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Genetic diversity studies for yield and its contributing traits in brinjal (*Solanum melongena* L.) Germplasm using PCA

Praveen P Yankanchi[1]*, Dhanalashmi TN[2], Lakshmana D[1], Prakash K[3], Onkarappa S[3]
[1] Department of Genetics and Plant breeding, College of Horticulture, Mudigere, UAHS, Shivamogga, Karnataka, India
[2] Department of Genetics and Plant breeding, College of Horticulture, Hiriyur, UAHS, Shivamogga, Karnataka, India
[3] Indian Council of Agricultural Research – Krishi Vigyan Kendra, Babbur Farm, Hiriyur, Karnataka, Inida

Abstract
Present experiment was conducted to assess the genetic divergence among brinjal (*Solanum melongena* L.) germplasm along with 3 check varieties in randomized complete block design (RCBD) with two replications by using Principle component analysis (PCA). Assessing and exploitation of existing variability among germplasm is the first principle of breeding on yield and its traits in brinjal. The principle components plant height, number of primary and secondary branches per plant had eigen values >1 and together accounted for 72.40 % of total variation. Genotypes were grouped into 6 clusters based on multivariate analysis and average value which emphasizing the relative contribution of 13 quantitative traits to total variability. The genotypes, R2580, H-9 and A-3 were grouped under cluster IV and were identified as potential donors that could be passed on to breeders for improvement in brinjal fruit yield. Also it indicates the genotypes grouped under this cluster were highly diversified and the genotype can be used for hybridization.

Keywords: genetic diversity, principle component analysis, eigenvalues

Introduction
Brinjal (*Solanum melongena* L.) is most important and popular vegetable crop belongs to solanaceae family and is widely cultivated in India and is considered to be primary center of origin (Vavilov, 1928). This also includes a number of other crop species, in particular Potato, Tomato, Chilli and Tobacco. It is grown in an area of 7.3 lack hectares with the production of 128.01 lack tonnes and the productivity is 17.54 tonnes per hectare (NHB, 2018) [2].

For an effective breeding program, the extent and nature of genetic diversity within a crop species is essential. Genetic diversity study also permits to select the parents having high genetic diversity, used to obtain the desirable recombinant in the segregating generations of brinjal, also helps for successful vegetable improvement especially hybridization programme.

Materials and methods
The present investigation was conducted at College of Horticulture, Hiriyur during *Kharif* season of 2019-20. The investigation consists of 30 brinjal genotypes along with 3 checks carried out in randomized complete block design (RCBD) with two replications.

Tray sowing was carried out in 4th week of August-2019. The seedlings were transplanted to main field after 35 days at a spacing of 60 cm between rows and 45 cm between plants. All recommended cultural practices and plant protection measures were followed and observations were recorded for the traits like plant height (cm), number of primary and secondary branches per plant, days to 50 % flowering, number of flowers per cluster, number of clusters per plant, days to first pick, number of fruits per plant, fruit length (cm), fruit girth (cm), fruit weight (g) and fruit yield per plant (kg).

Statistical analysis
The estimated values of the 13 quantitative traits subjected to statistical analysis. The germplasm in each of the qualitative traits category varied. The means of each of the 12 quantitative traits of the germplasm categorized based on field evaluation. The differences between means of 12 quantitative traits of the germplasm was tested for statistical significance using two-sample 't' test assuming unequal variances to examine the relationship. The following formula was used for calculation of t' statistic (Sokal *et al*. 1995) [4].

$$t' = \frac{\bar{x} - \bar{y} - \Delta_0}{\sqrt{\frac{S_1^2}{m} + \frac{S_2^2}{n}}}$$

Where
X: Mean quantitative traits of the germplasm in the 1st category
Y: Mean quantitative traits of the germplasm in the 2nd category
S^2_1 and S^2_2 are the variences of the quantitative traits of the germplasm in the 1st and 2nd categories 'm' and 'n' are the number of germplasm in each category.
The following formula is used to calculate the degrees of freedom.

$$df = \frac{\left(\frac{S_1^2}{m} + \frac{S_2^2}{n}\right)^2}{\frac{\left(S_1^2/m\right)^2}{m-1} + \frac{\left(S_2^2/n\right)^2}{n-1}}$$

Where,

S^2_1 and S^2_2 are the variences of the quantitative traits of the germplasm in the1st and 2nd categories. 'm' and 'n' are the number of germplasm in each category. The significance of t' statistic was tested by referring to the table t' value at the calculated degrees of freedom. Genetic diversity was assessed in 33 brinjal germplasm using principal components analysis as conceptualized by Pearson (1901) and described by Hotelling (1933) [1]. Adjusted, standardized and uncorrelated quantitative characters were used for Principal component analysis (PCA). Based on first two major principal components which explained maximum variability among the germplasm, a scatter graph was plotted. Based on the scatter plot, germplasm were grouped into different clusters.

Results and Discussion

The present study aimed at determining the genetic divergence of 33 brinjal germplasm for 13 quantitative traits by using Principal component analysis (PCA). PCA transforms a number of correlated variables into a number of uncorrelated variables called principle components. The first principle component accounts for as much of the variation in the data as possible, and each succeeding components depict for remaining portion of variability. The results indicated that PC1 (Plant height) explained 41.20 % of variation, whereas PC2 (number of primary branches per plant) and PC3 (number of secondary branches per plant) explained variations of 22.40 % and 8.80 % respectively (Table 2).

High diversity occurred among genotypes along with strong relationships (Fig. 1) indicated that the distribution of different genotypes were scattered and they were diverse in nature.

Similarly, Ullah *et al*. (2014) used PCA with eigenvalues to explain variation in brinjal genotypes. Maximum numbers of germplasm were grouped into cluster V (9) followed by cluster III (7), cluster I & II (6), cluster IV (4) and cluster VI (1) represented in table 3.

Table 1: Estimates of Mean, t-statistics for yield and its components in brinjal germplasm

SL. No.	Characters	Mean	T-Statistics
01	Plant height (cm)	51.20	-0.133
02	No. of primary branches/plant	4.70	1.434
03	No. of secondary branches/plant	12.22	1.377
04	Days to 50 % flowering	58.69	2.185
05	Number of flowers per cluster	2.89	-2.160
06	Number of clusters per plant	6.58	-0.717
07	Days to first picking	85.64	0.901
08	Number of fruits per plant	11.29	-0.281
09	Fruit length (cm)	10.64	0.470
10	Fruit girth (cm)	8.711	0.445
11	Fruit weight (g)	55.48	0.482
12	Fruit yield per plant (g)	593.18	-0.461
13	Fruit yield per hectare (t)	21.97	-0.461

Table 2: Number of principal components and their Eigen values and contribution to total variability for 13 characters in brinjal germplasm

Principal Components	Eigen values	Percent contribution to total variation (%)	Cumulative percent contribution to total variation (%)
01	5.772	41.20	41.20
02	3.139	22.40	63.60
03	1.229	8.80	72.40
04	0.903	6.50	78.90
05	0.708	5.10	83.90
06	0.603	4.30	88.20
07	0.444	3.20	91.40
08	0.363	2.60	94.00
09	0.336	2.40	96.40
10	0.209	1.50	97.90
11	0.167	1.20	99.10
12	0.109	0.80	99.99
13	0.000	0.00	100

Table 3: Grouping of brinjal germplasm in to different clusters on the basis of principal component analysis

No. of clusters	No. of germplasm	Germplasm code/name
I	06	Rampur local-1, F-2, H-5, I-9, K-1, R-2
II	06	A-2, F-11, Rampur local-3, M-3, C1, C3
III	07	D-3, D-4, H-3, Rampur local-2, J-7, L-2, L-5
IV	04	A-3, H-9, R-2580, C2
V	09	B-3, C-8, D-2, F-3, I-10, K-4, M-8, M-11, N-9
VI	01	K-8

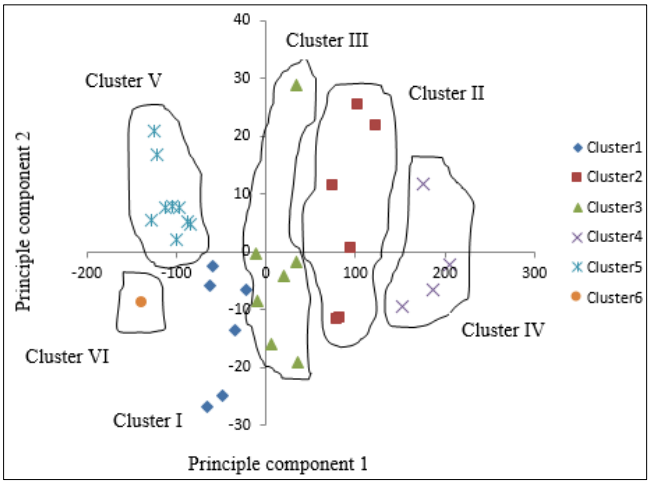

Fig 1: Grouping of brinjal germplasm into different clusters based on first and second principle components of yield and its traits

Conclusion

Based on determination of divergence, 33 brinjal germplasm were grouped into 6 clusters indicating the relative contribution of various quantitative traits to total variability. The genotypes, R2580, H-9 and A-3 were grouped under cluster IV and were identified as potential donors for further breeding programmes.

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