

**GENETIC DIVERGENCE STUDIES IN MUNGBEAN (*VIGNA RADIATA* L. WILCZEK)**

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**ABSTRACT:** Genetic divergence using  $D^2$  statistic of forty genotypes of various agro-climatic region for ten quantitative characters revealed existence of considerable genetic diversity in the material. The genotypes were grouped into eleven clusters. Cluster VIII contained the highest number of nine genotypes followed by cluster V with seven genotypes. The pattern of distribution of genotypes from different geographical location into eleven clusters were random, demonstrating that geographical isolation may not be the only factor causing genetic diversity. The highest intra-cluster distance was observed for cluster VI (112.02) and the lowest was observed for cluster II (6.24). While the highest inter-cluster distance was observed between cluster III and X (493.41). Harvest index contributed maximum to diversity. Cluster IX with WGG-66 recorded the highest mean for yield contributing characters viz., plant height, branches/plant, pods/plant and clusters/plant. Therefore it was suggested that more emphasis should be given this genotype as parents for crossing with genotypes of other clusters which may produce novel recombinants with desirable traits.

**Key words:** Mungbean, genetic divergence  $D^2$  analysis

**INTRODUCTION**

Mungbean (*Vigna radiata* L. Wilczek,  $2n = 22$ , Fabaceae) is an important short-duration grain legume crop which is widely-grown in south and Southeast Asia. It is an important source of inexpensive protein and iron, and is a good substitute for meat in most Asian diets and a significant component of various cropping systems (Rudy et al., 2006). However, yield per acre in the country is still marginal and there is a need of improvement in the existing mungbean varieties. Genetic diversity is one of the criteria of parent selection in the hybridization program to exploit maximum heterosis. The availability of transgressive segregants in any breeding program depends upon the diversity between the parents involves. Multivariate analysis using Mahalanobis  $D^2$  technique may be an efficient tool in the quantitative estimation of genetic diversity. Therefore, an attempt has been made in the present investigation with a view to select the divergent parents for future hybridization program.

**MATERIALS AND METHODS**

The present study was carried out at S.V.Agricultural College, Tirupati during rabi, 2012 in Randomized Block Design replicated twice with spacing of 30 cm between rows and 15 cm between plants. The recommended agronomic and plant protection practices were followed to maintain healthy stand of the plants. Data were recorded on five competitive plants in each genotype per replication and mean value plant basis were obtained for the characters viz., plant height (cm), number of branches per plant, number of pods per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod, 100 seed weight (g), biological yield of plant (g), harvest index (%) and seed yield (g). The data were subjected to Mahalanobis  $D^2$  statistics as per Mahalanobis (1936) method and genotypes were grouped into different clusters following Toucher's method as suggested by Rao (1952).

**RESULTS AND DISCUSSION**

The analysis of variance revealed highly significant differences among mungbean genotypes for all the characters studied indicating the existence of variability among the genotypes for the characters studied. Using Tocher's procedure, forty genotypes were grouped into eleven clusters (Table 1), among these, cluster VIII was the largest and consists of nine genotypes followed by cluster V with seven genotypes, cluster VI with six genotypes and cluster VII with four genotypes. Clusters I and IV, each had three genotypes, whereas cluster II, III and IX had two genotypes. Clusters X and XI were unique, since each had only one genotype. The random distribution of genotypes was evident from cluster VIII having maximum genotypes with wide distribution.

The genotypes of the same origin were distributed into different clusters indicating that there was no parallelism between clustering pattern and geographic distribution of genotypes. This might be due to difference in adoption, selection pressure and environmental condition. Similar findings were reported by Rahim *et al.*, (2010). Average intra and inter-cluster  $D^2$  values among forty genotypes were presented in Table 2, revealed that clusters X and IX showed minimum intra-cluster value (0). While cluster VI showed maximum intra cluster value (112.02) followed by cluster VII (96.90) and cluster V (93.79) revealing the existence of diverse genotypes in the experimental material and selection within the clusters might be implemented based on *per se* performance of the genotypes for the desirable traits. Inter cluster  $D^2$  values ranged from 60.15 between clusters III and V to 493.41 between clusters III and X. Minimum and maximum inter cluster  $D^2$  values indicated close relationship and maximum divergence between clusters, respectively. Crosses between divergent genotypes generate promising segregants with better heterotic effect (Piyada *et al.*, 2010).

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

Cluster No.	No. of genotypes	Genotypes
I	3	CO-6, MGG-360, MGG-369
II	2	MGG-374, MGG-386
III	2	LGG-551, MGG-347
IV	3	CO-7, SML-668, WGG-52
V	7	LGG-407, LGG-410, LGG-450, LGG-549, MGG-338, MGG-370, MGG-373
VI	6	MGG-341, MGG-348, MGG-359, MGG-371, PBM-1, PDGG-3
VII	4	MGG-376, MGG-380, MGG-397, WGG-2
VIII	9	MGG-388, MGG-395, ML-267, ML-613, Pant M-3, PDGG-1, PDGG-2, PDGG-4, PDGG-7
IX	2	PM-113, WGG-65
X	1	PM-103
XI	1	WGG-66

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

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
Cluster I	81.12 (9.01)	62.41 (7.90)	84.88 (9.21)	157.07 (12.53)	100.13 (10.01)	163.37 (12.78)	83.27 (9.13)	132.43 (11.51)	77.90 (8.83)	381.05 (19.52)	99.47 (9.97)
Cluster II		6.24 (2.50)	98.88 (9.94)	94.95 (9.74)	84.95 (9.22)	85.85 (9.27)	74.64 (8.64)	63.35 (7.96)	79.24 (8.90)	281.62 (16.78)	66.66 (8.17)
Cluster III			7.41 (2.72)	227.95 (15.10)	60.15 (7.76)	161.70 (12.72)	94.87 (9.74)	173.32 (13.17)	59.60 (7.72)	493.41 (22.21)	93.40 (9.66)
Cluster IV				70.52 (8.40)	197.09 (14.04)	152.90 (12.37)	169.29 (13.01)	81.37 (9.02)	140.95 (11.87)	135.40 (11.64)	179.57 (13.40)
Cluster V					93.79 (9.68)	155.58 (12.47)	100.85 (10.04)	150.91 (12.28)	75.69 (8.70)	411.91 (20.30)	117.95 (10.86)
Cluster VI						112.02 (10.58)	185.97 (13.64)	106.80 (10.34)	145.23 (12.05)	284.44 (16.87)	88.67 (9.42)
Cluster VII							96.90 (9.84)	148.11 (12.17)	76.60 (8.75)	396.29 (19.91)	159.72 (12.64)
Cluster VIII								79.99 (8.94)	120.64 (10.98)	183.86 (13.56)	120.03 (10.96)
Cluster IX									74.19 (8.61)	320.81 (17.91)	118.50 (10.89)
Cluster X										0.00 (0.00)	372.04 (19.29)
Cluster XI											0.00 (0.00)

Hence, hybridization between the genotypes included in these different clusters may give maximum hybrid vigour and eventually might result in better segregants. The average cluster means for all the ten characters were presented in Table 3. Cluster XI, with WGG-66, had maximum plant height (57.65 cm), branches/plant (3.40), pods/plant (30.10), and clusters/plant (10.20). Whereas cluster X, with PM-103 had maximum number of pods/cluster (3.80), 100 seed weight (5.44) and harvest index (65.81). Seed yield/plant (7.27) was highest in cluster VI, however seeds/pod (11.55) was highest in cluster II and mean for biological yield/plant (15.45) was highest in cluster V. Therefore parents from these clusters may be used in a breeding programme to combine the high yield potential. On the basis of mean and genetic divergence estimates it is suggested that the crosses between WGG-66 (cluster XI) and PM-103 (cluster X) may provide a base material for developing high yielding varieties.

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

Character / cluster	Plant height (cm)	No. of branches/plant	No. of pods/plant	No. of clusters/plant	No. of Pods/cluster	No. of seeds/pod	100 seed weight(g)	Biological Yield/plant (g)	Harvest index (%)	Seed yield/plant(g)
Cluster I	54.35	1.90	18.33	7.14	2.58	10.03	4.06	10.67	45.75	4.70
Cluster II	51.51	1.75	19.30	7.10	2.72	11.55	3.93	12.25	53.69	6.57
Cluster III	46.76	2.60	21.25	6.90	3.09	10.70	3.68	14.45	34.92	5.03
Cluster IV	37.38	1.46	17.03	6.53	2.62	10.02	4.72	8.60	60.57	5.09
Cluster V	49.72	1.84	21.04	6.92	3.04	11.11	3.87	15.45	39.25	5.95
Cluster VI	45.54	1.88	26.85	8.61	3.01	10.18	3.89	13.77	54.45	7.27
Cluster VII	47.70	1.45	14.65	6.15	2.37	11.01	4.05	12.45	40.95	5.12
Cluster VIII	42.47	1.52	20.26	6.63	3.05	10.22	4.22	10.91	56.74	6.11
Cluster IX	45.10	1.75	20.05	7.50	2.71	9.60	4.19	13.80	38.97	5.34
Cluster X	32.60	1.00	19.00	5.00	3.80	8.00	5.44	9.50	65.81	6.25
Cluster XI	57.65	3.40	30.10	10.20	2.92	9.90	4.21	13.60	53.71	7.13

The percent contribution of ten characters towards total genetic divergence was listed in Table 4. The highest contribution in manifestation of genetic divergence was exhibited by harvest index followed by biological yield/plant, pods/plant, seed yield/plant and seeds/pod also played considerable role in conditioning the genetic divergence. The lowest contribution towards total divergence was exerted by number of branches/plant. Rest of the characters *viz.*, clusters/plant, plant height, 100 seed weight and pods/cluster also has low contribution towards the expression of total genetic divergence; this might be due to genetic similarity among the genotypes for these traits. The present results are in contrast with studies of Singh *et al* 2009 this might be due to difference in the materials.

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

S. No.	Character	Times ranked first	Contribution (%)
1.	Plant height (cm)	24	3.08
2.	No. of branches/ plant	2	0.26
3.	No. of pods/ plant	73	9.36
4.	No. of clusters/ plant	25	3.21
5.	No. of pods/ cluster	3	0.38
6.	No. of seeds/ pod	35	4.49
7.	100 seed weight (g)	12	1.54
8.	Biological Yield/plant (g)	112	14.36
9.	Harvest index (%)	439	56.28
10.	Seed Yield (g)	55	7.05

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