LR-4568
[1-8]

RESEARCH ARTICLE Legume Research - An International Journal

Genetic Diversity and Principal Component Analysis in Mungbean [*Vigna radiata* (L.) Wilczek] under Rainfed Condition

Deepak Gupta[1], Suresh Muralia[2], N.K. Gupta[3], Sunita Gupta[4], M.L. Jakhar[5], J.S. Sandhu[6]

10.18805/LR-4568

ABSTRACT

Background: Mungbean is a short duration grain legume widely grown in south and Southeast Asia. The extent of variability through Principal Component Analysis (PCA) and cluster analysis in promising mungbean genotypes should be known for possible yield improvement. A study was undertaken to work out the extent of variability among twenty four mungbean genotypes through cluster analysis and Principal Component Analysis (PCA).

Methods: The experiment was laid out in a randomized block design with three replications during *kharif* 2018 and 2019 at the experimental field of Agricultural Research Station, Navgaon (Alwar) under rainfed condition.

Result: Principal component analysis revealed that the first three main PCAs amounted 78.80% of the total variation among genotypes for different traits. Out of total principal components, PC1 accounts for maximum variability in the data with respect to succeeding components. Number of branches per plant (28.62%), number of clusters per plant (23.55%) and seed yield (15.58%) showed maximum per cent contribution towards total genetic divergence on pooled basis. Cluster analysis showed that genotypes fall into seven different clusters and their inter and intra cluster distance showed genetic diversity between different genotypes. The maximum number of genotypes *i.e.,* 8 was found in cluster II followed by cluster III comprising of 6 genotypes. Genotypes RMG-1138 and IPM-02-03 representing the mono genotypic cluster signifies that it can be the most diverse variety and it would be the appropriate genotype for hybridization with ones present in other clusters to tailor the agriculturally important traits and ultimately to boost the seed yield in mungbean under rainfed conditions.

Key word: Genetic divergence, Genetic variability, Mungbean, Principal component analysis, Yield.

INTRODUCTION

Mungbean [*Vigna radiata* (L.) Wilczek] is the most important short duration pulse crop. It is an affordable supply of vegetable protein, vitamins, and minerals for a common person. It contains about 23.9% protein, which is nearly three times that of cereals (Thirumaran and Seralthan, 1988). It's rich in lysine, an essential amino acid that's normally low or deficient in cereals (Yimram *et al.*, 2009). Mungbean also improves the soil fertility status by fixing the environmental nitrogen (Joshi *et al.*, 2003).

In India, mungbean is important pulse crops grown in Kharif season. India alone accounts for 65% of its world acreage and 54% of the production. In Rajasthan, it is grown on an area of 23.27 lakh hectares with production of 13.04 lakh tonnes and productivity of 561 Kg/ha (Anonymous, 2019-20). The low productivity can be attributed to narrow genetic base and lack of suitable genotypes for different cropping situations (Dikshit *et al.,* 2009).

Yield is a complex quantitative trait in any crop because numerous morphological and physiological traits contribute towards it. These contributing components associate with each other demonstrating a complicated chain of relationship which is additionally impacted by the ecological conditions. Hence, in order to increase the productivity of mungbean, there is need to develop new mungbean varieties suitable for varied environmental conditions. As the simple genetic variation nears exploitation through selection, hybridization between parents with maximum genetic divergence is the alternate choice to release new genetic

---

[1]Department of Plant Breeding and Genetics, SKN College of Agriculture, Jobner-303 329, Jaipur, Rajasthan, India.
[2]Agriculture Research Station, Navgaon-Alwar-301 025, Rajasthan, India.
[3]Directorate of Education, SKN Agriculture University, Jobner-Jaipur-303 329, Rajasthan, India.
[4]Directorate of Prioritization, Monitoring and Evaluation, SKN Agriculture University, Jobner-303 329, Jaipur, Rajasthan, India.
[5]Directorate of Research, SKN Agriculture University, Jobner-303 329, Rajasthan, India.
[6]SKN Agriculture, University, Jobner-303 329, Rajasthan, India.

Corresponding Author: Deepak Gupta, Department of Plant Breeding and Genetics, Sri Karan Narendra College of Agriculture, Jobner-303 329, Jaipur, Rajasthan, India.
Email: deepakgupta.pbg@sknau.ac.in

How to cite this article: Gupta, D., Muralia, S., Gupta, N.K., Gupta, S., Jakhar, M.L. and Sandhu, J.S. (2021). Genetic Diversity and Principal Component Analysis in Mungbean [*Vigna radiata* (L.) Wilczek] under Rainfed Condition. Legume Research. DOI: 10.18805/LR-4568.

Submitted: 15-12-2020 **Accepted:** 07-06-2021 **Online:** 22-07-2021

variation for genetic improvement (Arunachalam, 1981 and Jakhar and Kumar, 2018).

Some appropriate strategies *viz.,* cluster analysis, factor analysis and principal component analysis helps in determination of genetic diversity. The PCA has been referred by various researchers for the decrease of multivariate data into a biplot which can be additionally utilized for grouping material. This approach is particularly significant for screening a large number of genetic resources by a large number of descriptor variables (Golbashy *et al*., 2010 and Beiragi *et al*., 2011).

The present investigation was therefore, planned to estimate the potential genetic diversity using cluster analysis through PCA based techniques for selection of parents. The study is expected to identify potential morphological traits that are better employed as selection criteria for developing high yielding mungbean genotypes. The findings may help mungbean breeders to breed better yielding new mungbean varieties suitable for certain conditions.

MATERIALS AND METHODS

Twenty four mungbean genotypes were evaluated in a randomized block design (RBD) with three replications during *Kharif* seasons in two consecutive years 2018 and 2019 at Agricultural Research Station, Navgaon, Alwar under rainfed conditions with standard cultural practices. Each plot consisted of five rows of 4 m length and 30 cm apart. The experimental area was quite uniform with respect to topography and fertility. The Agriculture Research Station, Navgaon-Alwar is situated at North East Corner of Rajasthan between 76°7'-28°2' N latitude. The average rainfall of the zone is 500 mm. The crop was grown under normal crop season. The details of name and origin/source 24 genotypes are given in Table 1. Eleven quantitative characters were taken into consideration for estimating relationship among mungbean genotypes. These quantitative characters included days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), 100-seed weight (g), pods per cluster, seeds per pod and seed yield (q/ha). The data collected were subjected to multivariate analysis utilizing Mahalanobis D^2 statistic as suggested by Mahalanobis (1936) and Rao (1952) using statistical software TNAUSTAT. Accessions were grouped into five clusters following Tocher's method as suggested by Rao (1952). The necessity of the principal component analysis (PCA) for measuring the degree of divergence has been established by SPSS 16.0 version.

RESULTS AND DISCUSSION

ANOVA indicated that there were significant differences among 24 mungbean genotypes for most of the traits studied in both the years indicating the existence of adequate genetic variability. The highest seed yield was observed in genotype IPM-205-07 followed by genotype IPM-410-03 and PDM-139 under rainfed conditions. The lowest yield was observed in genotype MH-421 (Table 2).

Significant high coefficient of variation (>10%) was observed for number of branches per plant accompanied by seed yield, number of clusters per plant and number of pods per plant suggesting substantial amount of genetic variability and are in accordance with the findings of Hemavathy *et. al.* (2003). Moderate variation (5-10%) was observed for plant height, number of pods per cluster, number of seeds per pod, 100-seed weight and pod length. Low variability (<5%) was found for days to 50% flowering and days to maturity. This variability among the mungbean genotypes could be attributed to the inherent genetic differences or differential adaptation to rainfed conditions. Comparable outcomes were accounted for by Shukla *et al.* (1997), Mehandi *et al.* (2015), Sarkar and Kundagrami (2016) and Kaur *et al.* (2017).

Under rainfed conditions, correlation coefficients for various quantitative characters reveals that seed yield significantly and positively correlated with number of clusters/plant, number of pods/plant, 100-seed weight, number of pods per cluster and number of seeds per pod and negatively significant correlated with days to 50% flowering, days to maturity and plant height (Table 3). Perusal of data further revealed that days to 50% flowering was

Table 1: Name and origin of genotypes.

Name of genotype	Origin	Name of genotype	Origin
IPM-410-3	IIPR, Kanpur	PDM-139	IIPR, Kanpur
RMG-1087	RARI, Durgapura	RMG-1148	RARI, Durgapura
MH-318	CCSHAU, Hisar	MSJ-118	RARI, Durgapura
RMG-1139	RARI, Durgapura	RMG-1154	RARI, Durgapura
RMG-492	RARI, Durgapura	RMG-1094	RARI, Durgapura
RMG-1132	RARI, Durgapura	MH-421	CCSHAU, Hisar
IPM-205-7	IIPR, Kanpur	RMG-1152	RARI, Durgapura
RMG-1137	RARI, Durgapura	MH-1-25	CCSHAU, Hisar
RMG-975	RARI, Durgapura	RMG-1147	RARI, Durgapura
MH-2-15	CCSHAU, Hisar	RMG-1138	RARI, Durgapura
RMG-1134	RARI, Durgapura	IPM-02-03	IIPR, Kanpur
IPM-2-14	IIPR, Kanpur	RMG-1098	RARI, Durgapura

Table 2: Variations in quantitative traits of 24 mungbean genotypes on pooled years basis.

Characters	Mean ± S.Em.	Coefficient of variance (%)	Range	
			Minimum	Maximum
Days to 50 per cent flowering	41.49±0.70	04.11	37.17	44.50
Days to maturity	69.22±0.77	02.73	65.67	72.33
Plant height (cm)	65.01±6.28	08.42	51.94	80.28
Number of branches per plant	07.59±0.37	11.99	05.33	12.00
Number of clusters per plant	11.49±0.48	10.29	07.50	17.25
Number of pods per plant	33.07±1.39	10.27	26.93	40.99
Pod length (cm)	07.08±0.18	06.29	06.13	08.05
100-seed weight (g)	04.70±0.13	06.71	03.65	05.47
Number of pods per cluster	04.68±0.14	07.09	03.88	05.82
Number of seeds per pod	09.81±0.28	06.96	08.77	11.32
Seed yield (q/ha)	08.21±0.38	11.19	06.57	11.39

Table 3: Correlation coefficients among 11 quantitative traits in mungbean genotypes.

	DF	DM	PH	Br	CP	PP	PL	SW	PC	SP	SY
DF	1.000	0.465*	0.509*	0.305	-0.725**	-0.469*	-0.578**	-0.246	-0.557**	-0.657**	-0.575**
DM		1.000	0.236	-0.104	-0.452*	-0.463*	-0.354	-0.485*	-0.556**	-0.483*	-0.538**
PH			1.000	0.158	0.590**	-0.200	-0.412*	-0.116	-0.434*	-0.467*	-0.502*
Br				1.000	-0.161	0.441*	0.020	-0.019	-0.052	-0.168	-0.051
CP					1.000	0.609**	0.645**	0.236	0.623**	0.668**	0.665**
PP						1.000	0.475*	0.369	0.531**	0.414*	0.572**
PL							1.000	-0.007	0.224	0.470*	0.325
SW								1.000	0.825**	0.605**	0.731**
PC									1.000	0.792**	0.893**
SP										1.000	0.750**
SY											1.000

* Significant at 5 per cent, ** Significant at 1 per cent.

DF-Days to 50%flowering, DM-Days to maturity, PH-Plant height (cm), Br-Number of branches/plant, CP- Number of clusters/plant, PP-Number of pods/plant, PL-Pod length (cm), SW-100-seed weight (g), PC- Number of pods per cluster, SP- Number of seeds per pod and SY-Seed yield (q/ha).

significantly and positively correlated with days to maturity and plant height but significantly and negatively correlated with number of clusters/plant, number of pods/plant, pod length, 100-seed weight, number of pods per cluster and number of seeds per pod. In other words the days to flowering was negatively correlated with all the yield attributes as well as yield. Plant height was significantly and positively correlated with number of clusters per plant while, number of branches per plant were significantly and positively correlated with number of pods per plant. Also, it was found that number of clusters per plant was significantly and positively correlated with number of pods/plant, pod length, number of pods per cluster and number of seeds per pod. Number of pods per plant was significantly and positively correlated with pod length, number of pods per cluster and number of seeds per pod. In other words, number of capsules per plant, number of pods per plant, 100-seed weight, number of seeds per cluster and number of seeds per pod attributes were positively correlated among themselves and these were also positively correlated with yield. It can therefore, be inferred that these characteristics will be valuable for future breeding programme in mungbean under rainfed situation. The results are in concurrence with Parsanna *et al.* (2013), Hemavathy *et al.* (2015), Baisakh *et al.* (2015) and Kaur *et al.* (2017).

Selection of suitable parents is important for any successful plant breeding program. Parents with more genetic distance are expected to generate wider variation in the progeny thus facilitating higher genetic gains from selection. Hence, genetic divergence analysis was performed. The dendrogram also observed the relative magnitude of resemblance among the different clusters (Fig 1). The distribution pattern of genotypes among various clusters showed that considerable genetic variability exists among the genotypes. The genotypes got distributed into seven distinct clusters (Table 4). Among these, clusters II was the largest with eight genotypes followed by cluster III with six genotypes and cluster I with four genotypes. Cluster IV and V comprised only two genotypes while the remaining clusters VI and VII were mono genotypic clusters indicating that these genotypes may be having completely different genetic makeup, thus leading to the formation of separate

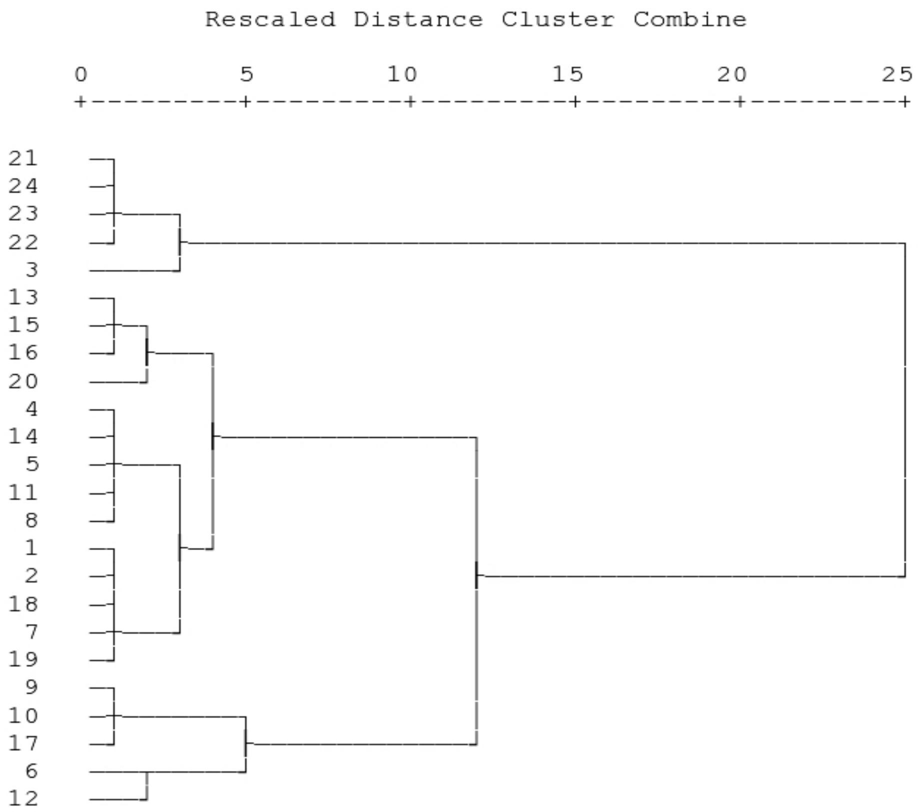

Fig 1: Dendogram based on 11 characters observed in mungbean genotypes.

Table 4: Clustering of 30 mungbean genotypes for various characters in mungbean.

Clusters	Number of genotypes	Composition of cluster
I	4	IPM-410-3, IPM-205-7, IPM-2-14, PDM-139
II	8	RMG-1087, RMG-1148, MSJ-118, RMG-1137, RMG-1154, MH-318, RMG-1139, RMG-1094
III	6	RMG-492, RMG-1132, RMG-975, RMG-1098, MH-2-15, RMG-1134
IV	2	RMG-1152, RMG-1147
V	2	MH-421, MH-1-25
VI	1	RMG-1138
VII	1	IPM-02-03

cluster. The genotype which belongs to the same cluster indicates to be more closely related than those belonging to different clusters under rainfed situation. Chaudhary *et al.* (2015), Garg *et al.* (2017) and Jakhar and Kumar (2018) also reported the similar results.

The intra and inter cluster D^2 values among 24 genotypes (Table 5) clearly show that inter cluster distances are more than intra cluster distances indicating the presence of narrow genetic variation within a cluster. Clusters VI and VII exhibiting an intra-cluster distance of 0.00 suggested them to be mono-genotypic and consequently less heterogeneous. Cluster IV exhibited minimum intra cluster D^2 value (20.84) which stipulates a minimum difference among the genotypes grouped in this cluster. The maximum intra cluster D^2 value was observed in cluster III (47.32) followed by cluster III (44.61), cluster I (27.44) and cluster IV (20.84) indicating that maximum differences exists among the genotypes that fall in these clusters. A critical analysis of data showed that the cluster diversity based on D^2 values was in a range of 63.55 to 231.55. Further, cluster III and IV showed minimum inter cluster distance of 63.55 which indicates close relationship among the genotypes present in these clusters. Cluster I and IV showed maximum inter cluster distance of 231.55, followed by cluster V and VII (199.74) and clusters III and VII (181.51) indicating that genotypes included in these clusters are genetically diverse. Results in similar lines were reported by Pandiyan *et al.* (2012), Mehandi *et al.* (2015) and Singh *et al.*, (2015).

Improvement in yield and other related characters is the basic objective in any breeding programme. So, cluster diversity for seed yield and its contributing attributes should to be considered for selection of genotypes. In present investigation considerable differences were observed among the clusters for most of the characters studied (Table 6). Cluster I had the highest mean value for number of clusters per plant (16.18), pod length (7.53), pods per cluster (5.69), seeds per pod (11.03) and seed yield (10.33). It had lowest mean value for days to 50% flowering (37.71), days to maturity (67.29) and plant height (54.34). Cluster VII showed the maximum mean value for number of branches per plant (11.63) and number of pods per plant (40.50). For 100-seed weight, the highest mean value was possessed by cluster VI (5.40). This comparison indicates that cluster I, VI and VII had better cluster means for most of the characters. Therefore, these clusters may be considered better for selecting genotypes with desirable characters. Similar findings were reported by Mehandi *et al.* (2015), Sarkar and Kundagrami (2016) and Garg *et al.* (2017).

The results obtained on per cent contribution of each character towards total diversity shows that number of seeds per pod has no contribution towards the total divergence, while pod length exhibited less contribution (<1%), indicating the possibility of green gram improvement through targeting this character (Table 5). The maximum contribution for total divergence was recorded from number of branches per plant, number of clusters per plant and seed yield. Consequently, considering both cluster mean and per cent contribution of each character, genotypes belonging to cluster I, VI and VII found promising for use as breeding material in future hybridization programme.

In present investigation, the principal component analysis (PCA) has been done to estimate effective contribution of various traits on seed yield and other characteristics (Table 7). Results showed that 3 principal components (PC) had eigen values more than unity and accounted for 78.80 per cent of the whole variance within the data. Among initial three PCs, PC1 accounted high proportions of total variance (51.16%) and therefore, the remaining 2 principal components *viz.*, PC2 and PC3 recorded 14.64 and 13.00 per cent of total variance respectively. Eigen values of 11 principal components are shown within the scree plot (Fig 2).

In order to understand the relationships among the measured traits in mungbean, the data has been diagrammatically displayed in a plot of PC1 and PC2 (Fig 2). It is inferred that the primary two PCAs mainly distinguish the traits for number of pods per plant, seed yield and pods per cluster as Group A and 100-seed weight as Group B. Similar trend on grouping of characters by multivariate methods has been reported by Sarkar and Kundagrami (2016).

In present investigation the results of hierarchical cluster analysis and PCA confirmed the findings of each other. Principal factor scores (PF scores) for all the 24 genotypes were estimated for all the three PCs. These scores may be utilized to construct precise selection indices based on variability exhibited by each of the principal factor. The genotypes were plotted for PC1 and PC2 which together explained 65.81 per cent variability and included the major grain yield characters (Table 8, Fig 3). Positive side of PC1 indicated the genotypes giving high seed yield, number of pods per cluster, number of seeds per pod, number of

Table 5: Intra and inter cluster average distances among clusters of green gram genotypes following Tochers method.

Clusters	I	II	III	IV	V	VI	VII
I	27.44	173.86	155.27	231.55	160.71	82.02	160.42
II		47.32	95.86	74.11	121.52	82.87	82.92
III			44.61	63.55	101.26	66.92	181.51
IV				20.84	86.40	103.77	164.41
V					25.57	116.22	199.74
VI						0.00	144.59
VII							0.00

Table 6: Mean values for yield and its components in various clusters.

Character	Clusters							Contribution
	I	II	III	IV	V	VI	VII	(%)
Days to 50 per cent flowering	37.71	43.23	41.39	43.33	41.25	44.17	37.17	5.80
Days to maturity	67.29	69.19	69.22	70.75	71.58	70.50	68.00	2.54
Plant height (cm)	54.34	69.58	69.94	60.95	60.25	63.50	60.93	4.71
Number of branches per plant	6.67	9.28	6.09	7.37	5.48	7.50	11.63	28.62
Number of clusters per plant	16.18	10.63	9.91	7.83	13.18	12.13	12.67	23.55
Number of pods per plant	37.13	33.97	30.37	28.42	30.17	33.63	40.50	2.54
Pod length (cm)	7.53	7.08	6.93	6.78	7.32	6.13	7.47	0.72
100-seed weight (g)	5.23	4.59	4.91	4.33	3.82	5.40	4.43	7.97
Number of pods per cluster	5.69	4.54	4.64	4.02	3.97	5.37	4.53	7.97
Number of seeds per pod	11.03	9.55	9.64	9.63	9.23	9.70	9.50	0.00
Seed yield (q/ha)	10.33	7.68	8.00	6.95	7.13	9.37	8.90	15.58

Table 7: Eigen value and percent of total variation for various principal components.

Component	Eigen values	Variance explained (%)	Cumulative (%)
PC1	5.63	51.16	51.16
PC2	1.61	14.64	65.80
PC3	1.43	13.00	78.80
PC4	0.67	6.11	84.91
PC5	0.53	4.80	89.71
PC6	0.40	3.59	93.30
PC7	0.26	2.38	95.68
PC8	0.22	1.99	97.67
PC9	0.12	1.12	98.79
PC10	0.09	0.83	99.62
PC11	0.04	0.39	100.00

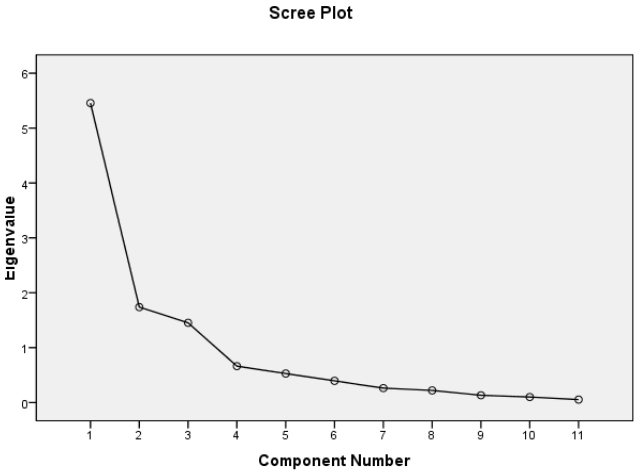

Fig 2: Scree plot showing the Eigen value variation for eleven quantitative traits of mungbean.

Table 8: Factor loadings of nine characters with respect to different PC's (Principal components).

Characters	PC1	PC2	PC3
Days to 50 per cent flowering	-0.782	0.397	0.008
Days to maturity	-0.667	-0.236	-0.128
Plant height (cm)	-0.592	0.439	0.053
Number of branches per plant	-0.073	0.546	0.753
Number of clusters per plant	0.839	-0.338	0.151
Number of pods per plant	0.674	0.251	0.571
Pod length (cm)	0.580	-0.465	0.472
100-seed weight (g)	0.634	0.610	-0.379
Number of pods per cluster	0.881	0.310	-0.251
Number of seeds per pod	0.861	-0.015	-0.199
Seed yield (q/ha)	0.894	0.211	-0.162

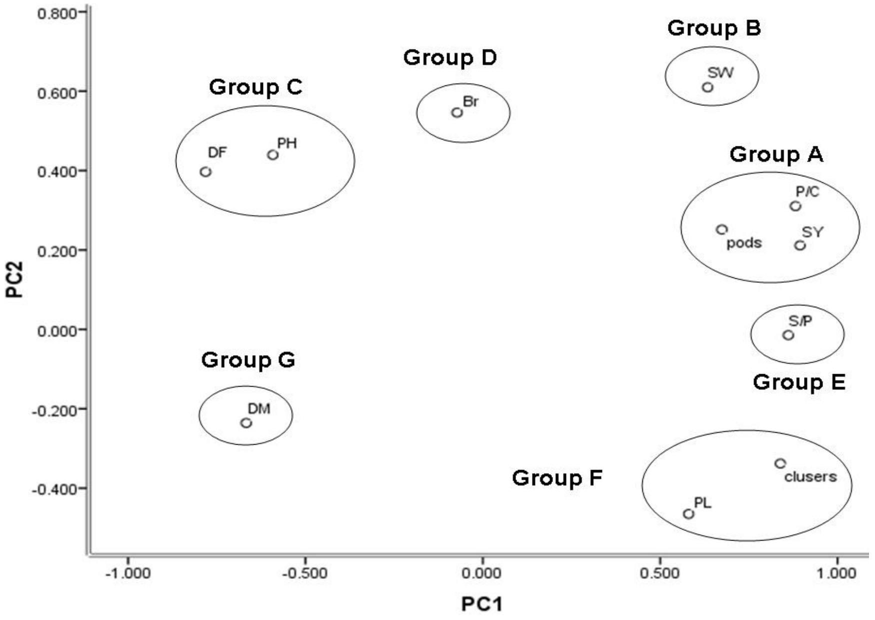

Fig 3: Plot of the first two PCAs indicating relation among various mungbean traits.

DF-Days to 50%flowering, DM-Days to maturity, PH-Plant height (cm), Br-Number of branches/plant, CP- Number of clusters/plant, PP-Number of pods/plant, PL-Pod length (cm), SW-100-seed weight (g), PC- Number of pods per cluster, SP- Number of seeds per pod and SY-Seed yield (q/ha).

clusters per plant, number of pods per plant, 100-seed weight as well as early flowering and maturity and short stature of plant which were indicative as 1 (RMG-492), 8 (RMG-1132), 9 (RMG-1134), 10 (RMG-1137) and 11 (RMG-1138). Similarly, positive values of PC 2 were 2 (RMG-975), 3 (IPM-02-03), 12 (RMG-1139), 18 (MH-318), 19 (MH-421) and 20 (MH-1-25) and these genotypes were combining for 100-seed weight and number of branches per plant. The genotypes 21 (IPM-410-3), 22 (IPM-205-7), 23 (IPM-2-14) and 24 (PDM-139) scored high and positively both for PC1 and PC2 *i.e*. the genotypes giving high yield and yield contributing characters. The grouping obtained in 3-D plot of principal components illustrates the accession distribution in the first three principal components clearly showed the separation of 24 genotypes evaluated (Fig 3). The pattern of clustering obtained with PCA was comparable to the UPGMA based analysis and distinguished the groups clearly and effectively. Also the results of PCA were closely in consonance with those of the cluster analysis. Accessions from diverse group will maximize opportunities to obtain transgressive segregants as there is a higher chance from genotypes to contribute

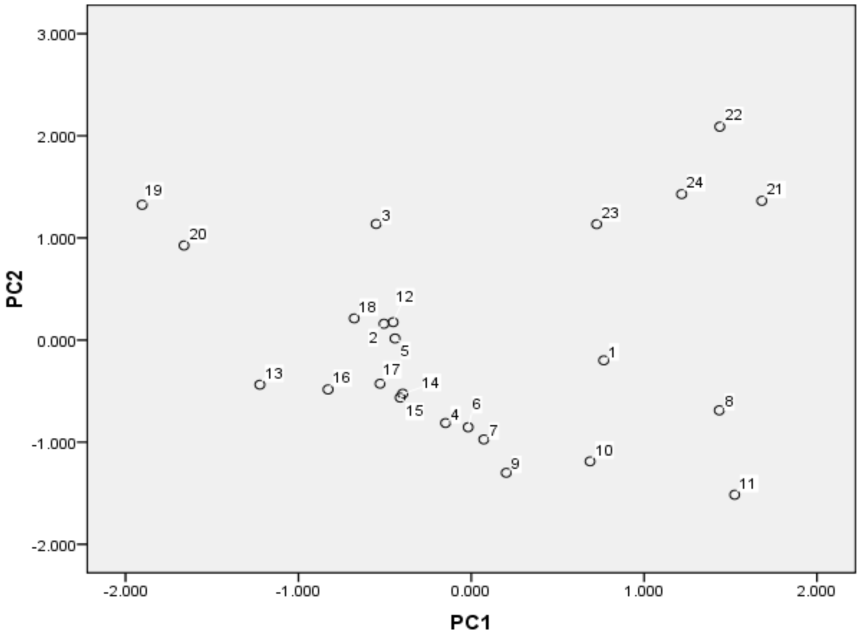

Fig 4: Genotypes plotted for PC 1 and PC 2.

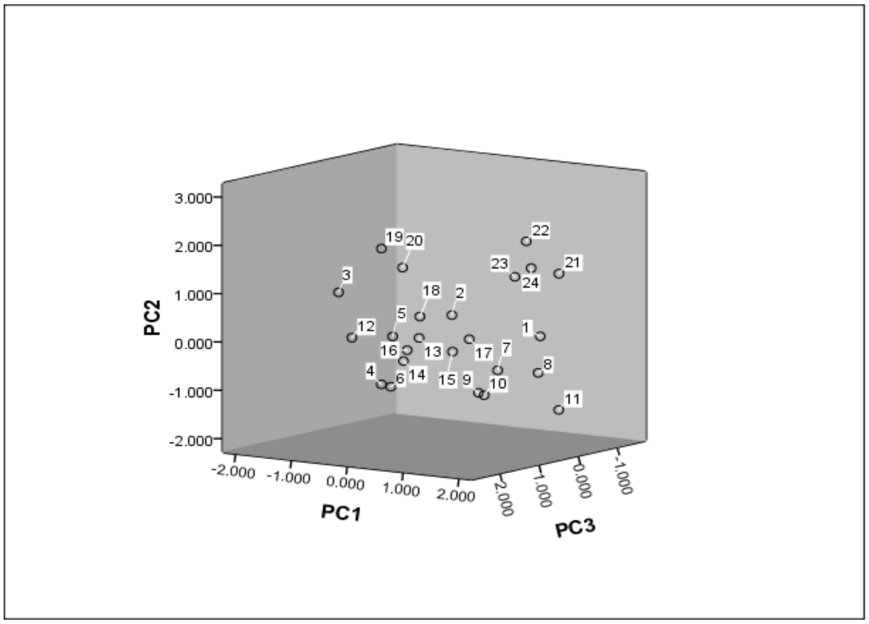

Fig 5: 3 D plot for first three principal component scores.

unique desirable alleles at various loci. These studies also suggest that it was possible to reduce large number of variables into only three principal factors and identify different lines better for different combinations of characters. Hence, indirect selection for seed yield based on component traits may lead to create better genetic recombinants for improving yield and yield attributing characters in mungbean.

REFERENCES

Anonymous. (2019-20). Vital Agriculture Statistics. Directorate of Agriculture, Rajasthan, Jaipur.

Arunachalam, V. (1981). Genetic distance in plant. Indian Journal of Genetics and Plant Breeding. 41: 226-236.

Baisakh, B., Swain, S.C., Panigrahi, K., Das, T.R. and Mohanty, A. (2015). Estimation of genetic variability and character association in micro mutant lines of greengram (*Vigna radiata* L.Wilczek) for yield attrib-utes and cold tolerance. Legume Genomics and Genetics. 7: 1-9.

Beiragi, M.A., Ebrahimi, M., Mostafavi, K., Golbashy, M. and Khorasani, S.K. (2011). A Study of Morphological Basis of corn (Zea mays L.) yield under drought stress condition using Correlation and Path Coefficient Analysis. Journal of Cereals Oilseeds. 2: 32-37

Chaudhary, S., Sagar, P., Hooda, B.K. and Arya, R.K. (2015). Multivariate analysis of pearl millet data to delineate genetic variation. Forage Research. 40 : 201-208.

Dikshit, H.K., Sharma, T.R., Singh, B.B. and Kumari, J. (2009). Molecular and morphological characterization of fixed lines from diverse cross in Munbean [*Vigna radiata* (L.) Wikzek]. Journal of Genetics. 88: 3.

Garg, G.K., Verma, P.K. and Kesh, H. (2017). Genetic Variability, Correlation and Path Analysis in Mungbean [*Vigna radiata* (L.) Wilczek]. International Journal of Current Microbiology and Applied Sciences. 6(11): 2166-2173.

Golbashy, M., Ebrahimi, M., Khorasani, K.S. and Choucan R. (2010). Evaluation of drought tolerance of some corn (*Zea mays* L.) hybrids in Iran. African Journal of Agricultural Research. 5(19): 2714-2719.

Hemavathy, A.T., Shunmugavalli, N. and Anand, G. (2015). Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilezek]. Legume Research. 38 (4): 442-446.

Jakhar, N.K. and Kumar, A. (2018). Principal component analysis and character association for yield components in green-gram [*Vigna radiata* (L.) Wilczek] genotypes. Journal of Pharmacognosy and Phytochemistry. 7(2): 3665-3669.

Joshi, K.D., Khanal, N., Khanal, N.P., Sherpa, L.T. and Giri, R.K. (2003). Promotion of mungbean in rice-wheat system of low hill and Nepal terai. Report of monitoring mungbean in rice-fallow *rabi* cropping project area, April-May, 2003.105-130.

Kaur, S., Bains, T.S. and Singh, P. (2017). Creating variability through interspecific hybridization and its utilization for genetic improvement in mungbean [*Vigna radiata* (L.) Wilczek]. Journal of Applied and Natural Science. 9 (2): 1101 -1106

Mahalanobis, P.C. (1936). On the generalized distance in statistics. Proceedings National Academy of Science India, 249-55.

Mehandi, S., Singh, I.P. Bohra A. and Singh, C.M. (2015). Multivariate analysis in green gram [*Vigna radiate* (L.) Wilczek]. Legume Research. 38: 758-762.

Pandiyan M, Senthil N, Packiaraj D, Thanga Pandian R, Suresh R, Jagadeesh S. **(**2012). Characterization and evaluation of 646 greengram (*Vigna radiate* L.) genotypes for constituting core collection. Wudpecker Journal of Agricultural Research. 1(8): 294-301.

Parsanna, B.L., Rao, P.J.M., Murthy, K.G.K. and Parkash, K.K. (2013) Genetic variability, correlation and path coefficient analysis in mungbean. Environment and Ecology. 31: 1782-88

Rao, C.R. (1952). Advance Statistical Method in Biometrical Research. John Wiley and Sons, Inc. New York.

Sarkar, M. and Kundagrami, S. (2016). Multivariate analysis in some genotypes of mungbean [*Vigna radiata* (L.) Wilczek] on the basis of agronomic traits of two consecutive growing cycles. Legume Research. 39: 523-527.

Singh, C.M., Mishra, S.B., Pandey A. and Arya, M. (2015). Multivariate analysis in mungbean [*Vigna radiata* (L.) Wilczek] to identify the genetic donors for pubescence and agro-morphological traits. Legume Research. 38: 767-771.

Shukla, D.S., Gupta, N.K., Kapashi, S.B., Deshmukh, P.S., Sairam, R.K. and Pande, P.C. (1997). Relationship between stem reserves and grain development in terminal heat stress susceptible and tolerant wheat genotypes. Indian Journal of Plant Physiology. 2:36-40.

Thirumaran, A.S. and Seralathan. M.A. (1988). Utilization of Mungbean. In: S. Shanmugasundaram and B. T. McLean (eds.) Mungbean: Proceedings of the second international symposium, Shanhua, Tainan, Asian Vegetable Research and Development Centre, AVRDC Publication No. 88-304. pp: 470-485.

Yimram, T., Somta, P., Srinives, P. (2009). Genetic variation in cultivated mungbean germplasm and its implication in breeding for high yield. Field Crops Research. 112**:** 260-266.