



Research Article

GENETIC VARIABILITY AND DIVERSITY ANALYSIS FOR THE SELECTION OF DIVERSE INBRED LINES IN MAIZE (*ZEAMAYS* L.) CROP

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Abstract: Wide range of genetic variation among the studied genotypes for genetic variability and diversity analysis was observed for traits viz. days to 50% tasseling, days to 50% silking, days to 80% maturity, final plant stand, plant height, ear height, ear length, ear girth, number of cobs per plot, number of kernel rows per cob, number of kernels per row, test weight, shelling percentage and grain yield. High heritability coupled with high genetic advance as percentage of mean was recorded for grain yield, test weight, ear height, number of cobs per plot, number of kernels per row, number of kernel rows per cob, ear length, ear girth and plant height. Maximum contribution in percentage towards total genetic divergence was obtained for trait number of kernel rows per cob followed by number of cobs per plot, test weight, number of kernels per row and ear length. On the basis of D^2 values, the 196 genotypes were grouped into 8 clusters. Cluster I and II were the largest clusters with 34 genotypes followed by cluster III (31 genotypes), cluster V (23 genotypes), cluster VII (21 genotypes), cluster VIII (20 genotypes), cluster VI (17 genotypes) and cluster IV with 12 genotypes. The cluster IV had the maximum D^2 value (2.950) followed by Cluster VIII ($D^2=2.856$) and Cluster III ($D^2=2.702$). The inter cluster D^2 values of the eight clusters revealed that highest inter cluster generalized distance ($D^2=6.765$) was between cluster IV and cluster VI, while the lowest ($D^2=2.257$) between cluster I and cluster VII.

Keywords: Genetic Variability, GCV, PCV, h^2 , Diversity, Cluster Analysis, D^2 , Cluster Distance

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Introduction

Maize (*Zea mays* L.) belongs to family Gramineae ($2n=2x=20$) and is an important staple food of many countries, particularly in the tropics and subtropics. This cereal is referred as Miracle crop and Queen of the Cereals due to its high productivity potential compared to other Poaceae family members. It is a cereal with a remarkable potential for production, it is the third most important grain crop after wheat and rice. It is a cereal with a remarkable potential for production, it is the third most important grain crop after wheat and rice. Maize (*Zea mays* L.) is an exciting and leading crop contributing significantly to world agriculture and more importantly to world's food basket of roughly 2000 million metric tons [1]. It contributes maximum among the food cereal crops i.e. 38% annually in the global food production as compared to 30% for wheat and 20% for rice. In India, presently it occupies about 8.69 million hectares area with the mean yield of 2.53 tons/hectare [2]. The availability of genetic variability is the basic pre-requisite for genetic improvement through systematic breeding programme. In crop plant, collection of germplasms and assessment of genetic variability is basic step in any crop improvement programme, which acts as a building block for generation of genetic variability. Evaluation and cataloguing of this variability is of paramount importance of its efficient utilization. Many modern cultivars in maize and in other crops as well, are often genetically similar, with a rather narrow genetic base. Therefore, in breeding we need to also utilize sources of new diversity. Knowledge on genetic divergence is very important in the selection of parents in hybridization programme for identifying heterotic crosses and obtaining desirable segregants. There are so many methods available for analysis of genetic diversity in germplasm accessions, breeding lines and populations. Among these the D^2 statistics is one of the best methods for assessment of genetic diversity in crop species. The concept of D^2 statistics was developed by P.C. Mahalanobis in 1928[3]. This technique is widely used for the assessment of genetic diversity in

the germplasm collections. This is a numerical approach which is used for measuring genetic divergence, in the germplasm collection. In D^2 statistics the genetic diversity is depicted by cluster diagram.

Material and Methods

A field experiment was conducted with standard agronomical package of practices at IGKV, RMD CARS, Research and Instructional Farm, Ajirma, Ambikapur (C.G.) during Kharif 2016 which is located at a latitude of $20^{\circ}8'N$, longitude of $83^{\circ}15'E$ and altitude of 592.62 m MSL (mean sea level). A field trial was conducted using 191 germplasms (95 inbreds & population received from WNC, Hyderabad; 82 inbred lines developed at RMD CARS Ambikapur and 14 local germplasm) and five checks. These varieties were sown during Kharif, 2016 in a Randomized Block Design replicated twice. Each variety was sown in double rows of 4 m row length adopting a spacing of 75 cm between rows and 20 cm between the plants. All the recommended agronomic package of practices was adopted during the entire crop growth period. In each replication, five plants were taken at random and the following 14 biometrical observations viz, days to 50 % tasselling, days to 50 % silking, days to 80 % brown husk maturity, plant height (cm), plant population per plot, ear height (cm), ear length (cm), ear girth (cm), no. of kernel rows per cob, no. of kernels per row, no. of cobs per plot, test weight (gm), shelling percentage, grain yield kg/plot were recorded.

Result and Discussion

Genetic Variability

The analysis of variance for different morphological traits was carried out to partition the total variance due to genotypes and other sources. Analysis of variance revealed highly significant differences among genotypes in respect of almost all the characters under studied at 1% and 5% level.

Table-1 Analysis of Variance for grain yield and its component in maize

SN	Characters	Mean sum of squares			Standard Error of mean (SEm $\pm$)	Coefficient of variation (%)
		Replication	Genotype	Error		
		1	195	195		
1	Days to 50% tasseling	3.31	34.28**	0.57	0.75	1.46
2	Days to 50% silking	2.87	32.36**	0.90	0.95	1.71
3	Days to 80% maturity	1.00	63.00**	0.79	0.89	0.95
4	Final plant stand	3.37	26.67**	1.21	1.10	7.42
5	Plant height (cm)	63.00	1438.00**	99.78	9.98	6.05
6	Ear height (cm)	1.56	408.70**	26.55	5.15	10.17
7	Ear length (cm)	0.72	12.74**	1.47	1.21	10.71
8	Ear girth (cm)	1.54	4.59**	0.54	0.74	6.45
9	No. of Cobs per plot	3.24	27.35**	1.10	1.05	7.40
10	No. of kernel rows per cob	0.01	4.25*	0.75	0.86	7.55
11	No. of kernels per row	11.87	71.18**	8.83	2.97	13.44
12	Test weight (100gm)	0.65	90.18**	2.04	1.43	5.90
13	Shelling percentage (%)	0.12	70.80*	11.24	3.35	4.62
14	Grain yield (kg per plot)	0.004	0.08**	0.002	0.05	11.01

* = significant of $p = 0.05$ level, ** = significant of $p = 0.01$ level

Table-2 Parameters of Genetic variability for different characters of maize genotypes

Character	Mean	Range		PCV %	GCV %	h^2	GA	GA as % of mean
		Minimum	Maximum					
Days to tasseling	51.48	41.50	64.50	8.11	7.97	96.70	8.32	16.16
Days to silking	55.74	47.00	66.50	7.32	7.11	94.50	7.94	14.25
Days to maturity	93.50	83.00	107.00	6.04	5.96	97.50	11.34	12.09
Final plant stand	14.82	10.00	21.50	25.19	24.07	91.30	7.02	46.98
Plant height	165.09	99.30	262.10	16.80	15.67	87.00	49.71	29.83
Ear height	50.66	19.20	94.80	29.12	27.29	87.80	26.68	51.93
Ear length	11.32	5.20	19.90	23.55	20.97	79.30	4.36	38.17
Ear girth	11.49	5.85	16.20	13.96	12.38	78.60	2.60	22.45
No. of cobs/plot	14.22	8.50	21.50	26.52	25.47	92.20	7.17	49.96
No. of kernel rows/cob	11.50	6.20	15.40	13.7	11.49	69.80	2.28	19.77
No. of kernels/row	22.10	9.70	43.40	28.61	25.26	77.90	10.15	45.19
Test weight	24.23	12.00	48.00	28.02	27.39	95.60	13.37	54.52
Shelling percentage	72.48	48.00	83.65	8.84	7.53	72.60	9.58	13.19
Grain yield (kg/plot)	0.45	0.16	2.44	46.44	32.55	70.09	0.40	81.63

Table-3 Contribution of grain yield and other characters towards divergence in maize (%)

SN	Character	Times ranked 1 st	Percentage contribution towards divergence (%)
1	Number of kernel rows per cob	32473	11.17
2	Number of cobs per plot	31299	10.76
3	Test weight	28121	9.67
4	Number of kernels per row	26728	9.19
5	Ear length	26180	9.00
6	Shelling percentage	26106	8.95
7	Ear girth	25775	8.86
8	Days to 50% silking	25403	8.74
9	Days to 50% tasseling	23801	8.18
10	Ear height	14796	5.09
11	Days to 80% maturity	12503	4.30
12	Final plant stand	6037	2.07
13	Plant height	5848	2.01
14	Grain yield	5657	1.94
15	Total	290637	100

Similar result was also reported earlier [4]. This indicated presence of substantial amount of genetic variability among the genotypes under study. The mean sum of squares of the genotypes for 14 characters is presented in table-1. The character wise variability i.e., estimates of coefficient of variation, range, mean, phenotypic and genotypic coefficient of variation, heritability in broad sense, genetic advance and genetic advance as percent of mean for all 14 characters studied are summarized in [Table-2]. In general, the values of phenotypic coefficient of variation were higher than that of genotypic coefficient of variation for all characters. The phenotypic coefficient of variation was estimated to be high for grain yield (46.44%), ear height (29.12%), number of kernels per row (28.61%), test weight (28.02%), number of cobs per plot (26.52%), final plant stand (25.19%) and ear length (23.55%), while, it was moderate for plant height (16.80%), ear girth (13.96%), number of kernel rows per cob (13.7%), and low for shelling percentage (8.84%), days to 50% tasseling (8.11%), days to 50% silking

(7.32%) and days to 80% maturity (6.04%). This was confirmed by earlier reports [8] and [9]. These characters with low magnitude of genetic variability may have limited utility in a programme of selection for their improvement. Genotypic coefficient of variation observed higher for grain yield (32.55%), test weight (27.39%), ear height (27.29%), number of cobs per plot (25.47%), number of kernels per row (25.26%), final plant stand (24.07%) and ear length (20.97%), while it was moderate for plant height (15.67%), ear girth (12.38%) and number of kernels rows per cob (11.49%), and low for days to 50% tasseling (7.97%), shelling percentage (7.53%), days to 50% silking (7.11%) and days to 80% maturity (5.96%). Higher PCV and GCV were reported previously for grain yield per plant [5], [6] and [7] for 100 grain weight. The heritability estimates are high for all the traits viz, days to 80% maturity (97.50%), days to 50% tasseling (96.70%), test weight (95.60%), days to 50% silking (94.50%), number of cobs per plot (92.20%), final plant stand (91.30%), ear height (87.80%), plant height (87.00%),

Table-4 Distribution of maize genotypes in different clusters

Cluster	No. of genotypes	Name of genotypes
I	34	DMSC 20, CAL 1441, Z484-32, IAMI-06, IAMI-16, IAMI-23, IAMI-30, CM-209, IAMI-3, PC-106(2011), IAMI-38, SC-104(2011), IAMI-57, IAMI-41, IAMI-7, CML-175, CM-209, Keshkal 1-6, IAMI-61, Pharasgaon I-1, Pharasgaon I-4, IAMI- 43, Kondagaon I-4, Jagdalpur I-2, IAMI-44, IAMI-64, Bijapur II-1, Pharasgaon II-1, IAMI-67, IAMI-46, BLD 7, IAMI-81, DMRQPM 03 -104, MRC PC 8
II	34	DMR 10 RYFWS 8105 (A), DMR 19 RYDWS 1247, DMR 11 R 0144, DMR 11 R 4785, DMRSCY 18 R 715, SNL 142851, CIL 1218, Z486-3, Z 486-7, Z 491-3, Z491-17, V941-25, Z490-24, Z489-144, IAMI- 04, IAMI- 14, IAMI- 15, IAMI- 21, IAMI- 25, IAMI- 53, IAMI- 52, HKI-1126, HKI-1342, DMHOC-15, S87(P56Q)-B-B-B-17-B-B-B, CML165-B-B, Chhindgaon II-3, Kate kalyan II-2, IAMI- 65, CM105, MRC PC 22, MRC SC 8, SC7-2-1-2-6-1, DMR T4
III	31	IAMI-34, BML 6, DMSC 6, IAMI-9, IAMI- 51, CAL 1468, CAL 1425, IAMI- 49, CML 425, CAL 14100, Z 487-4, Z491-50, V941-20, Z489-69, IAMI- 27, IAMI- 54, Z-49-45-CA-14514-2-1-2-B-B, SC-109(2011), Z-51-20, CM-209, IAMI-5, IAMI- 60, IAMI- 42, IAMI- 62, IAMI- 66, Pharasgaon II-2, IAMI- 69, IAMI- 19, IAMI-33, IAMI- 82, MRC PC 6
IV	12	DMR 10 RYFWS 8384 (B), CML 451 (P2), Z489-92, IAMI- 28, SOOTLYQ-HG-35-B-B-B, EC-611064, IAMI- 45, IAMI- 87, IAMI- 74, CM 104, MRC PC 13, SC-24-9(C12)-3-2-1-1
V	23	IAMI-11, IAMI-36, IAMI-18, BML 14, BML 8, CM 501, CAL 1454, CAL 1462, CAL 1480, CAL 14111, CAL14114, VL 121160, IAMI- 08, IAMI- 31, HKI-1324-1, Z-15-1, IAMI- 39, P-62-C6-B-B-B-31-B-B-B, CM-123, IAMI- 47, IAMI- 68, IAMI- 73, Pro 4212
VI	17	SC 7-2-1-2-1-6-1(N), IAMI-1, Z 485-4, Z485-17, Z491-28, Z490-23, IAMI- 55, Z-56-2-TL-SEOULA503446-B-B-B-1-B-B-B, IAMI-58, Baderajpur I-3, Keshkal I-8, Dantewada II-1, IAMI- 71, TNAU/CBE-98, PFSR R5, IAMI- 83
VII	21	SNL 142798, CML 161, CML 70, CML 162, Z491-35, Z489-134, IAMI- 10, IAMI- 12, IAMI- 22, S87(P66Q)-B-B-B-30-B-B-B, IAMI- 84, IAMI- 59, G33 QC20-B-B-B-1-B-B-B, SO1SIWQ-2-B-B-B-38-B-B-B, HKI SCT, IAMI- 20, IAMI-37, IAMI- 48, PFSR R3, MRC PC 29
VIII	20	DMR 10 RYFWS 8279 (B), IAMI-35, BML 15, CAL 1429 (VL 1043), IAMI-89, IAMI-17, IAMI-29, IAMI- 50, VL121230, IAMI-85, Z489-107, IAMI-02, IAMI- 32, IAMI- 40, P67-C1-B-B-B-37-B-B-B, CML289-B-B-B, EC440631, HK-193, IAMI-88, CM 212

Table-5 Intra (bold) and Inter cluster distance values in maize

Cluster	I	II	III	IV	V	VI	VII	VIII
I	2.232							
II	2.372	2.326						
III	3.860	3.711	2.702					
IV	4.141	3.118	4.320	2.950				
V	4.658	5.540	3.551	6.061	2.605			
VI	3.756	5.408	5.815	6.765	3.910	2.533		
VII	2.257	3.440	4.146	4.539	3.314	2.477	2.380	
VIII	4.812	4.341	4.669	4.178	4.109	5.169	3.439	2.856

Table-6 Mean performance of different clusters for grain yield and its component traits

Character Cluster	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
I	47.96	52.32	91.62	12.00	171.67	52.68	11.14	11.01	11.32	11.05	22.95	21.99	74.69	0.32
II	51.79	56.10	89.13	11.76	143.03	38.68	9.51	10.39	11.15	11.44	18.11	19.60	72.43	0.31
III	50.08	54.37	90.35	19.60	148.26	42.34	9.55	10.79	19.02	11.01	19.92	21.63	73.82	0.71
IV	52.92	57.67	94.42	13.67	149.70	39.44	9.06	9.82	12.79	9.29	13.67	23.88	59.55	0.37
V	51.96	56.02	96.50	20.04	185.87	60.63	13.14	12.84	19.57	12.32	26.52	29.78	74.74	0.74
VI	49.53	53.56	95.91	12.74	191.10	67.85	14.61	13.92	12.09	12.91	32.55	30.65	76.57	0.33
VII	51.71	56.24	94.17	13.38	180.82	62.41	13.36	12.11	12.90	11.82	24.53	26.21	72.65	0.36
VIII	59.12	62.92	102.32	15.40	164.26	48.87	11.80	12.02	14.88	12.04	19.41	26.33	68.33	0.46

X1- Days to 50% tasseling, X2- Days to 50% silking, X3- Days to 80% maturity, X4- Final plant stand, X5- Plant height (cm), X6- Ear height (cm), X7- Ear length (cm), X8- Ear girth (cm), X9- Number of cobs per plot, X10- Number of kernel rows per cob, X11- Number of kernels per row, X12- Test weight (100gm), X13- Shelling percentage (%), X14- Grain yield (kg/plot).

ear length (79.30%), ear girth (78.60%), number of kernels per row (77.90%), shelling percentage (72.60%), grain yield (70.09%), and number of kernel rows per cob (69.80%). High heritability estimate was also reported for days to 50 percent tasseling, days to 50 percent silking and grain yield per plant [6], for days to 50 percent tasseling, days to 50 per cent silking and plant height [8], for plant height, ear length, ear girth, and 100-grain weight [9]. The higher estimate of genetic advance as percent of mean was exhibited by grain yield (81.63%), test weight (54.52%), ear height (51.93%), number of cobs per plot (49.96%), number of kernels per row (45.19%), ear length (38.17%), plant height (29.83%), ear girth (22.45%) and number of kernel rows per cob (19.77%). However medium estimate of genetic advance as per cent of mean was exhibited by days to 50% tasseling (16.16%), days to 50% silking (14.25%), shelling percentage (13.19%) and days to 80% maturity (12.09%). These results were in consonance with the findings of [10] for 100-grain weight, grain yield per plant and cob diameter [7] for plant height and ear length [11] for ear weight [12].

Diversity Analysis

The quantitative assessment of genetic divergence has been studied using Mahalanobis's D^2 statistics on 196 genotypes over 14 yield and yield contributing characters. The percentage contribution towards genetic divergence by all the characters is presented in [Table-3]. The character number of kernel rows per cob contributed most towards genetic divergence (11.17%) followed by remaining characters in descending order viz, number of cobs per plot (10.76%), test weight (9.67%), number of kernels per row (9.19%), ear length (9.00%), shelling percentage (8.95%), ear girth (8.86%), days to 50% silking (8.74%), days to 50% tasseling (8.18), ear height (5.09%), days to 80% maturity (4.30%), final plant stand (2.07), plant height (2.01) and grain yield (1.94%). D^2 values, categorized 196 genotypes into 8 clusters. Cluster I and II are the largest clusters with 34 genotypes followed by cluster III (31 genotypes), cluster V (23 genotypes), cluster VII (21 genotypes), cluster VIII (20 genotypes), cluster VI (17 genotypes) and cluster IV with 12 genotypes [Table-4].

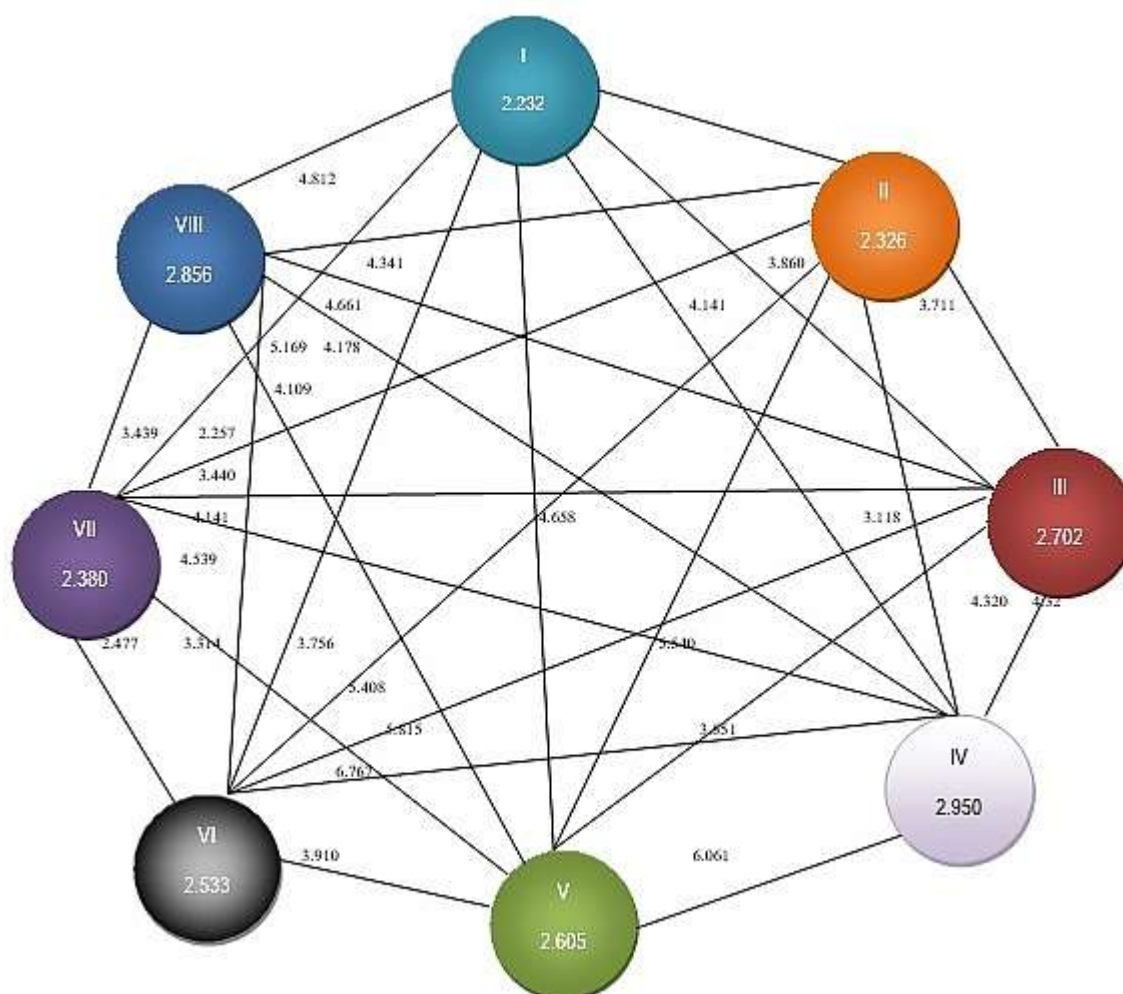


Fig-1 Intra (Bold) and inter cluster distances between clustered genotypes of maize Mahalanobis Euclidean² Distances

Earlier [13], [14] and [15] obtained only five, seven and four clusters of genotypes, from 110, 45 and 38 genotypes respectively, indicating presence of narrow genetic diversity in their materials. On the other hand, [16], [17], [18] reported formation of 15, 10 and 23 clusters from 135, 186 and 101 genotypes respectively, representing the availability of wide genetic diversity in the materials studied by them. The average intra and inter-cluster D^2 values estimated as per the procedure [19] are presented in [Table-5] & depicted by [Fig-1] and the cluster mean values are summarized in [Table-6]. The intra cluster D^2 value ranged from 2.232 to 2.950. Maximum D^2 value (2.950) was observed for cluster IV followed by Cluster VIII ($D^2=2.856$) and Cluster III ($D^2=2.702$). Highest inter cluster generalized distance ($D^2= 6.765$) was obtained between cluster IV and cluster VI, while the lowest ($D^2 = 2.257$) between cluster I and cluster VII. Cluster I was nearest to cluster VII (2.257) and distant from cluster VIII (4.812). Cluster II exhibited close proximity with cluster IV (3.118) and maximum divergence with cluster V (5.540). Cluster III was nearest to cluster V (3.551), while it was farthest from cluster VI (5.815). Cluster IV showed close proximity with cluster VIII (4.178) and maximum divergence with cluster VI (6.765). Cluster V exhibited intimate relation with cluster VII (3.314) and wide diversity with cluster VIII (4.109). Cluster VI was nearest to cluster VII (2.47) and distant from cluster IV (6.765). Cluster VII exhibited intimate relation with cluster I (2.257) and wide diversity with cluster IV (4.539). Nearest and farthest clusters for cluster VIII are VII (3.439) and VI (5.169) clusters, respectively. Cluster I recorded low values for days to 50% tasseling (47.96) and days to 50% silking (52.32). Cluster II showed lowest value for days to 80% maturity (89.13), final plant stand (11.76), plant height (143.03), ear height (38.68), number of cobs per plot (11.15), test weight (19.60) and grain yield (0.31). Cluster III recorded highest value for traits e.g., final plant stand (19.60) and number of cobs per plot (19.02). Cluster IV recorded low values for ear length (9.06), ear girth (9.82), number of kernel rows per cob (13.67) and shelling percentage (59.55). Cluster V recorded high values of cluster means for plant height (185.87)

and grain yield (0.74). Cluster VI recorded high values for ear height (67.85), ear length (14.61), ear girth (13.92), number of kernel rows per cob (12.91), number of kernels per row (32.55), test weight (30.65) and shelling percentage (76.57). Cluster VII not recorded any high or low values for any character. All the characters in this cluster recorded moderate values. Cluster VIII recorded high values of cluster means for days to 50% tasseling, days to 50% silking and days to 80% maturity. These results were in consonance with the findings [4]. From the above study diverse lines identified are CAL 14114, IAMI-73, CAL 1462, CAL 14111, Z490-23, TNAU/CBE-98, IAMI-44, BLD 7, PFSR R5, Pharasgaon I-4, Jagdalpur I-2, IAMI-7, SC-104(2011), IAMI-33, PC-106(2011), Pharasgaon I-I, IAMI-40, IAMI-29, IAMI-17, CML289-B-B-B, IAMI-22, IAMI-55, IAMI-35, VL121230, EC-611064 and Z489-92.

Application of research: These lines can be utilized for further breeding programme or development of suitable and promising maize hybrids for the Northern hill zone of Chhattisgarh.

Research Category: Cluster analysis

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Study area / Sample Collection: Research and Instructional Farm, Ajirma, Ambikapur

Cultivar / Variety name: Maize (*Zea mays* L.)

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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