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Studies on Genetic Diversity of Certain Inbred Genotypes of Maize (*Zea mays* L.) at Varanasi

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ABSTRACT

Genetic diversity for yield and yield attributing characters was studied in maize using thirty nine inbreds of maize. The thirty nine inbreds of maize were categorized into twelve clusters. Based on genetic divergence intra cluster values ranged from 0.00 (mono genotypic clusters III, IV, V, VI, VII, VIII, IX, XI and XII) to 9.25 (cluster X). The minimum inter cluster distance was observed between cluster VI and cluster VIII (8.21) followed by between Cluster III and cluster V (8.28). The maximum inter cluster distance was observed between cluster III and cluster XI (16.89) followed by between cluster III and cluster XII (16.54). The contribution of each character towards total genetic diversity, in that out of 12 characters, grain yield per plant (31.71%), days to 50% tasseling (22.81%) and 100 grain weight (18.62%) contributed high for divergence.

Keywords - *Genetic diversity, Zea mays, Genotypes, Hybrids .*

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INTRODUCTION

In any plant breeding programme, determining the genetic diversity is an essential first step for identifying suitable parents for hybridization. Obviously the diverse parents are expected to through higher frequency of heterotic hybrids besides generating a broad spectrum of variability in segregating generations. Among the statistical tools, the D^2 statistics is useful multi varietal statistical tool for effective discrimination among various genotypes on the basis of genetic diversity. In the present study an attempt was made to assess the genetic diversity in maize inbreds in order to identify divergent parents from distantly related clusters for fruitful hybridization.

MATERIAL AND METHODS

The experimental material consisting of 39 genotypes was evaluated in randomized block design with three replications. Each entry was sown as single row of 3 meter length with row-to-row and plant-to-plant distance of 60 cm and 20 cm respectively. The observations on twelve quantitative characters namely days to 50% silking, days to 50% tasseling, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), ear weight without husk (g). ear weight with husk (g), number of kernel rows per ear, number of kernels pr row, 100-seed weight and grain yield per palnt (g) were recorded. Observations were recorded on five plants selected at random from each genotype in each replication and were averaged. These data were subjected to diversity analysis[4]. Inter cluster and intra cluster variances were calculated. Contributions of each character to total divergence were also estimated.

RESULTS AND DISCUSSION

The data were subjected to RBD analysis, the results given in Table 1 indicate that the treatment differences were found significant for all twelve characters studied, this indicated sufficient variability existing among the germplasm lines of maize. In present investigation, the inter-cluster values were found greater in magnitude than intra cluster distance suggesting the presence of diversity among the clusters indicating that genotypes included in the same cluster are less divergent than those in different cluster. The 39 germplasm lines of maize were grouped into twelve clusters, the germplasm lines of each cluster is presented in Table 2. Average intra and inter cluster distances for twelve clusters in thirty nine germplasm lines of maize is represented in Table 3.

Table 1. Analysis of variance for twelve characters in maize

Source of variation	d.f	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Ear weight without husk (g)	Ear weight with husk (g)	Number of kernel rows per ear	Number of kernels per row	100 seed weight (g)	Grain yield per plant (g)
Replications	2	0.717	2.111	7.031	6.285	1.208	0.005	21.482	5.875	0.243	0.824	1.285	62.106
Genotypes	38	63.719**	74.418**	759.404**	141.866**	12.000**	0.304**	1903.889**	1897.656**	7.592**	65.268**	43.051**	756.831**
Error	76	0.726	1.076	15.567	8.419	0.594	0.046	17.227	21.447	0.620	1.492	0.622	20.763
S.E. m ±		0.492	0.598	2.278	1.675	0.445	0.123	2.396	2.673	0.454	0.705	0.455	2.630
C.V (%)		0.752	0.895	3.730	7.210	5.137	5.287	5.279	4.606	6.127	5.566	3.661	7.940
C.D (5%)		1.386	1.686	6.416	4.718	1.253	0.349	6.749	7.531	1.281	1.986	1.282	7.410

*Significant at 5 per cent level: **Significant at 1 percent level.

Table 2. Grouping of thirty nine maize genotypes based on D^2 analysis

Cluster	Number of genotypes	Genotypes
I	20	HK1 17-2, 17, DMSC-4, HUZM-67, LM-16, WIN PINK L5-1, 72149, HUZM -79, 1105, 102, 1033-1, LTP-3, HUZM-3, HUZQPM-7, 193-1, HUZM-446, HUZM-4, CML-161, HUZM-48 and HUZM-53
II	7	HUZM-185, HUZM-711, HUZM-536, HUZM-705, 323, HUZM-488 and 294
III	1	HUZM-77
IV	1	LM-6
V	1	HUZM-722
VI	1	HUZM-427
VII	1	HUZQPM-8
VIII	1	HUZM-329
IX	1	P -7421
X	3	HUZM-509, HUZM-1 and HUZM-65-1
XI	1	LM-10
XII	1	HUZM-70-1

Table 3. Average intra (bold) and inter cluster distances for twelve clusters in thirty nine genotypes of maize

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**8.7**	10.44	10.69	11.02	10.08	10.89	12.12	11.24	11.25	10.91	12.67	13.58
II		**8.22**	15.55	11.69	13.93	12.48	14.67	14.35	13.73	14.3	11.34	14.23
III			**0**	13.36	8.28	14.78	13.38	12.02	11.35	9.56	16.89	16.54
IV				**0**	10.89	11.34	8.9	8.85	9.97	11.59	10.28	9.91
V					**0**	14.35	11.23	10.06	10.82	12.14	14.16	12.1
VI						**0**	9.86	8.12	12.53	10.35	10.04	13.4
VII							**0**	8.65	9.21	10.23	3.18	12.4
VIII								**0**	10.24	10.64	9.51	12.43
IX									**0**	11.4	15.44	16.41
X										**9.25**	14.37	14.79
XI											**0**	11.43
XII												**0**

Maximum inter cluster distance was found between cluster III and cluster XI (16.89) followed by between cluster III and cluster XII (16.54). The high magnitude of D^2 values in the above case showed that genotypes in different clusters are genetically more divergent probably due to geographical and reproductive isolation and may provide basis for consideration in hybridization programme. The minimum inter cluster distance was observed between cluster VI and cluster VIII (8.21) followed by between Cluster III and cluster V (8.28). The minimum value indicates narrow genetic diversity among genotypes. The similarity in the base material from which they had been evolved might be the cause of genetic uniformity. Inter-crossing of genotypes from divergent groups would lead to greater opportunity for crossing- over, which release hidden variability by breaking linkage[6]. Emphasis should be laid on characters contributing maximum D values for choosing the cluster for the purpose of further selection and choice of parents for hybridization. The contribution of each character towards total genetic diversity was given in Table 4. Highest contribution towards divergence in this regard was put forth by grain yield per plant similar results were reported by Kumar and Singh[3], Dutta and Mukharjee[2], Beyene *et al.*[1]. The other characters with high contribution towards yield were days to 50% tasseling and 100 grain weight.

The above results imply that in order to select genetically diverse genotypes for hybridization, the material should be screened for important traits like grain yield per plant, days to 50% tasseling and 100 grain weight. Days to 50% tasseling, days to 50% silking, ear diameter and number of kernel rows per ear recorded maximum mean values in cluster VI. Plant height, Number of kernels per row and grain yield per plant recorded high mean values in cluster XII. Ear height exhibited maximum mean values in cluster VII. Cluster IV exhibited highest mean values for ear length. Ear weight without husk, ear weight with husk, and 100 grain weight recorded maximum mean values in cluster XI.

Hence, it is worthy to note that in calculating cluster means, the superiority of particular genotype with respect to a given character gets diluted by other genotypes that are related and grouped in the same cluster but which are inferior or intermediary for that character in question. Hence, apart from selecting genotypes from the clusters which have high inter cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence with respect to a particular character of interest. It means that, if a breeder's intention is to improve seed yield and oil content, one can select parents which are highly divergent with respect to these characters.

CONCLUSION

From the present investigation, it was concluded that the 39 inbred lines of maize were categorized into twelve clusters. Cluster III, IV, V, VI, VII, VIII, IX, XI and XII were monogenotypic, rest being polygenotypic clusters. Cluster I had highest number of genotypes (20), followed by cluster II (7) and cluster X (3). The inter cluster distances were found greater in magnitude than intra cluster distances suggesting the presence of diversity among the clusters indicating that genotypes included in the same cluster are less divergent than those in different cluster. Maximum inter cluster distance was between cluster III and XI.

Table 4. Per cent contribution of characters towards diversity in maize genotypes

Sl. No	Character	Times ranked 1st	Percent contribution
1	Days to 50 % tasseling	169	22.81
2	Days to 50 % silking	1	0.13
3	Plant height (cm)	55	7.42
4	Ear height (cm)	21	2.83
5	Ear length (cm)	18	2.43
6	Ear diameter (cm)	1	0.13
7	Ear weight without husk (g)	7	0.94
8	Ear weight with husk (g)	29	3.91
9	Number of kernel rows per ear	5	0.67
10	Number of kernels per row	62	8.37
11	100 seed weight (g)	138	18.62
12	Grain yield per plant (g)	235	31.71

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