SHORT COMMUNICATION

Evaluation of Mungbean Germplasm for Genetic Diversity

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Mungbean is one of the most important grain legume crops. It ranks third in total production amongst the pulses grown in the country after chickpea and pigeon pea. It is estimated that India's population will touch nearly 1.35 billion marks by 2020 AD and will require 30.3 million tonnes of pulses as against the present production of 12-14 million tonnes (Tiwari, 2004). Clearly a quantum jump is required in the total production of pulses to increase the per capita availability and to meet the challenges of increasing population. Conventional strategies for increasing the production of pulses include development and utilization of improved plant varieties, production technologies and plant protection procedures, which are expected to reduce the existing gap in production and requirement of pulses. The genetic reconstruction of plant type is required for developing high yielding varieties by improving yield component characters. The available germplasm serves as the most valuable natural reservoir for providing the desirable plant attributes for obtaining the high yielding crop varieties (Hawkes, 1981). The present study was conducted with an objective to select divergent parents for further use in improvement of mungbean.

The experiment was conducted during *kharif*, 2003 and 2004 at Crop Research Farm of Department of Genetics and Plant Breeding, Allahabad Agricultural Institute (Deemed University), Allahabad, comprising 132 mungbean genotypes. The experiment was laid in randomized complete block design in three replications of plot size 1x1 m^2 with 30 cm and 10 cm inter and intra-row spacing, respectively. Observations were recorded on 10 morphological characters, *viz.*, plant height (cm), number of primary branches, number of clusters plant^{-1}, number of pods cluster^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, pod length (cm), days to maturity, 100-seed weight (g) and seed yield plant^{-1}(g) on five randomly selected plants of each genotype. Recommended cultural practices and plant protection measures were followed to raise a healthy crop. The pooled data were subjected to multivariate analysis as suggested by Mahalanobis (1936) and genotypes were grouped into different clusters based on Euclidean distances by non- hierarchical cluster analysis (Spark, 1973).

The pooled analysis of variance showed a wide range of variation and significant differences for all 10 characters (Table 1). In the present study, 132 genotypes were grouped into 10 clusters. Cluster IV comprised 28 genotypes, evolving the largest cluster, followed by cluster I with 26 genotypes while, cluster VII emerged as mono genotypic and constituting only one genotype *i.e.* EC398889. Distribution of genotypes into different clusters, suggested the presence of substantial genetic divergence among the germplasm 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 grouping of genotypes originating from different eco-geographical regions into one cluster could be attributed to frequent exchange of breeding material and operation of similar forces of natural and artificial selection resulting in perpetuation, adaptation and stabilization of similar genotypes (Murty and Arunachalam, 1966). The perusal of clustering pattern of the genotypes clearly revealed the lack of relationship between geographic distribution and genetic diversity as the distribution of accessions into various clusters was fairly random (Loganathan *et al.*, 2001; Reddy *et al.*, 2004). Therefore, selection of parents for hybridization should be based on genetic diversity rather than geographic distribution.

The intra and inter-cluster average distances among 10 clusters were variable (Table 2). The maximum intra-cluster distance (D^2) was registered for cluster V (6.631) followed by cluster X (4.924) and cluster IX (4.343). Inter-cluster distance (D^2) was found the maximum between clusters VIII and IX (148.645) followed by

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Table 1. Distribution of 132 mungbean genotypes into different clusters

S. No	Cluster No.	Number of genotypes	Genotypes included
1	I	26	EC30400, EC393407, LM-497, K-1310, EC399223, V-4512, V-2815, K-1284, V-3957, ML-613, KM-2194, K-92-200, TARM-1, LLR-2, PUSA-103, NARP-280, BHUM-93-34, PUSA-9531, AKM-8802, PUSA-9132, MARP-280, AKM-9241, PM-9001, LM-407, LLR-3, LLR-4
2	II	14	IPRM-90, UPM-83-1, OUM-11-5, ML-5, SONAMUNG, ML-131, PUSABAISAKHI, PS-16, AKM-9243, PANT MUNG-1, AKM-9601, T-1, CO-9, LGG-478
3	III	15	OBGG-11, V-2070, MUM-1-1, K-1460-1, NP-28, WGG-37, T-44, OBGG-52, MGG-47, PUSA-105, TARM-2, V-2015, MH-90-1, MGG-295, LM-23
4	IV	28	SAMRAT, ML-390, ML-583, PDM-1, HUM-10, PS-10, ML-406, JYOTI, HUM-1, PDM-54, PUSA-9072, SUJATA, DPM-90-1, SABARMATI, HUM-8, LGG-420, PDM-89-226, MGG-347, MH-309, LGG-460, PDM-11, PDM-84-139, ML-803, HUM-7, LGG-410, HUM-14, PUSA-102, NM-1
5	V	13	WGG-2, KM-2197, PUSA-9871, PUSA-108, PDM-139, LM-1119, V-3561, KM-2192, LM-490, V-4589, K-2192, K-1284, LM-387
6	VI	4	EC398888, MSO-9, PUSA BOLD-2, MSO-8
7	VII	12	PUSA-9332, ML-955, ML-405, MUM-2, BHU-MGP-17, HUM-2, BDYR-MUM-2-1, OBGG-40, LLR-1, K-851, K-1310, DMG-1098-1
8	VIII	1	EC398889
9	IX	9	LGG-470, MP-28, PUSA-9071, PDM-84-143, NARENDRA M-1, PIMS-11/ 99, V-1133, DMG-1103, VC-3944
10	X	10	V-557, ML-287, ML-588, K-1084, ML-575, LGG-499, LGG-477, Lam M-2, LGG-491, LGG-476

Table 2. Intra (diagonal) and inter-cluster average distances (D^2) for 10 characters in mungbean

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**3.415**	10.511	5.272	4.661	7.5076	17.758	8.827	132.803	6.791	8.745
	(1.848)	(3.242)	(2.296)	(2.159)	(2.740)	(4.214)	(2.971)	(11.524)	(2.606)	(2.957)
II		**3.787**	17.181	8.341	18.473	19.625	27.552	134.885	13.786	11.042
		(1.946)	(4.145)	(2.888)	(4.298)	(4.430)	(5.249)	(11.614)	(3.713)	(3.323)
III			**3.516**	7.393	15.140	28.665	4.439	143.976	6.401	21.372
			(1.875)	(2.719)	(3.891)	(5.354)	(2.107)	(11.999)	(2.530)	(4.623)
IV				**3.003**	12.440	13.119	13.742	118.657	10.170	9.967
				(1.733)	(3.527)	(3.622)	(3.707)	(10.893)	(3.189)	(3.157)
V					**6.631**	31.349	16.728	138.086	7.209	10.036
					(2.575)	(5.599)	(4.090)	(11.751)	(2.684)	(3.168)
VI						**3.119**	37.259	99.341	34.751	14.846
						(1.766)	(6.104)	(9.967)	(5.895)	(3.853)
VII							**3.870**	145.010	13.542	31.776
							(1.967)	(12.042)	(3.681)	(5.637)
VIII								**0.000**	148.645	129.368
								(0.000)	(12.192)	(11.374)
IX									**4.343**	14.585
									(25.084)	(3.819)
X										**4.924**
										(2.219)

D^2 values are represented in parentheses

clusters VII and VIII (145.010). 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 hybridization programme.

Mean performance of different clusters revealed wide range of differences (Table 3). Cluster II included genotypes having the highest number of pods cluster^{-1} and number of pods plant^{-1} and cluster IV had early maturing genotypes which may serve as a suitable source for incorporation of earliness into other genotypes, cluster VI comprised genotypes with long pods, high 100-seed weight and seed yield plant^{-1}. However, cluster VII was characterized with dwarf plants.

Table 3. Mean values of 10 clusters for 10 characters in 132 mungbean genotypes

Cluster No./ Characters	Plant height (cm)	No. of primary branches/plant	No. of clusters/ plant	No. of pods/ cluster	No. of pods/ plant	No. of seeds/ pod	Pod length (cm)	Days to maturity	100-seed weight (g)	Seed yield/ plant (g)
I	47.04	3.50	15.36	2.78	38.72	10.14	6.64	82.55	3.49	9.68
II	53.74	3.40	14.07	5.36	53.24	11.05	7.11	79.93	3.91	13.49
III	41.64	2.64	12.02	3.07	31.73	7.91	6.08	75.47	3.41	9.38
IV	50.80	3.63	14.58	3.30	39.83	10.31	6.83	68.38	3.54	12.88
V	39.56	4.64	23.05	2.92	49.54	8.79	5.53	82.18	4.48	10.01
VI	59.42	3.92	16.58	2.83	37.67	11.25	10.73	72.75	4.88	14.72
VII	31.14	3.64	10.11	2.79	21.11	8.25	5.80	76.67	3.39	6.04
VIII	69.67	5.33	12.33	2.33	24.00	11.33	9.90	58.00	2.63	13.80
IX	43.37	3.96	14.59	3.74	43.63	7.19	5.11	82.22	3.46	11.30
X	65.53	4.20	21.87	3.00	54.73	10.03	7.24	83.03	3.66	13.84

Since choice of appropriate parents plays a vital role in hybridization programme, best performing genotypes from distant clusters like VII, VIII and IX should be selected. Progenies of genetically diverse parents are likely to produce a broad spectrum of variability in segregating generations which will facilitate the isolation of transgressive segregants and recombinants for improvement of mungbean crop.

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