Genetic divergence in eggplant *(Solanum melongena* L.)

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Abstract

Genetic divergence in brinjal was studied through non-hierarchical Euclidean cluster analysis. The results showed the presence of sufficient amount of genetic diversity as all the 192 test genotypes were grouped into five different clusters. Estimates of intra-cluster distances ranged from 0.00- 2.99. It was maximum in cluster I and minimum in cluster V. The maximum inter-cluster value (18.031) was obtained between cluster II and V. Minimum diversity was observed between cluster I and III (2.869) which suggested that members of these two clusters are genetically very close. The genotypes of heterogeneous origin are grouped together in some of the major clusters suggesting no parallelism between geographical and genetic diversity suggesting thereby that parents should be selected on the basis of total divergence for the characters used for an overall improvement in the yield.

Keywords: Cluster analysis, eggplant *(Solanum melongena* L.) and genetic diversity.

Introduction

Eggplant (*Solanum melongena* L.) is a major vegetable crop throughout the tropics and subtropics (Bose and Som,1986). Brinjal is native of India (Thompson and Kelly, 1957). It is a major vegetable crop grown throughout India for its tender fruits.

For an effective breeding program, information concerning the extent and nature of genetic diversity within a crop species is essential. It is particularly useful for characterizing individual accessions and cultivars and as a general guide in the selection of parents for hybridization (Furini and Wunder, 2004). Better knowledge on genetic diversity or genetic similarity could help to sustain long term selection gain (Choudhary *et al*., 2002). Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization program. A previous knowledge of the structure of the genetic diversity within a large collection of germplasm may be of great help to make decisions on management procedures, as well as on breeding strategies to use in current and future breeding programs. According to Sharma and Jana (2002), assessment of genetic variation in a species is a prerequisite for initiating an efficient breeding programme, as it provides a basis for tailoring desirable genotypes. Genetically diverse parents are likely to segregates/ 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, 1981). Genetic diversity study also permits to select the genetically divergent parents to obtain the desirable recombinant in the segregating generations of eggplants. The aim of the present study was to characterize eggplant genotypes collected from different regions of India and exotic sources to assess the genetic diversity within the germplasm.

Material and Methods

A total of 192 genotypes of brinjal from NBPGR, New Delhi, including indigenous and exotic lines were raised at Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand) in *kharif* (rainy season) 2011-2012, in augmented block design with checks repeated after every 8 test genotypes as per Federer (1956). Each genotype was sown in a single row of five meters length at 90 m spacing with 60 cm spacing from plant to plant. Data were recorded on five randomly selected plants for fifteen characters *viz*., days to 50% flowering, days to first fruit harvest, plant height (cm), number of primary branches per plant, number of shoots infested by shoot and fruit borer per plant, number of fruits infested by shoot and fruit borer per plant, number of fresh fruits per plant, total number

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of fruits per plant, average fruit weight (g), fruit length (cm), fruit diameter (cm), weight of infested fruits per plant (kg), weight of fresh fruits per plant (kg), total fruit weight per plant (kg) and total yield per hectare.

Genetic divergence of 192 test genotypes in augmented design was studied through non-hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973).

Results and Discussion

Non-hierarchical Euclidean cluster analysis was done to study the divergence in 192 genotypes in respect of various economic traits. The genotypes were grouped into 5 non-overlapping clusters.

Appropriate cluster arrangement was determined by using 'F' test. It was determined that cluster combination with 4 and 5 were most appropriate for the material, because the "F" value was significant at 5% level of significance than the expected "F" values. The averages inter and intra cluster distances have been presented in Table 2.

Table 1. Sequential F-ratio tests for comparison of cluster solutions

Cluster number	Degree of freedom (df¹)	Degree of freedom (df²)	'F' value
4 and 5	9	1683	5.48*

* Significance at 5% level of probability

Table 2. Average distance of intra- and inter-cluster centriods

	I	II	III	IV	V
I	2.992	4.669	2.869	4.889	17.310
II		2.500	2.985	3.109	18.031
III			2.788	3.482	17.421
IV				2.978	17.680
V					0.000

The maximum intra cluster distance was found in cluster I (2.992) and minimum in cluster V (0.00). Distribution in each cluster has been presented in Table 3. The clustering pattern does not correspond to their pedigree in general. The maximum inter cluster distance (18.031) was found in between clusters II and V, whereas minimum distance (2.869) was found between clusters I and III. The cluster number III had maximum number of genotypes (57) followed by cluster number II (53), I (43), IV (38), and V (1). The cluster mean has been presented in Table 4.

The genotypes with lowest mean value for days to 50% flowering (52.72) was recorded in cluster II while cluster IV had the genotypes with highest mean values for days to 50% flowering (73.53). Cluster number III had lowest mean value for days to first fruit harvest (62.63), while maximum value for days to first fruit harvest was found in cluster number V (88.00). Maximum mean value of plant height was observed in cluster V (83.11 cm) followed by cluster I (78.59 cm), IV (74.71 cm), III (71.87 cm) and II (65.00 cm). Cluster III had maximum mean value of average fruit weight (118.95g) and fruit diameter (5.29cm), while cluster V had minimum mean value of fruit weight (49.46g) and fruit diameter (3.53cm). Maximum mean value for number of primary branches per plant was found in cluster II (4.56) while cluster V had minimum mean value for primary branches per plant (2.19). Maximum mean value for number of shoots infested by shoot and fruit borer (1.09), number of fruits infested by shoot and fruit borer (1.89), number of fresh fruits per plant (4.80) and total number of fruits per plant (6.70) were recorded in cluster I, while minimum mean value for number of shoots infested by shoot and fruit borer (0.70), number of fruits infested by shoot and fruit borer

Table 3. Non-hierarchical clustering of 192 brinjal genotypes

Cluster number	Number of genotypes	Genotype
I	43	EC038474, EC038474, EC144139, EC169079, EC304072, EC305048, EC316230, EC384619, EC490062, IC023957, IC074194, IC074207, IC074224, IC089888, IC089912, IC090092, IC090806, IC090811, IC090871, IC090905, IC090915, IC090931, IC099712, IC112723, IC112738, IC112779, IC112814, IC112815, IC112851, IC139200, IC203399, IC249319, IC249437, IC265246, IC280961, IC304981, IC306236, IC332508, IC347779, IC354597, IC383107, IC383195, IC545884.
II	53	EC306226, EC305014, EC316242,IC089837, IC08910, IC090031, IC090035, IC090045, IC090051, IC090064, IC090085, IC090088, IC090093, IC090144, IC090260, IC090806, IC090810, IC090932, IC099731, IC104096, IC111010, IC111018, IC111037, IC111085, IC111409, IC111431, IC112315, IC112341, IC112728, IC112736, IC112750, IC112905, IC112993, IC281112, IC336793, IC343212, IC354612, IC354697, IC354707 IC374904, IC387807, IC397299, IC398212, IC398820, IC410129, IC413648, IC420656, IC427007, IC427017, IC427025, IC433547, IC433625, IC545256.
III	57	EC111317, EC305056, EC305070, EC316227, EC316244, EC316275, EC316284, EC378820, EC379244, EC393239, IC023971, IC089826, IC089890, IC089937, IC089949, IC090068, IC090940, IC090942, IC099675, IC099691, IC099726, IC112848, IC112950, IC261771, IC261803, IC261808, IC285125, IC316201, IC317422, IC329327, IC332516, IC336472, IC347750, IC354511, IC354512, IC354525, IC354538, IC354539, IC354562, IC354564, IC354578, IC354596, IC354633, IC354635, IC354637, IC354655, IC354676, IC354694, IC354701, IC361838, IC374912, IC374921, IC374942, IC383345, IC383392, IC545854, IC545928.
IV	38	EC169757, EC305163, IC023970, IC023969, IC089929, IC089947, IC090026, IC090132, IC090137, IC098735, IC099670, IC104083, IC104089, IC111062, IC111387, IC111443, IC112909, IC112934, IC218975, IC249185, IC249327, IC261788, IC261792, IC261793, IC264470, IC272904, IC279555, IC281115, IC310884, IC334558, IC345744, IC347962, IC374535, IC374867, IC383106, IC420406, IC467247, IC545844.
V	1	IC333527

(0.98), number of fresh fruits per plant (1.80) and total number of fruits per plant (2.79) were recorded in cluster IV. Cluster I had maximum mean value for fruit length (9.61), while minimum mean value for fruit length was found in cluster III (7.41). Maximum mean value for weight of infested fruits per plant (0.19kg), weight of fresh fruits per plant (0.46kg), total fruit weight of per plant (0.65kg) and total yield per hectare (119.90q) were found in cluster I, while cluster II had minimum mean value for weight of infested fruits per plant (0.07kg), weight of fresh fruits per plant (0.14kg), total fruit weight of per plant (0.20kg) and total yield per hectare (37.47q).

Information on genetic divergence among the available germplasm is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregates. It was also observed that the more diverse the parents, greater are the chances of obtaining high heterotic F_1s and broad spectrum of variability in the segregating generation (Arunachalam, 1981). Improvement in yield and quality is normally achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization programme. Some related results have been reported in eggplant by Begum *et al*., (2013), Quamruzzaman *et al*., (2009), Kumar *et al,*. (2000), Mohanti and Prusti (2001), Singh and Gapalakrishnan (1999), Chaudhary and Pathania (1998) and Tambe *et al*., (1993).

In present study differences were observed in cluster means for almost all the 15 characters in the 192 genotypes studied. Generally crosses involving parents belonging to most divergent clusters are expected to give maximum heterosis and create wide variability in genetic architecture. However, for a practical plant breeder, the objective is not only obtaining high heterosis but also to achieve high level of production with the shortest possible time.

Table 4. Cluster mean for different economic traits in brinjal

S.No.	Characters	I	II	III	IV	V
1	Days to 50% flowering	54.47	52.72	52.95	73.53	72.00
2	Days to 1st fruit harvest	65.72	63.81	62.63	87.26	88.00
3	Plant height (cm)	78.59	65.00	71.87	74.71	83.11
4	No. of primary branches/plant	3.45	3.56	3.30	3.52	2.19
5	No. of shoots infested by SFB/ plant	1.09	1.01	0.87	0.70	0.51
6	No. of fruits infested by SFB/ plant	1.89	0.99	1.80	0.98	3.00
7	No. of fresh fruits/ plant	4.80	2.08	2.41	1.80	4.40
8	No. of fruits/ plant	6.70	3.08	4.20	2.79	7.40
9	Average fruit weight (g)	98.79	69.93	118.95	111.29	49.46
10	Fruit length (cm)	9.61	7.55	7.41	7.80	8.16
11	Fruit diameter (cm)	4.50	4.05	5.29	4.47	3.53
12	Weight of infested fruits/ plant (kg)	0.19	0.07	0.21	0.11	0.15
13	Weight of fresh fruits/ plant (kg)	0.46	0.14	0.27	0.19	0.22
14	Total fruit weight/ plant (kg)	0.65	0.20	0.51	0.29	0.37
15	Total yield per hectare (q)	119.90	37.47	93.73	54.19	68.52

सारांश

बैंगन में आनुवांशिक विचलन का अध्ययन गैर श्रेणीबद्ध इयूक्लीडीन समूह विश्लेषण विधि से किया गया। परिणाम से स्पष्ट हुआ कि इनमें प्रचुर अनुवांशिक विविधता विधमान है जैसा कि सभी 192 परीक्षण प्रभेदों को कुल 5 विविध समूह में वर्गीकृत होने से पाया गया। अंतर समूह की औसत दूरी का आकलन 0.00–2.99 था। समूह–1 में सबसे अधिक एवं समूह–5 में सबसे कम वर्गीकृत हुए। सबसे अधिक अंतर–समूह मूल्य (18.031) समूह–2 एवं समूह–5 के मध्य पाया गया। सबसे कम विविधता मूल्य समूह–1 एवं समूह–3 (2.869) के मध्य पाया गया। जिससे सुझाव मिला कि इन दो समूहों के बीच प्रभेदों में अनुवांशिक निकटता सबसे कम है। असमलैंगिक उत्पत्ति वाले प्रभेद का समूहन एक साथ कुछ मुख्य समूह में होने से सुझाव मिला कि इनमें समानान्तरता भौगोलिक एवं अनुवांशिक विविधता के मध्य नहीं हैं। इससे स्पष्ट होता है कि पित्रों का चयन कुल विचलन के आधार पर करना चाहिए जिससे उपज में सम्पूर्ण उन्नयन वांछित गुणों को समाहित कर किया जा सके।

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