



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2023; 12(5): 1950-1953  
© 2023 TPI

[www.thepharmajournal.com](http://www.thepharmajournal.com)

Received: 02-03-2023

Accepted: 07-04-2023

## Deepak Kumar Mishra

Department of Plant Breeding and Genetics, Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India

## Birender Singh

Department of Plant Breeding and Genetics, Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India

## SS Mandal

Department of Plant Breeding and Genetics, Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India

## Kumari Rashmi

Department of Plant Breeding and Genetics, Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India

## Sumit Kumar Mishra

Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

## Corresponding Author:

### Sumit Kumar Mishra

Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi, Jharkhand, India

## Genetic diversity in maize inbred lines

**Deepak Kumar Mishra, Birender Singh, SS Mandal, Kumari Rashmi and Sumit Kumar Mishra**

### Abstract

In *Rabi*, 2019-20 the experiment was planned in a line  $\times$  tester mating pattern and 30 crosses were made. In *Kharif*, 2020 all 30 crosses along with their 13 parents and 2 checks were grown in Randomized Block Design with two replications and were evaluated. The experiment was carried out to study the diversity among the parents. Genetic divergence was analysed using  $D^2$  statistics. The 13 genotypes were grouped into four different clusters on the basis of inter-genetic distance. It indicates the presence of considerable diversity within the genotypes. The dendrogram representing the clustering of 13 genotypes was also examined. The cluster I showed ten genotypes, followed by one genotype in cluster II, cluster III and cluster IV each. The contribution of lines was found to be greater than that of testers and interaction to the total hybrid variance, which indicates that the lines are superior to the testers. The analysis of variance for combining ability revealed that both additive and non-additive gene actions were responsible for the inheritance for all the characters under study.

**Keywords:** Diversity, cluster, inbred lines, inter-genetic distance

### Introduction

Maize (*Zea mays* L.) plays a vital role in human and livestock nutrition worldwide. It has great yield potential and attained the leading position amongst cereals based on production and productivity. It is one of the world's most widely produced as well as consumed cereal crops. It is also called as a 'poor man's cereal crop'. In developing countries like Africa and Latin America, as the animal protein is very limited and expensive, which results in being unavailable to a huge number of the population, maize grains provide about 15-56% of total daily calories in people's diets. Maize production of world increased from 265 million thousand tonnes in 1970 to 1,148 million thousand tonnes in 2019 growing at an average annual rate of 3.41%. The global demand of maize from 2000 to 2020 has increased by 45% compared with 30% for wheat and 32% for rice. Among the maize growing countries, India ranks 4th in area and 7th in production, representing around 4% of world maize area and 2% of total production. During 2018-19 in India, the maize area has reached to 9.2 million ha (DACNET, 2020). During 1950-51 India used to produce 1.73 million MT maize, which has increased to 27.8 million MT by 2018-19, recording close to 16 times increase in production. The average productivity during the period has increased by 5.42 times from 547 kg ha<sup>-1</sup> to 2965 kg ha<sup>-1</sup>, while area increased nearly by 3 times. In India, Karnataka is the leading producer followed by Rajasthan and Madhya Pradesh. Bihar ranks sixth place, with a total production of 2.3 million tonnes in 2017-18. In India, productivity is found to be highest in rabi maize. Bihar has received Krishi Karman award for maize production in the year 2015-16 & 2016-2017.

The genetic diversity between the genotypes is essential as the diverse lines can produce high heterotic effect. The hybrid breeding is vital to select the cross combinations with high degree of SCA as well as parents with high GCA. Combining ability is an important tool in identifying the best combiners for hybridization especially, when more numbers of advance inbred lines are available and most promising are to be selected on the basis of their ability to give superior hybrids.

### Materials and Methods

Ten diverse lines were selected and crossed with three testers in line  $\times$  tester design in Rabi, 2019. In Kharif, 2020 all the 30 crosses and 13 parents were evaluated with 2 checks *viz.*, DHM 117, SHM 1. After land preparation, sowing was done in July 2020. Seeds were sown by hand dibbling with two seeds per hill and afterwards thinned to one plant per hill after

emergence to attain an optimum plant population density. Compound fertilizer was applied at the rate of 40 kg N, 60 kg P<sub>2</sub>O<sub>5</sub>, and 40 kg K<sub>2</sub>O ha<sup>-1</sup> at the time of sowing. An additional 40 kg ha<sup>-1</sup> N was applied in the form of urea as top dressing, at knee-high stage and another 40 kg ha<sup>-1</sup> N was applied at tasselling stage.

Field layout : Randomized Block Design (RBD)  
 Replication : 2  
 Row-to-row spacing : 0.60 m  
 Plant-to-plant spacing : 0.20 m  
 No. of rows : 2 per entry  
 Row length : 5 m each  
 Plot size : 6.0 m<sup>2</sup>

**Table 1:** Details of the lines

| S. No. | Code            | Name      | Source            |
|--------|-----------------|-----------|-------------------|
| 1.     | L <sub>1</sub>  | VL1016537 | CIMMYT, Hyderabad |
| 2.     | L <sub>2</sub>  | VL109476  | CIMMYT, Hyderabad |
| 3.     | L <sub>3</sub>  | VL1010763 | CIMMYT, Hyderabad |
| 4.     | L <sub>4</sub>  | VL1018419 | CIMMYT, Hyderabad |
| 5.     | L <sub>5</sub>  | VL109475  | CIMMYT, Hyderabad |
| 6.     | L <sub>6</sub>  | VL1017055 | CIMMYT, Hyderabad |
| 7.     | L <sub>7</sub>  | VL109353  | CIMMYT, Hyderabad |
| 8.     | L <sub>8</sub>  | VL1010848 | CIMMYT, Hyderabad |
| 9.     | L <sub>9</sub>  | VL109479  | CIMMYT, Hyderabad |
| 10.    | L <sub>10</sub> | VL1017524 | CIMMYT, Hyderabad |

**Table 2:** Details of the testers

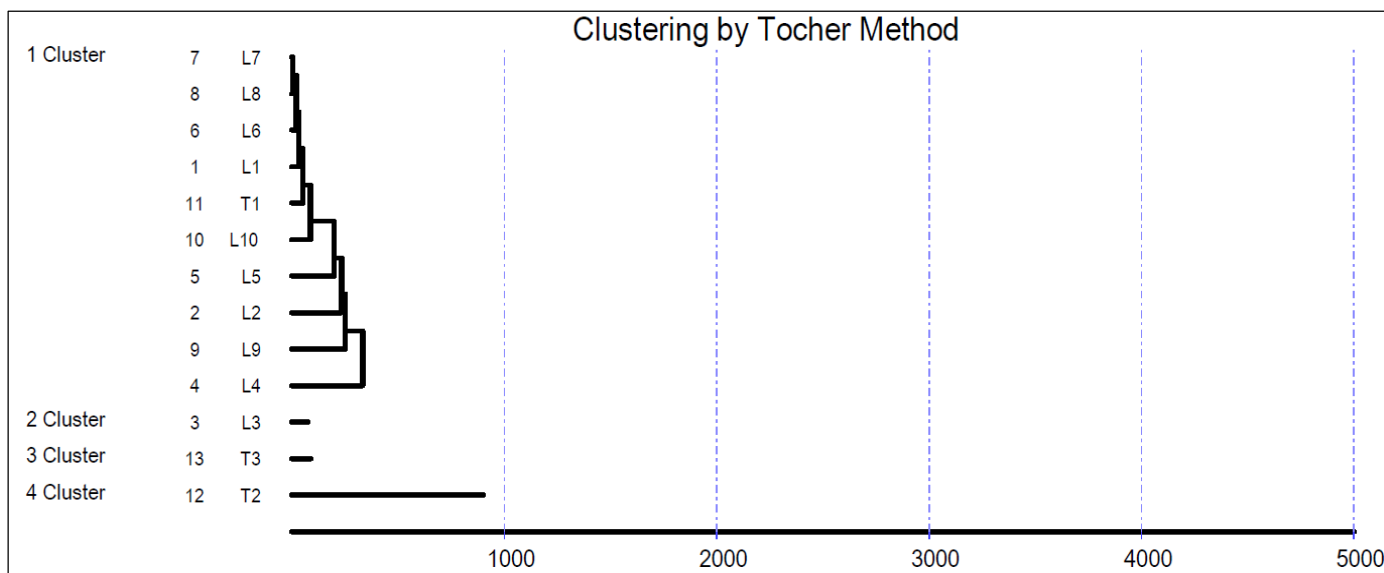
| S. No. | Code           | Name      | Source            |
|--------|----------------|-----------|-------------------|
| 1.     | T <sub>1</sub> | VL1016498 | CIMMYT, Hyderabad |
| 2.     | T <sub>2</sub> | VP15295   | CIMMYT, Hyderabad |
| 3.     | T <sub>3</sub> | SML-1     | BAU, Sabour       |

Pre harvest parameters such as days to 50% tasselling, days to 50% silking, Anthesis-Silking interval, days to 75% brown husk, Plant height, Ear height were recorded. Post-harvest parameters cob length (cm), cob girth (cm), number of rows per cob, number of grains per row, Test weight (g), Shelling percentage (%), Grain yield at 15% moisture content (Kg ha<sup>-1</sup>). Days to 50% tasseling, days to 50% silking and days to 75% brown husk were calculated from day of sowing. For plant height, Ear height, Cob length, Cob girth, No. of rows per cob, No. of grains per row five random plants were selected from each plot and data was recorded. For test weight One thousand grains of maize were also counted from composite sample of the produce from the five cobs from

each of the plot and weighed and recorded in gram separately. Average pith and grain weight of five randomly selected cobs were used to compute the shelling percentage.

**Results and Discussion**

Genetic divergence was analysed using D<sup>2</sup> statistics, Mahalanobis (1936) [13]. The 13 genotypes were grouped into four different clusters on the basis of inter-genetic distance. It indicates the presence of considerable diversity within the genotypes. The dendrogram representing the clustering of 13 genotypes is shown in figure 1. The cluster I showed ten genotypes, followed by one genotype in cluster II, cluster III and cluster IV each.



**Fig 1:** Dendrogram of 13 maize genotypes using Tocher’s method

**Table 3:** Grouping of 13 maize genotypes into four clusters by Tocher’s method

| Group | No. of genotypes | INBREDS  |
|-------|------------------|--|
| I     | 10               | VL109353, VL1010848, VL1017055, VL1016537, VL1017524, VL109475, VL109476, VL109479, VL1018419, VL1016498 |
| II    | 1                | VL1010763  |
| III   | 1                | SML-1  |
| IV    | 1                | VP15295  |

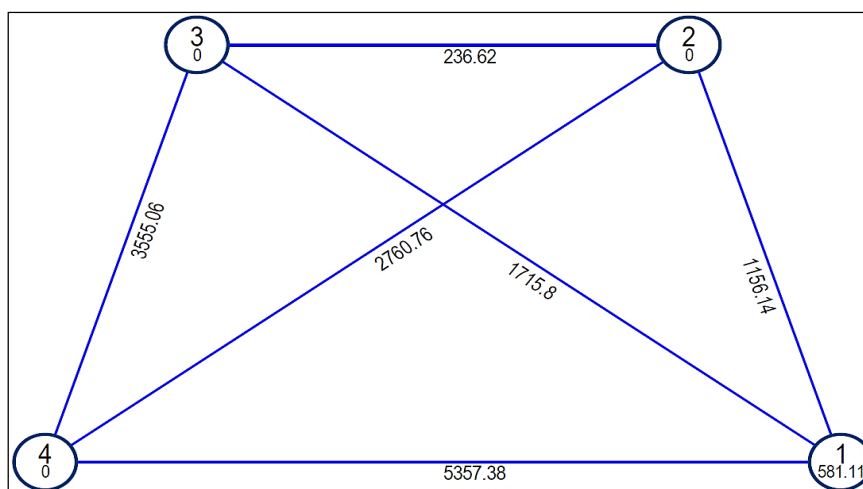
**Table 4:** Average intra and inter-cluster distance between the four clusters of 13 maize genotypes

| Cluster     | Cluster I | Cluster II | Cluster III | Cluster IV |
|-------------|-----------|------------|-------------|------------|
| Cluster I   | 581.11    | 1156.14    | 1715.8      | 5357.38    |
| Cluster II  |           | 0.00       | 236.62      | 2760.76    |
| Cluster III |           |            | 0.00        | 3555.06    |
| Cluster IV  |           |            |             | 0.00       |

Diagonal values are intra-cluster distances.

The intra and inter-cluster distances between the four clusters is presented in the table 2. The maximum inter-cluster distance was observed between cluster I and cluster IV

(5357.38), while the minimum inter-cluster distance was observed between cluster II and cluster III (236.62).



**Fig 2:** Mahalanobis Euclidean distance of 13 maize genotypes in four clusters

Diversity analysis of the parents, the 13 genotypes were grouped into 4 different clusters on the basis of inter-genetic distance. It shows the presence of considerable diversity within the genotypes. The maximum inter-cluster distance was observed between cluster I and cluster IV (5357.38),

while the minimum inter-cluster distance was observed between cluster II and cluster III (236.62). Similar results were also obtained by previous workers, Dubey *et al.* (2001) [6], Kumar *et al.* (2015) [12].

**Table 5:** Cluster mean values of morphological traits

| Cluster | Days to 50 per cent tasseling (day) | Days to 50 per cent silking (day) | Anthesis-silking interval (day) | Days to 75 per cent brown husk (day) | Plant height (cm) | Ear height (cm) |
|---------|-------------------------------------|-----------------------------------|---------------------------------|--------------------------------------|-------------------|-----------------|
| I       | 62.35                               | 67.50                             | 5.15                            | 88.65                                | 85.00             | 30.13           |
| II      | 65.00                               | 68.00                             | 3.00                            | 92.00                                | 67.50             | 22.50           |
| III     | 58.00                               | 63.00                             | 5.00                            | 89.00                                | 115.00            | 37.50           |
| IV      | 56.50                               | 62.00                             | 5.50                            | 84.00                                | 152.50            | 70.00           |

**Table 5B:** Cluster mean values of morphological traits

| Cluster | Cob length (cm) | Cob girth (cm) | Number of rows per cob | Number of grains per row | Test weight (g) | Shelling percentage (%) | Grain yield at 15% moisture (Kg/ha) |
|---------|-----------------|----------------|------------------------|--------------------------|-----------------|-------------------------|-------------------------------------|
| I       | 9.11            | 2.78           | 11.20                  | 14.35                    | 148.45          | 67.15                   | 1568.07                             |
| II      | 6.37            | 2.61           | 12.00                  | 15.50                    | 168.50          | 68.65                   | 2088.80                             |
| III     | 5.29            | 2.33           | 12.00                  | 11.00                    | 142.50          | 64.01                   | 1250.00                             |
| IV      | 14.16           | 4.23           | 13.00                  | 17.50                    | 159.00          | 77.92                   | 2410.40                             |

The diversity was also supported by the appreciable amount of variation among the cluster means of different characters (Table 3). For days to 50% tasseling minimum cluster mean was observed for the cluster IV (56.25 days), while the maximum cluster mean was observed for the cluster II (65.00 days). For days to 50% silking minimum cluster mean was observed for the cluster IV (62.00 days), while the maximum cluster mean was observed for the cluster II (68.00 days). For test weight minimum cluster mean was observed for the cluster III (142.50 g), while the maximum cluster mean was observed for the cluster II (168.50 g). For grain yield

minimum cluster mean was observed for the cluster III (1250.00 Kg/ha), while the maximum cluster mean was observed for the cluster IV (2410.40 Kg/ha). Similar results were also obtained by previous workers, Dubey *et al.* (2001) [6], Kumar *et al.* (2015) [12].

The parents for hybridization could be selected on the basis of their large intercluster distance for isolating useful recombinants in the segregating generations. The better performing genotypes from clusters I, II and III were identified for all the traits. Therefore, F1 derived from such diverse crosses are expected to show high yield. Hence, these

genotypes might be used in a multiple crossing programmes to recover high yielding hybrids.

## References

1. Amin MN, Amiruzzaman M, Ahmed A, Ali MR. Combining ability study in waterlogged tolerant maize (*Zea mays* L.). Bangladesh Journal of Agricultural Research. 2014;39(2):283-229.
2. Bisen, Amit Dadheech, Namrata, Omprakash Nagar, Ram Kunwar Meena. Exploitation of Heterosis in Single Cross Hybrids of Quality Protein Maize (*Zea maize* L.) for Yield and Quality Traits. International Journal of Bio-resource and Stress Management. 2017;8(1):012-019.
3. Chen ZH, Gao XA. Study on the combining ability and heterosis of suwan germplasm line. Scientica Agricultura Sinica. 2000;33(1):113-118.
4. Chahar S, Vyas M, Vijayan BR, Aruna V. Heterosis and Combining Ability Analysis for Yield and its Contributing Traits in Early Maturing Maize (*Zea mays* L.) Genotypes. Trends in Bioscience. 2014;7(14):1774-1777.
5. Darshan, Marker S. Heterosis and combining ability for grain yield and its component characters in quality protein maize (*Zea mays* L.) hybrids. Electronic Journal of Plant Breeding. 2019 Mar;10(1):111-118.
6. Dubey RB, Joshi VN, Pandiya NK. Heterosis and combining ability for quality, yield and maturity traits in conventional and non-conventional hybrids of maize. Indian Journal of Genetics. 2001;61(4):353-355.
7. Fisher RA, Yates F. Statistical tables for biological, agricultural and medical research. Biometrical journal; c1963.
8. Griffing B. Concept of general and specific combining ability in relation to diallel crossing system. Australian Journal of Biological Science. 1956;9:463-493.
9. Haddadi MH, Eesmaeilof M, Choukan R, Rameeh V. Combining ability analysis of days to silking, plant height, yield components and kernel yield in maize breeding lines. Journal of Agricultural Research. 2012;7(33):4685-4691.
10. Iqbal AM, Nehvi FA, Wani SA, Qadir R, Dar ZA. Combining ability analysis for yield and yield related traits in maize (*Zea mays* L.). International Journal of Plant Breeding and Genetics. 2007;1(2):101-105.
11. Kempthorne O. An introduction to statistics. John Wiley and Sons. Inc. New York; c1957. p. 468-471.
12. Kumar R, Mandal SS, Mishra AK, Smriti, Singh R, Kumar P. Heterosis and combining ability for yield and its contributing traits of *kharif* maize (*Zea mays* L.). The Bioscan. 2015;10(4):2049-2056.
13. Mahalanobis PC. The generalized distance in statistics. Proc. Nat. Acad. Sci. (India). 1936;2:79-85.
14. Sprague GF, Tatum LA. General vs specific combining ability in single crosses of corn. Journal American Society of Agronomy. 1942;34:923-932.