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Estimation of genetic divergence for agro morphological characters in mungbean [*Vigna radiata* (L.) Wilczek]

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Abstract
The genetic diversity in germplasm provides a good opportunity for plant breeders to create new and better genotypes with beneficial traits, which include both farmer-preferred traits (yield potential etc.) and breeders preferred traits (stress resistance / tolerance etc.). The present investigation was conducted to ascertain the information about the magnitude and extent of genetic diversity of agro-morphological characters in mungbean. A total of sixty genotypes of mungbean were evaluated during Kharif season 2018 with three replications adopting randomized compete block design. The observations of each genotype under each replication for phenological and yield attributing traits were recorded on the basis of per plot and five randomly selected plants, respectively. Based on the D^2 values, the sixty genotypes were divided into ten clusters. A maximum of 18 genotypes belongs to cluster I which evolved as the largest cluster, followed by cluster III with 16 genotypes, while cluster VII and IX were solitary. The highest intra-cluster distance was observed for cluster IX (17.20) and the lowest was observed for cluster V, VIII, X (0.0), while the maximum inter-cluster distance was observed between cluster IX and X (35.6). Within the twelve characters studied, the seed yield per plant contributed most to the divergence followed by the 100-seed weight. On the basis the results of this study, it was suggested that a successful hybridization programme could be performed between the genotypes of clusters *viz.* IX and V, VIII, X that exhibit maximum inter-cluster distance to produce new recombinants with desired traits.

Keywords: Genetic divergence, inter-cluster distance, intra-cluster distance, mungbean

1. Introduction

Mungbean (*Vigna radiata* L. Wilczek, 2x=2n=22), also known as green gram, belongs to the Leguminosae family. In India, mungbean has been cultivated since prehistoric times and served as a major source of dietary protein for most people. Being a short duration legume crop and its adaptability to all zones, it is cultivated in three different seasons *viz.*, Kharif, Rabi and Summer. However the maximum coverage of the area under cultivation is in the Kharif season (Sharma *et al.*, 2011) [12]. Mungbean seeds contain approximately 25 *per cent* protein, 1.0-1.5 *per cent* oil, 3.5-4.5 *per cent* fiber, 4.5-5.5 *per cent* ash and 62-65 *per cent* carbohydrates on a dry weight basis. Its protein is comparatively rich in the lysine which is mainly lacking amino acids in cereals. It adds about 42 kilogram nitrogen (N) per hectare because of its ability to fix atmospheric nitrogen to the soil. Mungbean is also used as green manuring, hay and cover crop. Mungbean is cultivated in 4.74 million hectares with a total production and productivity of 2.62 million tonnes and 553 kg per hectare, respectively in India. While in Madhya Pradesh, the cultivated area is 12.76 lakh hectares, with an annual production of 5.74 Lakh tonnes and a productivity of 450 kg per hectare (Anonymous 2020-21) [2]. Mungbean has a noteworthy contribution in diversifying Indian agriculture and its ability to meet the protein deficit of the country's vegetarian population, but its productivity in the country is still low and needs for improvement. Yield components are the primary objective under study for crop improvement as Grafius (1978) [6] suggested that there may not be genes for yield *per se* but for the various components, the multiplicative interactions of which resulting in the artifact of yield. Genetic diversity is the basic requirement in any crop improvement program which aimed to improve the crops genetically. Hence, the success of breeding depends entirely on the genetic diversity of desired traits and the great emphasis has been placed on the usefulness of multivariate analysis (Gadakh *et al.*, 2013) [4]. Genetic diversity is defined as the extent to which heritable material differ within a group of plants as a result of evolutionary forces, including domestication and plant breeding (Hintum and Van, 1995) [7].

Genetic diversity in plant genetic resources offers good opportunity to plant breeders to generate new and genetically ameliorated genotypes/cultivars with desirable traits, including farmer-preferred traits (high yield potential, large seed, earliness, dwarfness/tallness etc.) and breeder-preferred traits (pest and disease resistance, photosensitivity, nutritional quality etc.) (Bhandari *et al.*, 2017) [3].

The existence of genetic diversity represented in the form of wild species, related species, breeding stocks, mutant lines etc. can serve as a source of desirable alleles to plant breeders in developing climate resilient varieties because of these varieties are becoming more important in the scenario of climatic change. Genetic diversity analysis is the most appropriate statistical analysis to find out the level of divergence between biological populations and also to evaluate the relative endowment of dissimilar component traits for total divergence. The D^2 statistic (Mahalanobis, 1936) [9] is one of the effective techniques for evaluating genetic divergence. The technique measures the divergence at two levels, namely within clusters (intra-cluster) and between clusters (inter-cluster), which facilitates the selection of diverse parents for breeding programme. Many researchers *viz.* Gadakh *et al.*, 2013; Mishra *et al.*, 2014; Suhel *et al.*, 2015; Tripathy *et al.*, 2016; Aijaz *et al.*, 2016; Garg *et al.*, 2017 and Sharma *et al.*, 2018 [4, 10, 19, 20, 1, 5, 18] outlined the significance of genetic divergence studies in the selection of diverse parents for an effective crossing programme. Therefore, keeping the importance of genetic diversity in view, the present investigation was carried out to ascertain the genetic divergence among sixty genotypes of mungbean.

2. Material and Methods

The present investigation was carried out to ascertain the information on genetic divergence in mungbean during the Kharif season 2018. The experiment was laid out in randomized complete block design with three replications which was conducted in the experimental block of All India Coordinated Research Project on MULLaRP, R.A.K. College of Agriculture, Sehore (M.P.) which is situated in the western track of Vindhyan plateau agro climatic zone of Madhya Pradesh at the latitude of 23°-12´, North longitude of 77°-05´ and an altitude of 498.7 meters above the mean sea level with sub tropical climate.

The experimental material consisted of sixty genotypes of mungbean available at the centre (Table 1). Data on agro-morphological characters *viz.*, Days to 50% flowering and Days to maturity, were recorded on visual observations of plants on plot basis while data on Plant height (cm), Number of branches per plant, Number of clusters per plant, Pods per plant, Length of pods (cm), Number of Seeds per pod, 100-seed weight (g), Biological yield per plant (g), Seed yield per plant (g) and Harvest index (HI) were recorded from five randomly selected plants from middle of row of each genotype in each replication. The mean values used for statistical analysis that were recorded on five randomly selected plants for various characters. The genetic divergence calculated by following the Mahalanobis D^2 statistics analysis. Clustering of sixty genotypes was done based on the D^2 values by the use of Tocher's method as suggested by Rao (1952) [15].

3. Results and Discussion

The substantial magnitude of variability in the agro-morphological characters shows the wide scope of genetic diversity among the genotypes under study. The exalted magnitude of D^2 expressed wide scope of dissimilarity among the genotypes of mungbean. On the basis of D^2 values, the sixty genotypes were grouped into ten clusters which revealed that the genotypes indicate significantly substantial variation for all the characters. Cluster I which include 18 genotypes and evolved as the largest cluster followed by cluster III with 16 genotypes, cluster II with 9 genotypes, clusters IV and VI with 5 genotypes, cluster VII and cluster IX with 2 genotypes. Cluster V, VIII and X were found to be solitary (Table 1).

The mean performance of all characters in various clusters is presented in Table 3. The genotypes in cluster I were better average for the length of pod and 100-seed weight. The genotypes of cluster II were better average for Day to 50% flowering, plant height and 100-seed weight. The cluster III was consisted with sixteen genotypes which had better number of branches per plant and number of pods per plant. The cluster IV was consisted of five genotypes with average values of genotypes for day to 50% flowering, days to maturity, plant height, number of branches per plant, number of clusters per plant, length of pod, were superior than their respective population means. The cluster V includes one genotype with better average for the number of pods per plant, length of pod, number of seeds per pod, seed yield per plant and harvest index. The cluster VI was includes five genotypes, had better average for the characters days to 50% flowering, days to maturity, number of clusters per plant, number of seeds per pods and 100-seed weight. The average value of these characters were exceeded their respective population mean. The cluster VII includes two genotypes, had better average for the characters days to 50% flowering, days to maturity, plant height, number of branches per plant, number of pods per plant, length of pod and number of seeds per pods. The cluster VIII includes one genotype, had better average for the characters plant height and number of seed per pods. The average value of these characters were exceeded their respective population mean. The cluster IX includes two genotype, had better average for the characters number of clusters per plant, number of pods per plant, length of pod, number of seeds per pod, biological yield per plant, seed yield per plant, hundred seed weight and harvest index. The average value of these characters were exceeded their respective population mean. The cluster X includes one genotype, had better average for the characters plant height, number of branches per plant, length of pod and biological yield per plant. The average value of these characters were exceeded their respective population mean. Similar kind of results was reported by various researchers. Forty genotypes were grouped into eleven clusters (Narasimhulu *et al.*, 2013) [11], sixteen genotypes of green gram were grouped into three distinctive main clusters (Mishra *et al.*, 2014) [10], nine green gram genotypes grouped into five clusters (Panigrahi *et al.*, 2014) [13], thirty one green gram genotypes were grouped into eleven clusters (Sai Rekha *et al.*, 2015) [16] and twenty one genotypes of green gram were grouped into ten clusters (Suhel *et al.*, 2015) [19].

The average intra and inter-cluster distances (D) = ($\sqrt{D^2}$) are presented in table 2. The highest intra-cluster distance was observed for cluster IX (D=17.2) followed by cluster III (14.1), Cluster VI (D=13.8), cluster I (13), cluster IV (13.1), cluster II (12.0), cluster VII (10.8) and cluster V, VIII, X showed no intra cluster distance being solitary. The higher intra-cluster distance within a cluster showed higher degree of variability within the cluster, providing scope for evolution by different determination techniques. Thereby cluster IX showed highest degree of variability. A single group displays their autonomous identity and significance because one of those genotypes is involved in the character. These genotypes can satisfy as expectant parents for the breeding program.

The maximum inter-cluster distance was observed between cluster IX and X (35.6) followed by cluster II and V (D=34.4), cluster VII and IX (D=33.1),cluster V and VI (30.3), cluster III and IX (29.5), cluster II and VII (28.4), cluster II and III, cluster VI and IX (27.6) cluster VI and X (26.9), cluster I and V (26.8), cluster II and IV (26.7), cluster VIII and X (26.5), cluster VIII and IX (26.3), cluster VII and X and cluster I and IX (26.1), cluster III and X (25.9), cluster IV and V (25.0). The inter-cluster distances expressed the extent of genetic divergence between the clusters. This demonstrated that these clusters how genetically different from each other. Comparable findings have been reported by Katia and Kumar (2015), Sai Rekha *et.al* (2015) [16] and Suhel *et al.* (2015) [19].

The average performance of all the characters in different clusters is presented in Table 3. It can be seen from data that substantial divergence existed for all the characters under study. The data indicated that the genotypes in the cluster VIII (31.2 days) were early for the days to 50% flowering whereas late in cluster VI (48.2 days). Cluster mean for days to maturity varied between 66.6 days to 74.5 days with population mean of 69.2. The genotypes from cluster VIII and cluster VI were early and late for days to maturity, respectively. For plant height high cluster mean values were recorded by cluster VII (63.8) where as lower values were observed for cluster IV (41.1). Cluster mean for number of branches per plant ranged between 3.7 for cluster V to 8.6 for cluster VII. Cluster mean for number of clusters per plant ranged between 2.7 (cluster X) to 5.3 (cluster VII). The highest cluster mean of number of pods per plant was recorded by the genotypes in cluster V (36.6) with the population mean of 23.4. The highest cluster mean of pod length was recorded by the cluster VII (8.6). The highest cluster mean for number of seeds per pod was recorded by the cluster VIII (15.1) with population mean of 11.2. The cluster mean of biological yield per plant (g) was ranged between 22.9 (cluster I) to 30.2 (cluster X). The cluster mean for seed yield per plant (g) is between 1.4 (cluster X) to 15.0 (cluster IX). The highest cluster mean for 100-seed weight (g) was recorded by the genotypes in cluster II (4.3) while lowest by the genotypes in cluster X (2.1) with population mean of 3.0. The highest cluster mean of harvest index was recorded by the genotypes in cluster IX (53.5) and lowest by the genotypes in cluster IV (23.2) with population mean of 30.2.

Among the twelve characters studied, seed yield per plant contributed the highest (24.86) for divergence followed by number of pods per plant (22.05), 100 seed weight (18.5%), day to 50% flowering (12.56) however number of branches per plant, number of seeds per pod, number of clusters per plant, plant height, length of pod, harvest index and biological yield per plant recorded lowest contribution to divergence. Narasimhulu *et al.* (2013) [11] reported the character harvest index contributed maximum to diversity. Sen *et al.* (2017) [17] reported the *per cent* contribution towards genetic diversity was high for seed yield per plant. It is clear that the yield is a dependent character represented by some other yield contributing traits, which are affected by different conditions in various regions. As such, changes in character variability between genotypes for breeding cannot be based exclusively on yield potential. Thus to improve it, the selection should be done considering at seed yield per plant, number of pods per plant, 100 seed weight, day to 50 *per cent* flowering as their commitment towards absolute specificity is high. Similar findings were observed by Katiyar and Kumar (2015) [8], Aijaz *et al*. (2016) [1], Garg *et al.* (2017) [5], Punia *et al*. (2017) [14], Sen *et al.* (2017) [17] and Sharma *et al.* (2018) [18].

Table 1: Clustering of 60 genotypes of Mungbean into 10 clusters by Tocher's method.

Cluster No.	Number of genotypes	Name of the Genotypes
I	18	PK-5, PK5-5,Pusa-0971,M-981, MH-810,M-313,DMS-10,M-322, Ganga-1, M-409, HUM-2, M1053, IC-436763, MH-521, IC-282130, IPM-406-1, M-1209, KM-2241,
II	9	M-1131, M-1032, M-1334, M-1255, M-1199, M-1370, M-1156, M-989, IC-436637
III	16	M-880, KM-16-82, Ganga -8, IPM-205-4, M-729, Pusa-1131, KM-11-40, IPM-410-3, ML-512, KM-16-85, IC-282085, KM-16-75, IPM-288, M-204, KPS-3, M-313,
IV	5	M-678, M-684, Satya, TM-96-2, MH-96-1
V	1	KM-16-69
VI	5	M-1395, DMS-4, SPS-5, Bhutan-LM-2, MH-1442
VII	2	KM-16-81, Bhutan-LM-1
VIII	1	Pusa-1333
IX	2	M-1168, M-1372
X	1	PLM-67

Table 2: Average intra (bold) and inter cluster values of 10 clusters (D) = ($\sqrt{D^2}$) of from sixty genotypes of mungbean.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	13.0	18.7	19.4	17	26.8	18.4	20.8	15.5	26.1	24.9
II		12.0	27.6	26.7	34.4	20	28.4	22.8	23.5	31.9
III			14.1	17.2	17.5	23.9	19	17.5	29.5	25.9
IV				13.1	25	19.3	14.8	18.9	31.8	22.8
V					0.0	30.3	27.5	21.3	32.3	33.9
VI						13.8	20.4	21.2	27.6	26.9
VII							10.8	23.9	33.1	26.1
VIII								0.0	26.2	26.5
IX									17.2	35.6
X										0.0

Table 3: Cluster means performance for seed yield and its components characters in sixty genotypes of mungbean.

Characters	Clusters										Population Mean
	I	II	III	IV	V	VI	VII	VIII	IX	X	
Day to 50% flowering	33.0	37.6	34.4	38.4	32.9	48.2	46.7	31.2	33.3	34.7	37.0
Days to maturity	67.9	69.8	68.6	70.7	68.1	74.5	71.8	66.0	66.6	67.8	69.2
Plant Height (cm)	46.0	47.8	47.4	41.1	42.0	43.8	63.8	49.8	44.6	49.2	47.6
No. of Branches Plant^{-1}	5.7	6.9	6.7	6.0	3.7	5.3	8.6	4.2	5.9	6.5	5.9
No. of Clusters Plant^{-1}	4.0	3.2	3.8	4.6	3.8	4.3	5.3	3.5	4.9	2.7	4.0
No. of Pods Plant^{-1}	19.2	16.6	26.7	22.1	36.6	20.7	27.1	20.7	35.8	8.4	23.4
Length of pod (cm)	7.9	7.6	7.9	8.2	8.0	7.4	8.6	6.6	7.8	7.9	7.8
No. of Seeds Pod^{-1}	10.7	10.0	11.0	10.7	12.0	11.2	11.7	15.1	11.4	8.1	11.2
Biological Yield Plant^{-1} (gm)	22.9	24.6	23.7	23.2	24.8	25.0	25.3	25.5	29.9	30.2	25.5
Seed Yield Plant^{-1} (gm)	6.0	6.5	6.5	5.1	9.1	7.1	7.1	9.1	15.0	1.4	7.3
100-Seed Weight (gm)	3.4	4.3	2.5	2.4	2.3	3.5	2.5	3.2	4.1	2.1	3.0
Harvest Index (%)	27.7	27.9	28.9	23.2	39.1	29.9	29.4	38.1	53.0	4.6	30.2

Table 4: Contribution of various characters towards divergence in mungbean genotypes.

S. No.	Characters	*Per cent* contribution
1	Day to 50% flowering	12.56
2	Days to maturity	1.0
3	Plant Height (cm)	2.86
4	No. of Branches Plant^{-1}	7.2
5	No. of Clusters Plant^{-1}	2.71
6	No. of Pods Plant^{-1}	22.05
7	Length of pod (cm)	0.73
8	No. of Seeds Pod^{-1}	6.1
9	Biological Yield Plant^{-1} (gm)	0.23
10	Seed Yield Plant^{-1} (gm)	24.86
11	100-Seed Weight (gm)	18.5
12	Harvest Index (%)	1.2

4. Conclusions

The analysis of variance exhibited significant variation among the genotypes for all the characters studied. The sixty genotypes were divided into 10 clusters based on the D^2 values. Cluster I with 18 genotypes evolved as the largest cluster. The highest intra-cluster distance was observed for cluster IX; it shows a high degree of variability. The maximum inter-cluster distance was observed between clusters IX and X. Thus the genotypes M-1168, M-1372, PLM-67 and KM 16-69 may be used in the breeding programme to create new recombinants with desirable traits. Within the twelve characters studied the seed yield per plant followed by 100-seed weight made the substantial contribution towards the genetic divergence.

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