

Original Research Article

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## Parental Selection for Varietal Improvement through Genetic Divergence Analysis in Mungbean (*Vigna radiata* (L.) Wilczek)

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### ABSTRACT

Thirty five mungbean genotypes were evaluated to select superior parents with genetic diversity based on yield and physiological traits in order to develop high yielding varieties in mungbean. The results of multivariate analysis ( $D^2$ ) indicated the presence of considerable genetic divergence among these genotypes. The genotypes were grouped into seven clusters. Out of seven clusters, cluster I contained maximum number of thirteen genotypes, followed by cluster II with ten genotypes and cluster IV with seven genotypes. The maximum intra-cluster distance was recorded by cluster IV (34.70), while the minimum distance was noted in the clusters V, VI and VII (0.00) as they included single genotype each. The maximum inter-cluster  $D^2$  value was observed between cluster III and IV (153.62) followed by II and IV (145.11) and cluster IV and VII (110.29). While, the minimum  $D^2$  value was found between cluster V and VI (19.06). Based on genetic diversity studies hybridization programme might be initiated between GVIT-203 X WGG-42 (cluster III and IV) and KM-122 X EC-396117 (cluster II and IV) in order to get transgressive segregants, since these genotypes showed maximum diversity. The characters *viz.*, leaf area duration, chlorophyll content, seed yield per plant, 100 seed weight and net assimilation rate had maximum contribution to the total genetic divergence.

#### Keywords

Mungbean,  $D^2$  analysis, Diversity.

#### Article Info

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### Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is one of the important pulse crops grown in India. It is grown as kharif and summer crop. Among the wide array of pulse cultivation in India mungbean holds key position as it has established itself as highly valuable short duration crop having many desirable characters like high protein content, wider adaptability, low input requirement and ability to improve soil fertility. In spite of its importance, the productivity of this crop is relatively low. The major constrains in

achieving higher yield of this crop are lack of genetic variability, poor harvest index absence of suitable ideotypes for different cropping systems and susceptibility to diseases. Hence, the assessment of genetic diversity is an important step in a breeding program aimed at improving crop yields through development of high yielding cultivars with increased physiological efficiency. Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parental lines.

Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing promising parents for purposeful hybridization. Though several tools to measure genetic divergence are available, multivariate analysis by means of Mahalanobis  $D^2$  statistic is a powerful and simple tool in quantifying the divergence among genotypes. Understanding the genetic diversity among the genotypes helps in revealing genetic variation besides providing the information regarding the possibility of getting transgressive segregants. Characterization, evaluation and utilization of diverse genotypes are not only vital for improvement but also to safeguard the crop against its vulnerability to various abiotic and biotic stresses.

### Materials and Methods

The experimental material for the present study consisted of thirty five diverse genotypes of mungbean which were grown in randomized block design with three replications during *khari*, 2015 at Sri Venkateswara Agricultural College dry land farm, Tirupati. Each genotype was sown in three rows of 3m length with a spacing of 30 cm between rows and 10 cm between plants within rows. The observations on the fourteen characters were recorded on five competitive plants taken from each replication for plant height, number of clusters per plant, number of pods per cluster, number of seeds per pod, number of pods per plant, hundred seed weight, harvest index, seed yield per plant, net assimilation rate, leaf area duration, SPAD Chlorophyll meter reading (SCMR) and chlorophyll content. The characters *viz.*, days to 50% flowering and days to maturity were recorded on per plot basis. The data collected on the yield, yield component characters coupled with physiological traits among the thirty five genotypes of mungbean were subjected to Mahalanobis  $D^2$  analysis (Mahalanobis, 1936) as suggested by Rao

(1952) and the genetic diversity was estimated. The thirty five genotypes were grouped into respective clusters on the basis of  $D^2$  values using Tocher's method (Rao, 1952).

### Results and Discussion

For successful hybridization programme, selection of diverse parents is essential since the crosses involving genetically divergent parents are likely to produce good heterotic effects and also help in recovery of better segregants in the following segregating generations. The analysis of variance revealed highly significant differences among 35 genotypes for all the 14 characters studied. The thirty five genotypes were grouped into seven clusters and distribution of genotypes into each of seven clusters was presented in Table 1 and Figure 1. Out of seven clusters, cluster I contained maximum number of thirteen genotypes, followed by cluster II with ten genotypes, cluster IV with seven genotypes and cluster III with two genotypes. Whereas, clusters V, VI and VII comprised of only one genotype each. Critical analysis of clustering pattern revealed that the genotypes originating from different eco-geographical regions were grouped together into different clusters. The clustering pattern obtained in the present study indicated that the genotypes originating from different geographical regions grouped together into different clusters show no parallelism between genetic diversity and geographical distribution. The genetic diversity among the genotypes may be due to factors like history of selection, heterogeneity, selection under diverse environments and genetic drift. These results were also in conformity with Sunil *et al.*, (2011), Patel and Patel (2012), Ajay *et al.*, (2012), Vijay and Shekhawat (2012), Narasimhulu *et al.*, (2013), Garje *et al.*, (2013), Shweta (2013), Swathi (2013), Laxmi *et al.*, (2013), Paramesh *et al.*, (2014), Rekha *et al.*, (2015) and Aijaz *et al.*, (2016).

Genotypes grouped into the same cluster diverge little from one another when the aggregate of characters were measured. Statistical distances represent the index of genetic diversity among clusters. The average intra and inter-cluster  $D^2$  and  $D$  values of seven clusters were furnished in Table 2. Intra-cluster average  $D^2$  values were ranged from 0.00 to 34.70. In the present study, the intra-cluster distance was maximum for cluster IV (34.70) followed by cluster II (26.53), cluster I (21.05) and cluster III (10.13), while it was zero for cluster V, cluster VI and cluster VII as these clusters consisted of single genotype. The highest intra-cluster distance in cluster IV indicates the presence of considerable genetic diversity among the seven genotypes within the cluster.

The maximum inter-cluster distance was recorded between cluster III and IV (153.62) followed by II and IV (145.11), cluster IV and VII (110.29) and cluster IV and VI (106.42) and cluster IV and V (89.16) suggesting highest genetic divergence existing between the genotypes of these clusters and expected to give higher frequency of better transgressive segregants or desirable combinations for development of useful genetic stocks or varieties. The inter-cluster distance was minimum between cluster V and VI (19.06) followed by cluster I and V (36.49), cluster I and VI (39.46), cluster II and III (42.26) and cluster II and VII (43.87) indicating a close relationship and similar magnitude for most of the characters of the genotypes in these clusters.

A perusal of cluster means for different characters revealed the considerable differences among the clusters for all the characters (Table 3). Early flowering was observed in the genotypes of cluster V (32.33 days), while delayed flowering was noticed in the genotypes of cluster I (35.36 days). Days to maturity was ranged from 58.33 days in cluster V to 65.33 days in cluster III. The

plant height was maximum in cluster VI (60.07 cm) and minimum in cluster IV (52.17 cm). The cluster mean for number of clusters per plant ranged from 11.34 in cluster IV to 16.70 in cluster III. Number of pods per cluster ranged from 3.17 in cluster IV to 4.20 in cluster II. The genotypes in cluster III recorded high seed yield per plant (18.58g), while genotypes in cluster VII recorded low seed yield per plant (10.96 g).

The genotypes of cluster II exhibited highest cluster mean for number of pods per cluster, number of seeds per pod and leaf area duration, whereas the genotypes of cluster III exhibited higher number of clusters per plant, number of pods per plant and seed yield per plant. Similarly, maximum values were registered by the genotypes of cluster IV for 100 seed weight; cluster V for net assimilation rate and SCMR; cluster VI for plant height and cluster VII for harvest index and chlorophyll content.

Inter-crossing of the genotypes from these clusters could be suggested to generate a wide spectrum of variability followed by effective selection for these characters.

The performance of genotypes and the characters with maximum contribution towards divergence should also be considered for inclusion of genotypes in the hybridization programmes for improvement of mungbean. The number of times that each of the fourteen characters appeared in first rank and its respective per cent contribution towards diversity is presented in Table 4. Among all the characters studied, leaf area duration contributed the maximum (49.92%) to the diversity by taking first rank in 297 times, followed by chlorophyll content (19.33%) with 115 times ranked first, seed yield per plant (16.30%) with 97 times ranked first, 100 seed weight (3.87%) with 23 times ranked first and net assimilation rate (3.70%) with 22 times ranked first.

**Table.1** Cluster composition of thirty five mungbean genotypes (Tocher's method)

Cluster No.	No. of genotypes	Genotypes
I	13	MGG-295, ML-267, TM-96-2, ASHA, PM-115, ML-145, VG-6197A, MGG-350, PM-110, LGG-450, LGG-460, AKM-9904 and IPM-02-14.
II	10	LGG-407, PUSA VISHAL, IPM-02-13, MGG-380, RM-112, KM-8651, PUSA 9531, JBT37/150, KM-122 and WGG-37.
III	2	GVIT-203 and LM-95.
IV	7	IPM-02-19, RMG-9912, SML-1023, EC-396117, WGG-42, WGG-2 and VG-7098A.
V	1	TLM-7
VI	1	LGG-528
VII	1	MGG-347

**Table.2** Intra cluster (diagonal) and inter-cluster distances for seven clusters in mungbean

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	21.05 (4.59)	48.12 (6.94)	47.58 (6.90)	67.25 (8.20)	36.49 (6.04)	39.46 (6.28)	46.83 (6.84)
Cluster II		26.53 (5.15)	42.26 (6.50)	145.11 (12.05)	44.05 (6.64)	44.96 (6.71)	43.87 (6.62)
Cluster III			10.13 (3.18)	153.62 (12.39)	77.83 (8.82)	78.60 (8.87)	52.67 (7.26)
Cluster IV				34.70 (5.89)	89.16 (9.44)	106.42 (10.32)	110.29 (10.50)
Cluster V					0.00 (0.00)	19.06 (4.37)	68.11 (8.25)
Cluster VI						0.00 (0.00)	66.29 (8.14)
Cluster VII							0.00 (0.00)

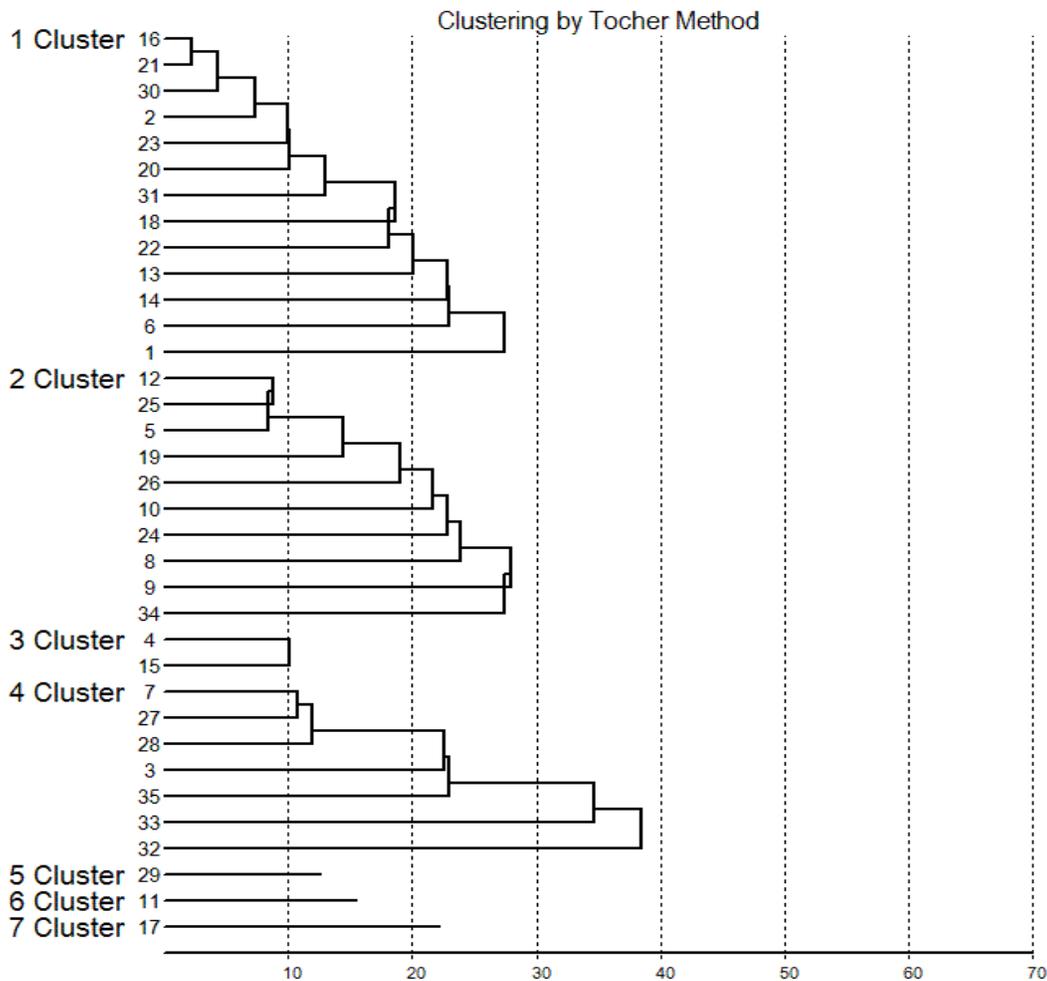
**Table.3** Mean performance of the clusters with respect to different characters

Character per cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of clusters plant <sup>-1</sup>	No. of Pods cluster <sup>-1</sup>	No. of seeds pod <sup>-1</sup>	No. of pods plant <sup>-1</sup>	100 seed weight (g)	Harvest index (%)	Net assimilation rate (g dm <sup>-2</sup> w <sup>-1</sup> )	Leaf area duration	SCMR	Chlorophyll content (mg g <sup>-1</sup> )	Seed yield per plant (g)
Cluster I	35.36	61.51	58.10	12.34	4.19	11.80	46.38	4.03	41.43	0.28	64.91	52.16	3.88	13.95
Cluster II	35.20	62.10	59.69	12.44	4.20	11.98	49.68	3.82	41.84	0.29	89.96	51.23	3.80	14.52
Cluster III	35.00	65.33	58.83	16.70	4.17	11.79	64.08	3.33	46.35	0.23	74.38	52.77	5.05	18.58
Cluster IV	33.33	60.81	52.17	11.34	3.17	11.60	29.95	4.62	51.43	0.35	51.81	54.01	3.75	13.11
Cluster V	32.33	58.33	55.67	13.53	4.13	11.40	54.97	4.38	46.52	0.36	77.10	54.87	2.73	14.49
Cluster VI	34.67	64.67	60.07	11.47	4.07	11.84	44.90	3.85	38.97	0.19	73.60	53.13	1.93	14.12
Cluster VII	35.00	61.00	55.53	11.93	4.11	11.72	45.03	3.96	51.72	0.14	84.70	53.83	4.15	10.96

**Table.4** Contribution of different quantitative characters to diversity in mungbean

S. No.	Character	Times ranked first	Contribution (%)
1.	Days to 50% flowering	0	0.00
2.	Days to maturity	0	0.00
3.	Plant height (cm)	0	0.00
4.	No. of clusters plant <sup>-1</sup>	5	0.84
5.	No. of pods cluster <sup>-1</sup>	9	1.51
6.	No. of seeds pod <sup>-1</sup>	6	1.01
7.	No. of pods plant <sup>-1</sup>	11	1.85
8.	100 seed weight (g)	23	3.87
9.	Harvest index (%)	8	1.34
10.	Net assimilation rate (g dm <sup>-2</sup> w <sup>-1</sup> )	22	3.70
11.	Leaf area duration	297	49.92
12.	SCMR	2	0.34
13.	Chlorophyll Content (mg g <sup>-1</sup> )	115	19.33
14.	Seed Yield plant <sup>-1</sup> (g)	97	16.30

**Fig.1** Dendrogram of thirty five mungbean genotypes obtained through Tocher's method of classification



Similar results were also reported by Sunil *et al.*, (2011), Narasimhulu *et al.*, (2013), Laxmi *et al.*, (2013) for seed yield; Mohan *et al.*, (2014), Gokulakrishnan *et al.*, (2012) for seed yield and 100 seed weight; Singh *et al.*, (2009) for 100 seed weight and Paramesh (2014) for chlorophyll content and seed yield per plant.

Theoretically, the maximum amount of heterosis and transgressive segregants would be manifested in cross combinations involving the parents belonging to the most divergent clusters. Based on present studies hybridization programme might be initiated

between GVIT-203 X WGG-42 (cluster III and IV), KM-122 X EC-396117 (cluster II and IV), IPM-02-19 X MGG-347 (cluster IV and VII), RMG- 9912 X LGG-528 (cluster IV and VI) and VG-7098A X TLM-7 (cluster IV and V) in order to get transgressive segregants, since, these genotypes showed maximum diversity.

In addition to diversity, genotypes belonging to different clusters having high means for desired characters may be successfully used in hybridization programmes. Similarly, the crosses between genotypes LM-95 X EC-396117 (cluster III and IV), WGG-37 X VG-

7098 A (cluster II and IV), VG-7098A X WGG-347 (cluster IV and VII) and EC-396117 X TLM-7 (cluster IV and V) could be suggested for the exploitation of transgressive segregants for yield and yield contributing characters like number of pods per plant, number of seeds per pod, 100 seed weight and seed yield per plant as the genotypes that are involved in the above said crosses viz., LM-95, WGG-37, TLM-7 and EC-396117 showed higher per se performance for the traits like number of clusters per plant, number of pods per plant, seed yield, days to maturity, days to 50% flowering SCMR and harvest index besides having maximum genetic divergence.

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