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Genetic Diversity For Grain Yield And Physiological Parameters Under Mild Water Stress Condition in Maize (*Zea mays* L.)

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ABSTRACT

The extent of genetic divergence between genotypes in the present experimental material was observed by Mahalanobis D^2 analysis. In the present investigation based on D^2 analysis, 49 genotypes were grouped into 8 clusters. The magnitude of D^2 values suggested that there was consideration amount of diversity in the experimental material used in investigation. Maximum divergence was found between cluster III and VIII, suggesting that the genotypes in these clusters could be fully exploited to explore the wide range of heterosis and to release good recombinant lines by intermating them in a definite design.

Key words : Maize D^2 analysis Cluster analysis Mild Water stress condition.

Maize (*Zea mays* L.) is one of the important food and industrial crops grown extensively in major parts of the world. The crop is cultivated in a wide range of environments than either Wheat or Rice because of its wider adaptability. There are several abiotic factors limiting maize production in different parts of the world. Among them, drought is one of most important factors limiting maize production. To stabilize the production for year, emphasis should be given to the screening and identification of genotypes under artificially created moisture stress condition and it is a pre-requisite to achieve the goals of high yield and moisture stress tolerance. Keeping with this in view, the present investigation was undertaken to study the extent of genetic diversity in 49 genotypes under mild water stress condition.

MATERIAL AND METHODS

The experiment material for the present investigation comprised of 49 genotypes including two checks viz., CM-211 and CM-119. The experiment material was sown in 7X7 simple lattice design with two replications. The trail was subjected to water stress at the flowering stage and further irrigation released as per schedule (four irrigations). each genotype sown in three rows of 5.0 m length with a spacing of 75X20 cm. Recommended package of practices were followed to raise a good crop. Data were recorded on five randomly selected plants in each entry in each replication for the following traits viz., Days to 50% tasseling, days to 50% silking, Anthesis-Silking interval (days), Chlorophyll content at 50% silking (SPAD-unit), Flag leaf area (cm2), No.of leaves above ear, Leaf Senescence (scored by visual rating using a scale of 1-no leaves senescenced to 5-all leaves senescenced), days to physiological maturity, Plant height (cm), Ear length (cm), Ear girth (cm), 100 seed wt (g) and Grain yield per plant (g). Data was subjected to Mahalanobis D^2 analysis to study genetic divergence between genotypes for various traits under study. Based on the D^2 values the inbreds were grouped into clusters of genetically closer related groups following the Tocher's method (Rao,1952).

RESULTS AND DISCUSSION

Forty-seven genotypes along with two checks which were subjected to D^2 analysis (Mahalanobis, 1939), revealed the presence of substantial amount of genetic diversity among them.

Based on D^2 values, 49 genotypes were grouped into 8 clusters, The distribution of genotypes into different clusters are presented in table 1. Data on cluster means is presented in table 2. From the data it was observed that considerable differences existed among the genotypes between

Table 1. Distribution of 49 genotypes into different clusters.

Cluster No.	No.of Genotypes	Genotypes
I	6	EI 30-1-1-1-2-1-1-2; BHOL-444-2-1-1-1; DMR-149-1-1-1-1-1-1-1-1; DMR-332-5-1-1-1-®; CM-119; CM-211
II	3	EI-28-2-1-1-1-1-1; BML-492-1-1-1-2-1- ; BSRL-12-1-1-;
III	1	BML-497-3-1-1-1
IV	8	DMV12-1-2-1-1-1-1-1-2; TQPM42-1-2-1-2-1-1-1; BHOL-444-1-1-1-1; BHOL-212-1-1-1-2-1; BML-483-1-1-1; BHOL-383-1-1-1; TQRM 27-1-1-1-3-1-1-1-1-1; TQPM27-2-1-1-2-1
V	14	BML-497-1-1-1; EI-10-2-1-1-1-; BML-497-2-1-1-1; DMR-33-3-1-1-1-; EI-17-1-1-1-1-1-1; BL-497-8-1-1-1-; PN24E-1-2-1-1-4-1-1-1-1-1; DMR40E-1-4-1-1-1-1-1-1-1; PN4E-1-3-2-1-1-1-1-1; DMR-156-2-1-1-3-1-1-1-1; BHOL 212-3-1-2-1-1-; TQPM 34-1-2-1-1-2-1-1-1-1; EI 10-1-1-1-1-1-1-1-1; QPM (KR)-1-1-1-
VI	8	BQL-258-1-1-1-1; BML-497-12-1-2-1-; PN24E-2-1-1-1—1; DMR-332-8-1-1-1-; HOL OP 10-1-3-1-1-1-1; BQL-344-1-1-1-1; BSRL-16-1-1-1-; BQL-349-1-1;
VII	8	BQL-321-1-1-1-1; TQPM 34-1-1-1-1; BSRL-2-1-1-; BSRL-7-1-1-; HOLOP 25-1-1-1-2-1-1; BSRL-12-1-1-1-; DMR-332-1-1-1-1-1-1-1-1-1; HOLOP 10-1-1-1-1-1-1-1;
VIII	1	BQL-326-1-1

Table 2. Means of physiological, grain yield and its components under mild water stress condition.

S. No.	Cluster group	Days to 50% tasselling	Days to 50% silking	A.S.I.	Plant height (cm)	Leaf above ear	Chlorophyll Content (SPAD-units)	Leaf area / plant (cm2)	Leaf senese-cence
1.	Cluster I	75.66	60.91	5.25	157.84	7.04	50.44	478.73	2.29
2.	Cluster II	76.66	82.16	5.50	165.63	7.47	41.80	526.63	2.16
3.	Cluster III	67.50	74.00	6.50	183.43	8.50	34.61	672.15	1.75
4.	Cluster IV	73.25	79.56	6.31	167.27	7.10	47.70	382.79	1.93
5.	Cluster V	75.21	80.60	5.39	133.06	5.92	42.27	398.13	2.42
6.	Cluster VI	73.06	79.68	6.62	139.15	6.03	43.81	332.12	2.50
7.	Cluster VII	73.25	78.68	5.43	127.74	5.84	50.04	296.71	2.56
8.	Cluster VIII	80.00	85.50	5.50	173.18	7.21	54.46	256.15	1.50

S. No.	Cluster group	Days to Phy Maturity	Ear length (cm)	Ear girth (cm)	100 seed Weight (g)	yield plant (g)
1.	Cluster I	107.55	13.472	12.30	14.76	54.74
2.	Cluster II	107.54	13.49	12.63	18.57	70.95
3.	Cluster III	102.67	13.92	13.18	16.95	68.57
4.	Cluster IV	105.62	14.93	12.75	17.99	71.39
5.	Cluster V	106.59	12.13	11.70	15.26	47.37
6.	Cluster VI	106.05	11.93	11.23	13.85	44.46
7.	Cluster VII	105.54	11.77	11.05	14.33	42.38
8.	Cluster VIII	111.06	10.36	12.86	17.79	91.32

Table 3. Average intra (bold values) and inter clusterD^2 values of 8 clusters for 49 genotypes of maize (*Zea mays* L.).

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster
1 Cluster	**53.640**	153.072	941.966	242.314	163.457	427.684	704.706	1146.002
2 Cluster		**127.957**	523.736	538.864	436.467	864.087	1251.725	1746.422
3 Cluster			**0.000**	1865.321	1650.397	2468.871	3110.287	3933.361
4 Cluster				**83.534**	110.081	122.946	267.154	472.472
5 Cluster					**58.023**	135.626	292.830	633.077
6 Cluster						**27.788**	78.461	274.358
7 Cluster							**56.892**	206.450
8 Cluster								**0.000**

Table 4. Contribution of physiological, grain yield and yield components towards genetic divergence.

Source	Times Ranked 1st	Contribution %
1. Days to 50% tasseling	78	6.63%
2. Days to 50% Silking	1	0.09%
3. Anthesis-Silking interval	0	0.00%
4. Plant height (cm)	100	8.50%
5. Leaves above Ear	0	0.00%
6. Chlorophyll Content	48	4.08%
7. Flag Leaf Area (cm2)	870	73.98%
8. Leaf Senescence	9	0.77%
9. Days to Physiological Maturity	25	2.13%
10.EarLength (cm)	7	0.6
11.Ear Girth (cm)	5	0.43%
12. 100 Seed Weight (g)	9	0.77%
13. Yield/plant (g)	24	2.04%

clusters. The cluster means for days to percent tasseling was highest in cluster VII (80.00) while cluster III recorded least value (67.50). Cluster VIII had the highest mean value for days to 50 per cent silking (85.50) while cluster III had the lowest value (74.00). Cluster VIII had the value (111.06) while cluster III recorded least value (102.67) for the trait days to physiological maturity. For yield, cluster VIII had (91.32) and cluster VIII (42.38) respectively.

The average intra and inter cluster D^2 values are presented in table 3. Intra cluster values ranged from 0.00 (cluster III and cluster VIII) to 127.957 (cluster II). From the inter cluster distances it can be inferred that highest divergence occurred between cluster III and cluster VIII (3933.361) and least between cluster VI and VII (78.461) indicating wider diversity between genotypes in these clusters. Selection of parents from these diverse genotypes for hybridization programme would help in achieving novel recombinants. Similar results were obtained by Prasad and Singh, (1990), Singh *et al*., (1999) and Mirianda *et al*., (2003).

Contribution of different characters towards genetic divergence is presented table 4. The maximum contribution towards genetic diversity was by flag leaf area per plant (73.98%) followed by plant height (8.50%). From the results it could be concluded that flag leaf area, plant height, days to 50% tasseling were important traits contributing towards genetic divergence and for the discriminating the genotypes. Similar results were

reported by Kumar and Sing, (2002) and Datta and Mukherjee, (2004).

The genotypes exhibited random pattern of distribution into various clusters showing that genetic diversity and geographical diversity is not related. This suggests that forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material plays an important role in the diversity of genotypes. Maximum divergence was found between cluster III and VIII, III and VII suggesting that the genotypes in these clusters with cross combinations i.e.,BML-497-3-1-1-1 with BQL-326-1-1 followed by 7 inbreds placed in VII cluster could be fully exploited to explore the wide range of heterosis and to release good recombinant lines to tolerate water stress condition by intermating them in a definite design.

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