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Research Article

Genetic divergence study in advanced breeding lines of mungbean in tarai region

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Abstract
The present investigation was conducted with an objective to study genetic diversity available in 35 advanced breeding lines of mungbean for the identification of genetically diverse and agronomical superior breeding lines. Different morphological and economic traits like plant height, pods per plant, hundred seed weight, biological yield, seed yield and harvest index exhibited considerable genetic variability. Metroglyph analysis distributed mungbean genotypes into 14 and 12 clusters in *kharif*, 2011 and *kharif*, 2012, respectively. Cluster I evolved as a major cluster in *kharif*, 2011 and II as a largest cluster in *kharif*, 2012 with 19 genotypes each. Nodule volume contributed maximum towards genetic divergence 2011, whereas Nitrogen fixation in 2012. These characters were considered to be most important for the genetic diversity. Distribution of genotypes into different clusters, suggested the presence of substantial genetic divergence among the germplasm. The crosses between diverse parents are generally the most responsive for genetic improvement in mungbean.

Key words
Mungbean, genetic diversity, metroglyph analysis, germplasm

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek; 2n=2x=22] is an important grain legume of the Indian subcontinent. The achievement of higher yields in self pollinated crops like mungbean is depend on genetic variability which can be achieve through hybridization between selected divergent parents producing desirable segregants for selection in the advanced breeding generations. Enhancement of genetic variability for traits of interest constitutes the key component of any breeding programme and is achieved mainly through intra and inter-specific hybridization. For efficient use of genetic variability in plant breeding programmes, assessment of genetic diversity is a pre-requisite. The crosses between the parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam 1981). Keeping in view the above perspectives, the present experiment was conducted to assess the magnitude of genetic divergence among advanced breeding lines of mungbean genotypes to know their behaviour under different environments/ seasons.

Material and methods

The present investigation was conducted at N. E. Borlaug Crop Research Center, G. B. Pant University of Agriculture and Technology, Pantnagar (29.0^0N latitude and 79.30^0E longitude and at an altitude of 243.84 m above the mean sea level). This region falls in the humid subtropical zone and situated in the Tarai belt in the foothills of Shivalik range of the great Himalayas. This investigation comprising of 35 advanced breeding lines of mungbean genotypes during *kharif*, 2011 and *kharif*, 2011. All the 35 genotypes were planted in randomized complete block design with three replications during both seasons. The genotypes were sown with 30cm and 10cm inter- and intra- row spacing, respectively. Recommended cultural practices and plant protection measures were followed to raise a healthy crop. Five randomly selected competitive plants of each genotype of each replication were taken for recording observations on 19 morphological characters *viz* days to 50% flowering, number of root nodules, nodule volume, root length, shoot length, nodule dry weight, days to maturity, plant height, number of primary branches, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, seed yield per plant, harvest index, seed protein, straw protein, nitrogen fixation and yield per plot. The data on days to 50% flowering and maturity were recorded on plot basis. The environment-wise data was subjected to multivariate analysis as suggested by Mahalanobis (1936) separately and genotypes were grouped into different clusters following Tocher's method (Rao, 1952) and character contribution towards diversity was estimated.

Result and discussions

In the present study, during 2011 the 35 genotypes were grouped into 14 clusters, whereas in 2012, it was grouped into 12 cluster (Table 1) based on D^2 statistic which are in agreement with earlier reports indicating substantial diversity in mungbean

material (Natarajan *et al.,* 1988; Naidu and Satyanarayana, 1991; Sharma *et al.,* 1996, Raje and Rao, 2001 and Abbas et.al. 2010). During 2011, maximum, 19 genotypes were grouped in the cluster I followed by cluster II and VI with two genotypes, whereas remaining cluster had one genotype each. While during 2012 the 35 genotypes could be grouped into twelve clusters. The maximum number of genotype 19 were found in cluster II followed by cluster III and IV with 3 genotype each, cluster I was having two genotypes and remaining cluster had one genotype each. Distribution of genotypes into different clusters, suggested the presence of substantial genetic divergence among the genotypes and indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable recombinants for seed yield as well as other characters (Raje and Rao, 2001).

The intra- and inter-cluster average distances among five clusters during *kharif*, 2011 and *kharif*, 2012 were variable. The maximum intra-cluster distance (D^2) was registered for cluster VI (121.18) and cluster I (140.15) for 2011 and 2012, respectively. Critical perusal of Table 2 revealed that during 2011, maximum inter-cluster distance (D^2) was found between cluster VII and VIII (426.20) followed by between cluster VIII and XIV (416.76), while Table 3 indicated that the inter-cluster average D^2-value was maximum between cluster I and VIII (288.02) followed by average D^2-value between cluster I and IV (248.94) during 2012. Clusters with maximum inter cluster distance were found to be highly divergent groups. Hence inter cluster distance must be taken into consideration while selecting the parents for a hybridization programme. It is assumed that maximum amount of heterosis is manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high-level of production.

The mean performance of all the characters in different cluster is presented in Table 4 and 5 for season 2011 and 2012, respectively. The results clearly underlines that different clusters showed wide variation from one another in respect of cluster means. This indicated that genotypes having distinctly different mean performance for various characters were separated in to different clusters. Mean performance of different clusters revealed wide range of differences between clusters. During 2011 the genotypes in the cluster X had maximum number pods per plant, pod length and 100 seed weight, whereas maximum number of seed per pod, plant height and yield per plot was revealed by the genotypes in the cluster VIII. Maximum amount of nitrogen fixation per plant was observed by the genotype of cluster V. During 2012 the genotypes in the cluster VIII had maximum days to maturity, plant height, primary branches, nitrogen fixation per plant, pod per plant and 100 seed weight. Whereas cluster XII had maximum number of seed per pod, yield per plant and harvest index. The shortest plant height was recorded for cluster XIV and VI for 2011 and 2012, respectively. Thus these genotypes hold great promise as parental stock to create genetic variability for selection as well as suitable donor for these characters in hybridization programme. Thus upon hybridization between these genotypes, we can create genetic variability for selection. The factors responsible for differentiation of intra- and inter-cluster levels were different in different environments as indicated by cluster means of various characters (Patil, *et al.,* 2003).

Nodule volume contributed maximum towards genetic divergence followed by nodule dry weight then nitrogen fixation in 2011 (Table 6), whereas in 2012 Nitrogen fixation contributed maximum towards genetic divergence followed by nodule dry weight and nodule volume. These characters were considered to be most important for the genetic diversity. Lowest contribution was made by days to maturity followed by days to 50 % flowering and seed protein,.

On the basis of this grouping it may be concluded that an effective hybridization program can be initiate that may include the genotypes of diverse group to produce better segregants which can be used for the development of high yielding mungbean varieties in future.

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Table 1. Clustering patterns of thirty five mungbean genotypes on the basis of D^2 analysis during two seasons

Cluster number	First season (2011)		Second season (2012)	
	Genotypes included	Number of genotypes	Genotypes included	Number of genotypes
I	PM 11-1, PM 11-2, PM 11-3, PM 11-5, PM 11-7, Pant mung- 4, PM 11-8, PM 11-9, Pant mung-5, PM 11-15, PM 11-16, PM 11-17, PM 11-19, PM 11-27, PM 11-21, PM 11-22, PM 11-23, PM 11-32, PM 11-28, PM 11-30	19	PM 11-1, PM 11-31	2
II	PM 11-4, PM 11-10	2	PM 11-2, PM 11-5, Pant mung-4, PM 11-6, PM 11-7, PM 11-9, PM 11-10, PM 11-13, PM 11-16, PM 11-17, PM 11-19, PM 11-20, PM 11-21, PM 11-22, PM 11-23, PM 11-24, PM 11-25, PM 11-32, PM 11-30	19
III	PM 11-6	1	PM 11-3, PM 11-4, PM 11-28	3
IV	PM 11-11	1	PM 11-8, PM 11-14, PM 11-15	3
V	PM 11-12	1	Pant mung-5	1
VI	PM 11-13, PM 11-25	2	PM 11-11	1
VII	PM 11-14	1	PM 11-12	1
VIII	Pant mung-6	1	Pant mung-6	1
IX	PM 11-18	1	PM 11-18	1
X	PM 11-20	1	PM 11-27	1
XI	PM 11-24	1	PM 11-26	1
XII	PM 11-26	1	PM 11-29	1
XIII	PM 11-29	1		
XIV	PM 11-31	1		

Table 2. Average inter and intra-cluster (diagonal) D^2 values in mungbean genotypes *kharif* 2011.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	118.02	104.19	166.95	140.37	162.90	33.99	149.24	277.63	124.05	23.45	123.73	119.45	127.93	140.12
II		16.05	63.95	52.21	73.25	136.22	251.69	179.45	227.61	123.65	213.77	221.36	231.82	242.50
III			0.00	62.78	62.72	198.45	314.09	127.78	290.34	185.78	275.28	284.46	294.65	304.75
IV				0.00	37.36	173.03	285.77	146.63	259.19	157.91	231.26	248.79	263.38	275.64
V					0.00	196.48	309.99	118.20	282.37	178.85	250.64	271.16	285.50	300.58
VI						121.18	116.49	311.28	93.06	28.53	109.73	92.68	97.88	107.66
VII							0.00	426.20	38.23	135.12	113.98	60.38	41.38	18.95
VIII								0.00	398.82	293.33	365.95	387.99	401.43	416.76
IX									0.00	107.65	81.26	26.87	14.44	29.24
X										0.00	107.62	102.18	110.54	125.39
XI											0.00	55.13	79.93	105.91
XII												0.00	28.03	51.71
XIII													0.00	36.11
XIV														0.00

Table 3. Average inter and intra-cluster (diagonal) D^2 values in mungbean genotypes *kharif* 2012.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	140.15	153.42	89.67	248.94	43.85	70.72	181.28	288.02	156.69	248.78	209.20	105.41
II		57.68	71.00	96.32	111.46	86.24	35.45	136.40	53.92	96.43	68.41	59.97
III			100.33	162.80	51.03	20.88	101.28	204.12	97.31	165.79	135.82	50.86
IV				93.94	206.65	180.41	74.14	49.43	119.18	24.20	70.51	151.76
V					0.00	34.24	138.10	244.90	116.56	206.13	167.22	63.51
VI						0.00	116.75	221.24	104.91	182.11	148.82	54.32
VII							0.00	107.46	52.20	69.25	40.55	79.57
VIII								0.00	147.23	43.23	91.44	186.49
IX									0.00	109.00	57.65	55.90
X										0.00	55.12	147.55
XI											0.00	105.60
XII												0.00

Table 4 Cluster mean values for different characters in mungbean during 2011

Clusters	50 % flowering	Root nodule number	Nodule volume (ml)	Root length (cm)	Shoot length(cm)	Nodule dry weigh (mg)	Maturity	Plant height (cm)	Primary branches	Pod per plant	Pod length (cm)	Seed per pod	100 seed weight (g)	Plant yield (g)	Harvest index (%)	Seed protein (%)	Straw protein (%)	Nitrogen fixation (%)	Yield per plot (g)
I	39.73	75.60	0.41	46.33	12.05	0.06	74.57	64.34	1.53	19.53	6.99	11.07	3.38	5.02	32.03	27.16	7.1	0.15	549
II	40.17	73.83	0.21	49.83	12.97	0.05	74.50	55.70	1.27	13.00	6.45	10.43	3.08	4.33	33.22	27.28	8.36	0.11	655
III	41.00	166.00	1.35	42.50	11.70	0.15	73.33	52.23	1.93	15.00	6.33	11.13	3.13	5.33	33.29	26.82	8.63	0.19	706.67
IV	41.50	94.00	1.25	40.00	10.30	0.10	74.67	45.17	1.87	15.27	7.23	11.3	3.17	5.00	31.20	27.39	5.05	0.11	680
V	41.00	101.33	0.20	49.33	12.37	0.07	74.33	73.27	1.73	16.13	7.03	11.63	3.53	5.67	24.97	27.36	8.9	0.30	703.33
VI	40.33	70.00	0.72	42.80	11.45	0.06	74.83	59.27	1.33	16.93	6.33	10.22	3.33	3.83	32.32	27.57	6.12	0.07	510.17
VII	40.33	80.00	0.37	51.67	12.70	0.05	73.33	49.90	1.47	14.93	6.43	9.73	3.47	4.00	27.24	26.51	8.16	0.12	395
VIII	41.00	88.83	0.40	54.17	13.10	0.05	75.00	88.97	1.90	22.66	7.10	12.1	3.69	5.67	33.82	27.5	6.52	0.18	819.17
IX	39.33	97.67	0.17	38.67	12.50	0.14	73.67	62.20	1.33	21.80	7.30	10.17	3.89	4.67	34.78	28.76	5.61	0.11	421.67
X	40.33	80.67	0.09	45.00	12.90	0.09	75.00	73.13	1.93	31.27	7.47	11.53	4.01	5.67	34.78	25.4	8.34	0.19	526.67
XI	40.67	165.67	1.27	42.33	11.80	0.15	74.67	80.93	1.87	24.27	7.08	11.6	3.51	5.33	34.78	28.39	6.78	0.17	461.67
XII	43.00	120.67	0.87	42.00	11.00	0.09	74.33	66.67	1.27	23.93	7.07	11.43	3.34	4.67	34.12	28.33	7.08	0.14	433.33
XIII	39.67	99.33	0.70	46.00	12.37	0.07	75.33	72.93	1.22	22.77	7.13	10.87	3.15	4.67	38.83	29.87	3.89	0.09	418.33
XIV	39.00	84.33	1.37	45.13	12.10	0.10	73.67	43.87	1.47	25.6	7.05	10.93	3.5	5.00	33.43	27.81	6.99	0.15	405

Table 5. Cluster mean values for different characters in mungbean during 2012

Clusters	50 % flowering	Root nodule number	Nodule volume (ml)	Root length (cm)	Shoot length(cm)	Nodule dry weigh (mg)	Maturity	Plant height (cm)	Primary branches	Pod per plant	Pod length (cm)	Seed per pod	100 seed weight (g)	Plant yield (g)	Harvest index (%)	Seed protein (%)	Straw protein (%)	Nitrogen fixation (%)	Yield per plot (g)
I	40.333	66.167	0.583	38.433	8.967	0.074	74.5	56.455	1.533	15.6	6.895	10.333	3.515	3.933	26.053	29.138	8.652	0.154	396
II	40.158	71.649	0.343	39.254	8.191	0.058	74.842	52.534	1.5	15.236	6.508	9.832	3.461	3.649	29.59	27.655	7.245	0.076	412.412
III	39.222	63.444	0.194	39.522	8.911	0.047	74.778	49.856	1.433	15.711	6.358	9.644	3.349	3.444	29.208	28.028	9.693	0.085	363.111
IV	39.889	65.778	0.2	43.133	8.633	0.053	74.778	50.556	1.444	16.26	5.532	8.989	3.299	3.778	29.342	28.457	10.02	0.13	435.556
V	40.167	77.667	0.6	41.867	7.758	0.051	74.333	54.353	1.367	14.433	5.857	9.45	3.235	3.667	27.639	28.304	8.04	0.072	299.167
VI	40.667	59.00	0.433	33.067	7.8	0.08	74.00	46.067	1.6	15.933	6.583	9.067	3.083	3.667	27.143	26.075	6.655	0.063	325
VII	40.00	87.00	0.2	42.067	8.3	0.077	75.667	62.44	1.733	16.00	5.757	10	2.643	4.333	30.187	29.033	8.999	0.177	436.667
VIII	41.667	81.667	0.225	41.667	9.6	0.048	76.00	71.467	2.033	18.733	6.8	10.983	3.728	4.333	23.734	29.395	7.425	0.192	543.333
IX	39.333	126.00	0.15	42.00	8.5	0.14	74.333	48.707	1.6	16.333	6.967	10.167	3.567	3.667	29.861	30.343	6.547	0.08	405
X	39.333	83.667	0.7	36.667	8.333	0.085	74.333	55.173	1.8	18.533	7.027	10.6	3.717	4.00	33.272	29.225	5.623	0.075	505
XI	42.333	116.667	0.45	41.00	8.00	0.08	74.00	51.707	1.333	15.067	7.05	9.467	3.277	3.333	30.455	31.864	7.282	0.073	461.667
XII	40.00	98.00	0.467	39.967	12.367	0.08	75.333	59.387	1.867	16.167	7.383	11.1	3.723	4.667	34.188	29.018	4.173	0.107	358.333

Table 6. Contribution of different characters towards divergence in mungbean

Sl No.	Character	Contribution (per cent) **2011** data	Contribution (per cent) **2012** data
1	50 % flowering	0.69	1.36
2	Root nodule number	8.63	4.19
3	Nodule volume (ml)	19.78	8.46
4	Root length (cm)	2.76	1.63
5	Shoot length(cm)	1.83	1.99
6	Nodule dry weigh (mg)	11.71	25.36
7	Maturity	0.24	1.23
8	Plant height (cm)	5.90	2.13
9	Primary branches	4.96	5.37
10	Pod per plant	7.20	1.05
11	Pod length (cm)	1.53	1.24
12	Seed per pod	1.69	0.84
13	100 seed weight (g)	2.25	3.62
14	Plant yield (g)	3.37	3.43
15	Harvest index (%)	2.86	1.52
16	Seed protein (%)	1.07	0.92
17	Straw protein (%)	5.83	2.98
18	Nitrogen fixation (%)	10.67	30.20
19	Yield per plot (g)	7.04	2.48

Fig 1: Dendrogram Kharif,2011

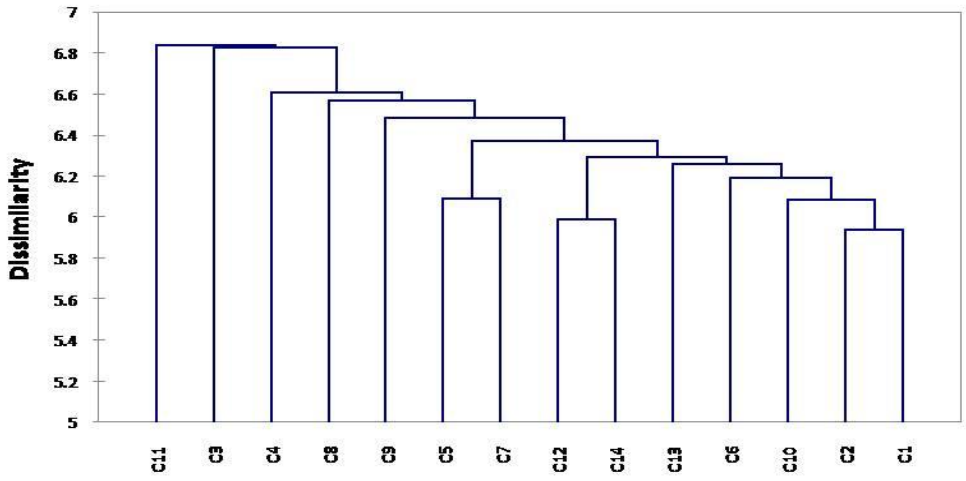

Fig 2:Dendrogram Kharif, 2012