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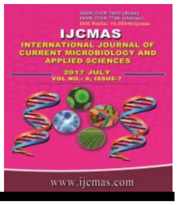

Original Research Article

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Multivariate analysis in Mungbean (*Vigna radiata* L. Wilczek) for Genetic Diversity under Acidic Soils of Manipur, India

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ABSTRACT

Keywords

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Mungbean is one of the significant summer pulse crop in India and Manipur. A study was carried out to evaluate 24 mungbean genotypes for variability available between them using nine quantitative traits. Analysis of variance revealed significant differences among the mungbean genotypes for the characters studied. The estimation of genetic variability in the 24 advanced mungbean breeding lines shows good amount of genetic variability. Genetic advance as percent of mean was moderate to high for all the characters studied. The seed yield was significantly, positively correlated with all the characters except days to 50% flowering, days to maturity and 100 seed weight. Path analysis revealed that, pod length and number of cluster/plant were the two important characters for yield improvement. Genotypes MH 921, BM 2012-9, Pusa 0672, PM-10-18, GM 05-08, IPM 312-19, MH 729A and ML 2410 formed a group in right top corner of the biplot shows positive values of both the PCs and the characters *viz*., Pod length, yield/plot, seed weight and seeds/pod are also placed in the same quadrant shows these characters were mostly influencing the grain yield. In the present study, cluster III having the highest mean yield, followed by the cluster IV, so genotypes corresponding to these clusters can be utilized for the future breeding programme. Based on the present investigation, correlation coefficient, path analysis, principal component and cluster analysis together were utilized for the selection of genotypes for future mungbean breeding programme.

Introduction

Mungbean (*Vigna radiata* L. Wilczek) is one of the important kharif pulse crops in India. In Manipur it is grown under acidic soils of upland and hill slopes. It belongs to Leguminosae family. Mungbean is an important source of easily digestible protein (up to 24%) and iron (40–70 ppm) for nutritionally balanced cereal-based diets in South and Southeast Asia (Bains *et al.*, 2003; Weinberger, 2005). The climatic conditions of India favour mungbean cultivation throughout the year. Now it is also grown during spring/summer season in northern parts and during *rabi* season in southern parts of India. Being a short duration crop, it fits well into the intensive rice–wheat cropping system of

Indo-Gangetic plains of India. It can also be grown as intercrop with sugarcane, pigeon pea, poplar and orchards. For any yield improvement programme selection of superior parents is an essential prerequisite i.e. possessing better heritability and genetic advance for various traits (Khan *et al.,* 2005). The knowledge of genetic variability present within the different parameters contributing to yield is also an important criterion for yield enhancement but in highly self-pollinated crops like mungbeans natural variation is narrow resulting in limited selection opportunity. The efficacy of selection depends upon the magnitude of genetic variability for yield and yield contributing traits in the breeding material. The knowledge of heritability and genetic advance guides the breeders to select superior parents to initiate an effective and fruitful crossing programme. Correlation analysis provides the information of association of important plant characters and hence, leads to a directional model for direct and/or indirect improvement in grain yield (Khan *et al.,* 2004). Current studies were conducted with two main objectives in mind. First, to estimate the genetic variability, heritability and association among yield and related traits in mungbean. Second is to find the characters influencing the yield and clustering pattern of the genotypes.

Materials and Methods

An experiment was performed to compare the performance and to estimate the genetic variability, heritability and association among yield and related traits in mungbean genotypes at Andro Research Farm, CAU, Imphal, Manipur during kharif season of the year 2015. Twenty four entries (including Pusa 0672 as a check) were sown in a plot size of 3.5m x 1.5 m using triplicated Randomized Complete Block Design maintaining row-to-row distance of 30 cm and plant to plant distance of 10cm. All the cultural practices were uniformly applied to all the experimental units to minimize the experimental error. Data were recorded for days to 50% flowering, days to maturity, plant height, number of cluster/plant, number of pods per plant, pod length, seeds/pod, 100 seed weight (g) and grain yield (kg/ha) from 5 well-guarded and randomly selected plants. The mean value of data were subjected to statistical analysis to obtain analysis of variance (Panse and Sukhatme, 1985).Genetic parameters like genotypic, phenotypic variances, heritability, genetic advance and genotypic phenotypic correlation and path co-efficient analysis were computed according to Singh and Chaudhary (1985). The Principal component and clustering analysis has been done through SAS 9.3 software.

Results and Discussion

The analysis of variance showed the significant variation among the genotypes for all the characters at 0.05% level (Table 2). In the present investigation phenotypic covariance was greater than the genotypic covariance shows the greater influence of the environmental factors. These results were corroboration with the Rahim *et al.,* (2010) and Kumar *et al.,* (2014) in mungbean.

Heritability (broad sense) estimates were moderate to high for all the characters (Table 3). The heritability were ranged from 58.73 (number of clusters/plant) to 94.38 (100 seed weight). The genetic advance was highest for the traits namely *viz*., plant height and yield. These results were agreement with the report of Kumar *et al.,* (2014) in blackgram. However, genetic advance as percent of mean is higher in number of pods/plant, 100 seed weight and number of cluster per plant (Table 3). These traits were much useful to estimate the heritability value with genetic advance in estimating the expected improvement to be achieved through selection. Therefore, high heritability coupled with high genetic advance over mean was obtained for number of pods/plant, 100 seed weight and yield/plot. Similar results were found by Jeberson *et al.,* (2016) for yield in Field pea.

Estimation of correlation coefficients between different pair of characters under the investigation shown that, not all the characters were correlated with each other or with seed yield/plant (Table 4).

The investigation revealed that the genotypic correlation is greater than the corresponding phenotypic correlations indicates the preponderance of the genetic variance in the expression of the traits. It shows that the prominence of additive and the additive x additive gene action (Falconer, 1981).

Seed yield was positively correlated with all the characters except days to 50% flowering. The seed yield was significantly, positively correlated with all the characters except days to 50% flowering, days to maturity and 100 seed weight. These results were corroborated with the findings of Singh and Singh (1994), Canci and Toker (2014) and Khaimichho *et al.,* (2014) in mungbean.

The path analysis shows the direct and indirect effects of the different traits were shown in the table 5. Pod length (cm) was shown highest direct effect on yield per plot followed by number of cluster per plant, seeds per pod and number of pods per plant. Number of pods per plant, seeds/pod, pod length, plant height and number of cluster per plant were indirectly highly influencing the seed yield through other characters. Based on the path analysis, pod length and number of cluster/plant were the two important characters for yield improvement. Similar results were obtained by Singh and Singh (1994) in blackgram and Rahim *et al.,* (2010) in mungbean.

Principal component analysis

Genetic variation is important for utilizing any genotype in any crop improvement program. In order to effectively utilizing the germplasm, characterization is important and principal component analysis give a good screening of the different genotypes as suggested by (Rabbani *et al.,* 1998). Multivariate analysis is considered as best method for choosing the parents for hybridization as suggested by Dasgupta and Das (1984).

Fig.1 Scree plot constructed for nine principal components

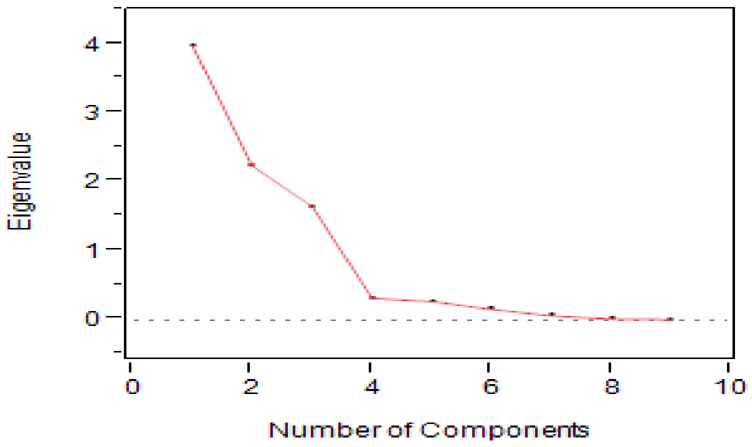

Fig.2 The Biplot of 24 mungbean genotypes for PC1 and PC2 (DFF-Days to 50% flowering, DM-Days to Maturity, Pht-Plant Height (cm), NC-Number of cluster, PPP-Pods per plant, PL-Pod length (cm), SPP-Seeds per pod, SW-seed weight (g) and Yd-Yield (Kg/ha)

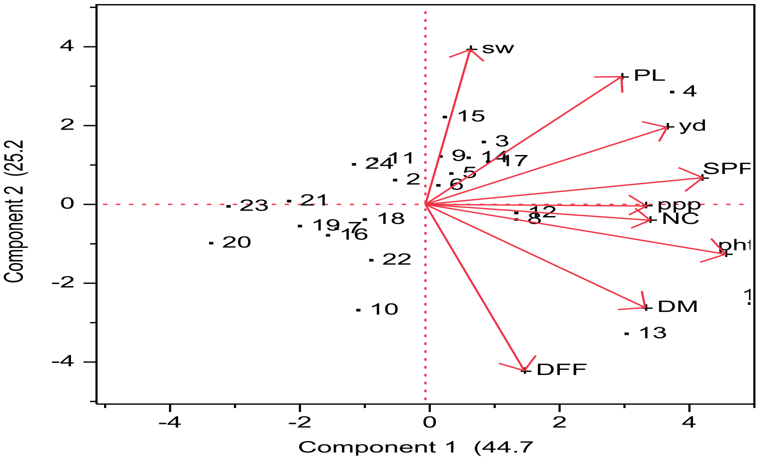

Fig.3 Dendrogram based on nine quantitative characters in mungbean genotypes

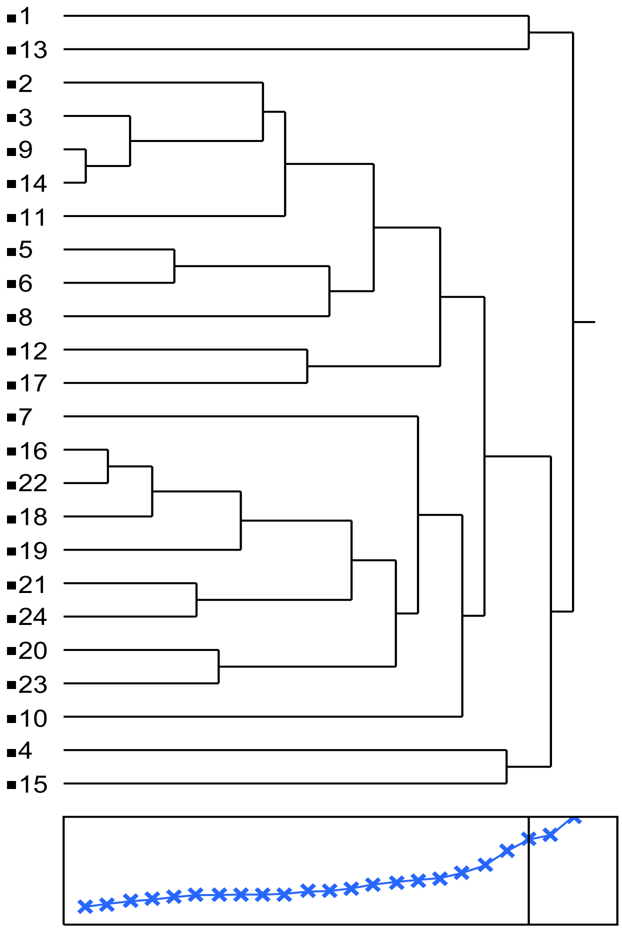

Table.1 Genotypes and their pedigrees

S.No	Genotypes	Pedigree	Sources
1.	Pant M6	Pant M2 x AMP 36	Pantnagar
2.	KM 2241	Samrat x PDM 54	CSAUA&T, Kanpur
3.	Pusa 0672	11/395 x ML 267	IARI, New Delhi
4.	MH 921	ML 96-1 x 2KM 114	CCS HAU, Hisar
5.	MH 729A	Selection from MH 729 (MH 98-1 x BDYR 2)	CCS HAU, Hisar
6.	ML 2410	ML 5 x PAU 911	PAU, Ludhiana
7.	ML 2412	ML 1349 x Mash 1-1	PAU, Ludhiana
8.	PM 12-2	BDYR-1 x IPR 99-40	GBPUA&T, Pantnagar
9.	PM 10-18	PM-4 x ML 818	GBPUA&T, Pantnagar
10.	VGG 10-008	PDM 139 x BB 2664	NPRC, Vamban
11.	COGG 11-02	COGG 912 x IPM 02-3	TNAU, Coimbatore
12.	NDMK 14-24	NDM 1 x Samrat	Faizabad
13.	LGG 574	LGG 460 x P 101-1	ARS, Lam
14.	GM 05-08	GM 9402 x E 92-3	S.K. Nagar
15.	BM 2012-9	Mutant of BPMR 145	Badnapur
16.	RMG 1082	RMG 492 x ML 818	Durgapura
17	IPM 312-19	IPM 03-1 x SPS 5	IIPR, Kanpur
18.	IPM 312-20	IPM 03-1 x SPS 5	IIPR, Kanpur
19.	KM 2348	KM 2195 x Pusa 9872	CSAUAT, Kanpur
20.	Pusa 1571	MUM 2 x Pusa Vishal	IARI, New Delhi
21.	Pusa 1572	Pusaratna x IPM02-1	IARI, New Delhi
22.	IGKM 06-4-2	Beliya x TARM 1	IGKV, Raipur
23.	NVL 825	NVL724 x NVL 810	Nirmal Seeds Pvt Ltd
24.	AKM 12-17	AKM 9911 x UPM 99-3	PDKV, Akola

Table.2 Analysis of variance for different morphological and economical characters in mungbean

S.No.	Characters	Sum of squares	Mean sum of squares	F value
1.	Days to 50% flowering	972.67	42.29	15.11**
2.	Days to maturity	1242.44	54.02	11.73**
3.	Plant height	7874.2	342.36	6.45*
4.	No. of cluster/plant	21.00	0.91	5.27*
5.	No of pods per plant	399.41	17.37	9.67*
6.	Pod length	29.83	1.30	5.68*
7.	Seeds/pod	120.35	5.23	6.67*
8	100 seed weight	16.03	0.70	51.42**
9.	Yield (g/plot)	868550	37763	20.16**

*, ** significant at 0.05 and 0.01 level of significance, respectively

Table.3 Genetic parameters for different traits in mungbean

S.No.	Characters	PV	GV	PCV%	GCV%	H^2	GA	GAM
1.	Days to 50% flowering	15.96	13.16	9.67	8.78	82.47	6.79	16.42
2.	Days to maturity	21.08	16.47	6.76	5.98	78.15	7.39	10.89
3.	Plant height	149.48	96.44	27.75	22.29	64.51	16.25	36.88
4.	No. of cluster/plant	0.42	0.25	20.98	16.08	58.73	0.78	25.38
5.	No of pods per plant	6.986	5.19	27.24	23.48	74.29	4.05	41.69
6.	Pod length	0.54	0.36	10.48	8.18	60.94	0.96	13.16
7.	Seeds/pod	2.27	1.48	14.10	11.40	65.36	2.03	18.99
8	100 seed weight	0.24	0.23	15.85	15.40	94.38	0.96	30.81
9.	Yield (g/plot)	13836.76	11963.13	28.29	26.31	86.46	209.51	50.39

Table.4 Estimation of genotypic and phenotypic correlation coefficient in Mungbean

Traits	**Genotypic/ Phenotypic correlation**	**Days to maturity**	**Plant height**	**No. of cluster/plant**	**No of pods per plant**	**Pod length**	**Seeds/pod**	**100 seed weight**	**Yield (g/plot)**
Days to 50% flowering	G	0.8880**	0.6572**	0.0509	-0.0341	-0.2535	0.2933	-0.4434	-0.1637
	P	0.6965**	0.3450	0.0187	-0.0817	-0.1810	0.2669	-0.4020	-0.2167
Days to maturity	G		0.8461**	0.3424	0.1640	0.2197	0.6659**	-0.1236	0.2316
	P		0.6278**	0.1983	0.1382	0.2015	0.5288**	-0.0914	0.2463
Plant height	G			0.6477**	0.6173**	0.4492*	0.8952**	-0.0623	0.5956**
	P			0.5215*	0.5613**	0.3430	0.5838**	-0.0184	0.5373**
No. of cluster/plant	G				0.9557**	0.1789	0.3554	-0.2332	0.5876**
	P				0.7184**	0.2023	0.2934	-0.1541	0.4182*
No of pods per plant	G					0.1571	0.4171	-0.2138	0.6310**
	P					0.1549	0.3056	-0.1600	0.5408**
Pod length	G						0.7429**	0.7124**	0.6178**
	P						0.7476**	0.5380**	0.4766*
Seeds/pod	G							0.3035	0.6197**
	P							0.2234	0.4689*
100 seed weight	G								0.2629
	P								0.2665

*, ** significant at 0.05 and 0.01 level of significance, respectively

Table.5 Direct (diagonal) and indirect effects of yield component traits on seed yield in Mungbean

Traits	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**No. of cluster/plant**	**No of pods per plant**	**Pod length**	**Seeds/pod**	**100 seed weight**	**Yield (g/plot)**
Days to 50% flowering	**0.1443**	-0.2411	-0.0427	0.0170	0.0076	-0.1020	0.0860	-0.0175	-0.1637
Days to maturity	0.1282	**-0.2715**	-0.0550	0.1143	0.0368	0.0884	0.1953	-0.0049	0.2316
Plant height	0.0948	-0.2297	**-0.0650**	0.2163	0.1385	0.1807	0.2625	-0.0025	0.5956
No. of cluster/plant	0.0073	-0.0929	-0.0421	**0.3340**	0.2144	0.0720	0.1042	-0.0092	0.5876
No of pods per plant	-0.0049	-0.0445	-0.0401	0.3191	**0.2243**	0.0632	0.1223	-0.0084	0.6310
Pod length	-0.0366	-0.0597	-0.0292	0.0597	0.0352	**0.4023**	0.2178	0.0281	0.6178
Seeds/pod	0.0423	-0.1808	-0.0582	0.1187	0.0936	0.2989	**0.2932**	0.0120	0.6197
100 seed weight	-0.0640	0.0335	0.0040	-0.0779	-0.0480	0.2866	0.0890	**0.0395**	0.2629

Table.6 Eigen values and percentage of variation in respect of 9 traits in 24 mungbean genotypes

Eigenvalues of the Correlation Matrix				
Sl.No,	**Eigenvalue**	**Difference**	**Proportion**	**Cumulative**
1	4.0178	1.7561	0.4464	0.4464
2	2.2616	0.5849	0.2513	0.6977
3	1.6767	1.3322	0.1863	0.8840
4	0.3445	0.0315	0.0383	0.9223
5	0.3130	0.1188	0.0348	0.9571
6	0.1943	0.1004	0.0216	0.9787
7	0.0939	0.0382	0.0104	0.9891
8	0.0557	0.0133	0.0062	0.9953
9	0.0424		0.0047	1.0000

Table.7 Contribution of nine characters towards total variance

Eigenvectors									
	PRIN1	**PRIN2**	**PRIN3**	**PRIN4**	**PRIN5**	**PRIN6**	**PRIN7**	**PRIN8**	**PRIN9**
DFF	0.1597	-0.5598	**0.3089**	-0.0236	0.1070	0.0885	-0.0181	-0.1725	0.7182
DM	**0.3424**	-0.3420	**0.3341**	-0.0954	0.2896	-0.3130	**0.3560**	**0.4384**	-0.3799
pht	**0.4635**	-0.1558	0.0510	-0.0449	0.0692	**0.3174**	-0.7381	-0.0326	-0.3238
NC	**0.3455**	-0.0442	-0.4730	**0.3970**	**0.3426**	-0.4556	0.0190	-0.4148	0.0111
PPP	**0.3407**	0.0071	-0.5240	0.1254	0.0071	**0.4854**	0.2585	**0.4913**	0.2229
PL	0.2963	**0.4284**	0.2726	**0.3094**	-0.2860	-0.3911	-0.2633	**0.3767**	**0.3356**
SPP	**0.4255**	0.0932	0.2753	0.2004	-0.4744	0.2558	**0.4220**	-0.4361	-0.1887
sw	0.0463	**0.5260**	**0.3408**	0.0695	**0.6886**	**0.3107**	0.0999	-0.1051	0.0918
yd	**0.3687**	0.2728	-0.1604	-0.8212	-0.0390	-0.1883	0.0605	-0.1430	0.1689

Table.8 Four clusters grouping field pea genotypes based on Nine (9) quantitative characters

Cluster	Frequency	Cluster Memberships
I	2	MH921 and Bm 2012-9
II	10	ML 2412, RMG 1082, IGKM 06-4-2, IPM 312-20, KM 2348, Pusa 1572, AKM 12-17, Pusa 1571, NVL 825 and VGG10-008
III	10	KM 2241, Pusa 0672, PM 10-18, GM 05-08, CoGG 11-02, MH 729A, ML 2410, PM-12-2, NDMK-14-24 and IPM 312-19
IV	2	Pant M6 and LGG 574

Table.9 Cluster means for nine traits in 24 mungbean genotypes

Traits/Clusters	**I**	**II**	**III**	**IV**
Days to 50% flowering	40.5	41.8	39.2	50.5
Days to Maturity	57.5	66.9	66.4	77.5
Plant Height (cm)	48.75	36.2	45.61	70.9
Number of cluster	3	2.84	3.21	3.9
Pods per plant	8.4	8.03	10.99	12.8
Pod Length (cm)	8.7	6.78	7.5	7.3
Seeds per pod	12.75	9.63	10.9	12
Seed Weight (g)	4.35	2.91	3.16	2.65
Yield/plot (Kg/ha)	728	674.2	905.6	878

According to the principal component analysis, three principal components have Eigen values more than unity and the variance accounted for 88.4% of the total variance in the data (Table 6). Among the three principal components, the PC1 shares high proportion of total variation 44.64% and the rest of the two principal components viz., PC2 and PC3 contributed 25.13% and 18.63% of the total variance respectively. Nine principal components have been showing Eigen values in the Scree plot (Fig 1). Similar findings were given by Divyaramakrishnan and Savithramma in mungbean (2014).

Criteria of Raji (2002) was taken to determine the critical limit for the coefficients of the proper vectors, according to this criterion, coefficients was greater than 0.3 as having large effect to be considered important, while characters having lesser coefficients value than 0.3 were not considered to have important effects in the overall variation observed in the present study. Eigen vectors of the first three PCs were presented in the table 7. The results shows that the plant height had the highest positive value (0.464) followed by seeds/pod (0.426), yield/plot(0.369), number of cluster per plant(0.345), days to maturity (0.347) and pods/plant (0.341) and all other traits are showing positive value in first PC.

In the second PC, only two characters are showing Eigen vector value more than 0.3 *viz*., 100 seed weight (0.526) and pod length (0.428). In the PC3 100 seed weight (0.341) followed by days to maturity (0.344) and days to 50% flowering (0.308) had the high positive value respectively. Similar results were given by Ghaffoor *et al.,* (2002) where they have taken first four component of PC with Eigen values >1 contributed 78.7% of the total variance among the 40 greengram genotype studied. Basnet *et al.,* (2014) also reported similar results in mungbean, while the first three PCs had contributing nearly 78% of the total variation with individual share of 40.60%, 23.30% and 14.70% respectively. The first two PCs were plotted against each other in biplot to observe the relation among the mungbean lines based on the observed yield attributing characters (Fig. 2). Genotypes MH 921, BM 2012-9, Pusa 0672, PM-10-18, GM 05-08, IPM 312-19, MH 729A and ML 2410 formed a group in right top corner of the biplot shows positive values of both the PCs and the characters *viz*., Pod length, yield/plot, seed weight and seeds/pod are also placed in the same quadrant shows these characters were mostly influencing the grain yield. Razzaque *et al.*, (2016) also observed similar kind of results in mungbean under nutrient stress in soil.

Cluster analysis

The 24 mungbean genotypes were grouped into four clusters based on average linkage distance method of hierarchical clustering as shown in the diagram (Figure3). There were four major groups, Clusters I, II, III and IV were consists of two, 10, 10 and two genotypes (Table 8). The mungbean genotypes of cluster III had highest mean value for yield, cluster IV had highest value for days to 50% flowering and cluster I had the lowest mean value of days to maturity (Table 9). For plant height, cluster IV having the highest mean value. For number of cluster character cluster IV having the highest mean value. For pods/plant cluster IV having the highest mean value. For pod length cluster I having the highest mean value. For seeds/pod, 100 seed weight cluster I is having highest value. The genotypes from different clusters can be selected based on the interest of the character to be improved. In the present study, cluster III having the highest mean seed yield, followed by the cluster IV, so the genotypes belongs to these clusters can be utilized for the future breeding programme. These results were similarity with the studies of Zubair *et al.*, (2007) and Razzaque *et al.*, (2016) in the crop mungbean.

In conclusion, Twenty four mungbean genotypes of Indian origin were utilized for genetic variability studies using the correlation, path analysis, principal component and cluster analysis techniques based on the nine quantitative characters. The seed yield was significantly, positively correlated with all the characters except days to 50% flowering, days to maturity and 100 seed weight.

Based on the path analysis, pod length and number of cluster/plant were the two important characters for yield improvement. Genotypes MH 921, BM 2012-9, Pusa 0672, PM-10-18, GM 05-08, IPM 312-19, MH 729A and ML 2410 formed a group in right top corner of the biplot shows positive values of both the PCs and the characters *viz*., Pod length, yield/plot, seed weight and seeds/pod are also placed in the same quadrant shows these characters were mostly influencing the grain yield.

In the present study, cluster III having the highest mean yield, followed by the cluster IV, so genotypes belongs to in these clusters can be utilized for the future breeding activities. These techniques were helped to indentify the superior genotypes for further crop improvement programme.

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References

Bains K, Yang R, Shanmugasundaram S (2003). High Iron Mungbean Recipes for North India. AVRDC-The World Vegetable Center AVRDC, Tainan.

Basnet, K.M., Adhikari, N.R. and Pandey, M.P. 2014. Multivariate analysis among the Napalese and exotic mungbean (*Vigna radiata* (L.) Wilczek) genotypes based on the qualitative parameters. Universal Journal of Agricultural Research, 2(5):147-155.

Canci, H. and Toker, C. 2014. Yield components in mungbean (*Vigna radiata* (L.) Wilczek). Turkish Journal of Field crops, 19(2): 258-261.

Dasgupta, T. and Das, P.K. 1984. Multivariate analysis and selection for hybridization in blackgram. Philippine Agriculturist, 57(10): 86-92.

Divyaramakrishnan, C.K. and Savithramma, D.L. 2014. Tailoring genetic diversity of mungbean (*Vigna radiata* (L.) Wilczek) germplasm through principal component and cluster analysis for yield and yield related traits. International Journal of Agronomy and Agricultural Research, 5(2):94-102.

Falconer, D.S. 1981. Introduction to Quantitative Genetics, edn 2, pp 281-284. Oliver & Boyd, London.

Jeberson, M.S., Shashidhar, K.S. and Iyanar, K., 2016.Estimation of genetic variability, expected genetic advance, correlation and path analysis in field pea (*Pisum sativum* L.). *Electronic Journal of Plant Breeding*, 7(4):1074-1078.

Khaimichho, E.B., Hijam, L., Sarkar, K.K. and Mukherjee, S.2014. Genetic control and character association estimates of yield and yield attributing traits some mungbean genotype. Journal Crop and Weed, 10(2):82-88.

Khan, M.D., I.H. Khalil, M.A. Khan and Ikramullah, 2004. Genetic divergence and association for yield and related traits in mash bean. *Sarhad J. Agric*., 20: 555–61.

Khan, M.Q., S.I. Awan and M.M. Mughal, 2005. Estimation of genetic parameters in spring wheat genotypes under rainfed conditions. *Indus J. Biol. Sci*., 2: 367–70.

Kumar, S. Singh, P., Kumar, R. and Singh, R. 2014. Evaluation of genetic divergence and heritability in urdbean (Vigna mungo L. Hepper). Legume Research, 37(5): 473-478.

Panse V.G. and Sukhatme, P.V. 1985. *Statistical Method for Agricultural Workers.* I.CAR. NewDelhi.

Rabbani, M.A., Iwabuchi, A., Murakami, Y., Suzuki, T. and Takayanagi, K. 1998. Phenotypic variation and the relations among mustard (*Brassiccajuncea*,L.) germplasm from Pakistan. Euphytica, 101:357-366.

Rahim, M.A., Mia, A.A., Mahud, F., Zeba, N. and Afrin, K.S. 2010. Genetic variability, Character association and genetic divergence in mungbean (*Vigna radiata* (L.) Wilczek). Plant Omics Journal, 3(1): 1-6.

Raji, A.A. 2002. Assessement of genetic diversity and heterotic relationship in African improved and local cassava (*Manihot esculenta* Crantz) germplasm. Phd Thesis, University of Ibadan, Nigeria.

Singh, G. and Singh, M. 1994. Correlation and path analysis in blackgram (*Vigna mungo* L.). Indian Journal of Agricultural Sciences, 64(7): 462-464.

Singh, R.K. and B.D. Chaudhary. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. Pp.303.

Weinberger K (2005). Assessment of the nutritional impact of agricultural research: the case of mungbean in Pakistan. *Food Nutr. Bul*. 26:287–294.

Zubair, M., Ajmal, S.U., Anwar, M. and Haqqani, A.M., 2007. Multivariate analysis for quantitative traits in mungbean (*Vigna radiata* L. Wilczek). *Pak.J. Bot.*, 39(1): 103-113.

Razzaque, M.A., Haque, M.M, Rahman, M.M., Bazzaz, M.M. and Khan, M.S.A. 2016. Screening of mungbean (*Vigna radiata* L. Wilczek) genotypes under nutrient stress in soil. Bangladesh J. Agril. Res, 41(2):377-386.

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