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Divergence studies in Brinjal for yield attributes and shoot and fruit borer incidence

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Abstract

Genetic divergence amongst fifty one brinjal germplasm was premeditated founded on sixteen qualitative and measurable characters. Significant variations were detected among the brinjal genotypes for all the traits studied. D^2 analysis resolved fifty one genotypes into eight clusters. Most of the genotypes existed in cluster III (23 genotypes); followed by cluster II (15 genotypes); cluster I (08 genotypes). The intra-cluster distance was extreme with the cluster III (78.16) followed by cluster II (50.78) and cluster I (25.46). The germplasm grouped in this cluster may also be diverse genetically. The minimum inter-cluster D^2 value was observed between cluster V and VI demonstrating the close relationship among the genotypes included in these clusters. The inter-cluster distance was high among the clusters V and cluster VIII. The genotypes grouped in these clusters might be altered genetically and utilized in crossing programme to get good heterotic hybrids or superior recombinants (segregants).

Keywords: Brinjal, D^2 statistics, Genetic diversity, cluster analysis

Introduction

Brinjal (*Solanum melongena* L.) is the utmost important herbaceous, tropical vegetable crop. It is perennial plant but raised as annual vegetable crop. It has been a foremost vegetable in our diet since ancient times and very usually used in all households. Being primary center of origin, India has wide range of variability in this crop. The area under brinjal cultivation in India is about 757.57 thousand hectares with production of 13153.52 thousand metric tonnes. The productivity was 17.36 metric tonnes per hectare (Indiastat, 2020) [3].

It is an important source of carbohydrates (4.0 g), protein (1.4 g), fiber (1.3 g), vitamin A (124 IU), phosphorus (47 mg), potassium (2 mg) and iron (0.3 mg) and recommended for diabetes, asthma, cholera and it protects the brain cell membranes from damage (Mangi *et al.*, 2017) [8]. Brinjal is an often-cross pollinated crop. Hence, opportunity of exploitation of heterosis in brinjal is very bright. A large indigenous biodiversity exists in eggplant with variation in plant type, stem colour, leaf size, leaf tip, midrib colour, fruit size, fruit shape, fruit colour, fruit quality, cooking quality and tolerance to pest and diseases (Ullah *et al.*, 2014). It is an established fact that genetically diverse parents are likely to yield desirable hybrids.

Selection of parents based on divergence study would be promising for a hybridization programme. It was observed that additional diverse the parents, high heterotic F_1 s and broad spectrum of variability in the segregating generation (Kumar *et al.*, 2013). Improvement in produce and quality is commonly reached by selecting genotypes with desired character combinations existing in the nature or by hybridization. Selection of parents on the basis of divergence study would be more promising for a hybridization programme. Among the several statistical methods developed for assessing the divergence between populaces, multivariate analysis (D^2 analysis) developed by Mahalanobis (1936) [7] has been establish to be a potent tool (Rao, 1952) [10]. Assessment of genetic diversity is an imperative step in crop enhancement programme through plant breeding.

Materials and Methods

The trial was conducted in the field of Vegetable Research Station, Agriculture Research Institute, Rajendrangar, Hyderabad. Fifty one genotypes were raised in Randomized Block Design with three replications during *Rabi*, 2015-16 at Vegetable Research Station, ARI, Rajendranagar, Hyderabad, Telangana. Each genotype was grown in a single row plot of 5 m length in each replication. Each plot consisted of one ridge alternating with furrow accommodating only one row of germplasm line. Row-to- row spacing of 60 cm and plant-to-plant spacing of 50 cm was retained.

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The recommended set of executive practices was monitored for raising the entire germplasm. Necessary prophylactic plant protection measures were conceded to safeguard the entire germplasm from pests and diseases.

The data on sixteen quantitative and qualitative traits were noted on five competitive and randomly selected plants in each replication for all the characters under study except days to 50% flowering, total number of fruits per plant, number of marketable fruits per plant, total yield per plant, marketable yield per plant, percentage of fruit and shoot borer effect on shoots and fruit and shoot borer effect on fruits, which were chronicled on whole plot basis.

Commended agronomic practices and need based plant protection measures were judiciously followed. Multivariate analysis (D^2 statistic) as outlined by Mahalanobis (1936) [7] was implemented. Grouping of genotypes into diverse clusters was conceded out by following Tocher's procedure (Rao, 1952) [10]. The relative impact of different characters towards entire genetic divergence was intended as per Singh and Choudhary (1985) [14].

Results and Discussion

Assemblage of genotypes in to different clusters

Present result of cluster analysis (Table 1) naked that the genotypes of brinjal under the study were grouped into eight unlike clusters showing significant variability for selecting different genotypes for advance breeding programmes. Out of eight clusters formed, cluster III was the biggest group containing of 23 genotypes, monitored by cluster II with 15 genotypes, cluster I with 8 genotypes, whereas clusters IV, V, VI, VII and VIII are monotypic.

Intra and inter-cluster distance

The intra and inter cluster distance was calculated for entire traits and are available in Table 2. Experimental outcomes revealed that the highest intra cluster distance was detected for cluster III (78.16) followed by cluster II (50.78) and cluster I (25.46). No intra cluster distance was witnessed in cluster IV, V, VI, VII and VIII as those were denoted by solitary genotype.

The inter cluster D^2 values of the eight clusters publicized that maximum inter cluster generalized distance (471.57) was among cluster V and cluster VIII, followed by VI and VIII (403.39) representing extensive genetic diversity among the genotypes while, the lowest (53.97) was between cluster V and cluster VI. Selection of parents from these diverse clusters for hybridization programme would help in attaining unique recombinants. Analogous remarks were stated by Rani *et al.*, 2019 [9] and Anbarasi and Priya (2021) [11].

Means of intra and inter cluster distance

The cluster means for sixteen quantitative characters in brinjal discovered considerable variance among all the clusters. Cluster wise mean and overall cluster mean for the characters are standing in Table 3. In provision with the current results Gupta *et al.* (2015) [2], Kaur *et al.* (2021) [4] and Leela and Emmanuel (2021) [6] also revealed the same results. From the contemporary study, it is evident that the highest mean value for plant height (101.61) the lowest mean value by cluster VII chronicled lowest plant height (68.87). Cluster VII (16.35) had more number of branches per plant and lowest mean value by cluster VI (10.95).

The genotypes of cluster IV (39.95) took least number of days

to first flowering while the genotypes of cluster VII took highest number of days for first flowering (48.66). The trait days to 50 percent flowering noted its lowermost mean value for the genotypes of cluster IV (43.20) while the genotypes of cluster VII (51.44) showed high mean value.

The genotypes of cluster IV (60.46) acquired less number of days to first fruit harvest while the genotypes of cluster III displayed more number of days for first fruit harvest (68.40). Utmost number of days taken to last fruit harvest was recorded in the genotypes of cluster VII (152.37) whereas lowest mean value was observed in cluster V (115.00).

The highest value for fruit length (cm) was noted in the genotypes of cluster VI (18.15) whereas lowest value was verified in the genotypes of cluster VIII (6.34). The genotypes of cluster VIII showed more fruit width (9.14 cm) while the genotypes of cluster V (2.64 cm) observed less fruit width. Highest mean value for average fruit weight (g) was recorded in the genotypes of cluster VIII (94.42) lowest mean value was noted in the genotypes of cluster V (36.17).

The genotypes of cluster VII recorded utmost mean value for total number of fruits per plant (43.49) while the genotypes of cluster VIII (20.81) recorded lowermost mean value. The character number of marketable fruits per plant registered its highest mean value in the genotypes of cluster VII (39.77), the least mean value was recorded in the genotypes of cluster V (15.85). The character total yield per plant (g) recorded its highest mean value in the genotypes of cluster VII (2326.63) whereas, the lowermost mean value was recorded in the genotypes of cluster V (764.89). The uppermost mean value for marketable yield per plant was recorded in the genotypes of cluster VII (2015.50). The lowermost mean value was documented in cluster V (584.50). The germplasm of cluster IV noted highest ascorbic acid content (8.80 mg/100g) and the lowest ascorbic acid content recorded in cluster II (4.74 mg/100g). Reduced amount of fruit and shoot borer infestation on shoots (%) was noted in the genotypes of cluster VII (10.71) monitored by cluster IV (13.86) whereas, more value was chronicled in the genotypes of cluster VI (23.00) followed by III (19.15). The genotypes of cluster VII stated less fruit and shoot borer infestation on fruits (17.00%) followed by cluster VI (23.49%), while the genotypes of cluster V (29.40%) recorded extreme fruit and shoot borer infestation on fruits followed by cluster IV (28.55%). The results were in consonance with the findings of Rekha and Celine (2015) [11] and Yadav *et al.* (2017) [12].

Relative influence of characters towards diversity

Number of times each of sixteen traits appeared in first rank and its respective per cent contribution towards genetic divergence are accessible in Table 4. The results presented that the character ascorbic acid content contributed maximum (44.24%) towards diversity by taking 564 times first ranking, followed by average fruit weight (31.14%) by 397 times, total number of fruits per plant (13.49%) by 172 times, fruit length (4.08%) by 52 times, days to first flowering (2.27%) by 29 times, fruit width (1.41%) by 18 times, plant height and number of marketable fruits per plant (0.86%) each by 11 times, marketable yield per plant (0.63%) by 8 times, Fruit and shoot borer infestation on shoots (0.39%) by 5 times and days to last fruit harvest (0.31%) by 4 times. Similarly, the character number of branches per plant and fruit and shoot borer infestation on fruits contributed 0.24% and 0.08% by 3 and 1 time respectively. In contrast, the traits days to 50 per

cent flowering, days to first fruit harvest and total yield per plant did not contribute towards total diversity. Sindhuja *et al.* (2019) [13], Valadares *et al.* (2019) [16] and Reshmika *et al.* (2015) [12] also observed such all-out participation of average fruit weight to total divergence. Apart from the high divergence, the performance of the genotypes and the characters with highest involvement towards divergence should also be assumed due consideration which appears as desirable for inclusion in brinjal improvement.

Multivariate analysis following D² statistics presented that significant genetic diversity present within and among the eight clusters. Average intra and inter cluster D² values among 51 genotypes revealed that cluster III exhibited extreme intra cluster D² value revealing the existence of

diverse genotypes in these clusters. The least inter cluster D² value was observed between cluster V and VI indicating the close relationship among the genotypes included in these clusters. The supreme inter cluster value was observed between cluster V and VIII indicating that the genotypes included in these clusters had maximum divergence. The characters, ascorbic acid content, average fruit weight, total number of marketable fruits per plant, fruit length and days to first flowering were the major characters which contributed towards divergence. Hence, hybridization between the genotypes included in these diverse clusters may give high heterotic responses and thus superior segregates are significantly suggested for selection and improvement of brinjal crop.

Table 1: Distribution of brinjal genotypes in different clusters (Tocher's method)

Cluster	No. of genotypes	Genotypes
I	8	A ₃₁ (Swarna Prathiba), A ₄₁ (IC-545948-3), A ₉ (IC-090783), A ₂₅ (IC-345333), A ₃₆ (IC-090783-3), A ₇ (IC-272927), A ₃₀ (IC-110667), A ₃₅ (IC-090783-2)
II	15	A ₄₅ (IC-090084-3), A ₄₆ (IC-545890), A ₃₃ (Surya), A ₁₇ (IC-136280), A ₁ (IC-90925), A ₂₆ (IC-545853), A ₄₇ (IC-090084-2), A ₄₈ (IC-090084-4), A ₈ (IC-104101), A ₅₁ (Bhagyamati), A ₂₂ (IC-127024), A ₁₁ (IC-090084), A ₂₉ (IC-111439), A ₁₆ (IC-090942), A ₄₂ (IC-446756)
III	23	A ₁₈ (IC-99701), A ₄₀ (IC-545948-1), A ₁₃ (IC-104086), A ₂₈ (IC-090915), A ₁₂ (IC-439263), A ₂ (IC-021621), A ₂₄ (IC-136056), A ₃₇ (IC-090783-4), A ₃₉ (IC-090784), A ₃₂ (IC-136056), A ₂₇ (IC-112322), A ₂₀ (IC-345747), A ₃₈ (IC-090783), A ₃₄ (IC-090783-1), A ₃ (IC-23771), A ₁₅ (IC-281112), A ₄₄ (IC-090084), A ₆ (IC-135929), A ₅ (IC-90785), A ₄₉ (IC-090084-5), A ₁₉ (IC-545948), A ₅₀ (IC-090084-6), A ₄₃ (IC-439263)
IV	1	A ₁₀ (IC-446756)
V	1	A ₄ (IC-281072)
VI	1	A ₂₁ (IC-345309)
VII	1	+ (IC-281104)
VIII	1	A ₂₃ (IC-111072)

Table 2: Average intra (bold) and inter-cluster D² values for eight clusters of brinjal genotypes. (Tocher's method)

	I	II	III	IV	V	VI	VII	VIII
I	25.46	55.78	80.29	160.19	135.89	120.13	157.17	155.89
II		50.78	121.67	169.47	99.99	82.15	135.68	283.51
III			78.16	128.90	195.63	177.73	160.93	159.36
IV				0.00	118.54	171.93	167.38	314.00
V					0.00	53.97	242.45	471.57
VI						0.00	221.52	403.39
VII							0.00	334.97
VIII								0.00

* Bold diagonal values indicate intra cluster distance, rest of the values show the inter cluster distance

Table 3: Percent contribution of different characters towards genetic divergence in Brinjal

S. No	Source	Times Ranked 1 st	Contribution %
1	Plant height (cm)	11	0.86
2	Number of branches/ plant	3	0.24
3	Days to first flowering	29	2.27
4	Days to 50% flowering	0	0.00
5	Days to first fruit harvest	0	0.00
6	Days to last fruit harvest	4	0.31
7	Fruit length (cm)	52	4.08
8	Fruit width(cm)	18	1.41
9	Average fruit weight(g)	397	31.14
10	Total number of fruits/ plant	172	13.49
11	Number of marketable fruits/ plant	11	0.86
12	Total yield/ plant (g)	0	0.00
13	Marketable yield/ plant (g)	8	0.63
14	Ascorbic acid content (mg/100g)	564	44.24
15	Fruit and shoot borer infestation on shoots (%)	5	0.39
16	Fruit and shoot borer infestation on fruits (%)	1	0.08

Table 4: Mean values of clusters for sixteen traits in 51 genotypes of brinjal (Tocher's method)

	Plant height (cm)	No. of branches / plant	Days to first flowering	Days to 50% flowering	Days to first fruit harvest	Days to last fruit harvest	Fruit length (cm)	Fruit width (cm)	Average fruit weight (g)	Total no. of fruits/plant	No. of marketable fruits/plant	Total yield/plant (g)	Marketable yield/plant (g)	Ascorbic acid content (mg/100g)	Fruit and shoot borer infest. on shoots (%)	Fruit and shoot borer infest. on fruits (%)
1	76.65	13.30	45.77	48.63	65.76	130.98	6.54	5.42	64.64	23.92	18.55	1544.69	1205.30	5.12	18.21	28.40
2	79.23	13.50	45.49	48.73	65.33	132.19	8.79	4.18	57.21	28.34	23.09	1628.75	1332.16	4.74	17.36	25.55
3	79.16	13.21	48.47	51.29	68.40	132.90	8.53	4.72	67.81	27.43	22.33	1893.53	1550.28	6.99	19.15	25.41
4	101.61	13.78	39.95	43.20	60.46	138.06	10.04	3.97	40.69	27.41	21.08	1190.33	862.89	8.80	13.86	28.55
5	80.18	13.17	42.06	45.90	64.50	115.00	11.66	2.64	36.17	21.11	15.85	764.89	584.50	5.61	18.37	29.40
6	79.83	10.95	47.25	49.94	66.42	127.34	18.15	2.66	56.19	23.44	19.64	1326.33	1117.88	4.81	23.00	23.49
7	68.87	16.35	48.66	51.44	67.76	152.37	6.84	5.10	50.53	43.49	39.77	2326.63	2015.50	6.54	10.71	17.00
8	73.65	12.56	44.91	47.69	64.77	129.94	6.34	9.14	94.42	20.81	16.19	1972.54	1541.91	6.76	19.12	28.04

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