



Genetic Diversity Studies in Maize (*Zea mays* L.) Germplasm from India

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Authors' contributions

This work was carried out in collaboration between all authors. Author SMP designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors DSJ and KK managed the analyses of the study. Author SM managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

In the present investigation D² values ranged from 36.84 to 369.02 and 40 genotype comprising 38 inbreds and 2 hybrids are grouped into seven and two clusters respectively. Among the clusters with inbred lines the cluster I with 16 inbreds emerged as dominating cluster followed by cluster III with 11 inbreds, cluster IV with 5 inbreds, cluster V with 3 inbreds and cluster II, VI, VIII were monogenotypic. The character grain yield per plant (46.15%) was the maximum contributor towards divergence followed by ear head height (37.69%), 100 grain weight (6.41%), and plant height (3.85%). On the basis of inter cluster distances, cluster means, per se performance observed in the present study the five genotypes viz Hyd 08R-2374-1, Hyd 08R-2614-2, GPM-320, GPM-35, and Hyd 08R-864-7 were found to be superior genotypes for further breeding programme.

Keywords: Genetic diversity; maize; *Zea mays* L.

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1. INTRODUCTION

Maize or corn (*Zea mays* L.) is a plant belonging to the family Poaceae and Tribe Maydeae. *Zea mays* is the only species in genus *Zea*. It is diploid species with chromosome number $2n = 20$. Central America (Mexico) is the origin of Maize. It is the native of America from where it was introduced in south East Asia by Portuguese traders in about 16th century. It is grown from 580 N to 400 S, from below sea level to altitudes higher than 3000 m, and in areas with 250 mm to more than 5000 mm of rainfall per year [1] and with a growing cycle ranging from 3 to 13 months. Maize is a good source of carbohydrates (starch), protein, fats and minerals, which are important in human diet. Several million people especially in the developing countries derive their protein and calories requirement from maize.

Maize is not only an important human nutrient, but also a basic element of animal feed and raw material for manufacture of many industrial products. The use of maize varies in different countries. In USA, EU, Canada and other developed countries, maize is used mainly to feed animals directly or sold to feed industry and as raw material for extractive/fermentation industries [2,3]. In developing countries use of maize is variable. In Latin America and Africa the main use of maize is for food while in Asia it is used for food and animal feed. In fact in many countries it is the basic staple food and an important ingredient in the diets of people. Globally, it has been estimated that approximately 21% of the total grain produced is consumed as food. Genetic diversity is variability available among the different genotypes of a species. The success in plant breeding depends upon the availability of germplasm resources and the amount of genetic variability available. For a crop improvement programme, it is prerequisite to maintain the genetic variability that allows identification of promising genotypes in the germplasm collection that can be incorporated in the breeding programme to develop promising cultivars. Therefore, the present investigation was undertaken to study genetic diversity in maize with the following objectives viz. to estimate the genetic divergence between different genotypes and group different genotypes in to suitable clusters.

2. MATERIALS AND METHODS

For the present study 40 genotypes (38 inbreds and 2 hybrids) of maize originating from different

geographic regions and showing phenotypic variability for different agronomic and yield characters were used from the germplasm maintained by AICRP on Maize, Kasba bawda, Kolhapur, India. Experiment was conducted at Post Graduate Research farm, College of Agriculture, Kolhapur during *Kharif* 2012. The experiment was laid out in randomized block design. The field was divided into three homogeneous replication blocks. Forty genotypes were randomly planted in three replications. Each entry was represented by a single row of 4 m length spaced at 75 cm between the rows and 20 cm between the plants within the rows. Two border rows were planted at both sides of blocks to reduce the border effects. Five random plants from each treatment in each replication were selected for recording observations. The selected plants were tagged at the age of 35 days. The following observations viz; days to 50 per cent tasselling, days to 50 per cent silking, days to maturity, plant height (cm), ear head height (cm), ear length (cm), ear circumference (cm), number of kernel rows per cob, number of kernels per row, 100 grain weight (g), shelling percentage and grain yield per plant (g) were recorded on the five plants from each genotype at different growth stages of crop and average values per plant were worked out. The ratio of total grain weight per cob to the total weight of ear head in percentage was worked out as shelling percentage. The analysis for divergence was done by following Mahalanobis [4] D^2 statistic. Tocher's method as described by Rao [5] was followed for cluster formation. Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster. The D^2 statistic also measures the degree of diversification and determines the relative proportion of each component character to the total divergence in Maize (*Zea mays* L.).

3. RESULTS AND DISCUSSION

The amount of diversity available in the crop decides the success of any crop improvement programme with manifested objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. The analysis of variance revealed highly significant differences for all the 12 characters studied. Clustering of genotypes following the Tocher's method as described by Rao [5] led to formation of 9 clusters in the present study. The D^2 values were estimated as per Mahalanobis [4] and described by Rao [5], based on twelve characters. The estimated of D^2

values ranged from 36.84 to 369.02. The aim of cluster formation in finding out intra and inter cluster divergence is to provide the basis for selection of parents for further hybridization programme. The crosses involving the parents with extreme divergence have also been reported to exhibit decrease in heterosis Mahalanobis [6]. Therefore, while selecting the parents by considering the genetic diversity, their *per se* performance and cluster mean for the character also need with due consideration in the crop improvement. Forty genotypes comprising 38 inbreds and 2 hybrids are grouped into seven and two clusters respectively (Table 1). Among the clusters with inbred lines the cluster I with 16 inbreds emerged as the largest cluster. The cluster III with 11 inbreds, cluster IV with 5

inbreds, cluster V with 3 inbreds and cluster II, VI, VIII were monogenotypic. Among the cluster with hybrids the cluster VII and IX were monogenotypic. Similar results were reported by Singh et al. [7], Khumkar and Singh [8] and Singh et al. [9] and Zaman and Alam [10]. Another study was carried out by Jakhar et al. [11] who reported that 40 chickpea genotypes could be classified into seven clusters. In the present investigation, highest statistical distance was found between the cluster IV and VIII (D=19.21) followed by cluster III and VIII (D=17.94), cluster IV and V (D=15.44), cluster III and VI (D=15.17), cluster II and VIII (D=15.03), cluster V and VIII (D=14.88), cluster IV and VI (D=14.57), and cluster II and V (D=14.11) (Table 2). Clustering pattern clearly

Table 1. Distribution of 38 inbreds and 2 hybrids of maize in to different clusters

Cluster number	Number of genotypes Included	Inbreds (38)	Hybrids (2)
I	16	GPM-35, Hyd 08R-291-1, Hyd 08R-378-1, Hyd 08R-2357-2, Hyd 08R-2570-3, Hyd 08R-321-1, Hyd 08R-2490-5, Hyd 08R-2374-1, N-8206-1, Hyd 08R-2474-1, Z-56-5, Hyd 08R-678-1, Hyd 08R661-1, N. 8213-48, Z. 059 37, GPM-320.	-
II	1	Hyd 06R-2082-1.	-
III	11	Hyd 08R-2473-3, Hyd 08R-2494-2, Hyd 06R -2086-2, N-4201-53, Hyd 08R-1083, Hyd 09R-468, GPM-67, Hyd 08R-573-1, GPM-293, Z. 53-10, Hyd 08R-2366-1.	-
IV	5	GPM-548, Hyd 06R-2208-2, Z.55-16, Hyd 08R-1210-1, Hyd 08R-626-1.	-
V	3	Hyd 08R-2066-3, Hyd 08R-681-2, V-632-144.	-
VI	1	Hyd 08R-864-7.	-
VII	1	-	Bio-9681 (C).
VIII	1	Hyd 08R-2614-2.	-
IX	1	-	Rajarshi (C).

Table 2. Average intra and inter cluster D² and D values of 9 clusters formed from 40 genotypes (38 inbreds and 2 hybrids) of maize

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	36.84 (6.07)	57.15 (7.56)	100.01 (10.01)	117.28 (10.83)	112.57 (10.61)	63.68 (7.98)	93.12 (9.65)	124.32 (11.15)	153.51 (12.39)
II		0.00 (0.00)	106.09 (10.30)	46.24 (6.80)	199.09 (14.11)	110.88 (10.53)	105.26 (10.26)	225.90 (15.03)	148.84 (12.20)
III			43.69 (6.61)	105.06 (10.25)	105.06 (10.38)	230.12 (15.17)	275.56 (16.60)	307.65 (17.94)	363.28 (19.06)
IV				37.08 (6.09)	238.39 (15.44)	212.28 (14.57)	230.73 (15.19)	369.02 (19.21)	267.64 (16.36)
V					50.69 (7.12)	192.37 (13.87)	292.75 (17.11)	221.41 (14.88)	350.43 (18.72)
VI						0.00 (0.00)	30.69 (5.54)	35.76 (5.98)	56.70 (7.53)
VII							0.00 (0.00)	68.22 (8.26)	54.90 (7.41)
VIII								0.00 (0.00)	104.24 (10.21)
IX									0.00 (0.00)

Table 3. Mean performance of clusters of 38 inbreds and 2 hybrids of maize

Characters	Days to 50% tasselling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear head height (cm)	Ear length (cm)	Ear circumference (cm)	No. of kernel rows per cob	No. of kernel per row	100 grain weight (g)	Shelling (%)	Grain yield/plant (g)
Clusters												
(A) Inbreds												
I	49.90	50.33	85.71	166.58	73.13	14.75	12.50	14.00	30.63	20.88	82.96	85.90
II	48.62	49.63	81.94	167.53	60.72	16.53	13.19	14.27	31.33	23.48	78.16	90.56
III	48.71	49.68	83.96	155.84	64.15	15.06	11.86	13.44	30.01	19.22	83.37	66.39
IV	47.74	49.17	85.54	145.99	54.07	14.74	12.62	12.94	30.44	22.03	82.47	84.51
V	50.17	51.06	86.44	160.67	80.27	12.54	11.93	14.31	23.82	23.09	85.54	66.77
VI	50.91	52.89	86.30	166.46	82.99	14.49	12.19	14.21	32.46	22.41	83.42	102.08
VIII	48.00	48.61	84.54	182.67	94.46	15.39	12.47	12.60	33.34	21.50	84.47	100.00
(B) Hybrids												
VII	51.00	52.26	85.39	182.47	76.97	17.12	13.33	14.28	37.53	21.00	84.13	106.40
IX	48.37	50.90	85.52	168.00	79.64	18.17	15.40	13.34	37.93	32.93	85.37	115.00

Table 4. Per cent contribution of 12 characters for divergence in maize

Sr. no.	Characters	No. of times appeared 1 st ranking	% Contribution
1	Days to 50% tasselling	0	0.00
2	Days to 50% silking	0	0.00
3	Days to 50% maturity	0	0.00
4	Plant height (cm)	30	3.85
5	Ear head height (cm)	294	37.69
6	Ear length (cm)	1	0.13
7	Ear circumference (cm)	0	0.00
8	Number of kernel rows per cob	1	0.13
9	Number of kernel per row	42	5.38
10	100 grain weight (g)	50	6.41
11	Shelling percentage (%)	2	0.26
12	Grain yield/Plant (g)	360	46.15
	Total	780	100.00

Table 5. Inbred lines suggested for hybridization programme

Sr. no.	Characters	Cluster combinations	Possible crosses
1	Plant height	VIII X I	Hyd 08R-2614-2 X GPM-320
2	Ear length	II X III	Hyd 06R-2082-1 X Hyd 08R-2494-2
3	Ear circumference	II X I	Hyd 06R-2082-1 X Hyd 08R-2374-1
4	Number of kernels per row	VIII X II	Hyd 08R-2614-2 X Hyd 06R-2082-1
5	100 grain weight (g)	II X V	Hyd 06R-2082-1 X Hyd 08R-2066-3
6	Grain yield/plant(g)	VI X VIII	Hyd 08R-864-7 X Hyd 08R-2614-2

suggested wide diversity between these genotypes. Intra cluster value was highest for cluster V ($D=7.12$) followed by cluster III ($D=6.61$) which indicates that these cluster are more heterogeneous. Cluster means for 12 characters were presented in Table 3. It revealed wide range of variability among the clusters for the characters plant height (cm), ear head height (cm), ear length (cm), ear circumference (cm), number of kernels per row, 100 grain weight (g), shelling percentage and grain yield per plant (g). Among the clusters, based on the mean cluster distance, it was observed that cluster VI and VIII are highly dissimilar for grain yield per plant and genotypes from these two groups could be evaluated for their combining ability and could be used as parents in heterosis breeding programmes in maize as suggested by Betrán et al. [12] in maize and Firoz Mahmuda et al. [13] in Brassica. The per cent contribution of 12 characters studied towards total divergence was presented in Table 4. It was observed that Grain yield per plant (g) contributed highest (46.15) for divergence, followed by Ear head height (cm) (37.69).

On the basis of inter cluster distance, cluster means and *per se* performance observed in the present study, the tentative hybridization

programme is suggested which involving the genotypes (Table 5) so that the better recombinants may be obtained in the segregating generations and as the most of the characters are showing the adequate gene action selection for these characters is more effective.

4. CONCLUSION

The D^2 study provides useful information that can be used in a breeding program for genetic improvement. On the basis of inter cluster distances, cluster means, *per se* performance observed in the present study the five genotypes viz Hyd 08R-2374-1, Hyd 08R-2614-2, GPM-320, GPM-35, and Hyd 08R-864-7 were found to be superior genotypes for further breeding programme.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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