



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2023; 12(3): 2210-2213  
© 2023 TPI

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

Received: 05-12-2022

Accepted: 13-01-2023

## Rumit Patel

Department of Agricultural  
Biotechnology, Anand  
Agricultural University, Anand,  
Gujarat, India

## Dipak A Patel

Department of Agricultural  
Biotechnology, Anand  
Agricultural University, Anand,  
Gujarat, India

## Juned Memon

Department of Genetics and  
Plant Breeding, B. A. College of  
Agriculture, Anand Agricultural  
University, Anand, Gujarat,  
India

## Arna Das

Department of Genetics and  
Plant Breeding, B. A. College of  
Agriculture, Anand Agricultural  
University, Anand, Gujarat,  
India

## Kalyanrao Patil

Department of Seed Science and  
Technology, Anand Agricultural  
University, Anand, Gujarat,  
India

## Corresponding Author:

### Rumit Patel

Department of Agricultural  
Biotechnology, Anand  
Agricultural University, Anand,  
Gujarat, India

## D<sup>2</sup> clustering of yield and yield accredited attributes for genetic diversity analysis in maize (*Zea mays* L.)

Rumit Patel, Dipak A Patel, Juned Memon, Arna Das and Kalyanrao Patil

### Abstract

Maize is an important crop having more diversity for various traits including different grain properties like colour, sweetness, protein and oil quantity. The current study provides information on morphological variety among chosen genotypes. D<sup>2</sup> values between all 1275 pairings varied from 28.52 to 29.52. The greatest inter-cluster distance (D = 722.50) was discovered between clusters 15 and 5, followed by 10 and 12 and 10 and 17. The shortest inter-cluster distance was found between clusters 21 and 11. For certain features, a wide range of mean values was reported among the clusters. Cluster 14 had the highest mean values for 50% silking and tasseling days. Cluster 13 outperformed the others in terms of ear length (18.41) and kernels per row (34.00). Similarly, the 14th cluster has a greater ear girth.

**Keywords:** Maize, diversity, cluster mean and distance

### Introduction

Maize (*Zea mays* L.) is an important cereal crop, which is a member of *Poaceae* family. It is grown under a wide range of environmental circumstances and it is the third most important food crop in India. Maize is seen as a viable choice for agricultural diversification in different agro-climatic zones. More than 4.5 billion people in 94 developing countries get at least 30% of their calories from three major cereal crops, rice, wheat, and maize. Maize is one of the preferred staple food worldwide. As a major crop for food, feed, and fodder, it helps to provide food security in most of the developing countries (Meena *et al.*, 2014) [5].

Estimation of genetic divergence between the parents is crucial because a cross between genetically diverse parents is likely to create a high level of heterosis, and more variability may be anticipated in segregating generations. Thus further, a classification of genotypes based on diversity analysis will allow the breeder to choose the parents with the greatest genetic diversity and utilize a few of the selected diverse parents in the hybridization programme. Evaluation of genetic divergence aids in reducing the number of breeding lines that have to be maintained. The genetic distance between different genotypes can be measured effectively using Mahalanobis (1936) [4] D<sup>2</sup> statistics. Finally, their genetic distance-based grouping offers a clear image of how the genotypes interact and helps in the selection of suitable genotypes for use in the hybridization programme.

The evaluation of genetic diversity is commonly employed by breeders as an alternative to the process of germplasm selection since it enables lines to be organized into groups that, when inter-crossed, would provide the most promising results and requires less time and resources. D<sup>2</sup> analysis is a helpful method for measuring the degree of genotypic divergence between biological populations and determining how much each component contributed to the overall divergence at both the intra and inter-cluster levels. Earlier scientists also studied diversity analysis in maize and classified the genotypes in different clusters (Meena *et al.*, 2014, Choudhary *et al.*, 2020) [5,21].

### Materials and Methods

The present investigation comprised of 51 diverse maize genotypes was carried out at Genetics and Plant Breeding Farm, B. A. College of Agriculture, A.A.U., Anand during Rabi 2020-21.

51 distinct maize genotypes were tested in a randomized complete block design with two replications. Each genotype was planted in a single row 5.0 m long, 30 cm apart, and 10 cm plant-to-plant. To prevent damage and border effects, the experiment was encircled by boundary rows.

To achieve a satisfactory output, agronomical and plant protection techniques were undertaken.

Plant height (PH), ear height (EH), ear length (EL), and ear girth (EG) were measured in centimeter, whilst ears per plant (EPP), number of kernel rows per ear (KRP), number of kernels per row (KPR), and number of kernels per ear (NKE) were counted, shelling percentage (SH) and test weight (TW). Grain yield was measured in grammes per plant. All observations for various maize descriptors were made on five randomly selected competitive plants of each genotype in each replicate (IBPGR, 1991). The phenological features tasseling (TA) and silking (SI) were recorded on plot basis. Genetic divergence was estimated by using  $D^2$  statistics of Mahalanobis (1936) [4] and Grouping of the genotypes in different clusters was done by using Tocher's method (Rao, 1952) [8]. The per cent contribution of characters towards genetic divergence was calculated according to Singh and Choudhary (1985) [2].

### Result and Discussion

The knowledge regarding the extent of variability and genetic diversity is of much importance while making improvement in a complex trait like yield. Therefore, while improving seed yield, selection of parents having wide genetic divergence for number of characters is of prime importance, which is assessed by multivariate technique  $D^2$ -statistics developed by Mahalanobis (1936) [4].

The  $D^2$  values between all 1275 pairs ranged from 28.52 (between PFSR5-3-5 and I-07-29-1-3) to 866.12 (between I-07-6-4-5 and GWQPM-26-3), which indicated the presence of high genetic diversity among the genotypes for all the traits (these  $D^2$  values were taken from matrix table, which is not given here).

The clustering pattern could be utilized in hybridization programme and deciding the cross combinations, which would generate the highest variability for various characters. The superior genotypes for breeding programme could also be selected on the basis of cluster mean and inter-cluster distance.

### Composition of clusters

Grouping of the genotypes was carried-out by following the Tocher's method (Rao, 1952) [8] with the assumption that the genotypes within cluster have smaller  $D^2$ -values among themselves than those from genotypes belonging to different clusters. In all, 22 clusters were formed from 51 genotypes. The composition of clusters is given in Table 1. The cluster I, II and III were the largest cluster with 7 genotypes all belonging to different groups. Cluster IV, V and VII, VIII was the second largest cluster with three genotypes each. Genotypes of cluster IV and VII belonged to the high-quality protein maize. The clusters VI, IX and X contained two genotypes. From the eleventh to twenty-two clusters were solitary cluster with single genotype. The mono-genotypic cluster indicated that genotypes belonging to these clusters had wide diversity from the rest as well as from each other. Thus, these genotypes have entirely different genetic make-up from the others. These results are in general agreements with the findings of Singh *et al.* (2009) [10], Singh *et al.* (2015) [9] and Patil *et al.* (2017) [7]. Similarly, Choudhary *et al.* (2020) [2] classified 70 single cross maize hybrids into 16 different clusters.

### Inter and intra-cluster distances

The inter-cluster and intra-cluster distances are shown in Table 2. The maximum inter-cluster distance ( $D = 722.50$ ) was found between cluster 15 and 5, followed by that between 10 and 12 ( $D = 718.86$ ) and 10 and 17 (677.60). The minimum inter-cluster distance was observed between cluster 21 and 11 ( $D = 94.65$ ). The intra-cluster distance ( $D$ ) ranged from 45.30 (cluster-6) to 78.92 (cluster-2). The twelve different clusters contained single genotype and therefore, their intra-cluster distance was zero. In general, intra-cluster distances were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other. The genotypes belonging to the clusters separated by high genetic distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. Similar result was reported by Patil *et al.* (2021) [6] during genetic diversity analysis of maize under drought stress condition.

### Cluster means of various characters

The cluster mean value for 14 characters are presented in Table 3. Wide range of mean values among the clusters were recorded for different traits. The cluster 14 manifested highest mean values for 50% days to silking and tasseling (77 and 83 days, respectively). cluster 13 was superior for ear length (18.41) and kernels per rows (34.00). Similarly, 14<sup>th</sup> cluster is higher for ear girth. Kernel rows per ear was higher for cluster 18, cluster 17 was higher for no of kernels per ear. Cluster 12 and 10 was higher for ear weight and shelling percent. Test weight and grain yield per plant were found superior for cluster 4 and 9, respectively. Therefore, intercrossing of such genotypes involved in these clusters would be useful for generating variability for the respective characters, and their rational improvement for increasing the seed yield. Similar result was observed by Choudhary *et al.* (2020) [2] in maize hybrids while Jakhar *et al.* (2018) [3] also reported similar result for maize.

### Characters contribution towards genetic divergence

The analysis of variance for each character was carried out using mean of the 51 genotypes. Estimation of inter and intra cluster variances, along with ratio of inter cluster variance to the total variance ( $R^2$ ) and inter cluster coefficient of variation (CVb) for 14 characters were worked out and presented in Table 3. Maximum value of  $R^2$  was observed for shelling percentage (0.973) followed by ear weight (0.915) and number of kernels per row (0.899), while minimum value of  $R^2$  was observed for ears per plant (0.636). From inter cluster coefficient of variation (CVb), it was observed that the ear weight contributed maximum (67.50%) towards the total divergence in yield. The next major contribution came from the yield per plant (59.30%) followed by number of kernels per ear (47.30%), ear height (43.00%) and kernels per row (41.30%).

The percent contribution towards genetic divergence by 14 quantitative characters (Figure 1) revealed that, shelling percentage contributed most towards genetic divergence followed by ear weight, number of kernels per row and days

to 50% tasseling. These characters were responsible for expressing maximum diversity between the clusters therefore, should be given due weightage during selection. Remaining characters exhibited very low or negligible contribution towards divergence. Fact has been well established that more the genetically diverse parents used in hybridization programme, the greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in

segregating generations (Arunachalam, 1981) [1]. It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. Therefore, in the present investigation, based upon high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from clusters 5 and 15, which may lead to produce broad spectrum of favorable genetic variability for yield improvement in maize.

**Table 1:** The distribution of the 51 maize genotypes into different clusters on the basis of D<sup>2</sup> statistics

Cluster no	Name of genotype
1	I-07-29-1-3, PFSR5-3-5, IL-14-28, IGI-1104, GYL-10, GWQPM-55-2, IL-15-39
2	IL-17-34, IL-17-44, I-07-66-1-2, I-07-60-4-3, IL-14-48, I-07-7-3-2, IGI-1102
3	I-07-56-4-3, LM-5, IL-17-28, I-07-54-3-2, I-07-13-1-3, GWQPM-26-3, I-07-9-5
4	GWQPM-40-5, GWQPM-46-2, GWQPM-5-3
5	I-07-28-3-2, IL-17-32, I-07-65-44-4
6	I-07-66-3-2, GWQPM-17-2
7	GWQPM-40-3, GWQPM-47-1, IL-14-60
8	I-07-14-1-2, IGI-1103, I-07-66-2-3
9	GWQPM-11, GWQPM-22-5
10	I-07-6-4-4, I-07-6-4-5
11	I-07-66-4-1
12	I-077-59-5
13	IL-15-11
14	IGI-1101
15	IGI-1103
16	CML-307
17	LTP-1-1
18	LM-B-2
19	H07R-1-3
20	GWQPM-26-1
21	GWQPM-67-2
22	GWQPM-68-4

**Table 2:** Average intra-cluster and inter-cluster distance for 51 genotypes of maize

Cluster	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1	71.58	184.82	342.51	113.88	483.01	334.44	178.29	366.41	101.98	137.44	167.84	376.49	270.05	182.62	119.33	158.40	433.11	199.19	113.49	132.22	336.54	292.91
2	184.82	78.92	156.91	191.84	164.00	136.45	166.11	193.53	180.97	322.78	121.65	235.07	200.17	116.30	308.34	214.91	161.17	120.15	110.13	265.95	165.74	262.90
3	342.51	156.91	73.68	365.04	156.17	175.94	174.13	112.53	387.71	641.91	167.18	104.37	157.44	183.54	577.72	491.16	107.25	304.69	269.92	396.40	147.76	154.99
4	113.88	191.84	365.04	57.97	482.46	275.95	173.62	429.91	126.02	199.44	228.98	390.77	367.48	251.07	153.11	98.40	476.19	208.60	127.03	140.39	409.96	383.59
5	483.01	164.00	156.17	482.46	66.38	138.22	314.42	202.43	457.33	690.84	239.78	260.35	307.56	211.33	722.50	508.45	117.13	300.59	293.55	597.41	161.44	353.98
6	334.44	136.45	175.94	275.95	138.22	45.30	148.73	193.68	373.84	553.42	212.68	242.40	337.23	116.19	526.67	289.67	259.20	294.06	146.75	418.79	168.25	289.54
7	178.29	166.11	174.13	173.62	314.42	148.73	69.09	166.46	261.87	419.28	179.85	138.97	189.00	97.93	370.57	275.59	326.47	326.83	156.12	196.70	202.50	136.50
8	366.41	193.53	112.53	429.91	202.43	193.68	166.46	64.26	450.53	677.39	240.16	95.95	98.69	126.91	596.00	516.26	177.14	354.99	322.24	359.14	133.56	142.70
9	101.98	180.97	387.71	126.02	457.33	373.84	261.87	450.53	59.56	113.44	172.55	467.06	323.08	239.23	183.85	180.78	398.28	179.65	128.90	228.46	333.55	398.78
10	137.44	322.78	641.91	199.44	690.84	553.42	419.28	677.39	113.44	68.21	327.03	718.87	506.02	357.03	106.40	156.22	677.60	247.95	204.45	243.15	567.87	607.47
11	167.84	121.65	167.18	228.98	239.78	212.68	179.85	240.16	172.55	327.03	0.00	309.58	239.21	154.25	346.17	326.97	209.34	210.22	112.98	345.56	94.65	133.66
12	376.49	235.07	104.37	390.77	260.35	242.40	138.97	95.95	467.06	718.87	309.58	0.00	104.40	207.68	633.36	544.33	193.28	427.80	386.07	314.88	255.79	155.39
13	270.05	200.17	157.44	367.48	307.56	337.23	189.00	98.69	323.08	506.02	239.21	104.40	0.00	168.50	448.86	472.35	204.57	295.74	348.21	212.56	201.04	152.05
14	182.62	116.30	183.54	251.07	211.33	116.19	97.93	126.91	239.23	357.03	154.25	207.68	168.50	0.00	371.11	256.17	275.53	251.77	101.33	255.12	116.30	178.65
15	119.33	308.34	577.72	153.11	722.50	526.67	370.57	596.00	183.85	106.40	346.17	633.36	448.86	371.11	0.00	113.01	656.81	177.21	213.51	131.91	615.19	568.54
16	158.40	214.91	491.16	98.40	508.45	289.67	275.59	516.26	180.78	156.22	326.97	544.33	472.35	256.17	113.01	0.00	566.12	189.08	127.88	178.22	497.96	557.99
17	433.11	161.17	107.25	476.19	117.13	259.20	326.47	177.14	398.28	677.60	209.34	193.28	204.57	275.53	656.81	566.12	0.00	262.26	346.16	538.92	175.92	296.67
18	199.19	120.15	304.69	208.60	300.59	294.06	326.83	354.99	179.65	247.95	210.22	427.80	295.74	251.77	177.21	189.08	262.26	0.00	149.77	269.68	355.66	482.34
19	113.49	110.13	269.92	127.03	293.55	146.75	156.12	322.23	128.90	204.45	112.98	386.07	348.21	101.33	213.51	127.88	346.16	149.77	0.00	279.13	228.75	317.95
20	132.22	265.95	396.40	140.39	597.41	418.79	196.70	359.14	228.46	243.15	345.56	314.88	212.56	255.12	131.91	178.22	538.92	269.68	279.13	0.00	487.90	344.65
21	336.54	165.74	147.76	409.96	161.44	168.25	202.50	133.56	333.55	567.87	94.65	255.79	201.04	116.30	615.19	497.96	175.92	355.66	228.75	487.90	0.00	121.45
22	292.91	262.90	154.99	383.59	353.98	289.54	136.50	142.70	398.78	607.47	133.66	155.39	152.05	178.65	568.54	557.99	296.67	482.34	317.95	344.65	121.45	0.00

**Table 3:** Cluster mean of different characters of maize

Cluster	No of Genotypes	TA	SI	PH	EH	EPP	EL	KPR	EG	KRP	NKE	EW	SH	TW	GY
1	8	68.37	74.75	133.25	54.33	1.43	13.93	28.67	11.24	13.51	387.91	92.95	71.86	18.89	76.29
2	6	71.08	76.83	115.00	43.46	1.35	12.05	21.94	11.54	13.88	307.11	55.70	65.17	15.54	53.16
3	7	69.85	76.36	130.36	53.64	1.62	12.97	28.25	10.61	13.34	374.76	87.56	58.42	19.16	67.14
4	3	57.83	64.33	131.33	47.93	1.28	12.76	21.97	10.17	12.85	282.02	70.66	72.78	25.23	74.84
5	3	74.00	80.50	80.48	33.38	1.38	11.57	19.29	12.41	13.65	263.92	39.89	58.19	13.02	44.72
6	2	68.00	73.75	93.53	42.62	1.46	12.07	14.17	10.59	12.80	182.77	57.83	65.17	19.21	32.34

7	3	63.83	71.00	131.99	55.85	1.28	15.70	25.09	10.40	12.78	325.54	107.57	66.69	21.29	69.28
8	3	74.16	79.50	137.88	51.67	1.33	15.26	23.85	11.57	13.54	321.15	112.17	58.01	15.49	49.61
9	2	65.75	71.50	136.04	54.77	1.08	16.78	32.79	11.24	14.08	461.04	54.56	70.98	17.89	106.67
10	2	69.75	76.25	109.01	41.74	1.67	14.86	29.57	12.34	14.00	413.88	61.64	77.93	16.41	73.22
11	1	71.50	78.00	157.65	74.88	1.66	11.59	25.00	14.30	14.17	349.50	62.50	65.75	19.49	61.00
12	1	63.5	71.50	119.20	40.16	1.17	16.28	31.16	10.75	14.00	437.22	130.51	57.17	17.13	81.52
13	1	70.00	76.50	147.90	46.68	2.00	18.42	34.00	11.29	13.24	448.92	114.22	58.63	9.49	86.15
14	1	77.00	83.00	111.45	50.19	1.33	15.75	24.08	8.80	10.27	247.71	77.74	67.32	13.10	40.58
15	1	70.00	76.00	139.53	44.93	2.00	9.83	21.50	11.50	14.34	309.11	92.43	77.84	19.93	53.28
16	1	65.50	71.00	97.55	27.70	2.00	9.95	14.98	8.07	9.14	136.67	42.50	76.63	17.58	27.19
17	1	71.50	76.50	122.40	44.77	1.00	12.16	29.80	12.64	15.78	471.24	64.14	54.45	9.64	60.62
18	1	74.00	81.00	126.40	38.47	1.50	8.95	17.50	11.75	16.00	270.56	45.95	67.82	12.09	41.27
19	1	74.00	81.00	117.90	57.40	1.50	12.42	22.00	9.57	13.17	290.05	54.17	73.10	19.36	56.67
20	1	62.00	68.00	130.98	34.71	1.83	14.13	26.75	8.67	9.76	264.60	112.11	70.90	20.15	54.61
21	1	72.00	76.00	149.55	72.06	1.50	15.99	24.84	14.08	13.54	335.58	63.81	59.95	10.67	57.71
22	1	67.00	73.50	172.05	78.97	1.67	15.00	29.50	13.84	12.47	369.27	121.22	61.22	18.48	62.16
R <sup>2</sup>		0.82	0.81	0.85	0.86	0.64	0.87	0.90	0.70	0.69	0.86	0.92	0.97	0.73	0.79
CV b%		13.40	11.84	31.22	42.95	31.28	30.64	41.34	22.71	18.49	47.29	67.48	21.81	45.16	59.26

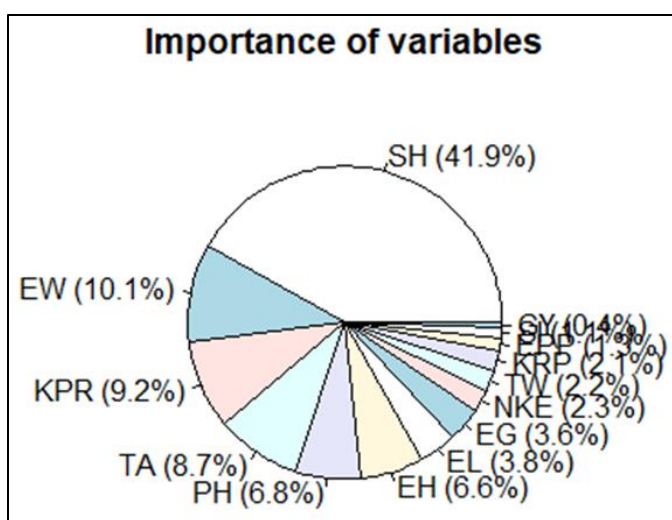


Fig 1: Contribution of different characters towards genetic divergence of 51 maize genotypes

- Mahalanobis PC. On the generalized distance in statistics. Proc. Nat. Inst. Sci. India. 1936;2:49-55.
- Meena MK, Singh R, Sharma A, Bhati PK. Diversity studies in selected maize (*Zea mays* L.) germplasm of eastern Uttar Pradesh. Research in Environment and Life Sciences. 2014;7(3):193-196.
- Patil NL, Shanthakumar G, Biradar BD. Genetic diversity analysis of Maize (*Zea mays* L.) inbred lines under drought stress using grain yield and yield related traits. Journal of Crop and Weed. 2021;17(3):192-198.
- Patil SM, Jakhar DS, Kumar K, Meena S. Genetic diversity studies in maize (*Zea mays* L.) germplasm from India. Int. J of Plant & Soil Sci. 2017;14(6):1-6.
- Rao CR. Advanced statistical methods in biometrical research. John Wiley and Sons Inc. New York; c1952. p. 390.
- Singh P, Salgotra SK, Singh AK, Sharma M, Gupta A, Sharma M, et al. Stability and genetic divergence study of single cross hybrids in maize (*Zea mays* L.). African Journal of Agricultural Research. 2015;10(31):3080-3085.
- Singh SB, Gupta BB, Singh AK. Genetic divergence for morpho-physiological traits and yield components associated with drought tolerance in maize (*Zea mays* L.) inbred. Indian J Plant Genet Res. 2009;22:102-107.

**Conclusion**

D-square analysis gave immense information regarding genetic diversity of morphological traits. The maximum inter-cluster distance was found between cluster 15 and 5, followed by that between 10 and 12 and 10 and 17. Suggest the utilization of these genotypes for getting more heterosis. In this study solitary clustered genotypes were more diverse and advised to use to select for specific characters based on the cluster mean analysis while grain yield and shelling percentage had maximum diversity among the population that can be utilized for further improvement.

**References**

- Arunachalam V. Genetic distance in plant breeding. Indian J Genet. 1981;41(2):226-236.
- Choudhary MK, Shahi JP, Kumawat G, Shikha K, Kilo GK. Diversity analysis of maize (*Zea mays* L.) genotypes under excess soil moisture condition. Journal of Pharmacognosy and Phytochemistry. 2020;9(4):3407-3413.
- Jakhar DH, Ray A, Singh R. Genetic Diversity Analysis in Maize (*Zea mays* L.) by D<sup>2</sup> Clustering of Yield and Yield Accredited Traits. International Journal of Agriculture, Environment and Biotechnology; c2018. p. 833-836.