The Bioscan 11(3):2031-2035,2016(Supplement on Genetics and Plant Breeding) www.thebioscan.com
AN INTERNATIONAL QUARTERLY JOURNAL OF LIFE SCIENCES

STUDIES ON GENETIC DIVERSITY FOR GRAIN YIELD AND PHYSIOLOGICAL PARAMETERS IN MAIZE (*ZEA MAYS* L.)

REKHA[1]*, H. D. MOHANKUMAR[1], G. Y. LOKESH[2] AND NETRAVATI[1]
Department of Genetics and Plant Breeding,
[1]University of Agricultural and Horticultural Sciences, Shivamogga - 577 204
[2]University of Agricultural Sciences, Raichur - 584 104
e-mail: rekha.sl.92@gmail.com

KEYWORDS
Kharif
maize
superior hybrids
leaf area

Received on :
01.03.2016

Accepted on :
24.06.2016

***Corresponding author**

ABSTRACT
The present investigation was carried out to assess the nature and magnitude of genetic diversity among the 43 new inbred lines of maize during *kharif* 2014 using Mahalanobis D^2 statistic. The analysis of variance revealed significant differences among the genotypes for all twenty one characters. The inbred lines were partitioned into ten clusters based on D^2 analysis. The cluster I is having highest number of genotypes (16). Maximum inter cluster distance was observed between cluster VI and X (838.65) and the highest intra cluster distance was in cluster VI (176.93) hence the genotypes belonging to this cluster 18600, 18704, 18477 and 18707 these genetically diverse inbreed lines used for developing superior hybrids. The characters like cob weight (31.67 %), leaf area index (17.83 %) and days to 50 % brown husk maturity (12.85 %) contributed more towards divergence.

INTRODUCTION

Maize (*Zea mays* L.; 2n = 20) is the third most important cereal crop in India after rice and wheat. Maize is native to Central America (Mexico) and it is a tropical crop and has adapted to temperate environments with much higher productivity.

Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin display a greater heterosis than those between closely related strains. For example in maize, increased genetic distance between inbred lines resulted in a greater heterosis in their hybrids. However, the maximum heterosis generally occurs at an optimal or intermediate level of diversity.

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 method used to study the genetic divergence and it was first time developed by Mahalanobis in 1928 in the study of Anthropometry and Psychometry. Rao (1952) suggested the application of this technique in plant breeding. D^2 statistic is used as a multi varietal statistical tool for effective discrimination among various genotypes on the basis of genetic diversity (Murthy and Arunachalam, 1966).

Yield components are the primary objectives under study for crop improvement as because Grafius (1978) suggested that there may not be genes for yield per se but rather for the various components, the multiplicative interactions of which result in the artifact of yield.

Moll *et al*. (1962) reported that heterosis in maize appears to increase with increased genetic divergence of the parent population over a wide range of diversity. Alom *et al*. (2003) studied the genetic diversity among twenty five genotypes of maize. The genotypes were proposed into seven clusters based on Mahalanobis D^2 statistic. The use of D^2 statistics has been emphasized by many workers (Kage *et al*., 2012, Alam *et al*., 2013 and Lingaiah *et al*., 2013).

The choice of the most efficient breeding scheme for improving maize population is dependent upon the relative amount and type of genetic variability involved (Kumar *et al*., 2013). The pace and magnitude of genetic improvement generally depend on the amount of genetic diversity present in a population. Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different traits (Kumar *et al*., 2015).

Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in F1 hybrids and broad spectrum of variability in segregating generations (Johnson *et al*., 2015). Keeping this in view, the present study was conducted to estimate the diversity among 43 inbredlines for selection of diverse genotypes for utilization in future breeding programmes.

MATERIALS AND METHODS

The present field experiment was carried out at the College of Agriculture, Navile, Shivamogga during *kharif* 2014. The experiment was comprised of forty three inbreed lines of maize, obtained from Indian institute of maize research, Hyderabad.

All 43 inbreed lines were grown and experiment was irrigated throughout the growing season and cultural operations, fertilization and weed control was conducted as per package of practices. The experiment was replicated twice in a randomized complete block design. The observation was recorded for 21 quantitative characters. Leaf area at 40, 60 and 90 days interval (Montgomery, 1911), leaf area index (Sestak *et al.*, 1971), days to 50 % tasseling, days to 50 % silking, days to 50 % brown husk maturity, stem girth, internodal distance, plant height, cob height, total chlorophyll content was estimated by following the method described by Arnon (1949), specific leaf weight, cob length, cob girth, cob weight, number of kernels per row, number of rows per cob, grain yield per plant and hundred grain weight. Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse and Sukhatme (1967). Diversity analysis was done using Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software WINDOSTAT 9.2)

RESULTS AND DISCUSSION

The strategy of developing superior hybrids in maize depends on the genetic diversity present in the available inbreed lines. Measure of genetic divergence reveals the differences in gene frequencies. Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating populations by considering a set of characters together. In addition to estimation of variability, cognizance of the genetic diversity of the germplasm is necessary for effective choice of parents for hybridization. The analysis of variance carried out for the yield and its component characters among 43 inbreed lines was presented in Table 1. The results revealed that all the genotypes differed highly significant for all characters.

The knowledge of genetic diversity among the genotypes is essential for selecting parents for hybridization programme, especially in a cross pollinated crop like maize. Genetic diversity considered to be an important tool for realizing heterotic response in F_1 and a broad spectrum of variability in segregating generations.

The D^2 analysis carried out involving 43 inbreed lines for 21 characters revealed that altogether 10 clusters have been formed (Table 2), wherein cluster I had maximum number of sixteen genotypes, cluster II had twelve genotypes, cluster IV had five genotypes, cluster VI had four genotypes and remaining clusters III, IV,VII, VIII, IX and X were all monogenotypic. The grouping of genotypes into so many clusters suggested the presence of high degree of diversity in the material evaluated. Earlier workers have also reported presence of substantial genetic diversity in maize (Kage *et al.*, 2012, Alam *et al.*, 2013 and Lingaiah *et al.*, 2013). The genotypes in these clusters are more genetically diverse and may be used as potential parents for breeding programmes to develop high yielding cultivars. It was also observed that geographical distance between the genotypes had no relation with the genetic divergence as the genotypes from same source had fallen into different clusters as well as the same cluster contained genotypes from different sources.

Contribution of individual character towards divergence among the characters studied (Table 3), cob weight (31.67 %), leaf area index (17.83 %) and days to 50 % brown husk maturity (12.85 %) contributed more towards divergence. Earlier Kage (2012) and Lingaiah (2013) also reported these characters to be responsible for diversity. Whereas, number of rows per cob (6.09 %), shelling percentage (4.54 %), plant height (4.32 %), stem girth (2.99 %), grain yield per plant (2.88 %), leaf area at 40 days after sowing (2.44 %), cob girth (2.33 %), 100 grain weight (1.66 %), number of kernels per row (1.44 %), days to 50 % tasseling (1.44 %), specific leaf weight (1.22 %) and cob length (1.22 %) contributed very little for divergence. Remaining traits did not contribute much to the divergence. Similar observations have been recorded by Reddy (2013), Kage (2012) and Lingaiah (2013).

Cob weight, leaf area index and days to 50 % brown husk

Table 1: ANOVA for yield and yield component characters in 43 inbred lines

Sl. No.	Characters	Replication	Treatments	Errors
1	Leaf area at 40 days after sowing	1048.23	9895.65**	03.67
2	Leaf area at 60 days after sowing	57097.46	5532.26**	2772.84
3	Leaf area at 90 days after sowing	663.42	10371.26**	3834.52
4	Leaf area index	0.0002	0.0032**	0.0012
5	Days to 50% tasseling	0.19	18.97*	1.71
6	Days to 50% silking	1.16	24.07**	2.09
7	Days to 50% brown husk maturity	1.41	29.63**	1.45
8	Stem girth	13.74	14.30**	7.63
9	Internodal distance	0.024	2.23**	1.09
10	Plant height	1366.42	887.82**	127.10
11	Cob height	115.47	326.07**	63.84
12	Chlorophyll content	0.0030	0.2875**	0.0097
13	Specific leaf weight	0.000003	0.000001**	0.0000001
14	Cob length	10.92	8.32**	2.18
15	Cob Girth	107.30	33.84**	9.56
16	Cob weight	1249.83	3382.32*	41.13
17	Number of kernels per row	44.40	53.18**	7.86
18	Number of rows per cob	2.69	2.52*	0.79
19	Grain yield per plant	623.60	2427.52*	213.61
20	100- grain weight	2.48	57.09**	9.86
21	Shelling percentage	0.32	25.07**	5.02

Table 2: Grouping of forty three maize genotypes based on D^2 analysis

Sl. No.	Clusters	No. of genotypes	Name of genotype
1	I	16	18168, 18169, 18500, 18078, 18577, 18698, 18005, 18587, 18241, 18635, 18627, 18026, 18494, 18850, 18328, 18838.
2	II	12	18206, 18342, 18710, 18740, 18657, 18484, 18209, 18857, 18851, 18844, 18037, 18095.
3	III	1	18832
4	IV	5	18171, 18854, 18666, 18847, 18697.
5	V	1	18458.
6	VI	4	18600, 18704, 18477, 18707.
7	VII	1	18570
8	VIII	1	18495
9	IX	1	18337
10	X	1	18861

Table 3: Percent contribution towards genetic diversity in maize

Sl. No.	Character	Contribution %
1	Cob weight	31.67
2	Leaf area index	17.83
3	Days to 50% brown husk maturity	12.85
4	No. of Row per cob	6.09
5	Days to 50% silking	4.76
6	Shelling percentage	4.54
7	Plant height	4.32
8	Stem girth	2.99
9	Grain yield per plant	2.88
10	Leaf area at 40 days after sowing	2.44
11	Cob girth	2.33
12	Test weight	1.66
13	Days to 50% tasseling	144
14	Number of kernels per row	1.44
15	Specific leaf weight	1.22
16	Cob length	1.22
17	Cob height	0.33

Table 4: Average intra and inter cluster D^2 values of clusters in maize

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	103.90	159.50	148.19	169.62	331.25	427.03	191.62	201.99	188.48	278.26
II		117.62	299.43	279.16	586.27	661.67	190.67	195.69	244.80	362.54
III			0.00	116.63	188.68	373.01	201.80	264.47	323.34	159.28
IV				128.61	254.21	364.29	300.79	243.22	279.82	240.07
V					0.00	136.50	557.49	625.17	377.11	585.23
VI						176.93	748.77	717.26	406.91	838.65
VII							0.00	233.22	321.11	247.61
VIII								0.00	243.90	213.20
IX									0.00	547.09
X										0.00

maturity were the important component character having higher contribution to the genetic divergence among genotypes studied (Table 3). It is interesting that the greater divergence in the present materials due to these characters will offer a good scope for improvement of yield and selection of parents for producing heterotic maize hybrids.

In general, inter cluster distance was much more than intra cluster distances. This suggesting that within cluster genotypes have same genetic constitution *i* e., homogeneous are less divergent than those occurred in a different cluster. The information on the degree of genetic divergence would be helpful in selecting parents for hybridization programme.

Results indicated that the inter cluster distances were larger than intra cluster distances in most of the cases suggesting wider genetic diversity among the genotypes of different groups. Reddy *et al*. (2013) also reported about the cluster by using D2-statiatics.

Based on the intra and inter cluster distances using D^2 values (Table 4), The maximum intra cluster distance was recorded within cluster VI (176.93), while it was lowest for the genotype of cluster I (103.90) indicating that the genotypes of these clusters might be differing marginally in their genetic architecture. The maximum inter cluster distance was observed between clusters VI and X (838.65) followed by cluster VI and VII (748.77), cluster VI and VIII (717.26) and clusters II and VI (661.67), the maximum inter cluster distance indicated the genotypes in these clusters were far diverse than those of other clusters.. The minimum inter cluster distance was observed

Table 5: Cluster mean analysis

Sl No	Cluster	N.G	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X13	X14	X15	X16	X17	X18	X19	X20	X21	Cluster score	cluster rank
1	I	16	221.47	337.38	367.48	0.2	59.31	60.53	95.06	20.32	7.51	169.41	56.55	0.76	0.01	13.45	39.05	92.58	25.47	12.55	112.48	25.69	85.11	102	IV
			-5	-3	-5	-5	-6	-6	-8	-5	-3	-6	-5	-3	-1	-5	-5	-6	-5	-6	-5	-4	-5		
2	II	12	207.86	292.02	332.59	0.18	58.25	59.5	92.13	19.49	7.02	162.47	55.54	0.68	0.01	13.3	34.94	64.96	24.75	12.54	84.63	20.01	85.88	131	IX
			-7	-8	-6	-6	-4	-4	-5	-7	-5	-7	-8	-6	(1)	-6	-10	-9	-6	-7	-8	-9	-2		
3	III	1	259.4	271.06	316.63	0.18	58	58	94	19.41	6.82	177.17	59.67	0.74	0.01	15.84	39.8	111.67	21.17	12.34	110.67	21.5	80.22	117	V
			-3	-10	-7	-6	-3	-2	-7	-8	-6	-5	-4	-4	-1	-3	-4	-4	-9	-8	-6	-8	-9		
4	IV	5	267.04	295.46	374.02	0.21	57.3	59	90.3	20.2	7.35	161.53	56.43	0.74	0.01	15.3	37.02	108.36	28.87	12.8	126.4	24.28	87.46	87	III
			-2	-7	-4	-4	-2	-3	-4	-6	-4	-8	-6	-4	-1	-4	-6	-5	-3	-4	-3	-6	-1		
5	V	1	257.95	350.8	405.8	0.23	58.5	60.5	95.5	21.22	8.34	192.67	74.83	0.61	0.01	16.5	42.12	186.61	33	11.83	161.83	29	85.54	75	II
			-4	-2	-3	-3	-5	-5	-9	-4	-2	-2	-1	-8	-1	-2	-3	-2	-2	-10	-2	-2	-3		
6	VI	4	372.26	405.77	507.49	0.28	55.38	55.88	95.63	23.22	8.73	205.87	72.21	0.72	0.01	17.87	45.9	192.86	33.54	14.12	164.96	30.25	81.24	43	I
			-1	-1	-1	-1	-1	-1	-10	-2	-1	-1	-2	-5	-1	-1	-1	-1	-1	-2	-1	-1	-7		
7	VII	1	142.64	310.4	304.51	0.17	59.5	62	85	28.69	7.51	192.33	43.67	0.66	0.01	13	36.03	77.35	24.34	11.84	117	25.5	85.33	122	VI
			-9	-6	-9	-7	-7	-8	-2	-1	-3	-3	-9	-7	-1	-7	-7	-7	-7	-9	-4	-5	-5		
8	VIII	1	213.83	288.99	310.5	0.17	66.5	68	89	21.53	6.03	192.17	64	0.97	0.01	13	35.86	69.12	27.17	13.5	58.83	23.17	78.98	127	VIII
			-6	-9	-8	-7	-8	-9	-3	-3	-8	-4	-3	-1	-1	-7	-8	-8	-4	-3	-10	-7	-10		
9	IX	1	202.43	323.88	449.39	0.25	66.5	68.5	83.5	19.11	6.54	138.17	56.17	0.58	0.01	12.83	43.48	116.17	20.67	12.67	109.17	26.17	80.77	124	VII
			-8	-5	-2	-2	-8	-10	-1	-1	-7	-9	-7	-9	-1	-8	-2	-3	-10	-5	-7	-3	-5		
10	X	1	129.95	331.07	261.31	0.15	58	61	93	17.3	6	137.5	35.17	0.82	0.01	11.84	35.3	62.72	23.84	14.67	75	14.67	84.45	152	X
			-10	-4	-10	-8	-6	-3	-7	-6	-9	-10	-10	-2	-1	-9	-9	-10	-8	-1	-9	-10	-6		

Figures in parenthesis, indicate the ranks based on cluster mean, highest (1) to lowest (10), except for days to 50% tasseling, days to 50% silking, days to 50% brown husk maturity where less value is given highest rank. Overall score is the summation of rank number for 21 characters;X1- Leaf area at 40 days after sowing, X2- Leaf area at 60 days after sowing, X3- Leaf area at 90 days after sowing, X4- Leaf area index, X5- Days to 50% tasseling X6- Days to 50% silking, X7- Days to 50% brown husk maturity, X8- Stem girth (mm), X9- Internodal distance (cm), X10- Plant height (cm), X11- cob height (cm), X12- Chlorophyll content, X13- Specific leaf weight (mg/cm^2), X14- cob length (cm), X15- cob girth (mm), X16- cob weight (gm), X17- number of kernels per row ,X18- Number of rows per cob, X19- Grain yield per plant (g), X20-100-seed weight (g), X21- Shelling percentage. (N.G- Number of genotypes)

between cluster III and IV (116.63) followed by cluster VI and V (136.50), clusters I and III (148.19), III and X (159.28) indicating a close relationship among the genotypes of these cluster. Suggesting higher intra and inter cluster distance indicating that high degree of genetic divergence within cluster and between clusters respectively.

These results revealed that the genotypes in cluster VI were distantly related; on the other hand the genotypes in cluster III, V, VII, VIII, IXand X were closely related. Therefore, genotypes belonging to these inter clusters may be used in hybridization programme to obtain transgressive segregants and to obtain higher magnitude of heterosis for the characters concerned. It is expected in our results that the crosses between the genotypes of cluster VI and X, VI and VII, VI and VIII would exhibit high heterosis and produce new combination with desirable traits. The genotypes of distant cluster could be used for further hybridization program. These results are in accordance with the finding of Alam *et al.,* 2013 and Lingaiah *et al.,* 2013. However, many earlier studies are of the opinion that hybrids between too divergent groups of parents are less successful in achieving required magnitude of heterosis (Arunachalam *et al.,* 1984).

The data on cluster means is presented in Table 5. From the data it is observed that considerable differences existed among the genotypes between the clusters. The cluster mean for leaf area at 40, 60 and 90 days after sowing, leaf area index, inter nodal distance, plant height, specific leaf weight, cob length, cob girth, cob weight, number of kernels per row, grain yield per plant and 100-seed weight was higher in cluster VI. Days to 50 % tasseling, days to 50 % silking recorded low mean values in cluster VI. So, the short duration and optimum yielding genotypes could be found VIth cluster. Days to 50 % brown husk maturity showed low mean values in cluster IX. Cluster VII exhibited highest mean values for stem girth, cob height exhibited highest mean value in cluster V and chlorophyll content exhibited highest mean value in cluster VIII. Cluster X exhibited highest mean values for number of rows per cob whereas shelling percentage recorded highest mean values in cluster IV. However, it is always desirable to look for genotypes having more than one desirable trait and belonging to different clusters as in case of clusters VI. Selection of genotypes from the clusters which have high inter-cluster distance for hybridization, one can also think of selecting parents based on extent of genetic divergence in respect to a particular character of interest.

REFERENCES

Alam, M. A., Khan, A. A., Islam, M. R., Ahmed, K. U. and Khaldun, A.B.M. 2013, Studies on genetic divergence in maize (*Zea mays*. L) inbreds. *J. Agric. Res.* **38(1):** 71-76.

Alom, A. K., Masum, M. M, Nazmun, A. S., Matin, M. A. and Pasha, M. J. 2003. Genetic divergence in maize (*Zea mays* L). *Pakisthan J. Biol. Sci.* **6(22):** 1910-1911.

Arnon, D. I. 1949. Copper enzyme in isolated chloroplasts polyphenol oxidase in *Beta vulgaris*. *Plant Physiology*. **24:** 1-15.

Arunachalam, V., Bandopadhya, A., Nigam, S. N. and Gibbons, R.W. 1984. Heterosis in relation to genetic genetic divergence and specific combining ability in groundnut. (*Arachis hypogaea* L.).

Euphytica. **33:** 33-39.

Grafius, J. E. 1964. A geometry of plant breeding. *Crop. Sci*. **4:** 241-246.

Johnson, P. L., Sharma, R. N. And Nanda, H. C. 2015, Genetic diversity and association analysis for yield traits chickpea (*cicer arietinum* L.) under rice based cropping system. *The Bioscan*. **10(2):** 879-884,

Kage, U. 2012. Genetic diversity and combining ability analysis of new inbred lines in maize (*Zea mays* L.), *M. Sc. (Agri.) Thesis,* Univ. Agril. Sci., Dharwad. p.186.

Kumar, N., Joshi, V. N. and Dagla, M. C. 2013. Estimation of components of genetic variance in maize (*Zea mays* L.). *The Bioscan*. **8(2):** 503-507.

Kumar, V. 2015. Genetic diversity and character association studies for some economic traits in rice (*Oryza sativa* L.), *The Bioscan*. **10(2):** 899-904.

Lingaiah, N., Bharathi, M. and Venkanna, V. 2013. Genetic diversity for grain yield and physiological parameters in maize (*Zea mays L.), International J.Applied Biology and Pharmaceutical Technology*. **4(3):**

Mahalanobis, P. C. 1936. On the generalized distance is statistic. *Proc. Natl. Acad. Sci. Indian*. **12:** 49-55.

Moll, R.H., Salhauna, W.S. And Robinson, 1962, Heterosis and genetic diversity in varietal crosses of maize. *Crop. Sci.* **2:**197-198.

Montgomery, E. G. 1911. Correlation studies in corn. Nebr. *Agriculture Experimental Station*. Annual Report, **24:** 108-159.

Murty, B. R. and Arunachalam. V. 1966. The nature of genetic divergence in relation to breeding system in crop plants. *Indian J. Genet.* **26A:** 188-198.

Panse, V. G. and Sukhatme, P. V. 1962. Statistical Methods for Agricultural Workers, ICAR Publication, New Delhi, p.145.

Rao, C. R. 1952. Advanced Statistical Methods in Biometrical Research. *John Wiley and Sons*. New York, pp.357-363.

Reddy, V. R., Jabeen, F. and Sudarshan, M. R. 2013. Genetic divergence in maize *(Zea mays L.). Progressive Agriculture.* **13(1):**14-18.

Sestak, Z., Catasky, J. and Jarvis, P.G. 1971. *Plant Photosynthetic Production: Manual of Methods*, Ed. Junk, N.V. The Hague Publishers, pp. 72-78.