

## Genetic divergence studies among inbred lines of maize (*Zea mays* L.)

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### ABSTRACT

The field experiment was conducted at Agricultural Research Station, Peddapuram, Kakinada during *rabi*, 2022-23 to study the genetic divergence among 112 maize inbred lines in alpha lattice design with two replications. The analysis of variance revealed significant genetic differences among the inbred lines for 18 characters under study.  $D^2$  analysis highlighted the significant contribution of kernel yield per plant, ear yield per plant, kernel rows per ear, number of kernels per row, ear height, days to 50% silking, ear position, tassel extrusion and tassel size towards overall divergence. This emphasizes the importance of these traits in selecting appropriate parents for hybridization programs. It was found that inbred lines from clusters III (CML 451), VI (PI 415, PI 424), VII (CL 02450) and VIII (PI 416) could be vital for such programs. The inbred lines PI 403, PL22398, PI 415, PI 424, PI 426, CML 451, CL 02450 are far apart from each other in the two dimension and three-dimension diagrams of principal component analysis. Hence, CML 451, PI 415, PI 424 and CL 02450 were found to be with sufficient genetic diversity in the studied lines as they have shown high inter cluster distances in  $D^2$  and they are also far apart from each other in the two-dimensional and three-dimensional graphs based on PCA scores may result in good  $F_1$  combinations to explore the heterosis or to produce transgressive segregants in their respective  $F_2$  and subsequent segregation generation.

**Key words:** Cluster means,  $D^2$  Analysis, Genetic divergence, PCA

Maize (*Zea mays* L.), ‘queen of cereal’, is one of the major cereals cultivated throughout the world after rice and wheat. Maize kernels contain 60 to 68% starch and 7 to 15% protein. Maize production in India has steadily increased over the years, especially with the development and release of heterotic hybrids at the beginning of the 21<sup>st</sup> century. Further, the focus on high-yielding hybrids has resulted in significant advancements in productivity. However, there is a need to develop varieties/ hybrids suitable to varied environmental challenges *i.e.*, climate change and emergence of varied biotic and abiotic stresses and agro ecosystems. Evaluating the germplasm/ inbreds for new traits along with important yield traits is need of the hour to select the parents and their utilization in plant breeding programmes.

The ability to pick genetically diverse parents is made possible by the quantification of genetic diversity using biometrical procedures. Crosses between genetically dissimilar parents yield more heterosis than crosses between closely related parents (Moll and Stuber, 1971). As a result, crop improvement

programmes require genetically diverse parents for the initiation of breeding programmes. For the examination of genetic diversity, Mahalanobis  $D^2$  statistic is one of the finest ways for measuring genetic diversity in a crop species. This assists in the grouping of germplasm/ inbred lines into appropriate groups for future breeding operations, as genetically diverse genotypes are known to exhibit high hybrid vigour. Principal component analysis (PCA) is a multivariate statistical method used to identify and extract the most significant axes of variation in a dataset. It calculates canonical vectors or roots, which represent these axes, along with their corresponding eigen values, indicating the amount of variance accounted by each axis. The term “principal component” roots from the fact that the technique highlights the primary contributors to the overall variation in the data.

### MATERIAL AND METHODS

The field experiment was conducted at Agricultural Research Station, Peddapuram, Kakinada during *rabi*, 2022-23 to study the genetic

divergence among 112 maize inbred lines in alpha lattice design with two replications. Each plot consisted of two rows of four meters each, spaced 60 cm row to row and 20 cm plant to plant. Statistical software WINDOSTAT version 9.2, created by Indostat Services Ltd., Hyderabad, India, was used to statistically analyze the data collected on eighteen traits.

The data was recorded on five plants taken from each replication on days to 50% anthesis, days to 50% silking, anthesis silking interval, plant height (cm), tassel height (cm), tassel extrusion, tassel size, ear height (cm), ear position, ear length (cm), ear girth (cm), days to maturity, kernel rows per ear, number of kernels per row, shelling percentage, 100-kernel weight (g), ear yield per plant (g) and kernel yield per plant (g). D<sup>2</sup> analysis was performed as per Mahalanobis (1936) by Tocher's method, Principal component analysis by Ward's minimum variance method through INDOSTAT software.

## RESULTS AND DISCUSSION

### D<sup>2</sup> Cluster analysis

The 112 inbred lines were grouped into eight clusters by using Tocher's method. The distribution of inbred lines into eight clusters is presented in Table 1 and illustrated in Figure 1. Cluster I had the highest number *i.e.*, 96 inbred lines while, cluster II had seven inbred lines. The clusters, III, V, VII and VIII had single inbred line *i.e.*, unitary clusters, while cluster IV had three inbred lines. The cluster VI had two inbred lines. Lone *et al.* (2017) and Pavithra *et al.* (2022) reported similar grouping pattern of maize inbred lines in their studies.

The eight clusters intra and inter-cluster distances are presented in Table 4.7 and 4.8. Intra-cluster average D<sup>2</sup> values ranged from 0 to 53.24. Among the clusters, cluster IV had the maximum intra-cluster distance (53.24) while, the minimum was recorded in cluster II (46.08). The intra cluster distance was zero in clusters III, V, VII and VIII as they had single inbred line each. The inbred lines of these solitary clusters may be unique and useful in plant breeding programme. The minimum inter-cluster D<sup>2</sup> values were recorded between the clusters III and IV (38.15) followed by II and VII (74.83). The highest D<sup>2</sup> value was recorded in-between the clusters VI and VII (273.04) followed by the clusters II and VI (236.25) indicating their usefulness in the

exploitation of heterosis. Similar trend of inter cluster and intra-cluster distances were reported by Singh *et al.* (2020) and Deepak *et al.* (2023).

The cluster means for each of 18 characters are furnished in Table 5. The cluster means for days to 50% anthesis ranged from 61 (Cluster VI) to 69.50 (Cluster VII). Days to 50% silking ranged from 62 (Cluster VI) to 72.5 (Cluster V). Anthesis-silking interval ranged from 0.50 (Cluster VII) to 5.00 (Cluster V). Plant height ranged from 122.86 (Cluster II) to 191.25 (Cluster VI). For tassel height, cluster means ranged from 29.50 (Cluster V) to 36 (Cluster III). Similarly, Tassel extrusion ranged from 1.87 (Cluster II) to 2.35 (Cluster III, V, VI, VII, VIII), for tassel size, the cluster means ranged from 1.58 (Cluster II and III). Whereas the ear height ranged from 42.93 (Cluster II) to 83.75 (Cluster VI) and ear position ranged from 0.33 (Cluster V) to 0.50 (Cluster VIII). The cluster mean for ear length ranged from 8.57 (Cluster II) to 15.34 (Cluster VI). The cluster mean for ear girth ranged from 11.0 (Cluster VII) to 15.88 (Cluster VI). The cluster mean for Days to maturity ranged from 89 (Cluster VII) to 127.50 (Cluster V) and for Kernel rows per ear ranged from 12.00 (Cluster VIII) to 14.85 (Cluster VI). The 100-Kernel weight ranged from 24.8 (Cluster VI) to 35.85 (Cluster VIII). The cluster mean for number of kernels per row ranged from 18.15 (Cluster V) to 33.53 (Cluster VI). Similarly, cluster mean for shelling percentage ranged from 465.34 (Cluster VIII) to 78.90 (Cluster III). Likewise, the cluster mean for ear yield per plant ranged from 62.70 (Cluster VII) to 233.00 (Cluster VI). The cluster mean for Kernel yield per plant ranged from 42.50 (Cluster VII) to 187.50 (Cluster VI).

Based on the cluster means, important clusters were cluster III (CML 451) for tassel height, tassel extrusion and shelling percentage. Cluster VI (PI 415, PI 424) is important for desired days to 50% anthesis, days to 50% silking, plant height, tassel size, ear height, ear length, ear girth, kernel rows per ear, number of kernels per row, ear yield per plant and kernel yield per plant. Cluster VIII (PI 416) is important for ear position and 100-kernel weight. Cluster VII (CL 02450) is important for anthesis-silking interval and days to maturity. This indicates that this genotype may be used in breeding for earliness. When these results were examined, it became clear that no cluster contained at least one

inbred line that possessed every desirable trait, which eliminated the option of choosing one inbred line for immediate use. Hybridization between the inbred lines chosen from divergent clusters is therefore necessary for the careful combination of all the targeted traits. Similar kind of results were reported by Kumar *et al.* (2015), Dubey *et al.* (2001) and Deepak *et al.* (2023).

### Relative Contribution of Individual Characters towards Divergence

The characters appeared in the first rank contribute more to towards diversity. Among all the characters, Kernel yield per plant (g) contributed the maximum (14.68%) to the diversity by taking the first rank in 920 times, followed by Ear yield per plant (g) (13.22%) with 828 times ranked first, Kernel rows per ear (9.78%) with 613 times ranked first and Ear height (cm) contributed 8.99% with 563 times ranked first. Number of kernels per row (6.26%) with 392 times ranked first.

Other characters viz., days to 50% anthesis, days to 50% silking, anthesis-silking interval, plant height (cm), tassel height (cm), tassel extrusion, tassel size, ear length (cm), ear position, ear girth (cm), days to maturity, shelling percentage, 100-kernel weight (g) contributed 3.18, 5.30, 2.95, 4.96, 6.00, 5.68, 5.67, 2.70, 4.50, 2.84, 1.36, 1.04 and 0.89 per cent, respectively, to the total genetic diversity. Similar kind of results were reported by Amin *et al.* (2013), Maruthi *et al.* (2015) and Lone *et al.* (2017).

### Principal Component Analysis

In the present study principal component analysis (PCA) was used to validate the clustering pattern obtained by Mahalanobis  $D^2$  statistic. Eigen values, variance (%) and cumulative variance (%) by the principal components (PCs) in maize inbred lines evaluated were given in Table 8. The results suggested the importance of the first seven PCs with Eigen values greater than or equal to 1.0 in discriminating the collection.

The results revealed that seven canonical roots accounted for 74.66 per cent of total divergence. PC<sub>2</sub> contributed maximum towards divergence (38.1 %) with Eigen value of 2.93. The first, third and fourth canonical vectors contributed 23.44%, 9.099% and 7.40% to total divergence, respectively. The remaining

canonical roots viz., fifth, sixth and seventh, accounts for 7.03 %, 6.54 % and 5.67 % respectively to total variability.

The scores of PCA with respect to the studied 112 inbred lines for the 1<sup>st</sup> three PCs were listed in Table 4.12. These scores of PCA were employed in plotting two- dimensional (Figure 3) and three-dimensional scatter diagrams (Figure 4) for the studied inbred lines. The hybrid combination with the diverse inbred lines numbered as 41 (PI 403), 45 (PL22398), 84 (PI 415), 94 (PI 424), 96 (PI 426), 102 (CML 451), 106 (CL 02450) which are far apart from each other in the two dimension and three-dimension diagrams may result in good F<sub>1</sub> combinations to explore the heterosis or to produce transgressive segregants in their respective F<sub>2</sub> and subsequent segregation generation.

Similar usage of PCA for obtaining 2D & 3D diagrams and in turn to understand the genetic diversity was earlier employed in maize by Javaid *et al.* (2023), Yadesa *et al.* (2022) and Devaux *et al.* (2023).

### CONCLUSION

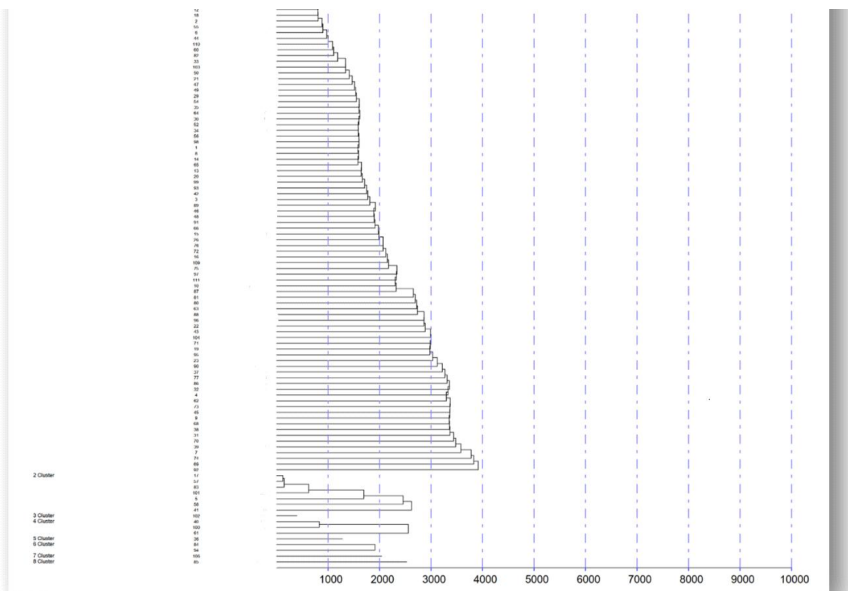
Genetic divergence studies revealed that CML 451, PI 415, PI 424 and CL 02450 were found to be with sufficient genetic diversity in the studied lines as they have shown high inter cluster distances in  $D^2$  and they are also far apart from each other in the two-dimensional and three-dimensional graphs based on PCA scores. Hence, these varieties may result in good F<sub>1</sub> combinations to explore the heterosis or to produce transgressive segregants in their respective F<sub>2</sub> and subsequent segregation generation.

### LITERATURE CITED

- Amin M N, Amiruzzaman M, Ahmed A, Rohman M M and Ali M R 2013.** The genetic diversity of white inbred lines of quality protein maize (QPM). *Eco-Friendly Agricultural Journal*. 6 (9): 13-17.
- Deepak K M, Birender S, Mandal S, Kumari R and Sumit K M 2023.** Genetic diversity in maize inbred lines. *The Pharma Innovation Journal*. 12 (5): 1950-1953.
- Devaux M F, Corcel M, Guillon F and Barron C, 2023.** Maize internode autofluorescence at the macroscopic scale: image

**Table 1. Clustering pattern by Tocher’s method in inbred lines of maize (*Zea mays* L.)**

Cluster Group	No.of Inbred lines	List of Inbred lines
I	96	PI UK, PL 22424, PL 22444, PL 22392, PI 404, PL 22439, PI 417, PL 22429, PL 22440, PL 22397, PI 405, PL 22409, PI 418, PL 22394, PL 22389, PL 22448, PL 22435, PL 22441, PI 419, PL 22396, PL 22408, PL 22399, PL 22398, PL 22411, PI 420, PL 22427, PL 22426, PL 22393, PL 22395, PL 22437, PI 421, PL 22421, PL 22449, PL 22417, PL 22414, PL 22430, PI 422, PL 22407, PL 22445, PL 22432, PL 22413, PL 22450, PI 423, PI 399, PL 22422, PL 22404, PL 22425, PL 22442, PI 425, PI 400, PL22428, PL 22416, PL 22420, PL 22447, PI 426, PI 401, PL 22431, PL 22402, PL 22400, PL 22410, PI 427, CML 451, PL 22434, PI 394, PL 22406, PL 22446, PI 428, CML 474, PL 22415, PI 395, PL 22433, PL 22403, CML 581, PL 22405, PI 1 ,PL 22443, PL 22438, CML582, LM 13, PI 397, PL 22419, PI 406, LM14, PL 22418, PI 407, BML 6 ,PL 22391, PI 408, BML 7, PI 409, BML 45, PI 410, CAL1812, PI 411, PI 412, PI 413
II	7	PL 22401, PL 22390, PI 414, CML 425, PL 22436, PL 22412 & PI 403
III	1	CML 451
IV	3	PI 402, UMI 1200 & PL 22423
V	1	PI 398
VI	2	PI 415, PI 424
VII	1	CL 02450
VIII	1	PI 416



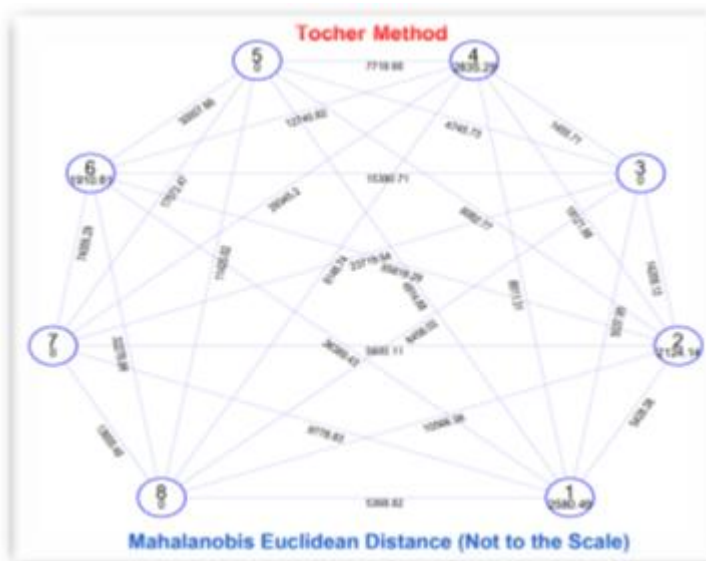
**Fig. 1. Dendrogram showing relationship based on Mahalanobis’D<sup>2</sup> values in eight clusters among 112 inbred lines of maize (*Zea mays* L.)**

**Table 2. Average intra(bold) and inter-cluster D<sub>2</sub> distance among 8 clusters of 112 maize inbred lines (*Zea mays* L.)**

Cluster Distances								
	I	II	III	IV	V	VI	VII	VIII
I	<b>2580.49</b> (50.79)	5428.38 (73.67)	5537.95 (74.41)	8811.31 (93.86)	4914.88 (70.10)	36389.43 (190.76)	9778.83 (98.88)	5368.82 (73.27)
II		<b>2124.14</b> (46.08)	14208.13 (119.19)	19121.98 (138.28)	8082.77 (89.89)	55818.29 (236.25)	5600.11 (74.833)	10566.38 (102.79)
III			<b>0.00</b> (0.00)	1455.71 (38.15)	4745.73 (68.88)	15380.71 (124.01)	23719.54 (154.00)	6458.02 (80.36)
IV				<b>2835.29</b> (53.24)	7718.66 (87.855)	12740.82 (112.87)	29345.20 (171.304)	8148.74 (90.27)
V					<b>0.00</b> (0.00)	30007.86 (173.22)	17572.47 (132.56)	11425.62 (106.89)
VI						<b>1910.81</b> (43.71)	74555.29 (273.04)	32278.89 (179.66)
VII							<b>0.00</b> (0.00)	13655.46 (116.85)
VIII								<b>0.00</b> (0.00)

**Table 3. The nearest and farthest clusters from each cluster based on D values in Maize inbred lines (*Zea mays* L.)**

Cluster no.	Nearest cluster with D values	Farthest cluster with D values
I	V (70.10)	VI (190.76)
II	VII (74.833)	VI (236.25)
III	IV (38.15)	VII (154.00)
IV	III (38.15)	VII (171.304)
V	III (68.89)	VI (173.22)
VI	IV (112.88)	VII (273.04)
VII	II (74.83)	VI (273.08)
VIII	I (73.2)	VI (179.6)



**Fig. 2. Intra and inter-cluster distances in eight clusters based on Tocher's method in maize (*Zea mays* L.)**

**Table 5. Cluster means of eight clusters estimated by Tocher's method in 112 maize inbred lines (*Zea mays* L.)**

cluster	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Plant height (cm)	Tassel height (cm)	Tassel extrusion	Tassel size	Ear height (cm)	Ear position
I	65.60	67.46	1.87	159.45	31.54	2.24	1.83	65.55	0.41
II	63.21	65.71	2.50	122.86	31.21	1.87	1.58	42.93	0.35
III	64.00	67.50	3.50	170.00	36.00	2.35	1.58	72.50	0.43
IV	64.33	65.33	1.00	171.67	30.33	2.12	1.83	83.33	0.48
V	69.50	72.50	5.00	145.00	29.50	2.35	1.82	47.50	0.33
VI	61.00	62.00	1.00	191.25	35.00	2.35	2.32	83.75	0.44
VII	67.00	68.00	0.50	152.50	34.50	2.35	2.12	60.00	0.40
VIII	63.00	64.00	1.00	167.50	31.50	2.35	2.12	82.50	0.50

cluster	Ear length (cm)	Ear girth (cm)	Days to maturity	Kernel rows per ear	Number of kernels per row	Shelling percentage	100 kernel weight (g)	Ear yield per plant (g)	Kernel yield per plant (g)
I	11.27	11.96	122.14	12.81	23.10	76.00	27.06	88.03	71.88
II	8.57	11.95	120.86	12.42	18.52	72.00	25.53	75.04	64.21
III	12.67	13.17	122.50	13.50	28.85	78.90	24.80	136.00	113.00
IV	12.14	12.83	120.17	12.62	25.50	74.79	33.22	148.33	121.17
V	10.09	12.17	127.50	12.35	18.15	69.20	26.50	99.35	74.00
VI	15.34	15.88	117.00	14.85	33.53	76.25	35.15	233.00	187.50
VII	11.00	11.00	89.00	13.50	20.50	77.80	26.20	62.70	42.50
VIII	10.84	12.75	119.00	12.00	22.70	65.34	35.85	128.00	48.50

**Table 6. Mean performance of top four clusters with selected inbred lines for hybridization and promising characters in inbred lines using Tocher's method in maize (*Zea mays* L.)**

S. No.	Cluster no.	Selected inbred lines for hybridization	Promising characters in inbred lines
1	VI	PI415, PI 424	Days to 50% anthesis, days to 50% silking, plant height, tassel size, ear height, ear length, ear girth, kernel rows per ear, number of kernels per row, ear yield per plant, kernel yield per plant.
2	III	CML451	Tassel height, tassel extrusion, shelling percentage
3	VII	CL 02450	Anthesis-silking interval and days to maturity
4	VIII	PI416	Ear position, 100-kernel weight

representation and principal component analysis of a series of large multispectral images. *Biomolecules*. 13 (7): 1104.

**Dubey R B, Joshi V N and Pandiya N K 2001.** Heterosis and combining ability for quality, yield and maturity traits in conventional and non-conventional hybrids of maize. *Indian Journal of Genetics*. 61 (4): 353-355.

**Javaid A, Razzaq H, Khan F A and Awan F S 2023.** Evaluation of maize accessions for drought tolerance through principal component analysis. *SABRAO Journal of Breeding & Genetics*. 55 (2): 45-76.

**Kumar R, Mandal S S, Mishra A K, Smriti Singh R and Kumar P 2015.** Heterosis and combining ability for yield and its contributing

**Table 7. The relative contribution of 18 characters to genetic diversity in 112 maize inbred lines (*Zea mays* L.)**

S. No.	Source	Contribution %	Times ranked 1st
1	Days to 50% anthesis	3.18	199
2	Days to 50% silking	5.30	332
3	Anthesis silking interval	2.95	185
4	Plant height (cm)	4.96	311
5	Tassel height (cm)	6.00	376
6	Tassel extrusion	5.68	356
7	Tassel size	5.67	355
8	Ear height (cm)	8.99	563
9	Ear position	4.50	282
10	Ear length (cm)	2.70	169
11	Ear girth (cm)	2.84	178
12	Days to maturity	1.36	85
13	Kernel rows per ear	9.78	613
14	Number of kernels per row	6.26	392
15	Shelling percentage	1.04	65
16	100-kernel weight (g)	0.89	56
17	Ear yield per plant (g)	13.22	828
18	Kernel yield per plant (g)	14.68	920

**Table 8. Canonical vectors for 18 characters in 112 inbred lines of maize (*Zea mays* L.)**

	PC <sub>1</sub>	PC <sub>2</sub>	PC <sub>3</sub>	PC <sub>4</sub>	PC <sub>5</sub>	PC <sub>6</sub>	PC <sub>7</sub>
<b>Eigene Value (Root)</b>	4.68983	2.93035	1.98031	1.48174	1.40767	1.30957	1.13438
<b>Variability %</b>	23.44916	14.65172	9.90157	7.40869	7.03835	6.54787	5.67188
<b>Cumulative variability %</b>	23.44916	38.10088	48.00244	55.41113	62.44947	68.99734	74.66923
<b>characters</b>							
<b>Days to 50% anthesis</b>	0.02813	<b>0.50269</b>	0.10195	0.19072	0.19162	0.04122	0.14434
<b>Days to 50% silking</b>	0.05670	<b>0.52890</b>	0.10562	-0.02767	0.10543	0.17124	0.08280
<b>Anthesis silking interval</b>	0.07538	0.10801	0.01436	-0.54213	-0.21306	<b>0.35098</b>	-0.10385
<b>Plant height (cm)</b>	-0.33438	0.05300	<b>0.28948</b>	0.12415	0.00295	0.04971	0.00613
<b>Tassel height (cm)</b>	0.02088	0.21963	-0.36696	<b>0.27223</b>	-0.12900	-0.13026	-0.32444
<b>Tassel extrusion</b>	-0.14940	-0.01371	0.18450	-0.27318	0.24616	-0.42280	<b>0.33085</b>
<b>Tassel size</b>	-0.07785	0.04747	-0.38233	0.14787	-0.09863	<b>0.32178</b>	-0.24287
<b>Ear height (cm)</b>	-0.34331	0.08368	<b>0.29949</b>	-0.07282	0.12644	-0.00640	-0.38349
<b>Ear position</b>	-0.21086	0.08060	0.19325	-0.27081	<b>0.17252</b>	-0.06128	-0.60488
<b>Ear length (cm)</b>	-0.33992	0.08328	0.01609	<b>0.27407</b>	-0.18633	-0.13371	0.09470
<b>Ear girth (cm)</b>	-0.27036	-0.02528	-0.35943	-0.24318	<b>0.26110</b>	0.15696	0.08707
<b>Days to maturity</b>	-0.00689	<b>0.37379</b>	0.08548	-0.14997	-0.15744	0.32913	0.24632
<b>Kernel rows per ear</b>	-0.05810	0.14733	-0.45273	-0.33692	<b>0.24570</b>	-0.24113	0.11851
<b>Number of kernels per row</b>	-0.32924	<b>0.14264</b>	-0.13600	0.08601	-0.22956	-0.27354	0.00547
<b>Shelling percentage (%)</b>	-0.06527	-0.01214	<b>0.13019</b>	-0.18213	-0.61924	-0.07634	0.11490
<b>100 kernel weight (g)</b>	-0.22356	-0.23010	0.16889	0.21696	0.20342	<b>0.39156</b>	0.15769
<b>Ear yield per plant (g)</b>	-0.40866	-0.05836	-0.16761	0.00244	0.03333	<b>0.12977</b>	0.11088
<b>Kernel yield per plant (g)</b>	-0.38498	-0.04180	-0.13621	-0.02838	-0.10339	0.16049	<b>0.18075</b>

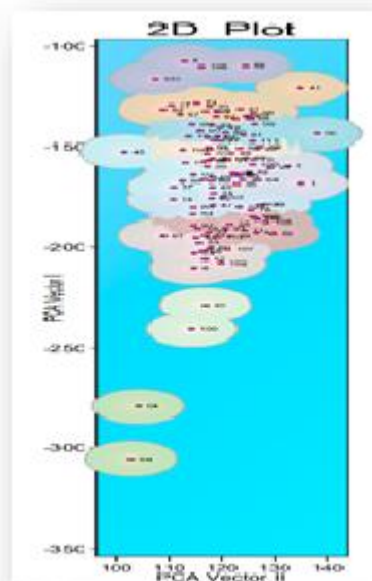
**Table 9. Mean values of canonical vectors for 112 inbred lines of maize (*Zea mays* L.)**

		<b>PCA I</b>	<b>PCA II</b>	<b>PCA III</b>
<b>SL.NO.</b>	<b>Inbred lines</b>	<b>X Vector</b>	<b>Y Vector</b>	<b>Z Vector</b>
1	PL 22424	-168.373	135.09	52.846
2	PL 22429	-201.329	117.433	74.84
3	PL 22394	-159.578	132.536	59.906
4	PL 22396	-134.608	124.54	56.867
5	PL 22436	-107.668	112.989	49.703
6	PL 22444	-210.116	114.819	68.415
7	PL 22440	-132.27	119.217	38.246
8	PL 22389	-163.773	123.066	51.077
9	PL 22408	-131.994	119.077	43.519
10	PL 22426	-146.97	118.397	57.302
11	PL 22449	-191.415	124.282	49.007
12	PL 22445	-206.138	116.866	68.355
13	PL 22422	-178.742	128.15	52.243
14	PL 22428	-176.134	110.758	48.645
15	PL 22431	-157.909	113.144	44.649
16	PL 22434	-156.013	120.768	62.364
17	PL 22401	-129.208	110.401	32.944
18	PL 22427	-190.624	115.559	72.481
19	PL 22421	-144.978	113.735	43.249
20	PL 22407	-159.84	117.199	54.354
21	PL 22390	-190.366	120.728	50.336
22	PL 22392	-149.83	127.386	67.347
23	PL 22397	-135.986	122.642	54.74
24	PL 22448	-203.204	114.859	59.172
25	PL 22399	-188.425	121.535	64.586
26	PL 22393	-153.153	117.173	53.266
27	PL 22417	-192.177	117.497	68.164
28	PL 22432	-194.286	121.639	65.858
29	PL 22404	-166.527	116.659	58.1
30	PL 22416	-164.178	122.336	59.981
31	PL 22402	-131.041	123.453	49.473
32	PI394	-139.237	118.186	68.624
33	PI 395	-193.913	116.846	78.954
34	PI 1	-173.007	118.436	60.254
35	PI 397	-166.607	123.854	59.711
36	PI 398	-168.651	122.839	42.269
37	PI 399	-169.955	110.837	37.895
38	PI 400	-132.863	126.022	55.513
39	PI 401	-129.733	117.643	53.591
40	PI 402	-228.71	116.952	46.308
41	PI 403	-120.788	134.947	65.069
42	PI 404	-162.715	125.164	63.974
43	PI 405	-140.493	119.693	53.828
44	PL 22435	-195.128	115.215	74.496

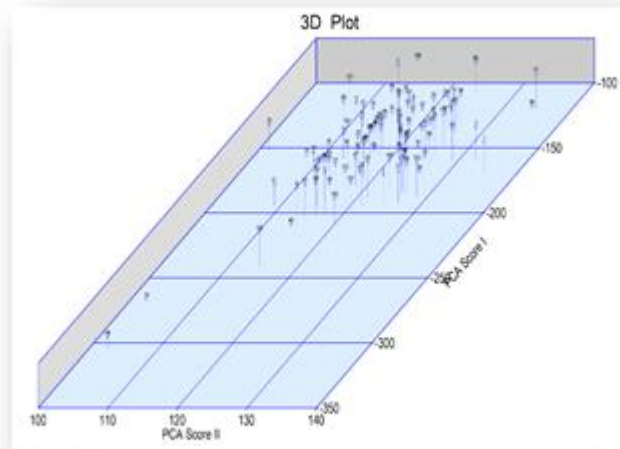


45	PL 22398	-152.482	101.635	47.779
46	PL 22395	-156.599	117.553	53.252
47	PL 22414	-179.174	118.333	49.04
48	PL 22413	-157.1	117.098	49.429
49	PL 22425	-170.02	118.196	57.381
50	PL 22420	-200.154	117.933	53.753
51	PL 22400	-192.543	126.583	57.619
52	PL 22406	-174.953	120.3	56.634
53	PL 22433	-197.871	115.734	66.592
54	PL 22443	-183.607	114.619	58.07
55	PL 22419	-202.302	116.338	59.975
56	PL 22418	-165.379	118.255	65.631
57	PL 22391	-133.646	112.13	36.499
58	PL 22412	-109.871	124.498	59.386
59	PL 22415	-193.191	129.747	58.613
60	PL 22405	-178.937	127.259	70.505
61	PL 22423	-194.177	109.013	37.721
62	PL 22439	-134.869	118.965	57.145
63	PL 22409	-145.225	119.097	47.843
64	PL 22441	-166.742	126.928	57.378
65	PL 22411	-164.641	123.28	49.539
66	PL 22437	-155.59	124.568	52.645
67	PL 22430	-188.981	114.771	65.177
68	PL 22450	-135.922	125.369	44.266
69	PL 22442	-142.203	115.937	34.688
70	PL 22447	-134.393	125.291	60.38
71	PL 22410	-145.359	117.279	45.777
72	PL 22446	-155.949	118.246	47.522
73	PL 22403	-132.192	116.931	52.8
74	PL 22438	-128.273	115.34	53.155
75	PI 406	-150.853	117.822	59.352
76	PI 407	-156.278	126.016	67.398
77	PI 408	-147.228	119.633	42.357
78	PI 409	-186.196	126.794	57.324
79	PI 410	-181.458	125.557	61.066
80	PI 411	-143.021	120.802	47.911
81	PI 412	-144.33	123.994	47.985
82	PI 413	-175.588	118.075	56.818
83	PI 414	-131.397	108.958	39.687
84	PI 415	-305.19	102.823	22.571
85	PI 416	-180.202	114.707	55.564
86	PI UK	-153.012	121.804	50.206
87	PI 417	-150.123	117.465	44.233
88	PI 418	-150.599	123.369	71.807
89	PI 419	-167.303	117.989	53.38
90	PI 420	-138.799	114.422	45.868

90	PI 420	-138.799	114.422	45.868
91	PI 421	-156.732	121.196	48.66
92	PI 422	-164.126	114.688	36.276
93	PI 423	-160.328	129.208	57.797
94	PI 424	-279.123	104.233	30.25
95	PI 425	-138.696	126.239	53.494
96	PI 426	-143.474	137.991	59.387
97	PI 427	-150.842	126.722	65.568
98	PI 428	-163.234	122.245	54.783
99	CML72	-167.203	112.563	44.62
100	UMI1200	-240.894	114.33	60.862
101	CML425	-116.274	107.422	41.96
102	CML451	-207.81	119.882	44.647
103	CML474	-180.027	123.306	49.298
104	CML581	-151.304	112.645	43.961
105	CML582	-184.938	125.876	55.169
106	CL02450	-110.129	116.166	65.102
107	LM13	-201.241	121.136	57.754
108	LM14	-187.552	128.452	62.788
109	BML6	-158.849	125.841	65.07
110	BML7	-185.677	126.31	71.73
111	BML45	-147.391	125.843	55.276
112	CAL1812	-194.84	119.304	63.32



**Fig. 3.** Two-dimensional graph showing relative positions of 112 inbred lines of maize (*Zea mays* L.) based on PCA scores



**Fig. 4. Three-dimensional graph showing relative positions of 112 inbred lines of maize (*Zea mays* L.) based on PCA scores**

traits of *kharif* maize (*Zea mays* L.). *The Bioscan*. 10 (4): 2049-2056.

**Lemi Y, Beyene A and Zelalem T 2022.** Genetic variability, heritability, correlation analysis, genetic advance and principal component analysis of grain yield and yield related traits of quality protein maize (*Zea mays* L.) inbred lines adapted to mid-altitude agroecology of Ethiopia. *EAS Journal of Nutrition and Food Sciences*. 10 (10): 281-289.

**Lone R A 2017.** Genetic diversity in maize (*Zea mays* L.) inbred lines from Kashmir. *International Journal of Pure Applied Bioscience*. 5 (1): 229-235.

**Mahalanobis PC 1928.** A statistical study at Chinese head measurement. *Journal of Asiatic Society*. Bangladesh. 25: 301-337.

**Maruthi R T and Rani K J 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.

**Moll R H and Stuber C W 1971.** Comparison of response to alternative selection procedure initiated with two population of maize (*Zea mays* L.). *Crop Science*. 11: 706-711.

**Pavithra A, Ganesan K N, Meenakumari B and Sivakumar S D 2022.** Genetic studies on green fodder yield and quality traits in fodder maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*. 13 (2): 432-439.

**Rao C R 1952.** *Advanced Statistical Methods in Biometrics Research*. John Wiley and Sons, New York. 236-272.

**Singh R K and Chaudhary B D 1977.** *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi. pp. 54-57.

**Singh S B, Kasana R K, Kumar S and Kumar R. 2020.** Assessing genetic diversity of newly developed winter maize (*Zea mays* L.) inbred lines. *Indian Journal of Plant Genetic Resources*. 33 (01): 68-76.