



Plant Archives

Journal homepage: <http://www.plantarchives.org>DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.1.199>

ASSESSMENT OF GENETIC DIVERGENCE FOR MORPHO-PHYSIOLOGICAL TRAITS AND YIELD COMPONENTS IN MAIZE (*ZEA MAYS* L.) FOR HYBRID DEVELOPMENT AND ADAPTATION TO TROPICAL ENVIRONMENTS

Lingaswamy Mukkaamula^{1&2*}, Sudheer Kumar S.¹, Venkatesh Selvarangam², Sai Harini¹, and Mahesh Gudla¹

¹Division of Genetics and Plant Breeding, School of Agricultural Sciences, Malla Reddy University, Hyderabad, Telangana, India.

²Pioneer Hi-Bred Pvt. Ltd, Corteva Agriscience, Multi Crop Research Center, Wargal, Hyderabad, Telangana, India.
Corresponding author E-mail: lingaswamyagrigo46@gmail.com; 2332ag010002@mallareddyuniversity.ac.in
(Date of Receiving-21-01-2025; Date of Acceptance-31-03-2025)

ABSTRACT

A total of 185 maize inbreds were evaluated for genetic divergence using Mahalanobis' D² statistic across 14 traits. Significant differences were observed among genotypes, which were grouped into 17 clusters. Cluster 1 had the largest number of genotypes (86), followed by cluster 2 (39), cluster 5 (24), and cluster 7 (23), while the remaining clusters contained one genotype each. The highest intra-cluster distance was found in cluster 7 (264.31), and the highest inter-cluster distance was between clusters 14 and 15 (1607.30), indicating substantial genetic variability. Genotypes from clusters with high inter-cluster distances were identified as potential candidates for hybridization to enhance heterosis and generate diverse segregants. Based on Tocher's clustering, 20 inbreds were recommended for crossing. Notably, ear height, plant height, and grain yield contributed most to genetic divergence. The selected genotypes offer valuable genetic resources for single and multiple crossing programs to develop high-yielding hybrids with broad adaptability.

Key words: Maize, Mahalanobis D² statistics, Tochers Clustering, Germplasm, genetic variability, and Genetic Divergence.

Introduction

Maize (*Zea mays* L.), known as the "Queen of Cereals," is a globally significant crop, ranking third in cereal production after wheat and rice. Originating from Mexico, maize thrives in diverse agro-climatic conditions, ranging from sea level to 3000 meters in altitude and annual rainfall from 250 mm to over 5000 mm, demonstrating its adaptability and high productivity (Shaw, 1988; Dowsell *et al.*, 1996).

As a C4 crop, maize exhibits efficient photosynthesis, supporting high yields across tropical, subtropical, and temperate regions. In India, it is the third most cultivated cereal, grown in kharif, rabi, and spring seasons, with major production in Maharashtra, Madhya Pradesh, Karnataka, Bihar, and other states. Globally, maize covers

202 million hectares, yielding 1217 million metric tonnes (FAOSTAT, 2024), while India produces 31.5 million metric tonnes from 9.89 million hectares (ICAR-IIMR, 2024). Beyond food, maize is a key industrial crop used in ethanol, animal feed, starch, biofuels, and processed foods, contributing significantly to trade, with exports of 1.44 million tonnes in 2023–24 (APEDA, 2024).

Despite its economic importance, climate change and yield stagnation pose challenges, exacerbated by limited genetic diversity in cultivated hybrids. Expanding the genetic base is essential for improving yield stability under varying environments. Genetic divergence analysis helps breeders select diverse parental lines, as greater divergence enhances heterosis and hybrid performance (Fuzzato *et al.*, 2002).

Among various methods, Mahalanobis' D^2 analysis (Mahalanobis, 1936) is widely used to quantify genetic variation and assess trait contributions to overall divergence. Understanding inter- and intra-cluster diversity optimizes hybrid selection and germplasm refinement for future breeding efforts.

This study evaluates the genetic divergence of maize inbred lines to identify diverse parental genotypes for developing superior hybrids with improved morpho-physiological traits and yield components.

Material and Methods

The study was conducted during the rainy season of 2024 at the Hyderabad Research Center, Corteva Agriscience, Hyderabad. A total of 185 maize inbred lines sourced from CIMMYT India and Corteva Agriscience were evaluated using a randomized block design (RBD) with three replications. Each genotype was sown in a single four-meter-long row with a spacing of 60 cm between rows and 20 cm between plants.

A recommended fertilizer dose of 180:70:60 kg ha⁻¹ (N:P:K) was applied, with the entire P, K, and half of the N applied as basal, while the remaining N was applied in two equal splits at the knee-height and tasseling stages. Standard agronomic practices, including weeding, irrigation, and pest and disease management, were followed.

Observations were recorded for 14 quantitative traits: days to 50% tasseling, days to 50% silking, anthesis-silking interval, days to maturity (brown husk), plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100-kernel weight, moisture content, stay greenness, and grain yield per plant. Data for days to tasseling, silking, maturity, 100-kernel weight, moisture content, and stay greenness were recorded on a plot basis, while the remaining traits were recorded from five randomly tagged plants per plot.

Genetic divergence among the genotypes was analyzed using Mahalanobis' D^2 analysis, and clustering was performed using Tocher's method (Rao, 1952) to categorize genotypes based on their genetic distance.

Results and Discussion

Genetic diversity assessment is a fundamental aspect of any crop improvement program, as it aids in identifying potential parents for hybridization. Genetic divergence among parents enhances the probability of obtaining superior heterotic hybrids while also generating a broad spectrum of variability in segregating generations. Mahalanobis' D^2 statistics is a widely used multivariate statistical tool for effectively distinguishing genotypes

based on genetic diversity (Murthy and Arunachalam, 1966).

The analysis of variance revealed significant differences among the studied genotypes for all the evaluated traits (Table 1), indicating substantial genetic variability within the germplasm. The presence of such diversity is crucial for crop improvement programs targeting specific agronomic and yield-related traits. Similar findings have been reported by Ganesan *et al.*, (2010), Azad *et al.*, (2012), Reddy *et al.*, (2012), Alam *et al.*, (2013), Lingaiah *et al.*, (2013), Monir *et al.*, (2014), Seshu *et al.*, (2014), Haydar *et al.*, (2015), Abirami and Vanniarajan (2016), Kumar *et al.*, (2018), Khan (2022), Patel *et al.*, (2023), James *et al.*, (2024), and Yogendra Prasad *et al.*, (2024).

A comprehensive genetic analysis was conducted on 185 maize inbred lines to assess the extent of variability for key morpho-physiological and yield-contributing traits. The significant mean sum of squares for all traits indicated substantial genetic variability. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were closely aligned for most traits, suggesting minimal environmental influence. High broad-sense heritability ($h^2 > 90\%$) was observed for traits such as days to 50% tasseling (0.977), days to 50% silking (0.98), plant height (0.982), ear height (0.992), and grain yield per plant (0.98), indicating strong genetic control over these characteristics.

The anthesis-silking interval (ASI) exhibited the highest GCV (120.735%) and PCV (127.149%), demonstrating substantial scope for selection, despite its moderate heritability (0.902). Traits directly associated with yield, such as ear length, ear girth, number of kernels per row, and 100-kernel weight, displayed considerable genetic variability and moderate to high heritability, suggesting their potential utility in selection and breeding programs. Grain yield per plant exhibited the highest genetic variance ($\sigma^2_g = 639.83$), coupled with high heritability (0.98) and substantial GCV (24.634%), confirming its suitability as a target trait for genetic improvement.

Correlation analysis revealed that ear length (0.1045), ear girth (0.1612), number of kernels per row (0.2327), and 100-kernel weight (0.0731) had significant positive genetic correlations with grain yield, highlighting their importance in selecting high-yielding genotypes. Conversely, early flowering traits such as days to tasseling and silking showed negligible correlations with yield, indicating their limited direct contribution to productivity.

Table 1. Estimates of Mean Sum of squares, mean, range, mean square, environment, phenotypic and genotypic coefficient of variation, heritability and genetic correlation with grain yield for different characters in maize for 185 maize inbred lines.

S. No.	Characters	Mean sum of squares genotypes (df=184)	Mean	Range Min	Range Max	ECV (%)	GCV (%)	PCV (%)	h ² (board sense)	rg with seed yield
1	Days to 50 per cent tasseling (Days)	29.26**	57.61	48.67	64.00	0.826	5.401	5.464	0.977	-0.0035
2	Days to 50 per cent Silking (Days)	32.6**	58.65	48.67	65.00	0.81	5.602	5.66	0.98	0.0007
3	Anthesis- Silking Interval (Days)	4.88**	1.04	-2.00	4.00	39.872	120.735	127.149	0.902	0.0186
4	Days to maturity (Brown husk) (Days)	60.17**	93.89	84.00	103.50	0.764	4.749	4.81	0.975	0.0164
5	Plant height (cm)	785.39**	169.43	126.80	212.00	1.274	9.521	9.606	0.982	0.006
6	Ear height (cm)	469.68**	73.99	43.50	104.50	1.524	16.887	16.956	0.992	-0.0019
7	Ear length (cm)	7.49**	12.36	7.63	16.98	3.532	12.619	13.104	0.927	0.1045
8	Ear girth (cm)	0.28**	3.69	2.99	4.58	2.846	8.225	8.704	0.893	0.1612
9	Number of Kernel Rows per Ear (Count)	4.78**	13.24	9.25	17.80	3.103	9.371	9.871	0.901	0.0157
10	Number of Kernels per Row (Count)	35.7**	20.58	11.00	30.20	6.214	16.376	17.515	0.874	0.2327
11	100-Kernel weight (g)	50.01**	24.94	15.50	35.50	3.836	16.219	16.667	0.947	0.0731
12	Moisture content (%)	12.99**	19.01	14.70	26.55	4.552	10.628	11.562	0.845	0.0471
13	Stay greenness (Score)-85DAS	3.01**	5.18	2.00	7.67	7.559	18.849	20.308	0.861	0.0038
14	Stay greenness (Score)-91DAS	3.55**	4.29	1.67	6.00	8.27	24.929	26.265	0.901	0.0342
15	Grain yield (g per plant)	639.83**	59.08	22.50	115.30	3.563	24.634	24.891	0.98

* Significant at 5% level; and ** Significant at 1% level.

These findings underscore the importance of selecting traits with high genetic variability and positive correlations with yield, particularly kernel number and ear traits, to enhance maize productivity and stability across diverse environments. The substantial genetic divergence observed among the studied germplasm suggests its potential utility in developing hybrids with improved adaptability and resilience, contributing to sustainable maize breeding programs.

Grouping of genotypes into various clusters (D² analysis)

A total of 185 maize genotypes were evaluated during Kharif 2024, and the data were subjected to D² analysis. The analysis of variance revealed highly significant differences among the genotypes for all fourteen characters, indicating substantial genetic variability within the experimental material.

Based on D² analysis, the 185 genotypes were grouped into seventeen clusters, as presented in Table 2. Cluster 1 was the largest, comprising 86 genotypes,

suggesting a high degree of genetic similarity among them. This was followed by Cluster 2 (39 genotypes), Cluster 5 (24 genotypes), and Cluster 7 (23 genotypes). The remaining clusters—Cluster 3, Cluster 4, Cluster 6, Cluster 8, Cluster 9, Cluster 10, Cluster 11, Cluster 12, Cluster 13, Cluster 14, Cluster 15, Cluster 16, and Cluster 17—each contained a single genotype.

Genetic diversity is often associated with geographical diversity; however, the two do not necessarily exhibit a direct correlation. In this study, genotypes within the same clusters originated from different geographical regions, indicating that genetic divergence did not align with geographical distribution. This pattern may be attributed to the continuous exchange of genetic material among different countries, leading to the dispersal of genetically similar material across various regions.

Average intra and inter cluster distances

The average intra- and inter-cluster D² values were estimated following the procedure given by Singh and

Table 2: Distribution of One Eighty-Five maize inbred lines in different clusters (Torcher's method).

Cluster information	Number of Genotypes in each cluster	Number of Genotypes selected from each group	Genotypes
Cluster 1	86	2	CIMVL18752, CIMVL18470 , CIMVL18917, CIMVL111354, CIMKL154749, CIMVL18898, CIMVL18812, CIMVL109524, CIMVL20140, SAB, 1N06, CIMVL186031, CIMKL154690, CIMVL18943, CIMVL172394, CIMVL162594, CIMVL175901, CIMVL18242, CIMVL18684, CIMKL155966, CIMVL109463, CIMVL171537, CIMVL18509, CIMVL181014, CIMVL18785, CIMVL18507, CIMVL18780, CIMVL143904, CIMVL176373, CIMVL175887, CIMVL144309, CIMSNI18743, CIMVL18935, CIMVL18760, CIMVL175899, CIMVL18262, CIMVL1017169, CIMVL18223, CIMKL155959, CIMVL162590, CIMVL18733, CIMVL108750, CIMVL1110501, CIMVL108303, CIMVL20118, CIMVL18820, CIMVL18624, CIMVL18698, CIMVL18938, CIMVL153882, CIMVL175815, CIMVL19978, CIMVL1110195, CIMVL18579, CIMVL191071, CIMVL175891, CIMKL155996, CIMVL153879, 27AC, CIMVL175830, CIMVL18488, CIMVL18572, CIMVL162333, CIMKL155990, CIMVL18897, CIMVL18782, CIMSNI172546, CIMVL20375, CIMVL18691, CIMCAL1440, CIMVL18310, CIMVL162208, CIMCAL1498, CIMCAL1421, CIMVL18905, CIMVL162541, CIMVL18473, CIMVL175115, CIMVL18563, CIMVL18813, CIMVL191001, CIMVL175828, CIMVL18313, CIMVL171522, CIMVL18481, CIMZL171614.
Cluster 2	39	2	CIMVL18682, CIMKL155991 , CIMVL1010764, CIMKL155992, CIMVL175817, CIMVL18790, CIMVL1047, CIMVL18900, CIMVL20111, CIMSNI146314, CIMVL18787, CIMVL18674, CIMVL172391, CIMVL145717, CIMVL175816, CIMVL172416, CIMVL18945, CIMVL18485, CIMVL192034, CIMVL175870, CIMVL18932, CIMKL153175, CIMVL1010964, CIMVL162212, CIMVL1051, CIMVL144011, CIMVL153904, CIMVL171530, CIMKL156001, CIMVL18571, CIMVL18680, CIMSNI172496, CIMVL175898, CIMZL155186, CIMSNI172563, CIMSNI146228, CIMKL156016, CIMVL18213, CIMVL18919.
Cluster 3	1	1	CIMVL19995
Cluster 4	1	1	CIMVL186246
Cluster 5	24	2	CIMSNI172487, CIMVL144287 , CIMVL18753, CIMVL18775, DMK, CIMVL109582, CIMKL153098, CIMVL20137, CIMVL18498, CIMVL19187, CIMCAL1514, CIMVL109344, CIMVL19961, CIMVL162290, CIMVL175824, CIMVL153209, CIMVL20107, CIMVL20117, CIMVL18789, CIMVL12332, CIMVL20106, CIMVL18930, M6T, CIMVL18232.
Cluster 6	1	1	CIMVL18482
Cluster 7	23	2	CIMVL109290, CIMVL175106 , CIMSNI172561, CIMSNI172566, CIMKL156023, CIMVL175858, CIMVL18201, CIMVL13682, CIMVL20363, CIMVL175849, CIMCAL1412, CIMVL1110517, CIMVL18211, CIMVL18467, CIMZL11953, CIMVL175841, CIMVL143994, CIMVL171488, CIMVL175864, CIMVL1110461, CIMVL20133, CIMVL18657, CIMZL11959.
Cluster 8	1	1	CIMVL1010968
Cluster 9	1	1	CIMVL20368
Cluster 10	1	1	CIMVL18569
Cluster 11	1	1	CIMVL20139
Cluster 12	1		4DYW
Cluster 13	1	1	CIMVL18300
Cluster 14	1	1	CIMVL18330
Cluster 15	1	1	CIMVL18574
Cluster 16	1	1	CIMKL155999
Cluster 17	1	1	CIMVL18492
Grand Total	185	20	

*The values in bold represent the accession numbers of the selected parents.

Table 3: Average inter and intra (diagonal) cluster D2 values among 17 clusters in maize (Tocher's method). Note: Bold values are intra cluster distances.

Cluster	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13	C14	C15	C16	C17
Cluster 1	149.17	240.45	233.88	193.44	275.73	193.15	275.31	428.37	270.90	255.84	336.67	272.22	334.08	487.07	530.52	449.65	443.33
Cluster 2		203.14	409.58	281.74	525.70	253.23	312.04	307.37	435.23	251.87	283.07	300.38	575.92	846.53	336.99	325.44	599.10
Cluster 3			0.00	513.38	248.37	410.57	267.65	704.58	355.73	436.73	708.59	481.51	220.89	360.98	843.11	883.43	728.55
Cluster 4				0.00	335.61	146.02	449.26	432.19	253.40	201.50	175.54	256.25	496.77	582.41	563.77	301.62	277.94
Cluster 5					199.16	325.48	444.79	736.46	346.42	495.46	596.22	534.03	311.29	332.21	968.25	828.45	460.29
Cluster 6						0.00	361.20	216.96	451.21	316.23	262.57	378.69	597.24	719.44	345.13	371.75	197.80
Cluster 7							264.31	441.64	509.74	442.15	472.90	478.47	502.56	755.90	491.12	599.08	685.39
Cluster 8								0.00	896.87	478.80	264.10	609.09	1091.12	1397.23	140.55	469.81	549.58
Cluster 9									0.00	191.16	426.57	232.92	131.13	206.49	1051.52	531.69	774.00
Cluster 10										0.00	182.09	255.16	425.32	610.16	648.86	350.95	754.55
Cluster 11											0.00	411.08	745.44	933.21	405.26	236.22	535.92
Cluster 12												0.00	422.82	600.22	643.06	340.81	721.37
Cluster 13													0.00	109.34	1257.54	837.42	925.01
Cluster 14														0.00	1607.30	1156.43	902.31
Cluster 15															0.00	392.82	619.01
Cluster 16																0.00	628.88
Cluster 17																	0.00

Chaudhary (1977). The intra- and inter-cluster distances among the seventeen clusters are presented in Table 3. The intra-cluster distances were lower than the inter-cluster distances, indicating that genotypes within the same cluster exhibited lower genetic diversity. The maximum intra-cluster distance (264.31) was observed in Cluster 7, followed by Cluster 2 (203.14), Cluster 5 (199.16), and Cluster 1 (149.17).

The highest inter-cluster distance (1607.30) was observed between Cluster 14 and Cluster 15, followed by Cluster 8 and Cluster 14 (1397.23), Cluster 13 and Cluster 15 (1257.54), Cluster 14 and Cluster 16 (1156.43), Cluster 8 and Cluster 13 (1091.12), Cluster 9 and Cluster 15 (1051.52), Cluster 5 and Cluster 15 (968.25), Cluster 11 and Cluster 14 (933.21), Cluster 13 and Cluster 17 (925.01), and Cluster 14 and Cluster 17 (902.31). These values suggest considerable genetic variability among the genotypes in these clusters.

The high inter-cluster distances indicate that genotypes from these clusters could be effectively utilized in hybridization programs to obtain a broad spectrum of variation among segregants. The presence of wide genetic diversity among these clusters suggests that crossing genotypes from distant clusters may yield desirable transgressive segregants with enhanced genetic potential.

The selection of a particular cluster and the choice of genotypes within that cluster are critical considerations before initiating a crossing program. Additionally, selected genotypes from diverse clusters may be utilized in diallel or line \times tester analyses to further evaluate their genetic potential. Hybrids derived from crosses between divergent genotypes across different clusters are expected to exhibit high heterosis, leading to the development of superior segregants. The data on inter-cluster distances, combined with the per se performance of genotypes, may be used to identify genetically diverse and agronomically superior genotypes. In this context, the following genotypes were selected for the hybridization program, as they are expected to produce highly heterotic crosses (Table 2) the genotypes are CIMVL18752 and CIMVL18470 from cluster 1, CIMVL18682 and CIMKL155991 from cluster 2, CIMVL19995 from cluster 3, CIMVL186246 from cluster 4, CIMSNI172487 and CIMVL144287 from cluster 5, CIMVL18482 from cluster 6, CIMVL109290 and CIMVL175106 from cluster 7, CIMVL1010968 from cluster 8, CIMVL20368 from cluster 9, CIMVL18569 from cluster 10, CIMVL20139 from cluster 11, CIMVL18300 from cluster 13, CIMVL18330 from cluster 14, CIMVL18574 from cluster 15, CIMKL155999 from cluster 16 and CIMVL18492 from cluster 17 were selected for hybridization

Table 4: Cluster means for fourteen characters in one eighty-five maize inbred lines (Tocher's method).

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
C 1	58.56	59.45	0.89	94.70	169.20	74.92	12.58	3.72	13.25	20.73	24.91	19.08	5.33	4.51	60.69
C 2	56.43	57.79	1.36	94.23	158.56	61.02	11.90	3.56	13.01	20.11	24.88	18.58	5.25	4.32	53.59
C 3	57.67	60.00	2.33	93.50	174.00	91.50	10.20	3.54	12.70	18.50	20.50	18.40	4.67	2.00	33.18
C 4	60.67	61.00	0.33	97.00	171.50	67.00	14.95	3.77	13.40	21.40	33.00	20.25	6.00	6.00	86.75
C 5	58.49	59.32	0.83	94.83	187.69	92.84	12.70	3.90	13.41	21.58	26.88	20.04	5.08	4.13	71.23
C 6	54.67	56.67	2.00	97.00	161.40	68.50	12.69	4.02	12.20	22.90	25.00	24.75	5.00	5.00	86.63
C 7	55.03	56.28	1.25	88.26	166.85	75.35	11.41	3.61	13.50	18.76	23.34	18.12	4.49	3.58	44.68
C 8	48.67	48.67	0.00	95.00	147.50	56.00	12.25	3.59	13.40	21.40	29.50	21.35	5.00	4.00	71.00
C 9	63.67	63.67	0.00	99.00	203.50	80.00	14.28	3.23	11.33	18.93	22.50	20.85	6.00	5.00	56.00
C 10	57.67	59.67	2.00	103.00	183.00	64.50	13.91	3.08	10.25	19.25	29.50	16.85	6.00	5.00	51.88
C 11	53.67	53.67	0.00	94.50	184.00	58.00	16.98	3.57	11.60	24.50	33.25	17.05	6.00	5.00	80.88
C 12	62.67	63.00	0.33	102.00	173.00	63.50	14.15	3.80	17.80	16.60	19.75	21.75	7.00	5.00	56.50
C 13	62.67	62.67	0.00	96.00	202.50	93.00	11.81	3.23	12.83	26.67	17.50	17.35	5.00	5.00	43.71
C 14	64.00	65.00	1.00	98.00	211.00	102.83	16.00	3.30	12.67	27.00	15.50	17.05	4.67	3.67	59.67
C 15	51.00	52.67	1.67	87.00	128.50	45.00	12.29	3.58	14.00	20.50	19.50	18.00	4.67	3.00	64.00
C 16	56.67	59.67	3.00	93.00	173.50	43.50	10.75	3.87	14.05	22.75	25.25	19.30	5.67	5.00	77.63
C 17	57.67	58.67	1.00	90.50	154.50	71.00	14.00	4.58	14.80	30.20	28.75	21.10	5.00	2.00	115.30
Note : C = Cluster 1: DAYSHD (Days); 2: DAYSLK (Days); 3: ASI (Days); 4: DAYSBHK (Days); 5: PLTHT (cm); 6: EARHT (cm); 7: EL(cm); 8: EG (cm); 9: NKRE (Count); 10: NKR (Count); 11: HKW (Gr); 12: MST (Moisture%); 13: SGNS85 (Score); 14: SGNS91(Score); 15: GY (Gr)															

programme as they were expected to produce high heterotic crosses as shown in Table 2. Inter-crossing these divergent groups is expected to create greater opportunities for recombination events, which could unlock hidden genetic variability by breaking genetic linkages (Thoday, 1960). Progenies derived from such diverse crosses are anticipated to exhibit a broad spectrum of genetic variability. Hence, these genotypes may be employed in single- as well as multiple-crossing programs for the development of superior hybrids.

The Mahalanobis D^2 analysis has been widely utilized to quantify genetic divergence in maize, as reported by Hemavathy *et al.*, (2006), Singh *et al.*, (2007), Alam and Alam (2009), Marker and Krupakar (2009), Ganesan *et al.*, (2010), Azad *et al.*, (2012), Reddy *et al.*, (2012), Alam *et al.*, (2013), Lingaiah *et al.*, (2013), Monir *et al.*, (2014), Seshu *et al.*, (2014), Haydar *et al.*, (2015), Abirami and Vanniarajan (2016), Kumar *et al.*, (2018), Khan (2022), Patel *et al.*, (2023), James *et al.*, (2024), and Prasad *et al.*, (2024). These studies support the concept that crossing genotypes from genetically divergent clusters is a promising strategy for exploiting heterosis and improving yield-related traits in maize.

Cluster means of characters

The cluster means of fourteen characters, as presented in Table 4, revealed a significant range of mean values for various traits among the clusters. Cluster 17 recorded the highest mean value for grain yield (115.30

g), while cluster 11 had the highest ear length (16.98 cm). Cluster 17 also exhibited the highest ear girth (4.58 cm), whereas cluster 12 recorded the maximum number of kernel rows per ear (17.80). The highest number of

Table 5: Contribution of characters towards divergence in maize inbred lines.

S.No.	Traits	Divergence Contribution %	Times ranked 1st
1	Days to 50 per cent tasseling (Days)	11.33%	1928
2	Days to 50 per cent silking (Days)	2.29%	389
3	Anthesis silking interval (Days)	0.18%	30
4	Days to maturity (Brown husk) (Days)	11.26%	1917
5	Plant height (cm)	19.42%	3305
6	Ear height (cm)	32.56%	5542
7	Ear length (cm)	0.97%	165
8	Ear girth (cm)	0.58%	99
9	Number of kernel rows per ear (Count)	0.45%	76
10	Number of kernels per row (Count)	0.18%	31
11	100-Kernel weight (g)	2.88%	490
12	Moisture content (%)	0.19%	33
13	Stay greenness (Score)	0.08%	14
14	Grain yield (g per plant)	17.55%	2987

kernels per row (30.20) was observed in cluster 17, and cluster 11 had the highest 100-kernel weight (33.25 g). For moisture content, cluster 6 had the highest value (24.75%), while stay greenness at 85 DAS was highest in cluster 12 (7 score) and at 91 DAS in cluster 4 (6 score). Cluster 14 recorded the maximum values for days to 50% tasseling (64 days), days to 50% silking (65 days), plant height (211 cm), and ear height (102.83 cm). Cluster 16 had the shortest anthesis-silking interval (3 days), whereas cluster 10 recorded the highest days to maturity (brown husk) at 103 days.

The wide range of variation observed for grain yield and its component traits suggests that genotypes from the most diverse clusters should be selected as parents in hybridization programs to develop high-yielding hybrids or varieties. It is well established that greater genetic diversity among parents leads to a higher likelihood of obtaining heterotic hybrids and a broad spectrum of variability in segregating generations. Furthermore, studies indicate that the most productive hybrids often originate from high-yielding parents with significant genetic diversity, emphasizing the importance of careful parental selection for breeding programs.

Percent Contribution of Characters Towards Divergence in 185 Maize Genotype

The contribution of various traits to total genetic diversity in 185 maize genotypes revealed that ear height contributed the most (32.56%), followed by plant height (19.42%) and grain yield (17.55%). Other significant contributors included days to 50% tasseling (11.33%), days to maturity (11.26%), 100-kernel weight (2.88%), and days to 50% silking (2.29%). Traits such as anthesis-silking interval, ear length, ear girth, number of kernel rows per ear, number of kernels per row, moisture content, and stay greenness did not significantly contribute to divergence. Based on large inter-cluster distances and high grain yield, along with optimum plant and ear height, 20 parents were selected from different clusters for a hybridization program. These selected genotypes included CIMVL18752 and CIMVL18470 from cluster 1, CIMVL18682 and CIMKL155991 from cluster 2, CIMVL19995 from cluster 3, CIMVL186246 from cluster 4, CIMSNI172487 and CIMVL144287 from cluster 5, CIMVL18482 from cluster 6, CIMVL109290 and CIMVL175106 from cluster 7, CIMVL1010968 from cluster 8, CIMVL20368 from cluster 9, CIMVL18569 from cluster 10, CIMVL20139 from cluster 11, CIMVL18300 from cluster 13, CIMVL18330 from cluster 14, CIMVL18574 from cluster 15, CIMKL155999 from cluster 16, and CIMVL18492 from cluster 17. These

genotypes are expected to produce highly heterotic crosses, as indicated in Table 5.

List of symbols and abbreviations

The abbreviations and symbols used in this study are as follows: RBD (Randomized Complete Block Design), CIMMYT (International Maize and Wheat Improvement Center), ANOVA (Analysis of Variance), FAOSTAT (Food and Agriculture Organization Corporate Statistical Database), ICAR-IIMR (Indian Council of Agricultural Research - Indian Institute of Maize Research), and APEDA (Agricultural and Processed Food Products Export Development Authority). The growth and phenotypic traits include DAYSHD (Days to 50% tasseling), DAYSLK (Days to 50% silking), ASI (Anthesis-silking interval), and DAYS BHK (Days to maturity, brown husk), all measured in days. Morphological parameters include PLTHT (Plant height, cm), EARHT (Ear height, cm), EL (Ear length, cm), and EG (Ear girth, cm). Yield-related traits include NKRE (Number of kernel rows per ear), NKR (Number of kernels per row), HKW (100-kernel weight, g), MST (Moisture content, %), SGNS85 (Stay greenness score at 85 DAS), SGNS91 (Stay greenness score at 91 DAS), and GY (Grain yield per plant, g).

References

- Abirami, S. and Vanniarajan C. (2016). Genetic diversity studies in maize (*Zea mays* L.). *Life Sciences Leaflets*, **72**, 5-13.
- Alam, M.S. and Alam M.F. (2009). Studies on combining ability in inbred lines of maize using line \times tester method. *International Journal of Sustainable Agricultural Technology*, **5**(3), 32-36.
- Alam, M.A., Khan A.A., Islam M.R., Ahmed K.U. and Khaldun B.M. (2013). Studies on genetic divergence in maize (*Zea mays* L.) inbreds. *Bangladesh Journal of Agricultural Research*, **38**(1), 71-76.
- Azad, M.A.K., Biswasi B., Alam M. and Alam S. (2012). Genetic diversity in maize (*Zea mays* L.) inbred lines. *A Scientific Journal of Krishi Foundation*, **10**(1), 64-70.
- Dowswell, C.R., Paliwal R.L. and Cantrell R.P. (1996). *Maize in the Third World*. Boulder: West View Press.
- Fuzzato, S.R., Ferreira D.F., Ramalho P.M.A. and Ribeiro P.H.E. (2002). Genetic divergence and its relationship with diallel crossing in maize crop. *Ciencia e Agrotechnologia*, **26**, 22-32.
- Ganesan, K.N., Nallathambi G., Safawo T., Senthil N. and Tamilarasi P.M. (2010). Genetic divergence analysis in indigenous maize germplasm (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **1**(4), 1241.
- Haydar, F.M.A., Paul N.K. and Khaleque M.A. (2015). D² statistical analysis of yield-contributing traits in maize (*Zea mays* L.) inbreds. *Bangladesh Journal of Botany*, **44**(4), 629-634.

- Hemavathy, A.T., Ibrahim S.M. and Aiswarya S. (2006). Genetic divergence studies in maize (*Zea mays* L.). *Agricultural Science Digest*, **26**(4), 303-305.
- James, M., Ajeesh Krishna T.P., Priyadarsini V., Angelin Gladina and Senthil P. Kumar (2024). Identification of diverse maize inbred lines using molecular and phenotypic genetic divergence analysis. *International Journal of Bio-resource and Stress Management*, **15**(10), 1-8.
- Kumar, A., Narayan A. and Kavita (2018). Morphological diversity in inbred lines of maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences*, **7**, 446-451.
- Khan, S., Mahmud F. and Ahmmmed T. (2022). Genetic diversity with cluster analysis of maize genotypes (*Zea mays* L.). *Advances in Bioscience and Biotechnology*, **13**, 273-283.
- Lingaiah, N., Bharathi M. and Venkanna V. (2013). Studies on genetic diversity for grain yield and physiological parameters in maize (*Zea mays* L.). *International Journal of Applied Biology and Pharmaceutical Technology*, **4**(3), 27-30.
- Marker, S. and Krupakar A. (2009). Genetic divergence in exotic maize germplasm (*Zea mays* L.). *ARPN Journal of Agricultural and Biological Science*, **4**(4), 44-47.
- Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proceedings of the National Institute of Sciences, India*, **12**, 49-55.
- Monir, H., Chowdhury F.N., Uddin M.S., Paul R.K. and Bhattacharjya D.K. (2014). Maintenance and characterization of new exotic inbred lines of maize (*Zea mays* L.). *IOSR Journal of Agriculture and Veterinary Science*, **7**(8), 62-66.
- Murthy, B.R. and Arunachalam V. (1966). Nature of genetic divergence in relation to breeding system in crop plants. *Indian Journal of Genetics*, **26**, 188-198.
- Patel, R., Memon J., Patel D.A., Patil K. and Borkhatariya T. (2023). Assessment of genetic diversity of sweet corn (*Zea mays* conva. *Saccharata* var. *rugosa*) genotypes using D² statistics. *The Pharma Innovation Journal*, **12**(3), 2642-2645.
- Rao, C.R. (1952). *Advanced Statistical Methods in Biometrical Research*. New York: John Wiley and Sons Inc., 236-272.
- Reddy, V.R., Jabeen F. and Sudarshan M.R. (2012). Genetic divergence in maize (*Zea mays* L.). *Crop Research*, **44**(3), 391-393.
- Seshu, G., Brahmeswara Rao M.V., Sudarshan M.R. and Eeswari K.B. (2014). Genetic divergence in sweet corn (*Zea mays* L. *saccharata*). *International Journal of Pure and Applied Biosciences*, **2**(1), 196-201.
- Singh, R.K. and Chaudhary B.D. (1977). *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani Publishers, 215-218.
- Singh, S.P. and Jha P.B. (2007). Influence of moisture regimes and sowing dates on heterotic potential of the flowering traits in winter maize. *Crop Improvement*, **31**(2), 27-32.
- Shaw, R.H. (1988). Climatic requirements. In: Sprague, G.F. and Dudley, J.W., eds. *Corn and Corn Improvement*. Madison, Wisconsin: American Society of Agronomy, 609-638.
- Prasad, Y., Kumar K., Kumar R., Kumar S., Prasash S., Izhar T., Ahmad E., Yadav N.P., Kumar S. and Dammame S.V. (2024). Genetic diversity studies in maize (*Zea mays* L.) for green fodder yield and its quality traits. *International Journal of Advanced Biochemistry Research*, **SP-8**(6), 111-114.