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GENETIC DIVERGENCE STUDIES IN MAIZE (*Zea mays* L.) ACCESSIONS

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ABSTRACT

Eighty eight genotypes of maize (*Zea mays* L.) were evaluated for genetic divergence to identify potential parents for hybridization programme in *kharif* 2018 at College of Agriculture, Nagpur.Mahalanobis D^2 statistics for nine characters *viz.*, days to 50% tasseling, days to 50% silking, days to maturity, plant height, cob length, cob girth, number of grains cob^{-1}, 100 grain weight and grain yield plant^{-1} were used in this study for computing genetic divergence. The eighty eight genotypes were grouped into twenty clusters by usingTocher's method. The maximum inter-cluster distance was recorded between cluster IV and cluster XX (D = 28.41) whereas, minimum inter-cluster distance was found between cluster VI and cluster VIII (D = 1.82). The canonical analysis and cluster means study revealed the importance of days to 50% tasseling, number of grains cob^{-1}, plant height, grain yield plant^{-1} and cob length were considered as criteria for selecting potential parents for hybridization programme and according to this criteria 28 genotypes *viz.*, 52202, 52623, 52025, 52201, 52014, 52291, 52087, 52115, 52196, 52020, 52140, 52327, 52285, 52180, 52497, 52552, 52347, 52045, 52597, 52353, 52095, 52081, 52065, 52219, 52263, 52250, 52603 and 52040 were identified to be used as parents for hybridization programme, which were suggested to be crossed in diallel fashion to obtain superior cross combinations. PKVM-Shatak as it is in separate cluster and distant from other clusters can be further improved to produce new hybrid by crossing with parents 52250, 52020, 52087, 52025, 52014, 52040, 52623, 52201, 52180, 52552, 52115 and 52202.

(Key words : Maize, genetic divergence, D^2 statistics, selection)

INTRODUCTION

Maize (*Zea mays* L.) is the world's important cereal crop after wheat and rice. Maize is known as queen of cereals because it has great yield potential, wider adaptability and attained the leading position among cereals in term of production as well as productivity. Maize can be grown in a wide range of climates, which is used as a food for human consumption and feed for cattle. It belongs to family Poaceae also called as Gramineae and subfamily Panicoideae. It is one of the first plant species identified to photosynthesize by C_4 pathway with high yield potential. Maize seed oil is also low in linolenic acid (0.7%) and contains a high level of flavour Rahangdale *et al.*, (2019) Maize provides many of the B vitamins and essential minerals along with fiber, but lacks some other nutrients, such as vitamin B12 and vitamin C, and is, in general, a poor source of calcium, folate and iron. Silage is prepared from green maize plants. Maize is not only used as food, feed and fodder but also used for some industrial purposes for manufacturing *viz*. starch, alcohol, acetic acid, glucose, paper, furfural, rayon, dyes, synthetic rubber and resin etc. (Pandit *et al.*, 2019).

Assessment of genetic diversity is an essential pre-requisite for identifying potential parents for hybridization. Diverse parents are expected to yield higher frequency of heterotic hybrids in addition to generating a broad spectrum of variability in segregating generations. D^2 statistic was one of the methods used to study the genetic divergence and it was first time developed by Mahalanobis in 1936. Maize breeders are consistently emphasizing on the importance of diversity among parental genotypes as a significant factor contributing to heterotic hybrids. D^2 analysis is a useful tool for quantifying the degree of divergence between biological population at genotypic level and in assessing relative contribution of different components to the total divergence both at intra and inter-cluster level (Murty and Arunachalam, 1966).

MATERIALS AND METHODS

The experimental material comprised of eighty eight germplasm obtained from principle scientist and I/C winter nursery centre/ICAR-IIMR/ Rajendranagar Hyderabad-30 and one check *viz*. PKVM-Shatak. These eighty eight genotypes were grown in Randomized Block Design in three

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replications with the spacing of 60 cm×20 cm accommodating 15 plants in each row for the estimation of genetic divergence analysis in *kharif* 2018-19. Eighty seven parents and one check viz. PKVM-Shatak was also raised in three replications adjacent to the parents for the estimation of genetic divergence.Recommended package of practices were followed to raise a good crop. The data were recorded on five randomly selected plants from each genotype on following six characters except days to 50% tasseling, days to 50% silking and days to maturity which were recorded on plot basis. The data recorded were subjected to D^2 statistics to know the genetic diversity among the germplasm as suggested by Mahalanobis (1936). Grouping of genotypes into clusters was done as per the method described by Rao (1952) and identifying the superior genotypes was as per the method described by Bhatt (1970).

RESULTS AND DISCUSSION

The analysis of variance for nine characters revealed highly significant differences among the genotypes for all the nine characters indicating presence of substantial genetic variability for the characters studied (Table 1). Based on the magnitude of D^2 values, 88 genotypes were grouped into 20 clusters (Table 2). Cluster I was the largest comprising of 65 genotypes. The next largest cluster was cluster IX which included 5 genotypes, cluster II, III, IV, V, VI, VII, VIII, X, XI, XII, XIII, XIV, XV, XVI, XVII, XVIII, XIX, XX included only one genotype each. Average intra and inter-cluster D^2 values were presented in table 3. The intra-cluster variation ranged from 0.00 to 5.46. Cluster IX possessed highest intra-cluster distance (D = 5.46) followed by cluster I (D = 4.96). The average inter-cluster distance was maximum between cluster IV and cluster XX (D = 28.41) followed by cluster XI and cluster XX (D = 26.12), cluster II and cluster XIX (D = 25.72), cluster XV and cluster XX (D = 25.56), cluster V and cluster XIX (D = 25.06), cluster IV and cluster XIX (D = 23.26) and cluster XVII and cluster XIX (D = 23.24). This suggests more variability in genetic makeup of genotypes included in these clusters. The inter-cluster distance was found to be minimum between cluster VI and cluster VIII (D = 1.82).

The per cent contribution of nine characters towards total genetic divergence (Table 4) showed that the per cent contribution of days to 50% tasseling to the total divergence was maximum (18.34%) followed by 100 grain weight (17.08%), plant height (14.47%), grain yield plant^{-1} (13.19%), cob girth (13.09%), days to maturity (11.05%), cob length (6.64%) and number of grains cob^{-1} (4.05%). Relatively days to 50% silking (2.09%) contributed less towards genetic divergence.Varaprasad and Shivani (2017) also in agreement with high contribution of number of kernels row^{-1} (22.56%), 100 kernel weight (20.19%), days to 50% tasseling (11.84%) and grain yield plant^{-1} (10.30%).

The value of first five canonical vectors and canonical roots are presented in table 5 and in table 6 respectively. The first three canonical roots accounted for 54.03% of the observed variability in material (λ_1 = 25.93%, λ_1 = 15.11% and λ_3 =12.99%). The overall contribution of the five canonical roots to total variability among 88 genotypes was 75.60% suggesting the completion of major portion of differentiation in first five phases. This indicated that differentiation for nine characters among 88 genotypes was nearly completed in five phases. Further the coefficients in the first five canonical vectors indicate that out of nine quantitative characters grain yield plant^{-1}, number of grains cob^{-1}, cob length, plant height, cob girth and 100 grain weight were important characters in the first vector which was major access of differentiation accounting for 25.93% of total variation. Days to 50% tasseling and cob length were important characters in secondary access of differentiation which accounted for 15.11% of total variation. Important characters in vector III were days to maturity, number of grains cob^{-1} and days to 50% silking accounting to 12.99% of variation. Plant height and cob girth were important characters in vector IV which accounted for 11.08% and days to 50% tasseling, days to maturity, 100 grain weight, plant height and cob girth were important source of variation in vector V accounting to 10.49% of variation. This suggested that parents selected on the basis of characters like days to 50% tasseling, number of grains cob^{-1}, plant height, cob girth and cob length may be expected to be genetically diverse. Akhi *et al.* (2017) and Varaprasad and Shivani (2017) also carried out the canonical analysis in maize and reported that days to 50% silking, plant height, cob length (cm), number of rows cob^{-1}, number of grains cob^{-1} for both the vectors I and II were positive and these are indication of the important components of genetic divergence.

Data regarding cluster means for all the nine characters are presented in table 7. The genotypes from cluster XII possessed the highest cluster mean for plant height, 100 grain weight and cob girth. Cluster XIX showed maximum mean for number of grains cob^{-1} and grain yield plant^{-1}. Cluster VII showed maximum mean for days to 50% tasseling and days to 50% silking. Cluster VIII showed maximum mean for cob length and cluster XIII for days to maturity, the genotypes with high mean values may be used as parents in future hybridization programme.

According to Bhatt (1970) the mean statistical distance may be considered arbitrarily as a guide line and crosses between parents belonging to different clusters having same or higher inter-cluster distance than the mean statistical distance may be attempted. The crosses should be chosen from widely distinct clusters. But, it is observed in the present study that there might be several genotypes included in such widely separated clusters. Then the question arise which of the genotypes from these more diverse clusters may be used for crossing. In that case preference for those genotypes which perform better for the characters (days to 50% tasseling, number of grains cob^{-1}, plant height, grain yield plant^{-1} and cob length) which contributed much towards divergence should be given. In

Table 1.Analysis of variance for various characters

			Mean squares								
Sr. No.	**Source of varience**	**d.f.**	**Days to 50% tasseling**	**Days to 50% silking**	**Days to maturity**	**Plant height (cm)**	**Cob length (cm)**	**Cob girth (cm)**	**Number of grains cob^{-1}**	**100 grain weight (g)**	**Grain yield $plant^{-1}$ (g)**
1.	Replication	2	0.03	2.40	4.10	543.40	2.94	0.11	2796.20	5.55	35.87
2.	Genotypes	87	8.97**	7.78**	10.63**	750.02**	8.47**	2.74**	5913.20**	9.73**	413.45**
3.	Error	174	2.44	2.46	3.15	196.88	2.65	0.68	1746.20	2.06	62.87

** Significant at 1% level

Table 2. Grouping of 88 genotypes of maize in different clusters

Cluster	Total number of genotypes	Genotypes
I	65	52042, 52377, 52070, 52483, 52549, 52340, 52399, 52149, 52068, 52098, 52262, 52540, 52274, 52536, 52383, 52058, 52361, 52185, 52077, 52370, 52019, 52292, 52342, 52329, 52266, 52310, 52409, 52597, 52349, 52099, 52389, 52048, 52556, 52059, 52631, 52066, 52032, 52317, 52205, 52060, 52545, 52615, 52031, 52214, 52217, 52638, 52208, 52353, 52041, 52568, 52461, 52184, 52278, 52049, 52169, 52095, 52459, 52507, 52081, 52065, DMR E 63, 52102, 52123, 52219, 52263
II	1	52025
III	1	52291
IV	1	52202
V	1	52014
VI	1	52285
VII	1	52140
VIII	1	52327
IX	5	52180, 52497, 52552, 52347, 52045
X	1	52623
XI	1	52196
XII	1	PKVM-SHATAK
XIII	1	52040
XIV	1	52020
XV	1	52201
XVI	1	52115
XVII	1	52087
XVIII	1	52234
XIX	1	52603
XX	1	52250

Table 3. Average intra and inter-cluster distance by Tocher's method

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX
I	**4.96**	6.69	6.56	6.94	9.16	8.32	7.55	8.30	7.66	7.70	6.71	7.56	6.84	7.55	7.81	6.98	8.77	9.20	13.57	16.35
II		**0.00**	8.53	2.13	8.76	17.52	10.55	18.19	10.83	5.75	6.39	14.47	7.44	4.79	8.91	6.79	6.25	9.08	25.72	20.31
III			**0.00**	7.38	12.84	7.99	12.27	10.37	11.99	13.59	8.40	10.66	3.43	6.85	4.00	11.74	8.31	11.15	11.13	23.48
IV				**0.00**	12.81	14.20	11.25	15.56	12.51	10.84	4.48	11.50	6.72	8.57	7.01	10.47	6.95	10.09	23.26	28.41
V					**0.00**	17.89	4.14	12.48	11.39	9.46	19.31	14.44	14.83	11.31	16.22	10.41	11.18	19.82	25.06	11.57
VI						**0.00**	13.79	1.82	7.40	14.90	10.42	6.09	7.71	15.57	10.90	16.60	12.92	10.56	5.94	18.35
VII							**0.00**	9.10	10.81	12.21	14.82	6.90	17.50	12.51	10.92	7.64	14.92	15.03	20.00	15.98
VIII								**0.00**	7.95	14.87	13.56	4.94	10.85	18.39	14.56	16.04	13.27	14.69	8.80	16.22
IX									**5.46**	8.58	12.18	11.60	9.76	8.83	12.07	9.63	10.89	9.27	16.56	10.72
X										**0.00**	8.01	12.19	10.81	8.54	15.84	7.83	10.06	7.72	18.09	8.00
XI											**0.00**	7.24	6.78	10.73	8.74	9.04	11.13	5.88	13.67	26.12
XII												**0.00**	14.25	18.34	11.81	11.51	18.24	8.79	8.69	21.30
XIII													**0.00**	7.17	8.60	12.65	5.30	12.40	13.68	22.52
XIV														**0.00**	5.00	5.68	8.97	9.86	20.72	15.86
XV															**0.00**	10.28	12.50	9.81	14.03	25.56
XVI																**0.00**	16.16	9.19	21.51	17.58
XVII																	**0.00**	16.06	23.24	18.62
XVIII																		**0.00**	16.22	18.14
XIX																			**0.00**	22.06
XX																				**0.00**

Table 4. Contribution of individual character to divergence

Sr.No.	Source	Time ranked 1st	Per cent contribution
1.	Days to 50% tasseling	702	18.34
2.	Days to 50% silking	80	2.09
3.	Days to maturity	423	11.05
4.	Plant height (cm)	554	14.47
5.	Cob length (cm)	254	6.64
6.	Cob girth (cm)	501	13.09
7.	Number of grains cob^{-1}	155	4.05
8.	100 grain weight (g)	654	17.08
9.	Grain yield plant^{-1} (g)	505	13.19
	Total	**3828**	**100**

Table 5. The value of canonical vectors

Vector	Days to 50% tasseling	Days to 50% silking	Days to Maturity	Plant Height (cm)	Cob Length (cm)	Cob Girth (cm)	Number of grains cob^{-1}	100 grains weight (g)	Grain yield plant^{-1} (g)
I	-0.076	-0.329	-0.045	0.289	0.456	0.180	0.510	0.104	0.538
II	0.574	-0.227	-0.178	0.061	0.163	-0.662	0.033	-0.342	0.012
III	-0.104	0.145	0.619	0.096	-0.102	0.035	0.350	-0.662	-0.053
IV	-0.018	-0.278	-0.416	0.608	-0.399	0.302	-0.078	-0.310	-0.162
V	0.631	-0.053	0.505	0.340	-0.046	0.248	-0.117	0.377	-0.089

Table 6. Value of five canonical root and their contribution expressed as per cent of the total variation

Root	Value	Contribution (%)
$ë_1$	2.334	25.93
$ë_2$	1.360	15.11
$ë_3$	1.169	12.99
$ë_4$	0.997	11.08
$ë_5$	0.944	10.49
Total	6.804	75.60
Sum of all canonical root	9.000	-
Residual	2.196	24.40

Table 7. Cluster means for nine characters in maize

Cluster	Days to 50% tasseling	Days to 50% silking	Days to Maturity	Plant Height (cm)	Cob Length (cm)	Cob Girth (cm)	Number of grains cob^{-1}	100 grains weight (g)	Grain yield $plant^{-1}$ (g)
I	54.46	57.72	86.12	149.32	13.30	10.74	280.79	18.68	51.44
II	52.67	56.33	86.00	136.87	11.98	10.35	202.93	17.31	27.49
III	54.00	57.00	88.67	115.80	14.15	11.32	332.27	20.99	57.85
IV	52.33	56.67	86.33	148.00	13.06	11.64	222.73	19.19	40.85
V	57.33	60.33	88.00	138.73	14.33	9.31	186.20	18.05	31.75
VI	55.00	58.33	87.33	168.40	16.98	12.44	403.90	19.11	77.11
VII	59.00	62.33	85.67	156.67	13.61	10.73	240.00	19.87	46.03
VIII	56.00	59.33	87.67	177.67	17.42	11.72	367.20	20.02	73.63
IX	55.93	59.07	87.33	161.93	13.71	10.80	309.11	15.48	49.02
X	52.67	55.67	82.33	152.87	14.04	9.83	258.07	15.29	35.63
XI	50.67	54.33	82.67	161.27	13.09	11.74	301.67	19.29	56.79
XII	55.67	58.67	82.67	182.13	16.87	12.87	341.70	21.26	69.63
XIII	51.00	54.33	89.33	131.13	13.44	10.52	296.50	18.49	55.16
XIV	55.33	58.33	87.67	109.53	9.53	9.69	253.60	15.76	34.56
XV	56.67	60.33	86.67	116.27	11.63	11.96	304.80	19.16	55.85
XVI	55.67	57.67	85.33	148.33	8.98	9.73	234.87	17.57	37.48
XVII	51.33	56.33	89.00	133.27	13.86	9.37	287.67	18.09	41.69
XVIII	54.33	57.00	82.67	162.40	14.61	12.82	370.60	16.83	47.54
XIX	55.00	57.67	83.00	144.60	17.07	12.33	414.30	20.03	89.69
XX	57.67	60.33	84.33	146.60	15.50	9.06	316.40	12.97	38.77
S. D.	**2.29**	**2.06**	**2.29**	**19.70**	**2.27**	**1.21**	**63.61**	**2.09**	**16.47**
Variance	**5.24**	**4.23**	**5.26**	**387.97**	**5.17**	**1.47**	**4045.73**	**4.37**	**271.13**

Table 8. Selection of cluster combinations, potential parents and cross combination on the basis of genetic diversity

Sr.No.	Cluster combination	Average inter-cluster distance	Cross Combination	Traits
1	IV × XX	28.41	52202 ×52250	Number of grains cob^{-1}
2	X × XX	26.12	52623 × 52250	Cob length
3	II × XIX	25.72	52025 × 52603	Grain yield plant^{-1}
4	XV × XX	25.56	52201 × 52250	Number of grains cob^{-1}
5	V × XIX	25.06	52014 × 52603	Grain yield plant^{-1}
6	III × XX	23.48	52291 × 52250	100 grain weight
7	IV × XIX	23.26	52202 × 52603	Grain yield plant^{-1}
8	XVII × XIX	23.24	52087 × 52603	Grain yield plant^{-1}
9	XII × XX	22.52	PKVM-Shatak × 52250	Cob girth
10	XIX × XX	22.06	52603 × 52250	Cob length
11	XVI × XIX	21.51	52115 × 52603	Grain yield plant^{-1}
12	XI × XX	21.30	52196 × 52250	Cob length
13	XIV × XIX	20.72	52020 × 52603	Grain yield plant^{-1}
14	II × XX	20.31	52025 × 52250	Cob girth
15	VII × XIX	20.00	52140 × 52603	Grain yield plant^{-1}
16	V × XVIII	19.82	52014 × 52234	Number of grains cob^{-1}
17	V × XI	19.31	52014 × 52196	Cob girth
18	XVII × XX	18.62	52087 × 52250	Number of grains cob^{-1}
19	VIII × XIV	18.39	52327 × 52020	Cob length
20	VI × XX	18.35	52285 × 52250	Grain yield plant^{-1}
21	XII × XIV	18.34	PKVM-Shatak × 52020	100 grain weight
22	XII × XVII	18.24	PKVM-Shatak × 52087	Cob girth
23	II × VIII	18.19	52025 × 52327	Cob length
24	XVIII × XX	18.14	52234 × 52250	Number of grains cob^{-1}
25	X × XIX	18.09	52623 × 52603	Grain yield plant^{-1}
26	V × VI	17.89	52014 × 52285	Grain yield plant^{-1}
27	XVI × XX	17.58	52115 × 52250	100 grain weight
28	III × VI	17.52	52291 × 52285	Grain yield plant^{-1}
29	VII × XIII	17.50	52140 × 52040	Number of grains cob^{-1}
30	VI × XVI	16.60	52285 × 52115	Number of grains cob^{-1}
31	IX × XIX	16.56	52180 52497 52552 x 52603 52347 52045	Grain yield plant^{-1}
32	I × XX	16.35	52196 52597 52353 52095 x 52250 52081 52065 52219 52219	Number of grains cob^{-1}
33	VIII × XX	16.22	52327 × 52250	Cob length
34	XVIII × XIX	16.22	52234 × 52603	Number of grains cob^{-1}
35	V × XV	16.22	52014 × 52201	100 grain weight
36	XVI × XVII	16.16	52115 × 52087	Cob girth
37	XVII × XVIII	16.06	52087 × 52234	Number of grains cob^{-1}
38	VIII × XVI	16.04	52327 × 52115	Cob girth
39	XIII × XX	15.86	52040 × 52250	Number of grains cob^{-1}
40	X × XV	15.84	52623 × 52201	Grain yield plant^{-1}

41	VI × XIV	15.57	52285 × 52020	Grain yield plant^{-1}
42	IV × VIII	15.56	52202 × 52327	Cob length
43	VII × XVIII	15.03	52140 × 52234	Number of grains cob^{-1}
44	VII × XVII	14.92	52140 × 52087	100 grain weight
45	VI × X	14.90	52285 × 52623	Cob girth
46	VIII × X	14.87	52327 × 52623	Grain yield plant^{-1}
47	V × XIII	14.83	52014 × 52040	Grain yield plant^{-1}
48	VII × XI	14.82	52140 × 52196	Cob girth
49	VIII × XVIII	14.69	52327 × 52234	Number of grains cob^{-1}
50	VIII × XV	14.56	52327 × 52201	Grain yield plant^{-1}
51	II × XII	14.47	52025 × PKVM-Shatak	Cob girth
52	V × XII	14.44	52014 × PKVM-Shatak	Cob girth
53	XII × XIII	14.25	PKVM-Shatak × 52040	Cob girth
54	IV × VI	14.20	52202 × 52285	Number of grains cob^{-1}
55	XV × XIX	14.03	52201 × 52603	Grain yield plant^{-1}
56	VI × VII	13.79	52285 × 52140	Cob length
57	XIII × XIX	13.68	52040 × 52603	Grain yield plant^{-1}
58	XI × XIX	13.67	52196 × 52603	Grain yield plant^{-1}
59	III × X	13.59	52291 × 52623	Cob girth
60	I × XIX	13.57	52196 52597 52353 52095 52081 52065 52219 52263 x 52603	Grain yield plant^{-1}
61	VIII × XI	13.56	52327 × 52196	100 grain weight
62	VIII × XVII	13.27	52327 × 52087	Cob girth
63	VI × XVII	12.92	52285 × 52087	Number of grains cob^{-1}
64	III × V	12.84	52291 × 52014	Cob girth
65	IV × V	12.81	52202 × 52014	Number of grains cob^{-1}
66	XIII × XVI	12.65	52040 × 52115	Number of grains cob^{-1}
67	VII × XIV	12.51	52140 × 52020	Grain yield plant^{-1}
68	IX × IV	12.51	52180 52497 52552 52347 52045 x 52202	Number of grains cob^{-1}
69	XV × XVII	12.50	52201 × 52087	Grain yield plant^{-1}
70	V × VIII	12.48	52014 × 52327	Cob girth
71	XIII × XVIII	12.40	52040 × 52234	Number of grains cob^{-1}
72	III × VII	12.27	52291 × 52140	Cob length
73	VII × X	12.21	52140 × 52623	Grain yield plant^{-1}
74	X × XII	12.19	52623 × PKVM-Shatak	Cob girth
75	IX × XI	12.18	52180 52497 52552 52347 52045 × 52196	Number of grains cob^{-1}
76	IX × XV	12.07	52180 52497 52552 52347 52045 × 52201	Number of grains cob^{-1}
77	IX × III	11.99	52180 52497 52552 52347 52045 × 52291	Grain yield plant^{-1}

78	XII × XV	11.81	PKVM-Shatak × 52201	Cob girth
79	III × XVI	11.74	52291 × 52115	Grain yield plant^{-1}
80	IX × XII	11.60	52180 52497 52552 52347 52045 × PKVM-Shatak	Grain yield plant^{-1}
81	V × XX	11.57	552014 × 52250	Grain yield plant^{-1}
82	XII × XVI	11.51	PKVM-Shatak × 52115	Cob girth
83	IV × XII	11.50	52202 × PKVM-Shatak	Cob girth
84	IX × V	11.39	52180 52497 52552 52347 52045 x 52014	Number of grains cob^{-1}
85	V × XIV	11.31	52014 × 52020	Grain yield plant^{-1}
86	IV × VII	11.25	52202 × 52140	Cob girth
87	V × XVII	11.18	52014 × 52087	Number of grains cob^{-1}
88	III × XVIII	11.15	52291 × 52234	Number of grains cob^{-1}
89	III × XIX	11.13	52291 × 52603	Grain yield plant^{-1}
90	XI × XVII	11.13	52196 × 52087	100 grain weight
91	VII × XV	10.92	52140 × 52201	Cob girth
92	VI × XV	10.90	52285 × 52201	Number of grains cob^{-1}
93	IX × XVII	10.89	52180 52497 52552 52347 52045 x 52087	Grain yield plant^{-1}
94	VIII × XIII	10.85	52327 × 52040	Cob length
95	IV × X	10.84	52202 × 52623	Cob length
96	IX × II	10.83	52180 52497 52552 52347 52045 x 52025	100 grain weight
97	X × XIII	10.81	52623 × 52040	Number of grains cob^{-1}
98	IX × VII	10.81	52180 52497 52552 52347 52045 x 52140	Grain yield plant^{-1}
99	XI × XIV	10.73	52196 × 52020	Number of grains cob^{-1}
100	IX × XX	10.72	52180 52497 52552 52347 52045 x 52250	Grain yield plant^{-1}

the present study all possible combinations beyond the mean inter-cluster distance (D = 10.70) formed from different clusters have been arranged in descending order of magnitude of genetic distance and promising hundred cluster combinations are presented in table 8. Other practical considerations like grain yield plant^{-1}, days to 50% tasseling, number of grains cob^{-1}, plant height and cob length were also taken into account while choosing the genotypes from the selected cluster combinations, which can be crossed in diallel fashion to obtain superior cross combinations.

Based on the above mentioned criteria 28 genotypes *viz.,* 52202, 52623, 52025, 52201, 52014, 52291, 52087, 52115, 52196, 52020, 52140, 52327, 52285, 52180, 52497, 52552, 52347, 52045, 52597, 52353, 52095, 52081, 52065, 52219, 52263, 52250, 52603 and 52040 were identified to be used as parents for hybridization programme, which were suggested to be crossed in diallel fashion to obtain superior cross combinations. PKVM-Shatak as it is in separate cluster and distant from other clusters can be further improved to produce new hybrid by crossing with parents 52250, 52020, 52087, 52025, 52014, 52040, 52623, 52201, 52180, 52552, 52115 and 52202.

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