1.6. COMBINING ABILITY IN MAIZE (ZEA MAYS L.) UNDER TWO NITROGEN RATES AND GENETIC DISTANCE DETERMINED BY RAPD

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ABSTRACT

A half diallel cross between 9 inbred lines of maize (*Zea mays* L.) was evaluated under two different nitrogen rates for six quantitative characters in RCBD with three replications. Nitrogen rates, genotypes, parents and hybrids mean squares were significant for all traits under study except, mean squares for parental inbred lines for ear height at high nitrogen rate and 100-kernel weight at both nitrogen rates and in the combined analysis. Significant genotypes x nitrogen rates interaction mean squares were obtained for days to 50% tasseling, ear height and grain yield/ plant, revealing that the performance of genotypes were differed from rate of nitrogen to another.Significant interaction mean squares between hybrids and nitrogen rates were obtained for days to 50% tasseling, ear height and grain yield/ plant. General and specific combing ability mean squares were found to be significant for all traits. The magnitudes of the ratios of GCA/SCA revealed that the additive and additive x additive types of gene action were the most important expressions for days to 50% tasseling at low rate of nitrogen fertilization, ear height at both nitrogen rates as well as the combined analysis. No. of rows /ear at high nitrogen rate as well as the combined analysis showed GCA/SCA ratios was found to be high than unity. The mean squares of interaction between nitrogen rates and both types of combining ability were significant for days to 50% tasseling and ear height. The ratio for SCA x D/SCA was higher than ratio of GCA x D/GCA for ear height. The parental inbred line no. P4 seemed to be the best general combiner for grain yield/plant and some of its components in the combined analysis of both nitrogen rates. The parental inbred line no. 3 appeared to be one of the good combiner for; days to 50% tasseling. For grain yield/ plant, the crosses P_1xP_4, P_1xP_5, P_1xP_6, P_1xP_9, P_2xP_3, P_2xP_4, P_2xP_5, P_2xP_6, P_2xP_8, P_3xP_4, P_3xP_5, P_3xP_6, P_3xP_7, P_3xP_8, P_4xP_5, 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 had the highest values for both SCA. Also, the three hybrids P3xP4, P4xP5 and P_4xP_6 were out yielded significantly the check hybrid S.C. G. 155. The nine RAPD primers generated 397 scorable bands across 9 inbred lines. These primers produced a total of 66 reproducible fragments, from which 39 (٥٩.٠٩%) were polymorphic. The mean of polymorphic bands per primer was 4.3. The lowest genetic similarity (0.55) was detected between P_1 and P_5 also, obtained between P_8 and P_9. While, the highest genetic similarity was (0.90) scorded between the two parental inbred lines P_4 and P_9. Non considerable values for 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.

INTRODUCTION

Maize (*Zea mays* L.) is considered as the third cereal crop after wheat and rice all over the world for production and conuumption. In addition to its use asa human food, it is also utilized as a poultry and livestock feed and also as a fodder. The amount of heterosis expressed in F_1 hybrid is mainly affected by the genetic diversity (Griffing and Lindstrom 1954; Moll *et al.*, 1965 and Hallauer *et al.*, 1988). Previous studies have shown a positive relationship between genetic distance, as measured by geographical distance and F_1 grain yield and grain yield heterosis in maize. East (1936), Hayes and Johnson (1939) and Moll *et al.*, (1962) stated that heterosis in maize appeared to increase with genetic divergence of the parents. Genetic diversity can be obtained from pedigree and heterosis data, from morphological traits or using molecular marker which detect variation at the DNA sequence level (Smith and smith 1992). In particular, DNA-based polymorphism is a powerful tool in the assessment of the genetic similarity between breeding stocks (Lee 1995). Molecular techniques are now a valuable tool for advances in genome research generating considerable interest in predicting hybrid performance. Molecular markers are of great value in genetic research and partial breeding programs since they reflect the genetic variation among individuals. Various PCR-based marker techniques have recently been successfully introduced in the fingerprinting of plant genomes (Kesseli *et al.*, 1994) and in genetic diversity studies (Tinker *et al.*, 1993). Among them random amplified polymorphic DNA (RAPD) analysis which is relatively simple rapid and cost effective. The genetic parameter estimates (GCA and SCA) are essential in developing breeding strategies. Furthermore, the magnitude of genetic components for a certain trait would depend mainly upon the environmental fluctions under which the breeding populations will be tested. Therefore, much efforts have been devoted by corn breeders to estimate the interactions between genetic components and environments. In this respect, many researchers (El Hosary and sedhom 1990, Mohamed 1993 and sedhom, 1994) concluded that the additive genetic variance was more affected by genotype x environment interaction that the non-additive variance for grain yield per plant. On the contrary, El-Hosary (2006), Nawar (2002) and Sedhom (2007) reported that the non-additive effects were more based by interaction with environments than the additive effects were more biased by interaction with environments than the additive effects for grain yield. The objectives of this investigation were (1) Establishing the magnitude of both general combining ability GCA and specific combining ability SCA effects and their interaction with the two

nitrogen rates. (2) Determining hybrid mean performance and heterosis for the nine selected inbred lines. (3) Determining the genetic similarity among nine selected inbred lines by using RAPD marker. (4) Obtaining a RAPD fingerprint for each line. (5) Determining the relationship between the RAPD-based distances of these inbred lines and mean performance of their single cross hybrids and heterosis for grain yield performance.

MATERIALS AND METHODS

Field experiment

Nine yellow inbred lines (*Zea mays* L.) were used as parents in this study. Moshtohor P_1 (313J), P_2 (202A), P_3 (319), P_4 (313A), P_5 (L156), P_6 (161), P_7 (210-2), P_8 (311-4) and P_9 (120-B-3) were developed at the Department of Agronomy, Fac. of Agric at Moshtohor, Benha Univ. by Prof. Dr. A.A.M. El-Hosary. In the 2008 season the nine inbred lines were split planted in 1st March, 10th and 20th to avoid differences in flowering time and to secure enough hybrid seed. A half diallel set of crosses was carried out between the nine inbred lines by hand method giving a total of 36 crosses. In 2009 season, two experiments were undertaken in two fertilizer rates (60 kg N/fed. and 120 kgN/fed.) at the Agricultural Research and Experimental Station of the Fac. of Agric., Moshtohor. Each experiment included the nine inbred lines and 36 crosses along with S.C. G 155 (check variety) were sown on 29th of May. A randomized complete block design with three replications was used. Each plot consisted of two ridges of six m length and 70 cm width. Hills were spaced by 25 cm with three kernels per hill on one side of the ridge. The seedlings were thinned to one plant per hill. The cultural practices were followed as usual for ordinary maize field in the area. Random sample of 10 guarded plants in each plot were taken to evaluate ear height (cm), no. of rows/ear, no. of kernels/row, 100-kernel weight and grain yield/plant which was adjusted for 15.5% moisture moreover days to 50% tasseling dates (days) in 50% of the plant tasseled.

DNA extraction

Leaf tissue from each genotype was collected from 5-7 days old germinated seedlings. Equal quantities of leaf tissue from 10 seedlings of each line were bulked, lyophilized, and ground with a mortar. Genomic DNA was isolated and extracted using the mi-Plant Genomic DNA Isolation Kit.

RAPD-PCR analysis

Amplifications were conducted with 10-mer primers from Operon Technologies Inc. (Alameda, Calif., USA). All PCR reactions were performed as reported by **Williams *et al.*, (1990)**, with minor modifications, using 25 ng of DNA. Controls were made by replacing DNA with water. Reaction mixtures (25 µl) contained 0.2 µM of primer, 2.0 units of Taq DNA polymerase, 2.5 µl

of 10 x supplied buffer, 0.2 mM of each dNTP, and 2.5 mM of MgCl2. The amplifications were carried out a PTC 200 DNA Thermal Cycler. DNA denaturation was done at 94˚c for 4 min., followed by 36-cycle amplification (94˚c, 30sec.; 36˚c, 1 min.; 72˚c, 2 min.) and by a final extension step at 72˚c for 10 min. amplification products were separated by electrophoresis on 1.2% agarose gels, stained with ethidium bromide, and photographed under uv light.

Data analysis

The obtained data were statistically analyzed for analysis of variance by using computer statistical program MSTAT-C. General and specific combining ability estimates were estimated according to **Griffing's (1956)** diallel cross analysis designated as method 2 model I for each experiment. The combined analysis of the two experiments was carried out whenever homogeneity of variance was detected **(Gomez and Gomez, 1984)**. Heterosis expressed as the percentage deviation of the F_1 mean performance from S.C. G.155 was determined. The obtained data of RAPD analysis was entered in a computer file as binary matrices where 0 stands for the absence of a band and 1 stands for the presence of a band in each individual sample. Similarity coefficients between a pair of inbred lines were produced for the RAPD data using **Nei and LI's** formula **(1979)**. A dendrogram tree was constructed by the UPGMA clustering algorithm from the SAHN option of NTSYS-PC version 2.1(Rohlf, 2000).

RESULTS AND DISCUSSION

The analysis of variance for ordinary analysis of the two nitrogen rates as well as the combined analysis for all traits is given in Table (1). Nitrogen rates mean squares were found to be significant for all traits under study except for number of rows/ ear, with mean values in high rate being higher than those in low rate of nitrogen for all traits. The increase in these traits at high rate of nitrogen might be due to the simulating effect of nitrogen on metabolic process in maize plant. These results are in agreement with those obtained by(Hassan, 1999, Medici *et al.* 2004 and Tamilarasi, and Vetriventhan, 2009).

Mean squares for genotypes, parental inbred lines, F_1 hybrids and parent *vs* crosses were found to be significant for all the studied traits studied in both nitrogen rates as well as the combined analysis except mean squares for parental inbred lines for ear height at high nitrogen rate and 100-kernel weight at both nitrogen rates and the combined analysis. This indicated the wide diversity between the parental lines used in the present study. Significant genotypesxnitrogen rates interaction mean squares were obtained for days to 50% tasseling, ear height and grain yield/ plant, revealing that the performance of genotypes were differed from rate of nitrogen to another.

Insignificant parent's x nitrogen rates mean squares were obtained for all traits except 100-kernel weight. This result might reveal higher repeatability of

performance of the parental inbred lines under different nitrogen rates. Also, insignificant interaction mean squares between hybrid and nitrogen rates were detected for all traits except days to 50% tasseling, ear height and grain yield/ plant, revealing that the performance of hybrids were responded similary to environmental changes.

Insignificant interaction between mean squares due to parent *vs* crosses and nitrogen rate were obtained for all traits except days to 50% tasseling and grain yield/ plant. This result indicates that the heterotic effects were not affected by the nitrogen changes.

Mean performances

The mean performances of the tested nine inbred lines and their 36 hybrids at each nitrogen rate and as an average over the nitrogen rates are present in Table (2).

For days to 50% tasseling, the inbred line P_1 at the combined analysis gave significant lowest value of this trait. However, inbred line P2 had significantly the latest one.

The inbred lines no. 1, 4, 6 and 7 for ear height gave the lowest mean values. However, inbred lines no. 2, 3 and 5 had the highest mean values for this trait. The inbred line no. 9 had significantly the highest mean values for no. of rows/ ear followed by inbred lines 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 higher number of kernels/ row. However, the parental inbred line no. 8 gave the lowest one for this trait. All inbred lines gave similar of 100-kernel weight.

The parental inbred lines no. 1, 7 and 4 in the first nitrogen rate, 7, 9 and 1 at high nitrogen rate and no. 1, 6, 9 and 4 in the combined analysis had the highest mean values of grain yield/ plant. These inbred lines exhibited high mean values for one or more of the traits contributing to grain yield. However, the parental inbred line no. 2 gave the lowest one for this trait in the combined analysis.

Mean performances of F_1 hybrids and S.C. G. 155 at each nitrogen rate as well as the combined analysis for grain yield and at the combined analysis for other traits are presented in table (2). None of the hybrids surpassed the late or the highest performing inbred lines for tasseling revealing that all hybrids were shifted towards the earliness direction. The earliness of tasseling date 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 favourable for escaping destructive injuries caused by *Sesamia cretica* ledi *chilo simplex* But and *Pyrausta nubilialis*.

As for ear height, four hybrids; P_1xP_7, P_2xP_5, P_3xP_7 and P_4xP_7 gave the lowest values in the combined analysis. However, the highest values were recorded by cross P_2xP_8 and S.C. G. 155. The lowest of ear in maize decreased the lodging degree and increased the yield potentiality. The two crosses P_5xP_7 and P_7xP_9 showed superiority over the check hybrid for number of rows/ ear. 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. G. 155. The crosses i.e. P_1xP_3, P_1xP_7, P_2xP_8, P_3xP_4 and P_4xP_6 gave the highest mean values for 100-kernel weight. However, the crossP_1xP_4 gave the lowest one for this trait.

Concerning grain yield/ plant the crosses P_3xP_4 and P_4xP_6 in low nitrogen rate, P_3xP_4, P_3xP_6, P_3xP_7, P_3xP_8 and P_4xP_6 in high nitrogen rate and P_3xP_4, P_4xP_6, P_4xP_5 and P_3xP_8 in the combined analysis had significant superiority over the best check hybrid (S.C. G. 155). These hybrids exhibited significant increase in one or more of traits contributing to grain yield (Table 2). The fluctuation of hybrids from nitrogen rate to another was detected for most traits. These results would be due to significant interaction between hybrids and nitrogen rates.

Heterosis:

Heterosis expressed as the percentage deviation of F_1 mean performance from S.C. G.155 value for grain yield/plant is presented in Table (2). With the exception of fifteen crosses P_1xP_2, P_1xP_3, P_1xP_7, P_1xP_8, P_1xP_9, P_2xP_3, P_2xP_7, P_2xP_9, P_3xP_9, P_4xP_7, P_4xP_9, P_5xP_6, P_5xP_9, P_6xP_8 and P_6xP_9, all hybrids gave significant positive or insignificant heterotic effects relative to S.C. G. 155. Also, the three hybrids P_3xP_4, P_4xP_5 and P_4xP_6 out yielded significantly the check hybrid S.C. G. 155. Meanwhile, other hybrids from 36 hybrids gave significant negative heterotic effects relative to the 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. Nawar *et al.* 2002, Shafey *et al.* 2003, Singh *et al.* 2004, El-Hosary *et al.*, 2006 and Sedhom *et al.* 2007.

Combining ability

The analysis of variance for combining ability at the combined analysis for all the studied traits is presented in Table (1). The variance 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 significant for all the studied traits.

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

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 case.

High ratios which largely exceeded the unity were obtained for days to 50% tasseling at low rate of nitrogen fertilization, 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 cases, GCA/SCA ratios, were less than unity. Therefore, it could be concluded that the large portion of the total genetic variability associated with these traits is due to non-additive gene action. Similar results were reported by (Amer, 2005, El-Hosary *et al.* 2006 and Sedhom *et al.* 2007)

The mean squares of interaction between nitrogen rates and both types of combining ability were significant for days to 50% tasseling and ear height. 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 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 days to 50% tasseling, reveling that additive and non- additive were similar changed by nitrogen rats.

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

As for grain yield/plant, insignificant mean squares of interaction between nitrogen rates and GCA along with significant SCAxnitrogen rate were detected, for 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 on. of rows/ear and no. of kernels/ row, revealing that all types of gene action did not appreciably fluctuate in magnitude from nitrogen rate to another. These finding confirm those obtained above from the ordinary analysis of variance. The interaction between both types of combining abilities and seasonal changes were reported to be significant for earliness, ear height and grain yield/plant (Mosa, 2003, Mosa, and Motawei, 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 the combined analysis are presented in Table (3) General combining ability effects estimated herein differ significantly from zero. High positive values would be of interest under all traits in question except days to 50% tassling and ear height where high negative effects would be useful from the breeder's point of view.

The parental inbred line no. 1 exhibited significant negative ($\hat{g}_i$) effects for; days to 50% tasseling and ear height indicating that this inbred line could be considered as a good combiner for developing early and lowest ear height genotypes to escape corn pests and decreased the lodging degree. Also, it showed significant positive effects ($\hat{g}_i$) for no. of rows/ ear. The parental inbred line no. 3 showed significant negative ($\hat{g}_i$) effects for days to 50% tasseling, indicating that this line could be considered as a good combiner for developing early genotypes. Also, it showed significant positive ($\hat{g}_i$) effects for no. of kernels/ row, 100-kernel weight and grain yield /plant. The parental inbred line no. 4 was a best combiner for no. of kernels/row and poor combiner for days to 50% tasseling. The parental inbred lines no. 5, 8 and 9 seemed to be a poor combiner for all traits. The parental inbred line no. 6 exhibited significant negative ($\hat{g}_i$) effects for; days to 50% tasseling. The parental inbred line no. 7 seemed to be the best combiner for; ear height and it seemed to be good combiner for no. of rows/ ear and no. of kernels/ row.

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.

From the previous result, it could be concluded that the parental inbred lines P4 seemed to be the best general combiner for grain yield/plant and some of its components.

Specific combining ability:

Specific combining ability effects $\hat{S}_{ij}$ for the studied 36 hybrids were computed for all the studied traits (Table 3). The most desirable inter and intra allelic interactions were presented by combinations: P_2xP_3, P_2xP_6, P_3xP_7, P_5xP_9, P_6xP_7 and P_8xP_9 for days to 50% tasseling, P_1xP_5, P_2xP_4, P_2xP_6, P_4xP_6, P_5xP_7, P_6xP_8 and P_7xP_9 for number of rows/ear, P_2xP_4, P_2xP_8, P_3xP_4, P_3xP_5, P_3xP_6, P_3xP_8, P_4xP_5, P_4xP_6 and P_8xP_9 for no. of kernels/ row, P_1xP_7, P_2xP_6, P_3xP_4, P_3xP_8 and P_4xP_6 for 100-kernel weight and P_1xP_4, P_1xP_5, P_1xP_6, P_1xP_9, P_2xP_3, P_2xP_4, P_2xP_5, P_2xP_6, P_2xP_8, P_3xP_4, P_3xP_5, P_3xP_6, P_3xP_7, P_3xP_8, P_4xP_5, p_4xP_6, P_4xP_8, P5xP7, P_5xP_8, P_6xP_7, P_7xP_8, P_7xP_9 and P_8xP_9 for grain yield/ plant. These crosses may be prime importance in breeding programmes either towards hybrid maize production or synthetic varieties composed of hybrids which involved the good combiners for the traits in view.

RAPD-PCR marker

RAPD experiments were conducted using twenty random primers. Eleven primers gave non-polymorphic fragment. On the other hand, nine primers (A12, A13, A14, A15, A17, A18, A19, A20 and Q11) gave polymorphic amplification products. The nine RAPD primers generated 397 scorable bands across 9 inbred lines (Table 5). These primers produced a total of 66 reproducible fragments, from which 39 (59.09%) were polymorphic (Table 5 and Fig. 1:9). Primer A12 produced eleven amplified fragment (ASF) ranged between 250b.p. and 2121b.p. and it produced four polymorphic fragments. The total number of scorable bands was 71 bands and gave six polymorphic fragments out of eleven, with 54.5% polymorphism. the primer A13 gave four fragments ranged between 319b.p. and 1115b.p. The total number of scorable bands was 30 bands and the primer gave two polymorphic fragments out of four, with 50% polymorphism. The primer A14 gave eight fragments between 543b.p. and 2133b.p and give 44 scorable bands and the primer gave six polymorphic fragments out of eight, with 75% polymorphism. 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. Primer A17, six fragments ranged between173b.p. and 1143 b.p. were produced by this primer. The total numbers of scorable bands were 37 bands and the primer gave three polymorphisms, the estimate of polymorphic for this primer was 50%. The primer A18 gave 50 bands in nine fragments ranged between 181b.p. and 1535b.p. Also, the primer gave eight polymorphic fragments out of nine, with 88.89% polymorphism. The primer A19 gave eight fragments ranged between 181b.p. and 1763b.p. showed that the total number of scorable bands was 65 bands and the primer gave two polymorphic fragments out of eight, with 25% polymorphism. 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, it gave non-monomorphic fragments out of six, with 100% polymorphism. 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%.

Genetic similarity:

The genetic similarity matrix was produced for the RAPD data using Nei and Li's formula (1979). Genetic similarity coefficient was presented in Table (6). The lowest genetic similarity (0.55) was detected between P_1 and P_5 also, obtained between P_8 and P_9. 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 represented in Fig. (10). The data collectively distinguished two main clusters. The first main cluster consists of eight inbred lines P1, P2, P3, P4, P6, P9, P8 and P7 and this cluster separated into two sub-clusters: the first sub-cluster contained six inbred lines P1, P2, P3, P4, P6 and P7. Meanwhile, the second sub cluster contained two inbred line P8 and P9. In addition, the first sub-cluster divided into two sub-sub clusters the first sub-sub cluster contained P1 and P2. While, the inbred lines P3, P4, P6 and P7 were belonging to the second sub-sub cluster as well as inbred lines P4 and P6 being closely. The second main cluster contains the inbred lines only P5. 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.

The correlation between genetic distance and each of mean performance and heterosis for grain yield/plant.

The correlation of GD and each of mean performance and heterosis for grain yield which computed for 36 hybrids combination studied are estimated and presented in table 6. The estimate value of correlation coefficient between GD, and each of mean performance and heterosis relative to the check variety S.C. G. 155 for grain yield/plant found positive (r = 0.06 and 0.03), respectively. Therefore, this specified tendency could be predicted about the relationship of GD and heterosis for grain yield/plant in this study. A similar finding was obtained by Lanza *et al.*, (1997). Melchinger (1999) showed that the correlation between marker-estimated genetic distance and heterosis in general is low or not high enough to be of predictive value. Parentoni *et al.*, (2001) and Salama *et al.*, (2001) found that the correlation between marker genetic distance for pair parents was moderate, low and positive. The higher correlation between marker distance, mean performance and heterosis has

been reported by Lee *et al.*, (1989) and Melchinger (1993) and sedhom *et al.*, (2007), Ajmone *et al.*, (1998), suggested that AFLPs are able to detect a larger number of polymorphisms in a more efficient was in comparison to RFLPs or SSRs due to much higher number of loci assayed in a single multiplex PCR reaction.

This study showed that GD can be used to precisely predict the yield performance and heterosis value for F_1 hybrids. The results indicated that RAPD marker can be used as a tool for determining fingerprint for each line and 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.

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Table (1): observed mean squares from ordinary analysis for the studied traits in both two rates of nitrogen as well as combined over them.

S.O.V.	d.f.		Dayes to 50% Tasseling (days)			Ear height (cm)			no. of rows/ear		
	S.	C.	60 KgN/ fed.	120 KgN/ fed.	Comb	60 KgN/ fed.	120 KgN/ fed.	Comb	60 KgN/ fed.	120 KgN/ fed.	Comb
Nitrogen (N)		1			340.03 * *			5733.46 * *			1.25
Rep/L	2	4	5.49	6.02	5.76 *	954.45 * *	2395.19 * *	1674.82 * *	0.02	0.97	0.50
Genotypes (G.)	44	44	24.19 * *	31.92 * *	51.20 * *	919.49 * *	1103.64 * *	1674.69 * *	7.92 * *	7.59 * *	14.78 * *
parent (P.)	8	8	7.33 * *	9.83 * *	15.75 * *	266.56 * *	209.91	371.42 * *	7.45 * *	5.32 * *	12.08 * *
Crosses (Cr.)	35	35	9.87 * *	10.90 * *	15.30 * *	443.92 * *	560.03 * *	592.82 * *	2.44 * *	3.36 * *	5.08 * *
P.vs.cr.	1	1	660.02 * *	944.07 * *	1591.41 *	22787.71 * *	27279.65 * *	49966.40 *	203.21 * *	173.57 * *	376.20 *
G. x N		44			4.90 * *			348.43 * *			0.72
P. x N		8			1.42			105.06			0.69
Cr. x N		35			5.48 * *			411.13 * *			0.73
P.vs.cr.Vs.N		1			12.68 *			100.96			0.58
Error	88	176	2.56	1.86	2.21	101.14	111.43	106.29	0.61	0.94	0.78
GCA	8	8	8.76 * *	7.33 * *	14.61 * *	383.77 * *	406.71 * *	669.09 * *	2.58 * *	2.93 * *	5.35 * *
SCA	36	36	7.91 * *	11.37 * *	17.61 * *	289.32 * *	359.25 * *	533.60 * *	2.65 * *	2.44 * *	4.83 * *
GCA x N		8			1.48 *			121.40 * *			0.16
SCA x N		36			1.67 * *			114.98 * *			0.26
Error	88	176	0.85	0.62	0.74	33.71	37.14	35.43	0.20	0.31	0.26
GCA/SCA			1.11	0.64	0.83	1.33	1.13	1.25	0.97	1.20	1.11
GCA x N/GCA					0.10			0.18			–
SCA x N/SCA					0.09			0.22			–

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

Table (1): observed mean squares Cont.

S.O.V.	d.f.		no. of kernels/ row			100-kernel weight (gm)			Grain yield / plant (gm)		
	S.	C.	60 KgN/ fed.	120 KgN/ fed.	Comb	60 KgN/ fed.	120 KgN/ fed.	Comb	60 KgN/ fed.	120 KgN/ fed.	Comb
Nitrogen (N)		1			935.84 * *			789.49 * *			26022.39 * *
Rep/L	2	4	16.62	6.15	11.39	38.26 *	2.04	20.15 *	71.41	258.24	164.82
Genotypes (G.)	44	44	107.53 * *	120.24 * *	222.29 * *	58.62 * *	56.86 * *	104.79 * *	5647.12 * *	6727.09 * *	12149.02 * *
parent (P.)	8	8	35.38 * *	70.14 * *	99.78 * *	9.79	13.47	6.27	320.18 *	708.35 * *	910.96 * *
Crosses (Cr.)	35	35	15.67 * *	26.74 * *	36.84 * *	27.27 * *	30.22 * *	48.06 * *	1449.65 * *	1289.36 * *	2523.52 * *
P.vs.cr.	1	1	3899.86 * *	3793.74 * *	7693.23 *	1546.27 * *	1336.29 * *	2878.73 *	195173.89 * *	245197.36 * *	438946.05 *
G. x N		44			5.48			10.68			225.19 * *
P. x N		8			5.74			16.99 *			117.58
Cr. x N		35			5.57			9.44			215.50 *
P.vs.cr.Vs.N		1			0.37			3.83			1425.20 *
Error	88	176	7.84	7.78	7.81	7.02	9.67	8.34	150.66	117.57	134.11
GCA	8	8	11.43 * *	20.75 * *	30.73 * *	11.77 * *	13.56 * *	18.14 * *	605.99 * *	449.70 * *	978.87 * *
SCA	36	36	41.27 * *	44.38 * *	83.73 * *	21.27 * *	20.15 * *	38.66 * *	2166.01 * *	2640.73 * *	4732.07 * *
GCA x N		8			1.45			7.18 * *			76.83
SCA x N		36			1.91			2.76			74.67 *
Error	88	176	2.61	2.59	2.60	2.34	3.22	2.78	50.22	39.19	44.70
GCA/SCA			0.28	0.47	0.37	0.55	0.67	0.47	0.28	0.17	0.21
GCA x N/GCA					–			–			–
SCA x N/SCA					–			–			–

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

Table (2): Mean performance of the genotype for all the studied traits over the two nitrogen rates and heterosis relative to SC G155 for grain yield/ plant.

Genotypes	tasseling date	ear height	no. of row s/ ear	no. of kernel s/ row	100-kernel weight	Grain yield/ plant			Heterosis % grain yield/ plant relative to SC G 155 in the combined analysis
						60 kgn	120 kgn	comb.	
1	58.83CE	68.53U	13.03LN	24.07O	29.03MO	69.90Q	78.90PQ	74.40PQ	
2	64.83A	92.58QS	9.033P	15.70QR	27.50NO	41.70S	42.50S	42.10S	
3	62.33B	84.70 ST	12.66LN	18.97PQ	26.83NO	51.10QS	54.60RS	52.90RS	
4	63.00 B	74.18 TU	11.30O	17.37 PR	26.67NO	62.70QS	63.40QR	63.10QR	
5	63.50AB	89.98 RS	11.27O	15.60QR	27.00NO	47.40QS	58.30RS	52.90RS	
6	62.00 B	74.82 TU	11.27O	19.18P	25.67O	55.70QS	67.70QR	61.70QR	
7	62.67B	76.57 TU	13.03LN	26.79NO	26.83NO	65.90QR	92.90P	79.40P	
8	61.67B	83.18ST	12.32N	14.36R	27.83NO	44.90RS	57.50RS	51.20RS	
9	62.17B	82.58 ST	13.67IM	19.12P	28.50MO	59.30QS	79.40PQ	69.40PQ	
x parent	62.33	80.79	11.97	19.02	27.32	48.26	63.78	56.02	
1x2	57.17 EK	125.3 AH	12.97LN	29.02KN	31.83JM	123.2NP	145.9NO	134.6NO	-22.92 **
1x3	54.83 MR	103.3MR	15.18BH	32.48DL	39.50AC	130.0JP	150.3MO	140.2LO	-19.71 **
1x4	55.17 KQ	115.9EM	14.63DJ	33.53DI	29.00MO	156.9CI	192.1BE	175.5DG	0.53
1x5	56.17 HN	119.2CL	16.07AB	30.50IM	33.79EK	148.0GM	163.9GN	155.9HL	-10.68
1x6	53.83PR	114.5 FN	15.80AD	32.70DL	37.50BG	172.3CF	182.7DG	177.5CF	1.70
1x7	56.50 GN	94.30 PS	15.55AE	32.02EM	39.17AC	148.4FL	151.7MO	150.1IN	-14.04 *
1x8	53.50 QR	108.8JO	14.95BH	30.76HM	36.83CI	137.8IO	158.5JO	148.0JO	-15.24 **
1x9	56.50 GN	107.1KP	15.42BG	30.50IM	34.73DJ	147.9GM	158.1JO	153.0HL	-12.35 *
2x3	53.00 R	121.5 BJ	12.78MN	30.67IM	36.00CI	150.9EL	160.2IN	155.6HL	-10.69 *
2x4	59.50 C	120.0CK	14.78CI	33.69DI	33.67FK	150.6EL	168.6FM	159.6GK	-8.57
2x5	57.50DI	137.2 A	13.68IM	30.72HM	34.17DJ	143.1HN	177.3DK	160.2GK	-8.22
2x6	54.50 NR	126.6AF	16.13AB	32.07DM	37.17CH	143.4HN	181.9DH	162.6FJ	-6.83
2x7	59.17CD	119.0CL	14.67DI	31.37FM	33.67FK	127.0LP	156.3KO	141.6LO	-18.66 **
2x8	57.50 DI	129.2 AE	14.27GK	33.50DI	37.83AE	153.4 DK	177.7 DJ	165.5EI	-5.17
2x9	58.83 CE	119.0CL	14.00HL	28.62MN	34.17DJ	123.9 MP	143.4NO	133.7O	-23.42 **
3x4	56.50GN	105.2LQ	14.58DJ	39.33A	41.33A	218.5A	224.8A	221.7A	26.97 **
3x5	55.83 HO	123.9 AI	15.10BH	35.91BD	37.17CH	152.3EK	183.2DG	167.7EH	-3.91
3x6	54.17 OR	111.2HO	14.37EK	34.84BG	37.00CH	161.8CI	197.1BE	179.4CE	2.79
3x7	54.00OR	94.18PS	14.30 FK	34.70BG	37.17CH	161.9CI	191.7BE	176.8CF	1.26
3x8	56.17HN	121.3BK	14.18 GK	34.20CI	41.17AB	176.6BD	205.6BC	191.0BC	9.40
3x9	55.50IP	101.1 NR	13.35 KN	28.92LN	36.17CI	132.1 JP	138.2O	135.2MO	-22.57 **
4x5	58.33 CG	125.8 AG	14.82CI	37.97AB	35.83CI	182.1BC	206.0B	194.1B	11.17 *
4x6	56.50 GN	110.3 IO	15.68AE	36.53BE	38.17AD	196.1B	197.6BD	196.8B	12.72 *
4x7	57.50DI	97.82 OR	14.67DI	32.83DK	29.67LN	118.3QP	154.5LO	136.4MO	-21.86 **
4x8	57.33DJ	121.0 BK	14.68DI	33.56DI	37.33DG	174.5CE	195.6BE	185.1BD	6.02
4x9	57.83CH	108.3LQ	14.24GK	33.58DI	30.16KN	143.6HN	147.5MO	145.6KO	-16.61 **
5x6	57.50 DI	111.4HO	15.95AC	29.54JN	37.00CH	149.6FL	161.4HN	155.5HL	-10.91 *
5x7	56.50GN	112.5FN	16.60A	31.37FM	35.67CJ	154.1DJ	177.0DK	165.6EI	-5.15
5x8	57.33 DJ	126.8 AF	15.42BG	31.10GM	33.50GK	147.8GM	175.6EL	161.7FJ	-7.37
5x9	55.83 HO	124.6 AI	15.27BG	28.62MN	33.83EK	109.2P	161.3HN	135.3MO	-22.52 **
6x7	54.50NR	109.3JO	15.27BG	34.02CI	34.83DJ	164.9CH	180.8DI	172.8DG	-0.99
6x8	57.00 EL	112.2GN	15.93AC	30.63IM	34.83DJ	129.1KP	143.9NO	136.5MO	-21.79 **
6x9	56.00 LQ	114.0FN	14.60DJ	30.63IM	36.00DJ	136.7IO	156.3JO	146.5JO	-14.55 **
7x8	56.83 FM	116.9DM	15.53AF	31.50FM	34.00EJ	141.1HO	186.0DG	163.6FJ	-6.60
7x9	56.33 GN	110.5 IO	16.68 A	31.03GM	32.83IL	146.8GN	178.2DJ	162.5FJ	-6.93
8x9	56.33 JQ	116.6DM	15.32BG	33.06DJ	36.67CJ	170.0CG	186.3CF	177.6CF	1.76
SC 155	58.50 CF	132.0 AC	15.07BH	33.28DJ	36.17CI	168.9CG	180.3DI	174.6DG	
x hybrid	56.32	115.27	14.93	32.39	35.50	145.39	170.10	157.75	
x Genotypes	57.50	108.52	14.35	29.77	33.90	126.39	149.30	137.84	

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

Table (3): General combining ability effects for all studied traits in two rates of nitrogen as well as the combined over them.

Parent	Dayes to 50% Tasseling (days)	Ear height (cm)	no. of rows /ear	no. of kernels/ row	100-kernel weight (gm)	Grain yield / plant (gm)
p1	-1.22 * *	-4.95 * *	0.30 *	0.25	0.18	-2.68
p2	1.10 * *	9.37 * *	-1.09 * *	-1.44 * *	-0.45	-10.73 * *
p3	-0.92 * *	-2.62	-0.34 *	1.10 *	1.88 * *	5.23 * *
p4	0.90 * *	-2.76	-0.25	1.62 * *	-0.91	11.37 * *
p5	0.66 * *	7.40 * *	0.19	-0.91 *	-0.32	-1.27
p6	-0.71 * *	-1.90	0.26	0.13	0.39	3.41
p7	0.17	-6.58 * *	0.54 * *	1.41 * *	-0.71	1.08
p8	-0.04	3.55 *	0.14	-0.90 *	0.76	1.38
p9	0.07	-1.53	0.26	-1.25 * *	-0.81	-7.79 * *
L.S.D ĝi 0.05	0.48	3.32	0.28	0.90	0.93	3.73
L.S.D ĝi 0.01	0.63	4.35	0.37	1.18	1.22	4.88
L.S.D ĝi-ĝj 0.05	0.72	4.97	0.43	1.35	1.39	5.59
L.S.D ĝi-ĝj 0.01	0.94	6.52	0.56	1.77	1.83	7.33

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

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

Crosses	Days to 50% Tasseling (days)	Ear height (cm)	no. of rows/ear	no. of kernels/ row	100kernel weight (gm)	Grain yield / plant (gm)
P1xP2	-0.18	12.88 *	-0.57	0.52	-1.74	6.40
P1xP3	-0.50	2.83	0.89	1.45	3.60 *	-3.95
P1xP4	-1.99 *	15.62 * *	0.25	1.97	-4.12 * *	25.24 * *
P1xP5	-0.75	8.78	1.25 * *	1.47	0.09	18.30 * *
P1xP6	-1.72 *	13.38 *	0.91 *	2.63	3.08 *	35.24 * *
P1xP7	0.07	-2.17	0.37	0.67	5.85 * *	10.09
P1xP8	-2.72 * *	2.23	0.18	1.72	2.05	7.70
P1xP9	0.18	5.61	0.52	1.81	1.52	21.52 * *
P2xP3	-4.65 * *	6.78	-0.12	1.33	0.72	19.49 * *
P2xP4	0.03	5.38	1.79 * *	3.82 * *	1.18	17.38 * *
P2xP5	-1.73 *	12.45 *	0.25	3.38 *	1.09	30.64 * *
P2xP6	-3.37 * *	11.16 *	2.63 * *	3.69 *	3.38 *	28.39 * *
P2xP7	0.42	8.21	0.88	1.71	0.98	9.75
P2xP8	-1.03	8.28	0.88	6.15 * *	3.68 *	33.32 * *
P2xP9	0.19	3.19	0.50	1.62	1.58	10.63
P3xP4	-0.96	2.60	0.84	6.92 * *	6.51 * *	63.45 * *
P3xP5	-1.38	11.17 *	0.92 *	6.03 * *	1.76	22.21 * *
P3xP6	-1.68 *	7.75	0.12	3.92 * *	0.88	29.23 * *
P3xP7	-2.73 * *	-4.62	-0.24	2.50	2.15	26.50 * *
P3xP8	-0.35	12.40 *	0.05	4.31 * *	4.68 * *	42.79 * *
P3xP9	-1.12	-2.76	-0.90	-0.62	1.25	-3.84
P4xP5	-0.70	13.11 *	0.54	7.56 * *	3.21 *	42.39 * *
P4xP6	-1.17	6.94	1.24 * *	4.09 * *	4.83 * *	40.42 * *
P4xP7	-1.05	-0.86	0.04	0.11	-2.56	-17.61 * *
P4xP8	-1.00	12.24 *	0.46	3.14 *	3.64 *	30.74 * *
P4xP9	-0.61	1.57	-0.10	3.51 *	-1.97	0.42
P5xP6	0.07	-2.13	1.17 *	0.63	3.08 *	11.82
P5xP7	-1.81 *	3.71	1.53 * *	1.18	2.85	24.15 * *
P5xP8	-0.76	7.87	0.75	3.22 *	-0.79	20.02 * *
P5xP9	-2.37 * *	10.68 *	0.48	1.08	1.12	2.75
P6xP7	-2.44 * *	9.81	0.13	2.79	1.30	26.78 * *
P6xP8	0.27	2.45	1.20 * *	1.71	-0.17	-9.83
P6xP9	-1.84 *	9.39	-0.25	2.06	1.57	11.28
P7xP8	-0.78	11.89 *	0.51	1.30	0.10	15.01 * *
P7xP9	-1.38	10.57	1.54 * *	1.18	0.51	27.61 * *
P8xP9	-2.17 * *	6.46	0.58	5.51 * *	1.87	42.48 * *
LSD5%(Sij)	1.53	10.61	0.91	2.88	2.97	11.92
LSD1%(Sij)	2.02	13.99	1.20	3.79	3.92	15.71
LSD5%(Sij-Sik)	2.26	15.65	1.34	4.24	4.38	17.58
LSD1%(Sij-Sik)	2.98	20.63	1.76	5.59	5.78	23.17
LSD5%(Sij-Skl)	2.14	14.85	1.27	4.02	4.16	16.68
LSD1%(Sij-Skl)	2.82	19.57	1.67	5.30	5.48	21.98

* and ** significance at 0.05 and 0.01 level of probability, respectively.

Table (5) name of primers, the nucleotides sequences of the applied primers, molecular weigh for RAPD loci found and total fragments detected by each primer and number of polymorphic fragments in nine maize inbred lines.

primer	Sequence	Molecular weigh (bp)	I*1	I*2	I*3	I*4	I*5	I*6	I*7	I*8	I*9	TSB	TF	NPF	PPF	Fig. (1-9): RAPD pattern
A12	TCA GGG AAA CC	2121	0	0	1	0	0	0	0	0	0	71	11	6	54.55	
		1898	1	1	0	1	1	1	1	1	1					
		1575	0	0	1	0	0	0	0	0	0					
		1347	0	0	0	1	1	1	0	1	0					
		1222	1	1	1	0	0	0	1	0	0					
		801	1	1	1	1	1	1	1	1	1					
		691	1	0	1	1	1	1	1	1	1					
		569	1	1	1	1	1	1	1	1	1					
		441	1	1	1	1	1	1	1	1	1					
		341	1	1	1	1	1	1	1	1	1					
		250	1	1	1	1	1	1	1	1	1					
A13	GAG GAC GGA CC	1115	1	1	1	1	1	1	1	1	1	30	4	2	50.00	
		619	0	1	1	1	1	1	1	1	1					
		504	0	0	0	1	1	0	0	1	1					
		319	1	1	1	1	1	1	1	1	1					
A14	TCT GTG CTG CC	2133	1	1	1	1	1	1	1	1	1	44	8	6	75.00	
		1462	0	0	0	0	1	1	0	0	0					
		1054	1	1	1	1	0	1	0	1	1					
		881	1	1	1	1	1	1	1	1	1					
		742	1	1	1	1	1	0	0	1	1					
		677	0	0	0	0	0	0	1	0	0					
		618	1	1	1	1	0	1	0	1	1					
		543	0	0	0	0	1	1	0	0	0					
A15	TTC CAA AG	2251	0	1	1	1	0	1	0	0	1	28	5	4	80.00	
		1434	0	0	1	0	0	0	0	0	0					
		1181	0	0	0	1	1	1	0	1	1					
		844	1	1	1	1	1	1	1	0	1					
		489	1	1	1	1	1	1	1	1	1					
A17	GAG GAC TTG TT	1143	0	0	0	0	0	0	1	0	0	37	6	3	50.00	
		890	1	1	1	1	1	1	1	1	1					
		698	1	1	1	1	1	1	1	1	1					
		421	0	0	0	0	1	0	0	0	1					
		308	1	1	1	1	1	1	1	1	1					
		173	0	1	1	1	1	0	1	1	1					
A18	AGG TAA CCC TT	1535	1	1	1	1	1	0	1	1	1	50	9	8	88.89	
		1259	0	0	1	1	1	0	0	1	1					
		1020	1	1	1	1	1	0	1	1	1					
		833	0	1	1	1	1	0	1	1	1					
		622	1	1	1	1	1	1	1	1	1					
		462	0	0	0	1	1	0	0	0	1					
		368	1	0	0	0	0	0	0	0	0					
		297	0	1	1	1	1	1	1	1	1					
		181	1	0	0	0	0	0	0	0	0					
A19	GAA AGG TCG CC	1763	1	1	1	1	1	1	1	1	1	65	8	2	25.00	
		1123	0	0	0	1	1	0	0	0	1					
		890	1	1	1	1	1	1	1	1	1					
		742	1	1	1	1	1	1	1	1	1					
		460	1	1	1	1	1	1	1	1	1					
		346	1	1	1	1	1	1	1	1	1					
		276	1	1	1	1	1	0	1	1	1					
		181	1	1	1	1	1	1	1	1	1					
A20	GTT GGG ATC CC	2020	0	1	1	1	1	1	1	1	0	30	6	0	100.00	
		1467	0	0	0	0	0	0	0	1	0					
		1317	1	1	1	1	1	1	1	0	1					
		900	0	0	0	0	0	0	0	1	0					
		813	1	1	1	1	1	1	1	0	1					
		422	0	0	1	1	1	1	0	0	1					
Cl1	TCT GCG CAA CC	2305	0	0	0	0	1	1	1	0	0	42	9	8	88.89	
		2036	1	1	1	1	0	0	1	1	1					
		1785	0	0	1	1	0	0	0	1	0					
		1500	1	1	1	1	1	1	1	1	1					
		1305	1	1	1	1	1	1	1	0	1					
		1237	0	0	0	0	0	0	0	1	0					
		715	0	0	0	0	1	1	1	0	0					
		633	1	1	1	1	0	0	0	1	1					
		363	0	0	0	0	1	1	0	0	0					
		Total										397	86	39	89.091	

TSB = Total number of scorable bands , TF = Total number of fragments , NPF = Number of polymorphic fragments.

and PPF = fragments per centage.

Table (6): Genetic similarity based on Jaccard coefficient for nine inbred lines in maize revealed by RAPI

	P1	P2	P3	P4	P5	P6	P7	P8	P9
P1	1.00								
P2	0.80	1.00							
P3	0.70	0.83	1.00						
P4	0.67	0.80	0.81	1.00					
P5	0.55	0.64	0.63	0.78	1.00				
P6	0.58	0.64	0.60	0.67	0.73	1.00			
P7	0.68	0.78	0.69	0.67	0.70	0.64	1.00		
P8	0.61	0.70	0.69	0.79	0.63	0.55	0.60	1.00	
P9	0.71	0.81	0.75	0.90	0.76	0.61	0.67	0.73	1.00

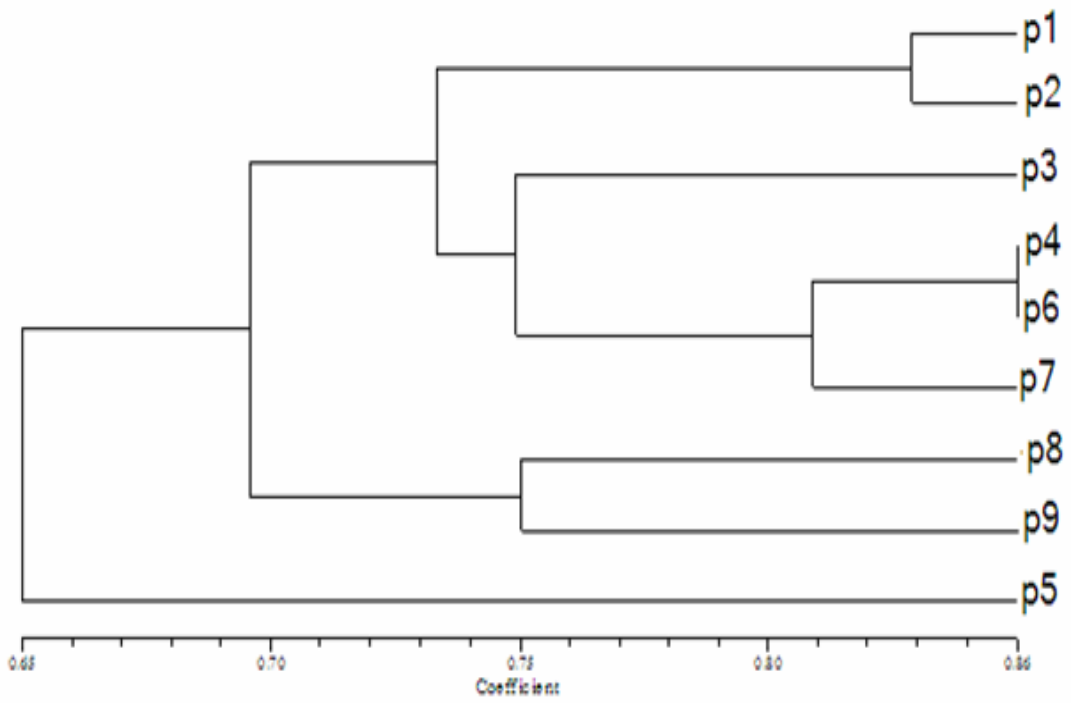

Fig. (1): Dendrogram of the genetic distance among the nine maize inbred lines based on RAPD analysis.

١.٦. قدرة التآلف فى الذرة الشامية تحت مستويى من التسميد النيتروجينى و التباعد الوراثى المقدرة بواسطة معلمات RAPD

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قسم المحاصيل - كلية زراعة بمشتهر – جامعة بنها

أجرى تقييم الهجن الناتجة من التهجين النصف دائرى لتسعة سلالات من الذرة الصفراء وذلك فى تحت مستويين من التسميد الازوتى (٦٠ و ١٢٠ كجم نيتروجين/ فدان) لستة صفات كمية فى تصميم قطاعات كاملة العشوائية. كانت متوسطات التباين لكل من مستويان التسميد والتراكيب الوراثية والآباء والهجن معنوية فى كل الصفات تحت الدراسة عدا التباين للاباء فى صفة ارتفاع الكوز فى مستوى التسميد المرتفع و صفة وزن ال ١٠٠ حبة فى كلا المستويين من التسميد و التحليل المشترك . كما كان متوسط التباين للتفاعل بين التراكيب الوراثية ومستويى التسميد معنوي لصفة عدد الايام حتى طرد ٥٠% من النورة المذكرة، ارتفاع الكوز و محصول الحبوب/ نبات. كما أظهر متوسط التباين للتفاعل بين الهجن ومستوى التسميد معنوية لصفات عدد الايام حتى طرد ٥٠% من النورة المذكرة، ارتفاع الكوز و محصول الحبوب/ نبات. و كانت التباينات للقدرة العامة والخاصة على التآلف معنوية لكل الصفات تحت الدراسة . وكانت النسبة بين القدرة العامة والقدرة الخاصة أكبر من الوحدة لكل من صفة عدد الايام حتى طرد ٥٠%من النورات المذكرة فى مستوى التسميد المنخفض ، صفة ارتفاع الكوز فى كل مستويى من التسميد و التحليل المشترك و عدد السطور فى الكوز فى مستوى التسميد العالى و التحليل التجميعى.

وكان متوسط التباين للتفاعل بين مستويى التسميد والقدرة العامة والخاصة معنويا لكل من عدد الايام حتى طرد ٥٠% من النورة المذكرة و ارتفاع الكوز. وكانت النسبة بين التفاعل فى القدرة العامة والتسميد للقدرة الخاصة عالية عن النسبة بين التفاعل للقدرة الخاصة والتسميد بالنسبة للقدرة العامة لصفة ارتفاع الكوز .

أظهرت السلالة الأبوية رقم ٤ قدرة جيدة عامة على التوافق لصفة محصول الحبوب /نبات و بعض مكونات المحصول . كما أظهرت السلالة رقم ٣ قدرة جيدة على التألف لعدد الايام حتى طرد ٥٠% من النورة المذكرة.

أعطت الهجن P1xP4, P1xP5 ، P1xP6، P1xP9، P2xP3، P2xP4، P2xP5، P2xP6، P2xP8، P3xP4، P3xP5، P3xP6، P3xP7، P3xP8 ، P4xP5، P4xP6، P4xP8، P5xP7، P5xP8، P6xP7، P7xP8، P7xP9 و P8xP9.أعلى القيم للقدرة الخاصة على التآلف محصول الحبوب/ نبات. و حققت الثلاثة هجن P3xP4، P4xP5 و P4xP6 تفوقا فى قوة الهجين عن الصنف التجارى جيزة ١٥٥. كان معدل عدد شظايا ال DNA الناتجة من خمس بادئات من RAPD لعشر سلالات أبوية هى ٣٩٧ شظية . وكان عدد المعلمات ٦٦ شظية حققت ٣٩ منهم عدد متباين من الإختلافات بنسبة ٥٩.٠٩ % وكان متوسط التباين أو الإختلاف للبادئ الواحد هى ٤.٣ . وكان أقل درجة تشابة بين السلالات الأبوية هى ٥٥ ,٠ بين السلالات الأبوية (p1 , p5) وبين السلالات الأبوية (p8 , p9) وأعلى درجة تشابة (٠.٩) بين السلالات الأبوية p4 , p9 . وكان الإرتباط موجبا بين التباعد الوراثى وكل من متوسط آداء وقوة الهجين لكل الهجن تحت الدراسة وهى (٠٦, . و ٠٣, .) على التوالى .

من خلال هذه الدراسة فأن RAPD كتكنيك من المعلمات الجزيئية يمكن أن يستخدم فى تحديد التباعد الوراثى بين سلالات الذرة الشامية وتقسيمها الى مجموعات واستخدام هذا التباعد فى التنبؤ بالمحصول وقوة الهجين للهجن الناتجة بين هذه السلالات ولكن بأستخدام عدد كبير من البادئات Primers .