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Association and cluster analysis in elite genotypes of eggplant

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Abstract

The present investigation was carried out in *summer spring* season of 2015. All the genotypes were grouped into seven clusters based on D^2 values. The intra-cluster distances ranged from 0 to 3180.79. The members of cluster 2 and 1 were least divergent. The intra-cluster distance was minimum for cluster 3 and maximum in cluster 4. The maximum distance at inter cluster level was between cluster 4 and 3 followed by cluster 6 and 1 which may serve as a potential genotypes for hybridization programme.

Keywords: brinjal, cluster, genetic divergence, breeding potential

Introduction

Brinjal (*Solanum melongena* L.) is an important vegetable of central, southern and southeast Asia (Kalloo, 1988) [2]. Brinjal is poor's man food and consumed as vegetable in every class of people because of its nutritive value (rich in Vitamin A and B) and low price (Lakshmi *et al.*, 2013) [3]. In India number of brinjal cultivars are available that showed diversity in shape, colour, taste and plant texture. To meet the market and consumer requirements, the strategy of the breeder is to produce not only varieties with high yield and pest resistance (especially BFB), but also with good fruit quality that has both commercial and nutritive value. Variability is the basic requirement within the members of the population for the success of any breeding programme because genetically diverse parents when crossed can bring together diversity of gene combinations either to cultivate heterosis or to obtain superior recombinants. Clustering genotypes according to their morphological and behavioural response helps breeder to draft a standing genetic variability (Hair *et al.* 1995) [1].

In plant breeding genetic diversity plays a very important role as it helps in selecting the suitable parents for hybridization programme resulting in superior hybrids and desirable recombinants. Therefore, prior to initiation of any breeding programme they should be tested and extent of variability present must be adequately assessed so that the breeding programme could yield the desired results. To employ or exploit the available variability present in the genetic material, the divergence studies based upon some desirable/suitable parameters is of very essential and of highest significance. Keeping in view the above facts present investigation was undertaken to work out genetic divergence and cluster analysis using D^2 statistics with the objectives to assess the variability present among the among 36 genotypes based on eleven important traits of brinjal, to help the breeders in selecting promising and genetically diverse parents for desired improvement programmes.

Use of Mahalanobis D^2 statistics to estimate or evaluate the net/total divergence in breeding for crop improvement has been indicated by number of workers in different crops. The use of genetically divergent parents in hybridization under transgressive breeding programme is dependent upon categorization of breeding material on the basis of appropriate criteria. Apart from providing requisite assistance or help in selection of divergent parents in hybridization, D^2 statistics also adequately assists in the measurement of diversification and the contribution of the relative proportion of each component trait towards the total genetic divergence or variation. Principal component analysis (PCA) provided with the information about the importance of the largest contributor to total variation at each axis of differentiation (Sharma, 1998) [6].

Materials and Methods

The present investigation was carried out at Vegetable Research Farm, Department of Horticulture, BAU, Sabour, Bhagalpur during 2015. The experimental materials comprised of thirty six indigenous genotypes of eggplant collected from NBPGR, IIVR IIHR, Sabour,

Odisha and West Bengal. The experiment was laid out in a randomized block design with three replications. Seeds were sown in the nursery bed in February and transplanting was done in March, 2015. All the recommended agronomic package of practices was followed. The observations were recorded on five randomly selected plants per replication for each genotype. Attention on twenty five quantitative and qualitative characters viz., (i) plant height (cm), (ii) number of primary branches/plant, (iii) days to first flowering, (iv) days to 50% flowering (v) days to first fruit set, (vi) fruit weight (g), (vii) fruit length (cm), (viii) fruit diameter (cm), (ix) number of fruits/plant, (x) fruit yield per plant, (xi) trichome density, (xii) shoot diameter (mm), (xiii) shoot borer incidence (%), (xiv) fruit borer incidence by number, and (xv) fruit borer incidence by weight (%) (xvi) total ascorbic acid content, (xvii) total sugar content, (xviii) total chlorophyll, (xix) total anthocyanin, (xx) Polyphenol oxidase activity, (xxi) total phenol, (xxii) total antioxidant were observed (Table 1). Mean across three replications were calculated for each traits and the analysis of variation was carried out. Multivariate analysis was done utilizing Mahalanobis D^2 statistic (Mahalanobis, 1936) [4] and genotypes were grouped into different population clusters following Tocher's method. The generalized distance between any two populations is given by formula:

$$D^2 = \sum \sum \lambda_{ij} \sigma_{ai} \sigma_{aj}$$

Where, D^2 = Square of generalized distance; λ_{ij} = Reciprocal of the common dispersal matrix; $\sigma_{ai} = (\mu_i - \mu)^2$; $\sigma_{aj} = (\mu_j - \mu)^2$; μ = General mean.

Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character mean (Xs) to standardized uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between pairs of corresponding uncorrelated (gs) values of any two uncorrelated genotype of D^2 value. All $n(n-1)/2$ D^2 value were clustered using Tocher's method described by Rao (1952) [5]. The intra cluster distances were calculated by the formula given by Singh and Choudhary (1997) [7]:

$$\text{Square of the intra cluster distance} = \sum D_i^2 / n$$

Where, $\sum D_i^2$ is the sum of distance between all possible combinations of the entries included in a cluster and n is number of all possible combinations.

The inter cluster distances were calculated by the formula described by Singh and Choudhary (1997) [7]:

$$\text{Square of the intra cluster distance} = \sum D_i^2 / n_i n_j$$

Where, $\sum D_i^2$ is the sum of distances between all possible combinations ($n_i n_j$) of the entries included in the clusters under study. n_i is number of entries in Cluster I and n_j is number of entries in cluster j. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster, at least on an average, show a small D^2 value than those belonging to two different clusters.

Results and Discussion

On the basis of D^2 values, all the 36 genotypes were grouped into seven highly divergent clusters by Euclidean (Table 2a)

and Tocher's (Table 2b) methods. The intra-cluster distances ranged from 0 to 3180.79 (Table 2a) indicating that the genotypes in clusters have dissimilarity for physico-biochemical features and performance. The members of cluster 4 and 3 exhibited maximum divergence (inter-cluster distance 9928.319) followed by the members of cluster 6 and 1 (inter-cluster distance 8424.096) and cluster 6 and 4 (inter-cluster distance 8091.233). The members of cluster 2 and 1 were least divergent (inter-cluster 2599.375).

Inter and intra cluster divergence values (D^2) by Tocher's method between and within seven clusters are presented in the Table 2b. Highest value of inter-cluster distance were exists between member of cluster VI and V (4398.70), followed by member of cluster VII and V (4002.25) and cluster VI and IV (3917.66) while it was lowest (704.21) between cluster II and I. The intra cluster distance was maximum (1343.73) for Cluster III and minimum (0.00) for Cluster IV, V, VI and VII. The mutual relationships among seven clusters are presented in diagram (Fig. 2).

The cluster divergence was proved by the high inter-cluster and low intra cluster D^2 values indicating a wider genetic diversity between genotypes of clusters with respect to trait considered. Maximum inter-cluster distance is indicative that germplasms falling in these clusters had wide diversity and can be used for improvement programme to get better recombinants in the segregating generations. Lowest inter cluster between clusters were indicative of close relationship and similarity for most traits in the genotypes hence selection of parents from these clusters is to be avoided.

On the basis of relative magnitude of D^2 values, the test genotypes were grouped into seven clusters (Table 3) based on different traits using Euclidian (1-7) and Tocher's (I-VII) method with variable number of entries in each cluster indicating the presence of genetic diversity in the genotypes of present study. Cluster-1 included highest number of genotypes (11) comprising (EC 169084, IC 261802, Swarna Shayamali, IC 89933, BRBR-01, DRNKV-03-26, RCMBL-04, Arka Neelkanth, BRBL-07, Pant Rituraj, IC 545920) followed by cluster-3 (8) comprising (IIHR 562, BSB 31, IIHR 563, Swarna Shree, BRBL-04, IIHR 586, BRBL-05, BRBL-08) while lowest number of genotypes included in cluster-5 and 7 (2) comprising (IC 215020, EC 384606 and Punjab Brinjal 67, Muktakeshi). Cluster-II had maximum number of hybrids (16) comprising (IC 89837, Swarna Mani, Pant Rituraj, PPC, IIHR 562, BRBL-07, IIHR 563, IC 90121, IIHR 586, IC 89933, Swarna Manjari, BRBL-04, IC 90087, BSB-31, Swarna Shree, IC 261802) followed by cluster-III (12) comprising (BRBL-05, BRBL-08, BRBL-02, PPL, EC 169084, RCMBL-04, BRBL-01, BRBL-06, IC 90148, IC 545920, EC 382524, IC 215020) whereas, cluster-IV, V, VI and VII had minimum number of genotypes (1) comprising (IC 107769), (EC 384606), (Muktakeshi) and (Punjab Brinjal 67) respectively. The dendrogram of 36 eggplant genotypes was constructed based on physical and biochemical data in order to examine the genetic diversity by Tocher's method (Fig.2). Genotypes grouped within the same cluster in the dendrogram were basically related to the original sources of the genotypes used as parents in the breeding program.

It is concluded that eggplant lines with wide genetic variation accompanied with useful characteristics could be efficiently employed in specific crosses with the hope that this would lead to the transmission of higher genetic gain for different reputed traits major being yield and fruit and shoot borer tolerance related traits from practical utility point of view.

Table 1: Characters of eggplant considered in the present study

S. No	Characters
1.	Plant height (cm)
2.	Number of primary branches/plant
3.	Days to first flowering
4.	Days to 50% flowering
5.	Days to first fruit set
6.	Average fruit weight (g)
7.	Fruit length (cm)
8.	Fruit diameter (cm)
9.	Number of fruits/plant
10.	Fruit yield per plant
11.	Trichome density
12.	Shoot diameter (mm)
13.	Shoot borer incidence (%)
14.	Fruit borer incidence by number
15.	Fruit borer incidence by weight (%)
16.	Total ascorbic acid content
17.	Total sugar content
18.	Total chlorophyll content of leaf
19.	Total chlorophyll content of fruit
20.	Total anthocyanin content of leaf
21.	Total anthocyanin content of fruit
22.	Polyphenol oxidase activity
23.	Total phenol content of leaf
24.	Total phenol content of fruit
25.	Total antioxidant

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

	Cluster1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster6	Cluster7
Cluster 1	1260.428	2599.375	6220.018	4855.709	4263.761	8424.096	3286.642
Cluster 2		1874.007	6516.052	4524.929	3024.873	6357.331	4577.272
Cluster 3			0	9928.319	6905.798	8029.120	6744.155
Cluster 4				3180.79	4734.992	8091.233	5737.075
Cluster 5					1739.397	3865.913	3391.559
Cluster 6						2123.256	5578.545
Cluster 7							1944.448

Table 2b: Inter & Intra Cluster Distances (Tocher's method)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	ClusterVI	ClusterVII
Cluster I	262.74	704.21	1482.40	1109.69	1411.30	1572.26	1497.18
Cluster II		669.84	1417.08	1764.73	1928.44	1701.68	1686.14
Cluster III			1343.73	2487.38	2326.42	2647.57	2449.00
Cluster IV				0.00	2580.48	3917.66	3312.53
Cluster V					0.00	4398.70	4002.25
Cluster VI						0.00	707.75
Cluster VII							0.00

Table 3: Mean inter and intra cluster distance among seven clusters in brinjal genotypes on the basis of D² Statistics by Euclidian method (1-7) and Tocher's Method (I-VII)

Cluster Euclidian method	No. of hybrids	Name of hybrids	Cluster Tocher's Method	No. of hybrids	Name of hybrids
C1	11	EC 169084, IC 261802, Swarna Shayamali, IC 89933, BRBR-01, DRNKV-03-26, RCMBL-04, Arka Neelkanth, BRBL-07, Pant Rituraj, IC 545920	CI	4	BRBR-01, Swarna Shyamli, Arka Neelkanth, DRNKV-03-26,
C2	7	IC 90121, Swarna Manjari, IC107769, EC 382524, IC 90087, IC 90148, BRBL-06	CII	16	IC 89837, Swarna Mani, Pant Rituraj, PPC, IIHR 562, BRBL-07, IIHR 563, IC 90121, IIHR 586, IC 89933, Swarna Manjari, BRBL-04, IC 90087, BSB-31, Swarna Shree, IC 261802
C3	8	IIHR 562, BSB 31, IIHR 563, Swarna Shree, BRBL-04, IIHR 586, BRBL-05, BRBL-08	CIII	12	BRBL-05, BRBL-08, BRBL-02, PPL, EC 169084, RCMBL-04, BRBL-01, BRBL-06, IC 90148, IC 545920, EC 382524, IC 215020
C4	3	Swarna Mani, PPC, IC 89837	CIV	1	IC 107769
C5	2	IC 215020, EC 384606	CV	1	EC 384606
C6	3	BRBL-02, BRBL-01, PPL	CVI	1	Muktakeshi
C7	2	Punjab Brinjal 67, Muktakeshi	CVII	1	Punjab Brinjal 67

Table 4: Cluster means for different characters of litchi among 18 hybrids by Euclidian and Tocher methods

Characters	Clusters [1-5 (Euclidian)/I-V (Tocher's method)]					6/VI	7/VII
	1/I	2/II	3/III	4/IV	5/V		
1	94.788	95.723	73.277	95.095	107.57	115.83	104.61
	104.19	102.67	91.95	107.45	109.67	118.89	112.78
2	3.84	3.96	3.33	3.68	4.68	5.33	4.127
	4.56	4.20	3.80	3.78	3.55	4.78	5.89
3	44.86	42.66	51.66	41.28	43.29	47.00	45.90
	45.75	43.92	43.42	46.33	35.67	48.67	45.33
4	56.33	56.38	59.33	55.57	55.79	58.83	56.57
	57.67	56.46	55.25	57.00	56.67	59.00	58.67
5	66.86	68.61	56.66	68.66	66.66	64.00	62.33
	66.25	66.19	66.14	67.67	67.67	71.33	56.67
6	4.70	4.82	4.91	4.67	4.99	4.99	4.64
	4.79	4.84	4.71	4.91	4.47	5.55	4.44
7	86.00	94.04	103.84	91.88	88.51	103.87	88.64
	82.59	90.73	92.95	92.27	80.18	111.36	96.39
8	9.01	9.34	9.65	8.79	9.34	9.84	10.83
	9.74	9.51	9.49	9.17	8.89	10.51	9.17
9	5.18	4.94	6.61	4.68	5.33	4.15	4.75
	4.96	5.19	4.77	4.94	5.72	3.70	4.62
10	69.60	69.64	76.88	69.26	76.92	106.02	68.86
	69.46	73.89	72.54	51.23	43.22	97.92	114.12
11	8.53	4.02	13.61	3.50	5.10	3.57	10.84
	4.12	6.68	7.72	1.57	4.08	5.60	1.55
12	583.41	290.13	1046.	235.6	392.5	362.3	742.7
	284.87	477.92	554.17	80.42	175.97	548.39	176.29
13	20.32	22.05	22.95	23.06	18.22	21.03	21.48
	18.44	19.96	22.32	22.31	31.30	23.67	18.39
14	46.39	44.78	29.63	36.96	42.80	34.74	37.25
	44.75	40.59	39.07	52.04	42.95	32.97	36.52
15	47.34	41.90	28.40	41.53	40.86	31.57	39.04
	42.79	40.46	41.21	45.30	49.08	29.69	33.45
16	23.97	24.45	21.12	26.46	28.46	25.78	27.36
	26.74	24.59	29.07	20.97	22.01	27.84	23.72
17	19.67	24.81	34.15	21.72	29.51	30.41	26.01
	27.07	27.32	22.40	17.61	19.87	38.55	22.29
18	7.91	10.66	9.61	12.41	8.32	6.04	13.00
	9.59	10.23	11.08	13.14	9.64	6.04	6.03
19	4.93	5.61	4.42	3.57	4.70	4.00	4.54
	4.30	4.69	3.94	3.10	3.76	5.22	6.01
20	1.31	1.16	0.87	1.23	0.79	0.40	0.75
	1.14	0.88	1.08	0.88	2.12	0.23	0.53
21	3.31	3.37	2.37	7.98	7.53	23.22	18.67
	6.97	10.80	6.86	1.60	1.31	29.09	17.34
22	2.31	4.50	4.68	11.56	21.68	21.85	18.94
	17.63	12.21	11.83	2.58	19.79	26.76	16.95
23	4.44	4.12	3.00	3.58	4.65	5.00	4.18
	4.00	4.37	4.09	3.28	3.26	4.04	5.96
24	2.15	3.12	1.75	2.97	2.55	1.64	1.89
	2.17	2.63	2.54	2.47	1.96	1.78	1.51
25	10.83	15.31	68.15	28.14	26.13	8.52	10.54
	8.71	11.93	35.74	25.02	14.33	2.80	14.25

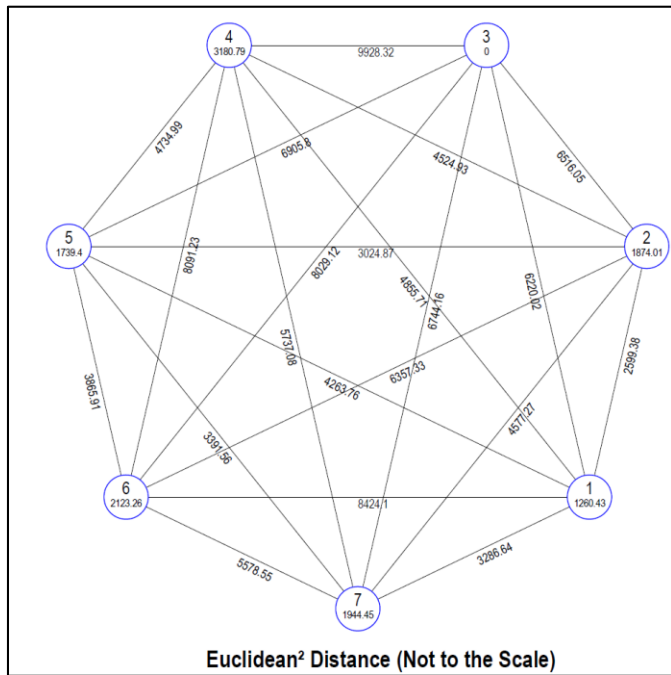


Fig 1: Mahalanobis Euclidean Distance (Not to scale)

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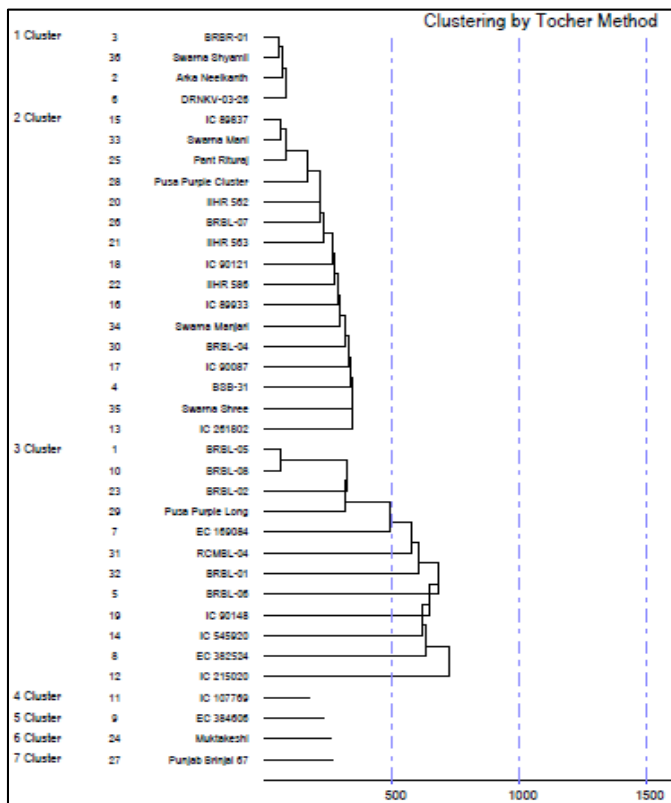


Fig 2: Clustering of genotypes by Tocher's method

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