Original Research Article

Morphological Diversity for Yield and its Component Traits in Mungbean [*Vigna radiata* (L.) Wilczek]

ABSTRACT:
The current experiment was held in Summer season, 2018 at rice upland 1, near rice borewell of Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India. The experiment was done by 36 mungbean genotypes at rice upland 1, near rice borewell of Bihar Agricultural University, Sabour, Bhagalpur in 2018. The analysis of variance (ANOVA) disclosed highly significant differences for all the traits studied in the experiment among all the genotypes. The genetic diversity was estimated by D^2 analysis. The 36 genotypes were grouped into 11 distinct clusters with cluster 4 to cluster 11 consisting of one genotype each. The maximum inter-cluster distance was found between cluster 11 and cluster 3 where maximum intracluster distance was found within cluster 2. The characters like Harvest index, the number of clusters per plant, seed yield per plant and days to maturity contribute maximum towards genetic divergence. The hybridization between the clusters 11 & 3 could give maximum heterosis and better desirable segregants.
Keywords: *Vigna radiata; Genetic divergence; D^2 statistics; Heterosis*

1. INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek], generally known as Green gram or Moong, is one of the important pulse crops grown in India. Being a short duration annual, it is grown as an inter-crop and increases cropping intensity. Therefore it became a good profit provider for marginal farmers. Mungbean is utilised as food legume and good protein diet for many vegetarians in India. It is an autogamous diploid plant with 2n =2x =22 chromosomes, having a genome size of 515 Mb (Tangphatsornruang S et al. 2009).

In India, the total area covered under mungbean is 30.41 lakh hectares with a total production of 14.24 lakh tonnes and productivity of 468 kg/ha (Tiwary and Shivhare 2016). The area covered under mungbean in Bihar is 1.57 lakh hectares with a production of 1.04 lakh tonnes and productivity of 664 kg/ha (Tiwary and Shivhare 2016). To increase production and productivity, there is a need for developing high yielding varieties in mungbean.

The production constraints mainly associated with the mungbean crop are as follows; Lack of high yielding varieties, fluctuating climatic conditions, asynchronous pod maturity, lack of disease-resistant or insect tolerant varieties (mainly for MYMV, pod borer, storage borer) etc. As mungbean is cultivated in all three seasons in India

namely- Kharif, Rabi and Zaid, it fits well in all cropping systems and increases the cropping intensity. For developing high yielding varieties, there is a need for variation in the tested germplasm.

Genetic diversity is an important element for any plant breeding programme. The hybridization programme between two genetically diverse parents is efficient in developing good Heterosis in F_1 and able to produce considerable variability in subsequent selfed generations. The genetic diversity is better estimated by D^2 analysis. Mahalanobis (1936) defined the distance between two populations as D^2 which was obtained by Tocher's method, described by Rao (1952). D^2 statistics analysis is used for the selection of genetically divergent parents for hybridization programme. In the present investigation, 36 genotypes were collected from different parts of India to study the genetic diversity in them and for future varietal development.

2. MATERIALS AND METHODS

The current investigation was held in Summer season, 2018 at rice upland 1, near rice borewell of Bihar Agricultural University, Sabour, Bhagalpur, Bihar. A total of 36 genotypes namely IC-39403, LM-249, Banka Local Mung-2, GP-276, DMG-1105-2-2, GG-1980, KL-1, Banka Local Mung-5, IPM-99-125, IC-314326, IC-16033, Meha, IPM-2-3, Banka Local Mung-4, Samrat (C), HUM-16 (C), DMG-1103, IC-369233, Pusa Vishal (C), HUM-12, IPM-205-7, IC-324012, BRM-8-1, Banka Local Mung-7, Banka Local Mung-1, SML-668, DMG-1105-1-2, IC-683, IPM-409-4, GM-99-25, LM-3, KL-4, LM-126, PM-5 (C), IPM-2-14 and BRM-1 were procured from different areas of Bihar, IIPR (Kanpur), G.B.P.U.A.&T (Pantnagar), NBPGR (New Delhi), Kashipur (Uttarakhand), BHU (Varanasi), CSKHPKV, Palampur. The observations were taken from five randomly selected plants of each genotype consisting of 14 quantitative characters like days to 50% flowering, days to maturity, plant height (cm), number of primary branches, number of secondary branches, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (gm), biological yield per plant (gm), harvest index (%) and seed yield per plant (gm). The estimation of genetic diversity was done by D^2 analysis. The genotypes were clustered into different clusters with the help of Tocher's method (Rao 1952).

3. RESULTS AND DISCUSSION

The analysis of variance (ANOVA) disclosed highly significant differences for all the traits studied in the experiment among all the genotypes (Table 1). The Mean, critical difference (CD), coefficient of variation (CV) of all the traits were indicating that there were considerable variations for all the characters which can be used in further breeding purpose.

Table 1. Mean, standard error (SE), critical difference (CD) and coefficient of variation (CV) of quantitative traits of Mungbean genotypes.

Sl.No.	Traits	Mean	Standa	Critical	Coefficient

			rd Error (SE)	Difference (CD) at 5%	of Variation (CV) (%)
1.	Days to 50% flowering	52.47	1.33	3.74	4.37
2.	Days to maturity	67.92	0.89	2.51	2.27
3.	Plant height (cm)	58.16	2.74	7.73	8.16
4.	Number of primary branches	2.5	0.12	0.35	8.63
5.	Number of secondary branches	2.5	0.15	0.42	10.34
6.	Number of clusters per plant	8.09	0.31	0.88	6.65
7.	Number of pods per cluster	3.69	0.21	0.59	9.75
8.	Number of pods per plant	18.53	0.95	2.69	8.92
9.	Pod length (cm)	6.86	0.14	0.4	3.54
10.	Number of seeds per pod	9.97	0.25	0.69	4.27
11.	100 seed weight (gm)	3.99	0.11	0.31	4.74
12	Biological yield per plant (gm)	23.34	1.14	3.22	8.47
13.	Harvest index (%)	31.26	1.61	4.54	8.93
14.	Seed yield per plant (gm)	7.00	0.17	0.47	4.09

Based on the morphological clustering by Tocher's method, the 36 genotypes of mungbean from different geographical locations all over India were clustered or grouped into 11 clusters in the current experiment as given in the (Table 2) and in (figure1). The genotypes present in the different clusters of dendrogram varied from one to sixteen genotypes. Among all the clusters, cluster 1 is largest, comprising of 16 genotypes followed by cluster 2 of 7 genotypes, cluster 3 of 5 genotypes and cluster 4, cluster 5, cluster 6, cluster 7, cluster 8, cluster 9, cluster 10, cluster 11 are comprising of one genotype each. The cluster 1 is consisting of 16 genotypes namely IC-39403, LM-249, Banka Local Mung-2, GP-276, DMG-1105-2-2, GG-1980, KL-1, Banka Local Mung-5, IPM-99-125, IC-314326, IC-16033, Meha, IPM-2-3, Banka Local Mung-4, Samrat (C), HUM-16 (C). The cluster 2 is consisting of 7 genotypes namely DMG-1103, IC-369233, Pusa Vishal (C), HUM-12, IPM-205-7, IC-324012, BRM-8-1. The cluster 3 is consisting of 5 genotypes namely Banka Local Mung-7, Banka Local Mung-1, SML-668, DMG-1105-1-2, IC-683. The cluster 4, cluster 5, cluster 6, cluster 7, cluster 8, cluster 9, cluster 10, cluster 11 are comprising of IPM-409-4, GM-99-25, LM-3, KL-4, LM-126, PM-5 (C), IPM-2-14 and BRM-1 respectively with one genotype in each cluster. From table 4, it was observed that the genotypes having the same origin were clustered in different clusters indicating that geographical location is not having much relation with genetic diversity. Similar results were reported by Jeevitha et al. 2018 and Chandra et al. 2017.

Table 2. Composition of Clusters based on Tocher's method (D^2 analysis) of 36 genotypes of Mungbean.

Clusters	**Number of Genotypes**	**Genotypes**

1	16	IC-39403, LM-249, Banka Local Mung-2, GP-276, DMG-1105-2-2, GG-1980, KL-1, Banka Local Mung-5, IPM-99-125, IC-314326, IC-16033, Meha, IPM-2-3, Banka Local Mung-4, Samrat (C), HUM-16 (C)
2	7	DMG-1103, IC-369233, Pusa Vishal (C), HUM-12, IPM-205-7, IC-324012, BRM-8-1
3	5	Banka Local Mung-7, Banka Local Mung-1, SML-668, DMG-1105-1-2, IC-683
4	1	IPM-409-4
5	1	GM-99-25
6	1	LM-3
7	1	KL-4
8	1	LM-126
9	1	PM-5 (C)
10	1	IPM-2-14
11	1	BRM-1

The results of intra and inter-cluster distances among all the 11 clusters in the experiment are given in the (Table 3). The maximum intracluster distance was found in cluster 2 (13.06) which was followed by cluster 3 (12.99) and cluster 1 (12.78) showing considerable genetic variability within these clusters. The remaining 8 clusters didn't have any intracluster distances as they contain only single genotype each. The maximum inter-cluster distance was found between cluster 11 and cluster 3 (32.03) which was followed by cluster 8 and cluster 3 (25.23), cluster 7 and cluster 3 (25.15), cluster 11 and cluster 10 (24.78), cluster 5 and cluster 3 (24.37) indicating wide genetic variability and hybridization between the above said clusters would be beneficial in mungbean breeding. The minimum inter-cluster distance was found between cluster 7 and cluster 5 (11.21).

Table 3. Average of Intra (diagonal) and Intercluster distance (Tocher's method- D^2 analysis) in Mungbean genotypes.

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**	**Cluster 7**	**Cluster 8**	**Cluster 9**	**Cluster 10**	**Cluster 11**
Cluster 1	**12.78**	14.58	17.38	15.49	16.07	15.95	17.52	16.63	17.42	16.47	21.37
Cluster 2		**13.06**	21.53	15.63	16.44	15.55	17.56	16.31	15.36	16.98	18.1
Cluster 3			**12.99**	22.05	24.37	23.55	25.15	25.23	24.06	21.29	32.03
Cluster 4				**0**	16.79	14.08	20.52	20.24	12.07	23.03	18.72
Cluster 5					**0**	16.41	11.21	17.55	18.71	16.61	16.61
Cluster 6						**0**	16.66	19.06	16.2	21.93	15.47
Cluster 7							**0**	21.18	22.16	12.4	18.84
Cluster 8								**0**	18.84	19.63	16.97
Cluster 9									**0**	23.58	20.51
Cluster 10										**0**	24.78
Cluster 11											**0**

The mean values of various clusters for 14 quantitative traits were given in table 4. There are recognizable differences in the cluster mean values for all the 14 characters dealt in the experiment. The current study disclosed that cluster 6 showed the highest mean values for days to 50% flowering (55.67), number of primary branches (3.4), number of clusters per plant (12.6), number of pods per cluster (4.44), number of seeds per pod (11.34) and lowest mean values for pod length (6.32). The cluster 7 showed highest mean values for 100 seed weight (5.2), harvest index (52.3) and lowest mean values for the number of secondary branches (1.87), the number of pods per cluster (2.8). The cluster 8 had highest mean values for pod length (7.67), biological yield per plant (37.78) and lowest mean values for days to maturity (58.33), the number of clusters per plant (5.4). The cluster 9 had the highest mean values for days to maturity (80), the number of pods per plant (30.33) and lowest mean values for harvest index (20.7). The cluster 4 had highest mean values for the number of secondary branches (3.47) and lowest mean values for days to 50% flowering (48), plant height (48.8) and 100 seed weight (3.47). The cluster 10 had the highest mean values for plant height (68.4) and lowest mean values for the number of primary branches (1.33), biological yield per plant (15.44). The cluster 3 had no highest mean values but showed lowest mean values for the number of pods per plant (11.75), the number of seeds per pod (8.85) and seed yield per plant (3.81). The cluster 11 had the highest mean value for seed yield per plant (11.53).

Table 4: Mean values of 11 clusters for 14 Quantitative characters in 36 Mungbean genotypes

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (gm)	Biological yield per plant (gm)	Harvest index (%)	Seed yield per plant (gm)
I	52.4	66.19	53.57	2.48	2.65	8.07	3.75	17.38	6.8	9.88	4.01	24.02	28.48	6.66
II	52.48	72.43	62.4	2.22	2.26	7.31	4	21.26	6.68	10.4	3.86	23.17	37.29	8.38
III	53.87	69.6	66.2	2.51	2.36	7.64	3.13	11.75	6.8	8.85	3.79	18.84	21.83	3.81
IV	48	72.67	48.8	2.93	3.47	11.33	4.27	27.93	7.43	10.43	3.47	21.27	32.43	6.86
V	49	59	52.93	3.33	2	7.93	3	23.67	7.05	10.19	4.18	17.11	48.57	8.28
VI	55.67	68.67	66.13	3.4	2.47	12.6	4.44	18.73	6.32	11.34	4.33	27.02	31.57	8.5
VII	51.33	64	61.33	2.07	1.87	10.07	2.8	17.53	6.81	10.06	5.2	17.02	52.3	8.84
VIII	52.67	58.33	59.47	2.93	3	5.4	4.21	21.87	7.67	9.44	3.69	37.78	23.5	8.81
IX	52.33	80	55.4	3.27	2.67	9.87	3.51	30.33	7.37	11.25	3.64	36.11	20.7	7.43
X	50.67	66.33	68.4	1.33	1.93	5.8	4.05	15.4	7.47	10.52	4.97	15.44	48.8	7.52
XI	54.33	62	56.27	2.8	2.53	9.73	3.09	25.8	7.11	10.58	3.9	27.79	41.73	11.53
Contribution towards genetic divergence (GD) (%)	**0.00**	**12.06**	**0.95**	**3.17**	**1.90**	**16.35**	**1.11**	**3.33**	**0.79**	**2.70**	**9.68**	**6.19**	**27.78**	**13.97**

The percentage contribution of each character towards total genetic divergence in 36 genotypes of mungbean are presented in the (Table 5). The parents are selected based on the contribution of characters towards genetic divergence. In the current experiment, the high contribution for genetic divergence were showed by the characters like harvest index (27.78) which was followed by number of clusters per plant (16.35), seed yield per plant (13.97), days to maturity (12.06), 100 seed weight (9.68), biological yield per plant (6.19). The low contribution for genetic divergence was shown by the characters like the number of pods per plant (3.33), number of primary branches (3.17), number of seeds per pod (2.70), number of secondary branches (1.90), number of pods per cluster (1.11), plant height (0.95), pod length (0.79). The days to 50% flowering showed no contribution towards genetic divergence. Similar results were reported by Vyas et al. 2018 and Jeevitha et al. 2018.

Table 5. Percentage contribution of each character towards total genetic divergence in 36 genotypes of Mungbean.

S.NO.	Characters	Times Ranked 1st	Contribution (%)
1.	Days to 50% flowering	0	0.00
2.	Days to maturity	76	12.06
3.	Plant height (cm)	6	0.95
4.	Number of primary branches	20	3.17
5.	Number of secondary branches	12	1.90
6.	Number of clusters per plant	103	16.35
7.	Number of pods per cluster	7	1.11
8.	Number of pods per plant	21	3.33
9.	Pod length (cm)	5	0.79
10.	Number of seeds per pod	17	2.70
11.	100 seed weight (gm)	61	9.68
12.	Biological yield per plant (gm)	39	6.19
13.	Harvest index (%)	175	27.78
14.	Seed yield per plant (gm)	88	13.97

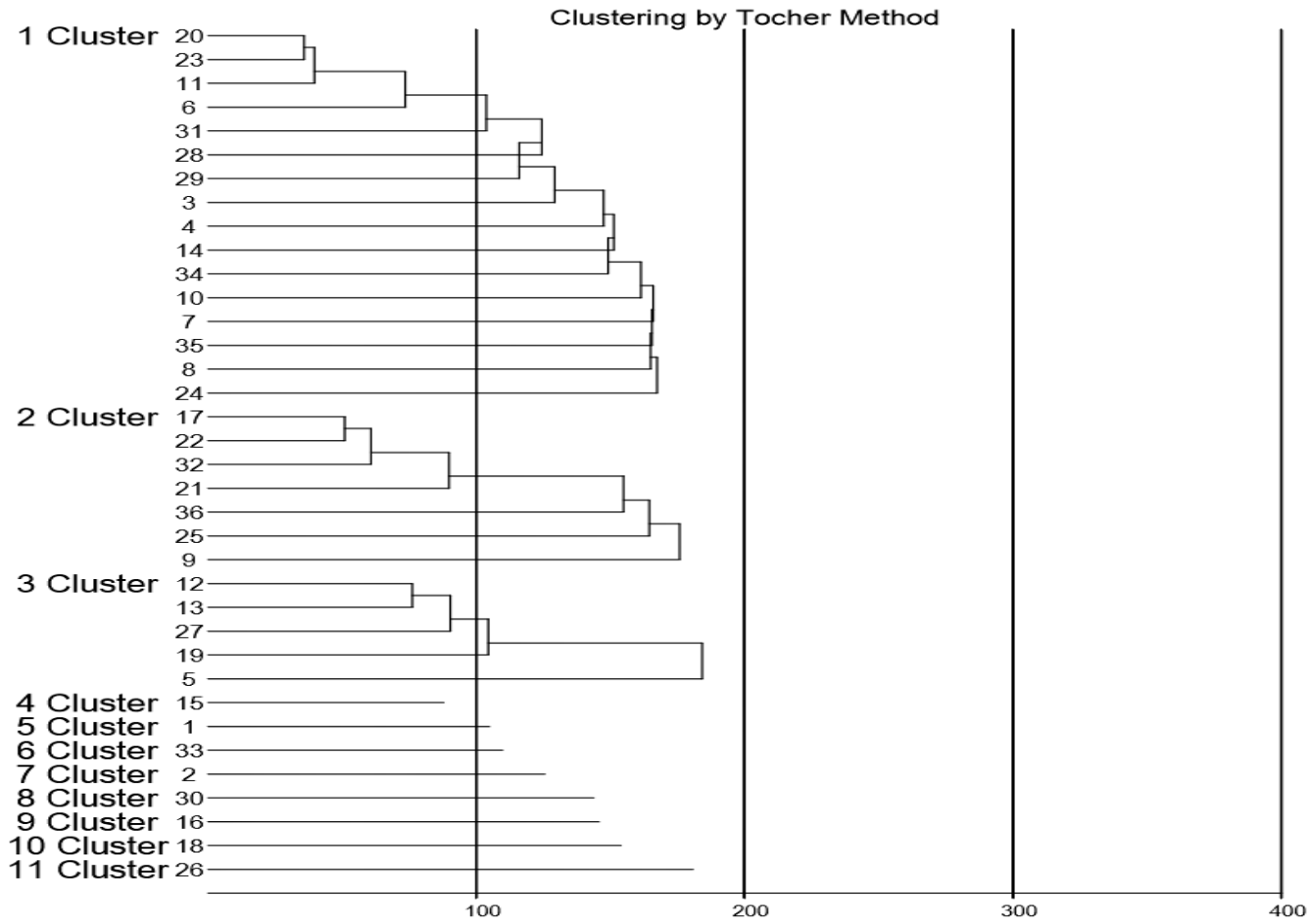

Figure 1. Dendrogram of Morphological clustering by Tocher's method.

CONCLUSION

The results show that the tested genotypes in the experiment had a significant level of variability which might be exploited in future breeding programmes. Based on cluster mean, intra and inter-cluster distances, the clusters 11, 3, 8 and 7 could be used for their desirable characters in the breeding programme of mungbean. The genotypes from these clusters could be inter-crossed to procure higher heterosis and to get desirable segregants.

REFERENCES

Chandra GS, Lavanya GR, Kulkarni SD, (2017) Studies on Genetic diversity in Greengram (*Vigna radiata* L. Wilczek) for seed yield characters. Journal of Pharmacognosy and Phytochemistry. 6(6):1765-7.

Gadakh SS, Dethe A.M, Kathale M. N, and Kahate N. S (2013). Genetic diversity for yield and its component traits in green gram [*Vigna radiata*(L.) Wilczek]. Journal of crop and weed, 9(1):106-109.

Jeevitha S, Karthikeyan R, Vignesh M, Malarkodi A, Tirumalai R, Nainu AJ, Anandan R, Prakash M, Murugan S, 2018. Estimation of morphological and molecular genetic diversity in blackgram [*Vigna mungo* (L.) Hepper] under YMV hotspot regime. Horticultural Biotechnology Research :06-9.

Kaur G, Joshi A, Jain D, Choudhary R and Vyas D (2016) Diversity analysis of green gram (*Vigna radiata* (L.) Wilczek) through morphological and molecular markers. Turkish Journal of Agriculture and Forestry 40(2): 229-240.

Kumar B, Singh CM and Jaiswal KK (2013) Genetic variability, association and diversity studies in bread wheat (*Triticum aestivum* L.). The Bioscan 8(1): 143-147.

Mahalanobis PC. on the generalized distance in statistics. Proceedings of National Institute of Science India, 1936; 2:49-55.

Palaniappan J and Murugaiah S (2012) Genetic diversity as assessed by morphological and microsatellite markers in greengram (*Vigna radiata* L.). African Journal of Biotechnology 11(84): 15091-15097.

Rao CR. Advanced Statistical Methods in Biometric Research. John Wiley and Sons Inc. New York. 1952, 390.

Tangphatsornruang S, Somta P, Uthaipaisanwong P, Chanprasert J, Sangsrakru D, Seehalak W, Sommanas W, Tragoonrung S, Srinives P (2009) Characterization of microsatellites and gene contents from genome shotgun sequences of mungbean (*Vigna radiata* (L.) Wilczek) BMC Plant Biology 9(1): 137.

Tiwari AK, Shivhare AK (2016) Pulses in India: Retrospect and prospects. Department of agriculture, cooperation and farmers welfare. DPD/Pub.1/Vol. 2/2016 pp 317.

Vyas D, Joshi A, Kedar OP. Genetic diversity analysis of black gram (*Vigna mungo* L.). Journal of Pharmacognosy and Phytochemistry. 2018;7(3):2535-8.