RESEARCH ARTICLE

D^2 ANALYSIS IN ADVANCED BREEDING LINES OF GREENGRAM (*VIGNA RADIATA* L.)

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Received-02.05.2021, Revised-11.05.2021, Accepted-23.05.2021

Abstract: Genetic divergence studies are very important to devise a hybridization strategy to exploit the variability present in the base population. In the present study, thirty genotypes of advanced breeding lines of greengram were evaluated to know divergence and use it the hybridization programme based on the inter cluster and high mean values of the clusters. The thirty genotypes were grouped into ten clusters. The cluster I was the largest cluster with 13 genotypes flowed by the cluster, II (6) and III (4). The clusters, IV to X were solitary clusters with single genotype each. The contribution of test weight towards divergence was maximum (78.39%) compared to other characters. The intra cluster distance was maximum in the cluster III (22.83) followed by the cluster II (21.52) and I (15.56).The inter cluster distance was maximum between the clusters VI and X (753.22) followed by IV and X (717.11), VII and X (552.56) and I and X (531.27) indicating their importance in the hybridization programmes for the generation of transgressive segregants. The cluster X mean value for test weight was maximum and can be utilized in the breeding programmes as it forms an important yield contributing trait for yield improvement.

Keywords: Advanced breeding lines, Divergence, Greengram

INTRODUCTION

Greengram (*Vigna radiata* (L.) Wilczek) popularly termed as mung bean, is extensively grown in tropical and sub-tropical regions of India. It constitutes a rich source of protein of vegetarian dietary people of India. India is the largest producer and consumer of greengram in the world. Greengram is a short duration pulse crop which fits well into the intensive rice–wheat cropping system of Indo-Gangetic plains of India and rice fallows (Brar *et al*., 2004). It can also be grown as intercrop with sugarcane and pigeonpea. Thus, there is a great scope of increasing area and production under mungbean (Sekhon *et al.,* 2007). Since, it is a highly self pollinated crop, variation existing within or between the species or varieties become important (Anamika *et al.,* 2017 and Mahalingam *et al.,*2018). The utilization of diverse genotypesin hybridization is suggested for attaining recombinants or transgressive segregants (Ram *et al*. (2002), Asha *et al*. (2013), Haritha and Lal Ahamed (2013), Jadhav *et al*. (2014), Tulasi *et al*. (2014), Radhika Ramya *et al*. (2017), Mounika *et al*. (2018), Roy *et al*. (2018), Sateesh Babu *et al*. (2019) and Shalini *et al*. (2020). The diversity studies in mungbean also helps to attain significant amount of genetic variability for yield improvement (Sandhiya and Saravanan, 2018). Genetic diversity is one of the criteria to estimate the variability before any breeding programme to be initiated (Marilene *et al.,* 2012). The quantification of genetic diversity through biometrical procedures such as Mahalanobis D^2 statistic analysis made possible to choose genetically diverged genotypes in breeding programmes for creating variability (Mahalanobis, 1936). Recent works indicated that the Mahalanobis generalized distance may be an efficient tool in the quantitative estimation of genetic diversity. Success of the hybridization followed by selection depends largely on the variation present in the base population for the traits of interest (Murthy and Arunachalam, 1966). The main objective of the present study was to know the genetic diversity among the advanced breeding lines of mungbean developed at Regional Agricultural Research Station, Lam, Guntur.

MATERIALS AND METHODS

The present investigation was carried out during *rabi*, 2019-20 at Regional Agricultural Research Station, Lam, Guntur with 30 genotypes of mungbean developed at RARS, Lam, Guntur. The experiment was conducted in a randomized block design with three replications and recommended package of practices were followed to raise the good crop. The spacing adopted was30 cm row to row and 10 cm between plant to plant. The data were recorded on ten randomly selected plants of each replication for eight quantitative characters *viz*., no. of branches/plant, no. of clusters/plant, no. of pods/plant, pod length, no. of seeds/pod, test weight, seed yield/ha along with the traits like days to 50% flowering and days to maturity, where the observations were recorded on plot basis. Data was subjected to statistical analysis using Mahalanobis'

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D^2 statistic to determine the genetic divergence among the genotypes in terms of generalised group distance (Mahalanobis, 1936). The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The average intra and inter cluster distances, cluster means and contribution of different traits to total divergence was estimated by the procedure given by Singh and Choudhary (1977).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) was carried out for 30 genotypes of greengram for all the traits viz., days to 50% of flowering, days to maturity, plant height, no. of branches/plant, no. of clusters/plant, no. of pods/plant, pod length, no. of seeds/pod, test weight and seed yield/ha and was significant indicating the presence of considerable genetic variability in the experimental material under study.

Based on D^2 analysis, 30 mungbean genotypes were grouped into 10 clusters (Table 1 and Fig.1). Cluster I had the maximum number of genotypes (13) followed by cluster II (6 genotypes) and cluster III (4). The clusters IV,V,VI,VII,VIII,IX and X were solitary consisting of only one genotype each. Similar results were also reported by Prasanna *et al*.(2013) for 50 greengram genotypes into 8 clusters; Garje *et al*.(2013) for 40 genotypes into 13 clusters; Ahmad *et al*.(2016) for35 genotypes into 7 clusters and Chandra *et al.*(2017) grouped 40 genotypes into 7 clusters.

The contribution of test weight was maximum (78.39%) towards divergence compared to other characters (Table 2). The contribution of days to 50% flowering was 7.59% followed by days to maturity (4.37%), seed yield per hectare (3.22%), number of clusters per plant (2.30%), number of branches per plant (1.84%)and number of pods per plant (1.15%). The traits, plant height (0.23%), number of seeds per plant (0.92%) and pod length (0) contribution towards divergence was negligible.

The intra and inter cluster distances are presented in Table 3.The maximum intra cluster distance was observed in the cluster III (22.83) followed by cluster II (21.52) and cluster I (15.56) indicating the presence of genetic variability among the genotypes present in these clusters and is of little importance. The inter cluster distances were more than the intra cluster distances indicating huge genetic diversity among the genotypes present in different clusters. The maximum inter cluster distance was observed between the clusters X and VI (753.22) followed by clusters VIand X (717.11), clusters VII and X (552.56) and clusters I and X (531.27) indicating the importance of genotypes present in these clusters for exploitation in the breeding programmes.

The cluster means of yield and yield traits are presented in table 4. The cluster IX showed the highest mean values for days to 50% of flowering (46.00), days to maturity (71.33) and pod length (9.29cm) while, cluster VII showed the highest mean performance for no. of clusters/plant (6.73), no. of pods/plant (16.73) and seed yield/ha (783.40kg). The results showed that the genotype in cluster VIII was early flowering type (39.00) while the genotype in cluster IX (46.00) was late flowering type. Genotype in cluster X (68.00) was early maturing while genotype in cluster IX (71.33) was late maturity. Cluster IV exhibited the highest mean performance for plant height (42.50) and cluster X showed the lowest mean (38.50). Cluster VIII showed the highest mean performance for no. of branches per plant (1.80) whereas in cluster IX showed the lowest mean (1.00). No. of clusters per plant observed were maximumin cluster VII (6.73) and were the lowest in cluster V and VI (1.53). The genotypes in cluster VII showed the highest mean performance (16.73) and genotypes in cluster IX showed the lowest mean performance (8.47) for no. of pods per plant. Pod length was the highest in cluster IX (9.29) and was the lowest in cluster IV (6.05). No. of seeds per pod was the highest in cluster III (11.03) whereas cluster X (8.40) recorded the lowest mean performance. The genotype in cluster X showed the highest mean performance for test weight (4.97g) and the cluster IV showed the lowest mean performance (3.35). Cluster V showed the highest mean performance for seed yield/ha (860.69kg) and cluster X showed the lowest mean performance (527.22).

These results suggest that the genotypes grouped in different clusters may be used as potential parental lines for hybridization programme. D^2 analysis is very much useful for the assessment of mungbean diversity to utilize them in crop improvement programmes (Muthusamy *et al.*, 2008; Arpita *et al.*, 2010; Ghulam *et al.*, 2010; Singh *et al.*, 2013; Vyas *et al.*, 2018).

Table 1. Clusters formed by the D^2 analysis in greengram (*Vigna mungo* L.)

S. No.	Cluster Number	Number of Genotypes	Genotypes
1	I	13	LGG 712, LGG 460, LGG 697, LGG 703, LGG 693, LGG 711, LGG 688, LGG 695, LGG 705, LGG 694, LGG 704, LGG 696, LGG 687

2	II	6	LGG 709, LGG 710, LGG 706, LGG 708, LGG 685, LGG 684
3	III	4	LGG 690, LGG 707, LGG 702, LGG 701
4	IV	1	LGG 692
5	V	1	LGG 700
6	VI	1	LGG 699
7	VII	1	LGG 691
8	VIII	1	LGG 689
9	IX	1	LGG 698
10	X	1	LGG 686

Table 2. Percentage contribution of different traits towards divergence in greengram (*Vigna mungo* L.)

S. No.	**Source**	**Number times ranked first**	**Percentage of contribution**
1	Days to 50% flowering	33	7.59%
2	Days to maturity	19	4.37%
3	Plant height	1	0.23%
4	Number of branches/plant	8	1.84%
5	Number of clusters/plant	10	2.30%
6	Number of pods/plant	5	1.15%
7	Pod length	0	0
8	Number of seeds/pod	4	0.92%
9	Test weight	341	78.39%
10	Seed yield/ ha	14	3.22%

Table 3. Intra and Inter Cluster distances of 30 genotypes using Mahalonobis D^2 analysis

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
Cluster 1	**15.56**	40.43	307.63	37.31	149.86	44.40	38.26	119.77	143.18	531.27
Cluster 2		**21.52**	170.63	101.95	68.88	112.95	58.89	45.29	63.34	337.47
Cluster 3			**22.83**	467.00	50.07	472.94	333.77	63.14	60.71	53.47
Cluster 4				**0.00**	263.28	24.97	55.90	215.77	250.08	717.11
Cluster 5					**0.00**	245.07	191.53	28.73	27.60	158.56
Cluster 6						**0.00**	82.31	238.43	267.61	753.22
Cluster 7							**0.00**	123.07	179.95	552.56
Cluster 8								**0.00**	30.31	162.62
Cluster 9									**0.00**	153.02
Cluster 10										**0.00**

Table 4. Cluster wise mean performance of 30 mungbean genotypes for yield and its related traits

Character / Trait	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
50% flowering	43.23	42.33	42.42	41.00	44.00	44.00	39.33	39.00	46.00	40.00
Days to maturity	70.56	69.67	69.33	68.67	71.00	71.00	63.67	67.00	71.33	68.00
Plant height (cm)	40.94	41.07	38.02	42.50	36.63	38.87	40.69	39.95	39.65	38.50
No. of branches/ plant	1.63	1.32	1.58	1.47	1.53	1.53	1.67	1.80	1.00	1.27
No. of clusters/plant	5.16	5.49	3.13	4.27	1.53	1.53	6.73	4.60	5.20	4.07
No. of pods/plant	14.40	15.16	13.40	9.67	15.13	16.07	16.73	13.67	8.47	8.80
Pod length	7.04	7.05	8.02	6.05	8.90	7.31	7.17	7.91	9.29	7.37
No. of seeds/pod	10.33	9.92	11.03	8.93	10.80	10.40	9.20	9.60	10.52	8.40
Test weight	3.63	3.91	4.66	3.35	4.32	3.37	3.59	4.21	4.30	4.97
Seed yield/ha	725.95	717.99	633.58	740.49	860.69	771.87	783.40	552.98	635.97	527.22

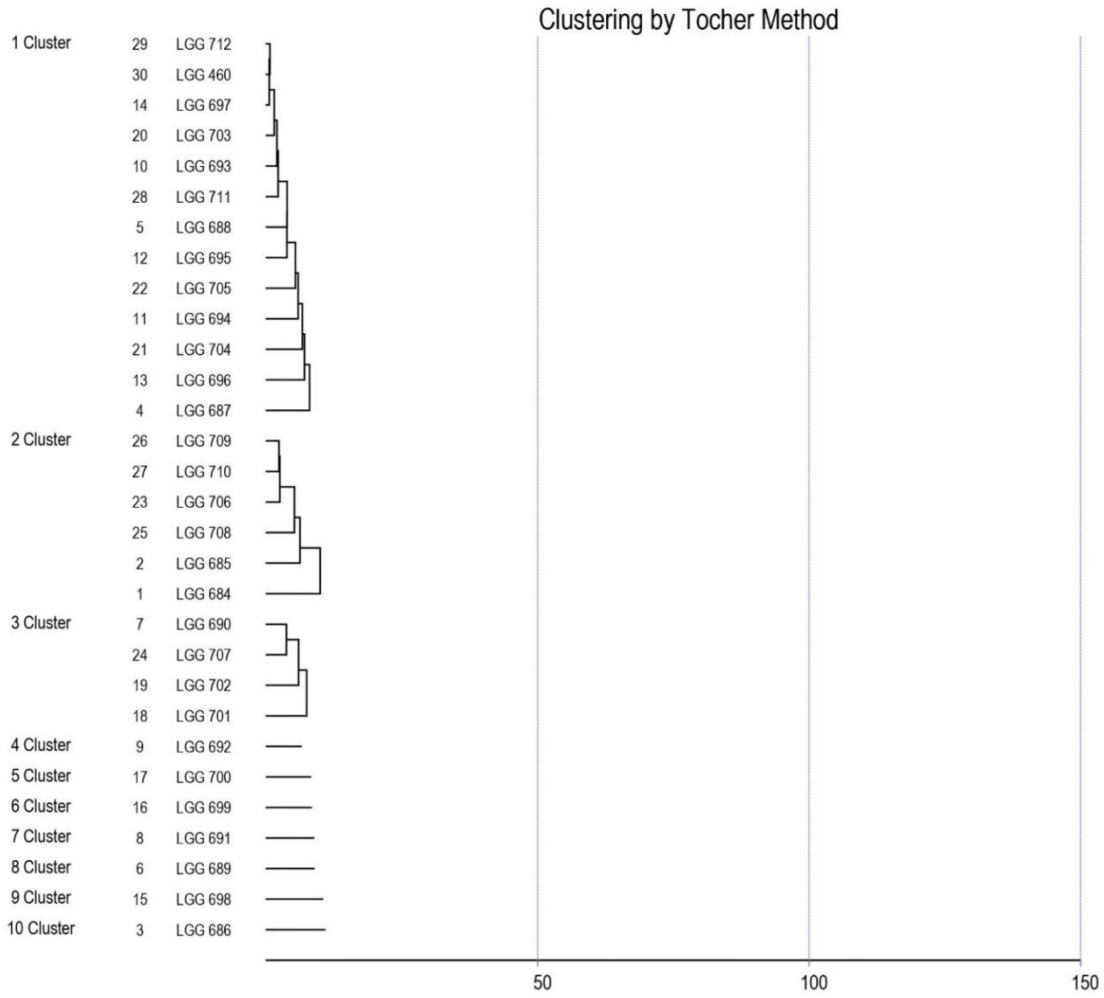

Fig. 1. Clustering of 30 genotypes of greengram by Tochers' method.

ACKNOWLEDGEMENTS

The first author is highly grateful to Acharya NG Ranga Agricultural University for providing the Fellowship during M. Sc (Ag.) programme.

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