concern, **Lanza *et al.* (1997)** and **Zhang *et al.* (1998)** indicated that RAPD technique can be used as a tool for determining the extent of genetic diversity among maize inbred lines, for allocating genotypes into different groups and is successful in confirming hypothesized relationship.

2- The second experiment:

This experiment was carried out to asses the genetic basis and to compare five methods using half diallel cross. For better persintation of the results, the obtained data for all studid traits are classified into the following main topics:

1- Analysis of variance, mean performance and heterosis.

2- Estimation of Genetic components and genetic-environmental interactions.

3- Comparison between methods:

2-1- Analysis of variance, mean performance and heterosis.

2-1-1-Analysis of variance.

The analysis of variance for all the studied traits are presented in **Tables (21and 22). Table 21**, represents the analysis of variance for one set of F_1's but neither parents nor reciprocals were included Griffing's method-4. While, the **table (22)**, represents the analysis of variance for parents and their F_1's without reciprocal (Griffing's method-2).

Data were recorded on all genotypes for yield, yield components and some agronomic traits, in each rate of nitrogen fertilization and their combined **(Tables 21 and 22)**.

Nitrogen rate mean squares were significant for all traits under study except for no. of rows/ear, with mean values in high rate being higher than those in low rate of nitrogen for all traits in both methods of analysis (M2 and M4) **(Table 23)**.

It is clear that number of days from sowing to tasseling or silking increased significantly with increasing nitrogen rates up to 120 Kg. N/ Fed. It coud be concluded that nitrogen fertilizer rates showed positive effect on the previous traits on maize.

The increase in these traits at high rate of nitrogen may be due to the stimulating effect of nitrogen on metabolic process in maize plant. These results are in agreement with those obtained by **El-Hefnawy and El-Zeir (1991), Mohamed (1993), Rizzi *et al.* (1993), GuangJauh *et al.* (1995), Hassan (1999), ZeHui *et al.* (2002), Ibrahim (2003), Ibrahim (2004), Medici *et al.* (2004) , Chun *et al.* (2005) and El-Hosary and El-Badawy (2005).**

In method-2, genotypes mean squares were significant for all traits in both rates of nitrogen as well as the combined analysis **(Table 22)**. This indicates the wide diversity between the parental materials used in the present study. Significant genotypes x nitrogen rate mean squares were obtained for all traits except ear diameter, no. of rows/ear, no. of kernels/row and 100-kernel weight, revealing that the performance of genotypes differed from rate to another of nitrogen.

Significant parents' mean squares were obtained for all cases except ear height at high nitrogen rate, 100-kernel weight at both nitrogen rates as well as combined analysis. **(Table 22)**. Insignificant interaction mean squares between parental inbred lines and nitrogen rates were detected for all traits studied except plant height, ear length, 100-kernel weight and shelling percentage **Table (22)**. This result may reveal higher repeatability of performance of the parental inbred lines under different nitrogen rates. For the exceptional traits on the contrary, significant interaction was obtained revealing that the parental inbred lines varied in their response to nitrogen rates.

Hybrids mean squares were significant for all traits in both rates of nitrogen as well as the combined analysis in both methods of Griffing **(Tables 21 and 22)**. This indicates the wide diversity between the parental materials used in present study.

Insignificant interaction mean squares between hybrid and nitrogen rates in both methods of Griffing (M2 and M4) were detected for all traits studied except, dayes to 50% tasselling, days to 50% sillking, ear height and shelling percentage in M4 revealing that the performance of hybrids responded similarly to environmental changes. For the exceptional traits, Significant interaction mean squares between hybrid and nitrogen rates were dwrwcted indicating that, these hybrids behaved some what differently from nitrogen rate to another.

2-1-2-Mean performance

The mean performances of the tested nine inbred lines and the tested 36 hybrids and two check hybrids SC Pionner 3084 and SC Giza 155 at each nitrogen rate and as an average over the nitrogen rates are presented in **(Table 23).**

For dayes to 50% tasseling, the inbred line P_1 at both nitrogen rates as well as the combined analysis significant gave the lowest value of this trait. However, inbred line P_2 significantly was the latest in both nitrogen rates and the combined analysis.

As for days to 50% silking, the inbred line P_1 behaved as the earliest inbred line at low, high nitrogen rates as well as the combined analysis. However, inbred lines no. 2, 4, 5, 7 and 8 in both nitrogen rates as well as the combined analysis.

For plant height the inbred lines no. 1, 6 and 9 and 1, 4. 6 and 7 for ear height gave the lowest mean values for plant and ear height in both nitrogen rates as well as the combined analysis. However, inbred lines no. 2, 3 and 5 had the highest mean values for both traits.

The parental inbred lines no. 3, 4 and 7 gave significantly higher mean values of ear length in both nitrogen rates and the combined analysis. However inbred line no. 8 had the lowest one for this trait.

The parental inbred lines no. 1, 4, 5 and 7 exhibited significant highest mean values for ear diameter in the combined analysis. However, the parental inbred line no. 6 had the lowest one for this trait.

The inbred line no. 9 had significantly the highest mean values for no. of rows/ ear followed by line no. 1, 3, 6 and 7. However, the inbred line no. 2 showed the lowest one for this trait.

The inbred lines no. 7 and 1 showed significant the highest number of kernels/ row in both nitrogen rates and over them. However, the parental inbred lines no. 8 gave the lowest one for this trait. All inbred lines gave similar 100-kernel weight.

The inbred line no. 1, 4 and 9 showed significantly the highest mean values for shelling percentage. However, inbred line no. 3 gave the lowest one.

The parental inbred lines no. 1, 6, 9 and 4 had the highest mean values of ear weight and grain yield/ plant in the combined analysis. These inbred lines exhibited high mean values for one or more of the traits contributing to grain yield. However, the parental inbred line no. 2 gave the lowest one for both traits.

Hybrid mean squares were significant for all traits, revealing over all differences between these hybrids.

Significant interaction mean squares between hybrids and nitrogen rates were obtained for days to 50% tasseling and silking and ear height, indicating that these hybrids behaved somewhat differently from nitrogen rate to another. For the other traits, insignificant interaction was obtained, reflecting that these hybrids responded similarly to environmental changes.

Mean performances of F_1 hybrids, S.C. G. 155 and SC Piooneer 3084 at each nitrogen rates as well as the combined analysis are presented in **table (23)**. None of the hybrids surpassed the late or the highest performing inbred lines for tasseling and silking dates revealing that all hybrids were shifted to wards the earliness direction. The earliness of tasseling and silking dates was detected by crosses P_1xP_3, P_1xP_6, P_1xP_8, P_2xP_3, P_2xP_6, P_3xP_6, P_3xP_7, P_6xP_7 and P_6xP_9.

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

As for plant and ear heights, four hybrids; P_1xP_7, P_2xP_5, P_3xP_7 and P_4xP_7 gave the lowest values in both nitrogen rates as well as the combined analysis. However, the highest values for both traits were recorded by cross P_2xP_8 , S.C. Pioneer 3084 and

S.C.G. 155 in both nitrogen rates as well as the combined analysis. Plant shortness in maize decreased the lodging degree and increased the yield potentiality.

The hybrids P_1xP_2, P_1xP_5, P_2xP_5, P_2xP_6, P_3xP_4, P3xP5, P_3xP_6, P_4xP_5 and S.C. Pioneer 3084 had the heighest mean values for ear length at both nitrogen rates as well as the combined. However the cross P_6xP_8 had the lowest one for this trait.

None of the hybrids showed superiority over the check hybrids for ear diameter. Twenty hybrids showed insignificant deference from the check hybrids for this trait in the combined analysis. The highest mean value was detected for cross P_6xP_8 for ear diameter in the combined analysis.

The two crosses P_5xP_7 and P_7xP_9 showed superiority over the two check hybrids for number of rows/ ear in the combined analysis. Also, the crosses P_1xP_5, P_1xP_6, P_1xP_7, P_2xP_6, P_4xP_6, P_5xP_6, P_5xP_7, P_6xP_8, P_7xP_8 and P_7xP_9 gave the highest mean values for this trait.

For number of kernels/ row, the hybrid P_3xP_4 had the highest number of kernels/ row followed by cross P_4xP_5 and then by S.C. Pioneer 3084 in the combined analysis.

The six crosses i.e. P_1xP_3, P_1xP_7, P_2xP_8, P_3xP_4, P_4xP_6 and S.C. Pioneer 3084 gave the highest mean values for 100-kernel weight in the combined analysis. However, the cross P_1xP_4 gave the lowest one for this trait.

For ear weight/ plant, the hybrids P_3xP_4, P_4xP_5, P_4xP_6 and P_4xP_6 showed significant high mean values than the best check hybrid S.C.G. 155 in the combined analysis. However, the lowest mean value was recorded by cross P_6xP_8 for this trait.

Concerning grain yield/ plant the crosses P_3xP_4, P_4xP_6, P_4xP_5 and P_3xP_8 in the combined analysis, P_3xP_4 and P_4xP_6 in low nitrogen rate and P_3xP_4, P_3xP_8 and P_4xP_5 in high nitrogen rate had significant superiority over the best check hybrid (S.C. G. 155). These hybrids exhibited significant increase of one or more of traits contributing to grain yield (**Table 23**). The fluctuation of hybrids from nitrogen rate to another was detected for most traits. These results would be due to significant interaction between hybrids and nitrogen rates.

For shelling percentage, the cross P_4xP_6 had the highest value for this trait. While, twenty eight hybrids did not differ from the best check hybrid in the combined analysis.

2-1-3-Heterosis

Significant mean squares for parents vs. hybrids were detected for all the studied traits in both nitrogen rates as well as the combined analysis as an indication of average heterosis. **Table (22)**. The largest heterotic magnitude expressed by the all traits as the deviation of particular F_1 mean values were significantly higher than parental means for all traits except tasseling and selling % where the parental means were significantly higher than F_1 mean values (**Table 23**).

Insignificant interaction between mean squares due to parents *vs.* crosses and nitrogen rate were obtained for all traits except dayes to 50% tasseling, dayes to 50% silking dates and plant height. These results indicated that the heterotic effects were not affected by the nitrogen changes.

Heterosis expressed as the percentage deviation of F_1 mean performance from each of S.C. G. 155 and S.C. Pioneer 3084 values for all traits studied at nitrogen rates as well as the combined analysis are presented in **Table (24).**

For dayes to 50% tasseling, the hybrids tended to deviate to wards earliness especially in low nitrogen rate. Earliness if found in corn is favorable for escaping destructive injuries caused by *Sesamia cretica ledi chilo simplex* But and *Pyrausta nubilialis*. Twenty two, eighteen and seventeen crosses exhibited significantly negative heterotic effects relative to S.C. Pioneer 3084 value, fourteen, seven and ten hybrids relative to S.C. G. 155 in low, high nitrogen rates as well as the combined analysis, respectively. The highest negative heterotic effects compared to two checks were P_1xP_6, P_1xP_8, P_3xP_6 and P_3xP_7.

For silking date, thirty one, twenty three and thirty hybrids exhibited significant negative heterotic effects relative to S.C. Pioneer 3084 at low, high nitrogen rate and the combined analysis, respectively. While, twenty, four and thirteen parental combinations gave significant negative heterotic effects relative to S.C. G. 155 in the same order. The best crosses were P_2xP_6, P_3xP_6 and P_3xP_7. Significant negative heterotic effects for earliness was detected by **Altinbas (1995), Khalil and Khattab (1998), Nawar *et al.* (1998), Abd El-Azeem (2000), Nawar *et al.* (2002), Singh *et al.* (2004) and El-Hosary *et al.* (2006).** On the other hand, **El-Zeir (1998), Shafey *et al.* (2003), El-Bagoury *et al.* (2004) and Motawei (2005)** found significant positive heterotic effects for earliness.

For plant height, seventeen, sixteen and nineteen crosses compared to S.C. Pioneer 3084 and twenty four, twenty and twenty three compared to S.C. G. 155 expressed significantly negative heterotic effects in low, high nitrogen rates as well as the combined analysis, respectively. The highest negative heterotic effects were detected by crosses P_1xP_7, P_1xP_3, P_1xP_9, P_3xP_7 and P_4xP_7 compared with the two check varieties.

As for ear height, sixteen, six and seven crosses compared with S.C. Pioneer 3084, and nineteen, six and nine hybrids compared with S.C. G. 155 expressed significantly negative heterotic effects in low, high nitrogen rates and the combined analysis, respectively. The highest negative heterotic effects were detected by crosses, P_1xP_7, P_4xP_7 and P_3xP_9 compared to the two check varieties. Similar results were reported by **Abd El-Azeem (2000), Nawar *et al.* (2002), and El-Hosary *et al.* (2006).**

As for ear length; zero, two and zero hybrids relative to S.C. Pioneer 3084 and six, twenty three and thirteen crosses relative to S.C. G. 155 gave significant positive heterotic effects in low, high nitrogen rates and the combined analysis, respectively.

For ear diameter five, seventeen and eight hybrids relative to S.C. Pioneer 3084 and zero, four and zero crosses relative to S.C. G. 155 exhibited significant positive heterotic effects in low, high nitrogen rates and the combined analysis, respectively. these results are in line with these reported by **El-Zeir (1998), Abd El-Azeem (2000), Nawar *et al.* (2002), El-Bagoury *et al.* (2004), Singh *et al.* (2004) and El-Hosary *et al.* (2006).**

Concerning no. of rows /ear; one, two and two crosses relative to S.C. Pioneer 3084 and zero, five and zero hybrids relative to S.C. G. 155 expressed significant positive heterotic effects in low, high nitrogen rates and the combined analysis, respectively.

For no. of grains/ row, non of the hybrids showed significant heterotic effects relative to S.C. Pioneer 3084 at both nitrogen rates and the combined analysis. While, zero, five and two hybrids expressed significant positive heterotic effects relative to S.C. G. 155.

For 100-kernel weight, zero, four and one crosses relative to S.C. Pioneer 3084 and zero, four and one compared with S.C. G. 155 exhibited significant positive heterotic effects in low, high nitrogen rate as well as the combined analysis, respectively. The most desirable heterotic effects were detected by cross P_3xP_4 compared with both checks and cross P_4xP_5 Relative to S.C.G. 155 in high nitrogen rate and the combined analysis.

For ear weight, eleven, eleven and fourteen hybrids relative to S.C. Pioneer 3084 and two, two and one crosses relative to S.C. G. 155 expressed significant positive heterotic effects in low, high nitrogen rates as well as the combined analysis, respectively. The highest positive heterotic effects were detected by cross P_3xP_4 compared to both checks in both nitrogen rates as well as the combined analysis.

Concerning grain yield/ plant, ten, fourteen and twelve parental combinations expressed significant positive heterotic effects relative to S.C. Pioneer 3084 in low, high nitrogen rates and the combined analysis, respectively. The cross P_3xP_4 gave significantly positive heterotic effects relative to S.C. G. 155 in both nitrogen rates as well as the combined analysis. Also, the crosses P_3xP_4 and P_4xP_6 in low nitrogen rate, P_3xP_4, P_3xP_8 and P_4xP_5 in high nitrogen rate and P_3xP_4, P_4xP_5 and P_4xP_6 in the combined analysis had significant out yielded than the best check hybrid (SC G. 155). In addition, the crosses P_1xP_4, P_1xP_6, P_2xP_3, P_2xP_4, P_2xP_8, P_3xP_5, P_3xP_6, P_3xP_7, P_3xP_8, P_4xP_5, P_4xP_8, P_5xP_6 P_5xP_7, P_6xP_7 and P_8xP_9 in low nitrogen rate, P_1xP_4, P_1xP_5, P_1xP_6, P_2xP_4, P_2xP_5, P_2xP_6, P_2xP_8, P_3xP_5, P_3xP_6, P_3xP_7, P_4xP_6, P_4xP_8, P_6xP_7 and P_8xP_9 in high nitrogen rate and P_1xP_4, P_1xP_5, P_1xP_6, P_2xP_4, P_2xP_5 P_2xP_6, P_2xP_8, P_3xP_5, P_3xP_6, P_3xP_7, P_4xP_6, P_4xP_8, P_5xP_7, P_5xP_8, P_6xP_7, P_7xP_8, P_7xP_9 and P_8xP_9 in the combined analysis gave insignificant out yielded the best check hybrid S.C. G. 155. Hence it could be concluded that these crosses offer possibility for improving grain yield of maize. Several investigators reported high heterosis for yield of maize; i.e. Several investigators reported high heterosis for yield of maize; i.e. **Sablijarevic (1997), El-Zeir (1998), Nawar *et al.* (1998), Abdel-sattar *et al.* (1999), Abd El-Azeem (2000), El-Bagoury *et al.* (2004), Nawar *et al.* (2002), and El-Hosary *et al.* (2006).**

For shelling percentage, the crosses P_3xP_8 and P_6xP_8 exhibited significant positive heterotic effects relative to S.C. G. 155 in high nitrogen rate. However, the two crosses P_2xP_6 and P_5xP_8 had significant negative heterotic effects relative to the two checks in low nitrogen rate. Meanwhile, the other hybrids showed insignificant heterotic effects relative to both checks in low, high nitrogen rates and the combined analysis. The correlation coefficients between genetic diversity (GD), and each of mean performance and heterosis relative to check variety S.C. G 155 for grain yield/ plant were positive (r = 0.06 and 0.03), respectively. The results indicated that RAPD marker can be used as a tool for determining the extent of genetic diversity among maize inbred lines. The results indicated that RAPD marker can be used as a tool for determining the extent of genetic diversity among maize inbred lines and for genotypes into different groups but when used a large number of primers to detect the variation over all DNA or used a new marker like SSR or AFLP.

2-2- Estimation of Genetic components

2-2-1- Griffing method 2 model 1, 1956.

The analysis of variance for combining ability for each nitrogen rates as well as the combined for all the studied traits is presented in **Table (22).**

The mean squares of general combining ability includes the additive and additive x additive genetic portion. While, specific combining ability represents the non additive genetic portion of the total variance arising largely from dominance and epistatic deviations. The mean squares due to general and specific combing ability were highly significant for all traits except mean square GCA for shelling% at low nitrogen rate. For the exceptional case, non additive type of gene action was important part of the total genetic variability.

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

Days to 50% silking at high nitrogen rate, plant height at low nitrogen rate and the combined analysis, ear length at the combined analysis and no. of rows/ear at the low nitrogen rate, had GCA/SCA ratio equal unity, indicating that additive and non-additive types of gene action have the same importance in the performance of these cases. High ratios which largely exceeded the unity were obtained for dayes to 50% tasseling at low rate of nitrogen fertilization, dayes to 50% sillking at low nitrogen rate as well as combined analysis, plant height, ear length and shelling% at high nitrogen rate, ear height at both nitrogen rates as well as the combined analysis, and no. of rows /ear at high nitrogen rate as well as the combined analysis, indicating that large part of the total genetic variability associated with these traits was additive and additive by additive gene action.

For the other remain traits, GCA/SCA ratios, were less than unity. Therefore, it could be concluded that the large portion of the total genetic variability associated with these traits is due to non-additive gene action. Similar results were reported by **El-Hosary and El-Badawy (2005), El-Shenawy (2005), Mosa and Motawei (2005), Motawei (2005), Soliman *et al.* (2005), El-Hosary *et al.* (2006), Sedhom *et al.* (2007), Akbar *et al.* (2008), Motawei and Mosa (2009) and GuangJauh (2009).**

The mean squares of interaction between nitrogen rates and both types of combining ability were significant for dayes to 50% tasseling and silking and ear hight and shelling %. Such results showed that the magnitude of all types of gene action varied from nitrogen rate to another. It is fairly evdent that ratio for SCAxN/SCA was higher that ratio of GCAxN/GCA for days to 50% silking and ear height. This result indicated that non additive effects were more influenced by nitrogen rates than additive genetic effects of both traits. This conclusion is in well agreement with those reported by **Gilbert (1958).** However, both ratios were equal for dayes to 50% tasseling, reveling that additive and non- additive were similar changed by nitrogen rates. Also, the ratio GCAxN/GCA was higher than ratio of SCAxN/SCA for shelling% indicating that additive effects were more influenced by nitrogen rates than non-additive effect.

As for plant height, 100-kernel weight and shelling percentage, the mean squares of interaction between nitrogen rates and GCA were significant. However, insignificant SCA by nitrogen rates mean squares were detected. Such result indicat that additive and additive by additive effect were more influenced by nitrogen rates than non-additive genetic one.

As for ear length and ear weight/plant, insignificant mean squares of interaction between nitrogen rates and GCA along with significant SCAxnitrogen rate were detected, revealing that non additive effects was more changed with nitrogen rates than additive genetic one.

On the other hand, insignificant mean squares of interaction between nitrogen rates and both combining ability was obtained for ear diameter, on. of rows/ear, no. of kernels/ row and grain yield / plant, revealing that all types of gene action did not appreciably fluctuate in magnitude from nitrogen rate to another. These finding confirm those obtained above from the ordinary analysis of variance. The interaction between both types of combining abilities and environmental changes were reported to be significant for earliness, plant height, ear height (**El-Hosry, 1989, El-Hosary *et al.* 2006 and sedhom *et al.* 2007** for ear height and earliness).

2-2-2-Griffing method 4

The analysis of variance for combining ability for each nitrogen rates as well as the combined for the studied traits is presented in **(Table 21)**.

The mean squares due to general and specific combining ability were highly significant for all traits except, the mean squares due to SCA for ear diameter and shelling% in the high nitrogen rate and no. of kernels/row in the low nitrogen rate. For the exceptional cases, additive type of gene action was important part of the total genetic variability for both cases.

While, in the other traits GCA/SCA ratio was used as measure to reveal the nature of genetic variance involved. High ratios which largely exceeded the unity were obtained, indicating that large part of the total genetic variability associated with these traits was additive and additive by additive gene action. Similar results were reported by **El-Hosary and El-Badawy (2005), El-Shenawy (2005), Mosa and Motawei (2005), Motawei (2005), Soliman *et al.* (2005), El-Hosary *et al.* (2006), Sedhom *et al.* (2007), Akbar *et al.* (2008), Motawei and Mosa (2009) and GuangJauh (2009).**

The mean squares of interaction between rates of nitrogen fertilization and both types of combining ability were insignificant for all studied traits except dayes to 50% taseling, dayes to 50% silking, ear height, ear weight/ plant and shilling percentage. For plant height and shelling% GCAxN was significant, along with insignificant SCAxN such results showed that magnitude of additive and additive x additive types of gene action influenced from nitrogen rate to another. It is fairly evident that the ratio for SCAxN/SCA was higher than ratio GCAxN/GCA for dayes to 50% tasseling, dayes to 50% sillking, ear height and ear weight/plant. This result indicate that non-additive effects were more influenced by the environmental conditions than non- additive effects. The genetic variance was previously reported to be mostly due to non-additive for plant and ear heights by **Sadek *et al.* (2000), Amer (2003), Shafey *et al.* (2003) and sedhom *et al.* (2007); no. of grains/row by Amer (2003), Shafey *et al.* (2003), El-Shenawy (2005) and sedhom *et al.* (2007) and grain yield/plant by Sadek *et al.* (2000), Soliman (2000), Dodiya and Joshi (2002), Amer (2003), Mosa (2003-a), Shafey *et al.* (2003), El-Hosary and El-Badawy (2005); El-Shenawy (2005) and El-Hosary *et al.* (2006) and sedhom *et al.* (2007).** On the other hand, the additive genetic variance was previously reported to be the most prevalent for earliness by **Sadek *et al.* (2000); Dubey *et al*. (2001); Amer (2003); Mosa (2003-a&b), El-Hosary and El-Badawy (2005), El-Shenawy (2005), El-Hosary *et al.* (2006) and sedhom *et al.* (2007);** no. of rows/ear by **Amer (2003); Mosa (2003-a), Shafey *et al.* (2003) and El-Hosary and El-Badawy (2005), El-Shenawy (2005) and sedhom *et al.* (2007);**100-kernel weight by **Dubey *et al.* (2001), Shafey *et al.* (2003), El-Hosary and El-Badawy (2005) and sedhom *et al.* (2007).**

General combining ability effects:

Estimations of GCA effects ($\hat{g}_i$) for individual parental inbred lines for each trait in both rates of nitrogen fertilization as well as their combined analysis in both methods (Griffing M-4 and 2) are presented in **Tables (25 and 26)**. General combining ability effects estimated herein were found to differ significantly from zero. High positive values would be of interest under all traits in question except silking, tassling days to 50% as well as plant and ear heights where high negative effects would be useful from the breeder's point of view.

The parental inbred line no. 1 exhibited the highest significant negative ($\hat{g}_i$) effects for; days to 50% tassling and plant height in both nitrogen rates as well as the combined analysis in both methods, ear height in method 2 in low nitrogen rate as well as the combined analysis and at low nitrogen rate in method 4. These results indicate that this inbred line could be considered as a good combiner for developing early and short genotypes. Earliness of inflorescence is required for developing early maturing genotypes to escape corn pest and shorter plant and ear heights are required for lodging resistance. Also, it gave significant positive ($\hat{g}_i$) effects for ear diameter in high rate of nitrogen and no. of rows/ear at high rate of nitrogen and the combined analysis in method-2 and shelling% in low nitrogen in both methods. Meanwhile, it gave undesirable ($\hat{g}_i$) effects for other cases in two methods (Method-2 and Method-4).

The parental inbred line no. 2 showed significant positive ($\hat{g}_i$) effects for ear length in both nitrogen rates as well as the combined analysis in two methods. Meanwhile, it gave undesirable ($\hat{g}_i$) effects for other traits, (Table 25 and 26).

The parental inbred line no. 3 gave significant desirable ($\hat{g}_i$) effects in both methods of analysis for days to 50 tasseling, days to 50% silking, 100-kernel weight ear weight/ plant and grain yield/plant in both nitrogen rates as well as the combined analysis and ear height at high nitrogen rate and the combined analysis in method 4. This inbred line could be considered as a good combiner for developing early genotypes and grain yield/ plant at high nitrogen rate in method-2 **(Table 26)**. Meanwhile, exhibited either significant undesirable or insignificant ($\hat{g}_i$) effects for other traits in both methods.

The parental inbred line no. 4 seemed to be a good combiner in both methods of analysis for; no. of kernels/ row, ear weight/ plant and grain yield/plant in both nitrogen rates as well as the combined analysis. However, it exhibited either significant undesirable or insignificant ($\hat{g}_i$) effects for the other traits, indicating that this line could be considered as excellent combiner for developing high yield hybrids.

The parental inbred line no. 5 gave significant positive ($\hat{g}_i$) effects for ear length at high rate and the combined analysis and ear weight/ plant at high nitrogen rate in method-2. While, it gave significant positive ($\hat{g}_i$) effects for ear length, no. of rows/ ear, ear weight/plant and grain yield/plant at high nitrogen rate and the combined analysis in method-4. However, it gave undesirable ($\hat{g}_i$) effects for other cases.

The parental inbred line no. 6 seemed to be good combiner for days to 50% tasseling, days to 50% silking and plant height in both nitrogen rates and the combined analysis in both methods of analysis. Also, it gave significant positive ($\hat{g}_i$) effects for 100-kernel weight, ear weight/plant and grain yield/plant at the low rate of nitrogen in method-2. On the other hand, it gave significant positive ($\hat{g}_i$) effects for ear diameter, number of rows/ear, grain yield/plant and shilling% in both rates of nitrogen and the combined analysis and ear weight/plant in low nitrogen rate and the combined analysis in method-4. Meanwhile, it was around the average of the other cases.

The parental inbred line no. 7 seemed to be the best combiner for; plant and ear heights, no. of rows/ ear in both nitrogen rates and the combined analysis in both methods of analysis, shelling % and grain yield/plant at high rate nitrogen and no. of kernels/row at both nitrogen rates and the combied analysis in method-2, and shelling % in high nitrogen rates as well as the combined analysis in method-4. On the other hand, it expressed either significant desirable or insignificant ($\hat{g}_i$) effects for other cases.

The parental inbred line no. 8 showed significant positive ($\hat{g}_i$) effects for; ear diameter at high rate of nitrogen and the combined analysis, no. of rows/ear at low nitrogen rate and 100-kernel and shelling% at high rate of nitrogen by the method-2. Meanwhile, ear diameter and ear weight/plant at both rates of nitrogen and the combined analysis, 100-kernel weight and shelling% at high rate of nitrogen and grain yield/ plant at high nitrogen rate and the combined analysis gave significant positive ($\hat{g}_i$) effects in method -4.

The parental inbred line no. 9 behaved as the best combiner for plant and ear heights and no. of rows/ear at low rate of nitrogen in method-2. Also, it gave significant desirable

($\hat{g}_i$) effects for ear height at low nitrogen rate in method-4. Meanwhile, it was around the average of the other cases.

It is worth noting that the inbred line which possessed high ($\hat{g}_i$) effects for grain yield per plant showed the desirable effect for one or more of the traits contributing to grain yield.

The same trend in both methods of analysis was obtained for ($\hat{g}_i$) effects for most studied traits.

In most traits, the values of ($\hat{g}_i$) effects mostly differed from nitrogen rate to another. This finding coincided with that reached above where significant GCA by rate of nitrogen mean squares were detected **Table (21 and 22)**.

From the previous result, it could be concluded that the parental inbred lines P_4 seemed to be the best general combiner for grain yield/plant and some of its components in the combined analysis of both nitrogen rates in both methods of analysis.

Specific combining ability effects ($\hat{S}_{ij}$):

Specific combining ability of the parental combinations were estimated for only when significant mean squares were obtained in both nitrogen rates as well as the combined analysis by two methods: Griffing's method-2 and method-4 **(Tables 27 and 28)**.

As for days to 50% tasseling; two, seven and three crosses in method-4, and eleven, sixteen and thirteen crosses in method-2 exhibited significantly negative $\hat{S}_{ij}$ effects in low and high rate of nitrogen as well as the combined analysis, respectively. Results indicated that the crosses P_1xP_8 and P_2xP_3 in both methods of analysis and P_2xP_6, P_3xP_7, P_5xP_9, P_6xP_7 and P_8xP_9 only in method-2 had the best desirable $\hat{S}_{ij}$ values, in both nitrogen rates as well as the combined analysis.

With regard to days to 50% sillking; nine, five and four crosses in method 4, and fifteen, fourteen and thirteen crosses in method-2 expressed significant negative $\hat{S}_{ij}$ effects in low, high nitrogen fertilization as well as the combined analysis, respectively. The other crosses had either significant positive or insignificant $\hat{S}_{ij}$ effects. Also, results indicated that the crosses P_2xP_6 and P_3xP_7 in both methods of analysis and P_5xP_7, P_5xP_9, P_6xP_7, P_6xP_9, and P_8xP_9 in method 2 exhibited the highest desirable $\hat{S}_{ij}$ effects in both nitrogen rates and the combined analysis.

For plant height; four, six and three crosses in method-4 expressed significantly negative $\hat{S}_{ij}$ effects at low, high nitrogen rates as well as the combined analysis, respectively. Meanwhile, none of the hybrids showed significant negative $\hat{S}_{ij}$ effects in method-2 in both nitrogen rates and the combined analysis. The crosses P_3xP_9, P_4xP_7, and P_5xP_6 gave the best $\hat{S}_{ij}$ effects for short plants at both nitrogen rate as well as the combined analysis in method-4. The other crosses gave significant positive or insignificant $\hat{S}_{ij}$ effects.

For ear height; four, four and one crosses in method-4, two, tow and zero crosses in method-2 expressed significantly negative $\hat{S}_{ij}$ effects at low, high rates of nitrogen and the combined analysis, respectively. However, five, five and zero crosses in method -4 and twelve and twelve and eleven crosses in method-2 gave significant positive $\hat{S}_{ij}$ effects in low, high nitrogen rates and the combined analysis, respectively.

For ear length, three, four and two crosses in method-4, fourteen, twelve and seventeen crosses in method-2 exhibited significant positive $\hat{S}_{ij}$ effects at low, high rates of nitrogen and the combined analysis, respectively. The cross P_3xP_6 and P_2xP_6 had the highest positive $\hat{S}_{ij}$ effects in both methods of analysis in low, high nitrogen rates and the combined analysis.

As for ear diameter; three, zero and zero crosses in method-4, eighteen, twelve and fourteen crosses in method-2 expressed significant positive $\hat{S}_{ij}$ effects at low, high nitrogen fertilization as well as the combined analysis, respectively. The crosses P_2xP_6, P_3xP_6, $P_6xP_8$and P_8xP_9 had the highest positive $\hat{S}_{ij}$ effects in both nitrogen rates and the combined analysis in method-2.

Regarding number of rows/ear; six, three and four crosses in method-4, thirteen, eight and ten crosses in method-2, expressed significant positive $\hat{S}_{ij}$ effects at low, high nitrogen rates as well as the combined analysis, respectively. The crosses P_2xP_4, P_2xP_6 and P_7xP_9 gave the highest desirable $\hat{S}_{ij}$ effects in both methods of analysis for this trait.

With regard to number of kernels/row; four crosses in high nitrogen rate and two crosses in the combined analysis expressed significant positive $\hat{S}_{ij}$ effects in method-4. While, fourteen, thirteen and fourteen crosses in method-2 expressed significant positive $\hat{S}_{ij}$ effects at low, high nitrogen rates as well as the combined analysis, respectively. The other crosses had either significant negative or insignificant $\hat{S}_{ij}$ effects. The results indicated that crosses P_4xP_5 recorded the highest desirable $\hat{S}_{ij}$ effects in both methods of analysis.

As for 100-kernel weight, five, three, and two crosses in method4, and eleven, nine and ten crosses in method-2 expressed significant positive $\hat{S}_{ij}$ effects at low, high nitrogen rates and the combined analysis, respectively. The other hybrids had either insignificant or significant negative $\hat{S}_{ij}$ effects. The two crosses P_1xP_7 and P_3xP_4 had the highest positive $\hat{S}_{ij}$ effects in both methods of analysis.

Regarding ear weight/ plant; twenty five, seventeen and twenty four crosses in method-2, eight, twelve and eight hybrids in method-4 exhibited significant positive $\hat{S}_{ij}$ effects at low, high nitrogen rates as well as the combined analysis, respectively. The other hybrids had either significant negative or insignificant $\hat{S}_{ij}$ effects. The crosses P_3xP_4, P_2xP_6, P_1xP_6, P_1xP_9 and P_8xP_9 gave the highest desirable $\hat{S}_{ij}$ effects in both methods of analysis.

With regard to grain yield/plant, twenty four, twenty six and twenty three crosses in method -2, seven, eleven and eight hybrids in the method-4, expressed significant positive $\hat{S}_{ij}$ effects at low, high nitrogen rates and the combined analysis, respectively. The crosses P_3xP_4, P_8xP_9, P_1xP_6, P_7xP_9, P_1xP_9, and P_3xP_8 had the highest significant desirable $\hat{S}_{ij}$ effects at both nitrogen rates as well as the combined analysis, in both methods of analysis. It could be concluded that the previous crosses seemed to be the best combinations.

For shelling percentage, six, two and one crosses in the method-2 in low, high nitrogen rates and the combined analysis, respectively and four and zero crosses in low and the combined analysis in method-4, exhibited significant positive $\hat{S}_{ij}$ effects .

In most traits, the values of SCA effects were mostly differed from nitrogen rate to another. This finding coincided with that reached before for SCA by nitrogen rates mean squares **Tables (21 and 22).**

It is worth noting that the most considerable specific combing ability effects were generally detected from combinations involving parental inbred lines that are very diverse in PCR, origin and widely differed in their mean performance.

If cross showing high specific combining ability involve only one good combiner such combinations would throw out desirable transgressive segregates providing that the additive genetic system present in the good combiner and complementary and epistatic effects present in the crosses act in the same direction to reduce undesirable plant characteristics and maximize the character in view. Therefore, the most previous crosses might be prime importance in breeding program for traditional breeding procedures.

2-2-3- The half diallel cross (Method of Jones, 1965):

The data obtained herein were subjected to the analysis of variance of diallel table as contrasted with **Hayman (1954a)** and modified by **Jones (1965)** to fit the half diallel, to test additive and dominance variation for the traits under study in both nitrogen rates and the combined analysis **(Table29**). The (a) component which primarily testes the significant of additive effects were significant in all traits in both nitrogen rates and the combined analysis. Significant of the component (b) which indicates the presence of non-additive effects at some of loci controlling the trait under study, was detected for all traits in both nitrogen rates as well as the combined analysis. This finding coincided with that already reached from the combining ability analysis (Griffing method-2 and method-4). The ratio of (a)/(b) was coincided with that obtained from GCA/SCA from Griffing method-2.

The sum of squares for non-additively (b) can be further sub divided into (b1), (b2) and (b3). The (b1) component testes the mean deviation of the F_1's from their mid parental values, it will only reach the significant level of probability of the dominance deviation of the genes that are prdominantely in one direction. The (b1) values were significant for all traits in both nitrogen rates and the combined analysis. These results coincided with those already reached for the corresponding parent *vs* crosses mean squares **(Table 22).**

The significant (b2) values were obtained for all traits in both nitrogen rates as well as combined analysis, except days to 50% tasseling, ear height and 100-kernel weight in low rate of nitrogen. Therefore, asummetry of gene frequencies for those traits having significant dominance might be indicated. Significant (b3) were detected for all traits in both nitrogen rates and the combined analysis except ear diameter in high rate of nitrogen and the combined analysis, number of kernels/ row and shelling percentage at low and high nitrogen rate, respectively. This indicated the existence of inconsistent allelic and or non allelic interaction for such traits **(Kersey, 1965).**

Generally, these results suggested the importance of both additive and non-additive genetic variance for these traits. The results obtained for additive, non additive and additive/ non additive confirmed the previous results which obtained from the previous methods (Griffing method 2 and 4).

The mean squares of interaction between nitrogen rates and both types of additive (a) and non-additive (b) were significant for days to 50% silking and tasseling and ear height. Such results showed that the magnitude of additive and non-additive types of gene action changed from nitrogen rate to another.

As for plant height, 100-kernel weight and shelling percentage, the mean squares of interaction between nitrogen rate and (a) component were significant. However, insignificant (b) component by nitrogen rates mean squares were detected. Such results indicated that additive and additive by additive were more changed by nitrogen rates than non-additive genetic effects.

As for ear length, ear weight/ plant and grain yield/ plant insignificant mean squares of interaction between nitrogen rates and (a) component along with significant (b) component with nitrogen rates were detected. Such result indicated that non-additive effects were more influenced with nitrogen rates than additive genetic one. On the other hand, insignificant mean squares of interaction between nitrogen rates and both (a) and (b) components were obtained for other traits, revealing that all types of gene action did not appreciably fluctuate in magnitude from nitrogen rate to another. These findings coincided with that already reached from the combing ability analysis (Griffing method-2 and M-4).

For days to 50% tassrling and silking, plant height, ear weight/ plant and grain yield/ plant where, significant mean squares of interaction between (b1) component and nitrogen rate were detected, indicating that mean deviation of the F_1's from their mid parental values was changed from nitrogen rate to another. However the other traits showed insignificant interaction mean squares between nitrogen rates and (b1), indicating that this component was stable from nitrogen rate to another.

Insignificant mean squares of interaction between (b2) and nitrogen rates were detected for all traits except, days to 50% silking, plant height and ear length and shelling%, revealing that (b2) component was stable from nitrogen rate to another.

Insignificant mean squares of interaction between (b3) and nitrogen rates were detected for all traits except days to 50% tasseling and silking, ear height, ear weight/ plant and grain yield/ plant, indicating that (b3) components did not differed from nitrogen rate to another.

2-2-4- Hayman,s method (1954b):

The half diallel analysis provides us with six genetic statistical parameters; these components are D, H1, H2, F, h2 and E **(Table 30)**. Also, several ratios could be derived from the diallel parameters as given by **Hayman (1954b)** and **Jinks (1954)** to provide futher information about each trait; these estimates were $(H1/D)^{0.5}$, H2/4H1, Kd/KR and heritability in narrow sense.

With the exception of ear height, 100-kernel weight and ear weight/plant in both nitrogen rates, dayes to 50% tasseling, number of kernels/row and grain yield/ plant in low rate of nitrogen, the additive component (D) reached the significant level of probability for all traits. For the exceptional cases, insignificant (D) value inspite of a highly significant GCA and / or (a) were obtained. Dominance may has a role in both items (GCA and as emphasized by **Jinks (1955)**. Also; (a) component as it is well known could be considered as a measure for only additive variation if dominance is absent **(Mather and Jinks, 1971)**. In addition, the computed t^2 was highly significant and of a larger magnitude for most traits **(Table 30)**. Moreover, the regression coefficients of the parental off spring covariance (wr) on the parental array variance (vr) were found in these traits to be less than unity, revealing the presence of complementary type of epistasis. Generally the decrease of (wr) disproporionally more than (vr) leading to an inflation in the relative magnitude of dominance to additive components **(Hayman, 1954b; Hayman and Mather 1955, and Mather and Jinks 1971)**. Therefore contradiction in magnitude detected herein beteewn (D) and both

GCA and (a) estimates for both traits could be attributed to the great role of both allelic and non-allelic interaction genetic types on the expression of these cases.

Highly significant values and larger in magnitude for the dominance component (H1) were obtained for all traits in both nitrogen rates. These results indicate that the largest part of the total genetic variability associated with all traits was a result of dominance type of gene action. Where the H1/D ratio was largely less than unity for all the studied traits (Table 30).

The dominance type of gene action was previously reported to be the most prevalent genetic type; for most traits under study **Nawar *et al.* (2002), Saleem *et al.* (2002), Abou-Deif (2003), Amer (2003), Barati *et al.* (2003) and Saleem *et al.* (2010).**

The overall dominance effects of heterozygous loci symbolized as (h2) were computed for all traits in both nitrogen rates **(Table 30)**. Significant (h2) values were detected for all the studied traits, indicating that dominance was unidirectional. This finding confirms the results showen above by parent vs crosses and (b1) items illustrated in **Tables (22 and 29)**. Heterotic effects was previously reported by **Sablijarevic (1997), El-Zeir (1998), Nawar *et al.* (1998), Abdel-sattar *et al.* (1999), Abd El-Azeem (2000), El-Bagoury *et al.* (2004), Nawar *et al.* (2002), and El-Hosary *et al.* (2006).**

The relative size of (D) and H1 was estimated as a weighted measure of the average degree of dominance at each locus. The result showed the presence of over dominance for all the studied traits. These results were previously reported by

Nawar *et al.* (2002), Saleem *et al.* (2002), Abou-Deif (2003), Amer (2003), Barati *et al.* (2003), Kalıtımı *et al.* (2006), Balc and Turgut (2007), Choukan *et al.* (2008), Irshad-ul-Haq *et al.* (2009) and Saleem *et al.* (2010).

The average frequency of negative *vs* positive alleles in parental population was detected by (H2/4H1). Values which largely deviate from one quarter were obtained for number of rows/ear and shelling percentage in both nitrogen rates and number of kernels/ row at high nitrogen rate, revealing that negative and positive alleles were unequally distributed among the parents for these traits. On the other hand, values of (H2/4H1) were nearly one quarter for other traits, reveling that negative and positive alleles were equally distributed among the parent. The symmetry vs. asymmetry in gene frequence was also examined by estimating the (F) component. Significantly positive (F) values were detected for number of rows/ear and shelling percentage in both nitrogen rates and number of kernels/ row and grain yield/ plant at high nitrogen rate, indicating asymmetry with dominant alleles being more frequent. Insignificant (F) values were detected for other cases, indicating that dominance and recessive alleles of loci exhibiting dominance were equally distributed among the parents. The same conclusion could be draw from the corresponding proportion $(4DH1)^{0.5} + F)/ (4DH1)^{0.5} - F)$.

Low heritability values were detected for all the studied traits in both nitrogen rates **(Table 30)**. This result indicate that the bulk method could be more efficient for obtaining desirable improvement

2-2-5-Graphical analysis

The data obtained herein were also subjected to genetic analysis by means of diallel cross graphs as contrasted by **Jinks (1954)**. According to this analysis, the parabola marks limits within which the variance-covariance points (Wr, Vr) should lie. If the regression coefficient (b) of (Wr, Vr) is not different from unity, the genetic system can be deduced to be additive without the complication of nonallelic interaction. Complementarey type of epistasis generally decreases the covariance disproportionally more than the variance causing the slope of the regression line to be less than unity. If dominance is complete, the regression line would pass through the origin. Over dominance causes the regression line to intersect the (Wr) axis below the origin, while partial dominances causes the regression line to intersect the (Wr) axis above the origin. The closness of the regression line of (Wr, Vr) points to the limiting parabola indicates little dominance. The position of the array points along the regression line depends on the relative proportion of dominant and recessive alleles present in the common parent of each array. Parents with preponderance of dominat alleles will have a low array variance and covariance and will lie near the origin. Highly recessive parents will have a large array variance and covariance and lie at the opposite end of the regression line. If the dominance effects of the genes are unequal, the position of an array point will be weighed in favour of genes with large dominance effect.

The regression of parent-offspring covariance (Wr) on parental array variances (Vr) and their limiting parabola of the nine parental inbred lines for all the studied traits are illustrated in **Fig 11-34**. Significant regression were obtained in all traits (in both nitrogen rates) and the slope of the regression lines significantly from unity. This result might revealed that complementary type of epistasis was involved. The regression lines were intercept the (Wr) axis below the origin, suggesting over dominance. This finding was coincide with obtained above by $(H1/D)^{0.5}$ **Table (30).**

The array points scattered along the regression line for all traits in both nitrogen rates in spite of the significant (Wr+Vr) array differences, corroborating with the results obtained herein for degree of dominance (over dominane) presented in **Table (30)**. The correlation coefficient between parental mean (Yr) and (wr+vr) for each array were significant positive values for dayes to 50% silking at both nitrogen rates, days to 50% tasselling in high rate of nitrogen and insignificant and high positive value in low nitrogen rate, indicating that decreases genes (earliness) were dominat over increases (Table 30). This indicates that earliness was dominate over lateness. The parental inbred line no 1 appeared to possess the largest number of dominate genes responsible for the expression of both traits, while, inbred line no. 2 seemed to contain most of the recessive ones in tasseling date in both nitrogen rates and silking date at high nitrogen rate. While, the P_7 contained most of the recessive one in low nitrogen rate for silking date. For the other traits, significant negative correlation estimates were obtained, revealing that increase of these traits appeared to be dominated.

For plant height, P_5 and P_9 contained the most dominant genes responsible for the expression of this trait in both nitrogen rates respectively. Meanwhile, P_9 and P_6 seemed to be carrying the most recessive ones in the same order. **(Fig, 15 and 16)**. For ear height, the parental inbred lines P_2 and P_5 in low nitrogen rate and P_9 in high nitrogen rate seemed to carry most of the dominant genes responsible for this trait. However, inbred lines P_1, P_4 and P_3 in both nitrogen rates possessed more recessive genes. **(Fig.s 17 and 18).**

The parental inbred lines P_1, P_3, P_7 and P_9 seemed to contain the largest number of dominant genes responsible for the expression in both nitrogen rates for ear length, ear diameter, no. of rows/ ear, number of kernels/ row and 100- kernel weight, respectively**. (Figs 19, 20, 21, 22, 23, 24, 25, 26, 27 and 28).** On the other side, P_6 and P_8 for ear length, P_6 and P_2 for ear diameter, P_2 for no. of rows/ear, P_5, P_4 and P_8 for number of kernels/ row and P_4 for 100-kernel weight.

The parental inbred lines P_1 and P_7 for ear weight and grain yield contained the most dominant genes responsible for the expression of both traits. Meanwhile, both inbred lines P_3 and P_8 seemed to carry the most recessive ones in both nitrogen rates.

For shelling% the parental inbred lines P_1 and P_4 in low nitrogen rate and P_7 and P_9 in high nitrogen rate contained the most dominant genes. However, P_5 and P_7 in low and P_3 and P_2 in high nitrogen rates, seemed to contain the most recessive genes.

2-2-6- Analysis of genetic-environmental interactions:

Stability of the genetic system under both nitrogen rates was investigated following the method proposed by **Allard (1956).** This method permits determination of the stability of three kinds of parameters, namely, additive effects (d), dominance effects (h), and epistatic effects (i). It is assumed that all of the basic diallel cross assumptions are valied except that of no epistasis. When epistasis occurs, the method is presumably capable of detecting it and assessing its stability in different environments.

Heritable differences between the homozygous parents, in the absence of nonallelic interaction, must result from the additive effects of gene (D). Hence, parental lines differing significantly from each other must carry genes with differing additive effects. Furthermore, constancy of the additive components of variation can be detected unambiguously by the parents x environments interaction item of an analysis of variance of parents. Significance provide evidence that they interact with environment and non significance is suggestive of the constancy of additive effects under different environmental conditions. When non allelic interactions are a feature of the genetic system, the situation is unambiguous if the parents x environments item is non significant. If this item is significant, however, the conclusions cannot be clear-cut without evidence from analysis of the variances (vr) and covariance's (Wr) of the arrays of the diallel table because the significance could result from inconsistency of the additive effects, from inconsistency of the interactions between homozygous genes under the different environmental circumstances or from both causes. The form of the analysis and the results for each variable are exactly similar to those illustrated before in **Table (22).**

For all traits, epistasis was already reported to be involved. For plant height, ear length and shelling% mean squares of parents and parent by nitrogen rate were found to be significant. Therefore it could be concluded that parental inbred lines differed in additive and additive x additive effects and/ or the interactions between homozygous genes were inconstant from fertilizer rate to another. The parental inbred line P_9, P_3 and P_7 for plant height, ear length and shelling%, respectively seemed to be the most unstable one in additive and additive by additive effects. P_5 and P_6 for plant height, P_8 and P_9 for ear length and P_4 for shelling %, on the contrarily, were the most stable in this respect. However, insignificant parent and parents x nitrogen rates mean squares were detected for 100-kernel weight and ear weight, revealing that parental inbred lines carried genes with the same of additive effects which seemed to be constant from rate of nitrogen to another.

On the other hand, the other traits significant mean squares associated with parents along with insignificant mean squares associated with parents by nitrogen rates mean squares were detected. This finding revealed that parental inbred lines carried genes with different additive and additive by additive effects which seemed to be constant from nitrogen rate to another.

To test the constancy of dominance and/ or additive x dominance and dominance x dominance effects an analysis of variance was performed on the 54 (vr) and 54 (wr) estimates for each trait from the nine arrays, three replications and two nitrogen rates at which the F_1 was studied. Individual (vr) and (Wr) terms within each replication were divided by the variance among the parents in that replication before analysis to minimize the additive components in the test and, in doing so, to increase the test's sensitivity. This rescaling also tends to minimize the fluctuation of basis variability between environments which is likely to mask between-environment comparisons in genetic systems. The form of analysis and the results for each trait are listed in **table (31).**

Fertilizers components of variation was calculated from the differences between the sums of (wr+vr) over all arrays and blocks for each nitrogen rate. In the absence of epistasis, it detects variation in (wr + vr), i.e. (D+H1 + F)/D over nitrogen rates after rescaling. Significance of this components of variation in such case can result from a change in mean dominance (H1) and or the relative proportion of dominat and recesive genetic effects (F), assuming that rescaling has aliminated inter-environmental differences in the additive effects of genes. In the presence of epistasis, this component of variation is influenced not only by changes in dominance but changes in nonallelic interactions. Non significance of this item can be taken as evidence that (H1), (F), and nonallelic interactions are stable and the rescaling was effective. Significance indicates that one or more of these postulates is incorrect.

Significant nitrogen rates (N) mean squares were detected for dayes to 50% tasseling, ear diameter, no. of kernels/ row and

100-kernel weight, revealing that one or more of (H1), F and I was changeable from nitrogen rate to another. However, for the other traits, insignificant nitrogen rates mean squares were detected, revealing that (H1), F and nonallilic interaction, are stable or the single points representing each nitrogen rate occupied the same position on the (Wr, Vr) graph **(Figs.: 11-34).**

The results obtained for this item agree to the same extent with those of SCA by nitrogen rates mean squares presented in **table (22).**

The dominance components of variation was calculated from the difference between the sum of (wr) and the sum of (vr) overall nitrogen rates, blocks and arrays. From diallel theory it is clear that the magnitude of this difference is only governed by the degree of dominance when epistasis is absent, the differences (wr-vr) providing a measure of (D-H1). The dominance component of variation can therefore be expected to be significant except when mean dominance is complete, at which point (wr) = (vr), and (D) = (H1). The dominance component of variation in the presence of epistasis is no longer concerned exclusively with mean dominance but is also influenced by nonallelic interactions.

For all traits, the dominance mean squares were significant. Therefore, on the scale of measurement used the average degree of dominance apparently not complete or epistasis was involved. This is consistent with previous evidence for average over dominance in these traits **(Table 30 and Figs 11-33).**

These results completely confirm that reached herein for SCA mean squares in the combined analysis presented in **Table (22).**

The dominance by nitrogen rates interaction item testes the consistency of mean dominance and or epistatic effects at both nitrogen rates. Significant mean squares associated with this item was found for days to 50% tasseling, number of kernels/row and 100-kernel weight, suggesting instability of dominance and/ or epistatic effects over both nitrogen rates for these traits.

The arrays mean squares was estimated from the sums of (wr+vr) for each array; taken over all blocks and nitrogen rates. It testes variation in (wr+vr) from one array to the next. The higher the level of dominance in a parent, the smaller will be its (wr+vr) value and vice versa. Thus (wr+vr) is an indicator of the average level of proportion of dominant and recessive alleles that are present in a particular parent. The (Wr+vr) value of a parent determines its rank along the regression line of the (vr, wr) graph. If epistatic effects are present, they too, will contribute to the apparent level of dominance in the different parents.

Significant of the array mean squares were detected for all traits except; days to 50% tasseling and sillking, ear length and shelling percentage. This result might revealed that the parental inbred lines exhibited different levels of dominance and/or possible different epistatic effects.

The mean squares for arrayes by nitrogen rates interaction tests the constancy of the average level of dominance and /or epistatic effects for each parent over the two nitrogen rates.

Insignificant variance of array x nitrogen were obtained for all traits, indicating that the posiontion of the parental arrays on the graphs were constant in different nitrogen rates.

The dominance x arrays component of variations is independent of fluctuation in the additive and dominance effects of genes with classical types of interaction systems. Since difference in (wr+vr) for array can occur only if $i \neq 0$ in such systems, significant of the dominance x arrays component provides evidence that epistatic is a feature of the genetic system. Significance of this item was obtained for all traits except dayes to 50% tasseling and silking and shelling percentage.

The insignificance of the dominance x arrays x nitrogen rates components of variation were detected in all traits except plant height revealing that the expression of this nonallelic interaction was the same in both nitrogen rates.

2-3-Comparison between methods of analysis:

2-3-1-Comparison between combining ability effects (M2 and M4 of Griffing)

The values of correlation coefficients between both Griffing's methods of analysis method-2 and method-4 for ($\hat{g}_i$) and ($\hat{S}_{ij}$) effects are presented in **table (32).**

The correlation coefficient between ($\hat{g}_i$) and ($\hat{S}_{ij}$) effects in two methods (Griffing's method-2 and 4) was significant for all traits, revealing a strong relation between the two Griffing methods in estimating ($\hat{g}_i$) and ($\hat{S}_{ij}$) effects. This finding conferms the results already shown by ($\hat{g}_i$) effects and ($\hat{S}_{ij}$) effects **(Tables 25:28).**

2-3-2-Relative efficiency of the four methods Griffing M2 and M-4, Jones 1965 and Hayman1954)

2-3-2-1-Additive

The relative efficiency of the four methods is presented in **table (33)**. The efficiency was computed based on F. test between these methods for additive, non- additive and their interaction as well as error mean squares. The F. test between the methods used in this study revealed that Griffing's method-2 and 4 and method of Jones reached similar results.

For additive gene effects, insignificant F-test was detected between all methods used in this concern for all traits, except days to 50% tasseling, days to 50% silking and shelling % in low nitrogen rate, plant height, ear height and 100 kernel weight in both nitrogen rates where method of **Hayman (1954b)** was cleared from other methods, 100-kernel weight in the combined analysis where method of **Hayman (1954b)** was changed from Griffing method-4. Also, shelling percentage in the combined analysis where **Hayman (1954b)** was differed from both methods of Griffing's method 2 and **Jones 1965**. For the exceptional cases, the F. ratio was significant between Hayman,s and other methods. Dominance has a role in GCA and (a) estimates as emphasized by **Jinks (1955)**. Moreover the computed t^2 and the regression coefficients of the parental offspring covariance (Wr) on the parental array variance (Vr) were found to be high large in both traits, revealing the presence of complementary type epistasis. Generally, decreases (Wr) disproportionally more than (Vr) leading to an inflation in the relative magnitude of dominance to additive components **(Hayman, 1954 b, Hayman and Mather, 1955 and Mather and Jinks 1971).**

The correlation coefficient of additive effects in four methods for all traits used in this study **(Table 34)** was highly significant between the four methods i.e. Griffing's method-2 and 4, **Jones 1965** and **Hayman 1954b**, indicating strength relation between the four diallel methods in the estimation of additive components.

The efficiency of the four diallel methods of analysis for additive x nitrogen interaction based on F. test presented in **Table (33).** Insignificant F. test was obtained between the four methods (Griffing's method-2 and4, **Jones 1965 and Allared 1956** used in this study for all traits except ear length and shelling percentage, where method of **Allared (1956)** was differed from the other methods, no. of rows/ ear and no. of kernels/ row where method of **Allard 1956** was changed from each Griffing method-2 and **Jones 1965**, and plant height, ear diameter and 100-kernel weight where the method of **Allared 1956** significantly differed than Griffing method-4. When insignificant additive x nitrogen rates interaction was obtained, indicating that these methods was similar.

The correlation coefficient of additive x nitrogen interaction for all traits is presented in **table (34)**. Significant correlation values between the four methods except between Griffing method 4 and **Allard 1956** was obtained between Griffing's method-2 and 4, Jones 1965 and **Allard 1956**. This result indicates strong relation between the four methods of diallel cross in estimating additive x nitrogen interaction.

2-3-2-2-Non additive

The efficiency of the four diallel methods of analysis for non additive gene effects based on F-test are presented in Table (33).

For comparison between the four methods (i.e G2/G4, G2/H, G4/J, G4/ Hayman and J/ Hayman), the results indicated that significant F. test was detected for all traits in both nitrogen rates as well as the combined analysis except Griffing Method 2 and **Jones 1965** in all traits in both nitrogen rates as well as the combined analysis, where M-2 did not differ than **Jones 1965**. Also, insignificant F. test was obtained between **Hayman 1954** and each of Griffing M-2 and **Jones 1965** for 100-kernel weight in the combined analysis, indicating that method of **Hayman**

1954 and each of Griffing M-2 and **Jones 1965** was similar in the combined analysis for 100-Kernel weight. The contradiction between the four methods of analysis for estimating non-additive effects may be due to use of parental inbred lines in method-2 of Griffing, Jones and Hayman, however the hybrids only used for analysis of Grigffing method-4. Also, the G/E of Hayman methods used Wr/Vr of parents. Moreover, the computed t^2 and the regression coefficient of the parental offspring covariance (Wr) on the parental array variance (Vr) were found to be significant in all traits, revealing the presence of complementary type of epistasis. Generally, decreases (Wr) disproportionally more than (Vr) leading, to inflation in the relative magnitude of dominance to additive components **(Hayman 1954b, Hayman and Mather, 1955 and Mather and Jinks 1971).**

Similar results were reached by **Dawood et al. (1994)** in corn, compared the relative efficiency of two Griffing diallel cross methods, i.e. method-2 and method-4. The results showed that the two methods of diallel cross draw approximately the same picture of gene action in the inbred lines under study, where they indicated that majority of σ^2 SCA than σ^2GCA especially for yield.

Consequently, when costs, efforts and time needed for conduct the experiments and to analysis the collect data will be taken into consideration, the perferability will be for method-4. In this respect, **Nawar (1985**) compared between seven analysis of diallell crosses in maize included the two Griffing’s method-2 and 4, Model II; the modified diallel crosses **(Matzinger and Kempthorne method (1956)**, **Gardner,s method 1967;** the half diallel cross **Jones (1965)**, the diallel method (by **Aksel and Johnson, 1959**); the regression method (wr/vr) method of **Jinks 1954 and Hayman 1954 a and b**. He showed that the genetic analysis which were carried out by different methods of analysis of diallel crosses in general, gave a similar picture with respect to gene action. Also, in case of grain yield per plant and silking date, the additive and dominance genetic effects were important in the expression of these traits. Moreover, the two half diallel methods, Gardner,s method, regression method analysis (wr/vr) and **Matzinger-Kempthorne method (1954)** may be more informative than the two Griffing's methods; however, they are more complicated since a high seed computer facilities are needed to do the calculations.

Griffing (1956) stated that the diallel crossing systems in which the parents are not included are generally the most useful in plant and animal fields. However, other system may be used in special situations.

The correlation coefficient of non-addiitive effects drived from four methods of diallel analysis over all traits in both nitrogen rates as well as the combined analysis were highly significant **(Table 34)**, indicating the strong relation between the four diallel methods in estimating non-additive genetic variance.

The efficiency of the four diallel methods of analysis for non-additive x nitrogen interaction based on F. test was obtained between the four methods (Griffing m-2, m-4, Jones and Allard) used in this study for all traits except days to 50% tasseling and silking, plant height, ear height, ear diameter, on. of rows/ear, no. of kernels/row, ear weight/plant, grain yield/plant and shelling%, where method of Allared was differed from the other methods i.e. Griffing m-4, m-2 and Jones. This result indicate that the three methods of analysis (Griffing method-2 and -4 and Jones reached similar results.

The correlation coefficient of non-additivex nitrogen interaction SCAxN/SCA for all traits is present in **Table (34).**

Significant correlation values of non-additive x nitrogen and SCAxN/SCA between the four methods were obtained for Griffing's method-2 and 4 and Jones, revealing that the closely relatiou between these methods of diallel crosses analysis in estimating non- additive x nitrogen and SCAxN/SCA ratio. **(Table 34).**

Insignificant correlation coefficients between Allaerd and each of three other methods for non-additive xN and non-additivexN/non-additive revealed that there is no relationship between Allared approach and other methods.

2-3-2-3-Error

For error mean squares insignificant F. test was detected between Griffing's method-2 and 4 for all traits except days to 50% tasseling in the combined analysis and shelling percentage in high nitrogen rate and the combined analysis, revealing that both methods did not differ between them.

Also, insignificant F. test between Griffing method-2 and Jones 1965 for all traits was obtained, indicating that coincided both methods for estimating error mean squares.

Insignificant F. test was obtained for **Hayman 1954** and each of Griffing method2 and **Jones 1965** for all traits except dayes to 50% tasseling in high nitrogen rate and the combined analysis, silking date at low nitrogen rate and the combined analysis and plant height, ear height, ear length, ear diameter, no. of rows/ear, no. of kernels/ row, 100-kernel weight, ear weight/plant, grain yield/ plant and shelling% in the combined analysis, revealing that Allared method differed from both methods Griffing method-2 and Jones). This result may be the estimation of error of Allared was obtained after rescaling Wr and Vr.

For comparison between Griffing method 4 and Jones, Insignificant F. test was detected for all traits except days to 50% silking in low nitrogen rate and shelling % in high nitrogen rate and combined analysis, revealing that the strong relation between two methods for estimating of error variance.

As for comparison between Griffing method4 and Hayman insignificant F. test was detected for all cases except, days to 50% tasseling in high nitrogen rate and the combined analysis, days to 50% silking, plant and ear heights, ear length and diameter, no. of row/ear, no. of kernels/row, ear weight/ plant and grain yield/ plant where the two methods differed in these cases.

Also, the correlation coefficient values of error mean squares between the four methods for all traits were significant between these methods, revealing the strong relation between the four methods used in this study for estimation of error variance **(Table 34).**

3- Six population's analysis. (Experiment III).

Seven genetic parameters were studied under 120kgN/fed. only in the present study. These were: 1-parental differences, 2-Heterosis, 3- Potence ratio, 4- Inbreeding depression, 5- Gene action, 6- Genetic coefficient of variability and 7- Heritability and genetic advance under selection.

The F_1 seeds of three crosses i.e. P_1xP_5 (high diversity), P_1xP_9 (moderate diversity) and P_4xP_9 (low diversity) with their inbred lines were sown and the F_1 plants were backcrossed to both inbred lines to produce Bc_1 (F_1x P_1) and Bc_2 (F_1x P_2) for each cross. In addition the F_2 seeds were obtained by selfeing of F_1-plants. This experiment involved parents, F_1, F_2, Bc_1 and Bc_2 populations of each of the three crosses.

3-1-parental differences:

Number of plants, mean, variance, variance of mean and coefficient of variation of the traits studied in the three crosses for parents, F_1, F_2, Bc_1 and Bc_2 are presented in **Table (35). Table (36)** shows the test of significance of parental mean performance and the genetic variance among F_2 populations in each cross for all traits studied. The difference between the two parents were significant in each of the three crosses for all studied characters except 100-kernel weight in the three crosses, ear length in the second and third cross, days to 50% tasseling in the third cross and no. of rows/ear in the first cross. Significant genetic variance was detected for all traits in the three crosses and therefore, other genetical parameters were estimated. The existence of significant genetic variability inspit of the significant differences between the parental inbred lines, obtained herein in most traits, may suggest that the genes of like effects were not completely associated in the parents, i.e., these genes are dispersed **(Mather and Jinks, 1971).**

3-2-Heterosis

Table (37) shows the percentages of heterosis for all traits in the studied three crosses. The results obtained herin indicated highly significant negative heterotic effects for days to 50% tasselling and silking in the three crosses, reflecting the possibility of producing earlier hybrids of corn. Earliness, if it is found in corn is favourable for escaping destructive injuries caused by *Sesamia cretica led, Chilio sinplex* But, and *Pyrausta nubilalis Hb*.

Highly significant positive heterotic effects, meanwhile, were detected for all the other traits. As it well known, number of rows and no. of kernels per row, and 100-kernel weight are the main components for grain yield in corn. Hence heterotic increase, if it is found in one or more of the three traits, may lead to considerable yield increase in hybrids. It is worth noting that heterotic effect for grain yield was larger in magnitude than for any one of its components which is logically expected. Also, heterosis associated with number of rows per ear was smaller in magnitude than those associated with the other two components, revealing its minor effect on the expression of heterosis for grain yield. The significance of heterotic effects show that non-additive genetic type of gene action affects such traits. These results were previously reported by **El-Shouny *et al.* (2005) and Abou-Deif (2007).**

3-3-Nature and degree of dominance.

Potence ratio (P) was calculated to study the nature and degree of dominance for all characters studied **(Table 37)**. The results indicated that (P) values exceeded the unity in all cases. Over dominance towards the lower parent was detected for days to 50% tasselling and silking suggesting that earliness dominated lateness. Over dominance towards the higher parent was detected for all other trait under test. Generally, potence values followed the same trend as heterotic effects for all traits. These results are in agreement with those obtained by **Sedhom 1984, El-Shouny *et al.* (2005) and Abou-Deif (2007).**

3-4- Inbreeding depression:

Table (37) shows the percentages of inbreeding depression for all traits in the studied the three crosses. Inbreeding depression was significant negative for no. of days to 50% tasselling and silking in the three crosses. Meanwhile, significant positive inbreeding depression was detected for other cases except shelling percentage in the first cross. Both heterosis and inbreeding depression effects as it is well known are two coincides to a same particular phenomenon. Therefore, it is logically to expect that heterosis in F_1 will be accompanied by appreciable reduction in the F_2 performance and vice versa. Similar results were obtained by **Sedhom 1984, El-Shouny et al. (2005) and Abou-Deif (2007).**

Table (37) shows the epistatic devitions of F_2 (E1) and backcrosses (E2) for all the studed traits. The results indicated that significant F_2 deviation (E1) were obtained for all the studied traits except plant height, no. of rows/ear and grain yield/

plant in the third cross, and plant height, ear diameter and 100-kernel weight in the first cross.

Significant backcrosses deviation (E2) were obtained for all traits except 100-kernel weight in the three crosses, days to 50% tasseling and shelling percentage in the third and the first cross, respectively. It is worthnoting that F_2 deviation was mostly accompanied by backcross deviation of significance. Also, the presence of appreciable epistatic deviations along with the large heterotic effects and the existence of overdominance detected herein in most cases may reveal the great role of interallelic gene effects on the performance of these cases.

3-5-Nature of gene action

Nature of gene action was studied according to the relationships illustrated by **Gamble (1962)**. The estimated values for each of the six parameters with their test of significance in all traits studied are shown in **table (38)**. In all cases, the estimated mean effect parameters (m), which reflects the contribution due to the over-all mean plus the locus effects and interaction of the fixed loci, was highly significant.

The additive gene effects (a) were significant for no. of days to 50% silking, ear height, ear weight/plant, grain yield/ plant and shelling percentage in the three crosses, no. of days to 50% tasseling in the first and third cross, plant height and 100-kernel weight in the first and second cross, ear length and no. of rows /ear in the third cross and ear diameter in the first cross. These results are in agreement with those obtained by **Sedhom 1984, El-Shouny *et al.* (2005) and Abou-Deif (2007).**

The dominance gene effect (d) was highly significant for all traits in the three crosses except the shelling percentage in the third cross. Dominance effects were higher in magnitude than additive gene effect. The negative value of dominance demonstrates that the smaller mean value parent had the dominant genes responsible for these cases.

Additive x additive (aa) epistatic type of gene action was significant for all traits, except ear height and ear length in the first cross. Also, additive x dominance gene effects were significant for all traits except no. of rows/ear in the three crosses, days to 50% silking in the first and second cross, no. of kernels/row in the first and third cross, and ear length and shelling percentage in the second cross. Dominance x dominance gene effects were significant for all traits in the three crosses except shelling % in the third cross. The majority of dominance x dominance gene effects were of negative values for most traits. The absolute relative magnitudes of the epistatic gene effects to mean effects were somewhat variable depending on the cross and traits studied. Generally, the absolute magnitude of the epistatic effects were larger than mean effects and approach the dominance effects for most cases. Therefore, it could be concluded that epistatic effect was important as a major contributor in the performance of these cases. These results agree with the idea that the inheritance of a quantitative characters is generally more complex than single qualitative characters. The significant values of epistasis in the three crosses were accompanied by significant estimates for E1 and E2.

The non-additive gene effects appears to be of primer importance in the inheritance of most traits, the large magnitude of both dominance and epistatic effects revealed that both types contribute in the expression of heterosis in most traits. These results well agree with those reported by **Gamble (1962)** from crosses between some inbred lines. **Sentz (1971)** who reported that dominance effects tended to be more important, and **Fadhi (1978)** who stated that dominance gene effects had the first rank of gene action and (aa) type of epistasis had the second rank with regard to grain yield. On the other hand, some workers stated that both additive and dominance effects had similar magnitude **Sedhom 1984, El-Shouny *et al.* (2005) and Abou-Deif (2007).** Most investigators reported that additive effects tended to be more important in the inheritance of yield **(Gardner 1961, Hallauer 1971, El-Rouby and Galal 1972 and shehata and Dawan 1975).**

3-6- Genetic coefficient of variability.

Table (38) shows high genetic coefficient of variation for ear diameter, no. of kernels/row ear weight/plant, grain yield/plant and shelling percentage, in the three crosses. However, moderate values were obtained for plant height, ear height, no. of rows/ear and 100-kernel weight, in the three crosses. Days to 50% silking and tasseling in the three crosses, had low values of G.C.V.% .

Using the genetic coefficient of variation alone, however, it is impossible to estimate the magnitude of heritable variation. The heritable portion of the variation could be found out with the help of heritability estimates and genetic gain under selection **(Swarup and chaugale, 1962).**

3-7- Heritability and genetic advance.

Table (38) shows heritability percentages in broad and narrow sense and genetic advance for all traits in the three cross. All traits in high heritability value in broad sense were detected for the three crosses except 100-kernel weight. For the exceptional case, moderate heritability values were obtained in the three crosses. These results are in agreement with those obtained by **Sedhom 1984, El-Shouny et al. (2005) and Abou-Deif (2007).**

Heritability in narrow sense was computed according to Mather's procedure on the basis of F_2 and back crosses. High heritability in narrow sense was detected for ear diameter and shelling percentage in the three crosses, no. of rows/ear, days to 50% tasseling and silking in the first cross and ear weight and grain yield/plant in third cross. Moderate to low heritability values in narrow sense were detected for the other cases in the three crosses.

For days to 50% tassling and no. of rows/ear in the first cross and ear diameter in the second cross, heritability values in narrow sense were high in magnitude and nearly equal its corresponding value in broad sense. This revealed that the genetic variance was mostly attributed to the additive effects of genes for these cases. As previously reported, non additive gene effects were found to be the major contributing factor in these traits **(Table 37)**. On these assumptions, heritability in narrow sense was excepted to be low, the exception which was not relized in the present study. **Comstock (1955)**, stated that the presence of epistatic gene effects will cause an upward bias in the estimate of additive genetic variance. **Gamble (1962)** also reported that genetic model assuming negligiable epistasis may be an important source of bias in the estimate of additive genetic variance and inclusion of epistasis in such models would perhaps decrease the amount of additive one.

For other or remaing case in the three crosses narrow sense heritability values were much lower than those of broad sense indicating that most of genetic variance was due to non-additive effects i.e., dominance and/ or epistasis. This finding ascertained the previously studies on the nature of gene action where the non-additive gene effects were found to have a great role in these traits **(Table 37)**. Such results are in agreement with that obtained by several investigators, **Sedhom 1984, El-Shouny *et al.* (2005) and Abou-Deif (2007)** who obtained high to moderate heritability values for date of tasselling and silking, plant and ear height, ear length and ear diameter. **Warner (1952), El- Ebrashy (1961) and Fadhi (1978)** reported low values of heritability in narrow sense for grain yield per plant.

Genetic advance upon selection:

Table (39) shows the genetic advance upon selection as the percentage of F_2 for all the studied traits in the three crosses. With the exception of days to 50% tasseling and silking in the second and third cross and plant height in the second cross, the results indicated that the predicted genetic advance expressed as the percentage of the mean was moderate to high for all the studied traits. For the exceptional cases, low GA% was low **(Table 38). Johanson et al. (1955)** reported that heritability estimates along with genetic gain are usually more useful than the heritability values alone in predicting the resultant effect for selecting the best individuals. On the other hand, heritability is not always associated with high genetic advance, but to make effective selection, high heritability should be associated with high genetic gain. In the present work relative high genetic gain was found to be associated with rather moderate heritability estimates for plant height in the first and third cross, ear height, ear length and ear diameter in the three crosses and no. of rows/ ear in the first cross. Therefore, selection for these cases in these particular population should be effective and satisfactory for successful breeding purposes.

For ear and grain yield/ plant, high genetic gain was associated with low heritability values. In spite of the relative low heritability in narrow sense computed in both traits, estimates of additive and additive x additive genetic effects were highly significant therefore, it could be suggested that selection for these traits in subsequent generations will be relatively more effective than in the early F_2 generation. It could be concluded that the highest genetic advance detected for both traits, in spite of low heritability estimates, may be due to a relatively range of variability in these populations.

For number of kernels/row and 100-kernel weight moderate genetic advance was associated with low to moderate heritability values. In spite of the relative low or moderate heritability in narrow sense computed in both traits, estimates of additive genetic effects was highly significant. Therefore, it could be suggested that selection for both traits in subsequent generations will be relatively more effective than the early F_2 generation. Relatively low genetic gain was associated with low heritability values in no. of rows/ear and plant height in the second cross. Hence, selection for these cases may be less effective.

For days to 50% tasselling and sellking low genetic gain was accompanied by high or moderate heritability values. As it well known, expected improvement of selection is directly proportional to heritability. Also, the expected response to selection varies with the phenotypic standred deviation of population means. This figure is a measure of the total variability in the trait and therefore, reflect, the total response that could be realized by breeding techniques. It is possible to visualize a situation where the heritability is high, but because of little potential for improvement (low δ^2 ph) little response can be expected. On this basis this situation could be explained.