Received: 10 Apr 2019 | Revised: 26 Jun 2020 | Accepted: 28 Jun 2020

Electronic Journal of Plant Breeding

Research Article

An appraisal of genetic divergence in some indigenous collections of mungbean (*Vigna radiata* (L.) Wileczek)

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Abstract
The present investigation was undertaken to retrieve information on the nature and extent of genetic diversity among 110 mungbean genotypes for yield related traits by using Mahalanobis's D^2 statistics. One hundred and ten genotypes could be grouped under 15 clusters, cluster XV showed maximum intra-cluster distance while the highest inter-cluster distance was observed between cluster VI and XIII. Seed yield exhibited a maximum contribution to genetic divergence (72.02 per cent) followed by days to 50 per cent flowering (15.33 per cent) and plant height (4.24 per cent) while the other traits *viz.,* the number of clusters per plant, the number of pods per cluster, pod length and seeds per pod exhibited insignificant values for contribution to genetic divergence. The maximum and minimum cluster value for seed yield ranged from 5.83 to 19.13. The greater the distance between two clusters, the wider the genetic diversity between the varieties. Keeping this in view, it is indicated that hybridization between the varieties (SML 171/1, AGG 11-013, FRM 1320, EC 396114 and SML 138) of cluster VI and cluster XIII (CO 4, VPM 50 and PLM 501), cluster VIII (V4, V2 and CO 7) and cluster VI (CO 4, VPM 50 and PLM 501), cluster II (AGG 10-850 and EC 396118) with cluster VI (SML 171/1, AGG 11-013, FRM 1320, EC 396114 and SML 138) would produce a better seed yield along with earliness in green gram.

Keywords
genetic diversity, green gram, Mahalanobis, D^2 analysis.

INTRODUCTION

Greengram (*Vigna radiata (L.)Wileczek*) most popularly termed as mungbean grown extensively over tropical and sub-tropical regions of India constituting a rich source for dietary protein. On an average, the seed have 24 per cent of protein and is rich in lysine which is predominantly deficient in cereal grains. Today, India identified as the largest producer and consumer of greengram in the world. Since, it is a highly self pollinated crop, variation existing within or between the species or varieties becomes important (Bisht *et al*., 2005 and Mahalingam *et al.,* 2018, Anamika *et al.,* 2017 and Suhel Mehandi, 2015). The utilization of diverse cultivars helps to tap significant amount of genetic variability for the trait based yield improvement in greengram (Sandhiya and Saravanan, 2018). The success of any breeding program depends on the immensity of the genetic variability present in these characters in the selected genotypes. Saravanan *et al*. (2017) reported the selection criteria for realising of higher seed yield through interpreting associated traits of yield. Multivariate analysis by means of the Mahalanobis generalized distance (D^2) statistic is a powerful tool in quantifying the degree of divergence at the genotypic level and might be an efficient tool in the quantitative estimation of genetic diversity in green gram genotypes (Mahalanobis, 1936). Hence, the present study was designed to assess the genetic divergence and clustering pattern among the greengram cultivars towards the identification of suitable parents for utilization in genetic introgression.

MATERIALS AND METHODS

The trial was conducted at D block farm of Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam during Rabi season of 2017-18. The experimental population includes 110 greengram cultivars (table 6.) of diverse origin and each entry is grown on a plot of 2.4m^2 in RBD design with a spacing of 30×10 cm in two replications. Observations are recorded on ten morphological characters *viz.,* days to 50% flowering (days), plant height (cm), the number of primary branches, the number of clusters per plant, the number of pods per cluster, the number of pods per plant, the number of seeds per pod, pod length (cm), 100 seed weight and single plant yield were recorded from five plants in the middle of the row excluding the border plants at appropriate crop stages.

The interpretation on genetic distance between the two populations (Mahalanobis, 1936 as D^2) was obtained by Tochers method. The contribution of individual characters towards divergence was estimated as per Singh and Chaudhary (1985). Further, grouping of cultivars into various clusters was made besides the average intra and inter cluster distance were estimated. Adopting the single factor analysis, the experimental data were subjected for statistical analysis and confirmed the existence of significant difference in mean values among the different genetic parameters taken for study.

RESULTS AND DISCUSSION

The assessment of genetic divergence among greengram cultivars would be useful in genetic interpretation of phenotypic traits, sorting cultivars on trait based expression besides the removal of any duplication in genetic stock. Genotypes of diverse geographic base are usually selected for gene introgression presuming their greater genetic distance. But, in contrast, the cultivars of different eco-geographical regions do necessarily have no relation for genetic diversenes (Saravanan *et al.,* 2017). In the present study, 110 greengram cultivars of diverse origin were subjected for appraisal of genetic divergence after the confirmation of significant difference among the test cultivars projecting the existence of genetic variation for ten yield related traits. Considering the clustering pattern (**Table 1**).

The maximum intra cluster distance was observed in cluster XV, followed by cluster XIV, signifying a minimal genetic divergence still existed among the varieties. This could be made use of in the yield improvement through recombination breeding. Considering the inter cluster D^2 values of fifteen clusters, it was interpreted that the highest divergence occurred between cluster VI and cluster XIII followed by cluster VIII and cluster XIII, cluster XII and cluster XIII and cluster II and cluster VI suggesting that the crosses involving lines from these clusters would

Table 1. Analysis of variance for different characters in green gram.

Source of Variation	Mean Sum of Squares										
	d.f.	Days to 50% flowering	Plant height (cm)	Number of primary branchs/ plant	Number of clusters/ plant	Number of pods/ cluster	Number of pods/ plant	Number of seeds/ pod	100 seed weight (g)	Pod length (cm)	Single plant yield (g)
Replication	1	0.86	5.21	0.07	0.32	032	54.36	0.21	0.18	0.13	2.33
Genotypes	109	103.8**	140.60**	0.64**	24.90**	0.46**	376.65**	2.46**	1.31**	1.69**	66.36**
Error	109	0.66	8.74	0.15	0.13	0.13	09.64	0.36	0.35	0.48	0.28
S.E.(d)		0.64	2.44	0.31	0.29	0.29	3.16	0.49	0.48	0.57	0.43
C.D(5%)		1.3	4.70	0.62	0.58	0.58	7.13	0.96	0.95	1.12	0.85

***** Significant at 1% level of significance***

give wider and desirable recombinations. The lowest divergence was noticed between cluster I and cluster X followed by cluster VI and cluster VIII. (Table 3)

It is expected that the maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective is not only high heterosis but other quality characters also. The greater the distance between two clusters, the wider the genetic diversity between the varieties. Keeping this in view, it is indicated that hybridization between the varieties (SML 171/1, AGG 11-013, FRM 1320, EC 396114 and SML 138) of cluster VI and cluster XIII (CO 4, VPM 50 and PLM 501), cluster VIII (V4, V2 and CO 7) and cluster VI (CO 4, VPM 50 and PLM 501) and cluster II (AGG 10-850 and EC 396118) with cluster VI (SML 171/1, AGG 11-013, FRM 1320, EC 396114 and SML 138) would produce encouraging results. The varieties of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity. Investigation on phylogenetic relationships among the greengram germplasm would help to realised necessary enriched vision for widening the genetic base besides protecting the conservation strategies for crops. (El. Esawi *et.al.*, 2016). Further, it is observed that hybridization between the diverse cultures/ germplasm would enable to get progenies holding broader genetic base with greater genetic potential on yield constituting traits (Mahalingam *et.al.,* 2018). Also, the cultures with wider genetic base could prove to broadening the genetic background of local breeding varieties (Wang *et al.,* 2018).

Table 2. Composition of D^2 cluster for greengram genotypes

Cluster number	No. of genotypes	Genotypes
I	2	LM -15, LM – 130
II	2	AGG-10-850, EC – 396118
III	3	MH- 565, LM – 154,AGG 11 012
IV	6	AGG-09-072, SML – 1077, IPM–2-14, EC–591388, AGG-09-063, AGG-11-004
V	33	AGG-09-073, PusaRatna, MH–309, CO-GG 980, Bing Mung–2, AGG-11-019, PHM-32, AGG-07-074, IPM-99125, AGG-10-091, AGG-10-085, EC-96100, CO-GG-930, AGG-11-010, FRM-131/9, Pusa- 0577, AGG-10-086, AGG- 11-01, LM- 30,AGG- 09- 087, FRM-1317,Annur- 2, AGG-09-074, AGG-10-091 (SR), AGG-10-087, AGG-10-088, GPB – 7784, EC –393612, Bing Mung– 1,Pusa Vishal, IC–39894, Annur– 3, EC 396114.
VI	5	SML - 171/1, AGG-11-013, FRM-1320, EC – 396114, SML – 138
VII	11	AGG-09-073, SML – 131,GPB-1784, CO GG 973, EC –396700, AGG 01 085, LM -109, AGG 09 077, AGG 10 092, VaraganesiPasi, AGG 10 087
VIII	2	V4/V2, CO – 7
IX	7	Annur- 1, PLS – 275, Erode Local, CO GG 365, CO – 27, AGG - 09 067, EC 591388
X	2	GM - 89 – 10, GPB GM 11887
XI	2	IC – 52077, EC- 396118
XII	8	LM – 130, MDU – 8379,IC – 39844, MH – 378, CO – 6, SML – 1151, MGG 329/1, GG 1734
XIII	3	CO – 4, VPM 50, PLM – 501
XIV	22	MDU–1, PLS – 2694,AGG 09 078, AGG 09 068, AGG 10 085, IC – 39317, IC – 52077, AGG 10 073, AGG - 10 091, PDM 86 199, LM – 104,SML – 1077,LM – 13, GM - 89 – 10, AC – 152, ML – 192, CO GG 11007, CO – 8, CO GG 365, GGPB 8897, EC 396126, AGG 09 075,PLS 302
XV	2	IPM – 029, GG – 107

Table 3. Average inter and intra cluster D^2 values for 110 greengram germplasm

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	2.07	6.63	17.96	12.47	12.44	25.82	17.40	23.98	11.48	4.65	9.82	22.70	11.19	16.55	13.94
II		2.92	21.91	12.47	15.03	29.68	20.91	28.27	13.34	8.58	15.19	26.82	11.41	19.54	15.49
III			17.67	23.64	18.47	16.49	15.63	14.52	19.91	16.99	12.46	16.35	24.70	17.02	22.09
IV				11.23	17.13	29.60	20.73	28.45	18.19	11.20	17.94	27.14	19.62	21.03	23.29
V					16.26	24.06	17.78	22.48	16.54	12.04	13.14	21.98	18.96	17.96	19.45
VI						11.41	17.19	8.97	26.72	24.04	18.42	14.96	33.56	20.32	29.92
VII							15.24	15.65	19.96	15.75	13.46	17.05	25.61	16.83	24.07
VIII								3.94	24.90	22.63	16.49	13.11	31.62	18.59	28.16
IX									16.63	12.62	13.93	24.09	15.95	19.15	16.82
X										3.96	9.15	21.35	14.25	15.73	16.25
XI											4.01	16.35	17.32	14.03	15.87
XII												17.35	29.97	19.48	26.97
XIII													9.03	23.36	13.11
XIV														18.22	22.14
XV															18.54

The cluster mean for days to 50% flowering was highest in cluster XV and the lowest in cluster IV. Higher and lower plant height was recorded in cluster XI and cluster II respectively. Cluster XII recorded the highest total number of primary branches per plant and the lowest number of primary branches per plant was in cluster II. While, cluster XII recorded the highest clusters per plant, lower cluster per plant was recorded in cluster XIII. The cluster mean for pods per cluster was highest in cluster VIII while cluster II and XV accommodated the lowest number of pods per cluster. Highest and lowest number of pods per plant showed in the clusters VIII and XIII respectively. The cluster means for seeds per pod was highest in cluster VIII and the cluster II exhibited the lowest value for seeds per pod. Pod length registered the highest value in cluster XIII while cluster II shown the lowest value for pod length.

Higher cluster mean value for 100 seed weight was obtained in the cluster XII and lowest value recorded by the cluster IV The maximum and minimum cluster value for seed yield ranged from 5.83 to 19.13 (Table 4).

Table 4. Cluster mean among green gram genotypes

	CHARACTERS									
Cluster	**Days to 50% flowering**	**Plant height (cm)**	**No. of primary**	**No. of clusters per plant**	**No. of pods per cluster**	**No. of Pods per plant**	**No. of seeds per pod**	**Pod length (cm)**	**100 seed weight (g)**	**Yield (g)**
I	40.33	44.43	3.13	13.53	2.97	40.50	9.70	6.82	2.12	8.37
II	40.17	32.38	2.70	11.67	2.73	31.43	8.57	5.84	2.26	5.83
III	38.11	46.04	3.42	15.42	3.47	52.64	9.84	7.20	2.86	15.00
IV	33.50	42.14	3.13	11.98	3.22	37.91	9.22	6.29	1.72	5.93
V	38.05	44.54	3.27	14.21	3.07	43.48	9.65	6.53	2.39	10.10
VI	33.60	45.92	3.23	15.47	3.47	53.53	10.32	6.27	3.22	18.38
VII	34.21	45.76	3.24	15.99	3.25	50.79	9.76	6.78	2.76	13.49
VIII	35.17	42.32	3.47	16.97	3.53	59.47	11.70	7.14	2.77	19.13
IX	41.48	41.53	2.82	13.83	3.15	43.71	9.33	6.03	2.24	9.34
X	37.67	46.63	3.23	13.00	3.23	40.60	9.23	6.73	2.29	8.62
XI	40.00	54.50	3.03	13.30	3.40	44.93	10.37	6.41	2.67	12.33
XII	35.67	50.04	3.59	17.24	3.51	59.40	10.18	6.97	3.40	16.99
XIII	47.00	42.30	2.73	9.96	3.00	29.87	10.58	7.38	2.18	6.67
XIV	37.12	41.50	3.10	14.28	3.33	47.59	9.84	6.73	2.72	12.70
XV	47.67	42.97	2.93	12.80	2.73	35.30	9.60	6.77	2.74	9.43

Table 5. Relative contribution of different characters to genetic divergence

CHARACTER	NO. OF FIRST RANK	% CONTRIBUTION
Days to 50% flowering	919	15.329
Plant height	254	4.237
No. of primary branches	24	0.400
No. of clusters per plant	35	0.584
No. of pods per cluster	51	0.851
No. of pods per plant	159	2.652
No. of seeds per pod	163	2.719
Pod length	35	0.584
100 seed weight	37	0.617
Yield	4318	72.027

Seed yield exhibited maximum contribution to genetic divergence (72.02 per cent) followed by days to 50 per cent flowering (15.33 per cent) and plant height (4.24 per cent) while the other traits *viz.,* the number of clusters per plant, the number of pods per cluster, pod length and seeds per pod exhibited insignificant values for contribution to genetic divergence (Table 5). Malli and Lavanya (2018) reported the maximum genetic divergence of cultures vide traits of seed yield /plant and seeds per pod. Further, no cluster contained at least one variety with all the desirable traits, which ruled out the possibility of selecting directly one variety for immediate use. Therefore, hybridization between the selected varieties from divergent clusters is essential to judiciously combine all the targeted traits (Aher *et al.,* 2018 and Singh *et al.,* 2012). It is observed that culivars in cluster VIII *viz*., V4, V2 and CO – 7 exhibited favourable cluster mean values for the key traits like the number of pods per cluster, pods per plant and seeds per pod and hence these cultivars can be better exploited for genetic introgression studies (Sen and De, 2017). The cluster VI is having a highest mean value for the number of primary branches per plant, the number of clusters per plant, pods per cluster, pods per plant, seeds per pod, 100 seed weight and seed yield followed by cluster 12 that exhibited significant cluster mean values for days to 50 per cent flowering, plant height, the number of primary branches per plant, the number of clusters per plant, the number of pods per cluster, the number of seeds

per pod, 100 seed weight and seed yield suggesting the utilization of cultivars accommodated in the said clusters in trait based breeding. Further, the clusters IV, VII and XIV do also exhibited favourable cluster mean values for most of the traits indicating the direct use of the cultivars clustered in these clusters or may be as parents in future hybridization programme (Table 5).

Table 6. Details of Green gram accessions utilized for the study

Sl. No.	Genotype	Source	Sl. No.	Genotype	Source	Sl. No.	Genotype	Source
1	AC-52	NPRC, Vamban	38	CO-27	TNAU, Coimbatore	75	IPM-0214	IIPR, Kanpur
2	AGG-09-067	NPRC, Vamban	39	CO–4	TNAU, Coimbatore	76	IPM–0219	IIPR, Kanpur
3	AGG-10-093	NPRC, Vamban	40	CO–6	TNAU, Coimbatore	77	IPM-99125	IIPR, Kanpur
4	AGG-01-085	NPRC, Vamban	41	CO–7	TNAU, Coimbatore	78	LM–109	Guntur
5	AGG-09-068	NPRC, Vamban	42	CO–8	TNAU, Coimbatore	79	LM–115	Guntur
6	AGG-09-072	NPRC, Vamban	43	CO GG 11 07	TNAU, Coimbatore	80	LM–13	Guntur
7	AGG-09-077	NPRC, Vamban	44	CO GG 11 03	TNAU, Coimbatore	81	LM–130	Guntur
8	AGG-09-078	NPRC, Vamban	45	CO GG 365	TNAU, Coimbatore	82	LM–15	Guntur
9	AGG-09-079	NPRC, Vamban	46	CO GG 973	TNAU, Coimbatore	83	LM–154	Guntur
10	AGG-10-074	NPRC, Vamban	47	CO-GG-930	TNAU, Coimbatore	84	LM-104	Guntur
11	AGG-10-084	NPRC, Vamban	48	CO-GG-980	TNAU, Coimbatore	85	LM-30	Guntur
12	AGG-10-090	NPRC, Vamban	49	EC-396114	NBPGR, New Delhi	86	MDU–1	TNAU, Madurai
13	AGG-10-092	NPRC, Vamban	50	EC-396121	NBPGR, New Delhi	87	MDU–8379	Madurai local, Tamil Nadu
14	AGG-11-002	NPRC, Vamban	51	EC-496841	NBPGR, New Delhi	88	MGG 329/1	Madurai local, Tamil Nadu
15	AGG-11-011	NPRC, Vamban	52	EC-591388	NBPGR, New Delhi	89	MH–318	HAU, Hisar
16	AGG-07-074	NPRC, Vamban	53	EC-93612	NBPGR, New Delhi	90	MH–378	HAU, Hisar
17	AGG-09-063	NPRC, Vamban	54	EC-96700	NBPGR, New Delhi	91	MH-565	HAU, Hisar
18	AGG-10-072	NPRC, Vamban	55	EC-396118	NBPGR, New Delhi	92	ML–192	HAU, Hisar
19	AGG-09-073	NPRC, Vamban	56	EC-396126	NBPGR, New Delhi	93	PDM 86 199	HAU, Hisar
20	AGG-09-076	NPRC, Vamban	57	EC-591389	NBPGR, New Delhi	94	PHM–32	PAU, Ludiana
21	AGG-09-074	NPRC, Vamban	58	EC-396100	NBPGR,New Delhi	95	PLM–501	Warangal
22	AGG-10- 089	NPRC, Vamban	59	Erode Local	Tamil Nadu	96	PLS 269A	NBPGR, New Delhi
23	AGG-10-085	NPRC, Vamban	60	FRM-131/7	NBPGR, New Delhi	97	PLS 275	PAU, Ludiana
24	AGG-10-086	NPRC, Vamban	61	FRM-1317-1	NBPGR, New Delhi	98	PLS 302	NBPGR, New Delhi
25	AGG-10-087	NPRC, Vamban	62	FRM-1320	NBPGR, New Delhi	99	Pusa-0577	IARI, New Delhi
26	AGG-10-088	NPRC, Vamban	63	GG–107	NPRC, Vamban	100	Pusa Ratna	IARI, New Delhi
27	AGG-10-091 (SR)	NPRC, Vamban	64	GG 1734	NPRC, Vamban	101	Pusa Vishal	IARI, New Delhi
28	AGG-10-092	NPRC, Vamban	65	GGPB 8897	NPRC, Vamban	102	SML–115	PAU, Ludiana
29	AGG-11-004	NPRC, Vamban	66	GM-89-10	NPRC, Vamban	103	SML–1151	PAU, Ludiana
30	AGG-11-010	NPRC, Vamban	67	GPB–7784	NPRC, Vamban	104	SML–131	PAU, Ludiana
31	AGG-11-013	NPRC, Vamban	68	GPB GM 11887	NPRC, Vamban	105	SML–138	PAU, Ludiana
32	AGG-11-019	NPRC, Vamban	69	GPB-1784	NPRC, Vamban	106	SML–171/1	PAU, Ludiana
33	Annur-1	Local variety, Tamil Nadu	70	IC–39317	NBPGR, New Delhi	107	SML-1077	PAU, Ludiana
34	Annur-2	Local variety, Tamil Nadu	71	IC–39344	NBPGR, New Delhi	108	V4/V2	Taiwan
35	Annur-3	Local variety, Tamil Nadu	72	IC–39894	NBPGR, New Delhi	109	Varaganesi pasi	NPRC, Vamban
36	Bing Mung- 1	Maharashtra	73	IC–39345	NBPGR, New Delhi	110	VPM 50	Tamil nadu
37	Bing Mung - 2	Maharashtra	74	IC–52077	NBPGR, New Delhi			

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