Received : 06 Feb 2020 | Revised : 18 Mar 2020 | Accepted : 19 Mar 2020

Electronic Journal of Plant Breeding

Research Article

Genetic divergence in advanced breeding lines and varieties of mungbean

P. Mathankumar, N. Manivannan*, A.Subramanian[1], P. Shanthi[2] and V. Babu Rajendra Prasad[3]

National Pulses Research Centre, Tamilnadu Agricultural University, Vamban-622 303, Tamil Nadu, India.
[1]Anbil Dharmalingam Agricultural College and Research Institute, TNAU, Trichy-620 027,Tamil Nadu, India.
[2]Agricultural College and Research Institute, TNAU, Kudumiyanmalai-622 104,Tamil Nadu, India.
[3]Department of Crop Physiology, TNAU, Coimbatore 641 003,Tamil Nadu, India.
***E-Mail:** nmvannan@gmail.com

Abstract

The present investigation was carried out to study the genetic divergence of 100 mungbean genotypes using Mahalanobis D^2 analysis. Among the traits studied, the number of branches contributed maximum percentage towards the total genetic divergence. The genotypes were grouped into fifteen clusters, with cluster I having the maximum number of genotypes. Maximum intra-cluster distance was recorded in cluster I indicating higher diversity among genotypes of this cluster. Cluster V and XV recorded maximum inter-cluster distance indicating wider divergence between genotypes of these clusters. Likewise, clusters III and XII also recorded wider divergence. Hybridization between genotypes of cluster V (VGG 16-035, VGG 17- 004) and cluster XV (VGG 17-009) followed by cluster III (VGG 18-012) and cluster XII (ADT 3) could yield better segregants. High mean performances for the number of clusters per plant, the number of pods per cluster, the total number of pods per plant and seed yield per plant was observed in cluster XIII (VGG 15-030). This genotype can be utilised for further crop improvement programmes in mungbean.

Keywords

Mungbean, diversity, clusters, hybridization

INTRODUCTION

Pulses play a vital role in sustainable agriculture because of their nutritional security and soil ameliorative properties. It contains 20-25 percent protein which is higher than cereals and hence, it is referred as poor man's meat (Tripathi *et al.*, 2019). Mungbean seeds are major and cheap source of protein and contains minerals, dietary fibre and vitamins (Hou *et al.*, 2019). Mungbean (*Vigna radiata* (L.) Wilczek) is one of the chief pulse crops grown in India after chickpea and pigeon pea (Soni*et al.*, 2020). In India, mungbean is cultivated in 4.26 million ha with a production of 2.01 million tonnes and productivity of 472 kg/ha (AICRP on MULLaRP, 2018-19). Grouping of mungbean genotypes based on genetic divergence for different characters will enable breeders for the better selection of parents during hybridization (Manivannan *et al.*, 1998). Hence an experiment was conducted to study the genetic divergence among mungbean genotypes.

MATERIAL AND METHODS

One hundred mungbean genotypes comprising of released varieties and pre-release cultures were used in the present study. The study was laid out at National Pulses Research Centre, Vamban in alpha lattice design with two replications. Each entry was raised in 1.5m row with 30x30 spacing. Morphological observations on days to 50% flowering, plant height, the number of branches per plant, the number of clusters per plant, the number of pods per cluster, the total number of pods per plant, pod length, the number of seeds per pod, 100-seed weight and seed yield per plant were recorded on five randomly selected plants from each replication. Genetic diversity among the genotypes was assessed by D^2 analysis (Mahalanobis,1936) and clustering was done by Tocher's method (Rao, 1952) with Indostat software.

https://doi.org/10.37992/2020.1101.044

RESULTS AND DISCUSSION

The test for significance was carried out using Wilk's static criterion which showed significant difference among the genotypes for all characters studied. The D^2 analysis grouped 100 mungbean genotypes into 15 clusters (**Table 1**). Thirteen out of fifteen clusters were with single genotypes. Among the clusters, cluster I (85) had maximum number of genotypes followed by cluster V (2). Similar type of more clustering pattern in mungbean was also observed by Sahu *et al.* (2014) and Das and Baisakh (2019).

Table 1. Distribution of mungbean genotypes into different clusters

S. No	Cluster	No. of Genotypes	Name of Genotypes
1	Cluster I	85	CO 6, CO 7, CO 8, HUM-1, IPM 2-14, LGG 607, MGG 385, MGG 387, NVL-722, OBGG 058, PUSA 9072, SAMRAT, TARM-18, VBN(Gg) 2, VBN(Gg) 3, VBN(Gg) 4, VBN 1, COGG 13019, COGG 13032, COGG 13039, VGG 15-013, VGG 15-029,VGG 16-027,VGG 16-029,VGG 16-036,VGG 16-054,VGG 16-055, VGG 16-058, VGG 17-001, VGG 17-002, VGG 17-010,VGG 17-015,VGG 17-019,VGG 17-026,VGG 17-038,VGG 17-039,VGG 17-040,VGG 17-042,VGG 17-043,VGG 17-045,VGG 17-048,VGG 17-049,VGG 17-050,VGG 17-076,VGG 17-102,VGG 17-105,VGG 17-106,VGG 18-003,VGG 18-004,VGG 18-005,VGG 18-006,VGG 18-007,VGG 18-013,VGG 18-015,VGG 18-019,VGG 18-020,VGG 18-021,VGG 18-024,VGG 18-025,VGG 18-026,VGG 18-027,VGG 18-028,VGG 18-029,VGG 18-030,VGG 18-031,VGG 18-032,VGG 18-033,VGG 18-034,VGG 19-001,VGG 19-002,VGG 19-003,VGG 19-004,VGG 19-005,VGG 19-006,VGG 19-007,VGG 19-008,VGG 19-009,VGG 19-010,VGG 19-011,VGG 19-012,VGG 19-013,VGG 19-014,VGG 19-015,VGG 19-016 and VGG 19-017
2	Cluster II	1	VGG 18-008
3	Cluster III	1	VGG 18-012
4	Cluster IV	1	VGG 17-109
5	Cluster V	2	VGG 16-035, VGG 17-004
6	Cluster VI	1	VGG 18-018
7	Cluster VII	1	VGG 17-003
8	Cluster VIII	1	VGG 18-010
9	Cluster IX	1	AGG 35
10	Cluster X	1	VGG 16-047
11	Cluster XI	1	OUM 11-5
12	Cluster XII	1	ADT 3
13	Cluster XIII	1	VGG 15-030
14	Cluster XIV	1	ADGG 13-009
15	Cluster XV	1	VGG 17-009

Inter and intra cluster distances were presented in **Table 2**. Among the 15 clusters, cluster I (7.37) had maximum intra cluster distance. This indicates that genotypes present in cluster I had wider variation among themselves. Maximum inter cluster distance was recorded between cluster V and cluster XV (21.46) followed by cluster III and cluster XII (20.88). This indicates the wider genetic divergence between these clusters. In view of the clustering pattern, VGG 16-035 and VGG 17-004 (cluster V) have wider variation from VGG 17-009 (cluster XV). Likewise, VGG 18-012 (cluster III) and ADT 3 (cluster XII) have wider variation. Hence, the crossing between these genotypes may create wide range of variability in segregating population (Abna *et al.*, 2012; Patel and Patel. 2012). The frequency of producing transgressive segregants among such divergent crosses are high (Sharma 2018; Das and Baisakh 2019).

Mean performance for various characters of clusters were presented in **Table 3**. Desirable mean value for days to 50% flowering (43.75) and plant height (67.90) was recorded in cluster XV and VIII respectively. Cluster XI recorded the highest mean value for the number of branches (2.75) whereas, superior mean performances for the number of clusters per plant (12.00), the number of pods per cluster (3.90), the total number of pods per plant (48.80) and seed yield per plant (10.40) were recorded in cluster XIII. Cluster IV recorded higher mean values for pod length (9.65) and 100-seed weight (5.60). Cluster II had superior performance for the number of seeds per pod (11.80). Thus, selecting genotypes from clusters with desirable mean value as parents could help in improving yield components in breeding programmes (Panigrahi and Baisakh, 2014).

Table 2. Intra cluster (diagonal values) and inter cluster distances based on D values

I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
7.37	9.48	9.63	10.22	9.94	10.23	10.07	9.37	10.94	10.30	13.40	14.57	12.55	12.64	15.30
	0	3.16	4.70	10.38	6.02	14.75	9.28	15.64	12.10	18.20	20.44	18.58	18.61	19.40
		0	4.81	10.18	5.24	15.30	9.48	16.25	12.59	18.96	20.88	18.65	19.20	19.70
			0	11.54	5.03	14.34	7.05	15.43	10.80	17.37	20.38	17.90	19.57	20.21
				3.77	13.69	12.11	13.24	13.29	12.81	18.07	18.33	16.59	16.10	21.46
					0	15.65	8.40	16.73	12.92	17.93	20.54	17.58	19.27	17.28
						0	9.91	4.72	6.69	7.55	9.75	7.63	9.18	16.34
							0	11.02	5.82	11.66	15.64	13.03	15.77	17.31
								0	6.86	6.52	7.29	9.96	8.02	17.41
									0	8.88	12.63	12.29	13.57	18.71
										0	6.56	9.03	10.07	15.86
											0	10.78	7.82	17.07
												0	9.19	12.23
													0	13.52
														0

Table 3. Mean performance of characters in various clusters

Cluster Numbers	Days to 50% Flowering	Plant Height (cm)	Number of Branches / Plant	Number of Clusters/ Plant	Number of Pods per Cluster	Total Number of Pods / Plant	Pod Length (cm)	Number of Seeds/ Pods	100- Seed Weight(g)	Seed Yield /Plant (g)
I	38.03	52.42	0.96	6.65	3.10	22.91	7.75	11.18	3.81	5.25
II	38.00	50.30	0.20	4.80	2.60	13.40	9.40	11.80	5.35	3.60
III	37.50	43.30	0.00	4.20	3.40	12.00	8.30	11.70	5.40	4.90
IV	38.50	49.60	0.50	4.90	3.10	16.50	9.65	11.30	5.60	7.05
V	43.75	67.90	0.20	6.05	3.55	25.60	7.35	11.00	3.47	6.00
VI	34.00	42.70	0.50	4.60	3.70	16.40	9.05	11.20	5.50	6.35
VII	42.50	61.30	2.00	9.40	3.70	39.70	7.25	11.10	3.55	6.80
VIII	38.50	39.30	1.35	6.65	2.75	22.40	8.10	10.75	5.40	7.50
IX	43.00	50.65	2.05	8.55	2.85	26.55	7.10	9.65	3.20	4.35
X	42.50	48.10	1.70	7.20	3.00	22.10	7.70	10.80	4.95	5.65
XI	40.00	52.55	2.75	8.10	2.30	27.25	7.90	10.65	3.45	5.20
XII	40.50	42.90	2.50	6.30	2.80	23.50	6.50	9.60	2.05	3.05
XIII	37.50	59.50	2.50	12.00	3.90	48.80	6.35	11.30	2.85	10.40
XIV	39.00	45.10	2.20	11.40	3.10	35.20	6.45	10.20	1.95	3.25
XV	27.50	65.80	2.30	11.60	3.30	37.70	7.20	11.30	3.20	4.70

The varying degree of contribution of characters to genetic diversity was observed in the study. The number of branches per plant (41.1%) contributed maximum to divergence followed by days to 50% flowering (23.01%) and 100-seed weight (18.75%) while the number of pods per cluster (0.77%) and the number of seeds per pod (0.83%) contributed minimum to diversity (**Table 4**). This indicates the presence of wider diversity for these traits in the study material. Hence, importance should be given for these traits in the selection of parents for further crop improvement. These findings are in agreement with the studies carried out by Manivannan *et al*. (2012), Chandra *et al.* (2017) and Das and Baisakh (2019) in mungbean.

Table 4. Contribution of various traits towards divergence in mungbean

S. No	Traits	Contribution(%)
1	Days to 50% flowering	23.01
2	Plant height (cm)	4.30
3	Number of branches per plant	41.17
4	Number of clusters per plant	1.43
5	Number of pods per cluster	0.77
6	Total number of pods per plant	1.74
7	Pod length (cm)	4.59
8	Number of seeds per pods	0.83
9	100-seed weight(g)	18.75
10	Seed yield per plant(g)	3.41

To conclude, hybridization between genotypes of clusters V (VGG 16-035, VGG 17- 004) and cluster XV (VGG 17-009) followed by clusters III (VGG 18-012) and cluster XII (ADT 3) could yield better segregants. The present study indicated that the traits number of branches contributed higher to the total divergence. Hence, it should be given importance during the choice of parents for crossing programme.

REFERENCES

Abna, F., Golam, F., and Bhassu, S. 2012. Estimation of genetic diversity of mungbean (*Vigna radiata* (L.)Wilczek) in Malaysian tropical environment. *African Journal of Microbiology Research*, **6**(8):1770-1775. [Cross Ref]

AICRP on MULLarp, 2018. Project Coordinator Report-(2017-18) All India Coordinated Research Project on MULLaRP, ICAR- Indian Institute of Pulses Research, Kanpur-208204, Uttar Pradesh, India, Pp 35-39.

Chandra, G.S., Lavanya, G.R., and Kulkarni, S.D. 2017. Studies on Genetic diversity in Greengram (*Vignaradiata* (L.)Wilczek) for seed yield characters. *Journal of Pharmacognosy and Phytochemistry*, **6**(6): 1765-1767.

Das, T.R. and Baisakh, B. 2019. Genetic divergence among mutant genotypes of greengram [*Vignaradiata* (L.)Wilczek]. *Electronic Journal of Plant Breeding*, **10**(1):160-166. [Cross Ref]

Hou, D., Yousaf, L., Xue, Y., Hu, J., Wu, J., Hu, X., Feng, N. and Shen, Q. 2019. Mung Bean (*Vigna radiata* L.): Bioactive Polyphenols, Polysaccharides, Peptides, and Health Benefits. *Nutrients*, **11**(6):1238. [Cross Ref]

Mahalanobis P.C. 1936. On the generalized distance in statistic.*Proceedings of National Institute of Sciences* (India), **2**:49 - 55.

Manivannan, N., Murugan, E., Viswanathan, PL. and Dhanakodi, C.V. 1998. Genetic divergence in greengram. *Legume Research*, **21**:131-133.

Manivannan, N. 2002. Genetic diversity in cross derivatives of greengram [*Vignaradiata* (L.)Wilczek]. *Legume Research*, **25**(1):50-52.

Panigrahi, K.K. and Baisakh, B. 2014. Genetic diversity assessment for yield contributing characters of green gram [*Vigna radiata* (L.)Wilczek] cultivars from Odisha. *Environment and Ecology*, **32**(1A): 294-297.

Patel, J.N. and Patel, N.K. 2012. Genetic divergence in *Vigna radiata* (L.)Wilczek. *Life science leaflets,***11**:53-56.

Rao, C.R. 1952. Advanced statistical methods in biometrical Research, *John Wiley and Sons*, New York. 236-272 pp

Sahu, H., Singh, S., Amadabade, J. and Barh, A. 2014. Genetic divergence study in advanced breeding lines of mungbean in tarai region. *Electronic Journal of Plant Breeding*, **5**(4):657-663.

Sharma, S.R. 2018. Assessment of Genetic Diversity in Mungbean[*Vigna radiata* (L.) Wilczek] Genotypes. *International Journal of Genetics,* **10**(7):471-474.

Soni, J. and Kushwaha, H.S. 2020. Effect of foliar spray of zinc and iron on productivity of mungbean [*Vigna radiata* (L.)Wilczeck]. *Journal of Pharmacognosy and Phytochemistry*, **9**(1):108-111.

Tripathi, A.K. 2019. Feeling the Pulse: Towards Production Expansion of Pulses in India. *Journal of Asian and African Studies*, **54**(6):894-912 [Cross Ref]