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RESEARCH ARTICLE

Genetic diversity analysis in mungbean [*Vigna radiata* (L.) Wilczek]

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SUMMARY

Seventy seven genotypes of mungbean were evaluated for ten different characters and mean values were worked for genetic diversity by Mahalanobis D^2 statistic. The results of multivariate analysis (D^2) indicated the presence of considerable genetic divergence among these genotypes. The genotypes were grouped into 9 clusters. Cluster III had maximum intra-cluster distance while inter-cluster distance was highest between clusters VIII and IX. cluster means indicated that none of the cluster was superior for all the characters studied. Therefore, hybridization between genotypes belonging to different clusters is suggested for development of superior genotypes.

Key Words : Divergence, mungbean

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Mungbean [*Vigna radiata* (L.) Wilczek] is one of widely grown short duration grain legume in India fitting well in also cropping systems. It is grown as *Kharif* (both as sole and intercrop) and summer crop. In any improvement programme, genetic diversity plays an important role and has been emphasized again and again by many workers (Joshi and Dawan, 1966, Murthy and Arunachalam, 1966). Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parental lines. More the diverse parents, greater are the chance of increased spectrum of variability, providing ample scope for selection of desired plant. Therefore, an effort was made to estimate the nature and magnitude of genetic diversity in a set of 77 genotypes of mungbean.

MATERIALS AND METHODS

The experimental material for the present study was consisted of seventy seven diverse to genotypes of mungbean procured from the germplasm stock maintained at the IIPR, Kanpur, were grown during the *Kharif* season of 2009 at regional research Centre, Saini of Chandra Shekhar Azad university of Agriculture and technology, Kanpur. The material was planted in a randomized block design with three replications. Each genotype was grown in three rows of 3 meter length with row to row and plant to plant spacing of 30 and 10 cm, respectively. the observations on the ten characters were recorded on five randomly selected plants in each of the three replications/blocks for days to first flowering, days to 50 per cent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, seeds per pod, pods per plant, seed yield per plant (g) and 100 seed weight (g). the replicated data were subjected to genetic divergence analysis using Mahalanobis's D^2- statistic (Mahalanobis, 1936) as suggested by Rao (1952). All the genotypes were grouped into respective cluster on the basis of D^2 values following Tocher's method.

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RESULTS AND DISCUSSION

The analysis of variance revealed highly significant variation among the genotypes for all the traits studied. These differences could be used in distinguishing genotypes on the basis of their morphology. Mahalanobis D^2 statistic was computed for all the ten characters in order to assess the genetic diversity present among the genotypes under study. in all, nine clusters were formed (Table 1). Cluster I was the biggest cluster having 15 genotypes which was followed by

Table 1: Distribution of 77 genotypes of mungbean on the basis of D^2 statistic

Cluster	Number of genotypes	Genotypes
I	15	DMG 1079, ML 1256, Ganga 8, Pusa 105, DMG 109-2, OBGG 52, DMG 080, Pusa 9072, DMG 1050-2, DPC 1020-2, HUM 1, DPC 057, BM 111, AKM 9910, DPC 1056
II	9	DMG 1080-1, HUM 12, RMG 344, Pratap, BM-11, Sona, HUM 6, ML 1059, Pusa 9531
III	13	E 3-8, EC 93162, Box 12-2, CDGG 912, MGG 295, CN 9058, Pant M-1, DMG 1081, DMG 11717, DMG 1065-2, K 851, BM 7, ML 818
IV	4	DM 071130-2, ML 512, BM 4, CN 8082
V	8	SML 32, EC 30400, AKM 8803, GM 4, DMG 1058, Pant M-5, HUM-12, DM 45-6
VI	9	RMG 62, Ganga 1, Pusa Vikas, IPM 99-125, Sujata, RO 669, HUM 2, GM 3, ML 131
VII	7	DMG 1166, DMG 1133-1, DMG 1058-1, RMG 268, VL 112, AKU 9904, RMG 32
VIII	6	Pusa Vishal, DMG 1127-2, DMG 1123-1, ML 613, BGG 1, PDM 11
IX	6	DMG 1090, Pusa 9531, DUM 11-5, EC 30000, SML 668, DMG 1102

Table 2: Intra-cluster (in-bold) and inter cluster distances in mungbean

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	1.995	2.993	2.306	3.743	2.414	3.144	3.376	4.366	3.164
II		1.736	3.899	3.022	3.779	2.553	5.631	4.766	3.165
III			2.100	3.684	2.595	3.532	2.851	4.007	4.732
IV				1.854	4.920	3.402	6.076	2.640	5.388
V					1.350	2.974	2.492	5.596	3.077
VI						1.919	5.084	4.117	3.186
VII							1.563	6.297	5.123
VIII								1.904	6.531
IX									1.660

Table 3: Cluster means for various characters in 77 genotypes of mungbean

Characters	Clusters									Overall mean
	I	II	III	IV	V	VI	VII	VIII	IX	
Days to 1st flowering	41.00	35.00	43.92	38.50	38.12	36.11	47.86	43.00	34.83	40.09
Days to 50% flowering	47.07	41.56	49.85	45.00	46.50	42.44	52.71	48.67	40.50	46.31
Days to maturity	68.80	56.78	71.00	65.00	69.75	60.67	72.86	70.33	58.00	66.36
Plant height	33.67	34.22	32.15	35.50	28.25	35.89	24.57	45.50	29.17	33.01
Primary branches/ plant	3.87	4.56	4.38	5.00	3.12	3.89	3.29	5.17	3.17	4.01
Secondary branches/ plant	4.60	5.56	7.54	9.25	4.50	7.00	3.71	9.33	3.83	5.95
Seeds per pod	7.40	6.89	7.69	7.00	8.62	9.44	8.43	8.50	8.50	8.00
Pods per plant	14.47	17.78	12.92	26.00	10.12	18.11	8.57	29.17	10.67	15.48
Seed yield/ plant	3.51	3.11	2.86	2.96	2.91	2.96	2.90	3.03	3.78	3.13
Seed weight	3.23	3.74	2.46	6.15	1.94	3.58	1.39	5.67	2.25	3.16

cluster III with 13 genotypes, cluster II and VI with 9 genotypes, respectively, cluster V with 8 genotypes, cluster VII with 7, cluster VIII and IX with 6 each and cluster IV with 4 genotypes. This indicated that there was a wide diversity among the mungbean genotypes for the characters studied. This may be attribute to the fact that these genotypes of mungbean were received from different breeding centres of the country (Birari and Ghanekar, 1992) that means there was no relationship between eco-geographical origin and genetic diversity present in these genotypes.

The average intra and inter cluster D^2 values (Table 2) indicated that cluster III with thirteen genotypes exhibited maximum intra cluster distance ($D^2 = 2.100$). this cluster was the most divergent group and genotypes falling in this cluster could be utilized as parents for hybridization. Cluster I ($D^2 = 1.995$) with fifteen genotypes and cluster VI ($D^2 = 1.919$) with nine genotypes were next most divergent groups. As far as inter-cluster divergence is concerned, the inter-cluster distance values ranged from 2.306 to 6.531. the member of cluster VIII and IX exhibited maximum divergence ($D^2 = 6.531$) followed by cluster VII and VIII ($D^2 = 6.297$), cluster IV and VII ($D^2 = 6.076$), cluster V and VIII ($D^2 = 5.596$), cluster IV and IX ($D^2 = 5.388$) indicating that genotypes belonging to these cluster were genetically more divergent that order. Parents selected from these individual groups showing maximum inter-cluster distance are likely to produce superior recombinants. Natarajan *et al.* (1988) have also opined that selection of parents for hybridization should be done based on the inter-cluster distance to get maximum variability. On the other hand, lowest inter-cluster D^2 value was observed between cluster I and III indicating that genotypes of these clusters are closer. Similar results were also observed by Murthy and Arunachalam (1966).

The cluster mean estimated for ten characters (Table 3) revealed that cluster means for days to 50 per cent flowering varied from 40.50 days in cluster IX to 52.71 days in cluster VII with overall mean of 46.31 days. cluster VIII had highest mean values for plant height, primary branches per plant, secondary branches per plant and pods per plant.Cluster VII had highest mean values for days to 1st flowering, days to 50 per cent flowering and days to maturity and lowest mean values for plant height. secondary branches per plant, pods per plant and 100 seed weight. cluster IX exhibited highest mean for seed yield per plant but lowest for days to 1st flowering and days to 50 per cent flowering. For seed yield per plant, highest mean was recorded for cluster IX and lowest for cluster III with over all mean of 3.16.

This indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Therefore, the result of the present study suggest that while selecting parents for hybridization inter-cluster distance must be taken into consideration that may provide wide spectrum of variation in the segregating generations.

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