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Genetic divergence in mung bean

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ABSTRACT

The present study was undertaken to provide information on the nature and magnitude of genetic diversity among 30 mung bean genotypes for yield traits by using Mahalanobis's D^2 statistics. Thirty genotypes could be grouped in 6 clusters, cluster VI showed maximum intra-cluster distance while the highest inter-cluster distance was observed between cluster III and VI. Cluster II recorded highest means for seeds per pod, 100 seed weight, seed yield per plant and shelling %. The percent contribution towards genetic diversity was highest for shelling percentage (17.70) followed by seed yield per plant (16.55) and number of clusters per plant (14.71). From the divergence analysis, it may be concluded that the genotypes belonging to different clusters separated by high estimated statistical distance may be used in the hybridization programme for developing high yielding mung bean varieties. Five genotypes *viz.*, PDM-11, TARM-2, TM-98-50, PDM 54 and Basanti could be identified as most useful in the future breeding programme.

Key words: Clustering, Divergence, Mungbean, Yield.

INTRODUCTION

Mung bean (*Vigna radiata* L.) is an important short season summer grain legume, well suited to small holder production under adverse climatic conditions and commonly used in Indian cuisine (Vijayalaksmi *et al*., 2003). India alone accounts for 65% of its world acreage and 54% of the production. Thus the production and productivity of Indian varieties are far below the world average. In India, according to the report published in 2010-11 by DES, DAC, Ministry of Agriculture, mungbean (*kharif* and *rabi*) was grown on an area of 35.082 lakh ha with a total production of 18.003lakh tons and total productivity of 942kg/ha. Though the crop can be grown in spring as well as in summer under irrigated northern plains and as *rabi* crop in southern and southeastern parts where the winter is quite mild, but it is mainly grown during the *kharif* season. Therefore, extensive breeding programme is urgently needed for developing lines suited to different crop seasons and simultaneous improvement in yield of the crop.

The success of the hybridization followed by selection depends largely on the selection of parents showing high genetic diversity for traits of interest (Murthy and Arunachalam, 1966). A large amount of genetic diversity has been reported in mung bean (Sinha *et al*. 1996; Francisco and Maeda, 1989) which indicates potential for genetic improvement of the crop.

The genetic variability present among the different genotypes of a species may arise either due to geographical separation or due to genetic barriers to crossability. One of the potent techniques of assessing genetic divergence is D^2 statistic proposed by Mahalanobis in 1936. This technique measures the forces of differentiation at two levels *viz*., intra cluster and inter cluster that helps selection of genetically divergent parents for exploitation in hybridization programmes. While selecting parents on the basis of D^2 statistic, three important points should be considered *viz*., i) the relative contribution of each character to the total genetic divergence, ii) the choice of clusters with the maximum statistical distance and iii) the selection of one or a few genotypes from such clusters. Evaluation of germplasm collection has the highest priority among germplasm functions. Germplasm enhancement embraces those activities required to aggregate useful genes and gene combinations into usable phenotypes (Evgenidis *et al*., 2011).

Thus the aim of the present study was to find out the genetic variability among different plant traits, direct and indirect contributions of these traits towards yield and to identify better combinations as selection criteria for developing high yielding fine mung bean genotypes.

MATERIALS AND METHODS

Thirty genotypes of mung bean, under study were subjected to classificatory analysis in respect of 13 characters. Among the thirty genotypes used in the experiment, genotypes WBM-659, B-105, Pant Mung 2, WBM-04-5, WBM-6-11-3, Pusa 9531, Hum-12, WBM-314, B-1, PDM-54, Basanti, PDM-84-139, PDM-11 and WBM-4-34-1-1 were collected from Pulses and Oilseeds Research Station, Berhampur, West Bengal while the genotypes

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TARM-2 and TM-98-50 were collected from Bhaba Atomic Research Station; WBM-220 was collected from NBPGR, Jodhpur Research Station and the rest of the genotypes viz. Midnapur Local, Radiata-5, BM-18, B-27, A-7, PDM-19-257, NP-28, Hinjalgunj, Malda-95-13, PS-16, K-851, SML-264 and SML-286 were collected from Department of Genetics and Plant Breeding, Bidhan Chandra Krishi Viswavidyalaya. The test entries were planted in the Departmental Farm at BCKV in February, 2010 and harvested during the last week of April, 2010. The experiment was conducted following Randomized Block Design with three replications. There were three rows of 2 m length for each genotype in each replication grown at a distance of 30 cm between lines and 10 cm between plants. All the recommended package of practices was followed to establish a good plant stand. Observations on 13 characters, namely days to first flowering, days to 50% flowering, plant height (cm), number of primary branches, number of fruiting cluster per plant, number of pods per cluster, Internode length (cm), total number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g) and shelling percentage were recorded from ten randomly selected competitive plants in each replication.Shelling percentage is one of the most important characters that indicate a plant's potentiality to partition and translocate photosynthates in the pods and seeds respectively (Injeti *et al*.,2008). Shelling percentage is calculated as weight of all seeds from 10 randomly selected pods divided by weight of 10 randomly selected pods, whole multiplied by 100. The mean data were subjected to statistical analysis and Mahalanobis D^2 (1928) statistics was used to study genetic divergence. The test of significance for the correlated variables had been done following Rao (1948) using 'V' statistic which in turn utilizes Wilk's criterion (value-6.227x10-20). Group constellation was performed according to the method suggested by Tocher (Rao, 1952). The contribution of individual trait towards genetic divergence was quantified on the basis of coefficient of variation at genotypic and inter-cluster levels (Vavilov, 1951).

RESULTS AND DISCUSSION

The analysis of variance showed highly significant difference among the genotypes for all the 13 characters and thus indicated the presence of appreciable amounts of diversity among the genotypes. The 30 genotypes could be grouped into six clusters (Table 1). Cluster I comprised the highest number of 22 genotypes, followed by cluster III and cluster VI comprising 3 and 2 genotypes respectively. The remaining three clusters were monogenotypic. The genotypes belonging to the same cluster indicate to be more closely related than those belonging to different clusters. Monogenotypic clusters indicate that such genotypes might have completely different genetic makeup from the remaining genotypes and from each other, thus leading to the formation of separate cluster. Cluster analysis of the 30 genotypes based on the characters under study has been illustrated by the dendogram as shown in the figure 2. This confirmed grouping of these genotypes into six clusters obtained by D^2 statistics. Earlier, Win *et al*. (2011) opined that such intra- and inter cluster distances might arise due to differential genetic makeup of the genotypes.

Average intra-cluster distance among 30 genotypes ranged between 0.00 and 17.50 (Table 2). The intra-cluster distance values indicate the closeness of the genotypes falling in the same cluster. The clusters exhibiting an intra-cluster distance of 0.00 reveal to be monogenotypic and

Table 1: Grouping of genotypes in different clusters

Clusters	Number of genotypes	Genotypes
I	22	WBM-04-5, B-27, A-7, B-1, Pant Mung 2, B-105, WBM-6-11-3, Pusa-9531, Hinjalgunj, PDM-19-257, WBM-314, SML-264, Radiata-5, PS-16, WBM-659, BM-18, NP-28, WBM-220, Malda-95-13, Midnapur local, SML-286, K-851.
II	1	PDM-11.
III	3	HUM-12, PDM-84-139, WBM-4-34-1-1.
IV	1	TARM-2.
V	1	TM-98-50.
VI	2	PDM-54, Basanti.

Table 2: Intra (diagonal) and inter cluster distance in the genotypes

Cluster	I	II	III	IV	V	VI
I	14.16					
II	17.60	0.00				
III	21.26	29.46	11.97			
IV	18.10	22.45	21.22	0.00		
V	22.94	23.06	29.41	24.45	0.00	
VI	28.63	21.33	39.39	29.12	19.90	17.50

consequently less heterogeneous; on the other hand, high intra cluster D^2 values indicate more genetic divergence between genotypes belonging to the same cluster and therefore more heterogeneous. Perusal of Table 2 indicated that cluster VI possessed highest intra cluster distance (17.50) followed by cluster I (14.16) and cluster III (11.97). According to Murthy and Arunachalam (1966) success of the hybridization followed by selection depends largely on the choice of parents showing high genetic diversity for traits of interest. Therefore, such intra cluster heterogeneity among the constituents' genotypes obtained in the present experiment might serve as guideline to choose parents for the recombination breeding programme.

The average of inter-cluster distance, however, varied from 17.60 to 39.39. The highest distance was observed between cluster III and VI, followed by cluster II and III (29.46), cluster III and V (29.41), IV and VI (29.12) and I and VI (28.63). It indicated that these cluster pairs were most divergent or in other words, the genotypic constituent of these cluster pairs comprised the genes from most distantly related parents in respect of the characters studied. The genotypes belonging to different clusters separated by high estimated statistical distance may be used in the hybridization programme for crop improvement as well as for studying the inheritance pattern of different characters in mung bean. Considering the individual genotype, those belonging to the cluster VI (PDM-54 and Basanti), cluster I (WBM-4-05, B-27, A-7, B-1, Pant-Mung-2, B-105, WBM-6-11-3, Pusa-9531, Hinjalgunj, PDM-19-257, WBM-314, SML-264, Radiata-5, PS-16, WBM-659, BM-18, NP-28, WBM-220, Malda-95-13, Midnapur local, SML-286 and K-851) and cluster III (HUM-12, PDM-84-139 and WBM-4-34-1-1) were found most divergent from those which belonged to cluster II (PDM-11), cluster IV (TARM-2) and cluster V (TM-98-50). The above results further reveal that considering individual character the genotypes were more divergent than that considering a constellation of characters.

Since improvement in yield and other related characters is a basic objective in any breeding programme, cluster means for seed yield per plant and its major components need to be considered for selection of genotypes. The means for number of cluster per plant varied from 2.27 in cluster III to 13.06 in cluster VI (Table 3). That with total pods per plant varied from 6.30 (cluster III) to 46.56 (cluster VI). Cluster means for number of primary branches, pods per cluster, internode length and pod length were recorded to be highest in cluster IV comprising the genotype TARM-2. The cluster means for different characters further indicate that cluster VI comprising PDM 54 and Basanti recorded highest or second highest cluster mean for six different characters like yield per plant, number of branches per plant, number of cluster per plant, number of pods per plant, number

Table 3: Cluster means for different characters

Cluster	Plant height (cm)	Number of primary branches	Number of cluster per plant	Pods per cluster	Inter-node length (cm)	Total pods per plant	Pod length (cm)	Seeds per pod	100seed weight (g)	Seed yield per plant (g)	Shelling %	Days to first flowering	Days to 50% flowering
I	45.18	1.71	5.60	3.70	6.07	20.88	6.77	10.62	3.13	3.45	54.74	38.66	42.70
II	52.02	1.61	7.44	3.05	6.42	22.68	6.84	10.91	4.07	5.96	75.94	40.00	43.67
III	31.54	1.22	2.27	2.82	3.91	6.30	7.02	8.30	2.92	2.32	37.66	38.04	41.71
IV	52.26	1.88	6.86	4.86	10.44	33.31	7.10	9.91	3.16	3.74	61.16	38.00	41.57
V	59.49	1.42	10.13	4.31	6.19	43.62	6.42	9.78	3.73	2.35	34.25	39.00	42.00
VI	56.77	1.82	13.06	3.53	6.30	46.56	6.36	10.35	3.10	4.60	58.51	39.78	43.90

of seeds per pod and shelling percentage; cluster V comprising one genotype *viz.*, TM-98-50 had similar mean for four different characters like number of cluster per plant, number of pods per cluster, number of pods per plant and 100 seed weight; cluster II comprising one genotype *viz.*, PDM-11 had highest cluster mean for four different characters like yield per plant, seeds per pod, 100 seed weight and shelling percentage. The above results thus indicated that there was no cluster containing genotypes with all the desirable characters which could be directly selected and utilized. Interestingly, most of the minimum and maximum mean values were distributed in relatively distant clusters. Recombination breeding between genotypes of different clusters has been suggested by Sonawane and Patil (1991). Since the genotypes under all the clusters had almost similar number of days to flower first or 50% therefore, the above five genotypes *viz.*, PDM-11, PDM 54, Basanti, TM-98-50 and TARM-2 may be considered for further use.

Perusal of the Table 4 regarding contribution of individual character toward total genotypic divergence revealed that the highest contribution was by the shelling percentage (17.70%) followed by seed yield per plant (16.55%), number of cluster per plant (14.71%). Conspicuously, total pods per plant (0.00%) revealed no contribution towards total genetic divergence. It may be mentioned here that the characters that contributed substantially toward total genetic divergence belonged to cluster II. The above results were confirmed when the parameter, number of times each character appeared first in rank is considered. The above characters that contributed significantly higher percentage of divergence toward total divergence in D^2 statistics also appeared higher number of times first in rank Percent contribution of individual characters towards divergence D^2 statistics has been represented with a pie diagram (Figure 1).

Therefore, selection of divergent parents based on these characters might be useful for heterosis breeding as well as to obtain large number segregants in the subsequent generations. Thus on the basis of inter-cluster distance, cluster means, characters with high contribution to D^2 values, dendrogram and by comparing the mean values of the all the genotypes; the following five genotypes *viz.*, PDM-11,TARM-2, TM-98-50, PDM 54 and Basanti would be the most useful in future breeding programme.

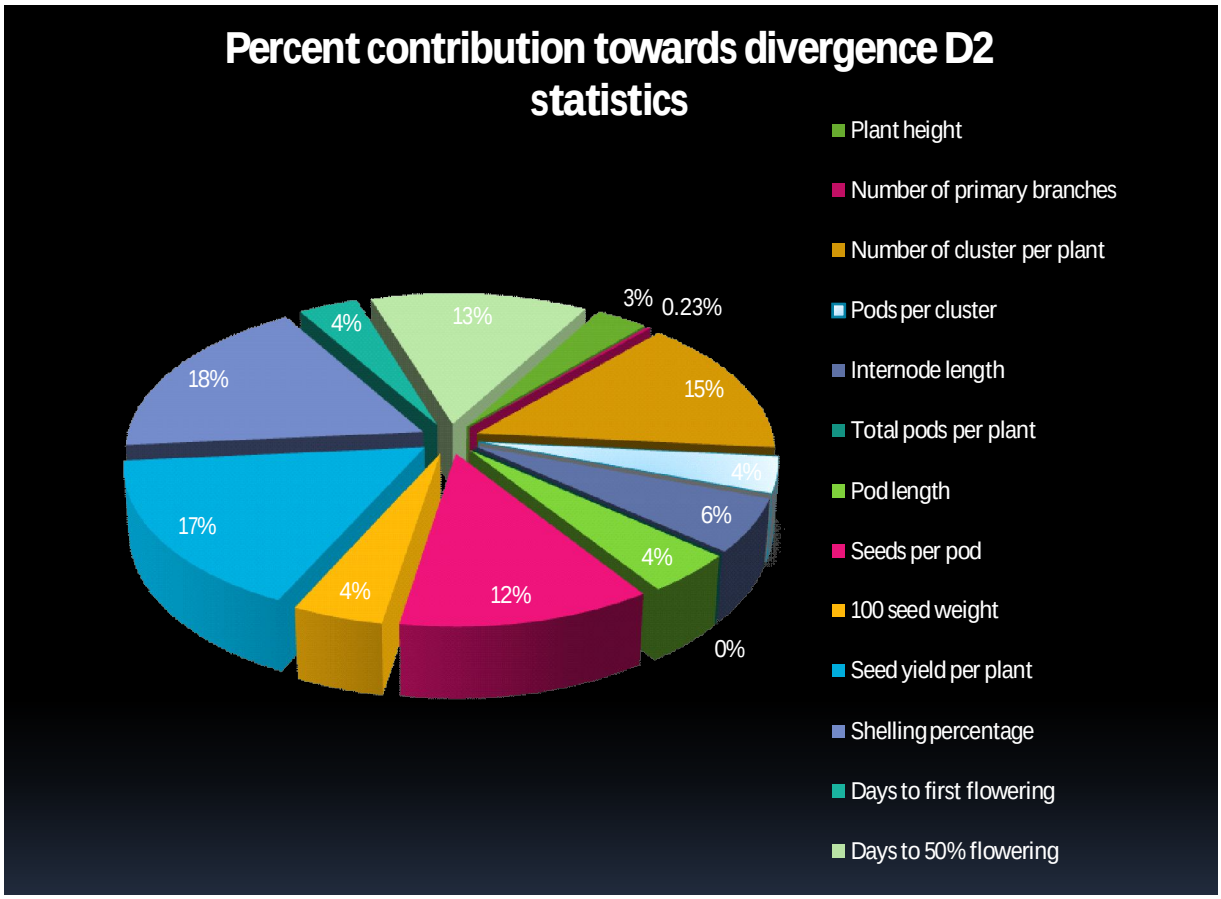
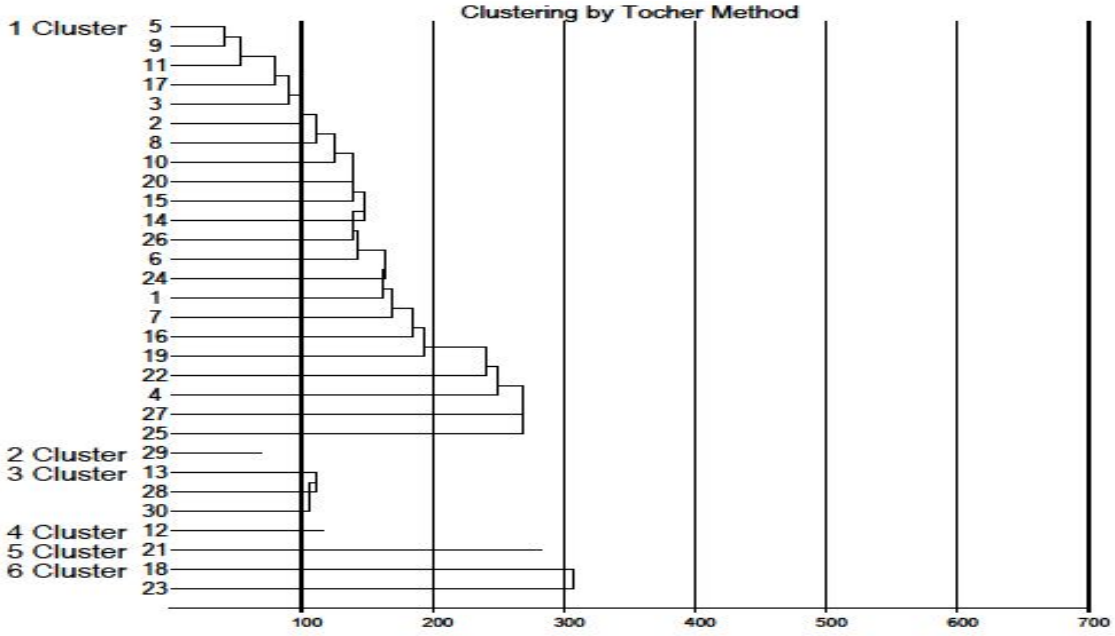


Fig 1: Percent contribution towards divergence D^2 statistics

Table 4: Contribution of individual characters towards total genotypic divergence in 30 genotypes of mung bean

Characters	Number of times appearing as first in rank	Percent contribution towards divergence D^2 statistics
Plant height (cm)	14	3.22
Number of primary branches	1	0.23
Number of cluster per plant	64	14.71
Pods per cluster	17	3.91
Internode length (cm)	25	5.75
Total pods per plant	0	0.00
Pod length (cm)	19	4.37
Seeds per pod	53	12.18
100 seed weight (g)	19	4.37
Seed yield per plant (g)	72	16.55
Shelling percentage	77	17.70
Days to first flowering	16	3.68
Days to 50% flowering	58	13.33



c1=WBM-659, 2=B-105, 3=Pant Mung 2, 4=Midnapur local, 5=WBM-04-5,6=Radiata-5,7=BM-18, 8=WBM-6-11-3, 9=B-27, 10=Pusa-9531, 11=A7, 12=TARM-2, 13=HUM-12, 14=WBM-314, 15=PDM-19-257, 16=NP-28, 17=B-1, 18=PDM-54, 19=WBM-220, 20=Hinjalgunj, 21=TM-98-50, 22=Malda-95-13, 23=Basanti, 24=PS-16, 25=K-851, 26=SML-264, 27=SML-286, 28=PDM-84-139, 29=PDM-11, 30=WBM-4-34-1-1.

Fig 2: Cluster analysis of the genotypes represented by dendogram

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