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K Mounika

Department of Genetics and Plant Breeding, Agricultural College, Bapatla, Acharya N G Ranga Agricultural University, Guntur, Andhra Pradesh, India

M Lal Ahamed

Department of Molecular Biology and Biotechnology, APGC, Lam, Guntur, Andhra Pradesh, India

Genetic divergence studies in maize (*Zea mays* L.) inbreds

K Mounika and M Lal Ahamed

Abstract

Selection of genetically diverse parents along with their per se yield performance is an important prerequisite to obtain better and desirable recombinants. Keeping this in view, forty seven maize inbred lines were characterized based on ten quantitative traits viz., days to 50% tasseling, days to 50% silking, days to maturity, plant height (cm), ear length (cm), ear height (cm), 100-seed weight (g), kernel rows per ear, number of kernels per row and grain yield per plant (g) using Mahalanobis D^2 statistic. D^2 analysis distributed the 47 genotypes into seven clusters of which cluster I was the largest with 12 genotypes. The highest intra-cluster distance was observed in the cluster IV (45.59). The maximum inter-cluster distance was observed between the clusters V and VII (436.57) indicating the importance of the genotypes present in these clusters for exploiting heterosis for the desirable traits of these clusters.

Keywords: Genetic divergence, inbreds, mahalanobis D^2 , maize

Introduction

Maize (*Zea mays* L.) is an important cereal crop belonging to tribe Maydeae of the grass family, Poaceae. Globally, maize is known as queen of cereals because it has the highest genetic yield potential among the cereals. It is the third most important cereal food crop of the world after wheat and rice which accounts for 9 per cent of the total food grain production. Being versatile, it also provides feed, fodder, fuel and serves as a source of basic raw material for a number of industrial products viz., starch, oil, protein, alcoholic beverages, food sweeteners, cosmetics and bio-fuel etc. and has occupied a prominent place in Indian agriculture.

In India it is cultivated over an area of 8.6 Mha with a production and productivity of 21.80 Mt and 2509 kg ha⁻¹, respectively. In Andhra Pradesh, maize is cultivated in an area of 0.23 Mha, with a production and productivity of 1.41 Mt and 6069 kg ha⁻¹, respectively (Director's Review 2016-17: ICAR-Indian Institute of Maize Research. www.iimr.res.in).

Success through hybridization followed by selection depends primarily on the selection of parents having genetic divergence for different characters. Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at the intra-cluster and inter-cluster levels (Murthy and Arunachalam, 1966)^[8]. D^2 statistic developed by Mahalanobis is a valuable tool in quantifying the degree of divergence. It helps the breeder to estimate the genetic divergence in the base population/germplasm and to classify the genetic stock into distinct groups for use in plant breeding programmes. Keeping this in view, the present investigation was planned with diverse inbreds developed and collected from different parts of the country for yield and yield components to know the genetic diversity among the genotypes.

Materials and Methods

The experimental material consisted of forty seven inbred lines of maize, was sown during rabi 2016-17 at Agriculture College Farm, Bapatla, Guntur district of Andhra Pradesh in a Randomized Block Design with three replications. Each entry was sown in two rows of 3 meter length with row-to-row and plant-to-plant spacing of 60 cm and 30cm, respectively. All the recommended package of practices were followed in order to raise a healthy crop. Observations were recorded on five randomly selected plants in each replication for yield traits like plant height, ear length, ear height, 100-seed weight, kernel rows per ear, number of kernels per row and grain yield per plant. However, observations for the characters namely

Correspondence

K Mounika

Department of Genetics and Plant Breeding, Agricultural College, Bapatla, Acharya N G Ranga Agricultural University, Guntur, Andhra Pradesh, India

days to 50 per cent tasseling, days to 50 per cent silking and days to maturity were recorded on plot basis.

Data was subjected to statistical analysis using Mahalanobis' D^2 statistic to determine the genetic divergence among the genotypes in terms of generalised group distance (Mahalanobis, 1928) [1]. The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952) [9]. The average intra and inter-cluster distances, cluster means and contribution of different traits to total divergence was estimated by the procedure given by Singh and Choudhary (1977) [10].

Results and Discussion

Pivotal condensation method measured the degree of diversification and determined the relative contribution of all the 10 characters to total divergence and was presented in Table 1. Among the characters studied 100-seed weight (34.51%) contributed maximum towards divergence followed by grain yield per plant (29.88%), ear height (12.21%), days to maturity (7.40%), number of kernels per row (6.29%), ear length (3.89%), days to 50% silking (2.59%), plant height (1.85%), kernel rows per ear (1.39%) and days to 50% tasseling (0.01%).

The forty seven genotypes were grouped into seven clusters using the Tocher's method (Table 2) with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values and the distribution of 47 genotypes into seven clusters is at random with maximum number of genotypes in cluster I (12 genotypes). The cluster III had eleven genotypes followed by cluster VII with eight genotypes, cluster IV with seven genotypes, cluster II with four genotypes, cluster V with three genotypes and cluster VI with two genotypes.

The average intra and inter-cluster D^2 values were presented in the Table 3. Intra-cluster D^2 values ranged from 0.00 (cluster III, V, VI and VII) to 45.59 (cluster IV). The high intra-cluster distance in cluster IV indicates the presence of wide genetic diversity among the genotypes present within this cluster. Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. The nearest and farthest clusters for each of the seven clusters are indicated in Table 4 and Figures 1 and 2.

The inter-cluster distances were worked out considering 10 characters and these distances were ranged from 20.68

(between clusters I and III) to 436.57 (between clusters V and VII). The maximum inter-cluster distance was observed between the clusters V and VII (436.57), followed by clusters III and VII (417.57), clusters VI and VII (380.37), clusters I and VII (358.57), clusters IV and VII (259.93) and cluster II and cluster VII (259.14) suggesting that there is wide genetic diversity between these clusters and crosses can be made between the genotypes of these clusters to obtain desirable transgressive segregants.

Cluster means indicated average performance of all genotypes present in a particular cluster. The cluster mean values for 10 characters are presented in Table 5. Days to 50% tasseling had a range of 54.33 days (clusters III and IV) to 61 days (cluster VI); days to 50% silking had a range of 61 days (cluster IV) to 67.67 days (cluster V); days to maturity had a range of 92 days (cluster III) to 103 days (cluster VI); plant height had a range of 148.69 cm (cluster II) to 204.47cm (cluster III); ear length had a range of 15.07 cm (cluster V) to 21.37 cm (cluster V)I; ear height values ranged from 51.20 cm (cluster V) to 70.13 cm (cluster III); 100-seed weight had a range of 12.85 g (cluster III) to 34.77 g (cluster VII); kernel rows per ear had a range of 11.87 (cluster V) to 17.87 (cluster VII); number of kernels per row had a range of 16.27 (cluster V) to 53.08 (cluster VI) and grain yield per plant ranged from 33.92 g (cluster V) to 170.96 g (cluster VII). The above results indicated a wide range of mean values between the clusters and these clusters can be exploited in the breeding programmes for the specific trait improvement.

For a successful breeding programme selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants. The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence in maize was already indicated by Lingaiah *et al.* (2013) [4], Hosen *et al.* (2014) [3], Maruthi and Jhansirani (2015) [7], Mani and Deshpande (2016) [6], Abhirami and Vanniarajan (2016) [1] and Varaprasad and Shivani (2017) [11].

Based on the inter-cluster distances, clusters V and VII are highly divergent and genotypes included in these clusters can be crossed. But as a rule along with genetic distance, *per se* yield and yield contributing characters should be taken into consideration. By considering these factors *i.e.*, genetic distance and *per se* performance, genotypes, CDM-342, C-2703-1, PDM-4251K and CM-138A-2, can be selected for the utilization in the breeding programmes as they had *per se* performance and present in divergent clusters.

Table 1: Contribution of different characters towards genetic divergence in 47 maize (*Zea mays* L.) inbreds.

S. No.	Source	No. of times ranked first	Per cent contribution
1.	Days to 50% tasseling	0	0.01
2.	Days to 50% silking	28	2.59
3.	Days to maturity	80	7.40
4.	Plant height (cm)	20	1.85
5.	Ear length (cm)	42	3.89
6.	Ear height (cm)	132	12.21
7.	100-seed weight (g)	373	34.51
8.	Kernels rows per ear	15	1.39
9.	Number of kernels per row	68	6.29
10.	Grain yield per plant (g)	323	29.88

Table 2: Clustering pattern of 47 maize (*Zea mays* L.) inbreds by Tocher's method.

Cluster number	No. of genotypes	Name of genotype (s)
I	12	PDM-260-2-1, PDM-4591, PDM-194-2, PDM-258-1, PDM-256-4, PDM-40-1, PDM-6508, PDM- 256-1R, PDM-4241, CDM-115, CDM-116, CDM-313
II	4	PDM-24-6A, PDM-3R, CDM-105, CDM-107
III	11	PDM-4441, PDM-24-3K, PDM-26-1A, PDM-4611, PDM-4131K, CM-1388, PDM-24-3R, PDM-6571, HK1-163-1, PDM-24-1, CDM-106
IV	7	PDM-71-2, PDM-84, PDM-113-2, PDM-203-1(PS-35-1), PDM-4131R-1, CDM-327, C-1746-1
V	3	PDM-4251K, CDM-342, C-2703-1
VI	2	CDM-320, CDM-306
VII	8	CM-138A-2, PDM-4351, PDM-96-1, CDM-309, CDM-311, C-2730-1, CDM-110, CDM-119

Table 3: Average intra and inter-cluster D² values among seven clusters with 47 maize (*Zea mays* L.) inbreds.

Cluster No.	I	II	III	IV	V	VI	VII
I	11.28	28.86	20.68	56.04	25.11	123.05	358.57
II		24.51	54.54	50.69	50.50	130.16	259.14
III			0.00	69.27	51.50	93.27	417.57
IV				45.59	97.27	132.32	259.93
V					0.00	177.82	436.57
VI						0.00	380.37
VII							0.00

Note: Diagonal values are intra-cluster distances. Off-diagonal values are inter-cluster distances

Table 4: The nearest and the farthest cluster from each cluster using Tocher's method in 47 inbreds of maize (*Zea mays* L.).

Cluster No.	Nearest cluster with D ² values	Farthest cluster with D ² values
I	III (20.68)	VII (358.57)
II	I (28.86)	VII (259.14)
III	I (20.68)	VII (417.57)
IV	II (50.69)	VII (259.93)
V	I (24.11)	VII (436.57)
VI	III (93.27)	VII (380.37)
VII	II (259.14)	V (436.57)

Table 5. Mean values of seven clusters estimated by Tocher's method from 47 maize (*Zea mays* L.) inbreds.

Cluster No.	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear length (cm)	Ear height (cm)	100 - seed weight (g)	Kernel rows per ear	No. of kernels per row	Grain yield per plant (g)
I	55.27	62.73	96.63	164.42	19.09	61.37	16.31	13.32	20.39	53.73
II	56.19	62.53	96.91	148.69	20.51	52.79	19.49	13.31	22.02	71.05
III	54.33	62.33	92.00	204.47	17.50	70.13	12.85	12.53	23.22	60.10
IV	54.33	61.00	93.12	165.38	20.64	62.10	19.19	14.83	24.49	81.57
V	60.67	67.67	102.67	150.20	15.07	51.20	16.47	11.87	16.27	33.92
VI	61.00	66.00	103.00	162.67	21.37	62.73	13.60	14.00	53.08	105.07
VII	56.33	61.33	96.00	182.27	17.13	66.40	34.77	17.87	27.27	170.96

Note: Bold figures indicate minimum and maximum values in each character

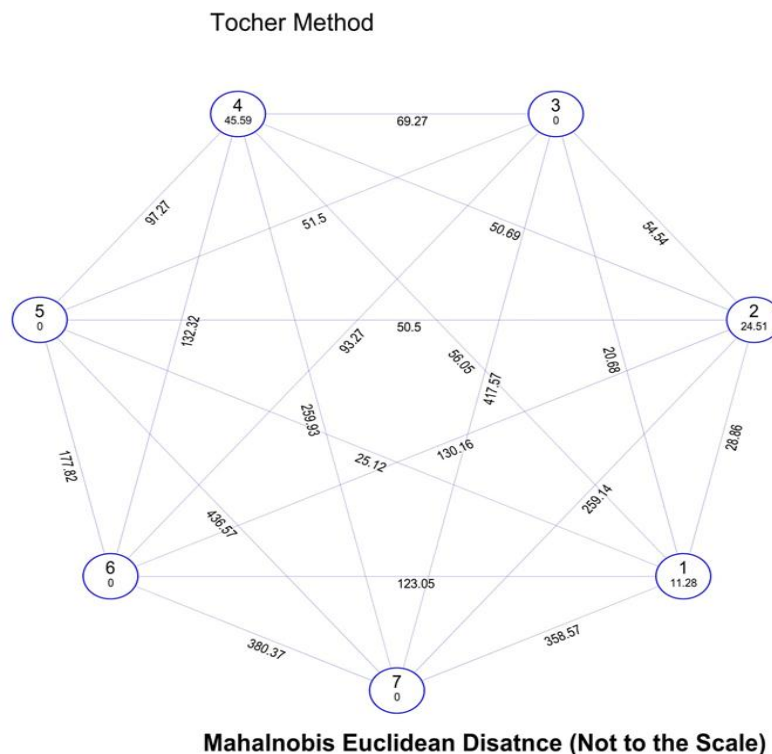


Fig 1: Intra and inter-cluster distance of 47 maize (*Zea mays* L.) inbreds in seven clusters based on Tocher's method

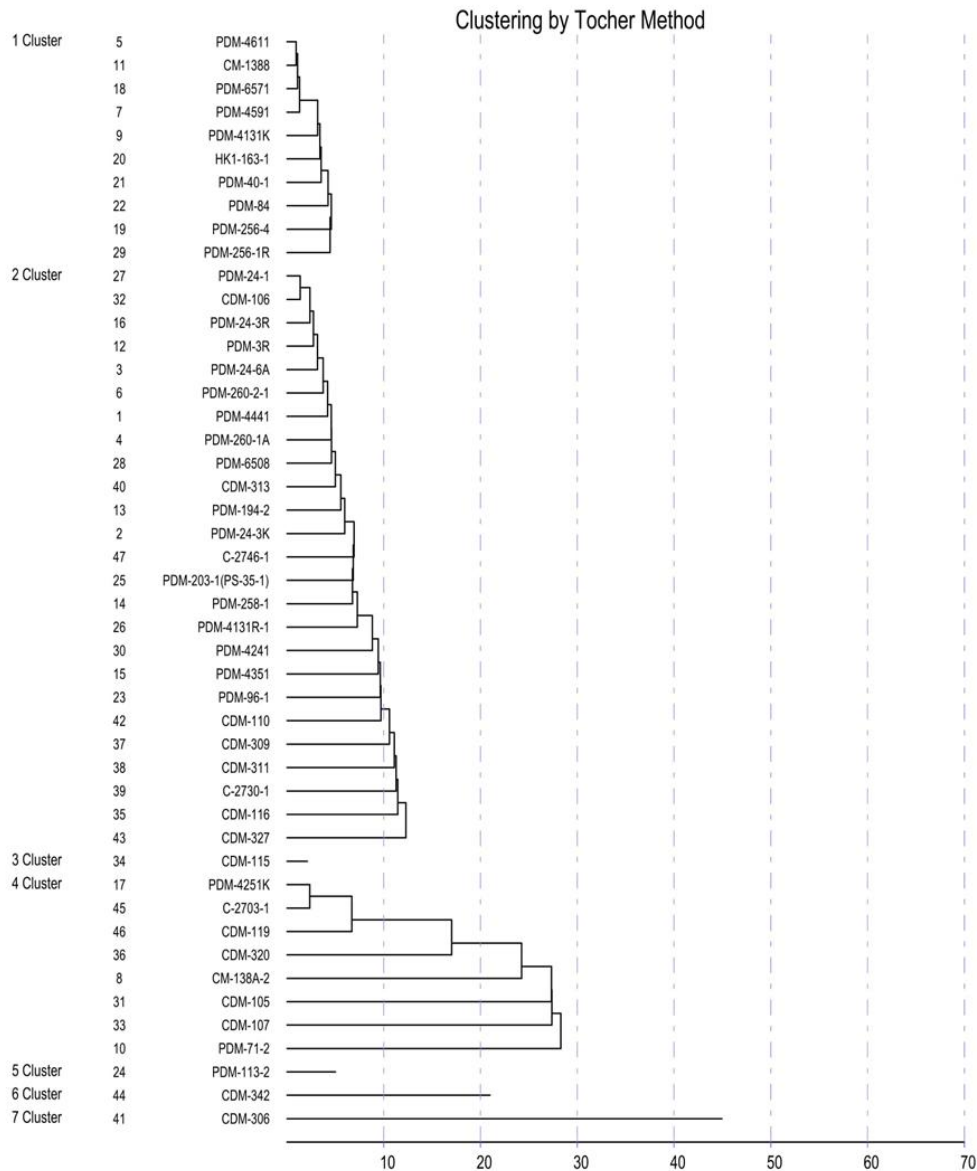


Fig 2: Dendrogram showing relationship among 47 maize (*Zea mays* L.) inbreds in seven clusters based on Mahalanobis' D^2 values.

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