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Principal component analysis and character association for yield components in greengram [*Vigna radiata* (L.) Wilczek] genotypes

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Abstract
The present investigation was carried out to determine the relationship and genetic diversity among thirty greengram germplasm accessions using principal component analysis for various quantitative traits. Principal component analysis (PCA) depicted that four components (PC1 to PC4) accounted for about more than 90% of the total variation for different traits. Out of total principal components retained PC1, PC2, PC3 and PC4 with values of 44.15%, 24.23%, 13.82% and 9.285 respectively. Biological yield (29%), seed index (28%) and plant height (17%) showed maximum percent contribution towards total genetic divergence. PCA based clustering showed that genotypes fall in to six different groups/clusters and their inter and intracluster distance showed genetic diversity between different genotypes. The Genotype G-04 which represents the mono genotypic cluster signifies that it could be the most diverse from other genotypes and it would be the suitable candidate for hybridization with genotypes present in other clusters to tailor the agriculturally important traits and ultimately to enhance the seed yield in green gram. Thus the results of principal component analysis revealed, wide genetic variability exists in this greengram germplasm accessions.

Keywords: principal component analysis, greengram, genetic diversity

Introduction
Mungbean/greengram [*Vigna radiata* (L.) Wilczek], one of the important grain-legume crops ranks third among the pulses grown in India after chickpea and pigeon pea. Being a leguminous crop, it is a good source of proteins in human diets along with providing quality food for livestocks (Karuppanapandian *et al.*, 2006) [5]. India alone accounts for 65% of its world acreage and 54% of the production. In India, production of pulses is around 13.5-15 million tonnes during the last decade, while annual domestic demand is 18-19 million tonnes. The yield of pulses has remained virtually stagnant for the last 40 year (539 kg/ha in 1961 to 544 kg/ha in 2001 to 651 kg/ha in 2013-14). India is short of supply by 2 to 3 million tonnes annually (Agropedia, 2015-16). In India, it is cultivated in Maharashtra, Andhra Pradesh, Rajasthan, Orissa, Karnataka and Uttar Pradesh. Greengram contributes 18.07 % of total pulses area and 11.48 % of total pulses production in India. Area, production and productivity of greengram in India are 34.4 lakh ha, 14 lakh tonnes and 406.98 kg/ha respectively. (Iipr.res.in, 2015-16). Mungbean has the potential to make up the gap of protein shortage, but its yield per hectare in the country is still low and there is a need for improvement. Yield, being a quantitative trait is a complex character in any crop. Various morphological and physiological plant characters contribute to yield. These yield contributing components are inter-related with each other showing a complex chain of relationship and also highly influenced by the environmental conditions.

Effective hybridization program between genetically diverse parents will lead to considerable amount of heterotic response in F_1 hybrids and broad spectrum of variability in segregating generations but appropriate selection of the parents is essential to be used in crossing to enhance the genetic recombination for potential yield increase (Islam 2004) [4]. Some appropriate methods *viz.*, factor analysis, cluster analysis and PCA helps in parental selection and genetic diversity identification. The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi 2002) [7]. Recently PCA has been cited by various authors for the reduction of multivariate data into a few artificial varieties which can be further used for classifying material. This approach is especially valuable for screening large number of genetic resources by a large number of descriptor variables (Beiragi *et al*. 2001 and Golbashy *et al*. 2010) [1, 3]. The main objective of this study was to assess the potential genetic diversity and correlation by using cluster analysis-PCA-

based methods for selection of parents in hybridization programme to obtain desirable segregants in advanced generation and to study the genetic parameters attributing to yield. The aim of present study was to to identify better combinations as selection criteria for developing high yielding fine mungbean genotypes. Such type of findings may help mungbean breeders and it could provide new opportunities for promoting the production of mungbean with better yield.

Materials and Methods

In present investigation, Thirty mungbean genotypes (Table 1) were grown following standard cultural practices for evaluation in a randomized block design (RBD) with three replications during *Kharif*- 2015 at the Field Experimentation Centre, Department of Genetics and Plant Breeding, SHIATS, Allahabad with spacing of 30 cm x 10 cm and plot size (0.6m x 2m) 1.2 m^2. Five competitive plants were selected to record data on 12 traits *viz.*, Days to 50% flowering, Days to 50% Pods setting, Plant height (cm), Number of branches per plant, Number of clusters per plant, Number of pods per plant, Pod length (cm), Number of seeds per pod, Days to maturity, Biological yield (g), Seed index (g) and Seed yield per plant (g).

The recorded data were analysed to assess the genetic divergence using cluster analysis-PCA-based methods with INDOSTAT computer software.

Table 1: List of greengram genotypes used in present investigation

S. No	Name of Genotypes	S.No.	Name of Genotypes
1.	RMG-1033	16.	HYM-03
2.	RMG-492	17.	RMG-268
3.	RMG-1004	18.	RMG-975
4.	RMG-1037	19.	RMG-1014
5.	GANGA-08	20.	RMG-1030
6.	RMG-157	21.	RMG-1052
7.	RMG-1010	22.	RMG-1063
8.	HYM-04	23.	RMG-1078
9.	VIRAT	24.	RMG-1062
10.	RMG-976	25.	MSJ-118
11.	RMG-62	26.	RMG-1094
12.	RMG-344	27.	RMG-1096
13.	RMG-1023	28	K-851
14.	G-4	29	MICRO-1008
15.	PDM-139	30.	SAMRAT (CHECK)

Results and Discussion

PCA analysis

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma 1998) [8]. To understand variable independence and balanced weighting of traits, principal component analysis (PCA) was done to estimate effective contribution of different traits on the basis of respective variation (Table 2). Five principal components (PC1 to PC5) which were extracted from the original data and having latent roots greater than one (except PC5) accounting more than 90% of the total variation. Suggesting these principal component scores might be used to summarize the original eight variables in any further analysis of the data. Out of total principal components retained PC1, PC2, PC3 and PC4 with values of 44.15%, 24.23%, 13.82% and 9.285 (Table 2) respectively contributed more to the total variation. According to Chahal *et al*. (2006) [2] traits 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.

Accordingly, the first principal component had positive component loading from days to 50% flowering (0.101), days to 50 % pod filling (0.171), plant height (0.126) and biological yield (0.145) and negative loading for primary branches per plant (-0.412) followed by pod length (0.406) (Table 2). The traits which load positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters. Hence, the major contributing traits for the diversity in the second principal component (PC2) were biological yield (0.493) followed by plant height (0.420). Similarly the traits which load positively or negatively in PC3 and PC4 contributed more to the diversity and they were the ones that most differentiated the clusters.

The PCA scores for 30 genotypes in the first four principal components with eigen value more than one were computed and presented in Table 3. The PCA scores for 30 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. 1 and Fig. 2).

Based on the PCA score trait which contributes maximum towards diversity seed index (29%) followed by biological yield (28%) and plant height (20%) (Table 3 and Fig 3). And based on PCA based clustering, 30 genotypes were grouped into 6 clusters in which maximum number of genotypes were fall in cluster 2 (9 genotypes) followed by cluster 5 (7 genotypes), whereas minimum number of genotypes were in cluster 4 (only 1 genotypes) (Table 4). Inter and intra cluster distance between different genotypes were showed were in (Table 5). On the basis of PCA based Tocher's method, the maximum intra-cluster distance was obtained for cluster 2 (11.003) followed by cluster 1 (10.859) while the highest inter cluster value was found between cluster 3 and 6 (136.929) followed by cluster 1 and 3 (97.868). This suggest that genotypes belonging to clusters separated by high statistical distance should be used in hybridization programme for obtaining a wide spectrum of variation among the segregants. Similar results were obtained in finding of Suhel *et el*. 2015 and Thippani *et el*. 2017 [9].

Table 2: Eigenvectors and eigenvalues of 5 principal components for 12 characters of 30 mungbean/ greengram genotypes

	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector
Eigene Value (Root)	5.330	2.908	1.658	1.113	0.456
% Var. Exp.	44.415	24.233	13.815	9.277	3.796
Cum. Var. Exp.	44.415	68.647	82.463	91.739	95.535
Days to 50% Flowering	0.101	0.349	0.513	0.078	0.491
Days to 50% Pods Setting	0.171	0.376	0.413	0.248	-0.016
Plant Height (cm)	0.126	0.420	-0.357	-0.326	0.273
Primary Branches/ Plant	-0.412	0.088	0.106	0.064	-0.141
Clusters/ Plant	-0.366	-0.040	0.350	0.212	0.039
Pods/ Plant	-0.304	0.369	-0.051	-0.175	-0.042
Pod Length (cm)	-0.406	0.096	-0.029	-0.153	-0.211

Seeds/ Pod	-0.401	0.167	0.005	-0.074	-0.014
Days to 50% Maturity	-0.287	-0.269	-0.151	-0.115	0.773
Seed Index (g)	-0.084	-0.129	0.421	-0.738	-0.113
Seed Yield/ Plant (g)	-0.336	0.213	-0.262	0.354	0.018
Biological Yield (g)	0.145	0.493	-0.182	-0.183	-0.078

Table 3: The PCA scores of genotypes of 30 genotypes of greengram (*Vigna radiata* (L.) Wilczek)

Genotype	PC1 (Vector 1)	PC1 (Vector 2)	PC3 (Vector 3)	PC4 (Vector 4)
RMG-1033	-29.772	36.304	12.044	-10.104
RMG-492	-29.785	36.445	10.112	-8.932
RMG-1004	-30.127	36.672	8.842	-8.744
RMG-1037	-30.507	35.214	12.423	-11.579
GANGA-08	-30.273	35.233	11.227	-10.386
RMG-157	-30.572	35.633	12.561	-10.754
RMG-1010	-28.476	38.463	8.588	-9.446
HYM-04	-29.423	36.397	8.811	-9.589
VIRAT	-28.142	37.211	10.943	-10.660
RMG-976	-27.320	38.509	10.873	-10.533
RMG-62	-29.964	36.610	10.144	-8.363
RMG-344	-29.380	36.985	11.415	-13.893
RMG-1023	-29.866	35.300	11.239	-12.034
G-04	-29.725	31.075	13.866	-9.769
PDM-139	-28.740	36.453	10.355	-8.337
HYM-03	-29.193	36.207	11.433	-10.294
RMG-268	-28.363	35.753	13.663	-11.183
RMG-975	-26.871	38.422	9.763	-10.912
RMG-1014	-35.676	39.935	11.037	-10.138
RMG-1030	-31.252	33.517	12.312	-11.602
RMG-1052	-37.543	39.653	11.434	-10.719
RMG-1063	-27.026	38.205	11.833	-12.530
RMG-1078	-26.414	38.776	9.939	-11.603
RMG-1062	-30.010	35.344	12.425	-9.185
MSJ-118	-29.720	35.087	11.118	-9.238
RMG-1094	-27.175	39.573	9.873	-8.934
RMG-1096	-28.039	38.328	11.488	-12.302
K-851	-27.232	38.842	7.739	-11.220
Micro-1008	-26.197	39.332	9.391	-12.747
Samrat(check)	-28.882	35.439	12.063	-7.682

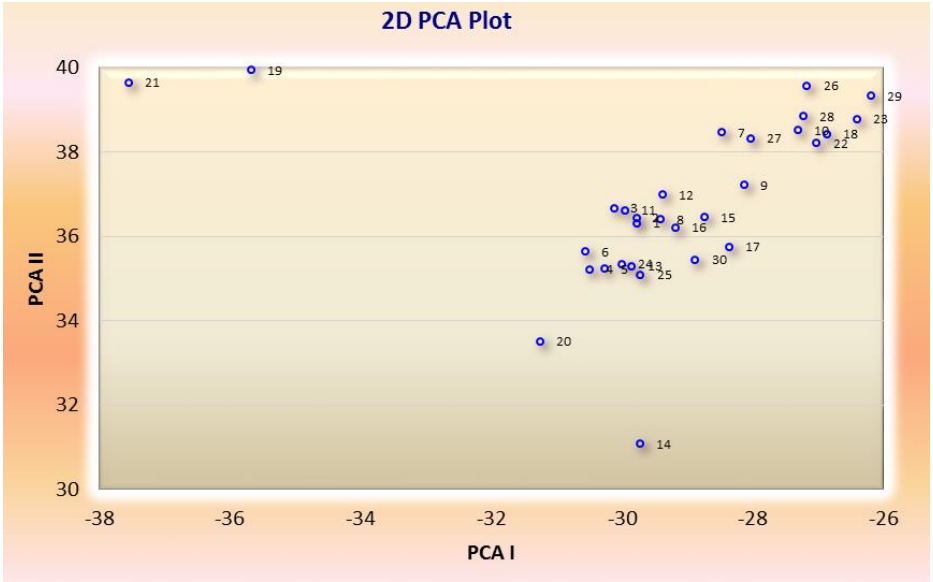

Fig 1: Two dimensional graph showing relative position of genotypes of greengrem based on PCA scores

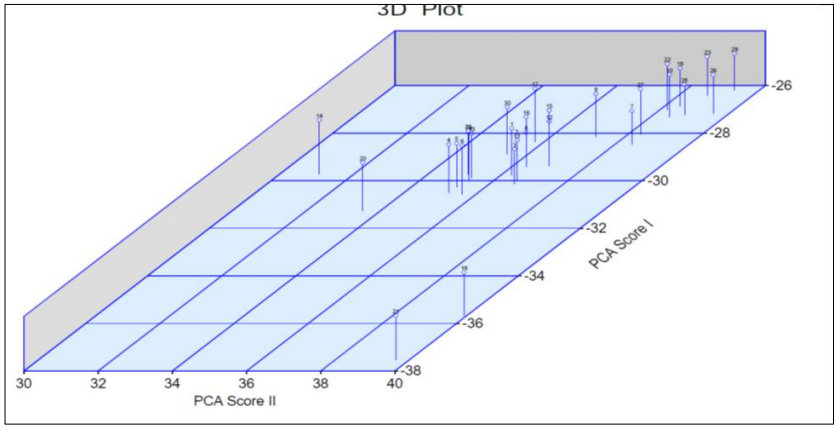

Fig 2: Three dimensional graph showing relative position of genotypes of greengrem based on PCA scores

Table 3 and Fig 3: Per cent contribution of 12 characters towards total genetic divergence

Characters	Times Ranked 1st	Contribution %
1 Days to 50% Flowering	4	0.92
2 Days to 50% Pods Setting	1	0.23
3 Plant Height (cm)	85	19.54
4 Primary Branches/ Plant	25	5.75
5 Clusters/ Plant	4	0.92
6 Pods/ Plant	3	0.69
7 Pod Length (cm)	15	3.45
8 Seeds/ Pod	5	1.15
9 Days to 50% Maturity	21	4.83
10 Seed Index (g)	128	29.43
11 Seed Yield/ Plant (g)	20	4.60
12 Biological Yield (g)	124	28.51

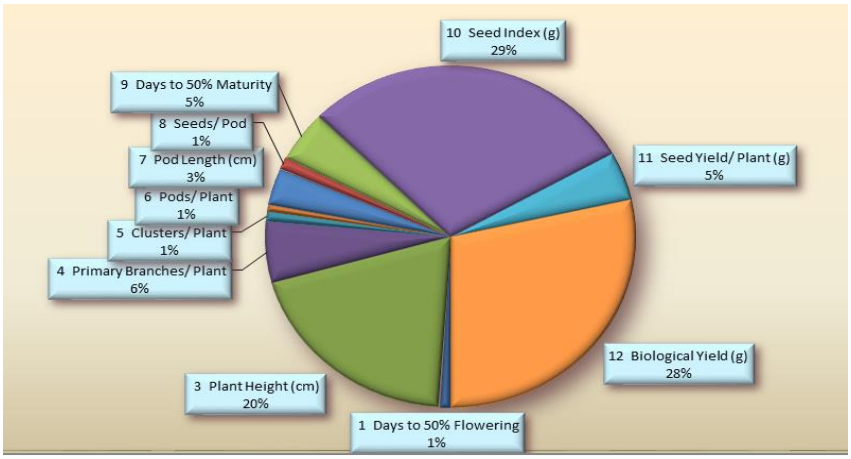

Fig 3: Contribution% towards Divergence

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

Clusters	Cluster Members	Genotypes
1	2	RMG-114 AND RMG-1052
2	9	RMG-1010, RMG- 976, RMG- 975, RMG- 1063, RMG- 1078, RMG- 1094, RMG- 1096, K-851 nad Micro- 1008
3	6	RMG-1033, RMG- 492, RMG-1004, HYM-04, RMG-62 and RMG-344
4	1	G-04
5	7	RMG-1037, GANGA-08, RMG-157, RMG-1023, RMG-1030, RMG-1062 and MSJ-118
6	5	Virat, PDM-139, HYM-03, RMG-268, SAMRAT

Table 5: Inter & Intra Cluster Distances

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	10.859	27.418	97.868	54.356	22.442	86.880
2 Cluster		11.003	72.732	19.064	24.557	36.787
3 Cluster			5.524	74.874	75.608	136.929
4 Cluster				0.000	24.757	14.975
5 Cluster					0.000	61.828
6 Cluster						0.000

Conclusion

There is significant genetic variability among tested genotypes that indicates the presence of excellent opportunities to bring about improvement through wide hybridization by crossing genotypes with high genetic distance. The information obtained from this study can be used to plan crosses and maximized the use of genetic diversity and expression of heterosis.

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