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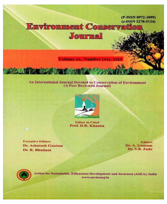

Genetic divergence studies for yield and its component traits in Mung bean (*Vigna radiata* L. Wilczek)

Sindoora Nalajala ✉
Department of Genetics and Plant breeding, College of Agriculture, Central Agricultural University, Imphal, Manipur, India.
N. Brajendra Singh
Department of Genetics and Plant breeding, College of Agriculture, Central Agricultural University, Imphal, Manipur, India.
M. Samuel Jeberson
Department of Genetics and Plant breeding, Agriculture University Jodhpur, Mandor, Jodhpur, Rajasthan, India.
Sonika Yumnam
Department of Genetics and Plant breeding, College of Agriculture, Central Agricultural University, Imphal, Manipur, India.
Bireshwar Sinha
Department of Plant Pathology, College of Agriculture, Central Agricultural University, Imphal, Manipur, India.

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ABSTRACT

The present investigation was carried out at Genetics and Plant Breeding (GPB) farm, College of Agriculture, Central Agricultural University, Imphal, Manipur during kharif 2021 using 60 genotypes of Mung bean. Mahalanobis D^2 statistics was used to evaluate the diversity. A total of fourteen clusters were formed with maximum number of genotypes in cluster I *i.e.*, 29 genotypes followed by cluster II with 17 genotypes, cluster XII with 3 genotypes, all the remaining clusters were mono genotypic. It was found that the pattern of genotype distribution into different clusters was random and unrelated to geographic diversity. Results on genotype diversity between clusters IV and IX revealed the greatest inter-cluster distances, whereas cluster XII had the greatest intra-cluster distances. The largest cluster mean for seed yield per plant was found in cluster IX. Further, maximum contribution towards divergence was by number of seeds per plant (52.49%) followed by seed yield (17.8%) and days to 50% flowering (7.34%), while minimum by pod length which had shown 0% contribution.

Introduction

In South and South-East Asia, the mung bean (*Vigna radiata* (L.) Wilczek) is one of the most significant food legumes. Pedigree analysis of the majority of the released cultivars showed that only a small number of parents with a close degree of relatedness were regularly used in breeding programmes. Amplified Fragment Length Polymorphism analysis, which is used to analyse genetic diversity, also reveals a high degree of similarity among mung bean varieties (Ghat *et al.*, 2005). ISSR research demonstrates that Indian cultivars have a small genetic foundation due to the continuous adoption of identical cultivars in their genealogy (Saini *et al.*,2004). So, Genetic divergence studies are essential for understanding the genetic variety among genotypes and are helpful in the selection of heterogeneous parents to achieve higher degrees of heterosis as well as a wide range of variability for efficient selection. When numerous traits are considered simultaneously, multivariate analysis, such as the Mahalanobis D^2 statistic, is a useful tool for determining the genetic diversity within a population. The difficulty of selecting various parents for hybridization programmes is brought into sharper focus by the discovery of the features important for genotype discrimination. In order to use these genotypes in crop improvement initiatives aiming at creating high yielding mung bean genotypes, it was decided to quantify the genetic diversity of the mung bean genotypes under study.

Corresponding author E-mail: *nalajalasindoora1@gmail.com*
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Material and Methods

The experiment was carried out on 60 genotypes of mung bean, the genotypes are selected based on visual diversity for seed shape, seed colour and seed lustre, at GPB Farm, College of Agriculture, Central Agricultural University, Imphal, Manipur during kharif 2021, following Randomized Block Design with three replications. Each row was 4 m × 30 cm size with a spacing of 30 cm x 10 cm between and within rows. All the other recommended package of practices were followed during the study for a good crop growth and the genotypes are harvested as and when pods matured. Ten randomly selected plants from each genotype in each replication were taken and observed for several traits i.e., days to 50 % flowering (number of days from sowing until 50% of plants in a genotype plot per replication had atleast one open flower), days to maturity (number of days was taken from sowing to 80% pods maturation on a plant), plant height (cm) (it was measured at maturity from ground level to tip of the main axis), number of primary branches (number of branches emerging directly from the main shoot), primary branch length (cm), number of clusters per plant (number of pod bearing clusters in a plant was calculated), number of pods per plant, Pod length (cm) (it was measured at the time of maturity), number of seeds per pod, number of seeds per plant, 100 seed weight (g), biological yield (g) (weight of all the above ground parts along with the roots was calculated after harvest), harvest index (%) (calculated by dividing total seed yield by biological yield per plant which is expressed as percentage) and seed yield per plant (g), the mean of all ten sampled plants from each genotype is drawn and used for further calculations. Using the D^2 statistics of Mahalanobis (1936), genetic divergence was assessed, and Tocher's approach was used to divide genotypes into several groups (Rao, 1952). The experimental data was analysed statistically by the method of analysis of variance for single factor and lastly to find out the significance mean difference between varieties different genetic parameters were estimated.

Results and Discussion

In the present investigation 60 genotypes of mung bean were grouped into fourteen different clusters using Tocher's clustering method.

Clustering pattern

The 60 mung bean genotypes used for the genetic divergence analysis varied greatly in terms of the 14 morphological traits examined. The cluster I contained maximum number of genotypes i.e., 29 followed by cluster II with 17 genotypes, cluster XII with 3 genotypes and one genotype in each of other eleven clusters which depicts a large amount of variation between and among the genotypes. Wide diversity was also reported by Das *et al.* (2010) grouped 23 genotypes in 8 clusters. The clusters and the contributing genotypes were presented in Table 1 and the dendrogram depicting the cluster pattern in Figure 1.

Table 1: **Showing clustering pattern of 60 genotypes of mung bean on the basis of D^2 statistics**

Cluster	Number of genotypes	Genotypes included
I	29	OBGG 109, BCM 18-2, DGGV 91, MH 1468, MH 1772, BCM 18-1, RVSM 18-1, SML 2015, KM 2241, CAU- GG-1, COGG 16-10, IPM 1610-1, Pusa BM6, RMG 1139, PM 1609, IIPM 20-2, Pusa M 2072, GM 6, IIPM 20-1, Pusa M 2071, Pusa 0672, KM 2419, MI 750-1, MGG 453, Pusa 1371, SML 1839, Pusa M 2132, VGG 17-049 and PM 504-20-27
II	17	RMG 1166, MH 1830, Pusa M 2131, Virat (IPM 205-7), IPMD 1604, IPM 99-125, TBMB 17-2, MHBC 20-7, MI 181-1, IPM 1604-1, SKNM 1705, RMG 1154, TCADM 20-5, SML 1115, PM 1624, Pusa BM 16 and IPMD 101-2
III	1	VGG 15-013
IV	1	IPM 604-1-2
V	1	IPM 1603-1
VI	1	PM 1603
VII	1	IPM 1103-1
VIII	1	Pant M6
IX	1	RMG 1132
X	1	TBMB 117-5
XI	1	IGKM 06-18-3
XII	3	PM 1605, MLS and SKNM 1514
XIII	1	MML 2568
XIV	1	LGG 600

Inter and intra cluster distances

Table 2 lists the typical inter and intra cluster distances between and within the fourteen clusters. In the majority of cases, the inter-cluster distances

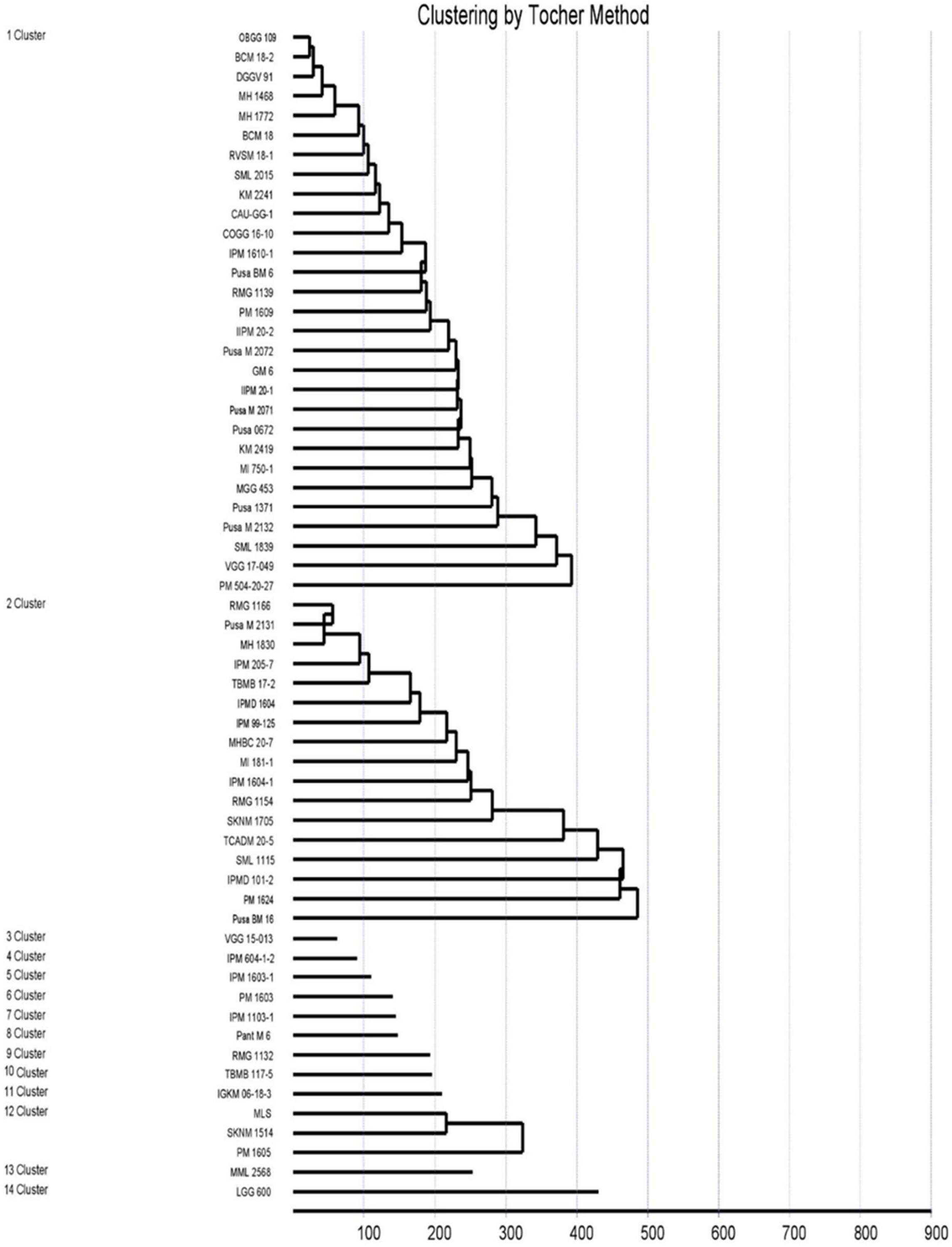

Figure 1: Dendrogram showing the cluster pattern of 60 genotypes of Mung bean

Table 2: Showing average intra & inter cluster distance among fourteen clusters of mung bean.

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	**XIV**
I	255.07	897.74	596.21	430.62	1800.82	478.72	1894.85	517.79	2196.17	852.45	536.23	620.61	1273.52	998.82
II		362.67	564.80	1793.12	650.70	1108.13	619.31	840.7	812.66	594.31	1152.62	802.31	645.6	1651.57
III			0	1144.51	1444.0	605.19	1401.53	147.11	1578.3	359.45	334.83	572.67	926.97	531.15
IV				0	3254.59	825.02	3340.27	78881	3718.04	1385.52	635.83	1209.72	2519.79	1160.75
V					0	1759.93	145.14	2060.57	193.06	1673.23	2450.31	1374.85	374.84	2930.3
VI						0	1921.47	646.14	1931.27	1382.23	655.78	401.91	845.24	515.77
VII							0	1915.77	197.55	1462.21	2489.09	1608.88	421.58	2918.85
VIII								0	2242.48	409.24	210.3	695.45	1363.79	504.41
IX									0	1934.56	2669.51	1499.89	426.34	2957.72
X										0	734.80	1104.08	1492.3	1246.61
XI											0	682.86	1613.74	430.33
XII												395.48	812.33	900.06
XIII													0	1703.41
XIV														0

Table 3: Cluster means for seed yield and its component traits in 60 genotypes of mung bean in 14 clusters.

	DF	**DM**	**PH**	**PB**	**PBL**	**NC**	**NPP**	**PLN**	**SPP**	**SPPL**	**TW**	**BY**	**HI**	**SY**
I	33.74	64.51	30.62	1.88	14.34	3.66	8.25	7.27	11.14	97.51	3.14	7.61	44.03	3.22
II	35.14	64.78	39.14	1.57	19.06	5.47	16.78	7.46	11.70	218.10	3.24	12.96	52.18	6.53
III	42.00	70.00	48.90	1.37	16.31	4.53	13.73	6.55	10.47	167.53	2.19	13.27	32.95	4.37
IV	32.00	62.67	23.27	2.60	17.10	2.17	5.23	5.55	10.27	43.53	2.08	2.87	32.67	0.93
V	34.33	64.33	30.33	1.20	13.20	7.13	18.47	8.47	13.73	265.43	3.39	21.27	45.94	9.77
VI	40.33	70.00	25.53	3.33	16.60	2.70	5.17	6.10	9.33	87.33	3.52	9.00	43.03	3.87
VII	36.00	64.67	25.73	1.00	11.20	6.73	15.10	7.89	11.93	285.47	3.65	13.93	68.80	9.60
VIII	40.33	69.33	36.35	1.00	27.20	4.27	11.33	6.27	6.40	132.60	2.21	6.67	45.14	2.97
IX	38.33	64.33	46.10	2.63	20.85	6.20	17.40	7.57	12.07	283.40	3.15	15.00	68.49	10.27
X	36.33	65.00	36.59	1.23	18.07	6.73	19.40	7.74	10.77	208.40	3.81	12.27	32.41	3.97
XI	40.00	69.67	49.10	1.30	42.33	5.67	6.87	6.95	12.20	90.07	2.39	6.30	31.76	2.00
XII	37.22	67.44	48.98	2.96	32.76	5.94	14.78	7.90	9.19	116.90	3.52	10.59	50.98	4.63
XIII	40.00	70.00	33.03	1.53	18.36	4.40	9.27	8.87	12.60	193.23	4.58	12.20	63.68	7.77
XIV	45.67	78.00	40.91	3.33	21.38	7.00	9.67	6.53	10.33	93.27	2.41	6.60	31.84	2.10

DF-Days to 50% flowering, DM- days to Maturity, PH-plant height, PB-number of Primary branches, PBL-primary branch length, NC-number of Clusters per plant, NPP-number of Pods per plant, PLN-Pod length, SPP-number of Seeds per pod, SPPL-number of Seeds per plant, TW-100 Seed weight, BY-biological yield, HI-harvest index and SY-seed yield per plant.

were greater than the intra-cluster distances, showing a significant amount of genetic variation. Maximum values at the intra-cluster level were found for cluster XII (395.48), cluster II (362.67), and cluster I (255.07), indicating that there is a significant genetic diversity among the genotypes of these clusters. Due to the presence of a single genotype in the other eleven clusters, intra cluster distances in these clusters were zero (0). The average inter-cluster values were minimum between cluster V and VI (145.14) and maximum between cluster IV and IX (3718.04). The cluster pairs exhibiting very high inter-cluster distance were between IV and IX (3718.04) followed by cluster IV and VII (3340.27) and cluster IV and V (3254.59) when crosses are made between genotypes of these clusters there may be increased chance of heterosis, So, it is desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield wide range of segregants on which selection can be done. While least inter-cluster distances were between cluster V and VII (145.14), cluster III and VIII (147.11), cluster V and IX (193.06), cluster VII and IX (197.55), cluster VIII and XI (210.3). The inter and intra-cluster distances were depicted in Figure 2.

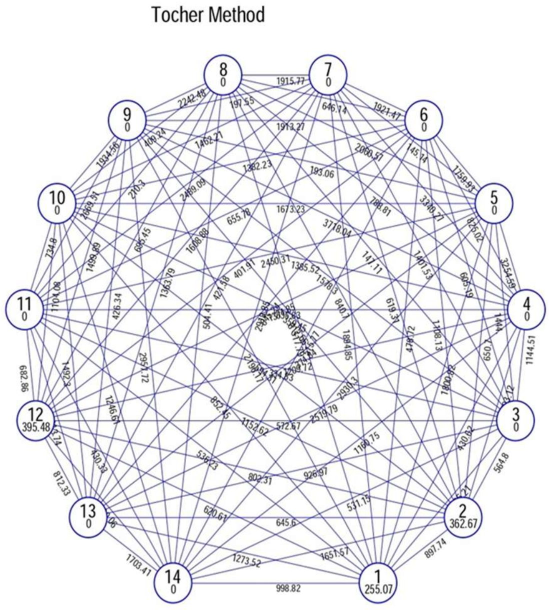

Figure 2: Average inter and intra cluster distance between fourteen clusters of 60 genotypes of Mung bean

Cluster means for different characters

Table 3 displays the cluster means for the fourteen morphological characters. For several features, there was a wide range in cluster mean values among the clusters. Cluster V had maximum cluster mean for number of clusters per plant (7.13), number of seeds per pod (13.73) and biological yield (21.27), whereas cluster XIV had maximum cluster means for days to 50% flowering (45.67), days to maturity (78.00) and number of primary branches (3.33). maximum cluster mean value for traits number of seeds per plant (285.47) and harvest index (68.8) was observed in cluster VII. While plant height (49.10) and primary branch length (42.33) in cluster XI and pod length (8.87) and 100 seed weight (4.58) had their highest means in cluster XIII. Cluster IX had maximum cluster mean for seed yield per plant (10.27) and cluster X had maximum cluster mean for number of pods per plant (19.4). Same trend was observed by Raje and Rao (2001) where cluster III had highest values for number of primary branches, number of clusters, number of pods per plant and number of seeds per plant., Haritha and Reddy (2002) observed maximum values in cluster VII, Yimram *et al.* (2009), Gokulakrishnan *et al.* (2012) observed cluster V recorded the highest mean for seed yield per plant, number of pods per plant, number of branches per plant, number of seeds per pod and 100 seed weight, Gadakh *et al.* (2013) reported cluster V had highest cluster mean for number of seeds per pod and biological yield, while cluster VII had highest cluster mean for pod length and 100 seed weight. Razzaque *et al.* (2016) cluster III had the highest cluster mean for pods per plant, seeds per pod, 1000 seed weight and seed yield, Sarkar and Kundagrami (2016) Cluster V showed the maximum mean value for plant height, number of pods per plant, seed per pod, seed yield and lowest values for days to 50% maturity and days to maturity, and Tiwari *et al.* (2022) reported similar results for clusters I to VII.

Relative contribution of the traits towards divergence

Percent contribution of 14 quantitative traits towards divergence by clustering is depicted in tabulated form Table 4 and pictorially in the Figure 3. Highest percentage contribution towards divergence was shown by trait number of seeds per

Table 4: Relative contribution of the fourteen characters studied towards the divergence

SN	Character	Percent contribution
1	Days to 50 % flowering	7.34
2	Days to maturity	1.07
3	Plant height (cm)	0.34
4	Number of primary branches	6.84
5	Primary branch length (cm)	3.95
6	Number of clusters per plant	0.11
7	Number of pods per plant	0.85
8	Pod length (cm)	0.00
9	Number of seeds per pod	0.51
10	Number of seeds per plant	52.49
11	100 seed weight (g)	1.53
12	Biological yield (g)	0.68
13	Harvest index (%)	6.5
14	Seed yield per plant (g)	17.8

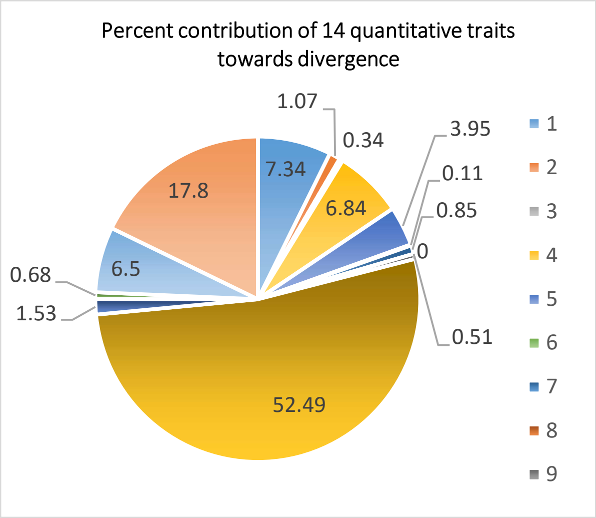

Figure 3: Percentage contribution of individual character towards divergence

plant (52.49%) followed by seed yield per plant (17.8%), days to 50% flowering (7.34%), number of primary branches (6.84%), harvest index (6.5%),primary branch length (3.95%), 100 seed weight (1.53%), days to maturity (1.07%), number of pods per plant (0.85), biological yield (0.68%), number of seeds per pod (0.51%) and plant height (0.34%). While lowest percentage contribution towards divergence was shown by number of clusters per plant (0.11%) and pod length had shown (0%) no contribution towards the divergence. Same trend was observed with the results of Jadhav *et al*. (2021) for PC1 TO PC7. The traits with more percentage contribution can be highlighted like number of seeds per plant and seed yield per plant to understand the variation between genotypes.

Conclusion

The 60 mung bean genotypes used in the current study were split into 14 clusters, with Clusters V and XIV having the highest cluster means for most of the variables and Clusters IV and IX having the maximum inter-cluster distance. According to the D^2 analysis of genetic diversity, which is based on significant inter-cluster distances, the genotypes were found to be diverse for most of the characters and it is advised to cross the genotypes from clusters IV and IX and cluster IV and VII, which may lead to a wide spectrum of favourable genetic variability for improving yield in mung bean.

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Conflict of interest

The authors declare that they have no conflict of interest.

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