GENETIC RELATIONSHIPS AMONG SOME MAIZE (*Zea mays* L.) GENOTYPES ON THE BASIS OF GENE ACTION AND RAPD MARKERS UNDER DROUGHT STRESS

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Maize (*Zea mays* L.) is one of the most important cereal crops in the world, especially in Egypt. The genetic information of a landrace can allow the possible explanation of genes for traits such as disease resistance, tolerance to environmental stresses by conservation of landraces which have high genetic variability with the fitness to the environments (Zeven, 1996). Maize is particularly sensitive to water stress at the flowering and grain filling periods (Grant *et al*., 1989). Phenotype is the result of genotype and environmental interaction. Therefore, assessment of desired genotypes is highly dependent on proper environmental conditions. Abiotic stresses (particularly drought, high temperature, salinity and others) generally reduce crop productivity. Of all the abiotic stresses that reduce crop productivity, drought is the most devastating one for stable production in developing countries (Ribaut *et al*., 2009). Simultaneously, drought resistance in crops is probably the most difficult trait to understand (Bruce *et al*., 2002; Ashraf, 2010). Hence, in the absence of thorough information related to the genetic mechanism of drought tolerance, grain yield under dry conditions is most often used to quantify the level of drought resistance of a genotype rather than a direct selection criterion, which can accurately measure the level of crop drought resistance (Farshadfar and Sutka, 2002). However, low heritability of grain yield and the complexity of genotype environment interactions limit the development of cultivars tolerant to water stress.

Non-additive type of gene action was more affected than the additive type of gene action by environment as published by Khaled (2008). Additive gene action with partial dominance was revealed for plant height, harvest index under normal and stress conditions, but over-dominance type of gene action was found for kernel per ear row, 100-grain weight (Imtiaz, 2009).

The genetic diversity has been assessed more efficiently relating polymorphism from the morphological, biochemical and DNA labels. Genetic variability in landraces has been studied by morphological traits (Louette and Smale, 2000; Ilarslan *et al*., 2002; Beyene *et al*., 2005). DNA polymorphism assays are powerful tools for characterizing and studying germplasm resources (Powell *et al*., 1996). In maize, random amplified polymorphic DNA (RAPD) markers have been used in describing genetic diversity be-

tween maize accessions (Moeller and Schall, 1999; Beyene *et al*., 2005). The level of association between agronomic characterization and DNA marker-based genetic similarity may vary among different crop species. In corn a close association was found (Messmer *et al.*, 1993). Therefore, it is necessary to determine within each species whether agronomic characterization and DNA marker-based genetic similarity provide similar information about the genetic distance among available germplasm.

The objectives of this study were: (1) to study the genetic systems controlling quantitative characters using a North Carolina Design II (NCDII) mating among nine maize lines and their 20 F_1's in two separate environments (normal and drought conditions), and (2) to evaluate genetic similarity determined by RAPD technique for the identification of the genetic relationship between the parental lines and the single cross hybrid 10 (S.C.10) used as a check.

MATERIALS AND METHODS

Field experiments

This study was carried out at the experimental farm of Faculty of Agriculture, Sohag University, Egypt during the successive seasons of 2010 and 2011. The genetic material used in the present investigation consisted of nine parental lines: A3 (B73, provided by ENS de Lyon, France), (B3, B5, B8 and B10) which are Egyptian lines produced by Department of Maize Research, Agricultural Research Center (ARC), Egypt and (C1, C12, C15 and C16) are sub-tropical maize produced by the International Maize and Wheat Improvement Center (CIMMYT) in Zimbabwe. The Single cross hybrid-10 (S.C.10) which is produced by the Ministry of Agriculture in Egypt is considered the best yielding hybrid in Egypt was used as a check.

In the summer season of 2010, the nine parental lines were arbitrary divided into four parents as males (B3, B5, C1, and C12) which were crossed with five parents (A3, B8, B10, C15 and C16) as females so as to produce 20 crosses in NCDII. All parental lines were self pollinated to obtain additional seed from each one.

In the summer season of 2011, the nine parental lines, the 20 F_1 crosses and the S.C.10, were sown in two contrasting conditions, under normal and drought conditions (15 May). The material was laid out in a RCBD with three replications. Each block consisted of 30 plots (9 plots for the parents, 20 plots for the F_1 hybrids and one plot for the S.C.10). Each plot consisted of three rows of 21 plants spaced 30 cm a part within the row, while the rows were set 70 cm a part. The irrigation was applied each 7 days in the normal conditions, and each 12 days in the drought conditions. All other agricultural practices were applied as recommended for maize production.

Data were recorded on five random plants/replicate (size of family, m = 15

plants) for number of days to pollen shedding and grain weight per plant.

Statistical and biometrical analyses

Data of the different measured traits for the parental lines and their 20 F_1's crosses were subjected to the conventional statistical analysis, the type of the analysis performed and the mean squares are as shown in Table (1). The NCDII analysis was performed for the 20 interlines crosses according to the method of (Mather and Jinks, 1971). The type of analysis employed and the expected mean squares (EMS) as shown in Table (2).

Genetic parameters were calculated as: $\sigma^2_f = \frac{1}{8}\ \sigma^2A$; $\sigma^2_m = \frac{1}{8}\ \sigma^2A$

$\sigma^2_{fm} = \frac{1}{16}\ \sigma^2D$

Heritability in narrow sense was calculated as:

$$h_n^2 = \frac{\sigma^2A}{\sigma^2A + \sigma^2D + \sigma^2W}$$

Where: σ^2A = additive variance
σ^2D = dominance variance
σ^2W = within families variance

Drought susceptibility index (DSI) is calculated according to the method of Fischer and Maurer (1978). Yield of individual genotypes is determined under drought stressed (Yd) and favorable (Yw) conditions. Data on average yield of all varieties under drought (Xd) and well-favorable conditions (Xw) are used to calculate drought intensity (D) as:

$$D = 1 - \frac{Xd}{Xw}$$

Then the drought susceptibility (S) of individual genotypes is calculated as:

$$Yd = Yw\ (1\text{-}SD),\ S = \frac{Yw - Yd}{YwD}$$

Genotypes with average susceptibility or resistance to drought have an "S" value of 1.0. Values of less than 1.0 indicate less susceptibility and greater resistance to drought. Meanwhile, a value of S=0 indicates maximum possible drought resistance (no effect of drought on yield).

Heterosis was calculated using the Mid-parent as:

$$H = \frac{\overline{F_1} - \overline{P}}{\overline{P}}\ X\ 100$$

Where; H= Heterosis, $\overline{F_1}$ = Mean of the F_1 crosses and $\overline{P}$ = Mid-parent value.

RAPD experiments

Fresh young leaves were harvested from three weeks old seedlings and immediately ground in liquid nitrogen. The total genomic DNA was extracted using cetyltrimethylammonium bromide (CTAB) protocol (Poresbski *et al*., 1997). The quality of the DNA was checked by electrophoresis in 1% agarose gels containing ethidium bromide (0.5 mg ml-1) in ½ x TBE [89 mM Tris-HCl, 89 mM boric acid, and 2 mM EDTA (ethylenediaminetetr-acetic acid)]. RAPD technique was conducted using 7 arbitrary 10-mer primers (Metabion International AG, Germany, Table 5).

Amplification was carried out in a DNA Thermal Cycler (Primus 25, Germa-

ny) according to the method described by Williams *et al.* (1990). The RAPD assay was performed in a 25 µl volume containing 12.5 µl of Go Taq® Green Master Mix (Promega, Madison, USA), 3.5 µl of primer 5 pmol, 7 µl of free nuclease water and 2 µl of 150 ng DNA template. A negative-DNA control was performed by adding 1 µ of sterile ultra pure deionized water. The Thermal Cycler was programmed by an initial denaturation cycle at 94°C for five minutes. The following 47 cycles were composed of: denaturation step at 94°C for 1 min, annealing step for 1 min 45 s at 38°C and elongation step at 72°C for 2 min. The final cycle of polymerization was performed at 72°C for 7 min. The amplification products were electrophoresed in a 1% agarose gel stained with 0.2 µl ethidium bromide. The amplified fragments were visualized and photographed using UVP Bio Doc-It imaging system (USA).

DNA banding pattern analysis

DNA banding patterns generated from RAPD experiments were analyzed by computer program, Gene Profiler (version 4.03). The presence (1) or absence (0) of each band was recorded for each parental lines and S.C.10 for the seven primers used. Genetic similarity estimates were determined using Nei & Li coefficient's (Nei and Li, 1979). Dendrogram was generated with the unweighted pair group method with arithmetic mean (UPGMA) algorithm using the computational package MVSP version 3.1.

Similarity matrix analysis

Data analysis based on the means of number of days to pollen shedding, grain weight, and values of drought susceptibility was initially performed using the similarity percent. The hierarchical cluster analysis (Kaufman and Rousseeuw, 1990) was used to investigate patterns of phenotypic diversity existing in these parental lines. Group average hierarchical cluster analysis by MVSP (version 3.1) program used to develop a dendrogram.

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance for number of days to pollen shedding and grain weight per plant under normal (N) and stress (D) conditions is presented in Table (1). Highly significant differences existed among genotypes (parents and their 20 F_1's crosses) under normal and drought stress conditions for studied traits, revealing a large amount of variability among them. Parents vs. crosses, as an indication of average heterosis over crosses, were highly significant under the two environments for the studied traits

Analysis of variance of North Carolina Design II under normal (N) and stress (D) conditions for all studied traits is presented in Table (2). The two main effects of “males” and “females” were highly significant under normal and drought stress conditions for the studied traits, reflecting the existing of additive

gene variance. Mean square due to the "males x females" interaction was also highly significant under both environments for the two studied traits, revealing the importance of dominance variance in the inheritance of these traits.

Mean performances

Mean performances of the parental lines and their respective 20 crosses for the two studied traits under normal (N) and stress (D) conditions are shown in Table (3). The results showed that the range of mean performance of days to pollen shedding for the nine parental lines was quite wide extending from extreme earliness of line A3 (55.7 days in favorable and 53.3 days in drought environments) to lateness of line C12 (84 days in favorable and 80.3 days in drought environments). The best cross for earliness was (A3 x B3) with the mean values of 54.3 days and 52.7 days under normal and drought stress conditions, respectively. As for grain weight per plant, mean performances ranged from 24.0 g for line B8 to 37.5 g for line B5 under normal conditions. While the range was narrower extending from 15.9 g to 22.1 g for B10 and B5 lines, respectively, under drought stress. The highest crosses for grain yield were (C16 x C12) under normal conditions and (B10 x B3) under drought stress. Therefore, these promising crosses among F_1 hybrids could be used for further breeding studies to improve these traits in maize.

Drought susceptibility index

The results of drought susceptibility index (DSI) (Table 3) indicated that the parental lines A3, B8, C12 and C16 showed DSI values of 0.39, 0.38, 0.74, and 0.99, respectively, revealing relative drought resistance. Maciej *et al.* (2012) showed that the variation of DSI for maize ranged from 0.381 to 0.65 and for triticale from 0.35 to 0.58. On the other hand, C1 and B10 parental lines were found to be the most susceptible. As for the F_1 crosses, nine out of the 20 F_1 crosses showed relative drought resistance (DSI<1). In general, the crosses that involved A3 as a common "female" were, on average, relatively tolerant to drought indicating that this trait is transmissible to progeny. In this direction, three particular crosses, namely (B10 x B3), (C15 x C12) and (C16 x C12) exhibited an excellent performance under drought conditions with the mean grain yield per plant approaching closely that of the check S.C.10 that displayed relative susceptible to drought with DSI value being 1.43. Similar results obtained by Stanisław (2001); Shirinzdeh *et al.* (2010) between maize hybrids**.** The intensity of drought was rather strong with grain yield per plant being reduced by 26% under drought.

Estimates of heterosis

Estimates of heterosis (Table 3) showed that flowering of, 9 and 10 out of 20 crosses were significant flowered than their mid-parents with negative heterosis values ranging from (-4.07% to -20.56%) and (-2.94% to -19.29%) under normal

and drought conditions, respectively. Concerning grain weight, estimates of heterosis were highly positive significant for all crosses under both environments. Heterotic values ranged from 28.45% to 208.36% for crosses (C16 x B5) and (C16 x C12), respectively under normal conditions. Whereas, the heterotic values were increased and ranged from 78.45% to 286.03% for crosses (C15 x B3) and (B10 x B3), respectively under drought conditions. Generally, the superiority of some crosses over their mid parents reflects the important role of non additive genetic variance in the inheritance of these traits.

Estimates of genetic parameters

Estimates of all types of gene action for the studied traits under two environments are presented in Table (4). The results showed that the magnitudes of non-additive genetic variance (σ^2D) were larger than those of additive ones (σ^2A) for number of days to pollen shedding under both environments. This finding reflects low estimates of narrow-sense heritability for this trait (0.07 and 0.04 under normal and drought conditions, respectively). Similar results were obtained by Shafey *et al*. (2002); Abd El-Maksoud *et al*. (2003); Fu *et al.* (2008) and Mahdi *et al*. (2011). Concerning grain yield per plant, the magnitudes of additive genetic variance (σ^2A) were larger than those of non additive ones (σ^2D) under normal conditions. On the contrary, the dominance component (σ^2D) was relatively slightly larger than additive (σ^2A) one under drought conditions. These results reflect the high narrow-sense heritability estimates obtained under normal environment (0.85), as opposed to the reduced estimates obtained under drought environment (0.38). These results are in agreement with those obtained by Bolaños and Edmeades (1996); Fu *et al.* (2008) and Imtiaz (2009). However, Mahdi *et al*. (2011) obtained results showed non-additive genetic effects, indicating preponderance of non-additive gene effects for inheritance of the grain weight trait under normal conditions.

RAPD analysis

Detecting DNA Polymorphism

After screening, only seven out of twenty one 10-mer arbitrary primers produced polymorphic bands. Okumus (2007) showed that 160 primers were screened and 14 of them were found to be valuable for RAPD analysis and were used to amplify genomic DNA of the 17 maize accessions. A total of 62 fragments were generated by 7 primers with an average of 8.86 fragments per primer (Table 5). Strong and weak bands were produced in the RAPD experiments (Fig. 1). The number of amplification bands (Table 5) by each primer varied from 5 (OPW-08) to 13 (OPAT-08), these fragments are in a range of 99 (OPW-08) to 943 bp (OPAT-08). Valdemar *et al.* (2004**)** obtained similar results in maize RAPD analysis, the fragments were in a range of 104 to 2270 bp, were scored with an average of 8 fragments per primer**.**

In order to test the differences of band patterns from different primers

among maize genotypes studied, similarity matrix was first calculated. A total of 48 bands was polymorphic across the entire samples were observed with the percentage of polymorphic bands ranged from 40% to 100% with an average of 76.14%. Similar results obtained by Heun and Helentjaris (1993); Lanza *et al*. (1997); Moeller and Schall (1999) and Valdemar *et el.* (2004), and in other species obtained by Tanttawi *et al.* (2007) in faba bean and Abdel-Sabour *et al.* (2010) in cowpea and phaseolus RAPD experiments. This result of polymorphic bands was smaller than (89%) obtained by Okumus (2007). Analysis of genetic diversity involving maize lines showed that 150 polymorphic fragments were sufficient to stabilize the dendrogram (Lanza *et al*., 1997; Pejic *et al*., 1998). However, according to Thormann *et al.* (1994), the number of bands giving a particular variation coefficient depends on the nature of the genotypes analyzed.

Phylogenetic tree based on RAPD

Values of similarity coefficient matrix for nine parental lines and the check S.C.10 were calculated and used for UPGMA cluster analysis (Fig. 2A). The phylogenetic tree showed that the nine parental lines and the check S.C.10 were separated into two main groups. The group (a) contained only line A3 which clustered at 77% level of similarity with the group (b). The group (b) sub-divided into four sub-groups. The sub-group 1 contained line B3 which clustered with line B10 at 92% level of similarity and line C1 which clustered with line C15 at 92% level of similarity. The B8 line formed in single branch, which clustered with (C1 and C15) at 90% level of similarity. The sub-group 2 contained line C16, which clustered with the sub-group 1 at 85% of similarity level. In the sub-group 3, B5 and C12 lines were separated at 92% level of similarity. The check S.C.10 formed in single branch belong sub-group 4, which clustered at 82% level of similarity with other sub-groups. There were close relationships among these genotypes (group b), which clustered with a similarity coefficient from 82% to 92%. Valdemar *et al*. (2004) obtained similar results with a similarity coefficient of between 82% and 90%. Moeller and Schall (1999**)** discussed the similarity index changing from 44% to 80% in Native American maize collections of Great Plains by RAPD markers. In Brazilian accessions had a similarity varied from 78% to 91% (Carvalho *et al*., 2004). The similarity in Turkish flint accessions was in range from 0.05 to 0.88 with high variability. ISSR and RAPD markers were also used to estimate the polymorphic indexes of diploid, tetraploid, and hexaploid wheat species **(**Nagaoka and Ogihara, 1997) and varieties of *Oriza sativa* (Beverley *et al*., 1997).

Phylogenetic tree analysis based on studied characters

The dendrogram analysis (Fig. 2B) showed that the genotypes created two distinct clusters at similarity percent of 58% between the S.C.10 in the first cluster

and the rest of genotypes that formed the second cluster. The second cluster created three sub-clusters. The sub-cluster 1 contained lines A3, B8 and C12. The sub-cluster 2 contained lines B10, C1, C15 and C16. The Egyptian lines B3 and B5 clustered at 91% level of similarity in the sub-cluster 3. Lines A3 and B8 clustered at 96% level of similarity in the sub-cluster 2, these two lines clustered with line C12 at similarity level of 87%. The CIMMYT Lines C1 and C16 clustered at the maximum level of similarity (97%) in the sub-cluster two.

The dendrograms based on RAPD technique and morphological characters showed a variations in genetic similarity between the S.C.10 and the nine parental lines. Parentoni *et al.* (2001) showed that there was an association between the dendrograms obtained by RAPD markers and morphological characteristics. Good agreement between known pedigree obtained by morphological data and phylogeny among open pollinated varieties estimated by RAPD has been reported by Yu and Pauls (1993) and Kongkiatngan *et al.* (1996).

SUMMARY

The range of mean performance of studied characters was quite wide among all genotypes under normal and drought conditions. Highly significant differences existed among nine parental maize lines and their 20 F_1's, revealing a large amount of variability among them under both environments. The significant of mean square of parents vs. crosses observed, indicating the importance of heterotic values and non additive genetic variance in the inheritance of these traits. Some lines and their F_1's crosses showed drought susceptibility index (DSI) values less than one revealing relative drought resistance. The results showed that the magnitudes of non-additive genetic variance (σ^2D) were larger than those of additive ones (σ^2A), indicating that non additive gene action was pronounced in the inheritance of traits. Therefore, these promising crosses could be used and utilized in maize breeding program to improve these traits under different conditions. This finding could be emphasized by the estimate values of narrow sense heritability. A total of 48 bands were polymorphic across the entire samples with an average of 76.14%. The phylogenetic tree based on RAPD markers showed that the genotypes were separated into two main groups, in which line A3 was separated from the other lines in the first group with a branched-off 77% level of similarity. The other lines were clustered together in the second group, which sub-divided into four sub-groups with a breached-off 82% genetic similarity. The phylogenetic tree based on morphological characters showed that the similarity percent ranged from 70.1% to 96.9%.

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Table (1): Analysis of variance of the 9-parental lines and the 20 F_1's crosses for studied traits under normal (N) and drought (D) conditions.

SV	d.f.		Number of days to pol-len-shedding		Grain yield	
			N	D	N	D
Replications	(r-1)	2	0.3	2.7**	330.9**	459.7**
Between entries	(b-1)	28	1884.3**	1854.9**	5877.1**	3846.3**
Among parents	(c-1)	8	1248.9**	1104.6**	354.5**	111.0**
Among F_1	(d-1)	19	2180.5**	2240.0**	3382.3**	1666.0**
Parents vs. F_1	(1)	1	1341.0**	539.8**	97459.3**	75154.4**
Error	b(m-1)	406	1.3	1.0	13.6	5.0

Where: r = number of replications; b = number of all entries (parents and F_1's); c = number of parental lines; d = number of F_1's; m = size of family. All items where tested against the error of mean square. (**, * Significant at 0.01 and 0.05 levels, respectively).

Table (2): North Carolina Design-II analysis of variance for studied traits under normal (N) and drought (D) conditions.

SV	d.f		Number of days to pollen-shedding		Grain yield	
			N	D	N	D
Replications	(r-1)	2	0.42 NS	2.07 NS	257.00	387.57*
Between males	(n1-1)	3	2446.95**	665.78**	9799.33**	2332.31**
Between females	(n2-1)	4	1767.46**	1999.78**	1875.35**	847.24**
Males x Females	(n1-1) (n2-1)	12	2336.68**	1957.24**	2110.50**	1655.39**
Within families	n1n2 (m-1)	280	0.44	0.48	3.2	2.5

Where: r = number of replications; n_1 = number of "females"; n_2 = number of "males" and m= size of family. (**, * Significant at 0.01 and 0.05 levels, respectively).

Table (3): Mean performances and heterosis of the studied traits under normal (N) and drought (D) conditions as well as DSI.

Genotypes		Mean performance				Heterosis				DSI
		Number of days to pol-len-shedding		Grain yield (gm)		Number of days to pollen-shedding		Grain yield (gm)		
		N	D	N	D	N	D	N	D	
Females	A3	55.7	53.3	24.8	21.5	-	-	-	-	0.39
	B8	74.3	71.7	24.0	20.9	-	-	-	-	0.38
	B10	68.7	64.7	28.2	15.9	-	-	-	-	1.28
	C15	80.7	77.3	32.2	20.0	-	-	-	-	1.11
	C16	82.7	79.3	32.1	21.3	-	-	-	-	0.99
Males	B3	81.0	77.3	31.7	19.9	-	-	-	-	1.09
	B5	80.0	72.0	37.5	22.1	-	-	-	-	1.21
	C1	78.0	73.3	30.4	16.4	-	-	-	-	1.35
	C12	84.0	80.3	25.3	18.9	-	-	-	-	0.74
A3 x B3		54.3	52.7	62.1	40.1	-20.56**	-19.29**	119.82**	93.72**	1.43
A3 x B5		70.0	65.3	42.5	40.8	3.17**	4.23**	36.44**	87.16**	0.16
A3 x C1		68.0	63.7	59.8	55.1	1.72**	0.63 n.s	116.67**	190.77**	0.31
A3 x C12		71.7	70.0	61.2	43.6	2.65**	4.79**	144.31**	115.84**	1.15
B8 x B3		78.0	70.0	55.6	37.2	0.45 n.s	-6.04**	99.64**	82.35**	1.32
B8 x B5		87.0	85.7	69.7	50.5	12.77**	19.28**	126.67**	134.88**	1.10
B8 x C1		73.0	66.0	66.8	51.9	-4.14**	-8.97**	145.59**	178.28**	0.89
B8 x C12		90.0	85.3	55.6	38.9	13.71**	12.24**	125.56**	95.48**	1.20
B10 x B3		79.3	61.0	79.4	69.1	5.95**	-14.08**	165.11**	286.03**	0.52
B10 x B5		74.7	71.7	50.3	36.7	0.47 n.s	4.90**	53.12**	93.16**	1.08
B10 x C1		66.3	62.7	66.7	52.5	-9.61**	-9.13**	127.65**	225.08**	0.85
B10 x C12		70.0	64.7	49.0	45.1	-8.32**	-10.76**	83.18**	159.19**	0.32
C15 x B3		91.7	89.7	46.5	35.6	13.41**	16.04**	45.54**	78.45**	0.94
C15 x B5		73.7	67.3	73.6	48.2	-8.28**	-9.85**	111.19**	128.97**	1.38
C15 x C1		83.7	81.7	82.9	47.5	5.48**	8.49**	164.86**	160.98**	1.71
C15 x C12		79.0	75.0	85.7	63.5	-4.07**	-4.82**	198.09**	226.48**	1.04
C16 x B3		80.0	76.0	54.3	43.0	-2.26**	-2.94**	70.22**	108.74**	0.83
C16 x B5		78.0	75.7	44.7	40.5	-4.12**	0.07 n.s	28.45**	86.64**	0.38
C16 x C1		91.7	86.3	69.5	44.4	14.13**	13.11**	122.4**	135.54**	1.44
C16 x C12		71.0	62.7	88.5	65.1	-7.62**	-16.04**	208.36**	223.88**	1.06
S.C.10		78.0	68.0	80.9	61.1	-	-	-	-	1.43

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

Table (4): Estimates of the genetic parameters for 20 F_1 crosses under normal (N) and drought (D) conditions.

Characters	Number of days to pollen shedding		Grain yield	
Genetic parameters	N	D	N	D
σ^2_f	22.05	-258.29	1537.70	135.4
σ^2_m	-142.31	10.64	-58.78	-202.05
σ^2_{fm}	155.75	130.45	140.5	110.2
σ^2_w	0.44	0.48	3.2	2.5
σ^2A	176.43	85.08	12302.6	1083.1
σ^2D	2492.0	2087.20	2247.8	1763
h_n^2	0.07	0.04	0.85	0.38

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

Table (5): Primers used in RAPD analysis, total number of fragments detected by each primer and polymorphism among nine parental lines and the S.C.10 of maize.

Primer Name	Primer Sequence (5'---------3')	Amplified bands		Polymorphic bands %	Fragment size base pair (bp)	
		Fragments number	Polymorphic		Larger	Smaller
OPAV-13	CTGACTTCCC	8	6	75%	507	191
OPW-08	GACTGCCTCT	5	3	60%	870	99
OPAT-08	TCCTCGTGGG	13	12	92%	943	223
OPP-05	CCCCGGTAAC	10	4	40%	400	100
OPW-13	CACAGCGACA	11	10	91%	637	137
OPAM-01	TCACGTACGG	7	7	100%	800	173
OPAR-05	CATACCTGCC	8	6	75%	935	282
Total		62	48			
Mean		8.86	6.86	76.14%		

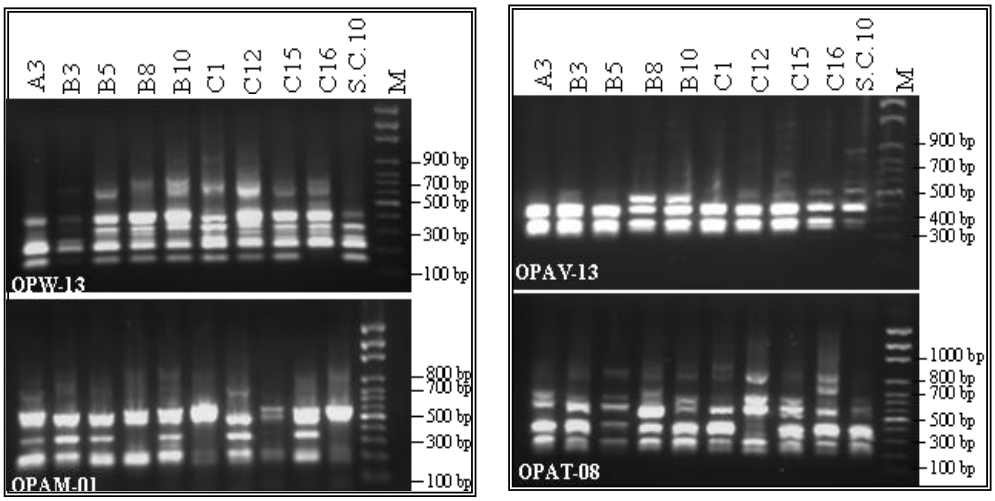

Fig. (1): RAPD profiles obtained for 10 maize genotypes amplified with some used primers, M=100 bp ladder size marker.

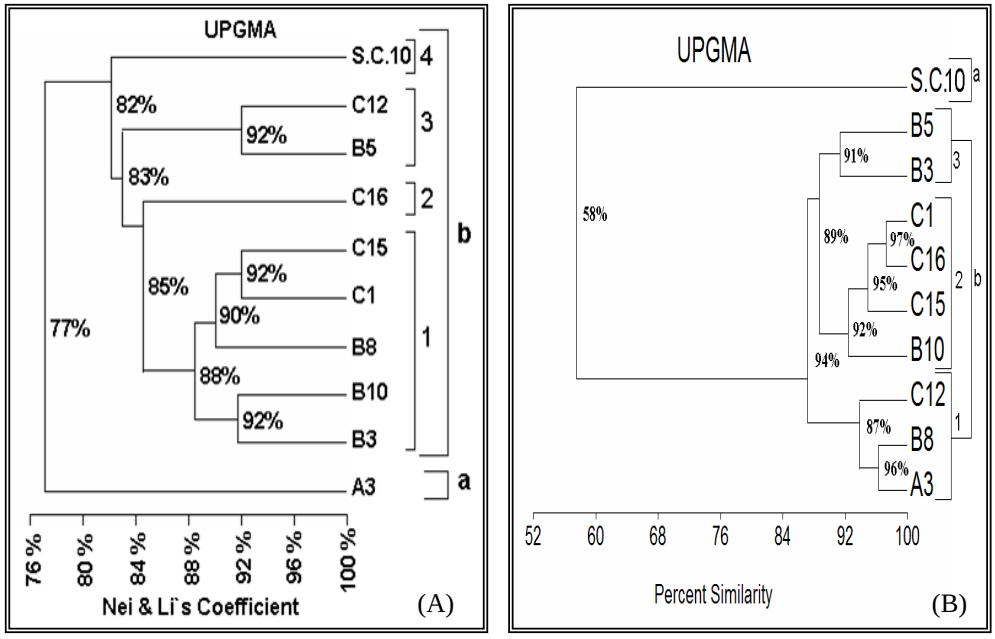

Fig. (2): Dendrograms generated by UPGMA cluster analysis using: (A) 62 RAPD fragments generated and (B) using values of characters studied among 9-parental lines and the check S.C.10.