

Multivariate analysis for study of genetic divergence in mungbean [*Vigna radiata* (L.) Wilczek] genotypes

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ARTICLE INFO	ABSTRACT
Received: 17 October 2022 Revised : 16 January 2023 Accepted : 22 January 2023 Available online: 12 April 2023 Key Words: Cluster analysis Greengram Mahalanobis D^2 PCA Tocher method	Forty mungbean genotypes were evaluated for fourteen quantitative traits, planted in Randomized Complete Block Design with three replications. Mahalanobis' generalised distance D^2 was used to assess the character data and Principal Component Analysis for estimating genetic diversity and identification of superior mungbean genotypes. Following Tocher's technique, the 40 genotypes were divided into 7 clusters in accordance with their genetic distance. Among them four clusters were polygenotypic and three were monogenotypic. The genotypes of cluster IV and VII showed highest (40.51) inter cluster distance followed by cluster III and VII (39.04). Cluster V has been discovered to have the largest intra-cluster distance. In order to increase the genetic diversity of <i>Vigna radiata</i>, genotypes from these clusters may be crossed. Based on Principal Component Analysis results, 5 PCs explained 75.87% of the variation among the 14 parameters and had eigen values greater than unit. Only six genotypes—TJM-37, TJM-134, TJM-140, TJM-235, Shikha, and PM-1632—contained with favourable yield and quality associated PCs, and had outstanding remark for yield traits—out of all genotypes contributing their existence in more than one PC with high PC score. These lines may be used in hybridization programmes to transmit desirable features, such as high yield and high quality, to recipient mungbean genotypes, resulting in the creation of promising cultivars.

Introduction

The mungbean (*Vigna radiata* (L.) Wilczek), which is indigenous to India or the Indo-Burman region, is the third-largest self-pollinated, short-duration grain legume crop, trailing chickpea and pigeonpea. Central Asia is regarded to be the main source of the genetic variety found in mungbeans (Kumar and Kumar, 2014). Mungbean has 22 chromosomes in the 2n set and a relatively modest (579 Mb) genome (Kang *et al.*, 2014). The names greensoy, greengram, greenbean, mashbean, and goldengram are also used to describe it (Markam *et al.*, 2018).

In Asia, mungbean is a vital and reasonably priced source of food protein, especially for the impoverished. It also plays a critical role in lowering protein insufficiency, particularly in developing countries. It is a great option for balanced diets because it contains a lot of readily digestible, high-quality protein (24%) that causes less flatulence and has a high iron level (40-70 ppm) (Vairam *et al.*, 2016). Central Asia is thought to be the main source of mungbean genetic diversity. The majority of the world's greengram

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comes from India, and it is grown in almost every states of India. According to 3rd advance estimates-2021-2022, the overall production of pulses in India to be 27.75 million tonnes. In India, total 2.85mt mungbean productions including 1.48mt in kharif and 1.37mt in *rabi*, accounting for 10% of all pulse production (Directorate of Economics and Statistics, Ministry of Agriculture and Farmers Welfare, 2022). The mungbean crop grows quickly in warm weather, requires little water, and nitrogen fixation provides good soil fertility enhancement (Yagoob and Yagoob, 2014).

Any crop improvement programme must have genetic diversity since it aids in the finding of outstanding segregants and makes their usage and control easier. Divergent lines from diverse, distant clusters are more likely to result in heterotic hybrids or superior offspring than parental lines from the same cluster or cluster with close genetic proximity. To comprehend the useful variation that exists among genotypes, it is crucial to organise or classify them using an appropriate scale. Principle component analysis is a widely used data reduction method. Finding the fewest possible components that could explain the most variability is the goal of principal component analysis (Rahangdale *et al.*, 2021). Given the significance of multivariate analysis, a study was conducted on 40 genotypes of *Vigna radiata* with the aim of analysing yield and yield-related inter-componential variables to gain specific data about the impact of character to genetic variability and to order the genotypes as per PC Score.

Material and Methods

This study was carried out at Breeder Seed Production Unit, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P) during summer season of 2021. Regarding geography and fertility, the trial region was quite uniform. The experimental material consists of 40 genotypes of mungbean obtained from BARC Project- Mutation breeding for mung and urd improvement, were planted in Randomized Complete Block Design with three replications. Each plot was consisted of four rows of two meter length with a spacing 30 cm row to row and 10 cm plant to plant. To record quantitative traits, middle five competitive plants from each plot were randomly selected and recorded the data at specific

growth stage. Days to 50% flowering and days to maturity were recorded on whole plot basis.

Statistical analysis

Utilizing mean values, statistical analysis was performed using INDOSTAT 8.1 and XLSTAT 2021.2.2 software. Mahalanobis' generalised distance D^2 was used to assess the character data. Tocher's method (Rao, 1952) was used to divide the populations into several clusters. In the present investigation, the principal components were extracted using a correlation matrix.

Results and Discussion

Genetic divergence:

The percentage contribution of all the characters towards genetic divergence is graphically presented in figure 1. The trait seed index (78.46%) contributed maximum to the genetic divergence followed by days to maturity, plant height, pod length, number of pods per plant, biological yield per plant, days to flowering, harvest index, number of seed per pod, seed yield per plant, leaf length, number of cluster per plant, number of primary branches. The trait number of pods per cluster had no contribution towards genetic divergence. In contrast to this result the findings of Gokulakrishnan *et al.* (2012) reported seed yield per plant had maximum contribution (63.67%) towards genetic divergence. These results were consonance by the findings of Win *et al.* (2020). The 40 genotypes were divided into 7 groups according to Tocher's technique based on genetic distance (table 1). The cluster I, II, IV and V were poly genotypic, while clusters III, VI and VII were mono genotypic (1 genotype in each). The average intra- and inter-cluster D^2 values determined using INDOSTAT software are shown in table 2, and the cluster mean values of several variables are reported in table 3. The average intra-cluster distance (D^2) values showed that Cluster V had the greatest intra-cluster distance ($D^2 = 10.72$), followed by Cluster IV ($D^2 = 9.62$), Cluster II ($D^2 = 9.58$), and Cluster I ($D^2 = 7.63$). Clusters IV and VII had the greatest intercluster distance ($D^2 = 40.51$) indicating, wide diversity between them and the hybridization between genotypes belonging to cluster IV and cluster VII (Hum-1) may lead to formation of superior recombinants. Findings of Goyal *et al.* (2021) showed highest inter cluster distance in cluster II and cluster IV. Gadakh *et al.*

Table 1: Clustering pattern of forty *Vigna radiata* genotypes as per Tocher Method

Cluster No.	Intra-Cluster Distance	No. of genotypes	Genotypes
I	7.63	10	TJM-37, TJM-111, TJM-160, TJM-236, PDM-11, PDM-139, LGG-460, Shikha, Kanika, Ganga-8
II	9.58	17	TJM-115, TJM-124, TJM-136, TJM-137, TJM-140, TJM-143, TJM-144, TJM-145, TJM-146, TJM-155, TJM-196, TJM-232, SML-668, Virat, MH-421, MH-903, PM-1623
III	0.00	1	TJM-37
IV	9.62	6	TJM-134, TJM-141, TJM-231, TJM-235, Pusa Vishal, Pusa B-51
V	10.72	4	IPM-430-1, PKVAM-4, TM-96-25, Urdi Local
VI	0.00	1	Yellow Mung
VII	0.00	1	Hum-1

Table 2: Average intra and inter cluster distance (D^2) among seven cluster in *Vigna radiata*

Clusters	I	II	III	IV	V	VI	VII
I	7.63	18.39	30.14	31.18	17.07	11.52	12.49
II		9.58	15.34	16.54	13.37	21.42	27.38
III			0.00	8.34	21.04	33.03	39.04
IV				9.62	21.96	33.56	40.51
V					10.72	16.45	23.38
VI						0.00	12.09
VII							0.00

Table 3: Cluster mean values showing performance of different traits

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
DF	42.37	42.71	44.67	42.78	43.67	40.67	43.67
DM	70.77	71.25	73.00	71.11	77.08	76.00	74.67
PH	35.70	35.80	40.00	37.94	42.38	48.00	44.33
LL	9.19	8.96	10.77	8.11	6.83	6.57	10.17
PL	7.40	7.58	7.87	8.36	6.07	7.23	7.17
NPB	2.07	2.25	1.67	2.28	2.92	2.67	2.00
NCPP	7.77	8.00	7.33	6.67	8.67	6.33	7.33
NPPC	4.73	3.92	4.00	4.06	3.58	3.67	4.33
NPPP	27.43	24.14	23.00	22.89	27.58	17.67	29.00
NSPP	10.70	10.86	11.67	10.50	8.50	8.67	9.00
SI	3.44	4.45	5.32	5.31	4.09	3.12	2.83
HI	23.34	21.61	24.71	21.71	27.36	21.31	29.52
BYPP	41.29	40.29	42.40	39.34	22.57	19.47	34.60
SYPP	9.16	8.41	10.47	7.80	6.20	4.13	10.20

DF (days to 50% flowering), DM (days to maturity), LL (leaf length), PH (plant height), PL (pod length), NPB (number of primary branch), NCPP (number of clusters per plant), NPPC (number of pods per cluster), NPPP (number of pods per plant), NSPP (number of seeds per pod), SI (seed index), HI (harvest index), BYPP (biological yield per plant), SYPP (seed yield per plant)

(2013) reported that the genotypes from cluster III and cluster IV may be utilized in hybridization programme as they had highest intercluster distance. Garg *et al.* (2017) reported cluster I and V were highest cluster distance followed by cluster III and VI and cluster II and IV. Cluster mean values showing performance of different characters on particular cluster present in table 3. Cluster I define

high value for number of pods per cluster whereas lowest cluster mean for days to maturity and plant height. Similarly, cluster III and cluster V recorded highest mean values of many yield related traits such as number of seeds per pod, seed index, biological yield per plant, seed yield per plant, number of primary branches and number of cluster per plant. Phenological traits such as days to

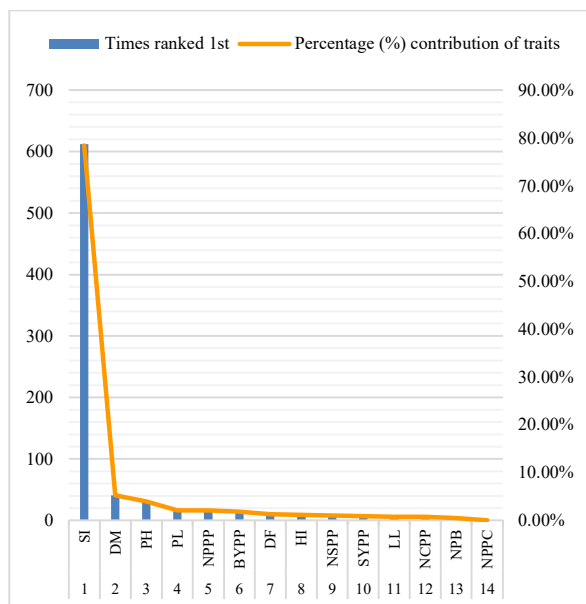


Figure 1: Graphical Representation of Contribution of Different Characters towards Divergence

Notations: SI (seed index), DM (days to maturity), PH (plant height), PL (pod length), NPPP (number of pods per plant), BYPP (biological yield per plant), DF (days to 50% flowering), HI (harvest index), NSPP (number of seeds per pod), SYPP (seed yield per plant), LL (leaf length), NCPP (number of clusters per plant), NPB (number of primary branch), NPPC (number of pods per cluster)

flowering and days to maturity were highest in cluster III and cluster V, respectively. Mostly, yield related traits had lowest performance in cluster VI, consequently, genotypes associated with this cluster may not be used in a hybridization programme as a donor for yield contribution. As per the high mean value of yield related traits recorded on cluster III, IV and V, the genotypes belonging to these clusters can be utilized for improvement in yield through selection for the characters having highest cluster mean values. Gupta *et al.* (2021) reported similar result and these results were also supported by the findings of Gokulakrishnan *et al.* (2012) recorded highest mean value of yield related traits in cluster IV and V.

Variability on the basis of PCA analysis:

Utilizing yield and yield attributing components on greengram genotypes, principal component analysis was carried out. Only five of the forty investigated traits' principal components (PCs) had an Eigen value greater than 1.0 and represented 75.87% of all the cumulative variability among the traits

(figure-2). Among the genotypes under research, the PC1 displayed 26.74% variability, while the PC2, PC3, PC4, and PC5 shown 19.05%, 12.35%, 10.41%, and 7.33% variability, respectively. PC1 exhibited highest eigen value 3.74 which then declined gradually as 2.67, 1.73, 1.46 and 1.03 so on with successive PCs. Out of the eleven PCs, Gupta *et al.* (2021) found that the first three accounted for 78.80% of the overall variation among genotypes for various characteristics. Divyaramakrishnan and Savithamma (2014) reported that, out of twelve PCs, four displayed more than 1.0 eigenvalues and shown a total variability of 63.86% among twelve characters of 374 mungbean germplasm (Fig. 3). According to Fetemeh *et al.* (2012), three factors accounted for about 79% of the total variability among 20 genotypes.

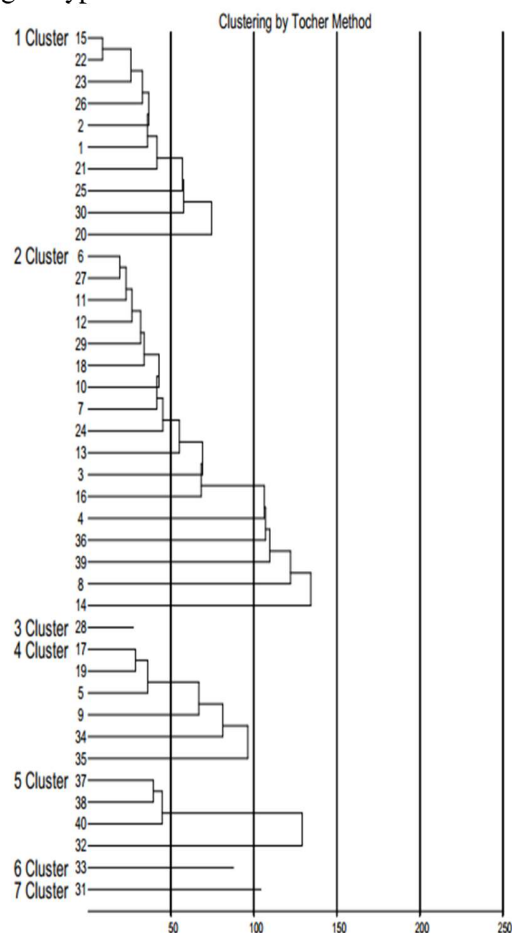


Figure 2: Dendrogram of forty genotypes of *Vigna radiate* based on Euclidean distance using quantitative traits

Rotated component matrix:

Rotated component matrix for fourteen yield attributing traits is depicted in Table 4 and figure 4, represented that the PC 1 which reported maximum variability (26.74%) was associated with yield related traits like number of seeds per pod, biological yield per plant and morphological trait leaf length. The PC 2 was dominated by yield related traits like number of pods per plant, number of clusters per plant, number of pods per cluster and number of primary branch. The PC3 was dominated by phenological traits such as days to flowering, days to maturity, plant height and pod length. The PC 4 contributed to grain quality character seed index. Similarly, PC5 was dominated by seed yield traits like seed yield per plant and harvest index. These findings were in partial consonance with the results of Gupta *et al.* (2021) and Jadhav *et al.* (2021). As per Mahalingam *et al.* (2020), the traits found in the first four PCs—such as pod length, number of seeds per pod (PC 2), number of pods per cluster (PC 3), and single plant yield (PC 4)—were a significant factor in the diversity between germplasm collections.

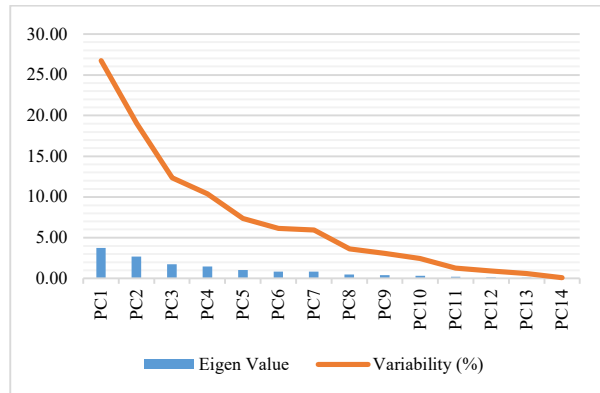


Figure 3: Graphical representation of eigen value and variance percentage of principle component

In this study, the genotypes contributing their presence in more than one principal components and also have >1.5 PC score were selected here for further consideration (table 5). PCA Scores of forty genotypes of *Vigna radiata* is schematically presented in figure 5.

From this study, it was reported that PC2 and PC5 were constituted by most of the yield attributing traits, hence genotypes belonging to these PCs like

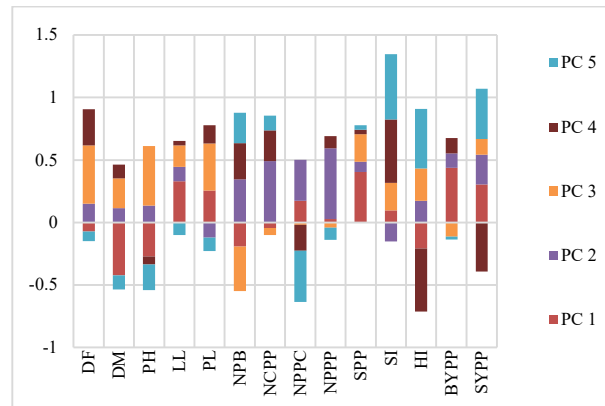


Figure 4: Rotated component matrix for fourteen yield attributing traits of *Vigna radiata*

Table 4: Interpretation of rotated component matrix for the traits having highest value in each PCs

	PC1	PC2	PC3	PC4	PC5
Traits	Number of seeds per pod	Number of pods per plant	Days to 50% flowering	Seed index	Seed yield per plant
	Biological yield per plant	Number of clusters per plant	Days to maturity		Harvest index
	Leaf length	Number of pods per cluster	Plant height		
		Number of primary branch	Pod length		

Table 5: Genotypes selected on the basis of high PC score (>1.5) in each component contributing positive values

PC 1	PC 2	PC 3	PC 4	PC 5
TJM-37	TJM-37	TJM-140	TJM-144	TJM-134
TJM-134	Shikha	GAM-5	TJM-145	PM-1623
TJM-140	Ganga-8	Pusa Vishal	TJM-231	
TJM-146	Virat	Pusa B-51	TJM-235	
TJM-155	TM-96-25	IPM-430-1	Urdu Local	
TJM-196	PM-1623	PKVAM-4		
TJM-232				
TJM-235				
Kanika				
Shikha				

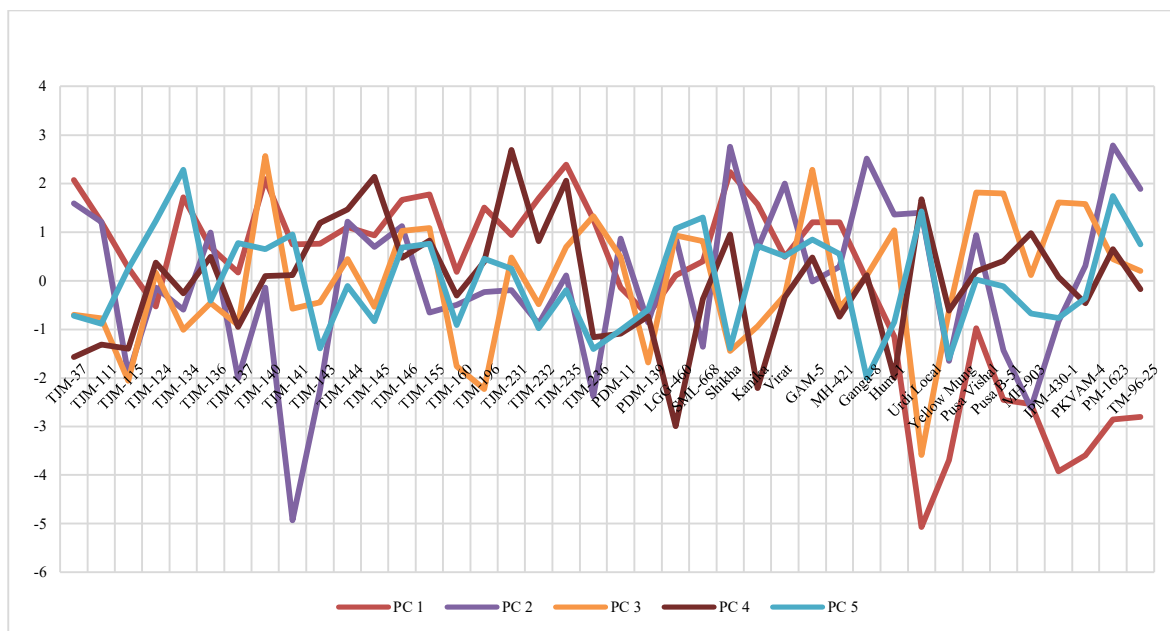


Figure 5: PCA Scores of forty genotypes of *Vigna radiate*

TJM-37, TJM-134, Shikha, Ganga-8, Virat, TM-96-25 and PM-1623 should be used for development of high yielding promising genotypes. Similarly, PC4 reported for the seed quality attributing trait seed index, hence genotypes like TJM-144, TJM-145, TJM-231, TJM-235 and Urdu Local should be selected from these PCs can be utilized for quality improvement programme. Genotypes recorded common share of presence in more than one PCs are TJM-37, TJM-134, TJM-140, TJM-235, Shikha and PM-1632 (table-5). The characters with the most variability are highlighted by PC analysis, it can be concluded. Therefore, rigorous selection techniques can be created to quickly increase yield and quality defining traits.

Conclusion

The trend of grouping generated using PCA was comparable to the analysis based on the Tocher's method and readily and successfully differentiated the groups. Additionally, the results of PCA and cluster analysis were quite comparable. Genotypes from diverse groups will increase the likelihood of obtaining transgressive segregants because different genotypes are more likely to contribute favourable, unique alleles at different loci. Genetic divergence and clustering trend of

forty genotypes of *Vigna radiata* concluded that the genotypes of cluster IV (TJM-134, TJM-141, TJM-231, TJM-235, Pusa Vishal, Pusa B-51) and cluster VII (Hum-1) can be crossed to utilized in hybridization programme as they showed highest inter cluster distance in order to increase the genetic diversity of mungbean. The selection of genotypes on the basis of PCA ranking and contributing their presence in more than one PC dominated with yield and quality traits, the genotypes TJM-37, TJM-134, TJM-140, TJM-235, Shikha and PM-1632 will be selected as donor for improving the yield and yield related trait in mungbean. These studies also suggest that improved genetic recombinants for yield and yield-attributing qualities in mungbean may result via indirect selection for seed yield based on component traits.

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The authors declare no known conflict of interests that could have appeared to influence the work reported in this paper.

Conflict of interest

The authors declare that they have no conflict of interest.

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