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GENETIC DIVERSITY UNDER DIFFERENT ENVIRONMENTS IN MAIZE (*ZEA MAYS* L.)

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ABSTRACT

Sixty four genotypes of maize (*Zea mays* L.) belonging to different geographical regions of the world were tested under six different environments with a view to assess the impact of environments on the expression of genetic diversity. There was better expression of genetic diversity under winter environment than in rainy season, which indicated the need to conduct such analysis under more favourable environmental conditions to have a better picture of genetic differentiation between genotypes. The results also reflected that pairs of genotypes showing consistent D^2 value across the environments should be utilized in the breeding programme to evolve high yielding stable varieties.

Key words: Genetic diversity, Mahalanobis' D^2 statistic, stability, combining ability, maize.

The knowledge of genetic diversity in crop plants is of paramount importance for any breeding programme. The corn breeders are consistently emphasizing the use of diverse genotypes as a significant factor contributing to high yielding hybrids [1–3]. However, numerical data in terms of genetic distance (D^2 value) between genotypes showing the impact of environment in the expression of genetic diversity are lacking in maize. Therefore, an effort has been made here to study the role of environment in the genetic differentiation of genotypes under six different environments. This study will also help the breeders in identifying the most suitable environments under which D^2 analysis should be conducted to have a more realistic picture of genetic divergence.

MATERIALS AND METHODS

The experimental materials consisted of 64 genotypes of maize (*Zea mays* L.) from six different geographical regions of the world, viz U.S.A., Mexico, Thailand, Indonesia,

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Pakistan and India. These 64 genotypes were random mating populations maintained under isolation, except three hybrids. They were tested at three locations in Bihar during winter season of 1982–83 and rainy season of 1983.

The trials were conducted in R.B.D. with two replications under uniform cultural and manurial practices. The data recorded on 12 quantitative characters, viz days to tassel, days to silk, days to brown husk, plant height, ear height, ear length, ear girth, kernel rows, kernels/row, shelling per cent, 1000-kernel weight, and grain yield, were subjected to multivariate analysis using Mahalanobis' D^2 technique, while the grouping of 64 genotypes into different clusters was done using Tocher's method [4].

RESULTS AND DISCUSSION

The ANOVA of different characters indicated that higher significant differences existed among the genotypes for all the characters in all the six environments. Wilk's 'λ' test [5] also revealed highly significant differences among the genotypes for the aggregate effect of all the characters under each of the six environments (Z value in E_1=41.04,** E_2=42.85,** E_3=36.80,** E_4=35.39,** E_5=42.90,** and E_6=41.20**). Thus, both the tests revealed considerable divergence among the genotypes.

The mean values based on all the 64 genotypes for the different traits varied from environment to environment, which indicates differential impact of environment on the gene expression which ultimately affected the phenotypic expression (Table 1). The mean

Table 1. Mean values (64 maize genotypes) of different traits under different environments

Character	Character means in different environments					
	E_1	E_2	E_3	E_4	E_5	E_6
Grain yield (kg/ha)	4229.0	4399.0	2325.0	735.0	875.0	2462.0
Days to tassel	96.0	93.3	107.6	54.5	52.5	50.4
Days to silk	102.5	99.2	113.3	61.5	58.5	56.8
Days to brown husk	151.6	145.3	155.8	85.3	86.7	86.1
Plant height (cm)	120.0	182.9	124.3	124.4	142.5	156.5
Ear height (cm)	44.9	62.7	51.2	50.3	58.4	68.7
Ear length (cm)	13.0	15.4	13.9	9.0	10.8	12.6
Ear girth (cm)	4.1	4.7	4.3	3.1	3.5	3.8
Kernel rows/ear	13.4	13.5	12.9	12.0	12.2	12.9
Kernels per row	27.5	32.4	30.1	22.5	25.0	29.4
Shelling per cent	81.1	82.4	82.0	76.9	77.7	82.8
1000-kernel weight	282.0	320.0	241.6	167.4	187.6	212.7

values were higher for almost all the traits for the winter season environments (E_1–E_3) than for the rainy season environments (E_4–E_6). The favourable interaction of genotypes with winter season environments might be because of increased photosynthesis under availability of sun-shine for a longer period, better availability of nutrients, and less natural hazards.

The expression of genetic diversity was better in the winter season environments as compared to rainy season. The D^2 values for the different pairs of genotypes varied from 5.2 to 1022.2 in the winter season environment E_2, whereas the same varied from 3.2 to 240.5 in the rainy season environment E_4. Further, the D^2 values even for the same pairs of genotypes varied from environment to environment (Table 2). It may be noted that D^2 values for only 5 out of 2016 pairs of combinations of 64 genotypes have been recorded just to show the trend of variation of D^2 value for the same pairs of genotypes in different environments. These results clearly indicated that environments played a significant role in the expression of genetic diversity between genotypes and there was better expression of genetic differentiation under winter season environments as compared to rainy season environments.

Table 2. D^2 values for five pairs of genotypes under six environments

Pairs of genotypes	D^2 in different environments					
	E_1	E_2	E_3	E_4	E_5	E_6
EC123540–EC123536	70.8	18.5	56.2	22.5	96.3	58.5
EC123536–OLO 73	649.3	743.5	679.3	199.4	510.9	613.8
EC123540–Pool 24	698.6	788.2	675.1	159.3	646.1	774.3
EC123540–Hi-starch	637.8	1022.2	672.2	152.8	359.3	643.8
EC123540–Ganga-5	752.6	844.8	612.5	171.1	515.2	859.8

The intra- and intercluster distances for one winter season environment (E_2) and one rainy season environment (E_4) are shown in Table 3. The maximum intra- and intercluster distances (D^2 values) in E_2 were found to be 65.2 and 982.1, respectively, while the same in E_4 were only 34.7 and 199.8, respectively. The larger intra- and intercluster distances under winter season environments reflected that there was better expression of genetic differentiation under winter season environments. Frey [6] also reported that nonstress environments led to very low G x E interaction effects in oats (*Avena sativa* L.) and gave a better picture of divergence at genotypic level. Singh and Gupta [7] and Varma and Gulati [8] also observed that estimates of genetic divergence in an environment conducive to maximal expression of genetic potential of strains in respect of various characters may provide the most realistic picture of genetic divergence. It was further observed that intra- and intercluster distances were larger under irrigated environments as compared to rainfed

environments and suggested that it would be more appropriate to study genetic diversity under favourable environments.

Table 3. Average intracluster and intercluster D^2 values in environments 2 and 4

Clusters		I	II	III	IV	V	VI	VII	VIII	IX
I	E_2	**47.8**	136.2	201.5	545.0	318.8	102.7	156.3	70.3	81.6
	E_4	**31.7**	131.6	102.0	62.9					
II	E_2	—	**50.4**	87.9	227.4	95.6	292.8	377.9	90.3	95.5
	E_4	—	**34.7**	181.0	137.6					
III	E_2	—	—	**15.3**	175.6	95.4	343.0	492.3	241.9	152.3
	E_4	—	—	**0.0**	199.8					
IV	E_2	—	—	—	**18.5**	89.6	839.8	982.1	419.4	496.5
	E_4	—	—	—	**0.0**					
V	E_2	—	—	—	—	**55.4**	524.2	658.9	245.3	215.7
VI	E_2	—	—	—	—	—	**65.2**	123.7	192.5	152.4
VII	E_2	—	—	—	—	—	—	**0.0**	233.3	265.9
VIII	E_2	—	—	—	—	—	—	—	**0.0**	109.8
IX	E_2	—	—	—	—	—	—	—	—	**0.0**

Note: The diagonal values (in bold) indicate intracluster distance.

E_2 — environment 2 (winter); E_4 — environment 4 (rainy season).

In spite of large variations in mean performance and D^2 values, a few genotypes, viz EC 123355, EC 123356, EC 123020, EC 123024, EC 123027, EC 120144, EC 120145, EC 120147, Across 7532 x D 743, Dholi 7633, Dholi 7742, TIWF, TLWD, TYFD, CM 601, CM 400 x CM 300, Lakshmi, M_3, Suwan White, Suwan Yellow, Soan White, and D 772 consistently occupied the same cluster in all the six environments, indicating that they are relatively stable and can be utilized in the breeding programme to evolve high yielding stable varieties. Two of the above genotypes, CM 601 and CM 400 x CM 300, have been used in the production of a double top cross hybrid (CM 400 x CM 300) x CM 601, which is at present the most popular hybrid for winter cultivation in Bihar. The other two genotypes, viz Lakshmi and Suwan Yellow are the composite varieties developed at the Rajendra Agricultural University, Bihar, which are, respectively, the most adapted varieties for winter and kharif cultivation in Bihar.

Thus, on the basis of the results discussed above, the genotypes should be tested under more favourable environments to have a better picture of genetic divergence between them. Also, the pairs of genotypes showing stability in their D^2 values across the environments should be used to evolve hybrids with wider adaptability.

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