

# Genetic Diversity Studies in Selected Mungbean (Vigna radiata (L.) Wilczek) Cultivars under Summer Conditions

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### ABSTRACT

Genetic divergence among thirty one mungbean genotypes grown under summer conditions was estimated using Mahalanobi's D<sup>2</sup> statistic and total of eight clusters were obtained. Cluster I was the largest with twenty four genotypes. Except cluster I, all other clusters *viz.*, cluster II, cluster III, cluster IV, cluster V, cluster VI, cluster VII and cluster VIII had one genotype each. Cluster V recorded the highest mean for seed yield per plant followed by harvest index and relative injury percentage. The highest inter cluster distance was observed between cluster III and VII (1768.20). 100 seed weight contributed maximum towards diversity. Therefore, it was concluded that more emphasis should be given on these clusters for selecting genotypes as parents for crossing which may produce new recombinants with desired traits.

## Key words: Diversity, D<sup>2</sup> Analysis, Mungbean, Physiological Traits.

Mungbean is currently grown on about 6 million hectares, mainly in South and Southeast Asia, but increasingly extends into Australia, USA, Canada and Ethiopia. It is a cheap source of carbohydrates and easily digestible protein and contributes folate and iron to the diet (Roland et al., 2015). It has strong tap root system to cope up with low moisture stress and nodulation in roots to fix atmospheric nitrogen in the soil and so it is most suitable to grow in water deficient places. The production of mungbean is reducing due to vary biotic and abiotic stresses. Thus, there is a need to increase production and productivity of mungbean in the country by more intensive interventions. Traditionally mungbean is grown during kharif and summer seasons. A number of varieties have been developed and released for *kharif* season for its commercial cultivation but not much work has been done for summer season. Therefore, in the present study efforts have been made to evaluate germplasm during summer for morphological traits and physiological traits that can be used in the breeding programme. So far no sincere efforts have been made to screen germplasm during summer season and consequently no variety is released for summer cultivation of mungbean. The cultivation of mungbean in summer can benefit farmers in two ways: I) extra income can be generated by the

summer crop as fields lie vacant during summer and II) by improving soil fertility for the next *kharif* crop as mungbean is a leguminous crop and it fixes atmospheric nitrogen in the soils through the swellings in its roots (Om and Singh, 2016).

The crosses between the parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam, 1981) and this leads to successful mungbean crossing programme. In the present study genetic diversity was evaluated among these 31 mungbean genotypes based on morphological characters and physiological characters through Mahalanobi's  $D^2$  analysis under summer condition.

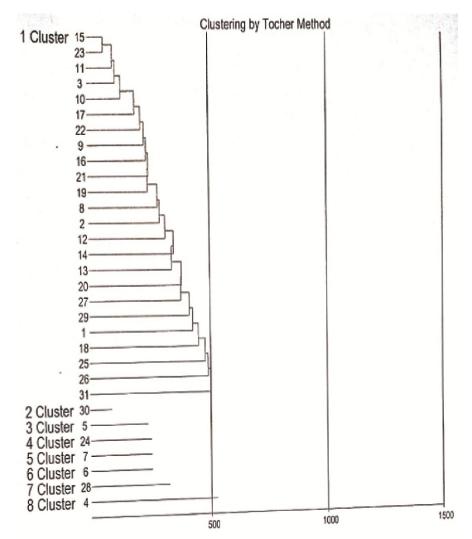
## **MATERIAL AND METHODS**

The experimental material for the present investigation consisted of thirty one mungbean genotypes obtained from Regional Agricultural Research Station, Lam, Guntur and Agricultural Research Station, Madira. The experiment was conducted in randomized block design (RBD) with three replications during summer, 2013-14 at wet land farm, Sri Venkateswara Agricultural College, Tirupati. Each genotype was sown in three rows of 4 m length with a spacing of 30 cm between rows and 10 cms between plants within rows. Observations were recorded on five randomly selected plants per replication for traits namely plant

Cluster No.	No. of genotypes	Genotypes
Ι	24	MGG 295, PUSA 9531, LGG 410, COGG 974, LGG 407, MGG 350, PM 110,
		KM-122, MGG 347, ML-267, MH-565, KM-8-657, ASHA, LGG 450, LGG
		528, LGG 460, ML-145, TM 96-2, VG 7098A, AKM 9904, MH-3-18, RMG
		492, TLM-7, WGG 37
II	1	WGG 2
III	1	GVIT 203
IV	1	PUSA VISHAL
V	1	IPM-02-19
VI	1	IPM-02-03
VII	1	VG-6197A
VIII	1	EC-396117

 Table 1. Cluster composition of thirty one mungbean genotypes (Tocher's method) under summer condition.

Fig. 1. Dendrogram of thirty one mungbean genotypes obtained through Tocher's method of classification under summer condition.

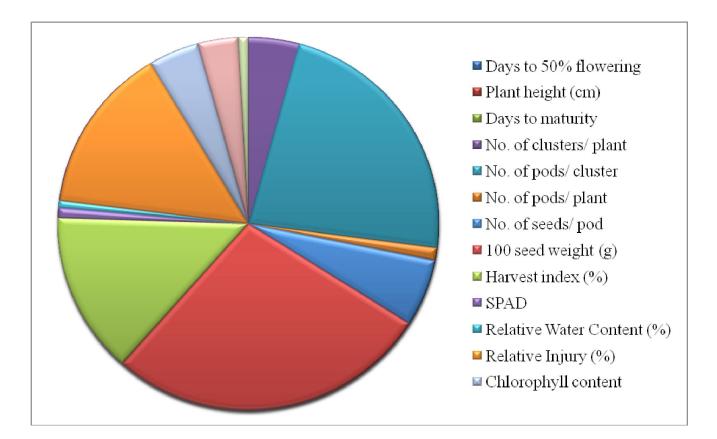


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	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	394.42	549.90	750.21	683.82	577.92	595.85	979.06	1085.70
	(19.86)	(23.45)	(27.39)	(26.15)	(24.04)	(24.41)	(31.29)	(32.95)
Cluster II		0.00	1419.78	894.01	470.02	349.69	325.44	1066.02
		(0.00)	(37.68)	(29.9)	(21.68)	(18.70)	(18.04)	(32.65)
Cluster III			0.00	444.37	773.95	1739.72	1768.20	860.25
			(0.00)	(21.08)	(27.82)	(41.71)	(42.05)	(29.33)
Cluster IV				0.00	900.00	1182.67	1341.76	808.26
				(0.00)	(30.00)	(34.39)	(36.63)	(28.43)
Cluster V					0.00	909.62	576.00	860.25
					(0.00)	(30.16)	(24.00)	(29.33)
Cluster VI						0.00	731.70	1351.29
						(0.00)	(27.05)	(36.76)
Cluster VII							0.00	678.6
							(0.00)	0(26.05)
Cluster VIII								0.00
								(0.00)

 Table 2. Intra cluster (diagonal) and inter-cluster distances for eight clusters in mungbean under summer condition.

Fig. 2. Relative contribution of different grain yield and physiological characters to diversity in mungbean under summer condition.



	100- Harvest SUMK KWC Kelative SLA (C Seed Seed index injury yield weight (%)	34.36 46.22 84.31 27.24 127.25 2.62	5.37 41.90 46.93 80.71 24.06 128.61 2.00 10.65	37.81 45.20 86.51 21.67 156.45 2.95	33.55 42.70 84.10 15.64 90.27 2.21	48.18 49.68 83.58 45.24 114.99 2.57	25.49 47.43 81.53 40.45 102.47 2.89	43.29 51.30 82.62 37.86 124.28 2.62	32.63 49.32 85.45 26.86 122.02
SLA									
	Kelauve injury (%)	27.24	24.06	21.67	15.64	45.24	40.45	37.86	26.86
	KWC	84.31	80.71	86.51	84.10	83.58	81.53	82.62	85.45
	SUMIK	46.22	46.93	45.20	42.70	49.68	47.43	51.30	49.32
	Harvest index	34.36	41.90	37.81	33.55	48.18	25.49	43.29	32.63
001	100- seed weight	3.85	5.37	3.45	4.06	4.60	4.25	6.34	5.61
-	Number of seeds per pod	10.11	9.41	11.79	10.52	10.59	9.00	10.14	12.88
	Number of pods per plant	23.26	30.33	24.67	26.33	27.33	30.00	20.00	21.00
-	Number of pods per cluster	3.77	3.03	5.96	6.73	3.49	2.91	3.85	6.20
	Number of clusters per plant	9.85	12.00	8.33	7.67	10.67	11.33	10.00	9.33
2	Plant height (cm)	56.22	54.77	62.67	57.52	62.55	47.96	48.44	47.56
Ĺ	Daysto maturity	68.78	69.33	69.33	69.67	69.33	65.33	70.67	68.33
ļ	Days to 50% flowering	43.54	42.00	43.00	44.67	42.67	40.33	45.00	44.00
	Character / Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII

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height, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 seed weight, harvest index, SPAD chlorophyll meter reading (SCMR), Relative Water Injury (RWC), Relative Injury Percentage (RI), Chlorophyll content and Specific Leaf Area (SLA). Whereas, traits days to 50 % flowering and days to maturity observations were recorded on plot basis. The mean values for each trait over the replications were subjected to the analysis of variance. Estimates of genetic divergence was done by following Mahalanobi's  $D^2$  (1936) analysis and based on the  $D^2$  values the thirty one genotypes were grouped into different clusters following Tocher's method as suggested by Rao (1952).

### **RESULTS AND DISCUSSION**

The analysis of variance showed significant differences between mungbean genotypes for all the characters studied and hence considered for estimation of D<sup>2</sup> values clustering. The thirty one genotypes were grouped into eight clusters using Tocher's method (Rao, 1952) and distribution of genotypes into each of eight clusters is presented in Table 1 and illustrated in Fig 1. Cluster I was the largest with twenty four genotypes. Except cluster I, all other clusters viz., cluster II, cluster III, cluster IV, cluster V, cluster VI, cluster VII and cluster VIII had one genotype each.

The intra and inter cluster  $D^2$  and D values among 8 clusters were presented given in Table 2. Intra-cluster average D<sup>2</sup> values ranged from 0.00 to 394.42. Among the clusters, cluster I had the maximum intra cluster distance (394.42), while the clusters II, III, IV, V, VI, VII and VIII had recorded zero values as they included only single genotype in each cluster. The maximum inter cluster D<sup>2</sup> value was recorded between cluster III and VII (1768.20), followed by between cluster III and VI (1739.72). The genotypes in these clusters may serve as potential parents and crossing between these genotypes may result in novel recombinants. Manivannan et al (1998) and Patel and Patel (2012) made similar study in mungbean to identify genotypes resulting in heterotic expression for yield components.

Cluster means for different characters showed considerable differences between the clusters for all the characters (Table 3). Cluster VII registered maximum values for days to 50% flowering, days to maturity, 100-seed weight and SCMR. Cluster VIII recorded maximum mean values for number of seeds per pod, RWC and chlorophyll content. Cluster II recorded maximum values for number of clusters per plant and number of pods per plant. Similarly, cluster III for plant height and specific leaf area; cluster IV for number of pods per cluster and cluster V for harvest index, seed yield per plant and relative injury showed maximum mean values. Inter-crossing the genotypes from these clusters could be suggested to generate wide range of variability subsequently followed by effective selection for these characters.

The contribution of each character towards divergence is presented in Table 4 and Fig 2. Among all the characters studied 100-seed weight contributed maximum (27.53%) to the diversity 2017

S.No.	Character	Times ranked first	Contribution (%)		
1.	Days to 50% flowering	0	0.00		
2.	Plant height (cm)	0	0.00		
3.	Days to maturity	20	4.30		
4.	No. of clusters/ plant	0	0.00		
5.	No. of pods/ cluster	106	22.80		
6.	No. of pods/ plant	5	1.08		
7.	No. of seeds/ pod	27	5.81		
8.	100 seed weight (g)	128	27.53		
9.	Harvest index (%)	65	13.98		
10.	SPAD	4	0.86		
11.	Relative Water Content (%)	3	0.65		
12.	Relative Injury (%)	67	14.41		
13.	Chlorophyll content	20	4.30		
14.	Specific leaf area (cm <sup>2</sup> g <sup>-1</sup> )	16	3.44		
15.	Seed Yield (g)	4	0.86		

 Table 4. Contribution of different quantitative characters to diversity in mungbean under summer condition.

by taking first rank in 128 times out of 465 combinations, followed by number of pods per cluster (22.80% with 106 times ranked first), relative injury (14.41% with 67 times ranked first) and harvest index (13.98% with 65 times ranked first). The characters *viz.*, number of seeds per pod, plant height, chlorophyll content, specific leaf area, number of pods per plant, SCMR, seed yield and RWC contributed 5.81%, 4.30%, 3.44%, 1.08%, 0.86% and 0.65%, respectively to the genetic divergence in decreasing order. On contrary, number of clusters per plant, days to 50% flowering and days to maturity had negligible contribution towards genetic divergence.

Based on this genetic diversity studies hybridization programme may be initiated between GVIT 203 X VG 6197A (cluster III × cluster VII) in order to get transgressive segregants since, these genotypes showed maximum diversity among themselves with desirable physiological traits parameters and can consider for drought tolerance. Similarly, the crosses between genotypes WGG 2 X GVIT 203 (cluster II × cluster III), IPM-02-03 X EC-396117 (cluster VI × cluster VIII) and PUSA VISHAL X VG-6197A (cluster IV × cluster VII) could be suggested for the exploitation of transgressive segregants for high yield coupled with good physiological traits under summer conditions.

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