Plant Archives Volume 20 No. 2, 2020 pp. 3585-3590 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

PRINCIPAL COMPONENT ANALYSIS FOR YIELD CONTRIBUTING TRAITS IN MUNGBEAN [*VIGNA RADIATA* (L.) WILCZEK] GENOTYPES

Nainu A.J.*, S. Murugan, N. Senthil Kumar And D. John Christopher

Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar - 608 002 (Tamil Nadu), India.

Abstract

In order to determine the relationship and genetic diversity among 81 mungbean accessions a field study was conducted under natural conditions at Bhuvanagiri in Cuddalore district during *Kharif*, 2019. Principal component analysis for various yield contributing traits was done to evaluate diversity and some quantitative traits which had more effects on diversity. The first five components obtained from Principal component analysis (PC1 to PC5) accounted for about more than 78% of the total variation for eleven quantitative traits. Out of total principal components retained PC1, PC2, PC3,PC4 and PC5 with values of 33.65%, 17.22%, 9.96%, 9.74% and 7.98% respectively. The traits showed maximum percent of contribution towards total genetic divergence includes Percentage of disease infection (44.41), single plant seed yield (33.15%) and number of pods per plant (10.37%). Based on PCA the extent of genetic divergence showed that these genotypes could be categorized into nine discrete groups/clusters. Their inter and intra-cluster distance displayed genetic diversity between different genotypes. The Genotypes IC398746, EC398953, EC396419 and PLM506 represents the mono genotypic cluster which indicates that it could be the most diverse genotypes from others. The clustering of mungbean genotypes based on different yield attributing traits would be valuable to recognize the hopeful genotypes for effective utilization in forthcoming breeding programmes. The results of principal component analysis revealed that wide genetic variability exists between these mungbean genotypes and suggested their potential value in mungbean yield improvement.

Key words : principle component analysis, genetic divergence, yield, mungbean, PCA.

Introduction

Mungbean [*Vigna radiata* (L.) Wilczek] is extensively cultivated in the southern half of Asia. India is known as the largest producer of mungbean in the world with more than 50 % of the production. An area of 43.0 lakh hectares with annual production of 20.7 lakh tons and an average productivity of 481 kg per hectare based on Annual Report, DPD 2016-2017. Mungbean is considered as one of the important legume crop because of its adaptation to short growing seasons, low water supply, soil fertility conditions, particular crop rotation and crop mixtures (Baldev, 1988; Sadaphal, 1988). It ranks third among the pulses grown in India after chickpea and pigeon pea. Mungbean is a good source of proteins in human diets besides it supplies quality food for live stocks (Karuppanapandian *et al*., 2006) and also it improves soil fertility by fixing the atmospheric nitrogen. Even though it has high economic importance, the productivity of mungbean remains low due to various biotic and abiotic stresses such as disease, insects, drought, high temperature, salinity and heavy metals. Yellow Mosaic Virus disease is considered as a major threat to mungbean which can cause 85% of yield loss. It is essential to break the yield barriers to meet out the ever-increasing demand for mungbean by developing high yield and biotic/abiotic stress resistant varieties. Yield is an intricate character which is manipulated by several characters. These dependent characters are again interrelated with each other. Improvement of yield is only possible through selecting crops based on yield dependent traits which show a complex chain of relationships. These traits are highly influenced by the environmental conditions also.

Principle component analysis and cluster analysis

Author for correspondence : E-mail: nainutitus@gmail.com

helps in parental selection and genetic diversity identification. More information about genetic diversity aids a breeder to execute targeted and precise hybridization (Jain and Patel, 2016). Generally, parents with maximum genetic divergence are crossed to obtain the most responsive for genetic improvement (Arunachalam, 1981). In recent times many authors cited PCA for the reduction of multivariate data into a few artificial strains which can be further utilized for sorting materials. This method is particularly valuable for screening large number of genetic resources by a large number of descriptor variables (Beiragi *et al*., 2001 and Golbashy *et al*., 2010). Principal component analysis (PCA) can be used to reveal similarities between variables and classify the genotypes, while on the other hand cluster analysis is involved with classifying previously unclassified materials (Leonard and Peter, 2009). The conventional technique based on selecting yield attributes needs extensive observation of mature plants but they cannot serve as unambiguous markers (Wrigley *et al*.,1987). Considering all these facts, a study was carried out to assess genetic diversity among mungbean genotypes and the results may help mungbean breeders with new prospects for promoting the production of mungbean with better yield.

Materials and Methods

Experiment site

The experiment was laid out in a Randomized Block Design with three replications during kharif 2019 at Bhuvanagiri, Cuddalore district of Tamil Nadu. Plants were grown in single row with a length of 4 meters and a spacing of 30 X 10 cm. One row of YMV infector line was raised with paiyur-1 after every five test entries in order to estimate the PDI (percentage of disease infection).

Plant material

Experimental plant material includes 81 mungbean genotypes in which 45 of them are cultures obtained from NPBGR, New Delhi and the remaining varieties are from National Pulses Research Centre, Vamban. Five competitive plants were selected to record data on eleven traits *viz.*, Days to 50% flowering, Plant height (cm), Number of primary branches per plant, Number of clusters per plant, Number of pods per cluster, Number of pods per plant, Pod length (cm), Number of seeds per pod, Percentage of disease infection, Hundred seed weight (g), Single plant seed yield (g).

Methods

The standardized values obtained were used to evaluate the genetic divergence using cluster analysis-PCA-based techniques with INDOSTAT computer software. In PCA the reduction is achieved by linear transformation of the original characters into a set of uncorrelated variables known as Principal components (PCs). Eigen roots and eigenvectors were also computed for various principal components.2D and 3D Plots were drawn using the first two principal components to distinguish the most diverse accessions in different clusters.

Results and Discussion

PCA analysis

Principal component analysis (PCA) signifies the importance of the major contributor to the total variation at each axis of distinction (Sharma, 1998). It evaluates the significance and contribution of each factor to total variance whereas each coefficient of proper vector shows the degree of contribution of every original variable with each principal component it is related. The results of PCA explained the genetic diversity of the eighty one genotypes under study. Five principal components (PC1 to PC5) were extracted from the original data accounting for more than 78% of the total variation. Suggesting these five principal component scores might be used to review the

Table 1: The eigen value, per cent variance and percent cumulative variance for five principal components (PCs) and factor loading between PCs and traits studied in mungbean.

	PC1	PC2	PC3	PC4	PC5
Eigen Value (Root)	3.7	1.89	1.1	1.07	0.88
% Var. Exp.	33.65	17.22	9.96	9.74	7.98
Cum.Var.Exp.	33.65	50.87	60.83	70.57	78.55
Traits	Factor loadings				
DFF	0.216	0.106	0.014	0.807	0.012
PH	0.210	0.450	-0.320	0.022	-0.128
NPB.P	0.440	-0.098	0.117	0.066	-0.047
NCPP	0.417	-0.021	0.057	0.053	0.116
NPPC	0.272	-0.366	0.333	-0.385	-0.050
NPPP	0.392	-0.344	0.083	0.130	-0.169
PL	0.235	0.407	0.144	-0.328	0.104
NSPP	0.253	0.513	-0.015	-0.190	0.058
PDI	-0.223	0.162	0.248	0.027	-0.865
100SW	0.067	-0.263	-0.812	-0.156	-0.164
SPSY	0.375	-0.008	-0.144	-0.093	-0.384

DFF-Days to 50% flowering, PH- Plant height (cm), NPB.P- Number of primary branches per plant, NCPP-Number of clusters per plant, NPPC-Number of pods per cluster, NPPP-Number of pods per plant, PL-Pod length (cm), NSPP-Number of seeds per pod, PDI-Percentage of disease infection, 100SW-Hundred seed weight (g), SPSY-Single plant seed yield (g).

original eleven variables in any further analysis. Correspondingly, Pandiyan *et al*., (2012) showed that 63.79% variation was justified by the first 3 principal components for 18 quantitative and 37 qualitative characters of 646 mungbean accessions subjected to multivariate analysis. Out of total principal components maintained PC1, PC2, PC3, PC4 and PC5 with values 33.65%, 17.22%, 9.96%, 9.74% and 7.98% (Table 1 and Fig. 1) respectively were contributed more to the total variation. Chahal *et al*., (2002) proposed that attributes with lower absolute value closer to zero influence the clustering less than those with largest absolute value closer to unity within the first principal component.

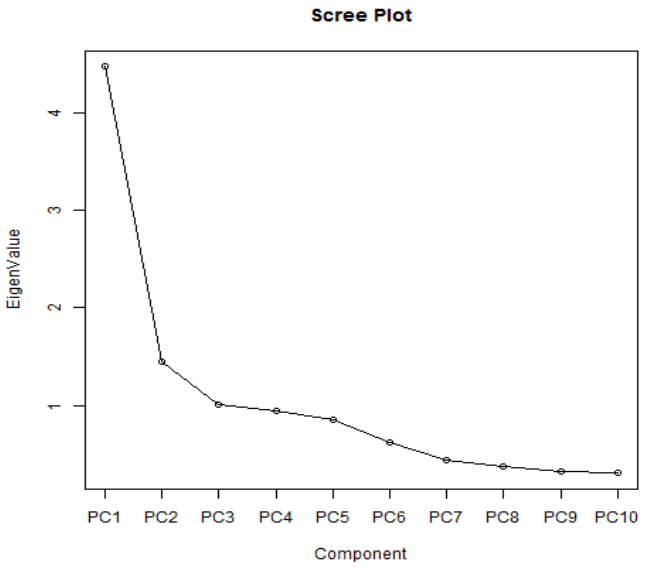

Fig. 1: Scree plot showing Eigen value variation.

The first principal component contributed maximum towards variability (33.65%). Characters *viz.*, Number of primary branches per plant (0.440), Number of clusters per plant (0.417), number of pods per plant (0.392), yield per plant (0.375) and number of pods per cluster (0.272) explained the maximum variance in first principal component (PC1). This suggest that this component reflects high number of primary branches per plant and clusters per plant of each accession. Similar results were obtained by Mehandi *et al.*, (2015) with the study of twenty one mungbean genotypes and reported that PC1 was positively contributed by short plant height and number of seeds per pod. The second principal component (PC2), which described 17.22 per cent of the total variance reflected significant loadings of number of seeds per pod (0.513) and pod length (0.407) which were positively correlated. This suggest that this component indicates high number of seeds per pod and pod length for each accession. The third principal component (PC3) was categorized clearly by negative high loading of hundred seed weight (-0.812) followed by positive number of pods per cluster (0.333). The traits which load positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters. Similarly, the traits which load positively or negatively in PC4 and PC5 affected more to the diversity and they were the ones that most distinguished the clusters.

The PCA scores for 81 genotypes in the first three principal components with eigen value more than one

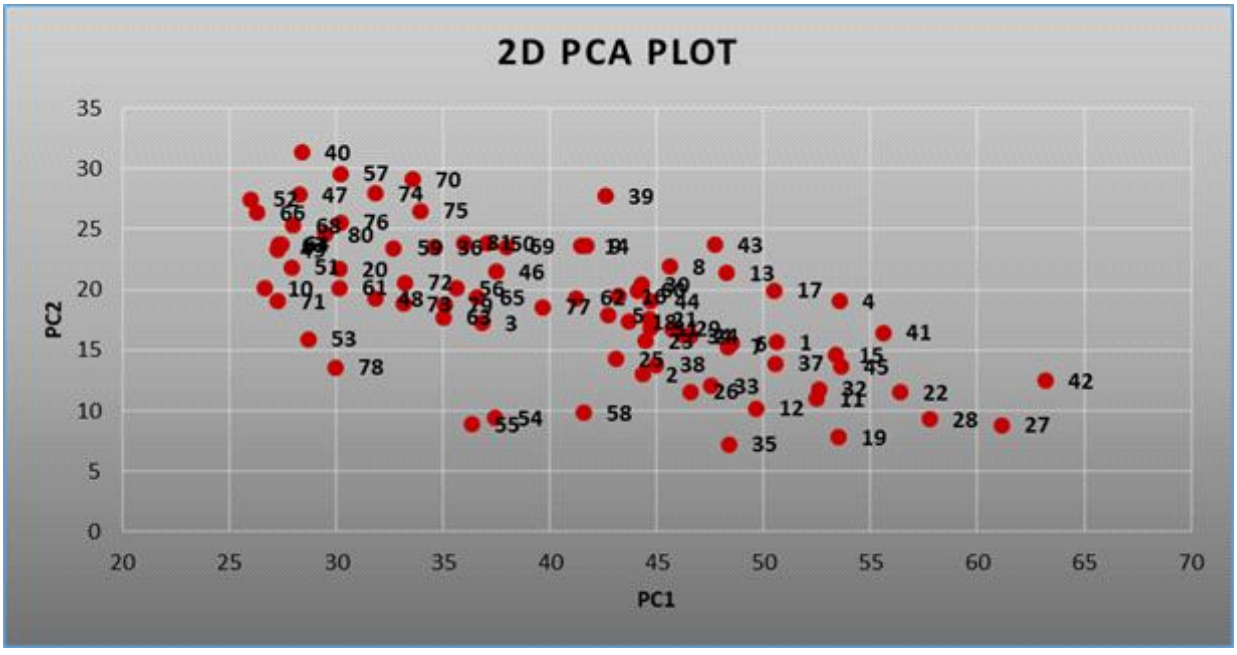

Fig. 2: Two-dimensional graph showing relative position of genotypes of mungbean based on PCA scores.

Table 2: The PCA scores of genotypes of 81 genotypes of mungbean (*Vigna radiata* (L.) Wilczek).

Genotype	PC1	PC2	PC3	Genotype	PC1	PC2	PC3
PLM634	53.768	18.268	-15.685	EC398881	62.28	14.345	-29.44
PLM776	45.26	18.845	-22.349	EC398953	52.368	26.897	-29.08
IC76417	38.973	21.286	-13.853	EC396419	49.846	29.817	-13.203
IC76381	57.307	22.886	-21.325	IC119020-2	54.269	17.065	-24.729
PLM350-1	43.492	21.558	-11.413	VBN 1	38.209	23.762	-16.905
IC76361	45.117	20.602	-21.281	AKM0503	27.59	28.284	-10.493
IC76322	48.807	18.429	-9.696	POM 262	29.78	21.84	-10.376
IC76441	49.474	25.22	-16.506	CO 9016	26.163	25.751	-4.97
PLM188	42.618	26.015	-23.61	UTKARSH	37.878	27.008	-16.564
IC76477	28.453	24.485	-5.208	AKM 1507	27.446	24.298	-9.393
IC39563	48.12	13.185	-21.754	TARM 2	30.503	27.588	-12.821
PLM746	46.944	14.289	-17.149	K 851	30.543	14.959	-15.142
1C76491	50.156	20.797	-18.788	NIRMAL 465	36.287	10.419	-24.158
PLM232	46.799	27.459	-7.199	CO 7	35.364	13.828	-19.505
PLM420	50.719	18.285	-16.39	VRM 1	36.689	18.869	-19.427
PLM858	42.456	22.993	-13.712	ADT-3	29.996	31.038	-13.165
PLM506	60.018	22.241	-24.932	CO 6	40.085	9.291	-25.467
PLM350-2	42.469	21.65	-20.648	VBN 3	33.683	23.539	-13.306
IC119020-1	55.486	14.585	-23.414	CO 8	41.415	23.296	-20.745
PLM614	31.179	26.873	-3.632	AKM 1502	27.709	21.753	-12.95
IC121233	52.749	22.571	-16.346	AKM 4	41.666	20.965	-24.31
PLM475	52.026	15.615	-20.389	AKM 8803	33.874	17.436	-22.055
IC314804	44.979	20.204	-16.267	KAMBAM	27.177	25.991	-10.284
IC398746	46.907	22.503	-6.053	PUSA VISHAL	38.483	21.861	-20.057
IC102913	41.297	15.487	-20.784	TAP 7	29.443	27.025	-13.969
IC546476	45.803	17.179	-19.263	MAYILADUDURAI	27.841	26.059	-10.024
PLM490	57.289	14.279	-20.731	VIRUDHUNAGAR	28.365	27.748	-8.589
IC282110	60.235	15.661	-23.863	IPM99 125	39.443	25.955	-20.609
IC314919	43.385	20.726	-15.073	K 17 2	33.295	27.163	-13.302
IC282095	47.17	26.782	-11.153	K 17 3	32.454	17.806	-17.123
IC148401	47.505	23.669	-13.982	KM 2	33.392	18.698	-18.044
IC565301	49.122	16.202	-24.666	ADT 2	28.998	19.296	-11.551
IC148403	43.114	14.967	-18.449	VAIBHAV	33.01	28.51	-16.253
IC75200	44.066	24.091	-12.237	CO 4	37.029	26.912	-13.617
IC148423	43.111	10.63	-21.773	VBN 2	27.831	24.753	-14.466
IC148419	39.573	31.066	-2.707	VRMGG 1	40.874	21.445	-24.747
IC149428	50.873	20.732	-15.911	K 17 1	32.565	11.066	-20.076
IC314291	41.864	16.094	-13.246	KM 1	36.013	18.712	-19.604
EC398952	49.364	28.032	-17.322	ML 5	27.302	24.651	-17.825
EC398413	36.277	32.968	-9.799	PAIYUR	35.22	22.74	-18.486
EC398893	56.042	18.197	-26.239				

were computed and presented in table 2. Likewise, Ghafoor *et al*., (2001) in his studies taken first four components of PCA with eigen values >1 contributed 78.7 percent of the total variance amongst 40 mungbean genotypes. The PCA scores for 81 genotypes plotted in graph to get the 2D (PCA I as X axis and PCA II as Y axis) and 3D (PCA I as X axis, PCA II as Y axis and PCA III as Z axis) scatter diagram (Fig. 2 and Fig. 3). PCA score of traits which contributes maximum towards percentage of disease infection (44.41%) followed by

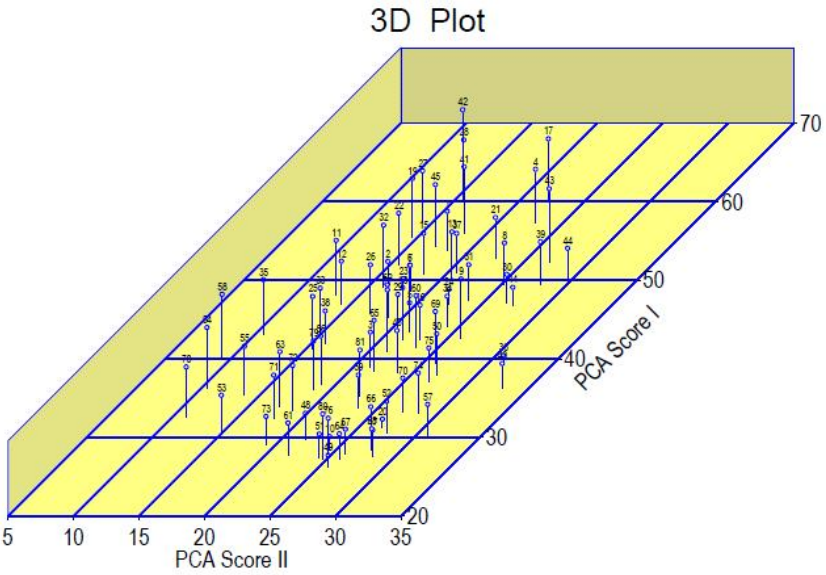

Fig. 3: Three-dimensional graph showing relative position of genotypes of mungbean based on PCA scores.

Table 3: Per cent contribution of 11 characters towards total genetic divergence.

S.No.	Characters	Contribution %
1	Days to 50% flowering	0.62%
2	Plant Height(cm)	0.15%
3	Number of primary branches	0%
4	Number of clusters per plant	0.25%
5	Number of pods per cluster	0%
6	Number of pods per plant	10.37%
7	Pod length(cm)	6.36%
8	Number of seeds per pod	0.15%
9	Percentage of diseases infection	44.41%
10	Hundred seed weight(g)	4.54%
11	Single plant seed yield(g)	33.15%

single plant seed yield (33.15%) (Table 3). On PCA based clustering, 81 genotypes were grouped into 9 clusters in which maximum number of genotypes were fall in cluster 2 (30 genotypes) followed by cluster 1 (21 genotypes), whereas clusters 5,7,8 and 9 were solitary clusters specified to be more diverse from other clusters (Table 4). Inter and intra cluster distance between different genotypes were showed in table 5. On PCA based Tocher's method, the maximum intra-cluster distance was obtained for cluster 4 (438.31) followed by cluster 3 (398.54**)** while the highest inter cluster value was found between cluster 1 and 9 (3074.17) followed by cluster 2 and 9 (2182.47). This result proposes that genotypes in clusters which are separated by high statistical distance should be utilized in potential hybridization programmes.

Table 4: Clustering patterns of mungbean genotypes on the basis of PCA based clustering.

Cluster	Number of Genotypes	Name of the Genotypes
Cluster –I	21	MAYILADUDURAI, VIRUDHUNAGAR, KAMBAM, AKM 1507, POM 262, AKM 0503, IC76477, AKM 1502, ADT 2, CO 9016, VBN 2, TAP 7, VAIBHAV, PAIYUR, K 17 2, VBN 3, TARM 2, ADT 3, VBN 1, ML 5, KM 1
Cluster- II	30	AKM 4, VRMGG 1, PLM 188, PLM 350-2, PLM 776, C0 8, IC76361, IPM 99 125, UTKARSH, PUSA VISHAL, AKM 8803, IC314804, IC102913, IC314919, IC76417, IC546476, PLM746, IC565301, NIRMAL465, IC39563, IC148403, C07, IC148423, PLM475, IC149428, IC148401, PLM 858, VBN 3, PLM350-1, IC75200
Cluster –III	12	IC119020-1, IC1190202, IC282110, EC398881, EC398893, PLM490, IC76381, IC76441, IC76491, PLM420, IC282095, PLM 634
Cluster –IV	10	K851, K 17 1, K 17 3, VRM 1, KM2, CO4, IC314291, IC76322, IC148419, PLM641
Cluster–V	1	IC398746
Cluster- VI	4	ICI21233, EC398952, PLM232, EC398413
Cluster-VII	1	EC398953
Cluster-VIII	1	EC396419
Cluster-IX	1	PLM 506

Table 5: Inter and Intra Cluster Distances.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	227.87	778.71	1519.82	498.68	832.97	1311.54	1341.28	1358.48	3074.17
II		295.75	698.01	956.22	606.44	1658.46	851.80	804.36	2182.47
III			398.54	1242.66	546.44	1211.60	594.67	835.43	963.36
IV				438.31	736.10	816.96	1077.65	1356.48	2263.99
V					0.00	898.95	993.93	858.92	1482.35
VI						393.61	845.84	1333.42	1157.13
VII							0.00	535.15	992.82
VIII								0.00	1785.50
IX									0.00

A broad range of variation among the segregants can be obtained. Similar results were attained by Suhel *et al*., (2015) and Thippani *et al*., (2017). The genetic variability present among the tested genotypes suggests the presence of outstanding prospects to bring development to crop through wide hybridization by crossing genotypes with high genetic distance.

References

Annual Report, D.P.D. (2016-17). Directorate of Pulses Development, Ministry of Agriculture and Farmers Welfare, Government of India. DPD/Pub/TR/19/2016-17.

Arunachalam, V. (1981). Genetic distance in plant. *Indian J. Genet.*, **41:** 226-236.

Baldev, B. (1988). Cropping patterns. In *Puke Crops (Grain Legumes)*, 513-557. Eds B Baldev, S Ramanujam and H K Jain. Oxford and IBH Publishing Co. Pvt Ltd.

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

Chahal, G.S. and S.S. Gosal (2002). Principles and Procedures of Plant Breeding: Biotechnological and Conventional Approaches. *Alpha science international*, 604-646.

Ghafoor, A.A., Z. Sharif, M.A. Ahmad, Zahid and A.A. Rabbani (2001). Genetic diversity in black gram (*Vigna mungo* (L.) Hepper). *Field Crops Res.*, **69:** 183-190.

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

Jain, S.K. and P.R. Patel (2016). Genetic diversity and principle component analyses for fodder yield and their component traits in genotypes of forage sorghum (*Sorghum bicolor* L. Moench). *A. Ar. Zone*, **55:**17-23.

Karuppanapandian, T., T. Karuppudurai, P.B. Sinha, H.A. Kamarul and K. Monoharan (2006). Genetic diversity in greengram [*Vigna radiata* (L.)] landraces analysed by using random amplified polymorphic DNA (RAPD). *African J. Biotech.*, **5(13):** 1214-1219.

Leonard, K. and R.J. Peter (2009). Finding Groups in data: An Introduction to cluster Analysis, 344.

Mehandi, S., I.P. Singh, A. Bohra and C.M. Singh (2015). Multivariate analysis in green gram [*Vigna radiata* (L.) Wilczek] *Legume Research*, **38(6):**758-762.

Pandiyan, M., N. Senthil, D. Packiaraj, R. ThangaPandian, R. Suresh and S. Jagadeesh (2012). Characterization and evaluation of greengram (*Vigna radiata* L.) genotypes for constituting core collection. *Wudpecker J. of Agri. Res.*, **1(8):** 294 –301

Sadaphal, M.N. (1988). Agronomy of pulses. In *Pulse Crops (Grain Legumes)*, 456-512.

Sharma, J.R. (1998). Statistical and biometrical techniques in plant breeding. *New Age International*, New Delhi, 432.

Mehandi, S., I.P. Singh, A. Bohra and C.M. Singh (2015). Multivariate analysis in green gram [*Vigna radiata* (L.) Wilczek]. *Legume Res.*, **38(6):** 758-762.

Thippani, S., K.B. Eshwari and M.H.V. Bhave (2017). Principal component analysis for yield components in Greengram Accessions (*Vigna radiata* L.). *Int. J. Pure App. Biosci.*, **5(4):** 246-253.

Wrigley, C.W., I.L. Batey and J.H. Skerrilt (1987). Complementing traditional methods of identifying cereal varieties with novel procedures. *Seed Sci. Technol.*, **15:** 679-688.