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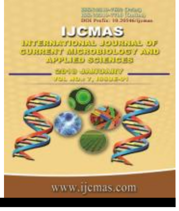

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Morphological Characterization of Different Genotype of Brinjal (*Solanum Melongena*)

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A B S T R A C T

Genetic divergence among 30 eggplant (*Solanum melongena* L.) genotypes was estimated using Mahalanobis D^2 Statistics. The 30 genotypes were grouped into six distinct clusters. Among the different clusters, cluster III consisted maximum number of genotypes (8 genotypes) followed by cluster I and VI (5 genotypes), cluster II, IV and V contained (4 genotypes). The highest intra-cluster distance was recorded for cluster I (1250.024) followed by cluster II (1217.052) and the lowest intra-cluster distance was recorded for cluster-V (389.277). However, the highest inter-cluster distance was observed between cluster IV and V (6815.521) while it was lowest between cluster III and IV (1149.46). The highest contribution in manifestation of genetic divergence was exhibited by days to first flowering, followed by days to 50 % flowering, fruit set percentage and fruit girth. The cluster III showed moderate mean values for all the characters under study except for number of primary branches. Cluster II had highest mean values for number of primary branches and fruit set percentage, Cluster I showed higher mean values for number of fruits per plant, Cluster IV showed higher mean values for plant height and fruit yield per plant, Cluster V showed higher mean values for fruit length, petiole length and test weight while cluster VI had higher mean values for fruit weight, plant spread, days to first flowering, days to 50 % flowering, fruit girth, days to first harvest. Considering the genetic divergence, clustering pattern and mean performance of genotypes for fruit yield and contributing characters 9 genotypes comprising EC-467273, 71-19, Rajendra Baigan-2, Pusa purple long, JB-15, IC-89933, Pant Rituraj and Muktakeshi may be considered as elite genotypes and hybridization involving these genotypes are likely to give desirable segregants for yield and its components characters.

Keywords

Eggplant, Cluster analysis, D^2 Statistics, Principle component, Dendogram

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Introduction

Eggplant (*Solanum melongena* L.) or brinjal, worldwide known as aubergine or guinea squash, is one of the most popular and major vegetable crops in India and other parts of the world, belonging to the nightshade family Solanaceae. It is an often cross pollinated annual herbaceous plant, originated in India and shows secondary diversity in South East Asia (Haushna, 2009). Brinjal fruits are rich sources of minerals like calcium, magnesium, potassium, iron, zinc and copper. It is also a fair source of fatty acids and it is used for medicinal purposes in curing diabetes, asthma, cholera, bronchitis and diarrhoea. It is reported to stimulate the intra-peptic metabolism of blood cholesterol. Leaf and fruit, fresh or dry produce marked drop in blood cholesterol level. The hypo cholesterolemic action is attributed to the presence of polyunsaturated fatty acids (lionleic and linolenic) which are present in flesh and seeds of the fruit in higher amount (65.1 %) (Timmapur, 2007). The multivariate analysis provides valuable information on the extent of variation present in the crop under improvement and helps a plant breeder in choosing desirable parents for breeding programme (Singh, *et al.*, 2006). Also inclusion of genetically diverse parents in any breeding programme is essential to generate new variability and desirable recombinants. Involvement of genetically diverse parents is essential to generate new variability and to look for desirable recombinants with respect to enhanced yield, quality and resistance to several important diseases. Genetically diverse parents are likely to segregates and or to produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic F_1s and broad spectrum of variability in segregating generations (Arunachalam, 1984). Cluster analysis and PC (principal component) analysis are the important genetic diversity measuring tools employed for exhibiting relative genetic differences among the genotype collection of various crop species. The aim of forming clusters and finding the intra and inter cluster divergence is to provide the base of selecting parents for a planned breeding programme.

Materials and Methods

The experimental material comprised of 30 genotypes and the field experiment was conducted at Vegetable Research Farm, BAU, Sabour, Bhagalpur in the *kharif* season during 2013-14. Each entry was sown at spacing of 60 X 60 cm with three replications accommodating 12 seedlings in each plot. All the recommended cultural practices and plant protection measures were followed data were recorded for 12 characters viz., plant height (cm), plant spread (cm), number of primary branches, fruit set percentage, days to first flowering, days to 50% flowering, fruit length (cm), fruit girth (cm), fruit weight (gm), test weight (gm), petiole length (cm), fruit yield per plant (Kg) and twelve quality parameters like leaf blade colour, leaf pubescence, presence of prickles on upper leaf, calyx colour, corolla colour, plant growth habit, fruit pedicel prickles, calyx spininess, fruit shape, fruit colour, seediness and seed colour. Cluster and PC analysis of 30 brinjal genotypes based on yield and its 12 component traits to assess the magnitude of genetic variation was performed by using statistical software Windostat version 8.6 from Indostat services. Genetic diversity is estimated using Mahalanobis D2 statistics. After this a method (Ward's minimum variance method) suggested by Ward (1963) is used for cluster formation.

Results and Discussion

The 30 genotypes taken for genetic divergence analysis and clustered for 14 quantitative characters into different group based on Mahalanobis D^2 statistics. On the basis of D^2 values, the 30 genotypes were cluster into six clusters, presented in Table 1. Among the different clusters, cluster III consisted maximum number of genotypes (8 genotypes) followed by cluster I and VI (5 genotypes), cluster II, IV and V contained (4 genotypes). Similar type of findings was reported by Goloni *et al.*, (2007). The inter and intra cluster distance D values which shows the index of genetic diversity among clusters were computed for 14 characters. A perusal of Table 2 shows that the highest intra-cluster distance was recorded for cluster I (1250.024) followed by cluster II (1217.052) while cluster V recorded minimum intra-cluster distance of 389.27. Similar types of results were obtained by Muniappan *et al.,* (2010). The inter-cluster distance ranged from 1149.46 to 6815.521 between cluster III and IV and cluster IV and V respectively. However, the highest inter-cluster distance was observed between cluster IV and V (6815.521) followed by cluster II and V (4230.82), cluster IV and VI (4064.033) cluster III and V (3869.051) and cluster I and V (3394.939) indicating wider genetic diversity among the genotypes between these groups. Similar types of findings were reported by Mohanty and Prusuti (2001), Jagtar Singh *et al.,* (2006).

A comparison of the mean values of different clusters for 14 characters, presented in Table 3 and it was observed that Cluster II had highest mean values for number of primary branches (5.301) and fruit set percentage (51.527) and lowest mean values for days to first harvest (92.801), Cluster I showed higher mean values for number of fruits per plant (12.783) and lowest mean values for fruit weight (92.178), plant spread (65.196) and fruit yield per plant (1.168). Cluster IV showed higher mean values for plant height (71.517), fruit yield per plant (1.775) and lower mean values for test weight (4.826), Cluster V showed higher mean values for fruit length (27.503), petiole length (3.503), test weight (5.650) and lower mean values for plant height (51.003), days to first flowering (37.00), days to 50 % flowering (50.00), fruit girth (9.317), while cluster VI had higher mean values for fruit weight (210.980), plant spread (92.250), days to first flowering (50.00), days to 50 % flowering (60.00), fruit girth (20.933), days to first harvest (112.00) and had showed lower mean values for fruit length (8.503), petiole length (2.750), number of fruits per plant (7.503) and fruit set percentage (32.640). The similar result was reported by Das *et al.,* (2010), Munshi *et al.,* (2011). High cluster mean for most of the yield contributing traits coupled with inter cluster distance was found in cluster VI and cluster V which indicate the possibility of obtaining high heterotic vigour and selection of superior segregants by inter crossing genotypes from these clusters. In the present investigation the highest contribution in manifestation of genetic divergence was exhibited by days to first flowering, followed by days to 50 % flowering, fruit set percentage, fruit girth, plant spread, test weight and number of primary branches. Fruit yield, days to first harvest, petiole length and plant height contributing least towards genetic divergence, presented in Table 4. The importance of fruit girth in genetic divergence of brinjal had been observed by Prabakaran (2010). Similar conclusions were drawn by Tambe *et al.,* (1993); Yadav *et al.,* (1996); Samaik and Verma (1999); Sharma and Maurya (2004); Chandrasekhar *et al.,* (2012) and Goloni *et al.,* (2007). The PCA of the fourteen traits in 30 brinjal genotypes is shown in Table 5. The first four PCs having Eigen values greater than one accounted for 88.04% of total variation amongst brinjal genotypes. Moreover, the first 5 PCs contributed 93.41 % of the total variation with proportionate contribution values of 39.52, 24.72, 15.49, 8.30 and 5.38 % respectively. Two dimensional ordinations of 30 brinjal genotypes on PC axis 1 and 2 are represented in Figure 1, which revealed scattered diagram of genotypic distribution pattern on axis. The first PC has positive association with fruit length, days to 1st flowering, days to 1st harvest, fruit set% and fruit girth while negative association with plant spread, test weight and number of primary branches. The second PC has positive association with fruit weight, days to 1st flowering and fruit girth while negative association with plant height, number of fruits per plant and days to 50 % flowering.

Table.1 Composition of clusters based on Ward's minimum variance of 30 genotypes

Clusters	Number of genotypes	Cluster members
Cluster I	5	JB-9, EC-384970, KS-331, Punjab Sadabahar, Nurkee
Cluster II	4	Swarna Mani, Muktakeshi, IC-261802, JB-15
Cluster III	8	IVBL-10, EC-305105, JB-8, IC-354666, IC-90149, IC-215018, IC-89910-K, IC-112341
Cluster IV	4	EC-169084, EC-467273, EC-305013, IC-90933
Cluster V	4	71-19, Rajendra Baigan-2,Pusa Purple Long, PB-67
Cluster VI	5	IC-89837, IC-89933, PB-70, Pant Rituraj, Pusa Shyamla

Table.2 Average of intra (diagonal) and inter cluster distance

Euclidean^2 : Cluster Distances : Ward						
	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	1250.024	2036.938	1707.588	1936.803	3394.939	2357.767
2 Cluster		1217.052	2082.03	2342.741	4230.82	2377.791
3 Cluster			553.821	1149.46	3869.051	1905.471
4 Cluster				420.647	6815.521	4064.033
5 Cluster					389.277	1223.943
6 Cluster						740.226

Table.3 Mean values of six cluster for 14 morphological characters in brinjal genotypes

Characters	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
Plant height (cm)	11.127	14.802	20.380	16.079	27.503	8.503
Plant spread (cm)	92.178	114.199	133.723	167.067	106.413	210.980
No. of primary branches	12.783	13.382	11.522	9.468	12.027	7.503
Fruit set %	2.753	2.753	3.038	3.189	3.503	2.750
Days to 1st flowering	62.130	70.271	68.370	71.517	51.003	60.247
Days to 50 % flowering	65.196	76.533	68.067	73.720	68.003	92.250
Petiole length (cm)	4.500	5.301	4.041	4.444	4.500	4.500
Days to 1st harvest	43.125	40.001	47.143	44.375	37.000	50.000
Fruit length (cm)	53.751	50.003	57.573	55.375	50.000	60.000
Fruit girth (cm)	96.877	92.801	103.143	101.126	96.000	112.000
No. of fruits/plant	4.831	5.070	5.121	4.826	5.650	5.200
Fruit weight (g)	1.168	1.523	1.522	1.775	1.330	1.517
Test weight (g)	13.263	15.343	15.794	18.258	9.317	20.933
Fruit yield/ plant (Kg)	49.757	51.527	45.397	38.977	42.050	32.640

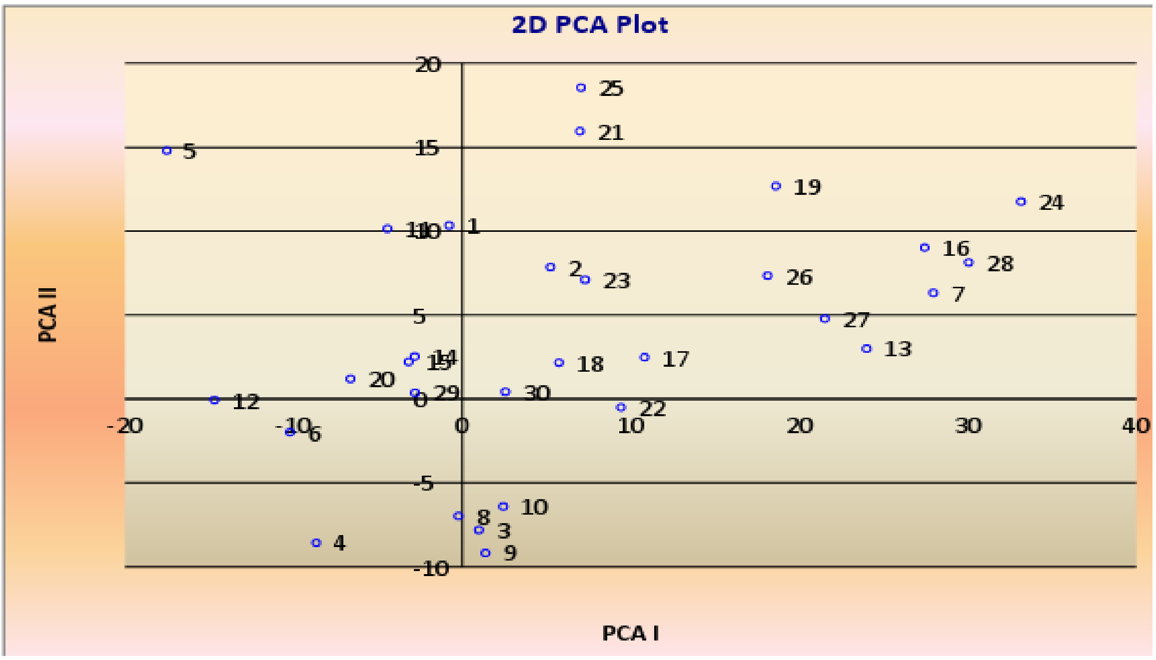
Table.4 Percentage contribution of each character towards total genetic divergence in 30 genotypes

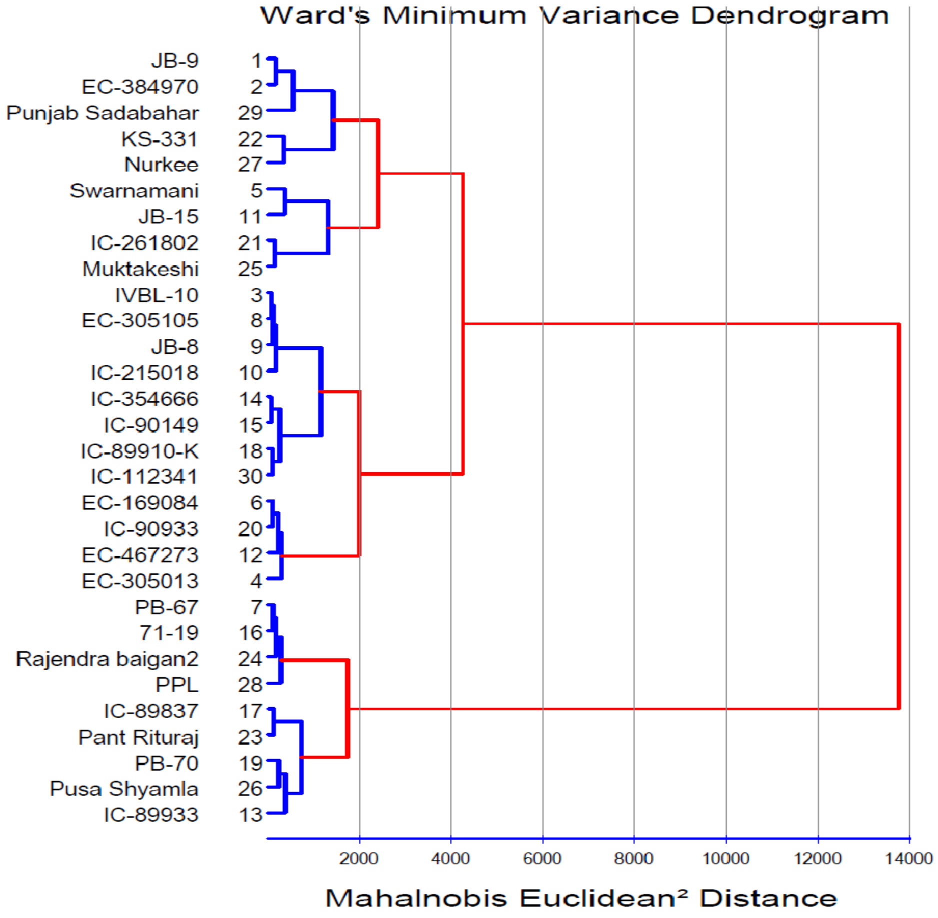
Characters	Times Ranked 1st	Contribution %
1. Fruit length (cm)	0	0.00
2. Fruit Weight (gm)	0	0.00
3. fruits/ plant	0	0.00
4. Petiole length (cm)	1	0.23
5. Plant height (cm)	1	0.23
6. Plant spread (cm)	16	3.68
7. primary branches	12	2.76
8. Days to 1st flowering	202	46.44
9. Days to 50% flowering	67	15.40
10. Days to 1st harvest	1	0.23
11. Test weight (gm)	15	3.45
12. Fruit yield/ plant (Kg)	5	1.15
13. Fruit Girth (cm)	54	12.41
14. Fruit Set %	61	14.02

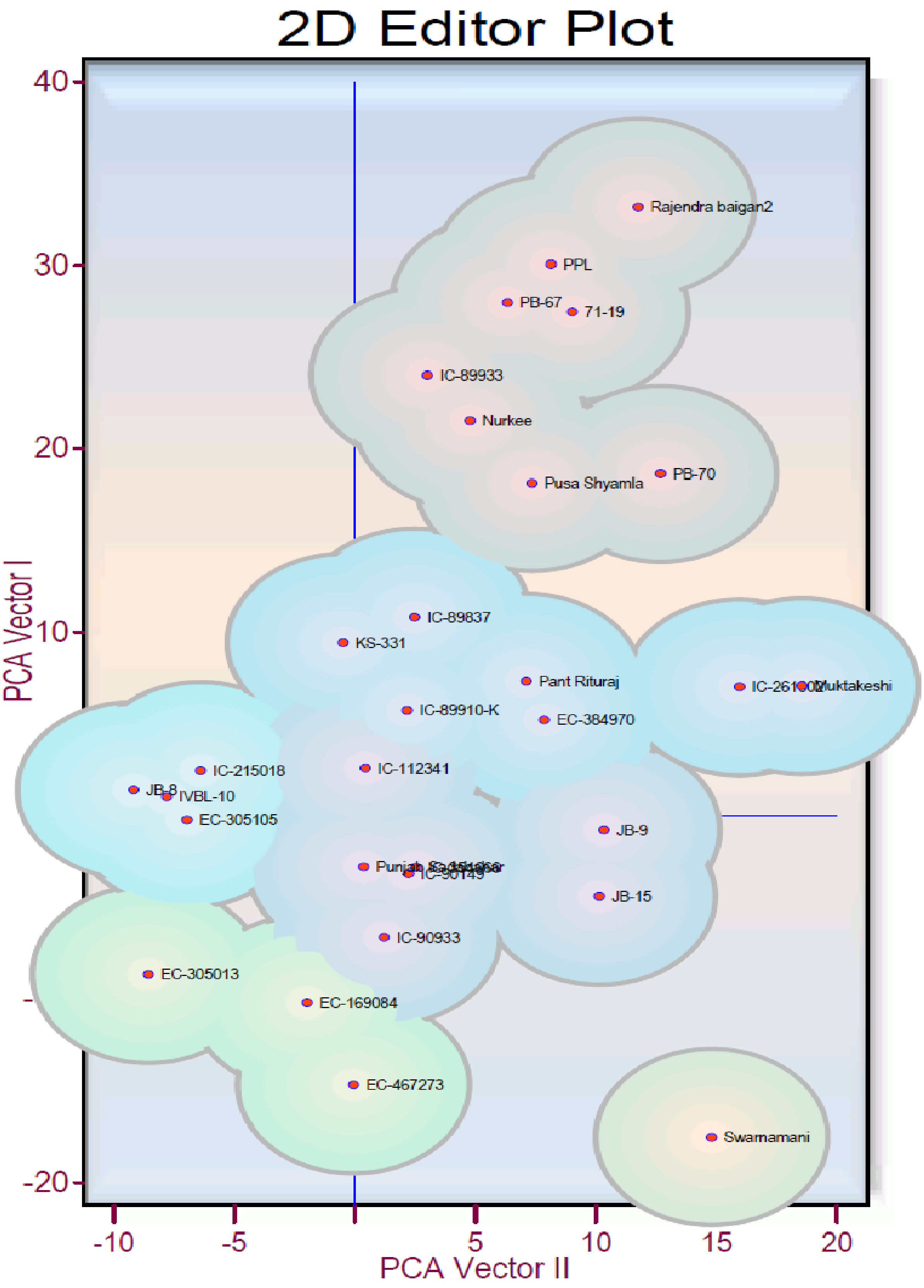
Table.5 Principal component analysis for 14 traits in 30 brinjal genotypes

	1 Vector	2 Vector	3 Vector	4 Vector	5 Vector
Eigene Value (Root)	**5.533**	**3.461**	**2.169**	**1.162**	**0.753**
% Var. Exp.	**39.523**	**24.724**	**15.491**	**8.303**	**5.379**
Cum. Var. Exp.	**39.523**	**64.247**	**79.738**	**88.040**	**93.419**
Fruit length (cm)	0.315	0.126	0.387	0.150	0.027
Fruit Weight (gm)	-0.036	0.500	0.041	-0.213	0.081
fruits/ plant	0.146	-0.428	0.253	0.019	-0.181
Petiole length (cm)	-0.165	-0.224	-0.293	-0.078	0.788
Plant height (cm)	0.136	-0.427	0.051	0.088	-0.066
Plant spread (cm)	-0.356	0.093	-0.202	0.195	-0.354
primary branches	-0.381	0.108	-0.097	-0.036	-0.045
Days to 1st flowering	0.385	0.193	-0.146	0.003	-0.022
Days to 50% flowering	0.181	-0.256	-0.476	0.234	-0.155
Days to 1st harvest	0.303	0.123	-0.427	-0.102	0.095
Test weight (gm)	-0.335	-0.078	-0.282	-0.163	-0.339
Fruit yield/ plant (Kg)	0.006	-0.162	0.122	-0.851	-0.116
Fruit Girth (cm)	0.277	0.348	-0.191	-0.047	-0.150
Fruit Set %	0.314	-0.163	-0.292	-0.244	-0.151

Fig.1 Scattered diagram: two dimensional ordination of 30 brinjal genotypes based on PC (principal component) axis 1 and 2






2D Editor Plot
PCA Vector I
PCA Vector II
40
30
20
10
-20
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-5
5
10
15
20
Rajendra baigan2
PPL
PB-67
71-19
IC-89933
Nurkee
Pusa Shyamla
PB-70
IC-89837
KS-331
Pant Rituraj
IC-89910-K
EC-384970
IC-261002
Muktakeshi
IC-215018
JB-8
IVBL-10
EC-305105
IC-112341
JB-9
Punjab Sadabahar
IC-90149
JB-15
IC-90933
EC-305013
EC-169084
EC-467273
Swarnamani

The third PC has positive association with fruit length, fruit weight, number of fruits per plant, while negative association with days to 50% flowering, days to 1st harvest, fruit set% & test weight.

The fourth PC has positive association with days to 50 % flowering and plant spread while negative association with fruit yield/plant, fruit set% and fruit weight. The fifth PC has positive association with petiole length while negative association with plant spread and test weight.

The traits of brinjal that demonstrated positive association with PCs have major role in genetic diversity analysis and explaining total genetic variation are in agreement with findings of Kundu *et al.*, (2012). For future experiment, traits contributing maximum to genetic diversity such as days to 1st flowering, days to 50% flowering and fruit set % should be given top priority as selection parameters and diverse genotypes identified in the present study may be utilized for attempting heterotic cross combination and developing hybrid varieties.

The results suggest a possibility for obtaining greater variation in the segregating generations derived from the hybridization of EC-467273 (Cluster IV) with 71-19, Rajendra Baigan-2, Pusa purple long (Cluster V). JB-15, Swarna Mani and Muktakeshi (Cluster II) with 71-19, Rajendra Baigan-2, Pusa purple long (Cluster V) and EC-467273 (Cluster IV) with IC-89933, Pant Rituraj, Pusa Shyamla and PB-70 (Cluster VI) because of maximum genetic distance of these combinations. High cluster mean for most of the yield contributing traits coupled with inter cluster distance indicate the possibility of obtaining high heterotic vigour and selection of superior segregants by inter crossing genotypes from these clusters as reported by Mehta *et al.*, (2004).

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