MULTIVARIATE ANALYSIS IN MUNGBEAN (*VIGNA RADIATA*) FOR GENETIC DIVERSITY UNDER RAINFED CONDITION

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SUMMARY

The present study was undertaken to provide information on nature and magnitude of genetic diversity among promising genotypes of mungbean using Mahalanobis's D^2 statistic planted in the research area of the Department of Dryland Agriculture, Chaudhry Charan Singh Haryana Agricultural University, Hisar (Haryana) during kharif 2014. These genotypes were grouped into six clusters. The highest intra-cluster distance was observed for cluster III (3.874) and the lowest was observed for cluster II (3.537). While the highest inter-cluster distance was observed between cluster I and VI (6.315). Cluster IV formed monogenotypic cluster. Cluster III showed the maximum mean value (35.407) for harvest index, plant height (31.85) and seed yield (2.51). The highest contribution toward the total genetic divergence was recorded for harvest index, plant height, days to maturity and biological yield per plant. Selection index (I) aimed at selection on several characters simultaneously indicated that genotypes, RMG-991, MH-539, ML-776, MH-560, MH-934, ML-682 and Pusa-0672 had performed better and are important for further breeding programme aimed at improvement of yield.

Keywords : Mungbean, genetic diversity, cluster analysis, rainfed condition

Mungbean, a warm-season leguminous species, has a short life cycle (approximately 60 days) and is mainly cultivated on small farms in South, East, and Southeast. As mungbean roots fix atmospheric nitrogen through symbiosis with nitrogen-fixing rhizobia, this crop is valuable both economically and nutritionally because it can improve soil quality and reduce the amount of nitrogen fertilizer required in the soil when grown in rotation with cereals, thereby increasing cereal grain and straw yields due to its residual effects (Yaqub *et al.*, 2010).

Mungbean is grown mostly in marginal and rainfed areas and the major constraint for higher productivity is inadequacy of moisture. Moisture deficit hampers the rate of carbon assimilation which results in decreased growth and yield of most crops (Mafakheri *et al.*, 2010). Water stress during the flowering and pod filling growth stages of mungbeen significantly reduced pod initiation, pod growth rates, shortened plant height, and decrease the period of maturing, yield and yield components (Moradi *et al.*, 2009). Hence, developing a moisture stress tolerant mungbean is necessary for cultivation in these areas. Even though it thrives moderately under drought prone condition, greater variability exists for yield performance of different genotypes (Prakash *et al.*,

2017). Thus, there exists ample scope to evaluate mungbean genotypes that have inherent capability for producing higher yield under rainfed conditions.

Genetic diversity is one of the criteria of parent selection in the hybridization programme. The availability of transgressive segregants in any breeding program depends upon the diversity between the parents involves. The multivariate techniques, such as cluster analysis and principal component analysis may be an efficient tool in the quantitative estimation of genetic variation. 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. Therefore the present study was conducted to evaluate the extent of genetic variation in mungbean genotypes on the basis of agronomic traits to screen superior genotypes for their utilization as parents in future hybridization programme.

MATERIALS AND METHODS

The present investigation was conducted with 30 genotypes of mungbean (Table 1) to access the

TABLE 1
List of 30 genotypes selected for the study

S. No.	Genotypes	Origin/Source	S. No.	Genotypes	Origin/Source
1.	LGG-460	ARS, Lamm	16.	Pusa Ratna	IARI, New Delhi
2.	BDYR-1	AVRDC, Taiwan	17.	Pusa-0871	IARI, New Delhi
3.	BDYR-2	AVRDC, Taiwan	18.	Pusa-0672	IARI, New Delhi
4.	MH-934	CCS HAU, Hisar	19.	IPM-02-3	IIPR, Kanpur
5.	Sattya	CCS HAU, Hisar	20.	IPM-06-5	IIPR, Kanpur
6.	Basanti	CCS HAU, Hisar	21.	KM-2241	IIPR, Kanpur
7.	MH-421	CCS HAU, Hisar	22.	NVL-638	Nirmal Seeds
8.	GP-69	CCS HAU, Hisar	23.	Vamban-2	NPRC, Vamban
9.	GP-248	CCS HAU, Hisar	24.	ML-682	PAU, Ludhiana
10.	GP-182	CCS HAU, Hisar	25.	ML-776	PAU, Ludhiana
11.	MH-805	CCS HAU, Hisar	26.	SML-668	PAU, Ludhiana
12.	MH-539	CCS HAU, Hisar	27.	SML-1018	PAU, Ludhiana
13.	MH-560	CCS HAU, Hisar	28.	AKM-9904	PRU, Akola
14.	EC-393410	Exotic collection	29.	RMG-991	RAU, Pusa
15.	EC-581523	Exotic collection	30.	TBM-11	TNAU, Coimbatore

degree of divergence and to isolate the suitable parent(s) for future hybridization. The genotypes were planted in the research area of the Department of Dryland Agriculture, Chaudhry Charan Singh Haryana Agricultural University, Hisar (Haryana) during kharif 2014. 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. Each genotype was sown in two rows of 3 meter length spaced at 45 cm; and 10 cm between the plants. All the recommended package of practices was followed to establish a good plant stand. Observations for all the traits (except days to 50% flowering and days to maturity) were recorded by taking five plants per plot. The days to 50% flowering and days to maturity were computed on plot basis. The data on eleven morphological characters viz. days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, pod length were recorded at the time of maturity, whereas observation on days to 50%

flowering was recorded for different genotypes when they attained 50% flowering stage. The 100-seed weight (g) and seed yield/plant (g), biological yield/plant (g) and harvest index (%) were recorded after threshing the crop. Mahalanobis (1936) D^2 analysis was used for assessing the genetic divergence among the test genotypes. 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 30 mungbean genotypes were grouped into six clusters based on the relative magnitude of their D^2 values, in such a way that genotypes within each cluster had smaller D2 value than between the clusters. Table 2 revealed the distribution pattern of genotypes in different clusters. Cluster pattern exhibited that cluster V was the largest ones with eight genotypes, followed by cluster I and II with five genotypes, cluster VI with four genotypes, cluster III

TABLE 2
Clustering of 30 mungbean genotypes for various characters in mungbean

Cluster No.	No. of genotype (s)	Name of genotype (s)
I	5	ML-682, Basanti, ML-776, MH-934, BDYR-2
II	5	IPM-02-3, MH-805, Pusa-0672, BDYR-1, EC-581523
III	3	MH-539, MH-560, RMG-991
IV	1	KM-2241
V	8	IPM-06-5, NVL-638, SML-668, SML-1018, LGG-460, Sattya, GP-69, Vamban-2, GP-248, GP-182, EC-393410, TBM-11
VI	4	AKM-9904, Pusa Ratna, MH-421, Pusa-0871

with three genotypes and clusters IV with one genotype. 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. Lavanya *et al.*, (2007) and Chaudhary *et al.*, (2015) also reported the same results. Because a breeding program mainly depends upon the magnitude of genetic variability, morphological characterizations as an important step in description and classification of crop germplasm (Piyada *et al.* (2010).

The intra and inter cluster D² values among 30 genotypes are given in Table 3. The Table shows that inter cluster distances are more than intra cluster distances which indicates the presence of narrow genetic variation within a cluster. The cluster IV exhibiting an intra-cluster distance of 0.00 reveal to be monogenotypic and consequently less heterogeneous. Cluster II had the minimum intra cluster value (3.537) indicating a minimum difference among the genotypes grouped in this cluster. While the maximum intra cluster D2 value was observed for cluster III (3.874), followed by cluster I (3.691), cluster VI (3.583) and cluster V (3.581), which reveals the existence of maximum differences among the genotypes that fall in these clusters. When diversity was studied among the clusters based on the inter cluster D2 values, it showed a range of 4.13 to 6.31. Cluster V and VI showed minimum inter cluster distance of 4.13 indicating close relationship among the genotypes included in these clusters. Cluster I and VI showed maximum inter cluster distance of 6.31, followed by cluster III and VI (6.12) and clusters IV and VI (5.98), which indicates that genotypes included in these clusters are genetically diverse. Similar results were also observed by Mehandi *et al.*, (2015) and Singh *et al.*, (2015).

TABLE 3

Average intra (diagonal) and inter (above diagonal) cluster D² values for various characters in mungbean

Cluster	I	II	III	IV	V	VI
I	**3.691**	4.197	4.615	5.736	5.089	6.315
II		**3.537**	4.764	5.630	4.471	4.890
III			**3.874**	5.264	5.446	6.123
IV				**0.000**	5.213	5.982
V					**3.581**	4.128
VI						**3.583**

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 data revealed considerable differences among all the clusters for most of the characters studied (Table 4). The cluster means for days to 50 per cent flowering varied from 35.07 days in cluster II to 38.17 days in cluster VI with overall mean of 36.42 days. Cluster I had the highest mean value for number of branches per plant (3.313) and biological yield (11.827). Cluster III showed the maximum mean value (35.407) for harvest index, plant height (31.85) and seed yield (2.51). For pods per plant, the highest mean value was possessed by cluster II (3.089). Cluster IV recorded the highest mean value of seeds per pod (9.200) and pod length (7.500) while cluster VI recorded the lowest (7.567) and (5.067) value for both the traits respectively. This comparison indicates that cluster I, III and IV had better cluster means for most of the characters. Therefore, cluster I, III and IV might be considered better for selecting genotypes. Similar findings were reported by Singh *et al.*, (2009) and Sarkar and Kundagrami (2016)

The per cent contribution of seed yield and various agro-morphological traits towards total divergence and ranking of traits are presented in Table 5. The results obtained with respect to per cent

TABLE 4

Mean values of different clusters for various characters in mungbean

Cluster No.	DF	DM	PH	NB	BY	HI	PPP	PL	SPP	100SW	SY
I	35.80	52.80	31.05	3.31	11.83	21.58	2.92	6.32	8.70	3.50	2.50
II	35.07	52.40	26.31	2.51	9.61	21.33	3.09	6.02	7.94	3.15	1.99
III	36.44	48.67	31.85	2.86	7.23	35.41	2.71	6.65	8.28	4.06	2.51
IV	36.00	47.33	23.25	2.70	8.00	16.84	1.64	7.50	9.20	5.31	1.34
V	36.69	55.67	26.51	2.87	6.91	17.35	1.83	5.72	7.76	3.56	1.18
VI	38.17	54.00	23.30	2.17	5.13	17.73	2.42	5.07	7.57	3.47	0.86
Mean	36.42	53.44	27.23	2.79	8.01	20.56	2.38	5.93	8.02	3.58	1.63

Abbrevations: DF- Days to flowering (50%), DM- Days to maturity, PH- Plant height (cm), NB- Number of branches/plant, BY-Biological yield/plant (g), HI- Harvest index (%), PPP- Number of pods/plant, PL- Pod length (cm), SPP- Number of seeds/pod, 100SW- 100-seed weight (g), SY- Seed yield/plant (g).

TABLE 5
Contribution of various traits towards divergence

S. No.	Agronomic traits	No. of times ranked 1st	Contribution towards divergence (%)
1.	Days to flowering (50%)	27	6.62
2.	Days to maturity	57	13.97
3.	Plant height (cm)	70	17.16
4.	Number of branches/plant	1	0.25
5.	Biological yield/plant (g)	43	10.54
6.	Harvest index (%)	124	30.39
7.	Number of pods/plant	4	0.98
8.	Pod length (cm)	20	4.90
9.	Number of seeds/pod	12	2.94
10.	100-seed weight (g)	8	1.96
11.	Seed yield/plant (g)	40	9.80

TABLE 6
Diverse and promising genotypes selected from different clusters for various traits in mungbean

S. No.	Genotypes	Cluster No.	Genotypic worth of genotypes
1	RMG-591	III	59.82
2	MH-539	III	55.36
3	ML-776	I	51.12
4	MH-560	III	48.63
5	MH-934	I	47.96
6	ML-682	I	47.70
7	Pusa-0672	II	47.16
8	Basanti-(C)	I	43.72

contribution of each character toward total diversity indicated that the characters like number of pods per plant (0.98) and number of branches per plant, contributed very little for divergence which illustrates that the possibility of improvement of green gram targeting these traits is remarkably low. The contribution of harvest index was found maximum (30.39%), followed by plant height (17.16%), days to maturity (13.97%), biological yield per plant (10.54%), days to flowering (50%) (6.62%), pod length (4.90%) and number of seeds per pod (2.94%). Similar results were reported by Gokulakrishnan *et al.*, (2012), Tiwari *et al.*, (2012) and Sen and De (2017).

The promising genotypes selected from different clusters in Table 6 along with their genotypic worth for characters seed yield, biological yield, harvest index, pod per branch and pod length. The genotypes namely, RMG-991, MH-539, ML-776, MH-560, MH-934, ML-682, Pusa-0672 and Basanti were found promising on the basis of their performance for different characters, and to be included in crossing programme to further expand genetic variability among

populations with improved yield under rainfed conditions.

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