

Original Research Article

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## Genetic Divergence Studies in Maize (*Zea mays* L.)

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### ABSTRACT

#### Keywords

Maize, Genetic divergence, D2-statistics.

#### Article Info

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Thirty genotypes of maize were evaluated for genetic diversity using Mahalanobis D<sup>2</sup> statistics for various morpho physiological traits during *kharif*, 2013. The data on 21 quantitative traits were recorded and on the basis of Mahalanobis' D<sup>2</sup> statistics, all the 30 genotypes of the present study were grouped into six clusters. Maximum number of genotypes (11) were included in cluster III followed by cluster-II (9), cluster-I (7) and remaining clusters were solitary with single genotype. Considering the inter cluster distances, it was highest between cluster IV and V (361.39) followed by IV and VI (357.02). Among the 21 characters studied, grain yield plant<sup>-1</sup>, stover yield plant<sup>-1</sup>, kernels per row, ear height contributed maximum towards the total divergence and were found to be responsible for primary differentiation.

## Introduction

Maize (*Zea mays* L.) plays a significant role in human and livestock nutrition world-wide. Among the cereal crops over the world, maize ranks first in total production followed by wheat and rice. This cereal is referred as Miracle crop and Queen of the Cereals due to its high productivity potential compared to other Gramineae family members.

On global front, maize has gained tremendous importance due to raising demand from diversified sectors like food, feed and ethanol

production. As a result, since last one decade, the acreage under maize cultivation is continuously on increasing trend. India stands in fifth position in the world in terms of corn production.

Assessment on genetic diversity among the genotypes is important for planning an effective hybrid breeding programme as the genetically diverse genotypes are known to produce high heterotic effects. It has become possible to quantify magnitude of genetic

diversity among germplasm with the help of advanced biometrical methods such as multivariate analysis (Rao, 1952) based on Mahalanobis' (1936)  $D^2$  statistics.

## **Materials and Methods**

Seeds of 30 maize inbred lines were obtained from Maize Research Centre, ARI, Hyderabad and were raised in Randomized Block Design (RBD) with three replications. Observations regarding 21 agronomic and physiological traits *viz.*, days to 50% flowering, days to 50% silking, days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, no of kernels per row, 100 kernel weight (g), grain yield per plant (g), leaf area index at 30, 60 and at 90 DAS, LAD at 30-60 and at 60-90 DAS, SCMR, RGR at 30-60 and at 60-90 DAS, harvest index and stover yield/plant (g) were recorded on five randomly selected plants in each replication.

The genetic divergence among the genotypes was computed by means of Mahalanobis'  $D^2$ -statistics.

Intra and inter cluster distance, cluster means and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985).

## **Results and Discussion**

The ANOVA revealed highly significant differences among the thirty genotypes for twenty one characters indicating the existence of sufficient amount of diversity among genotypes.

The statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion*  $\hat{\Lambda}$ . The *Wilk's criterion* thus

obtained was used in calculations of 'V' statistic. The statistic was highly significant indicating that genotypes differ significantly when all the characters were considered simultaneously. The value of 'V' statistic was 1834.83 in the present investigation.

The 30 genotypes were grouped into six clusters using Tocher's method with a criterion that the intra cluster average  $D^2$  values should be less than the inter-cluster  $D^2$  values.

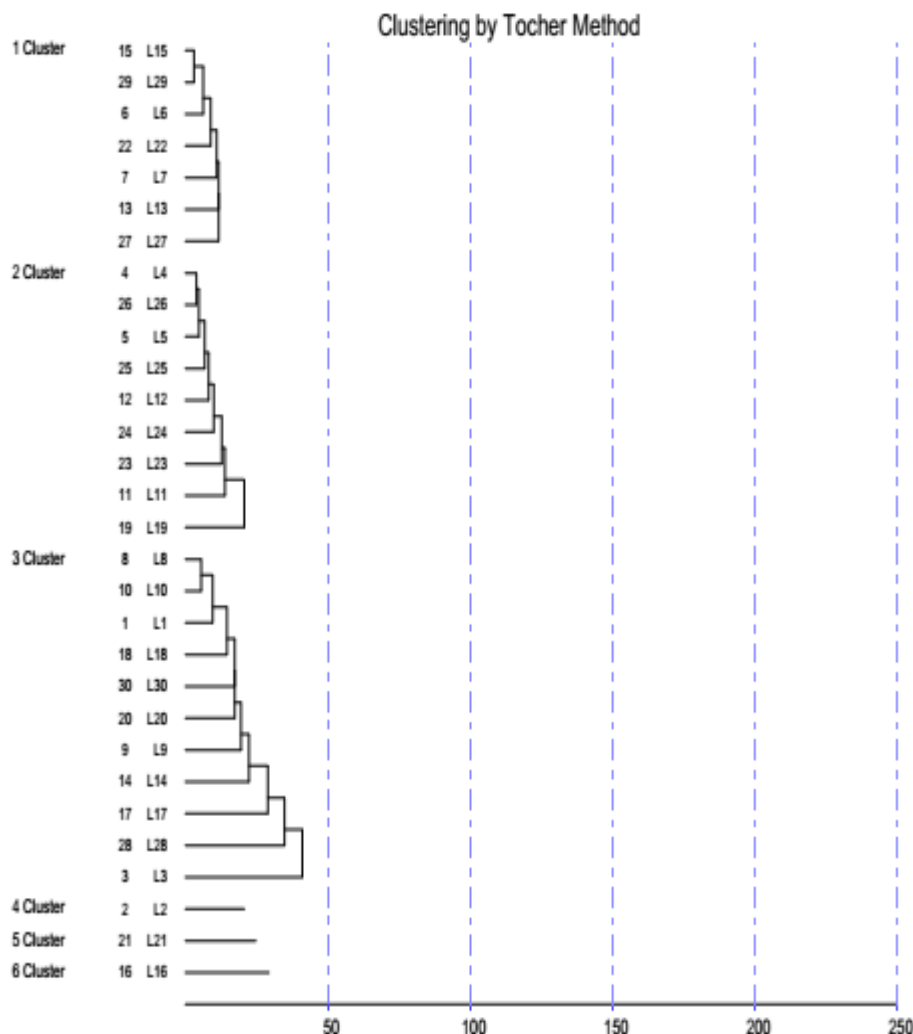
The distribution of 30 genotypes into six clusters was at random with maximum number of eleven genotypes grouped in cluster III followed by Cluster II with nine genotypes and cluster I with seven genotypes.

Clusters IV, V and VI were monogenotypic clusters with nil intra-cluster  $D^2$  values (Table 1). The mutual relationships between the clusters were represented diagrammatically by taking average intra and inter cluster  $D^2$  values. The tree like structure called dendrogram was constructed based on clustering by Tocher's method (Fig. 1).

The average intra and inter cluster  $D^2$  values were presented in table 2. The intra and inter cluster distances revealed that inter cluster distance was greater than intra cluster distance.

The maximum intra cluster distance was observed in the cluster III (60.43) followed by cluster II (39.50) and cluster I (33.57) while, it was zero for clusters IV, V and VI as they are solitary. The intra cluster distance in cluster III was highest indicating the presence of wide genetic diversity among the genotypes present within this cluster. Genotypes grouped in the same cluster presumably differ little from one another as the aggregate of characters measured.

**Fig.1** Dendrogram showing relationship of 30 maize inbred lines (Tochers method)



**Table.1** Distribution of thirty maize inbred lines in different clusters (Tocher’s method)

Cluster No.	No. of genotypes	Genotypes
I	7	MRC- 151, MRC- 203, MRC- 186, MRC- 197, MRC- 184, MRC- 167, MRC- 194.
II	9	MRC- 152, MRC- 191, MRC- 170, MRC- 163, MRC-180, MRC-134, MRC-219, MRC-190, MRC-157.
III	11	MRC- 153, MRC- 130, MRC- 142, MRC- 206, MRC- 179, MRC- 132, MRC-160, MRC-147, MRC-126, MRC-168, MRC-185.
IV	1	MRC- 127
V	1	MRC- 216.
VI	1	MRC-139

**Table.2** Average inter and intra (diagonal) cluster  $D^2$  and D values among six clusters in maize (Tochers method)

Cluster	I	II	III	IV	V	VI
I	<b>33.57</b> (5.79)	180.37 (13.43)	63.27 (7.75)	75.60 (8.69)	229.04 (15.13)	231.97 (15.23)
II		<b>39.50</b> (6.28)	159.62 (12.63)	315.65 (17.76)	95.90 (9.79)	117.00 (10.81)
III			<b>60.43</b> (7.77)	133.29 (11.54)	214.69 (14.65)	188.73 (13.73)
IV				<b>0.00</b> (0.00)	361.39 (19.01)	357.02 (18.89)
V					<b>0.00</b> (0.00)	150.91 (12.28)
VI						<b>0.00</b> (0.00)

Figures in parenthesis are D values

**Table.3** Contribution of characters towards divergence in maize inbred lines

S. No.	Character	Times ranked first	Percent contribution
1	Days to 50% tasseling	16	3.68
2	Days to 50% silking	0	0.00
3	Days to maturity	0	0.00
4	Plant height (cm)	2	0.46
5	Ear height (cm)	23	5.29
6	Ear length (cm)	1	0.23
7	Ear girth (cm)	0	0.00
8	No. of kernel rows per ear	8	1.84
9	No of Kernels per row	33	7.59
10	100 Kernel weight (g)	20	4.60
11	Grain yield/ plant (g)	196	45.06
12	Leaf area index at 30 DAS	11	2.53
13	Leaf area index at 60 DAS	33	7.59
14	Leaf area index at 90 DAS	14	3.22
15	LAD at 30-60	0	0.00
16	LAD at 60-90	0	0.00
17	SCMR	17	3.91
18	RGR at 30-60 DAS	0	0.00
19	RGR at 60-90 DAS	0	0.00
20	Harvest index (%)	3	0.69
21	Stover yield/ plant (g)	58	13.33

**Table.4** Cluster means for twenty one characters in thirty inbred lines of maize (Tocher's method)

	Days to 50% tasseling	Days to 50% silking	Days to maturity	plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	No of kernel rows/ear	No of Kernels/row	100 Kernel weight (g)	Grain yield/ plant (g)
1 Cluster	55.33	58.43	89.90	133.33	49.86	11.36	10.59	12.67	20.58	12.74	30.26
2 Cluster	54.78	58.00	89.15	146.26	52.59	15.54	12.24	13.40	29.39	19.93	74.71
3 Cluster	58.64	61.73	94.12	134.03	48.73	12.52	10.83	12.27	22.99	14.32	39.05
4 Cluster	55.33	58.33	92.00	115.33	35.33	9.00	9.25	15.42	11.75	15.46	21.14
5 Cluster	48.33	51.67	84.00	165.00	57.67	17.33	12.58	11.92	32.42	21.50	91.31
6 Cluster	55.67	59.00	89.67	110.00	33.00	15.33	12.50	15.83	36.92	16.25	83.90

	Leaf area index at 30 DAS	Leaf area index at 60 DAS	Leaf area index at 90 DAS	LAD at 30-60 DAS	LAD at 60-90 DAS	SCMR	RGR at 30-60 DAS	RGR at 60-90 DAS	Harvest index (%)	Stover yield/ plant (g)
1 Cluster	0.15	2.19	1.23	37.81	83.00	42.90	0.026	0.004	37.25	29.14
2 Cluster	0.17	2.86	1.61	47.39	108.92	47.03	0.025	0.004	35.47	26.89
3 Cluster	0.14	2.18	1.24	37.32	83.10	43.71	0.026	0.004	34.96	28.55
4 Cluster	0.13	2.02	1.10	34.54	75.58	51.37	0.025	0.005	39.33	31.52
5 Cluster	0.17	2.05	1.14	37.72	77.50	47.03	0.024	0.004	39.28	38.72
6 Cluster	0.16	2.34	1.08	40.98	81.49	29.27	0.027	0.004	38.64	27.59

The per cent contribution towards genetic divergence by all the twenty one contributing characters is presented in table 3. The knowledge on characters influencing divergence is an important aspect to a breeder. Character wise rank has shown that no single character alone had a greater contribution to total genetic divergence. The maximum contribution towards genetic divergence was displayed by grain yield per plant (45.06 %) followed by stover yield per plant (13.33%), number of kernels per row, leaf area index at 60 DAS (7.59%), ear height (5.29%), 100 kernel weight (4.60), SCMR (3.91), days to 50% tasseling (3.68%), leaf area index at 90 DAS (3.22%), leaf area index at 30 DAS (2.53%), number of kernel rows per ear (1.84), harvest index % (0.69), plant height (0.46) and ear length (0.23) in the decreasing order of values, respectively.

The cluster mean values for twenty one characters are presented in table 4. High mean values for ear length, ear girth were seen in cluster V, number of kernel rows per ear and number of kernels per row were seen in cluster VI, and high means for 100 kernel weight were seen in cluster V which are the major contributors for improving the grain yield per plant. Similar results were reported by Marker and Krupakar (2009), Zaman *et al.*, (2013), Nataraj *et al.*, (2014) and Maruthi and Jhansi Rani (2015). Thus involving the genotypes of outstanding mean performance from these clusters will be useful in development of high yield with better quality.

## References

- Marker, S and Krupakar, A. 2009. Genetic divergence in exotic maize germplasm (*Zea mays* L.). *ARPJ Journal of Agricultural and Biological Science*. 4(4): 44-47.
- Nataraj, V., Shahi, J. P. and Raghunandan, K. 2014. Studies on genetic diversity of certain inbred genotypes of maize (*Zea mays* L.) at Varanasi. *Int. J. Pure App. Biosci.* 2 (1): 71-76.
- Zaman, M. A and Alam, M. A. 2013. Genetic diversity in exotic maize (*Zea mays* L.) hybrids. *Bangladesh J. Agril. Res.* 38(2): 335-341.
- Maruthi, R. T. and Jhansi Rani, K. 2015. Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) inbred lines. *Journal of Applied and Natural Science* 7 (1): 149 – 154.
- Rao, C. R. 1952. *Advanced Statistical Methods in Biometric Research*. Edn I. John Wiley and Sons, New York. Pp. 36-38.
- Singh, R.K and Chaudhary, B.D. 1985. *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi. pp. 102-157.
- Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of National Institute of Sciences (India)*. 12: 49.

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