Available online at www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.2451

ISSN: 2320 – 7051

Int. J. Pure App. Biosci. **5 (1):** 489-497 (2017)

Research Article

International Journal of Pure & Applied Bioscience

OPEN ACCESS

Morphological Diversity Analysis of Novel Inbred Lines of Maize (*Zea Mays* L.) for Development of Single Cross Hybrids

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Received: 12.01.2017 | Revised: 23.01.2017 | Accepted: 25.01.2017

ABSTRACT

An investigation was carried out to assess the genetic divergence of the newly developed inbred lines of maize in compassing of thirty inbred lines and three testers were evaluated in RCBD during Kharif 2012. Observations documented on fourteen quantitative and unique morpho-physiological traits and analysis of variance reveal highly significant difference among all inbred lines. In addition inbred lines were further grouped into six clusters, indicating the presence of genetic diversity among the inbreds. The cluster I is having highest number of genotypes (17) and the maximum inter cluster distance was observed between clusters II and III (17.08). Highest intra cluster distance was being observed in cluster I (8.09) and wide range of variation was observed in cluster mean performance for the characters studied. These genetically diverse inbred lines can be further used for developing superior hybrids for improved productivity.

Key words: *Genetic diversity, Morph-physiological traits Variance, Inbred lines, Cluster and Hybrids.*

INTRODUCTION

Maize (*Zea mays* L.) is the third most important cereal crop in the world after rice and wheat. It is cultivated in range of environments than other staple crops because of its wider adaptability[1]. India is the fifth largest producer of maize in the world contributing three per cent of the global production. It's covers cropped an area of 9.19 million hectares with total production of 24.17 million tones and productivity of 2632 kg ha^{-1}. Karnataka being first in the maize growing area (3.13 m ha), its production (4.09 mt) and productivity of 2894 kg ha^{-1}[2].

Cite this article: Naveenkumar, K.L., Shanthakumar, G., Krishnappa, R., Brunda, S.M. and Harish, G.D., Morphological Diversity Analysis of Novel Inbred Lines of Maize (*Zea Mays* L.) for Development of Single Cross Hybrids, *Int. J. Pure App. Biosci.* **5(1):** 489-497 (2017). doi: http://dx.doi.org/10.18782/2320-7051.2451

Germplasm, being a prerequisite for success of any breeding programme, serves as it serves as a valuable treasure and it provides ample scope for building up desired genetic variability. Study of variability heritability and genetic advance in any given germplasm is a imminent exercise to ascertain the real potential value of the any genotype. Different methodologies have been used to characterize inherent genetic diversity in the maize germplasm, starting from morphological characters, pedigree analysis, heterosis and the detection of variation at the DNA level using array of genetic markers. Genetic diversity plays an important role in plant breeding because hybrids between inbred lines of diverse origin display a greater heterosis than those between closely related strains. For example in maize, increased genetic difference 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. With this background, the present study primarily aims at assessing the divergence of newly developed maize lines based on morphological characters using Mahalanobis D^2statistical analysis which is very useful tool in studying and understanding the nature and cause of diversity prevalent in the available germplasm.

MATERIALS AND METHODS

The present investigation was carried out during kharif season of 2012 at Main Agriculture Research Station (MARS), UAS, Dharwad, Karnataka, India. The experimental comprised of newly derived 30 maize inbred lines *viz.,* DMIL103, DMIL218, DMIL233, DMIL247, DMIL130, DMIL136, DMIL318, DMIL326, DMIL466, DMIL145, DMIL147, DMIL152, DMIL497, DMIL516, DMIL559, DMIL561, DMIL606, DMIL630, DMIL639, DMIL 655, DMIL688, DMIL699, DMIL703, DMIL736, DMIL749, DMIL762, DMIL765, DMIL767, DMIL769 and DMIL771.These new inbred lines were derived from different source populations through pedigree method and these inbred lines were used along with three testers viz., DMIL011, DMIL021 and DMIL031 to study the genetic diversity. All 33 inbred lines were grown as per the package of practice and the experiment was replicated twice in a randomized complete block design with a 4 m row length and spacing 60 cm between the rows and with intra row distance of 20 cm.

The observations were recorded from five plants randomly selected from each plot for 14 quantitative morpho-physiological traits *viz.,* days to 50 per cent tasseling, days to 50 per cent silking, plant height (cm), ear height (cm), days to 75 per cent dry husk, ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, test weight (g), shelling percentage, grain yield (q/ha), canopy temperature and SPAD value. Diversity analysis was calculated using Mahalanobis D^2 statistics and inter cluster distance was calculated by the formulae described by[3].

RESULTS AND DISCUSSION

For crop like maize, the strategy of developing superior hybrids depends on the extent of genetic diversity present in the available inbred lines which is of immense value for imminent crop improvement with trait of interest. For development of superior hybrids, one needs to select superior inbreds which possess higher directional dominance, genetic diversity and allelic differentiation for most of the traits. The genetic divergence estimated by adopting an effective statistical tool, Mahalanobis D^2 statistic, which elucidate the nature of the diversity of the population precisely. The analysis of variance carried out for the yield and its component characters among 33 inbred lines was presented in Table1. The results revealed that all the genotypes differed significantly for all assessed characters except days to 75 per cent dry husk and ear length.

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 import ant tool for realizing heterotic response in F_1 and a broad spectrum of variability in segregating generations. The D^2 analysis carried out involving 33 inbreds for 14 characters revealed that altogether six clusters have been formed (Table.2, Figure.1), where in cluster I had a maximum of seventeen genotypes, cluster II have twelve genotypes and remaining clusters III, IV, V and VI were figured as solitary. The genotypes which are within the clusters by and large exhibit a narrow range of genetic variability.

While studying the contribution of individual characters towards divergence among 14 characters studied, days to 75 per cent brown husk (19.25%) and grain yield ha^{-1} (17.99%) contributed high for divergence (Table. 3). Therefore, these characters should be given due recognition, for selecting diverse parents for breeding programme. However, other characters like test weight (13.64%), SPAD value (10.23%), shelling percentage (7.20%), canopy temperature (6.49%), number of kernels per row (6.19%), days to 50 per cent tasseling (4.95%), number of rows per ear (4.25%), days to 50 per cent silking (3.08%), ear height (1.76%), ear length (2.19%), ear girth (1.60%) and plant height (1.00%), have contributed very tepidly for divergence. [4], reported that leaf area per plant, plant height and days to 50 per cent flowering were the major contributors towards divergence. But while studying forage maize, more than 90 per cent contribution to divergence was reported from days to 50 per cent flowering, plant height and number of kernels per row. These observations were contradicted in the present investigation.

Based on the intra and inter cluster distances using D^2 values (Table. 4), the maximum intra cluster distance was recorded within cluster I, indicating that the genotypes of these clusters might be differing marginally in their genetic architecture and it can be considered that the genotypes belonging to cluster II and III, followed by cluster II and IV, cluster III and V and cluster II and VI, having highest inter cluster distances, which suggest that crosses between divergent groups may lead to higher magnitude of heterosis for the characters in consideration. However, many previous studies are of the opinion that crosses between too divergent groups of parents are less successful in achieving required magnitude of heterosis[5]. On the other hand, the crosses between genotypes exhibiting a narrow range of variability as revealed by short inter cluster distances may not be worthwhile to get desired extent of heterosis. This is probably because of parents with similarity may possess common alleles governing the characters and may not help in complementation in the crosses combination. Similarly, parents exhibiting greater divergence may also lack nick well ability. This is specially being observed in distant crosses (inter specific) for yield related traits. However, many studies are on the record that whenever parents with moderate divergence are used for crossing, throw out significant level of desired heterosis[6].

These findings reveal the presence of divergent genotype within the different cluster *viz.*, I, II, IV and VI, whereas all the three testers were grouped under different cluster that is cluster I, III and V. The inter cluster distance between these clusters was considerably high; therefore we got heterosis for the yield and its component traits.

Among fourteen quantitative characters studied, the most important characters contributing to divergence were considered to be days to 75 per cent dry husk, grain yield per hectare, test weight fallowed by shelling percentage, number of kernels per row, days to 50 per cent tasseling, number of rows per ear, days to 50 per cent silking, ear height, ear length, ear girth and plant height. Similar kind of results were reported and corroborated by the[7, 8, 9,10, 11,12] emphasizing plant height and days to 50 per cent flowering as the major contributors towards divergence, while studying forage maize. More than 90 per cent contribution to divergence was reported from days to 50 per cent flowering, plant height and number of kernels per row. This result seems to be contradicting the present investigation.

The study of mean values for fourteen economic traits in the maize might give an insight into the cluster characteristics for each of the six clusters studied (Table. 5). In the present study the inbreds in cluster IV and V had less number of days to 50 per cent tasseling, whereas cluster IV for days to 50 per cent silking, for plant height in cluster VI, for ear height, ear length and ear girth in cluster V, for days to 75 per cent dry husk in cluster I, for number of kernels per ear in cluster V, for test weight in cluster II and cluster III for grain yield per hectare coupled with high number of kernel rows per row, for shelling percentage in cluster III. In case of canopy temperature cluster IV and V and for SPAD value in cluster VI as also investigated by other researchers[12,13,14,15].

However, it is always desirable to search genotypes having more than one desirable trait and belonging to different clusters as in case of clusters I, III and IV, which are being grouped with genotypes different in days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent dry husk, ear girth, number of kernel rows per ear and number of kernels per row. Most interesting thing that all fourteen characters studied exhibited their contribution towards divergence and none of the characters showed zero or less contribution to the divergence.

Table 1: Analysis of variance for yield and its components traits, of parents and hybrids of maize during *kharif* 2012 at MARS Dharwad

Source of variation Characters	Replications	Parents	Error
Df	**1**	**32**	**32**
Days to 50 per cent tasseling	13.67**	4.69**	1.47
Days to 50 per cent silking	14.15**	4.43**	1.40
Plant height (cm)	9.6	1129.67**	128.24
Ear height (cm)	9.25	458.68**	80.69
Days to 75 per cent dry husk	0.04	1.46	1.41
Ear length (cm)	2.08	7.81	6.28
Ear girth (cm)	0.55	4.58 **	2.07
No. Kernels rows /Ear	2.34	2.42	2.90
No. Kernels /row	21.66	54.50*	31.92
Test weight (g)	6.13	80.98**	9.93
Shelling percentage	2.72	279.40**	39.32
Grain yield (q/ha)	2.36	164.48**	18.94
Canopy temperature (^{0}C)	19.98**	8.71**	2.84
SPAD value (%)	0.46	22.45**	9.95

* - Significant at 5% level ** - Significant at 1% level

Table 2: Distribution of thirty three inbred maize lines in to six different clusters

Sl. No.	Cluster	No of genotypes	Name of genotypes
1	I	17	DMIL136, DMIL769, DMIL466, DMIL218, DMIL011, DMIL152, DMIL233, DMIL699, DMIL147, DMIL749, DMIL606, DMIL762, DMIL 145, DMIL655, DMIL 630, DMIL 497, DMIL 561
2	II	12	DMIL103, DMIL639, DMIL736, DMIL703, DMIL771, DMIL559, DMIL767, DMIL247, DMIL765, DMIL318, DMIL688, DMIL516
3	III	1	DMIL021
4	IV	1	DMIL031
5	V	1	DMIL336
6	VI	1	DMIL130

Table 3: Per cent contribution of character towards divergence in thirty inbred lines with three testers

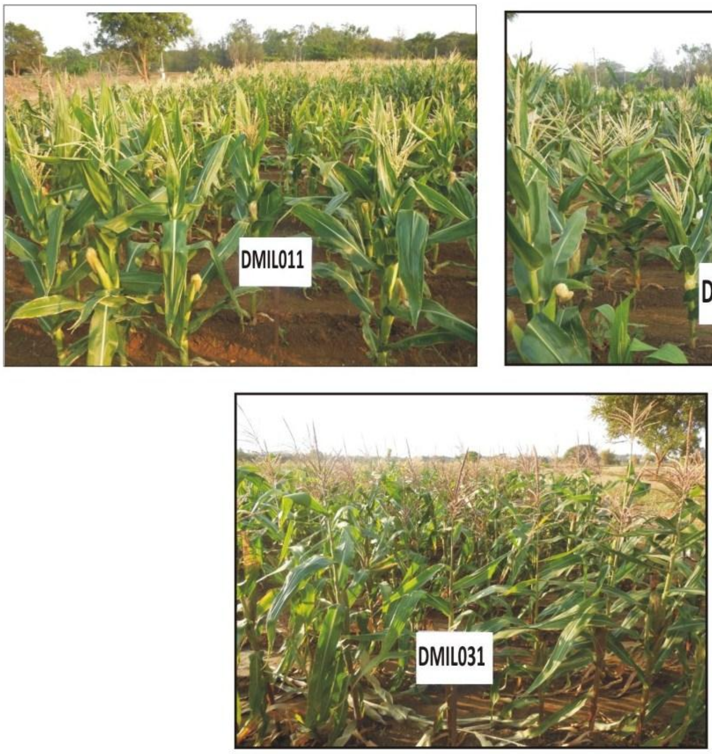
Sl. No.	Characters	Characters Contribution (%)
1	Days to 50 per cent tasseling	4.95
2	Days to 50 per cent silking	3.08
3	Plant height (cm)	1..00
4	Ear height (cm)	1.76
5	Days to 75 per cent dry husk	19.25
6	Ear length (cm)	2.19
7	Ear girth (cm)	1.60
8	No. of kernel rows per ear	4.25
9	No. of kernels per row	6.19
10	Test weight (g)	13.64
11	Shelling percentage	7.20
12	Grain yield (q/ha)	17.99
13	Canopy temperature (^{0}C)	6.49
14	SPAD value (%)	10.23

Table 4: Average intra and inter cluster distance values of thirty three maize inbred lines

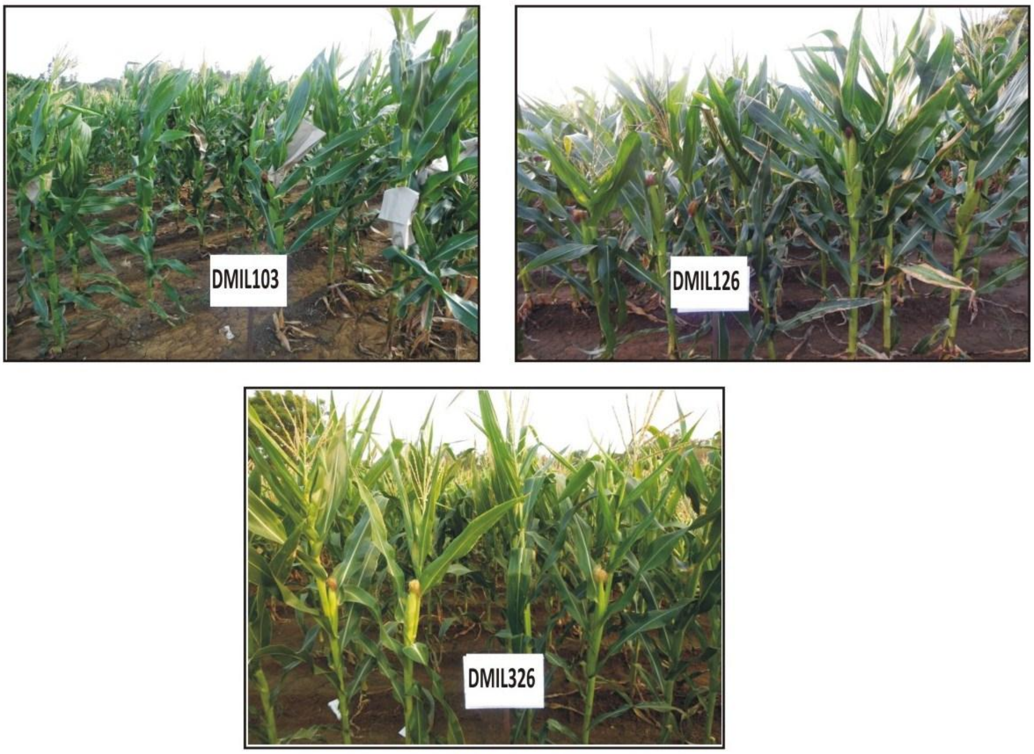
Clusters	I	II	III	IV	V	VI
I	8.09 (65.45)	11.27 (127.01)	10.53 (110.88)	10.95 (119.90)	10.49 (110.04)	11.27 (127.01)
II		7.56 (57.15)	17.08 (291.73)	15.97 (255.04)	8.11 (65.77)	14.75 (217.56)
III			0	8.86 (78.50)	15.58 (242.74)	11.02 (121.88)
IV				0	15.46 (239.01)	7.82 (61.15)
V					0	14.90 (222.01)
VI						0

Table 5: Cluster means of thirty three maize inbred lines for fourteen morph-physiological characters

Cluster	Days to 50 per cent tasseling	Days to 50 per cent silking	Plant height (cm)	Ear height (cm)	Days to 75 per cent dry husk	Ear length (cm)	Ear girth (cm)	No. of kernel row/ ear	No. of kernels /row	Test weight (g)	Shelling per centage	Grain yield (q/ha)	Canopy tempe rature (^{0}C)	SPAD value (%)
I	59.41	60.91	156.70	79.52	84.13	14.76	13.25	14.12	29.26	26.87	64.35	36.37	27.65	43.23
II	59.33	60.71	149.56	75.30	90.00	14.25	15.15	13.83	27.42	30.85	62.03	22.79	26.80	43.95
III	59.00	60.00	132.25	81.70	89.50	15.50	15.60	14.00	16.00	27.60	65.39	38.07	27.20	44.80
IV	57.50	59.00	142.30	70.10	89.50	16.50	13.70	16.00	25.00	28.50	67.00	40.64	24.25	41.70
V	57.50	59.50	153.15	65.25	88.00	17.25	16.25	13.00	35.00	18.60	44.86	33.78	24.25	41.55
VI	59.00	60.00	170.30	68.35	90.50	14.00	14.25	14.00	20.00	26.50	23.28	38.34	28.95	47.40



Testers



Lines

Plate 1: Parents used in the experiment for hybrid production

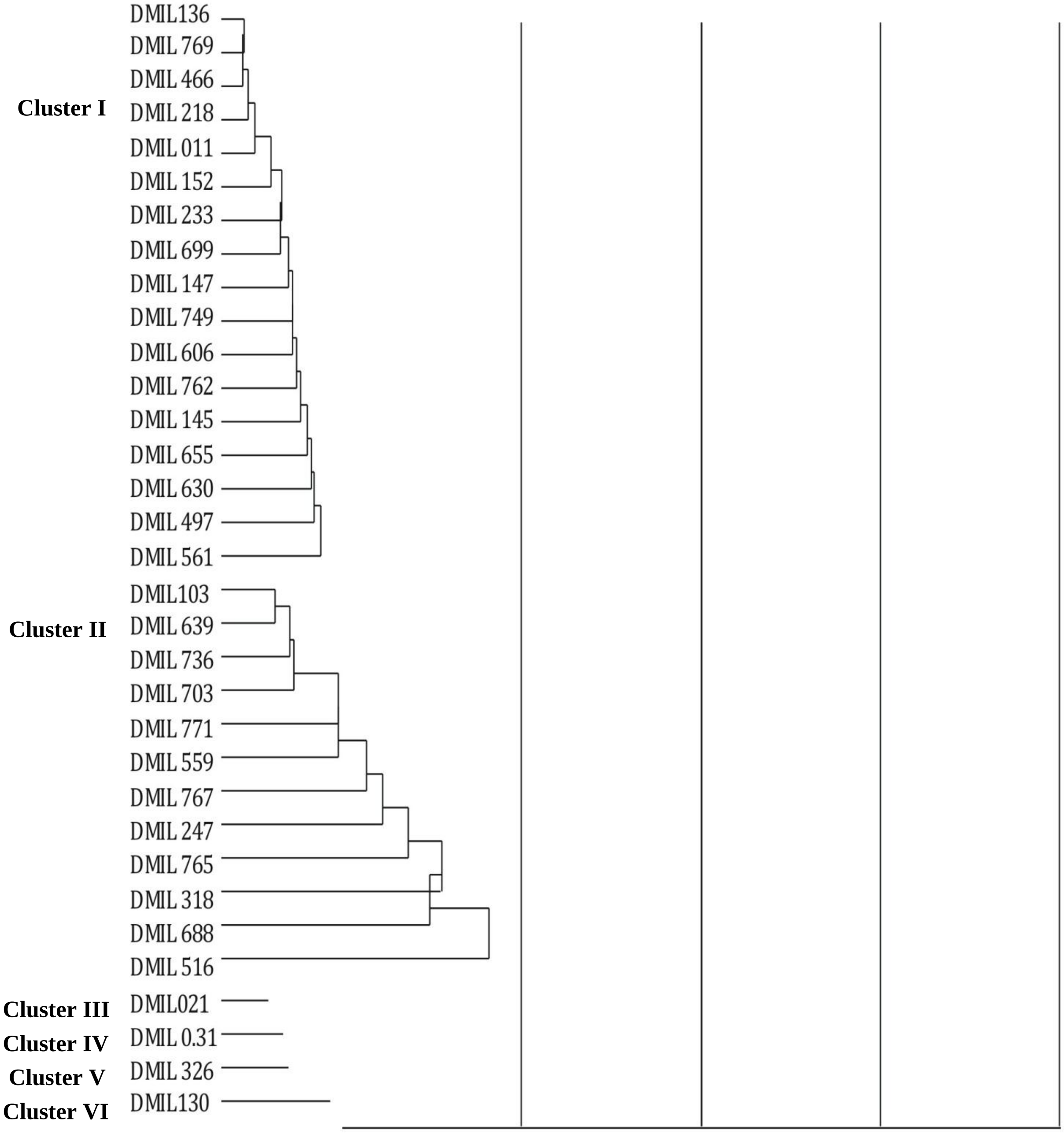
a) First high yielding F_1 hybrid

b) Second high yielding F_1 hybrid

c) Third high yielding F_1 hybrid

Plate 2: Promising hybrid identified during summer

Fig. 1: Dendrogram showing clusters by Tocher's method



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