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Genetic divergence in maize (*Zea mays* L.) genotypes through cluster analysis

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Abstract
Genetic divergence plays a crucial role in maize breeding programmes by identifying genetically diverse parental lines that can produce superior hybrids. The present study evaluated 42 maize genotypes including 39 inbred lines and 3 checks to estimate the magnitude of genetic variability using Mahalanobis D^2 statistics. The analysis revealed significant variation among genotypes for all yield and yield-related traits. Cluster analysis grouped the genotypes into thirteen distinct clusters with considerable inter and intra cluster divergence. Traits such as cob weight, 1000-kernel weight, plant height and kernel rows per cob contributed most substantially to the overall divergence. The presence of wide genetic distances between clusters indicates the potential for selecting highly divergent parents for hybridization which can lead to the development of heterotic crosses and superior hybrids. This study emphasizes the importance of genetic divergence analysis in maize improvement programmes. By identifying and utilizing genetically diverse inbreds, breeders can enhance selection efficiency broaden the genetic base of breeding material and accelerate the development of high yielding and stress resilient maize hybrids suited for diverse agro ecological conditions in India.

Keywords: Genetic divergence, Mahalanobis D^2, maize inbreds, cluster analysis, yield traits

Introduction

Maize (*Zea mays* L.) popularly known as the 'Queen of Cereals', is one of the most important cereal crops cultivated worldwide for food, feed and industrial purposes. In India maize ranks third after rice and wheat and its demand is increasing due to its role in food, feed and biofuel production. However the national average productivity of maize is still lower compared to major producing countries such as the United States and China. This necessitates the development of superior maize hybrids with enhanced yield potential, stress tolerance and adaptability to diverse environments. Genetic divergence which refers to the extent of variability among genotypes is a key factor in breeding programmes. Understanding the genetic divergence among inbred lines helps breeders identify distantly related parents that, when crossed, are more likely to exhibit heterosis. It has become possible to quantify magnitude of genetic diversity among genotypes with the help of advanced method such as torchers method (Rao, 1952) [16] based on Mahalanobis (1936) [10] D^2 statistics. It enables breeders to measure the contribution of various traits to overall diversity and classify genotypes into distinct clusters. Such classification facilitates the selection of genetically diverse parents for effective hybridization.

Materials and Methods

The study was carried out at AICRP on Maize, Kasba Bawada, Kolhapur during *Rabi* 2024. The experimental material consisted of 42 genotypes, including 39 maize inbred lines and 3 checks. The trial was conducted in a Randomized Block Design (RBD) with three replications. Each entry was sown in a single row of 3 m length, with row-to-row spacing of 60 cm and plant-to-plant spacing of 20 cm. Standard agronomic practices were followed to raise a healthy crop. Data were recorded on the following traits such as days to 50% tasseling, days to 50% silking, plant height (cm), cob height (cm), cob length (cm), cob girth (cm), number of kernel rows per cob, number of kernels per row, cob weight (g), 1000-kernel weight (g), grain yield per plant (g) and protein content (%).

(%). Statistical analysis was performed using Mahalanobis D^2 statistics to quantify genetic divergence. Intra and inter cluster distances, cluster mean and percent contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985) [23].

Results

Cluster analysis was performed using Tocher's method, as described by Rao (1952) [16]. Based on the genetic divergence data the 42 inbreds (comprising 39 inbreds and 3 checks) were grouped into thirteen clusters. The distribution of these genotypes into different clusters are presented in Table 1. Cluster II was the largest, containing 16 inbreds followed by Cluster I with 10 inbreds (including 8 inbreds and 2 checks), Cluster X with 4 inbreds and Cluster VIII (including 2 inbreds and 1 check). The remaining clusters III, IV, V, VI, VII, IX, X, XI, XII and XIII were solitary. Average intra and inter cluster distance of thirteen clusters are presented in Table 2. The highest intra-cluster distance was observed in cluster X (D^2 = 16.03) followed by cluster VIII (D^2 = 13.47) and cluster II (D^2 = 11.90) indicates the presence of wide genetic diversity among inbreds within these clusters. Whereas, the lowest intra-cluster distance was observed in cluster I ((D^2 = 9.93). The Clusters III, IV, V, VI, VII, IX, X, XI, XII and XII showed no intra-cluster distances due to being mono-genotypic in nature. The presence of several mono-genotypic clusters indicates a limited genetic diversity among certain genotypes based on earlier reports on the occurrence of such clusters in maize (Patil *et al*., 2017) [15]. The maximum inter-cluster distance was observed in between clusters VIII and IX (D^2= 38.68) followed by clusters IX and XIII (D^2 = 34.93), clusters VIII and XI (D^2 = 34.58), clusters V and VIII (D^2 = 30.94) and clusters XI and XIII (D^2 = 30.24) indicates that the greater the distance between two clusters the greater will be the genetic divergence. The minimum inter-cluster distances were observed between clusters V and IX (D^2 = 8.99) followed by clusters V and XI (D^2 = 9.26), clusters IV and V (D^2 = 9.48) and clusters VI and XII (D^2 = 9.89) indicating proximity with each other. The percent contribution of the thirteen characters to the total divergence is presented in table 3.The analysis showed that cob weight was the largest contributor to divergence, accounting for 43.55 percent followed by protein percent (34.15%), thousand kernel weight (9.64%), days to 50 percent tasseling (4.99%), cob length (2.56%), number of kernels per row (2.09%) and cob width (1.28%) contributed more than 80 percent towards total divergence. The characters plant height (0.58%), cob height, number of kernel rows per cob (0.46%), grain yield per plant (0.23%) contributed minimally. Days to 50 percent silking had no contribution. Based on these findings it is recommended to select parent lines exhibiting maximum genetic divergence, with particular focusing on traits such as cob weight, protein content, thousand kernel weight, days to 50% tasseling, cob length and cob width, for effective hybridization planning. Based on the mean performance of the clusters (Table 4) the following inbreds were selected as superior. For the trait days to 50 percent tasseling, inbreds from clusters IX and XII performed better requiring fewer days to reach 50 percent tasseling. Similarly, for days to 50 percent silking, inbreds in clusters IX and XII showed a shorter duration to reach 50 percent silking. The inbreds from clusters IX and XI showed the lowest plant height and those from the same clusters exhibited the shortest cob height making these clusters suitable for selection in future breeding programs. For cob length the inbreds in clusters VIII and I had the longest cobs which is a desirable trait. Similarly, clusters VIII and VII included inbreds with the maximum cob width making them ideal for selection. The inbreds that had highest number of kernel rows per cob are from the clusters VIII and IX. The highest number of kernel rows per cob are from clusters III and VIII. The inbreds with the highest cob weight was found in clusters VIII and XIII. The inbreds under the clusters III and IX had maximum thousand kernel weight and inbreds having higher protein comes under clusters VI, XIII. The inbreds which had the maximum grain yield per plant are from clusters VIII, XIII. Therefore selecting inbreds from these clusters based on these traits would significantly contribute to improving yield. Considering all the characters it appears that the genotypes in cluster VIII and cluster IX showed good performance. The performance of individual lines is presented in Table 5.

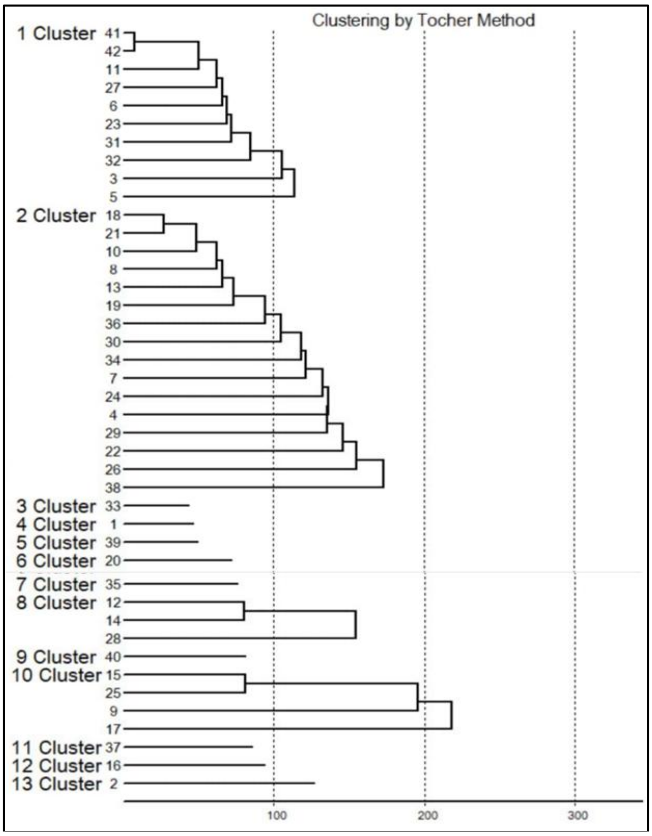

Fig 1: Cluster diagram of 42 genotypes of maize into thirteen clusters by Torcher Method

Table 1: Distribution of 42 genotypes of maize into 13 different clusters

Clusters	No. of genotypes/inbreds included	Name of genotypes/inbreds	Specific Character
I	10	Phule Maharshi, Phule Champion, QMI 24207, QMI 24051, QMI 24180, QMI 24277, QMI 24079, QMI 24088, QMI 24159, QMI 24156.	Highest cob length, moderate plant height and no. of kernel rows.
II	16	QMI 24245, QMI 24263, QMI 24193, QMI 24192, QMI 24199, QMI 24257, QMI 24124, QMI 24080, QMI 24096, QMI 24171, QMI 24282, QMI 24175, QMI 24040, QMI 24276, QMI 24010, QMI 24128.	Moderate Days to maturity, cob width, and cob length.
III	1	QMI 24027	High no. of kernels per row and thousand kernel weight.
IV	1	QMI 24147	lowest thousand kernel weight and grain yield per plant
V	1	QMI 24130	Moderate yield per plant (g)
VI	1	QMI 24259	Highest protein percent
VII	1	QMI 24122	Highest plant height and Lowest protein percent
VIII	3	QMI 24190, QMI 24216, Aarambh.	High Cob width, No. of kernel rows per cob, cob weight, grain yield per plant.
IX	1	QMI 24141	Early maturity, highest no. of kernel rows per cob.
X	4	QMI 24222, QMI 24009, QMI 24194, QMI 24230	Moderate plant height, no. of kernel per row.
XI	1	QMI 24125	Late maturity, highest no. of kernel rows per cob.
XII	1	QMI 24232	Highest cob height, lowest no. of kernel rows per cob
XIII	1	QMI 24155	high protein percent

Table 2: Average intra and inter cluster D^2 and D values of thirteen clusters formed from 42 genotypes of maize.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	9.93 (3.15)	16.66 (4.08)	16.71 (4.09)	21.26 (4.61)	22.24 (4.71)	20.85 (4.57)	14.58 (3.82)	14.90 (3.86)	30.23 (5.50)	20.82 (4.56)	25.68 (5.07)	16.08 (4.01)	14.87 (3.86)
II		11.90 (3.45)	13.82 (3.72)	16.02 (4.00)	14.77 (3.84)	16.58 (4.07)	21.02 (4.58)	26.06 (5.10)	21.50 (4.64)	17.73 (4.21)	17.37 (4.17)	16.07 (4.01)	19.57 (4.42)
III			0	21.73 (4.66)	22.02 (4.69)	11.69 (3.42)	24.75 (4.97)	26.11 (5.11)	28.67 (5.35)	22.52 (4.75)	24.18 (4.92)	12.10 (3.48)	16.19 (4.02)
IV				0	9.48 (93.08)	23.26 (4.82)	20.56 (4.53)	29.46 (5.43)	15.61 (3.95)	16.45 (4.06)	11.93 (3.45)	22.27 (4.72)	27.78 (5.27)
V					0	22.15 (4.71)	22.55 (4.74)	30.94 (5.56)	8.99 (3.00)	15.40 (3.92)	9.26 (3.04)	21.74 (4.66)	27.11 (5.21)
VI						0	29.81 (5.46)	29.25 (5.40)	28.14 (5.30)	27.35 (5.23)	25.39 (5.04)	9.89 (3.14)	14.47 (3.80)
VII							0	17.10 (4.13)	29.72 (5.45)	17.89 (4.23)	26.09 (5.11)	25.42 (5.04)	25.25 (5.02)
VIII								13.47 (3.67)	38.68 (6.22)	28.31 (5.32)	34.58 (5.88)	23.70 (4.87)	19.44 (4.41)
IX									0	20.04 (4.48)	12.86 (3.59)	28.74 (5.36)	34.93 (5.01)
X										16.03 (4.00)	18.84 (4.34)	25.18 (5.02)	29.03 (5.39)
XI											0	26.06 (5.10)	30.24 (5.50)
XII												0	11.27 (3.36)
XIII													0

Table 3: Percent contribution of various characters for divergence

Sr. No.	Source	Times ranked 1st	Contribution (%)
1	Days to 50% tasseling	43	4.99
2	Days to 50% silking	0	0.00
3	Plant height (cm)	5	0.58
4	Cob height (cm)	4	0.46
5	Cob length (cm)	22	2.56
6	Cob width (cm)	11	1.28
7	No. of kernel rows per cob	4	0.46
8	No. of kernel per row	18	2.09
9	Cob Weight (g)	375	43.55
10	Thousand kernel weight (g)	83	9.64
11	protein	294	34.15
12	Grain yield per plant(g)	2	0.23
		Total	100

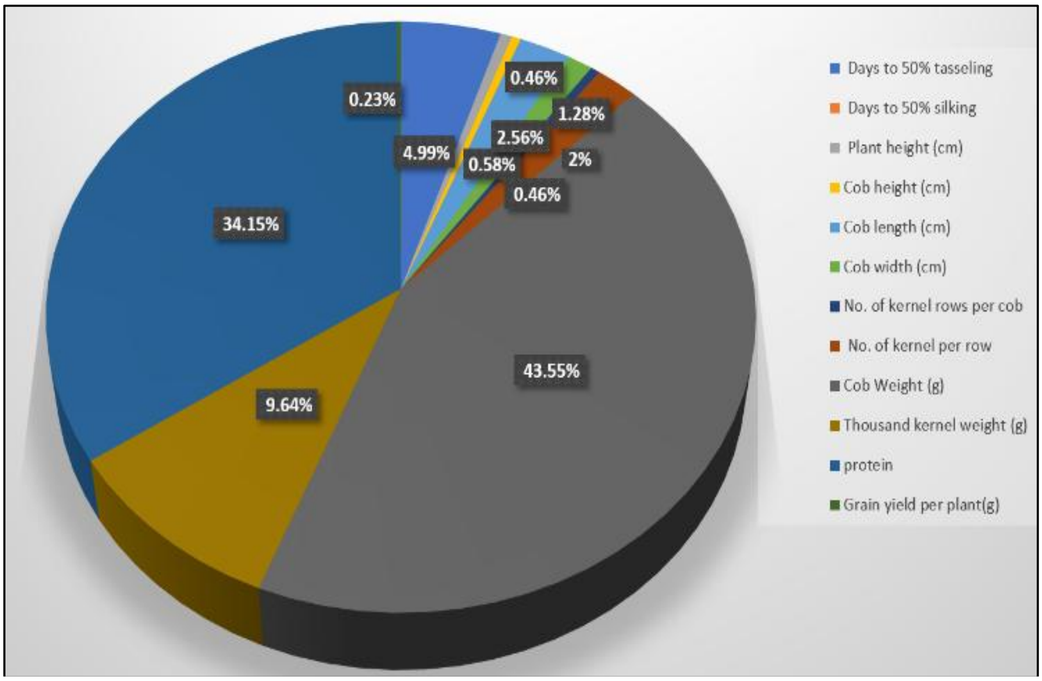

Fig 2: Percent Contribution of Various Characters for Divergence

Table 4: Mean performance of 13 clusters for 12 characters in maize.

Cluster	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Cob height (cm)	Cob length (cm)	Cob width (cm)	No. of kernel rows per cob	No. of kernels per row	Cob weight (g)	1000 kernel weight	Protein (%)	Grain yield per plant (g)
I	57.40	59.67	189.33	103.23	17.41	14.98	14.27	29.65	163.40	271.27	7.74	122.25
II	57.13	59.69	188.46	96.10	14.09	13.06	13.75	26.33	93.70	259.62	8.03	99.81
III	54.00	56.00	202.00	100.00	16.33	14.00	14.67	35.00	95.00	293.00	9.00	106.67
IV	55.00	57.33	205.33	84.33	14.25	14.50	14.00	29.00	66.00	161.83	6.90	62.33
V	54.00	56.00	155.00	85.33	10.97	11.33	13.33	22.00	79.33	201.67	7.10	86.73
VI	52.00	54.33	209.00	92.67	13.23	12.33	13.33	26.33	95.00	236.67	9.80	104.50
VII	58.00	61.00	210.17	105.67	15.23	15.17	12.00	31.00	169.33	270.67	5.67	129.17
VIII	57.67	60.00	185.44	101.89	18.91	16.39	15.33	30.56	225.56	273.89	7.39	140.89
IX	51.00	53.00	133.00	78.67	8.40	9.67	15.33	19.00	55.17	203.33	6.73	64.33
X	54.25	56.67	168.17	92.08	14.53	12.87	12.50	27.33	98.46	280.08	6.22	98.88
XI	61.67	64.33	153.33	80.33	9.77	10.67	15.33	28.33	60.83	184.67	7.33	72.17
XII	51.00	53.33	180.17	114.33	15.27	14.50	12.00	27.33	128.33	241.67	9.40	89.90
XIII	58.00	60.00	188.33	105.00	15.23	14.50	13.33	25.67	172.00	261.67	9.63	137.67

Table 5: Mean performance of 42 genotypes (39 inbreds and 3 hybrids) for 12 characters in maize

Sr. No	Genotypes/Inbreeds	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Cob height (cm)	Cob length (cm)	Cob width (cm)	No. of kernel rows per cob	No. of kernels per row	Cob weight (g)	Thousand kernel weight (g)	Protein percent (%)	Grain yield per plant(g)
1	QMI 24147	55.00	57.33	205.33	84.33	14.25	14.50	14.00	29.00	66.00	161.83	6.90	62.33
2	QMI 24155	58.00	60.00	188.33	105.00	15.23	14.50	13.33	25.67	172.00	261.67	9.63	137.67
3	QMI 24159	60.33	62.33	186.83	96.00	17.60	15.83	13.33	29.67	120.33	245.33	8.23	113.00
4	QMI 24175	54.00	56.67	189.67	88.33	14.87	12.25	10.67	29.00	80.50	201.67	7.17	83.80
5	QMI 24156	63.33	65.67	193.67	108.33	15.17	15.50	13.33	34.00	167.67	306.67	8.10	136.00
6	QMI 24180	59.00	61.33	179.33	100.67	16.93	14.93	14.67	29.67	155.33	266.67	7.33	122.83
7	QMI 24171	52.33	54.33	203.33	89.00	16.00	15.50	14.67	29.00	80.00	240.00	8.47	85.40
8	QMI 24192	59.00	61.33	195.00	94.33	12.50	11.83	14.67	22.00	94.50	288.80	8.13	101.57
9	QMI 24194	53.00	56.00	205.17	67.00	13.75	14.50	11.33	27.67	59.67	310.00	6.40	70.17
10	QMI 24193	57.00	59.67	189.17	85.67	11.37	12.50	14.67	21.00	87.33	236.67	7.13	94.10
11	QMI 24207	56.00	58.33	168.33	115.00	15.50	15.00	14.00	25.33	172.33	265.00	7.90	135.67
12	QMI 24190	59.00	61.33	173.50	99.67	16.32	15.33	16.67	28.33	235.00	248.33	7.43	126.67
13	QMI 24199	55.00	57.67	205.00	101.67	13.07	12.83	16.67	25.00	89.33	245.00	7.63	116.50
14	QMI 24216	57.00	59.00	168.67	111.00	20.27	15.50	13.33	27.33	250.00	273.33	8.13	141.67
15	QMI 24222	55.00	57.33	165.33	99.33	15.37	13.17	11.33	30.67	126.67	240.00	5.80	104.67
16	QMI 24232	51.00	53.33	180.17	114.33	15.27	14.50	12.00	27.33	128.33	241.67	9.40	89.90
17	QMI 24230	56.00	58.33	150.83	99.33	11.23	10.00	12.00	18.00	65.17	285.33	6.07	101.53
18	QMI 24245	60.00	62.67	198.33	89.00	14.83	14.00	11.33	23.33	81.67	275.00	7.10	101.23
19	QMI 24257	55.00	58.00	180.00	93.33	11.27	11.67	11.33	21.67	129.33	296.67	7.27	103.30
20	QMI 24259	52.00	54.33	209.00	92.67	13.23	12.33	13.33	26.33	95.00	236.67	9.80	104.50
21	QMI 24263	62.00	64.00	195.00	89.00	11.37	14.25	13.33	27.00	99.67	287.00	7.17	98.47
22	QMI 24276	59.00	61.00	202.67	95.33	15.27	11.33	16.00	31.00	105.00	278.33	8.93	106.90
23	QMI 24277	53.33	55.67	181.33	98.33	15.10	13.67	13.33	26.83	155.00	291.33	7.60	110.00
24	QMI 24282	58.00	60.67	157.50	95.00	15.27	17.00	16.00	27.00	95.00	213.50	8.40	101.17
25	QMI 24009	53.00	55.00	151.33	102.67	17.75	13.83	15.33	33.00	142.33	285.00	6.60	119.17
26	QMI 24010	60.00	62.00	171.17	102.67	14.77	12.50	15.33	31.33	88.50	331.67	8.30	105.40
27	QMI 24051	59.00	61.00	200.00	100.00	16.20	13.17	13.33	30.00	176.67	236.33	7.43	132.90
28	QMI 24040	54.00	56.00	173.33	106.00	15.70	13.50	13.33	29.00	96.67	205.00	8.60	102.00
29	QMI 24080	59.33	61.67	175.00	115.00	14.33	10.83	11.33	27.33	85.00	276.33	8.23	94.23
30	QMI 24079	59.00	61.33	198.33	105.00	19.00	14.83	13.33	32.33	154.00	300.00	7.90	112.00
31	QMI 24088	57.00	59.00	196.67	107.33	20.30	15.17	14.00	28.00	169.67	276.33	6.70	121.93
32	QMI 24027	54.00	56.00	202.00	100.00	16.33	14.00	14.67	35.00	95.00	293.00	9.00	106.67
33	QMI 24096	53.33	56.00	200.00	93.33	15.77	14.67	12.67	29.00	100.00	296.67	8.40	98.27
34	QMI 24122	58.00	61.00	210.17	105.67	15.23	15.17	12.00	31.00	169.33	270.67	5.67	129.17
35	QMI 24124	61.00	65.33	203.50	100.00	17.30	11.17	13.33	26.33	91.67	265.00	8.17	101.00
36	QMI 24125	61.67	64.33	153.33	80.33	9.77	10.67	15.33	28.33	60.83	184.67	7.33	72.17
37	QMI 24128	55.00	58.00	176.67	100.00	11.73	13.17	14.67	22.33	95.00	216.67	9.30	103.63
38	QMI 24130	54.00	56.00	155.00	85.33	10.97	11.33	13.33	22.00	79.33	201.67	7.10	86.73
39	QMI 24141	51.00	53.00	133.00	78.67	8.40	9.67	15.33	19.00	55.17	203.33	6.73	64.33
40	Aarambh (C)	57.00	59.67	214.17	95.00	20.13	18.33	16.00	36.00	191.67	300.00	6.60	154.33
41	Phule Maharshi (C)	53.00	55.67	192.17	99.67	19.67	15.33	16.67	31.00	176.33	265.00	8.07	119.83
42	Phule Champion (C)	54.00	56.33	196.67	102.00	18.67	16.33	16.67	29.67	186.67	260.00	8.10	118.33
	Mean	56.49	58.90	185.09	97.39	15.07	13.72	13.86	27.68	122.01	258.66	7.72	106.93
	C.V.%	1.91	2.53	4.83	5.35	6.12	7.12	7.94	5.56	6.39	4.07	2.18	9.06
	S.E	0.62	0.86	5.16	3.01	0.53	0.56	0.63	0.89	4.50	6.09	0.10	5.60
	C.D at. (5%)	1.75	2.42	14.53	8.47	1.50	1.59	1.79	2.40	12.66	17.12	0.27	15.74

Conclusion

The study highlighted the presence of substantial genetic divergence among maize inbred lines, as revealed by Mahalanobis D^2 statistics. The wide inter-cluster distances provide opportunities for selecting diverse parents to enhance heterosis. Traits such as cob weight, 1000-kernel weight, plant height and kernel rows per cob were the major contributors to genetic divergence. The selection of parents from highly divergent clusters is expected to generate superior recombinants and high-yielding hybrids. Thus, genetic divergence analysis serves as a valuable tool for maize breeders to design effective selection strategies, broaden the genetic base and develop resilient hybrids capable of adapting to diverse environmental conditions. The D^2 analysis proved to be an effective tool for identifying genetic diversity among the genotypes evaluated in this study. Based on inter-cluster distances, cluster means and the individual performance of inbreds several entries were identified as superior. The genotypes QMI 24141, QMI 24232, QMI 24125, QMI 24216, QMI 24088, Aarambh, QMI 24122, QMI 24190, QMI 24027, QMI 24155, QMI 24194 and QMI 24259 were identified as superior in desirable traits and performance. These inbred lines may be considered as promising candidates for use as parents in future maize improvement programs subject to confirmation through multilocation testing.

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