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RESEARCH ARTICLE

Studies on genetic divergence in brinjal (*Solanum melongena* L.) for yield attributes and shoot and fruit borer (*Leucinodes arbonalis*) incidence

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SUMMARY

Genetic divergence study was carried out with sixty brinjal genotypes for sixteen characters in Department of Horticulture during Feburary 2015. These genotypes were grouped into five clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. Cluster V was the largest cluster comprised of 43 genotypes followed by cluster I which consisted of eleven genotypes. Cluster II, III and IV consisted of two genotypes each. As regard to cluster means, cluster V and II performed better in most of the biometric characters studied. The maximum inter-cluster distance was observed in cluster III and V. The intra cluster distance was the maximum in cluster V followed by cluster I and cluster IV. Cluster II had the least intra cluster distance.

Key Words : Brinjal, Genetic divergence, D^2 statistics

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Brinjal is an important solanaceous vegetable crop widely cultivated in India. Brinjal (*Solanum melongena* L.) also known as eggplant or aubergine or guinea squash is an economically important vegetable crop widely cultivated in tropics, sub tropics and warm temperate regions throughout the year. The regional specific F_1 hybrids development is needed because consumer preference in eggplant is region specific (Kalloo,1994). Genetic divergence is essentially the first step in plant breeding for crop improvement and exploitation of variability is of great importance and is a pre-requisite for the effective screening of superior genotypes. Mahalanobi's D^2 statistics is a powerful tool for determining degree of divergence between populations and relative contribution of different components to the total divergence, in isolation of suitable parents. This technique provides a basic for selection of genetically divergent parents in a hybridization programme. Therefore, the present investigation was carried out to examine the nature and magnitude of genetic divergence in sixty brinjal genotypes with different geographical origins and

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distribution.

MATERIAL AND METHODS

Sixty genotypes of brinjal having diverse origin were evaluated at the Department of Horticulture, Faculty of Agriculture, Annamalai University, Chidambaram, during the period Feb-June 2015, using Randomized Block Design, with three replications. Plants were grown at a spacing of 60 cm x 45 cm adopting the package of practices recommended by Tamil Nadu Agriculture University (TNAU). Observations were recorded on five randomly selected plants of each genotype in each replication for sixteen characters *viz.*, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of long styled flowers per plant, number of medium styled flowers per plant, number of short styled flowers per plant, number of flowers per plant, number of days to 1st flowering, number of days to first harvesting, fruit set percentage, number of fruits per plant, shoot and fruit borer incidence (%), fruit length (cm), fruit girth (cm), fruit weight (g) and fruit yield per plant (g). Genetic divergence was estimated using D^2 statistics of Mahalanobis (1936) and the populations were grouped into clusters as per Rao (1952).

RESULTS AND DISCUSSION

General analysis of variance showed significant differences among the sixty genotypes of brinjal for all the sixteen characters studied. Having computed D^2 values for all possible pairs, the sixty genotypes were classified into five groups of gene constellations. These indicated a large genetic diversity (Table 1).

Cluster V was the largest cluster comprised of 43 genotypes, followed by cluster I which consisted of 11 genotypes. Clusters, II, III and IV consisted of two genotypes each. This result showed that almost all commercially cultivated varieties of brinjal in our country may have originated from closely related sources. Brinjal accessions *viz.*, IC 136177 and IC 136143 from cluster II, IC 127216 and Melapalayam local from cluster III, IC 127071 and IC 127063 from cluster IV, CO_1, CO_2, Thiruthurai puundi, Green round, Andarkulam local, Thovalai local, Long green, Pechiparai 1, Kamapuram local, Kamapuram red local and Sivanthipatti local from cluster I were distinctly different from the rest of the germplasm studied.

Intra and inter-cluster distances are an index of genetic diversity among cluster as shown in Table 2. Intra and inter cluster distance were computed for V clusters and are presented in Table 2. The intra cluster

Table 1 : Grouping of 60 brinjal genotypes into clusters

Cluster number	Number of genotypes	Name of the genotypes
I	11	CO_1, CO_2, Thiruthuraipoondi local, Green round, Andarkulam local, Thovalai local, Long green, Pechiparai 1, Kamapuram local, Kamapuram red local and Sivanthipatti local.
II	2	IC 136177 and IC 136143
III	2	IC 127216 and Melapalayam local
IV	2	IC 127071 and IC 127063
V	43	Pusa purple long, Kaliyakavilai local, Karungal palur local, Karungal local, Bihar local, Lalima, Brinjal long green, Gulabi, Pusakranti, Nagercoil local, Perunchilambu local, Kadapa local, Green small brinjal, Vellore local, Namakkal local, Mothiramalai local, Nagamalai Local, Purple long, Muktakeshi, IC 127237, IC 127162, IC 127074, IC 126918, IC 316258, IC 316291, IC 316276, IC 316236, IC 316234, IC 316223, IC 136210, IC 315014, IC 136204, IC 136200, IC 313088, IC 305046, IC 305044, IC 305020, IC 136179, IC 136172, IC 304981, Madurai local, Keeranur local and Annamalai 1.

Table 2 : Average intra and inter cluster distance in sixty genotypes of brinjal

	I	II	III	IV	V
I	1152.27 (33.94)	745.98 (27.31)	1263.03 (35.53)	933.73 (30.55)	1396.72 (37.37)
II		54.55 (7.38)	602.43 (34.54)	352.19 (18.76)	825.61 (28.73)
III			94.36 (9.71)	796.40 (28.22)	1406.13 (37.49)
IV				115.73 (10.75)	992.30 (31.50)
V					1373.66 (37.06)

Diagonal elements: Intra-cluster values; Off-diagonal elements: Inter-cluster values distance ranged from 7.38 to 37.06. Cluster V showed the maximum intra cluster distance of 37.06, followed by cluster I (33.94) and cluster IV (10.75). Cluster II had the least intra cluster distance of 7.38. The maximum inter cluster distance was found between clusters III and V (37.49), while the inter cluster distance was the least between cluster II and IV (18.76). Genetic distance (D^2) between clusters III and V was larger. The minimum inter cluster distance was observed between cluster II and IV indicating close relationship among genotypes. Data clearly indicated that the genotypes did not cluster according to their geographical distribution. In general, the pattern of distribution of genotypes from various regions into different clusters was seen to be random. The maximum inter cluster distance was found between clusters III and V (37.49), followed by clusters II and IV (30.55). This indicated that the genotypes included in these clusters can be used as a parent in the hybridization programmes to get higher heterotic hybrids from the segregating populations. In brinjal similar results were reported by Babu and Patil (2004); Mahta *et al*. (2004); Rathi *et al*. (2011); Singh *et al*. (2006); Sherly Roosevelt and Shanthi (2009) and Nalini Dharwad *et al.* (2011). In tomato similar result was reported by Rai *et al.* (2003). Genetic divergence (D^2) among thirty five accessions of (*Solanum melongena* L.) resulted in the formation of five divergent groups. The maximum inter cluster distance was observed between cluster III and IV (20.38) as reported by Sarnaik *et al*. (1998). Similar findings were reported by Kumar *et al.* (1998), Silva *et al*. (1999), Mohanty and Prusti (2000), Thirumurugan *et al*. (1998) and Yadav *et al*. (1996) in brinjal. Kurian and Peter (1994) observed similar findings in tomato. Absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin (such as exchange of genetic material, genetic drift, natural mutation, spontaneous variation or natural and artificial selection) may be responsible for the genetic diversity. Another possibility may be that estimates of diversity based on characters used in the present investigation may not be sufficient to account for variability caused by some other traits of physiological/biochemical nature (which could be important in depicting the total genetic diversity in a population). Therefore, selection of genotypes for hybridization should be based on genetic diversity other than geographic divergence.

Cluster means of sixty genotypes (Table 3) showed that mean values of clusters varied in magnitude for all the sixteen characters studied.

Cluster I consisted of eleven genotypes with the maximum number of secondary branches per plant, high number of medium styled flowers, days to 1st flowering, more number of fruits per plant, highest shoot and fruit borer resistance. Cluster II had two genotypes, with more number of short styled flowers and more number of flowers per plant and the minimum days to 1st harvesting. Cluster III comprised of two genotypes with the highest

Table 3 : Cluster means of sixteen quantitative traits in brinjal

Clusters	Plant height	Number of primary branches per plant	Number of secondary branches per plant	Number of long styled flowers per plant	Number of medium styled flowers per plant	Number of short styled flowers per plant	Number of flowers per plant	No. of days to Ist flowering
I	71.36	3.59	10.33	25.03	22.67	18.58	66.13	29.28
II	73.81	4.18	6.37	23.07	22.50	21.08	66.65	33.85
III	73.88	3.16	7.30	25.09	15.63	15.33	56.05	32.34
IV	57.87	3.57	8.98	21.46	15.61	18.75	55.81	36.11
V	75.22	4.57	8.70	24.82	20.62	18.41	63.84	32.83

Table 3 : Contd……….

Clusters	No. of days to Ist harvesting	Fruit set percentage	Number of fruits per plant	Shoot and fruit borer incidence	Fruit length	Fruit girth	Fruit weight	Fruit yield per plant
I	50.85	44.41	29.49	55.83	6.54	5.20	78.47	2294.52
II	49.30	44.03	29.14	66.49	7.44	4.58	67.81	1824.01
III	53.13	30.03	16.79	72.98	5.29	3.67	44.61	715.70
IV	51.78	52.93	29.43	71.97	7.02	5.54	94.90	2634.50
V	52.35	42.92	27.71	63.15	8.76	5.18	95.30	2714.05

number of long styled flowers, lowest fruit set percentage, lowest number of fruits per plant, highest shoot and fruit borer incidence and lowest fruit yield per plant. Cluster IV consisted of two genotypes with the maximum days to 1st flowering, maximum fruit set percentage and maximum fruit girth. Cluster V consisted of forty three genotypes of highest plant height, more number of primary branches per plant, highest fruit length, fruit weight and fruit yield per plant. The best cluster with yield and other component characters was represented by cluster V followed by cluster I.

Based on these results, Mahalnobis's D^2 was found to be a useful tool in grouping genotypes phenotypically and geographically. Findings revealed that in brinjal, there is a vast scope for developing new varieties with greater yield potential and to better other attributes of economic importance, using this elite germplasm. In crop improvement programmes, intercrossing among genotypes with outstanding mean performance for these characters were proved to be effective. To develop early varieties with higher yield, selection from cluster V would be effective, as it showed higher fruit yield per plant. To develop an early flowering as well as shoot and fruit borer resistance variety, selection from cluster I would be effective as it showed minimum days to 1st flowering and minimum shoot and fruit borer incidence. It is clear that to develop a variety with more number of short styled flowers and early maturity, cluster II would be a good candidate. To breed good varieties for long styled flowers and early maturity, selection from cluster III will prove to be highly useful and selection from cluster IV will be useful for breeding medium sized fruited varieties with higher demand in specific regions of India.

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