Research Paper

GENOTYPE CLUSTERING OF MAIZE (*Zea mays* L.) GERMPLASM USING MAHALANOBIS D² STATISTIC

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Abstract

The data collected from 45 genotypes of maize on eleven biometric characters *viz.,* days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, 100-seed weight (g) and grain yield per plant (g) were used to study genetic divergence. The 45 genotypes of maize were grouped into fifteen clusters with cluster II as the largest having 20 genotypes indicating genetic similarity among them. The highest inter-cluster distance of 13.33 was observed between cluster VIII and cluster XV suggested more variability in genetic makeup of the genotypes included in these clusters. Out of 11 characters studied, number of kernels per row, test weight, days to 50% tasseling and yield per plant contributed high for genetic divergence. The intra cluster distance in clusters from III to XV is 0.00 indicating that these are solitary clusters with single genotypes in them.
Key words: Germplasm, Mahalanobis D², genetic variability, maize.

INTRODUCTION

Maize (*Zea mays* L.) is an important cereal crop, popularly known as Queen of cereals because of its highest yield potential and wider adaptability. In India, maize is the third important cereal crop after rice and wheat. It is mainly grown in Uttar Pradesh, Bihar, Rajasthan, Madhya Pradesh, Punjab, Karnataka and Andhra Pradesh. In India, maize ranks third next to rice and wheat, with an area of 8.67 million hectares, production of 22.26 million tonnes and productivity of 2567 kg/ha. In Andhra Pradesh, maize occupies an area of 0.90 million hectares with a production of 4.80 million tonnes at an average productivity of 4995 kg/ha (CMIE, 2013).
Maize being a C_4 plant, is physiologically more efficient, has higher grain yield and wider adaptation over a wide range of environmental conditions. It is widely grown in India suggesting its wide adaptability. The crop has assumed a place of prominence in Indian agriculture owing to its varied uses.
The crop is grown under diverse agro production situations, across the climatic and geographic boundaries which necessitated the development of more productive

varieties of diverse origin. Plant breeders are always interested in assessing genetic divergence among the varieties or advanced breeding lines available with them so as to utilize in direct breeding programme because genetically diverse parents are likely to produce high heterotic effects and the distinctly related parents within species, when utilized in cross breeding programme, are likely to produce wide spectrum of variability (Arunachalam, 1981). D² statistic developed by Mahalanobis (1936) was used to measure genetic divergence and to classify the genetic stock into distinct groups.

MATERIAL AND METHODS

The present investigation was carried out during *kharif,* 2016 at Agricultural Research Station Madhira, Khammam district using 45 maize genotypes collected from Maize Research Institute, Rajendranagar. Data was collected on yield and yield contributing characters and was subjected to analysis of variance. Genetic divergence was computed by multivariate analysis using Mahalanobis D² technique and the genotypes were grouped into clusters following Euclidean method as described by Rao, (1952).

RESULTS AND DISCUSSION

Forty five genotypes were evaluated during *kharif,* 2016 and the data was subjected to D² analysis. The analysis of variance revealed highly significant differences among the genotypes for all the eleven characters indicating the existence of genetic variability among the experimental material. The 45 genotypes of maize were grouped into fifteen clusters, out of which cluster II was the largest having 20 genotypes indicating genetic similarity among them. Clusters III to XV are solitary clusters containing only one genotype indicating the uniqueness of the genotypes included in those clusters when compared to other genotypes included in the study. Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographical distribution. The genotypes within the same clusters were originated from different geographical regions of the world, which indicated the geographical distribution and genetic divergence did not follow the same trend which might be due to continuous exchange of genetic material among the countries of the world.

Average intra and inter cluster distances

The intra and inter-cluster values among the eleven clusters are presented in Table 1. The intra-cluster distances were lower than the inter-cluster distances. Thus the genotypes included within a cluster had less diversity among them. The maximum intra-cluster distance (3.63) was observed in cluster I followed by cluster II (3.32). The intra cluster distance from cluster III to cluster XV is 0.00 indicating that these are solitary clusters with single genotype in them indicating the uniqueness of those genotypes when compared to other genotypes included in the study.

The highest inter-cluster distance (13.33) was observed between cluster VIII and cluster XV followed by cluster VII and XV (12.86), cluster VIII and XIV (12.29) and cluster IV and XV (12.24), suggesting more variability in genetic makeup of the genotypes included in these clusters IV, VII, VIII, XIV and XV. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. The lowest inter cluster distance of 2.50 was observed between clusters IV and V followed by 2.81 between cluster VII and VIII indicating genetic closeness of the genotypes

included in these clusters. In this context, genotypes from cluster III, V, VII, VIII and IX exhibited highest cluster mean values were selected as parents in hybridization programme for yield improvement. These findings are in conformity with the findings of Alam and Alam, (2009), Marker and Krupakar (2009), Ganesan *et al.*(2010), Azad *et al.* (2012), Uday Kumar *et al.* (2013), Zaman and Alam (2013), Mehrnaz Tanavar *et al.* (2014), Praveen Kumar *et al.* (2014) and Seshu *et al.* (2014).

Cluster means of characters

The cluster means of eleven characters are presented in Table 3 and greatest range of mean values among the cluster was recorded for different traits. Cluster VIII recorded highest mean values for plant height (212.98), ear height (124.72) and grain yield per plant (146.52) followed by cluster IX and cluster III for grain yield, 154.34 and 142.06, respectively. Cluster XI exhibited highest cluster mean value for days to 50% tasselling (60.33) and days to 50% silking (63.00) indicating greater flowering period for the genotype included in that cluster. Genotype in cluster V recorded highest value for test weight (30.86) while the least was recorded by cluster XV (16.77). The genotypes with average grain yield are included in cluster I as indicated by average cluster mean value of 116.57 for that trait.

Based on cluster means, wide range of genetic variation for grain yield and its components was reported in maize. Therefore, it is suggested that lines from most diverse clusters may be used as parents in hybridization programme to develop high yielding hybrids or varieties. It has been well established that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad spectrum of variability in segregating generations. It has also been observed that the most productive hybrids may come from high yielding parents with high genetic diversity.

Percent contribution of character towards divergence in 45 maize genotypes

The contribution of each character towards total genetic diversity is presented in Table 4. Out of 11 characters studied, number of kernels per row (22.56%), 100 kernel weight (20.19%), days to 50% tasseling (11.84%) and grain yield per plant (10.30%) contributed high for divergence (More *et al.* 2006), whereas, days to 50% silking (1.31%), maturity (3.92%), ear girth (3.82%) and ear length (3.96%) contributed low for divergence. Based on percent contribution towards genetic divergence, emphasis can be made on selection of those characters with more contribution towards genetic divergence for creating variability in the population. Further parents with characters have more genetic diversity can be utilized in crossing programmes for creation of variability and development of transgressive segregants in the population.

Table 1: Average intra and inter cluster distances (D² values) for fifteen clusters of maize germplasm

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV
Cluster I	3.32	6.93	4.21	4.09	4.20	4.03	4.58	5.50	4.29	4.41	7.13	5.17	5.27	8.66	9.80
Cluster II	6.93	3.63	8.66	8.90	7.86	5.59	9.62	10.19	8.83	6.84	4.76	6.04	5.93	5.25	5.08
Cluster III	4.21	8.66	0.00	4.64	5.26	5.40	3.60	4.44	4.05	3.83	8.47	6.80	6.72	10.55	11.57
Cluster IV	4.09	8.90	4.64	0.00	2.50	5.75	3.61	5.08	3.12	5.31	8.96	5.83	6.54	10.66	12.24
Cluster V	4.20	7.86	5.26	2.50	0.00	5.10	4.47	5.47	4.12	5.12	8.17	5.87	5.65	10.11	11.36
Cluster VI	4.03	5.59	5.40	5.75	5.10	0.00	5.77	6.38	4.85	4.47	5.34	5.90	5.43	7.89	8.19
Cluster VII	4.58	9.62	3.60	3.61	4.47	5.77	0.00	2.81	3.47	4.61	9.30	7.99	6.90	11.87	12.86
Cluster VIII	5.50	10.19	4.44	5.08	5.47	6.38	2.81	0.00	5.10	4.83	9.18	8.66	6.85	12.29	13.33
Cluster IX	4.29	8.83	4.05	3.12	4.12	4.85	3.47	5.10	0.00	4.96	8.91	6.93	6.60	11.10	11.89
Cluster X	4.41	6.84	3.83	5.31	5.12	4.47	4.61	4.83	4.96	0.00	5.99	6.10	5.67	9.45	10.25
Cluster XI	7.13	4.76	8.47	8.96	8.17	5.34	9.30	9.18	8.91	5.99	0.00	6.13	6.45	6.27	6.40
Cluster XII	5.17	6.04	6.80	5.83	5.87	5.90	7.99	8.66	6.93	6.10	6.13	0.00	6.06	6.51	8.39
Cluster XIII	5.27	5.93	6.72	6.54	5.65	5.43	6.90	6.85	6.60	5.67	6.45	6.06	0.00	7.95	8.13
Cluster XIV	8.66	5.25	10.55	10.66	10.11	7.89	11.87	12.29	11.10	9.45	6.27	6.51	7.95	0.00	4.32
Cluster XV	9.80	5.08	11.57	12.24	11.36	8.19	12.86	13.33	11.89	10.25	6.40	8.39	8.13	4.32	0.00

Table 2: Eigene values, proportion of the total variance represented by first three principal components, cumulative percent variance and component loading of different characters in maize germplasm

Canonical roots analysis (PCA)			
	PC1	**PC2**	**PC3**
Eigene value (root)	**577.06230**	**99.36088**	**63.91712**
Percent Var. Exp.	**59.34792**	**10.21876**	**6.57355**
Cumulative variance explained	**59.34792**	**69.56668**	**76.14023**
Days to 50% tasseling	0.25191	0.63961	0.12071
Days to 50% silking	0.14143	0.30720	0.12173
Days to maturity	-0.03216	-0.04343	-0.15060
Plant height (cm)	-0.30959	0.33680	0.23648
Ear height (cm)	-0.19254	0.48826	0.02663
Ear length (cm)	-0.17071	-0.04129	-0.01910
Ear girth (cm)	-0.26519	0.06083	-0.00930
Number of kernel rows	-0.16967	-0.01817	-0.39820
Number of kernels per row	-0.51899	0.28531	-0.42236
Test weight (g)	-0.43532	-0.16479	0.73448
Seed yield / plant (g)	-0.44213	-0.16885	-0.12013

Table 3: Cluster means of forty five germplasm accessions for eleven quantitative traits in maize

	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear lenght (cm)	Ear girth (cm)	Number of kernel rows	Number of kernels per row	Test weight (g)	Seed yield / plant (g)
Cluster I	54.00	56.45	91.10	166.07	76.21	16.41	14.55	14.91	33.25	26.15	116.57
Cluster II	59.06	61.92	91.81	139.10	60.88	12.83	12.49	12.57	24.56	22.36	65.18
Cluster III	55.33	58.00	91.33	169.25	78.64	17.29	14.71	13.21	43.75	27.54	142.06
Cluster IV	52.67	56.00	88.33	186.92	77.61	17.46	15.17	15.25	32.08	30.64	136.54
Cluster V	54.67	58.33	92.00	203.19	8.43	13.88	14.71	14.50	29.42	30.86	109.56
Cluster VI	58.67	61.00	92.00	182.02	70.86	13.71	14.37	16.29	32.42	23.48	105.28
Cluster VII	54.33	58.00	91.33	207.93	108.30	20.53	14.52	15.00	37.16	28.98	146.56
Cluster VIII	55.67	57.00	89.33	212.98	124.72	17.04	14.46	14.50	38.72	27.86	131.47
Cluster IX	58.00	59.67	91.00	177.95	73.28	18.78	15.74	16.17	36.33	30.35	154.34
Cluster X	59.00	61.33	88.33	186.53	94.05	18.36	14.61	12.00	36.75	26.59	106.99
Cluster XI	60.33	63.00	85.67	170.72	83.47	11.20	13.45	12.35	24.20	18.31	80.67
Cluster XII	51.67	55.33	85.00	116.83	50.38	13.54	15.81	13.67	27.08	24.45	96.33
Cluster XIII	58.00	59.00	92.67	125.47	100.95	12.63	12.91	13.08	25.58	27.11	92.66
Cluster XIV	53.67	56.00	84.67	89.20	33.33	9.57	9.78	13.17	24.92	18.47	56.35
Cluster XV	59.33	62.00	93.00	81.93	45.78	9.34	11.21	13.33	21.25	16.77	60.25

Table 4: Percent contribution of different characters towards genetic divergence

Source	Times ranked 1st	Percent contribution
Days to 50% tasseling	254	11.84%
Days to 50% silking	28	1.31%
Days to maturity	84	3.92%
Plant height (cm)	152	7.09%
Ear height (cm)	178	8.30%
Ear length (cm)	85	3.96%
Ear girth (cm)	82	3.82%
Number of kernal rows	144	6.71%
Number of kernals per row	484	22.56%
Test weight (g)	433	20.19%
Yield per plant	221	10.30%
Tocher cut-off value =16.23		

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