Biological Forum – An International Journal **14(2a): 261-265(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Assessment of Genetic Diversity in 62 Maize Genotypes for Yield and Yield Accredited Traits

Anusha G.[1*], Bhadru D.[2], Vanisri S.[3], Usha Rani G.[4], Mallaiah B.[5] and Sridhar V.[6]
[1]Department of Genetics and Plant Breeding, College of Agriculture,
PJTSAU, Rajendranagar, Hyderabad (Telangana), India
[2]Senior Scientist, Plant Breeding, Maize Research Center,
ARI, PJTSAU, Rajendranagar, Hyderabad (Telangana), India.
[3]Professor, Molecular Biology and Biotechnology, Institute of Biotechnology,
PJTSAU, Rajendranagar, Hyderabad (Telangana), India.
[4]Scientist, Plant Breeding, Agricultural Research Station,
PJTSAU, Karimnagar (Telangana), India.
[5]Senior Scientist, Plant Pathology, Agricultural Research Institute,
PJTSAU, Rajendranagar, Hyderabad, (Telangana), India.
[6]Assistant Professor, Genetics and Plant Breeding, Agricultural Polytechnic,
PJTSAU Kampasagar (Telangana), India.

(Corresponding author: Anusha G.)*
(Received 03 May 2022, Accepted 23 June, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Genetic diversity is an essential element for the development of new inbred lines of maize because it has pivotal importance for hybrid combinations in maize breeding. The present experiment was carried out to determine the genetic diversity of 62 maize genotypes by using D^2 cluster analysis. Analysis of variance revealed the existence of significant variability among the genotypes. The sixty-two maize genotypes were grouped into five clusters *i.e.*, I, II, III which comprised 28, 23, and 9 genotypes respectively. Whereas cluster IV and cluster V are solitary clusters. Cluster I (312.76) exhibited the highest intra-cluster distance. The highest inter-cluster distance of 9470.22 was found between cluster III (MGC-13, GP-111, MGC-68, GP-215, PFSR-151, BML-13, MGC-39, MGC-90 and MGC-109) and cluster V (BML-30F). The genotypes included in clusters III and V exhibited high genetic diversity along with high per se performance, suggesting the utilization of these genotypes for future maize improvement programs.

Keywords: Maize, Genetic diversity, Variability, Cluster analysis.

INTRODUCTION

Maize (*Zea mays* L.) is the third most important cereal crop after wheat and rice in the world, contributing to food security and income in tropical and sub-tropical environments. It is a versatile crop grown over a range of agro-climatic zones due to its wider adaptability. Globally Maize occupies an area of 193.7 million hectares with a production of 1147.7 million tonnes and productivity of 5.75 tonnes per hectare (FAO STAT 2020). In India maize is cultivated in an area of 9.89million hectares with a production of 31.65 million tonnes and productivity of 31.99quintals per hectare (INDIA STAT, 2020-2021). The demand for maize global production as a source of food, forage, oil, and biofuel is increasing for the ever-increasing world human population. However, the number of maize landraces decreases in farmers' fields over time, threatening the availability of genetic resources for the future. The assessment of diversity among the maize germplasm is important for identifying parental lines for successful breeding programs and hybrid development (Mengistu, 2021; Soliman *et al.*, 2021). Genetic diversity may arise due to geographical separation or genetical barriers to crossability or due to different patterns of evolution. Thus, the study of diversity in inbreds of different origins may either complement or highlight new features of variation in the maize breeding program. The significance of genetically diverse genotypes as a source of obtaining transgressive segregants with desirable combinations has been reported by several researchers (Singh and Narayanan 2013; Hassan *et al.*, 2018).

As a cross-pollinated crop, maize has maintained heterozygous balance under open population and exhibits heterosis in recombinants, particularly when inbreds differing for many genes affecting yield or some other characters of importance are used as parents. Inbred lines derived from the diverse genetic base were found to be more productive than crosses of inbred lines derived from closely related stocks (Moll *et al.*, 1965; Vasal, 1998; Uday Kumar *et al.*, 2013). To develop high-yielding hybrids in maize, inbred lines need to be evaluated for their genetic diversity which is important for planning an effective hybrid breeding program as genetically diverse parents are known to produce high heterotic effects (Matin *et al.*, 2017). Further, the study of genetic divergence in the maize inbreds will help to ascertain the real potential value of the genotype.

Characterization of morphological variability allows the breeder to identify accessions with desirable characters and avoid duplication of accessions in available germplasm collection and their utilization in varietal improvement programs. Various biometrical techniques dealing with the genetic analysis of important characteristics guided the plant breeders in identifying the best genotypes for diverse environments. The estimation of genetic diversity through biometrical procedures such as Mahalanobis's D^2 statistics has made it possible to select genetically diverse parents for a breeding program. It also measures the degree of divergence and determines the relative proportion of each of the component characters to the total divergence.

Therefore, in view of the above context, the present investigation was undertaken to assess the extent of genetic diversity in 62 maize inbred lines which will help to select prospective parents to develop superior hybrids

MATERIAL AND METHODS

The present research work was undertaken at Maize Research Center (MRC), Rajendranagar, Hyderabad (27.2046°N, 77.4977°E) during *Rabi*, 2020-2021. A total of 62 maize genotypes (Table 1) were evaluated for yield and yield traits in a Randomized Block Design with two replications. Each entry was sown in two rows of 4min length and followed a spacing of 0.6m × 0.2m between row to row and plant to plant respectively. The standard agronomic management practices and plant protection measures were followed throughout the crop growing period to maintain proper plant stand. The observations for various characteristics like days to maturity, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), kernel rows per ear, number of kernels per row, and 100-seed weight (g) were recorded on five randomly selected plants from each plot. Whereas, the characters *i.e*., days to 50 percent tasseling, days to 50 percent silking, and grain yield per plant were recorded on a plot basis. Data were subjected to analysis of Mahalanobis' D^2-statistics (Mahalanobis, 1936), and intra-cluster and inter-cluster distance, cluster mean and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985). Clustering of genotypes was done by using Tocher's method (Rao, 1952). The cluster distance was estimated by the formula given by Singh and Chaudhary (1977).

Table 1: List of 62 maize genotypes used in the present study.

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	MGC-9	21.	MGC-15	41.	GP-170	61.	LM-13
2.	MGC-30	22.	MGC-137	42.	GP-35	62.	LM-14
3.	MGC-32	23.	MGC-144	43.	GP-16		
4.	MGC-40	24.	MGC-72	44.	GP-88		
5.	MGC-47	25.	MGC-81	45.	GP-99		
6.	MGC-52	26.	MGC-82	46.	GP-27		
7.	MGC-68	27.	PFSR-90	47.	GP-111		
8.	MGC-46	28.	PFSR-51	48.	GP-221		
9.	MGC-49	29.	PFSR-150	49.	GP-265		
10.	MGC-63	30.	PFSR-151	50.	BML-30F		
11.	MGC-13	31.	PFSR-46	51.	BML-11		
12.	MGC-93	32.	PFSR-275	52.	BML-51		
13.	MGC 90	33.	PFSR-256	53.	BML-32-2		
14.	MGC-125	34.	PFSR-129	54.	BML-20		
15.	MGC-39	35.	PFSR-157	55.	BML-10		
16.	MGC-130	36.	PFSR-32	56.	BML-2		
17.	MGC-109	37.	PFSR-49	57.	BML-13		
18.	MGC-103	38.	PFSR-95	58.	Z-63-45		
19.	MGC-114	39.	PFSR-68	59.	CM-105		
20.	MGC-161	40.	GP-215	60.	5125		

RESULTS AND DISCUSSION

Cluster analysis. The analysis of variance revealed significant differences among the 62 inbred lines for all the eleven characters, indicating the existence of sufficient genetic variability among the tested genotypes (Table 2). These findings are in accordance with those reported by Matin *et al.*, (2017); Mounika *et al.* (2018). The sixty-two maize genotypes were grouped into 5 clusters based on various agro-morphological characters (Table 3 and Fig. 1). Cluster I comprised 28 genotypes, cluster II consisted of 23 genotypes, clusters III included 9 genotypes, and the remaining two clusters IV and V are the solitary clusters having only one inbred line indicating the uniqueness of the genotypes included in those clusters when compared to the other genotypes in the present study. Similar results pertaining to a grouping of maize germplasm were reported by Ivy *et al*. (2007); Talukder *et al.* (2012); Kumari *et al*. (2017).

Average intra and inter-cluster distance. The highest intra-cluster distance was observed in cluster I (312.76) followed by cluster III (268.68) and cluster II (261.91). The intra-cluster distance was not observed in clusters IV and V as these clusters had only one genotype each (Table 4 and Fig. 2). These results are in accordance with the findings reported by Singh *et al.* (2005); Patil *et al.* (2017). The highest intra-cluster distance indicated the presence of significant genetic diversity between the genotypes which were grouped together in those clusters. Hence, there is a great possibility for the exchange of genes among genotypes within these clusters. With regard to inter-cluster distance, cluster III and cluster V were found to be most diverse with each other as the distance between them was9470.22, which denotes that the crossing between these genotypes would provide good segregation for selection. The lowest inter-cluster distance was observed between clusters IV and V (461.48) which indicates that the genotypes included in those clusters were not very distant, but could not be grouped together based on these traits.

Cluster means showed a wide range of variation for 11 characters (Table 5). Cluster I exhibited the highest mean value for plant height and ear height, cluster II had the highest mean value for days to 50 percent silking and cluster III showed the highest mean value for days to 50 percent tasseling and days to maturity. Cluster IV had the highest mean value for ear length and the number of kernels rows per ear and cluster V showed the highest mean value for ear girth, the number of kernels per row, 100 seed weight, and grain yield (kg/ha). Cluster IV and V contained one genotype each, which exhibited the highest mean value for most of the yield-related traits. Thus these genotypes can be further used to improve the grain yield in future maize breeding programs. Most of the studies have reported that cluster analysis is found to be effective to classify the genotypes under different environmental conditions and helpful for the selection of superior parents for hybrid breeding programs (Al-Naggar *et al*., 2020; Bhatti *et al.*, 2020 ; Khalid *et al*., 2020).

Table 2: Analysis of variance for yield and yield attributing traits in 62 maize genotypes.

Character /Source of variation	Mean sum of squares of		
	Replications	Genotypes	Error
d.f.	1	61	61
Days to 50 per cent tasseling	2.42	14.46 *	0.74
Days to 50 per cent silking	2.55	16.45*	0.97
Days to maturity	0.86	37.75**	1.92
Plant height (cm)	2.44	774.08**	3.38
Ear height (cm)	14.23	122.27**	4.05
Ear length (cm)	0.07	1.65**	0.24
Ear girth (cm)	0.04	1.49**	0.32
Number of kernels rows per ear	0.04	1.12**	0.16
Number of kernels per row	0.14	7.60**	0.53
100 seed weight (g)	0.01	16.77**	0.46
Grain yield (kg/ha)	19153.54	505466.71**	13770.05

*and** indicates significance at 5% and 1 % level respectively, df= degrees of freedom

Table 3: Clustering of genotypes based on diversity of 62 Maize genotypes.

Cluster No.	No. of inbreds	Names of the inbreds
I	28	MGC-30, MGC-137, MGC-15, LM-13, MGC-82, MGC-103, MGC-52, 5125, MGC-47, MGC-9, BML-2, CM-105, Z-63-45, MGC-40, BML-10, MGC-161, BML-11, MGC-114, MGC-130, PFSR-68, PFSR-49, GP-16, MGC-49, MGC-32, PFSR-256, BML-51, BML-20, PFSR-46
II	23	MGC-81, PFSR-51, GP-99, PFSR-129, PFSR-150, MGC-72, GP-265, GP-35, MGC-93, LM-14, PFSR-157, PFSR-275, GP-27, PFSR-32, PFSR-95, MGC-144, GP-88, BML-32-2, GP-170, GP-221, MGC-63, MGC-125, MGC-46
III	9	MGC-13, GP-111, MGC-68, GP-215, PFSR-151, BML-13, MGC-39, MGC-90, MGC-109
IV	1	PFSR-90
V	1	BML-30F

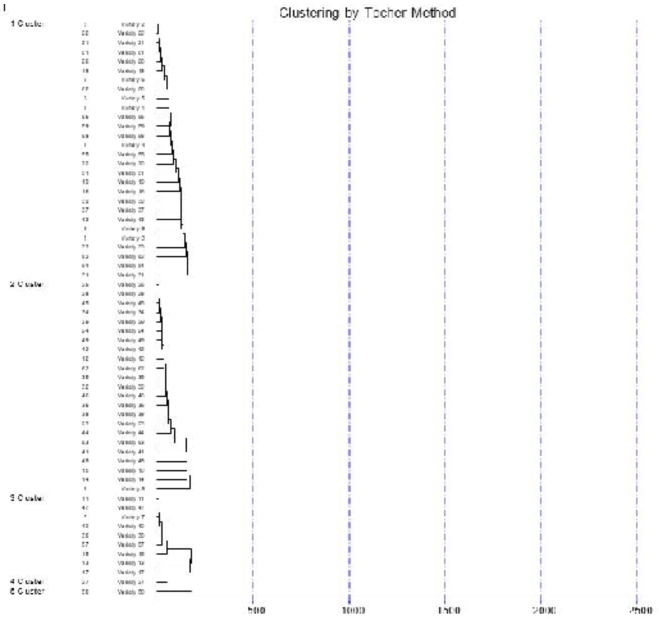

Fig. 1. Clustering pattern among 62 Parental lines of Maize (Tocher's method)

Table 4: Average intra and inter-cluster Euclidean^2 values among five clusters in 62 maize (*Zea mays* L.) inbreds.

Cluster No.	I	II	III	IV	V
I	312.76	1151.83	679.86	3407.00	6255.26
II		261.91	2591.94	894.12	2493.46
III			268.68	5897.78	9470.22
IV				0.00	461.48
V					0.00

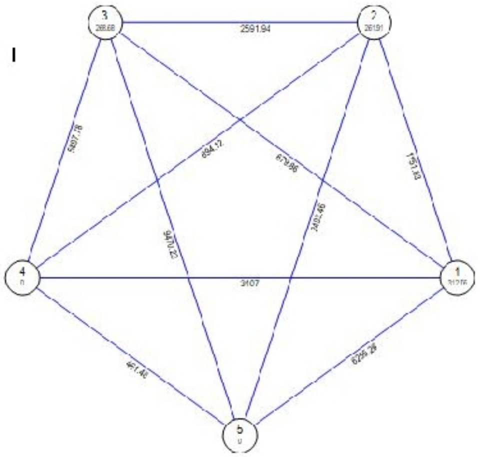

Fig. 2. Cluster diagram: Clusters and their interrelationships.

Table 5: Cluster means of eleven characters in 62 maize genotypes.

Clusters	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	No. of kernels rows per ear	No. of kernels per row	100 Seed weight (g)	Grain yield (kg/ha)
I	60.04	62.70	103.32	**152.00**	**59.00**	10.46	10.63	11.11	15.39	18.68	1910.14
II	60.57	**63.52**	104.91	132.98	51.74	11.33	11.50	11.59	17.70	22.87	2566.41
III	**60.83**	62.94	**105.33**	132.67	51.78	9.61	10.33	10.44	13.61	16.33	1470.28
IV	60.50	63.50	104.50	136.50	53.00	**13.10**	11.50	**12.50**	19.00	24.00	3228.00
V	59.00	60.50	101.50	116.00	48.18	13.00	**13.00**	12.00	**21.00**	**27.00**	**3693.50**

CONCLUSION

The results revealed the existence of highly significant differences among maize for grain yield and yield-related traits and 62 maize genotypes were classified into five groups based on the torcher method. The development of hybrids between identified divergent clusters III and V could yield heterotic hybrids. The genotype BML-30F was identified as high yielding and divergent genotype based on cluster analysis and per se performance.

FUTURE SCOPE

The above information on genetic diversity helps in the identification of heterotic patterns among diverse parents and the development of heterotic pools, which can be utilized to produce the best cross combination for one or multiple desirable traits.

Acknowledgment. I extend my sincere thanks to the Senior scientist (Dr.) D. Bhadru (major advisor) and my advisory committee members for giving me proper guidance throughout the course of my study. I also sincerely thank Professor Jayashankar Telangana State Agricultural University, Hyderabad for the academic and financial (stipend) support and Maize Research Center, Agricultural Research Institute, Rajendranagar for research support extended.

Conflict of Interest. None.

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How to cite this article: Anusha G., Bhadru D., Vanisri S., Usha Rani G., Mallaiah B. and Sridhar V. (2022). Assessment of Genetic Diversity in 62 Maize Genotypes for Yield and Yield Accredited Traits. *Biological Forum – An International Journal, 14*(2a): 261-265.