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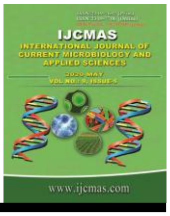

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Principal Component Analysis in Rainfed Green Gram Genotypes [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

The present investigation entitled "Principal component analysis in rainfed green gram genotypes [*Vigna radiata* (L.) Wilczek]" was carried out to determine the relationship and genetic diversity among 16 green gram genotypes using principal component analysis for various characters during *Kharif,* 2019 at Agricultural Research Station, Fatehpur - Shekhawati, Sikar (Rajasthan) under rainfed conduction. Principal component analysis (PCA) depicted that three components (PC1 to PC3) accounted for about more than 90% of the total variation for different characters. Out of total principal components retained V1, V2, V3 and V4 with values of 39.15%, 25.29%, 15.72% and 10.79 respectively. PCA based clustering showed that genotypes fall in to five different clusters showed genetic diversity between different genotypes. The Genotypes MSJ-118 and RMG-1094 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 characters and ultimately to enhance the seed yield in green gram. Thus the results of principal component analysis revealed, wide genetic variability exists in these green gram genotypes. Hence these could be utilized as parental material in future breeding programme for green gram improvement.

Keywords

principal component analysis, green gram, genotypes

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Introduction

Green gram (*Vigna radiata* (L.) Wilczek) is one of the important pulse crops in arid region because of its short growth duration, adaptation to low water requirement and low soil fertility (Raturi *et al*., 2015). It is favored for consumption due to its easy digestibility and low production of flatulence.

Pulses are extensively grown in tropical regions of the world as a major protein rich crop bringing considerable improvement in human diet (Muthuswamy *et al*., 2019 and Rahim *et al*., 2010).

Average protein content in the seed is around 24 per cent. The protein is comparatively rich in the amino acid lysine but predominantly deficient in cereal grains (Baskaran *et al.*, 2009 Garg *et al.*, 2017 and Dhanajay *et al.*, 2009). Presently, the yield of green gram is well below the optimum level compare to other pulses. Green gram (*Vigna radiata* (L.) Wilczek) is one of the chief pulse crops grown in India after chickpea and pigeon pea. In India, green gram is cultivated in 4.26 million ha with a production of 2.01 million tonnes and productivity of 472 kg/ha (AICRP on MULLaRP, 2018-19).

The average yield of green gram is very low not only in India but in entire tropical and sub-tropical Asia (Pratap *et al.*, 2012 and Kumar *et al.*, 2005).Grouping of green gram genotypes based on genetic divergence for different characters will enable breeders for the better selection of parents during hybridization (Tripathi,2019).

In plant breeding, genetic diversity plays an important role because hybrids between genetically diverse parents manifest greater heterosis than those between more closely related parents (Mahalingam *et al.*, 2018). Some appropriate methods *viz.*, factor analysis, cluster analysis and PCA helps in parental selection and genetic diversity identification. 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. 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 identify better combinations as selection criteria for developing high yielding fine green gram genotypes. Such type of findings may help green gram breeders and it could provide new opportunities for promoting the production of green gram with better yield.

Materials and Methods

The present investigation entitled “Principal component analysis in rainfed green gram genotypes [*Vigna radiata* (L.) Wilczek]” was under taken to study the different parameters of divergence. Sixteen genotypes of green gram were sown in randomized block design with three replications during *Kharif*, 2019 at research farm of Agricultural Research Station, Fatehpur-Shekhawati, Sikar (Rajasthan) under rainfed conduction. These genotypes of green gram were obtained from All India Coordinated Research Project on MULLaRP, RARI, Durgapur (Jaipur) is as under:

1.RMG-492	5.RMG-1087	9.RMG-1134	13.RMG-1147
2.RMG-975	6.RMG-1094	10.RMG-1137	14.RMG-1148
3.IPM-02-3	7.RMG-1098	11.RMG-1138	15.RMG-1152
4.MSJ-118	8.RMG-1132	12.RMG-1139	16.RMG-1154

Each genotype was given in a four row plot of 4 m length with a spacing of 30 cm between rows and 10 cm between plants. Ten plants were selected at random from each plot and data were recorded on 8 characters viz., plant height, pod length, number of seeds per pod, Test weight, seed yield per plot and seed yield per hectors whereas for days to 50% flowering and days to maturity data were recorded on whole plot basis.

The data so obtained were subjected to analysis of variance and genetic divergence using cluster analysis-PCA-based methods.

Results and Discussion

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation (Sharma, 1998). To understand variable independence and balanced weighting of characters, principal component analysis (PCA) was done to estimate effective contribution of different characters on the basis of respective variation (Table-1).Three principal components (PC1 to PC3) which were extracted from the original data and having latent roots greater than one 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 V1, V2, V3 and V4 with values of 39.15%, 25.29%, 15.72% and 10.79 (Table-1) respectively contributed more to the total variation. According to Chahal *et al.*, (2002) and Hadavani *et al.*, (2018) characters 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 (V1) had positive component loading from days to 50% flowering (0.528), days to maturity (0.270), pod length (0.191) and no. of seeds per pod (0.449) and negative loading for plant height (-0.428) followed by seed yield per plot (-0.353),test weight (-0.014) and seed yield kg per hectare (Table-1). The characters which load positively or negatively contributed more to the diversity and they were the ones that most differentiated the clusters.

Table.1 Eigenvectors and eigene values of principal components for 8 characters of green gram genotypes

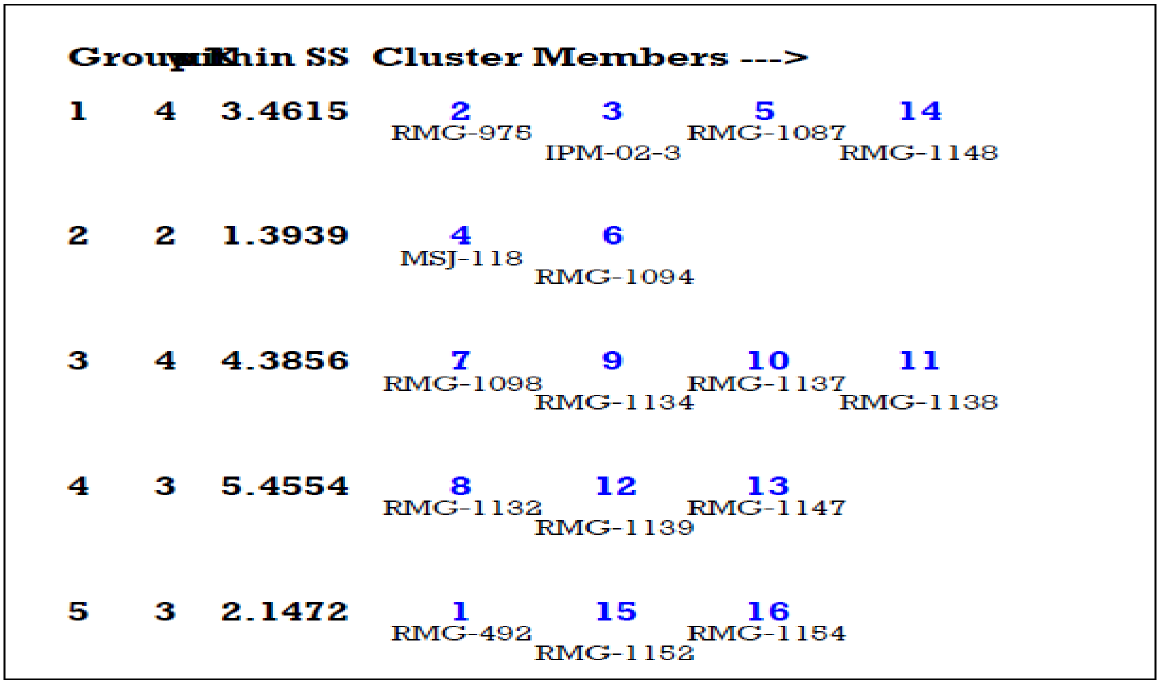
PC **Characters**	**1 Vector (PC1)**	**2 Vector (PC2)**	**3 Vector (PC3)**	**4 Vector (PC4)**
Eigene Value (Root)	3.13230	2.02368	1.25790	0.86395
% Var. Exp.	39.15380	25.29599	15.72374	10.79940
Cum. Var. Exp.	39.15380	64.44978	80.17352	90.97292
1. D50%F	0.52870	0.06268	0.09757	0.17231
2. DM	0.27085	0.28276	0.64504	-0.06027
3. PH (cm)	-0.42871	0.05651	0.40266	-0.27115
4. PL(cm)	0.19186	-0.57640	-0.06372	0.22409
5. No. of S/P	0.44940	0.24967	0.09027	0.34440
6. SY/Plot (g)	-0.35346	-0.20077	0.14473	0.75830
7. TW(g)	-0.01408	-0.45500	0.61164	-0.03680
8. SY(kg/ha)	-0.31530	0.52059	0.07075	0.38464

Table.2 The PCA scores of 16 genotypes of green gram

Genotypes	**PCA I (X Vector)**	**PCA II (Y Vector)**	**PCA III (Z Vector)**
1 | RMG-492	22.846	-10.636	54.930
2 | RMG-975	22.294	-12.615	56.403
3 | IPM-02-3	23.467	-13.328	58.283
4 | MSJ-118	24.342	-13.224	58.531
5 | RMG-1087	22.005	-13.213	57.716
6 | RMG-1094	25.162	-14.678	55.080
7 | RMG-1098	19.406	-12.754	55.639
8 | RMG-1132	17.980	-15.340	60.584
9 | RMG-1134	19.831	-11.219	56.220
10 | RMG-1137	20.192	-13.971	56.584
11 | RMG-1138	19.386	-13.077	56.551
12 | RMG-1139	20.947	-15.390	58.473
13 | RMG-1147	18.470	-16.134	60.325
14 | RMG-1148	22.782	-14.661	59.039
15 | RMG-1152	23.823	-11.891	57.842
16 | RMG-1154	23.619	-12.379	58.908

Table.3 K means clustering for 8 characters of green gram genotypes

K Mean Clustering								
Characters	D50%F	DM	PH (cm)	PL (cm)	No. of S/P	SY/ Plot (g)	TW (g)	SY (kg/ ha)
1 Cluster	40.500	61.667	41.875	7.708	10.667	217.917	32.800	605.323
2 Cluster	42.667	61.167	35.000	7.867	11.833	234.167	32.667	650.458
3 Cluster	37.333	59.833	44.208	7.658	10.833	280.000	30.758	777.774
4 Cluster	38.222	60.889	45.222	8.011	10.611	368.889	33.944	1020.572
5 Cluster	41.778	62.667	41.389	7.533	11.722	222.778	31.356	618.826



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Group  Within SS  Cluster Members --->

1    4   3.4615     2          3          5          14
                  RMG-975             RMG-1087
                             IPM-02-3              RMG-1148

2    2   1.3939     4          6
                  MSJ-118
                             RMG-1094

3    4   4.3856     7          9          10         11
                  RMG-1098            RMG-1137
                             RMG-1134              RMG-1138

4    3   5.4554     8          12         13
                  RMG-1132            RMG-1147
                             RMG-1139

5    3   2.1472     1          15         16
                  RMG-492             RMG-1154
                             RMG-1152
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Figure.1 Clustering of green gram genotypes by K means clustering method

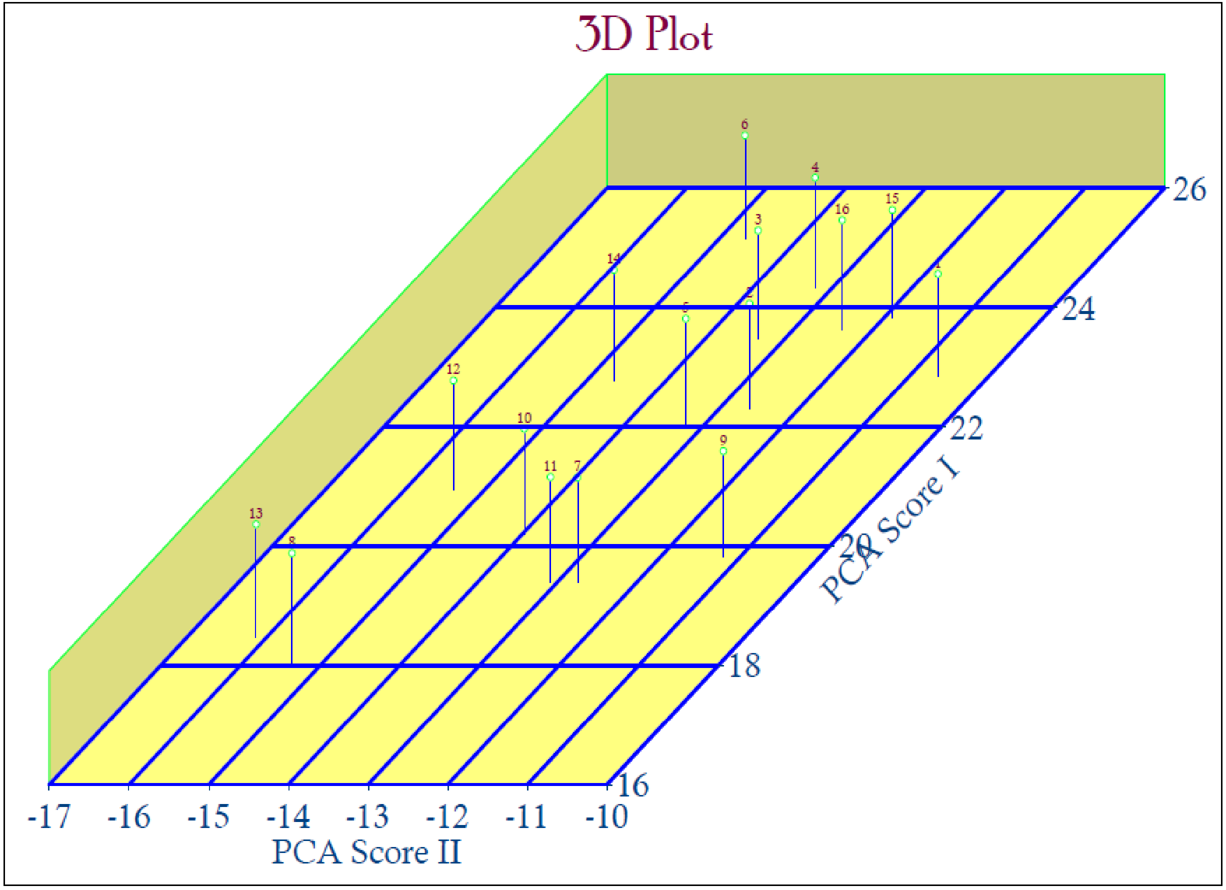

Figure.2 Three dimensional graph showing relative position of green gram genotypes based on PCA scores

Hence, the major contributing characters for the diversity in the second principal component (V2) were days to flowering, days to maturity, plant height, no. of seeds per plant and seed yield kg per hectare (0.062, 0.282, 0.056, 0.249 and 0.520) while pod length, seed yield per plot and test weight (-0.576, -0.200 and -0.455). Only pod length (-0.063) load negative contributed and other characters positive contributed load for third principal component (V3).

Similarly the characters days to flowering, pod length, no. of seeds per pod, seed yield per plot and seed yield kg per hectare (0.172, 0.224, 0.344, 0.758, 0.384) which load positively while days to maturity, plant height and test weight (-0.060, -0.271and -0.036) negatively in fourth principal component (V4) contributed more to the diversity and they were the ones that most differentiated the clusters. Similar results were obtained in finding of Mahalingam *et al.,* (2020) and Thippani *et al.,* (2017).

The PCA scores for 16 genotypes in the first three principal components with eigen value more than one were computed and presented in Table-2. The PCA scores for 16 genotypes plotted in 3D (PCA I as X axis, PCA II as Y axis and PCA III as Z axis) scatter diagram (Fig.-2).

On the PCA based clustering, 16 genotypes were grouped into 5 clusters in which maximum number of genotypes were fall in cluster 1 and 3 (4 genotypes) followed by cluster 4 and 5 (3 genotypes), whereas minimum number of genotypes were in cluster 2 (2 genotypes) (Table-3 and Figure-1). On the basis of PCA, the maximum cluster distance was obtained for cluster 4 (5.455) followed by cluster 3 (4.385), cluster 1(3.461), cluster 5 (2.147) while minimum cluster distance was obtained for cluster 2 (1.393).

These 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 Jakhar and Kumar, 2018 and Thippani *et al.,* 2017.

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. Hence these could be utilized as parental material in future breeding programme for green gram improvement.

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