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Genetic Diversity Studies in Mungbean (*Vigna ridiata (L.) Wilezek*)

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Abstract

The present investigation was undertaken to assess the genetic diversity of fifty-one diverse genotypes for the yield, yield related and quality traits in mungbean. The observations were recorded on 13 morphological / quality attributes. Results of the analysis of variance revealed significant differences for all the characters studied and thereby offering an ample opportunity for selecting suitable genotypes with desired traits. Based on diversity studies, all the 51 genotypes were grouped into 9 clusters, with Cluster I having the maximum number of genotypes (21) which was followed by Cluster II (9 genotypes) and Cluster IV (8 genotypes) while Clusters III, VI, VIII, and IX showed solitary nature with 1 genotype each. Cluster mean for cluster VI surpassed the population mean for most of the yield contributing characters viz., - primary branches plant^{-1}, clusters plant^{-1}, pods plant^{-1}, number of seeds pod^{-1}, 100 seed weight, seed yield plant^{-1}, biological yield plant^{-1} and harvest index. Maximum intra cluster distance was recorded in cluster VII (247.06). Similarly, highest inter-cluster distance was recorded between cluster IX and cluster II while the lowest inter-cluster distance was recorded between cluster VIII and cluster III (154.53). The highest contribution towards divergence was shown by pod length (27.18%) while as the minimum contribution towards divergence was shown by harvest index (0.62). However, the genotypes viz., MH-560, HUM-16, MH-919, MH-421, Satya, MH-2-15, Pusa-95, IPM-02-03, MH-534, and MH-934 showed the superior *per se* performance as well as the most diverse genotypes and thus could be utilized as potent parents for exploitation in further breeding programme to get better heterotic combinations.

Keywords: Genetic Diversity; Cluster Analysis; Yield; Mungbean

Introduction

Pulses are the main source of vegetable protein in human diet and a part of balanced diet in association with other cereals. Pulses also occupy an important position both in crop rotation and cropping system because of their ideal plant type, maturity duration, low water and nutritional requirement and due to ability to tolerate drought conditions. Mungbean (*Vigna radiata* L.) also known as greengram, bean is the third most important pulse crop after chickpea and pigeonpea. It plays a vital role Indian agriculture for treating malnutrition among the Indian as it is a rich source of digestible proteins. It is grown in all the seasons; however, maximum area is under kharif cultivation where intercropping with pearl millet, maize, sorghum etc., is very popular.

High range of variation was observed in the average yield of mungbean which that leads to design breeding programme which increase productivity and stabilize the yield For attaining high yield progenies, genetic divergence play an important role among crop improvement strategies, which is main pre-requisite for hybridization. Wide range of genetic diversity available in India has not been fully exploited to improve the yield of green gram. Multivariate analysis using D^2statistics based on Mahalanobis and quantification of the magnitude of divergence among diverse population helps the plant breeders to recognize the genetic diversity in selecting the genetically diverse parents for purposeful hybridization programme. For evaluating genetic diversity among biological population multivariate analysis has been greatly emphasized [**1, 2**]. Presence of high genetic diversity in this crop offers much scope for its improvement. Hence, an attempt was made to assess the potential genetic difference in respect to desirable traits in fifty-one genotypes of mungbean on the basis of their degree of total genetic divergence as measured by multivariate analysis.

Materials and Method

The experiment was laid out on Research Farm, Division of Genetics and Plant Breeding (GPB), Faculty of Agriculture (FoA), Wadura, Sopore, Sher-e-Kashmir University of Agricultural sciences and Technology Kashmir (SKUAST-K), to evaluate the 51 genotypes of mungbean for genetic diversity with respect to yield, yield contributing and quality traits. The design adopted for this experiment was Randomized Block Design with 3 replications. In this experiment, genotypes are sown at the spacing of 30 cm between rows and 10 cm between plants. Standard recommended package of practices were adopted to attain a good crop. The observations were recorded for all the morphological and quality attributes (except days to 50% flowering and days to maturity) by taking ten randomly selected plants from each replication. Days to 50% flowering and days to maturity were evaluated on plot basis. The data of thirteen morphological and quality traits *viz* plant height(cm), days to maturity, number of clusters plant^{-1}, number of branches plant^{-1}, number of pods plant^{-1}, pod length (cm), number of seeds pod^{-1}, biological yield per plant^{-1}(g), seed yield plant^{-1}(g), 100-seed weight(g), harvest index (%) and protein content(%) were recorded at the time of maturity, whereas, observation on days to 50% flowering for different genotypes was calculated when they attained 50% flowering stage. The mean values were subjected to the analysis of variances and multivariate analysis using the protocol as explained by Rao (1952) and Singh and Choudhary (1985).

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Results and Discussion

Analysis of variance and mean performance

Selection on the basis of yield is not effective as yield gets highly effected by different environmental conditions and is governed by polygenes with small, similar and cumulative effects and highly influenced by environment, selection based on yield alone is not effective.SO, in order to prevent this, breeders adopt indirect selection by observing yield attributes that possess high heritability which counteract the effect of environmental on yield.

The mean sum of squares with respect morphological traits has been given in **(Table-2).** The results revealed that the replication effects were in general non-significant for all the traits, whereas genotype effects were significant for all the characters under study *viz* days to 50% flowering, days to maturity, Plant height (cm),number of branches plant^{-1}, number of clusters plant^{-1}, number of pods plant^{-1}, Pod length (cm), number of seeds pod^{-1},100-seed weight(g),Seed yield plant^{-1}(g),Biological yield plant^{-1}(g), Harvest index (%) and protein content(%) indicating the presence of sufficient amount of genetic variability and all the genotypes differed from each other in respect of characters, which open a way for improvement in the material through selection. Similar finding was also reported by [**3, 4, 5, 6, 7**]. The means performance of the genotypes showed a wide range of variability for all the parameters studied **(Table 1)**. The variation was highest for Plant height (cm) followed by biological yield per plant^{-1} (g), number of pods plant^{-1} and the seed yield plant^{-1}(g). This may be due to the existence of diversity in genotypes evaluated. The range and coefficient of variation were higher for seed yield and number of branches/plant, and medium to low values were observed for biological yield per plant (g), Pod length (cm), number of pods plant-1, number of seeds pod-1, 100-seed weight (g), Harvest index (%), Plant height (cm) and days to flowering/ maturity The presence of considerable variability among genotypes for various economic traits indicated the wide scope for utilization of these genotypes in improvement of mungbean. Similar finding was also reported by [**8, 9, 10**].

Genetic divergence

Studying genetic diversity provides a platform for identifying the genotypes required for hybridization by stratified sampling of breeding population [**11**]. Genetically different individuals offer an opportunity for grouping gene constellation that possesses desirable potential segreggants in advanced generations. For classification of huge number of potential genotypes into small groups of homogenous clusters, the D^2 statistic of Mahalanobis (1936) is commonly used in plant breeding as depicted by different researchers. [**12, 13**] as it leads to precise comparison among two populations in any category before effecting actual crosses. Multi-variate analysis measures the level of divergence among populations in order to so as to recognize the pattern of their evolutionary process and thus to estimate the contribution percentage of various components in divergence together with nature of forces operating at intra and inter-cluster levels.

In the present study, 51 mungbean genotypes were grouped into 9 clusters with respect to various economic traits **(Table 3 & Figure 1)** using Mahalanabis D^2 statistic by employing Tocher's clustering method [**14**]. The cluster number I had maximum number of genotypes (21) which was followed by cluster number IV (9), cluster II (8), cluster V (5), Cluster VII (4), while four remaining clusters contained only one genotype **(Table 4 and Figure 1).** [**15**] reported that sixty genotypes of mung bean were grouped into eight clusters and [**15**] studied fourty mung bean genotypes and found 8 clusters. Similarly, [**16, 17, 18**] also recorded number of clusters in their studies on mungbean. In the present study, the pattern of group constellations revealed that geographical diversity was not an important criterion to group the genotypes into one particular that belongs from particular source. This means that, geographical diversity, though important, was not the only factor in determining the genetic divergence [**19, 20**]. Different workers explained the role of genetic drift, selection pressure and environment in imparting diversity rather than geographical distance [**12, 21**]. Thus, it can be concluded that Genetic diversity is the result of various factors along with geographical origin. Therefore, selection of parents that act as index of genetic diversity should be done on genetic diversity not on the basis of geographical diversity.

The intra-cluster values vary between 1.550 and 2.596 **(Table 4 & Figure 2)**. Highest average intra cluster distance was observed in cluster VII (247.07) while, least intra cluster distance was observed in Cluster I (82.19) which might be as a result of gene exchange or selection practices among the genotypes for diverse characters [**22**]. The clusters viz., III, VI, VIII and IX showed no intra cluster distance being solitary, thereby indicating highest degree of variability within cluster VII. Similar results obtained in mungbean [**23**]. The solitary

Table 1: List of 51 genotypes selected for the study of Mungbean.

S.No	Genotypes	S.No	Genotypes	S.No	Genotypes
1	MH-919	18	MH-534	35	EC-399223
2	ML-2037	19	SML-1817	36	PM-14-3
3	Samrat	20	EC-30400	37	SML-668
4	Pusa Ratna	21	EC-581523	38	IPM-99-125
5	KM-2241	22	SM-2	39	MH-925
6	Pusa-95	23	SM-1	40	MH-934
7	HUM-16	24	RMG-268	41	Basmati
8	IPM-02-03	25	IPM-06-5	42	IPM-02-14
9	MH-1010	26	ML-818	43	MH-421
10	Pusa Mishal	27	MH-929	44	GM-11-02
11	Satya MH-2-15	28	IPM-410-3	45	EC-470095
12	MH-926	29	COGG-8	46	EC-2511552
13	TMB-131	30	MH-560	47	SML-1018
14	IPM-205	31	LGG-460	48	TMB-13
15	MH-539	32	MH-921	49	TMB-37
16	EC-581523-B	33	EC-393410	50	SML-832
17	NDMZ-15-2	34	AKM-4	51	EC-581523

Table 2: Estimates of variability parameters for different traits of Mungbean .

Characters	Mean sum of squares due to genotypes (DF=50)	Mean sum of squares due to errors (DF=100)	Mean ± SE	Range	CV (%)
Days to 50% flowering	19.071**	3.104	42.76±0.19	38.00-47.00	4.12
Days to maturity	23.038**	2.694	70.78±0.18	65.67-75.66	2.32
Plant height (cm)	343.284**	13.579	78.26±0.44	61.00-114.00	4.71
Primary branches plant^{-1}	1.985*	0.306	2.31±0.47	1.33-3.66	23.95
Clusters plant^{-1}	8.204**	1.475	6.26 ±0.75	4.33-11.66	19.40
Number of pods plant^{-1}	49.971**	3.356	11.97±1.06	6.67-23.00	15.30
Pod length (cm)	13.223**	2.027	8.28±0.06	5.97-11.70	17.19
Number of seeds pod^{-1}	14.957**	1.031	11.55±0.76	8.00-15.67	8.79
100 seed weight (g)	2.033**	0.166	5.00±0.15	4.17-6.83	8.15
Seed yield plant^{-1} (g)	36.756**	4.194	6.92±0.75	3.34-18.08	29.59
Biological yield plant^{-1} (g)	137.251**	14.121	19.31±2.25	9.63-40.33	19.46
Harvest index (%)	43.756**	4.973	35.60±2.42	30.95-45.99	6.26
Protein content (%)	1.996*	0.124	20.76±0.58	20.18-22.02	2.28

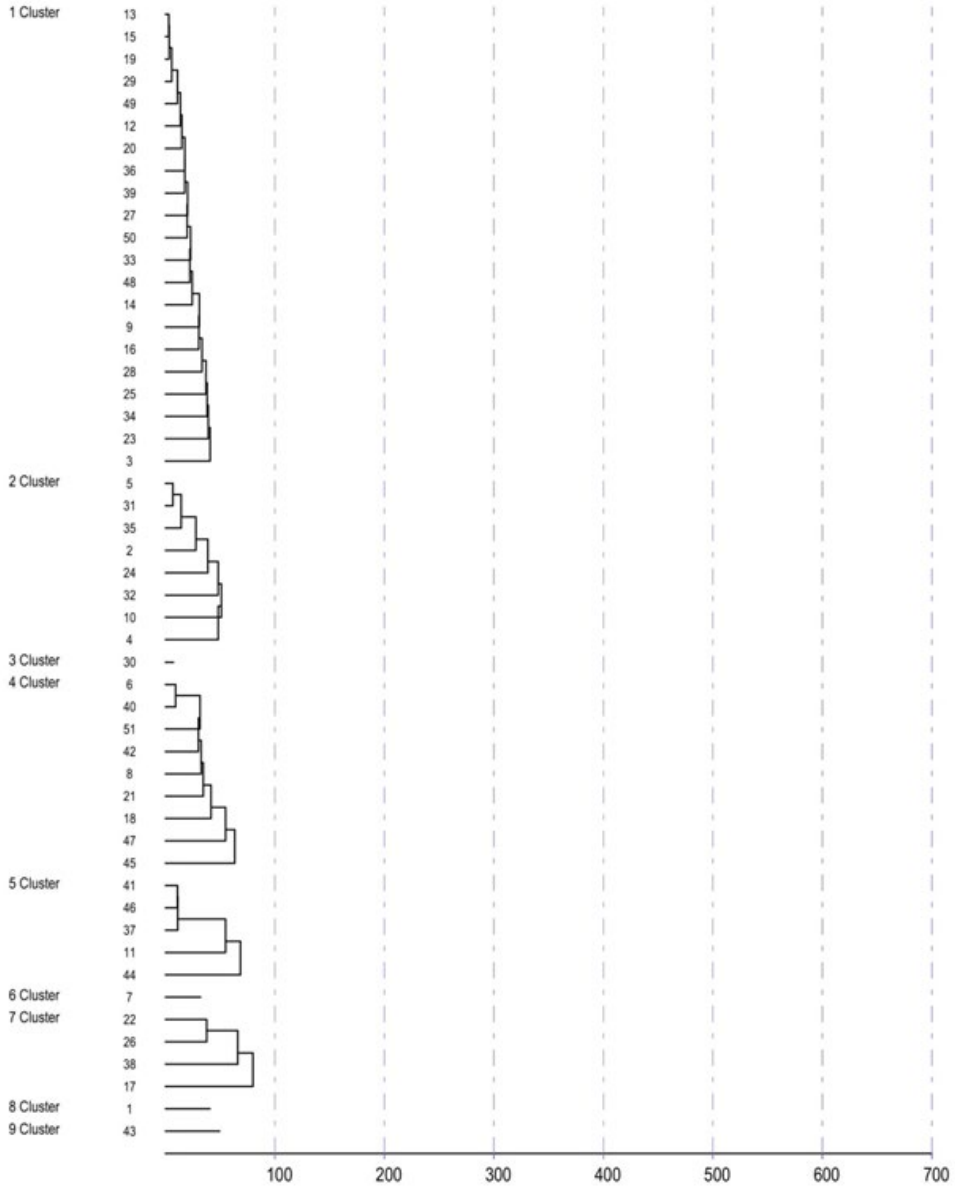

Figure 1: Diagram illustrating the clustering pattern by Tocher method.

Table 3: Grouping of genotypes into different clusters by Tocher method.

Clusters	No. of genotypes	Name of genotypes
Cluster I	21	Samrat, MH-1010, MH-926, TMB-131, IPM205, MH539, EC-581523B, SML-1817, EC-30400, SM-1, IPM-06-5, MH-929, IPM-410-3, COGG-8, EC-393410, AKM-4, PM14-3, MH-925, TMB-13, TMB-37, SML-832
Cluster II	8	ML-2037, Pusa Ratna, KM-2241, Pusa Mishal, RM-G268, LGG-460, MH-921, EC-399223
Cluster III	1	MH-560
Cluster IV	9	Pusa-95, IPM-02-03, MH-534, EC-581523, MH-934, IPM02-14, EC-470095, SML-1018, EC-581523
Cluster V	5	Satya MH-2-15, SML-668, Basmati, GM-11-02, EC-2511552
Cluster VI	1	HUM-16
Cluster VII	4	NDMZ-15-2, SM-2, ML-818, IPM-99-125
Cluster VIII	1	MH-919
Cluster IX	1	MH-421

Table 4: Average intra (Bold) and inter cluster values in 6 clusters (D^2) in Mungbean.

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9
Cluster 1	**82.19**	175.35	157.32	501.84	201.34	354.06	819.56	288.55	1957.82
Cluster 2	175.35	**132.20**	314.56	535.79	410.57	493.19	1030.67	264.60	2311.69
Cluster 3	157.32	314.56	**0.00**	399.65	219.12	181.60	446.89	154.53	1250.42
Cluster 4	501.84	535.79	399.65	**140.49**	473.38	230.89	494.10	347.48	1095.04
Cluster 5	201.34	410.57	219.12	473.38	**162.07**	366.59	806.50	520.76	1722.48
Cluster 6	354.06	493.19	181.60	230.89	366.59	**0.00**	253.89	204.70	834.52

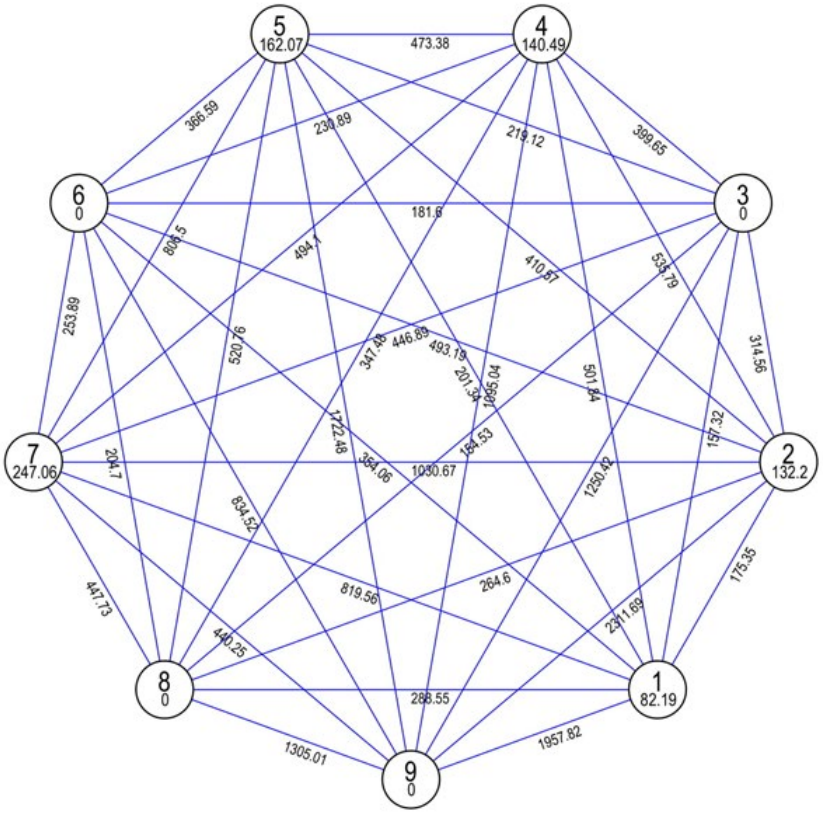

Figure 2: Configuration of clusters and their mutual relationship by Mahalanobis D2 statistic method.

cluster depicts the identity independent and hence plays a vital role for the unique characters constituted by those genotypes that serve as a potential source for breeding purpose.

The inter-cluster studies indicated magnitude of genetic divergence between the clusters. It showed that, how much this clusters were genetically diverse from each other. In the present investigation, maximum inter cluster distance was observed between clusters II and IX (2311.69) which was followed by cluster I and IX (1957.82), clusters V and IX (1722.48), clusters VIII and IX (1305.01), clusters III and IX (1250.42), clusters IV and IX (1095.04) and clusters II and VII (1030.67) indicating that the genotypes of these clusters were diverse to each other while, the minimum inter cluster distance was observed between cluster III and VIII (154.53). The higher distance between two clusters depicted higher genetic diversity among genotypes. The purpose of

genetic diversity indicates that crossing between highly genetic diverse leads to more heterosis than the closely related parents **[35]**.

Considering the cluster means for various qualitative and quantitative traits, the experimental material under the present investigation revealed that significant amount of genetic variation is present for all the quantitative and qualitative traits **(Table 5)**. The lowest cluster mean for days to 50% flowering (38.87 days) was observed in cluster V, similarly for day to maturity (87.53 days) in cluster V; plant height (114.0 cms) in cluster IX; primary branches per plant (2.67) in cluster VI; number of clusters per plant (8.00) in cluster VI; number of pods per plant (20.67) in cluster VI; pod length (11.07 cm) in cluster IX; number of seeds per pod (13.67) in cluster VI, 100-seed weight (6.57 g) in cluster VI, seed yield per plant (18.08 g) in cluster VI, biological yield per plant (39.47 g) in cluster VI and protein content (20.92%) in cluster IX. Cluster means revealed the identification of characters to be selected for hybridization. The present results are supported by the findings of **[24]** who observed that cluster means and coefficient of variation are the most important criteria to identify the nature of diversity.

Results further revealed that cluster VI showed higher mean values and statistical distance and thus act as a potential source for breeding stock for crossing the genotypes in these clusters selected for specific component traits and thus proved helpful for attaining new gene pool and increased the level of adaptation. Continuous selection in advance generation resulted in developing lines with high yield desires. Earlier workers like **[22, 17, 25, 26, 27]**, have also indicated the significance of genetic divergence in mungbean.

D^2 values estimates the magnitude of divergence between two clusters. Breeder get a platform for observing the total diversity and the characters mainly responsible for the total divergence. Besides it is significant for selecting the parents in breeding programme. The relative per cent contribution of each character towards total genetic divergence among the genotype was presented in Table 6. Perusal of the data revealed that out of 13 characters studied the pod length happened to be the major trait with 27.18 percent contribution for the whole divergence followed by plant height (15.94%), pods per plant (13.71%), days to 50% flowering (11.35%) and 100-seed weight (6.54%). However lowest contribution towards divergence was exhibited by harvest index (0.62%) followed by seeds per pod (1.08%) and protein content (1.23%). Rest of the traits contributed 3.0 to 5.0 per cent towards divergence. **[28]** reported that the trait 100-seed weight had highest contribution to genetic divergence. **[29]** Reported that days to maturity, 100-seed weight, number of pods per plant and total dry matter contributed maximum towards diversity. It is clear from the results that the yield got affected by different environmental conditions and dependent on various yield contributing characters. Hence, selection on the basis of variability in yield character. However, it should be done in response to plant height, days to 50% flowering, pods per plant, pod length, and 100-seed weight as they contribute greatly in total divergence. Divergence is contributed by various characters and vary from crop to crop **[30, 28]** **revealed** that that traits with maximum D^2 value should be considered for selection of clusters and choice of parents for hybridization. For successful hybridization programme, selection of parents that possess high genetic variability plays an important role for varietal improvement. So, it is advisable to select parents from different clusters that possess wider inter-cluster distance and from those clusters with good performance of the traits that are associated with the divergence **[31]** revealed that probability of successful crosses can be improved by selecting parents that possess medium to high divergence. As observed in mungbean maximum divergence has been noticed among the following characters as days to maturity, number of pods per plant and 100-seed weight **[28, 29, 15, 32]**.

Table 5: Cluster means performance for 13 characters in 51 genotypes of Mungbean.

Clusters	Days to 50% flowering	Days to Maturity	Plant height (cm)	Primary branches / plant	No. of Clusters plant	No. of Pods / plant	Pod length (cm)	No. of seeds/ pod	100-seed weight (gm)	Seed yield/ plant (gm)	Biological yield / plant (gm)	Harvest index (%)	Protein content (%)
Cluster 1	42.83	70.63	75.73	2.60	6.63	11.98	7.21	11.21	4.91	6.46	18.32	35.76	20.79
Cluster 2	44.88	73.42	69.63	2.25	6.25	10.79	7.94	11.96	5.10	6.70	18.78	34.75	20.75
Cluster 3	41.00	72.00	86.67	2.00	5.00	9.00	7.60	10.00	4.27	3.74	10.67	35.00	20.22
Cluster 4	42.41	70.11	76.67	1.89	5.70	12.85	10.56	12.15	5.01	7.69	21.36	35.85	20.76
Cluster 5	38.87	67.53	76.93	2.33	5.80	10.40	7.57	11.07	5.37	6.27	18.44	33.68	20.89
Cluster 6	43.00	70.00	87.67	2.67	8.00	20.67	9.00	13.67	6.57	18.08	39.47	45.99	20.78
Cluster 7	44.08	70.83	99.25	2.00	6.00	11.83	9.49	11.75	4.69	6.68	18.15	36.30	20.64
Cluster 8	45.67	75.67	84.00	2.00	6.33	14.00	8.80	12.67	4.47	7.86	21.17	37.06	20.22

Table 6: Per cent contribution of various characters towards divergence in Mungbean.

Characters	Times ranked 1st	Rank	Contribution%
Days to 50% flowering	145	IV	11.35
Days to maturity	60	VIII	4.69
Plant height (cm)	203	II	15.94
Primary branches plant^{-1}	71	VI	5.53
Clusters plant^{-1}	49	IX	3.85
Number of pods plant^{-1}	175	III	13.71
Pod length (cm)	347	I	27.18
Number of seeds pod^{-1}	14	XIII	1.08
100 seed weight (g)	83	V	6.54
Seed yield plant^{-1} (g)	61	V11	4.82
Biological yield plant^{-1} (g)	44	X	3.46
Harvest index (%)	8	XII	0.62
Protein content (%)	16	XI	1.23

Conclusion

The results obtained in present investigation showed a good amount of variability and diversity for all the agro-morphological traits present in the tested material leads to converging of the elite resources by systemic breeding and selection to recover high yielding segregants with good quality characteristics **[33, 34, 35]**. Further wider inter-cluster distance offers a platform for hybridization between genotypes that possess a high level of variation in the segregating generation. Thus, crosses between genotypes of the cluster VI and cluster IX *viz*; MH-560, HUM-16, MH-919, MH-421, Satya, MH-2-15, Pusa-95, IPM-02-03, MH-534, and MH-934 are likely to possess high heterosis and thus recombinants with superior traits should be selected for future breeding programme in mungbean.

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