IJBPAS, March, 2019, 8(3): 574-581

ISSN: 2277–4998

International Journal of Biology, Pharmacy and Allied Sciences (IJBPAS)

'A Bridge Between Laboratory and Reader'

www.ijbpas.com

GENETIC DIVERSITY STUDIES IN MAIZE (*ZEA MAYS* L.) INBRED LINES

D.B. LAD[1], A. A. BHAGAT[2] AND A.M. TIRMALI[3]

1: Associate Professor of Botany, NARP, Ganeshkhind, Pune-411067

2: Assistant Professor of Statistics, NARP, Ganeshkhind, Pune-411067

3: Assistant Professor of Agriculture Microbiology, NARP, Ganeshkhind, Pune-411067

Received 15th Oct. 2018; Revised 16th Nov. 2018; Accepted 21st Nov. 2018; Available online 1st March 2019

https://doi.org/10.31032/IJBPAS/2019/8.3.4668

ABSTRACT

In the present investigation forty inbred lines of maize procured from AICRP on Maize, Kolhapur was evaluated in Randomized Block Design during *kharif,* 2014. The D^2 values ranged from 125.88 to 1664.64. All the fourty inbreds evaluated were grouped into six clusters in which cluster I accommodating maximum 15 inbreds followed by cluster II and III with 8 inbreds and cluster IV with 7 inbreds. The cluster V and VI were monogenotypic indicating wide divergence from other clusters. The maximum intra-cluster distance was observed in the cluster IV (212.86) followed by cluster III (174.24) and cluster II (131.56), suggesting that inbreds present in these clusters possesses varied genetic architecture and might have originated from different genetic pool. The maximum inter cluster distance were observed between cluster V and cluster VI (1664.64) followed by cluster III and cluster VI (982.19) and cluster IV and cluster VI (804.85), indicating wide divergence among the clusters, which suggested that the genetic architecture of the inbreds in one cluster differ entirely from those included in the other cluster. On the basis of inter cluster distances, cluster means, *per se* performance observed in the present study, inbreds QMI-1427, QMI-1464, QMI – 1455, QMI -1457, QMI-1440, QMI-1432, QMI-1444,QMI-1437, QMI-1461 were found to be promising, suggested for future breeding programme.

Keywords: Inter and intra cluster, divergence, inbreds, monogenotypic maize

INTRODUCTION

Maize (*Zea mays* L.) popularly known as corn, is well known cereal crop of global importance and is believed to have originated in central Mexico 7000 years ago from a wild grass, and Native Americans transformed maize into a better source of food. Maize contains approximately 72% starch, 10% protein, and 4% fat, supplying an energy density of 365 Kcal/100 g and is grown throughout the world, with the United States, China, and Brazil being the top three maize-producing countries in the world, producing approximately 563 of the 717 million metric ton/year. Maize can be processed into a variety of food and industrial products, including starch, sweeteners, oil, beverages, glue, industrial alcohol, and fuel ethanol. It belongs to family Poacae and Tribe Maydeae. Maize is cross pollinated crop with 95 to 100 per cent cross pollination. It is used as livestock feed in a variety of ways. It may be used as grain, silage, hogging down, grazing and forage. Genetic diversity is variability available among the different genotypes of a species. D^2 statistic is useful multivariate statistical tool for effective discrimination among various genotypes. (Murty and Arunachalam, 1966). This technique measures the forces of differentiation at intra and inter cluster levels and thus helps in the selection of genetically divergent parents for their exploitation in hybridization programme. The D^2 also measures the degree of diversification and determines the relative proportion of each components character to the total divergence in maize. The present investigation was carried out to study the nature of extent and pattern of genetic variation in available inbreds of maize.

MATERIALS AND METHODS

In the present investigation, 40 inbreds of maize procured from AICRP on Maize, Kolhapur were evaluated to study nature of extent and pattern of genetic diversity. The experiment was laid out in Randomized Block Design (RBD) with three replications. Forty inbreds were randomly planted in three replications. Each entry was represented by a single row of 4.00 m length spaced at 75 cm between the rows and 20 cm between the plants within the rows. Two border rows were planted at both sides of blocks to reduce the border effects. Five random plants from each treatment in each replication were selected for recording observations. The selected plants were tagged at the age of 35 days. The observations were recorded on days to 50% tasselling, days to 50% silking, plant height (cm), days to 50% maturity, ear head height, ear length, number of grain per cob, 100 grain weight, shelling per cent, number of cobs per plant, protein content (%) and seed yield per plant. The D^2 analysis as described by Mahalanobis (1936) was utilized to assess the genetic diversity among 40 inbreds of maize and Tochers' method was employed for grouping the genotypes into different clusters as described by Rao (1952).

RESULTS AND DISCUSSION

Genetic divergence among 40 inbred of maize for 12 characters were made by using Mahalanobis D^2 analysis as per Rao (1952). Based on Mahalanobis D^2 analysis, 40 inbreds of maize were grouped into six clusters (Table 1). The D^2 values were ranged from 125.88 to 1664.64. The largest cluster I consisted 15 inbreds followed by cluster II and III with 8 inbreds and cluster IV with 7 inbreds. The monogenotypic nature of V and VI clusters indicated maximum divergence from other groups. Similar, results were reported by Khumkar and Singh (2012), Singh and Chaudhary (2012), Saxennna and Sandhu (2008), and Singh *et al*. (2008). The intra and inter cluster D^2 and D values were worked out and depicted in (Table 2). The maximum intra cluster distance was observed for cluster IV (212.86) followed by cluster III (174.24) suggesting that inbreds included in these clusters might have different genetical architecture. However, the lowest intra cluster distance was observed in cluster I (125.88) indicating that the inbreds of these clusters resembled one another genetically and from common gene pool. The clusters V and VI were monogenotypic and showed no intra cluster distances.

The maximum inter cluster distance was observed between cluster V and VI (1664.64) followed by cluster III and VI (982.19), cluster IV and VI (804.85),cluster II and cluster V (754.60), cluster I and V (754.60), cluster IV and V (418.80), cluster III and V (446.05). These clusters are divergent form each other and the inbreds belonging to them can be used for hybridization programme because crosses between inbreds belonging to the clusters having maximum inter cluster distance, will give high heterotic response and yield better recombinants (Bhatt, 1970). The inter cluster distance between cluster I and II (235.31) was comparatively low suggesting that the genetic constitution of the inbreds in one cluster were in close proximity with the inbreds in other cluster of the pair. Singh *et al* (2011) reported that inter-cluster distance were higher than intra-cluster distance, suggesting wide genetic diversity among the inbreds of different groups.

Cluster means for different characters indicated that none of the cluster contained inbreds with all desirable characters and so recombinant breeding between inbreds of different clusters is needed (Table 3). Cluster VI (100.67 g) with one inbreds recorded highest mean seed yield per plant followed by cluster II (87.52 g), cluster V (84.33 g) and cluster IV (80.58 g). Whereas cluster I (78.94 g) and cluster III (73.94 g) recorded lowest value. Out of 12 characters studied, cluster mean for 50 per cent tasselling varied between cluster III (47.74 days) to cluster I (49.64 days). The cluster mean for 50 per cent silking varied between cluster III (48.49 days) to cluster V (53.98 days). The inbreds involved in cluster III (48.49 days) appeared early silking as this group has taken minimum number of days for silking followed by cluster IV (48.88) and cluster II (49.88). Apart from cluster V (53.98), cluster VI (50.57) and cluster I (50.53) indicated late silking inbreds. The highest mean plant height was observed in cluster VI (187 cm) followed by cluster II (167.90 cm) and cluster I (167.74 cm). Days to 50 per cent maturity was ranged between cluster V (83.34) to cluster I (86.06). The highest mean for days to 50 per cent flowering was observed in cluster I (86.06) followed by cluster II (85.42) and least in cluster V (83.34). Ear head height varied between cluster V (46.32 cm) to cluster VI (94.24 cm). The cluster VI (94.24 cm) showed highest ear head height followed by cluster II (73.03 cm). The maximum mean ear length was recorded in cluster I (16.53 cm) followed by cluster VI (15.33 cm) and cluster II (14.75 cm). The highest number of grains per cob was recorded in cluster VI (510.79) followed by cluster II (504.30) and cluster V (450.50). The clusters mean for 100 grain weight was maximum for cluster IV (23.63 g) followed by cluster V (22.68 g). The cluster VI (84.60) recorded highest shelling percentage followed by cluster II (83.59) and cluster I (83.55). The maximum number of cobs per plant was observed in cluster VI (2.17) followed by cluster II (1.57). The minimum cluster mean was observed only one in cluster III, cluster IV and cluster V. The highest mean of per cent protein content was observed in cluster IV (9.13 %) followed by cluster III (8.94%) and cluster I (8.91%). Considerable amount of variability for seed yield per plant was observed within cluster mean for this character. Cluster VI (100.67 g) showed highest cluster mean followed by cluster II (87.52 g), cluster V (84.33 g) and cluster IV (80.58 g). The positive contribution of these yield components in genetic divergence may be considerably help in selecting inbreds for yield and yield attributing traits. Based on cluster means Singh and Chaudhary (2003) also reported wide range of variation for grain yield and its components in maize. The present results are in agreement with those of Tang *et. al* (2002).

The percent contribution of 12 characters for divergence in maize inbreds is presented in (Table 4). Out of 12 characters studied the character 100 grain weight (26.41%) contributed highest divergence followed by Plant height (22.31%), Ear head height (21.15%), Number of grain per cob (18.33%), Shelling per cent (6.15%), Seed yield per plant (3.08%), Protein content (1.79%). The contribution of number of cobs (0.64%), days to 50 per cent maturity (0.13%) were low magnitude and days to 50 per cent tasselling, days to 50 per cent silking, ear length did not contributed towards divergence. Similar results were reported by Datta and Mukharjee (2014), for contribution of ear weight and ear length towards divergence. William and Hauller (2011) reported that grain yield provided meaningful estimates towards divergence.

Table 1: Distribution of 40 inbreds of maize into different clusters

Cluster Number	Number of inbreds included	Inbreds
I	**15**	**QMI-1443, QMI-1446, QMI-1447, QMI-1428, QMI-1429, QMI-1450, QMI-1455, QMI-1426, QMI-1436, QMI-1463, QMI-1431, QMI-1435, QMI-1460, QMI-1442, QMI-1464**
II	**8**	**QMI-1444, QMI-1445, QMI-1441, QMI-1434, QMI-1433, QMI-1437, QMI-1457, QMI-1452**
III	**8**	**QMI- 1448, QMI-1462, QMI-1456, QMI-1454, QMI-1429, QMI-1459, QMI-1461, QMI-1451**
IV	**7**	**QMI-1425, QMI-1430, QMI-1438, QMI-1453, QMI-1458, QMI-1427, QMI-1439**
V	**1**	**QMI-1440**
VI	**1**	**QMI-1432**

Table 2: Average intra and inter cluster D^2 values from 40 inbreds of maize.

Clusters	I	II	III	IV	V	VI
I	**125.88 (11.22)**	**235.31 (15.34)**	**371.71 (19.28)**	**252.17 (15.88)**	**754.60 (27.47)**	**430.56 (20.75)**
II		**131.56 (11.47)**	**322.92 (17.97)**	**434.72 (20.85)**	**754.60 (27.47)**	**278.22 (16.68)**
III			**174.24 (13.20)**	**439.74 (20.97)**	**446.05 (21.12)**	**982.19 (31.34)**
IV				**212.86 (14.59)**	**481.80 (21.95)**	**804.85 (28.37)**
V					**(0.00)**	**1664.64 (40.88)**
VI						**(0.00)**

Figures in parenthesis indicate D values.

Table 3: Cluster mean performance for 40 inbreds of maize

Clusters	Days to 50% tasselling	Days to 50% silking	Plant Height (cm)	Days to 50% maturity	Ear head height (cm)	Ear length (cm)	Number of grain per cob	100 grain weight (g)	Shelling per cent	Number of cobs per plant	Protein content (%)	Seed yield per plant(g)
I	49.64	50.35	167.74	86.06	72.82	16.53	359.67	21.41	83.55	1.22	8.91	78.94
II	48.87	49.88	167.90	85.42	73.03	14.75	504.30	19.05	83.59	1.57	8.56	87.52
III	47.74	48.49	150.07	84.14	59.76	14.60	428.64	17.18	83.26	1.00	8.94	73.94
IV	47.89	48.88	158.42	83.88	64.50	13.92	353.23	23.63	80.98	1.00	9.13	80.58
V	49.52	53.98	133.00	83.34	46.32	13.33	450.23	22.68	81.70	1.00	8.41	84.33
VI	49.11	50.57	187.00	84.56	94.24	15.33	510.79	21.53	84.60	2.17	8.53	100.67

Table 4: Per cent contribution of 12 characters for divergence in maize inbreds

Sr. No.	Characters	Per cent contribution
1	Days to 50% tasselling	0.00
2	Days to 50% silking	0.00
3	Plant height (cm)	22.31
4	Days to 50% maturity	0.13
5	Ear head height (cm)	21.15
6	Ear length (cm)	0.00
7	Number of grain per cob	18.33
8	100 grain weight (g)	26.41
9	Shelling per cent	6.15
10	Number of cobs per plant	0.64
11	Protein content (%)	1.79
12	Seed yield per plant (g)	3.08
	Total	100

CONCLUSION

The hybridization among genetically diverse parental inbreds for specific trait may be helpful in bringing the new gene pool in population and expanding the range of adaptation. Hence from present study, on the basis of cluster distances , cluster means, *per se* performance the inbreds QMI- 1427, QMI- 1464, QMI- 1455, QMI- 1457, QMI-1440, QMI- 1432, QMI- 1444, QMI- 1437 and QMI- 1461 were found promising inbreds for future breeding programme.

REFERENCES

[1] Bhatt, G. M. 1970. Multivariate analysis approach to selection of parents for hybridization aiming at yield improvement in self pollinated crops. *Australian Res.* 21: 1-7.

[2] Data, D. and B. K. Mukharjee, 2014. Genetic divergence among maize and restricted traits for group constellation. *Ind.J. of Genetics* .64 (3): 201-207

[3] Khumkar, M.S. and R. D. Singh 2012. Divergence analysis of elite inbred lines of maize (*zea mays L.)Anals. of Agril. Res.* 23(4): 595-601.

[4] Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of Natural Inst. of Sci.*, India 2:49-55.

[5] Murthy, B. R. and V. Arunachalam 1966. The nature of divergence in relation to breeding system in some crop plants. *Indian J. of Genet and Plant Breed*. 26A:188-198.

[6] Rao, C. R. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley and Sons. Inc. New York.

[7] Saxena V. K. and A. S. Sandhu, 2008. Divergence analysis in maize. Crop improvement. 16 (2) : 154-158

[8] Singh, P. K. and P. B. Jha and Kumar P. 2008. Genetic divergence in fodder maize. *J. of Applied Biology*. 13(1/2): 24-28.

[9] Singh P. K. and B. D. Chaudhary 2012. Genetic divergence in maize *(Zea mays L.)* J. *of Res. Birsa Agril. Univ.* 13 (2): 193-195

[10] Singh, P. Sain Das, V. K. Dwivedi, O. Kumar and Y. Sangwan 2011. Genetic divergence studies in maize. *Annals of Agril.Bio. Res.*10 (1) : 43-46.

[11] Tang D. F., A. G.Yang, Pan G. T. and Rang T. Z. 2002. Study of combining ability and clustering analysis of CIMMYT maize population in China. J. Agric. Univ. 20(4): 317-320.

[12] Willaims, T. R. and A. R. Hauller 2011. Genetic divergence in maize hybrids. *Maydica J.* 45(3): 163-171.