SHORT COMMUNICATION

Studies in Brinjal Genotypes: Part II–Genetic Divergence

B Ramesh Babu and RV Patil
Department of Horticulture, University of Agricultural Sciences, Dharwad–580005 (Karnataka)
Email : rameshmanj@yahoo.com

Mahalanobis's D^2 statistics was used to study genetic divergence for 20 characters in a collection of 90 brinjal genotypes. These 90 genotypes were grouped into 7 clusters on the basis of relative magnitude of D^2 values. The maximum contribution towards the total genetic divergence was from yield per plant. It has been observed that no close correspondence is evident between geographical distribution to genetic divergence as estimated by D^2 statistics. The maximum inter cluster distance was observed between cluster IV and VII, while minimum was recorded between III and IV.

Key Words : Brinjal, Cluster Analysis, Divergence

A successful breeding programme is associated with diversity of parents. More diverse the parents, better are the chances of improving economic characters. This genetic divergence existing in the population helps in selecting the suitable parents for hybridization programme resulting superior hybrids and desirable recombinants. Mahalanobis's (1936) genaralized distance estimated by D^2 statistics was employed to assess the amount of genetic diversity for 90 brinjal genotypes.

Ninety brinjal genotypes from the germplasm maintained at Department of Horticulture, UAS Dharwad were evaluated during 2000-2001 in a Randomized Block Design with two replications in Vegetable Section of Golden Jubilee Block, Kumbapur Farm, Dharwad. Ten plants of each genotype were transplanted in each replication in a single row. The recommended cultural practices were adopted as per the UAS, Dharwad. The observations for 20 characters were recorded on three plants selected randomly. The mean values were used for Mahalanobis D^2 statistics to know the genetic divergence as described by Tocher's method (Rao, 1952).

Analysis of variance indicated highly significant differences among the genotypes for all the characters except fruit pedicel thickness. On the basis of D^2 analysis, the 90 genotypes were grouped into 7 clusters. The maximum number of genotypes were found in cluster I (38) followed by cluster V (20), cluster II(18), Cluster III(10) and Cluster IV (2). Cluster VI and VII were solitary consisting only one genotype in each. The clustering pattern of these genotypes under the study suggested that geographic diversity may not be necessarily related with genetic diversity. Similar findings were also reported by Yadav *et al.* (1996) and Rajeshkumar *et al.* (1998).

Contribution of different plant characters for total genetic divergence is important for the purpose of further selection and choice of parents for hybridization. The maximum contribution was found from yield per plant (97.95%) followed by fruit weight (1.34%) leaf area (0.56%), plant height at 50 per cent flowering (0.07%), days to 50 per cent flowering (0.05%) and leaf length (0.02%). However, Rajeskumar *et al.*, (1998) have reported fruit width followed by fruit length and yield per plot as responsible for grouping of germplasm. The differences in the contributing factors for genetic divergence is attributed to different genotypes under study, grouping patterns of the genotypes based upon colour and shape of fruits, method of analysis etc.

Intracluster distance was minimum (D^2 = 61.275) in the cluster IV, while maximum (D^2 = 255.48) in cluster V (Table 1). The highest genetic diversity in cluster V may due to both natural and artificial selection forces among the genotypes. Intracluster distance was

Table 1. Intra- and inter-cluster distance in 7 clusters

Clusters	I	II	III	IV	V	VI	VII
I	237.72	564.73	1390.00	935.76	684.30	999.359	2050.15
II		191.38	1905.68	419.49	1184.03	1514.65	2570.33
III			230.17	2296.932	768.02	417.28	690.43
IV				61.275	1570.36	1905.98	2963.86
V					255.48	389.06	1414.90
VI						0.00	1058.24
VII							0.00

Table 2. Cluster means for 20 quantitative characters in brinjal

Sl. No.	Character	Clusters						
		I	II	III	IV	V	VI	VII
1	Petiole length (cm)	1.97	2.18	1.99	2.57	2.22	1.90	1.49
2	Leaf length (cm)	11.87	12.19	11.21	10.815	11.37	10.00	11.15
3	Leaf breadth (cm)	8.28	8.49	7.5	7.45	7.42	5.79	7.08
4	Leaf area (cm)	47.66	39.92	47.94	39.51	43.52	34.23	50.90
5	Stem girth (cm)	1.72	1.81	1.75	2.44	1.86	1.65	2.35
6	Plant height at 50% flowering	23.73	22.22	25.84	26.72	24.11	17.92	22.60
7	Number of branches per plant	6.76	6.4	8.19	6.66	6.47	9.83	8.00
8	Days to 50% flowering	50	49.22	43.65	48.0	47.75	47	44
9	Number of flowers per cluster	3.20	2.64	3.14	2.33	2.08	3.33	3.50
10	Number of fruits per cluster	1.43	2.07	1.06	1.0	1.52	2.66	1.0
11	Flower length (cm)	3.48	3.72	4.14	3.50	3.46	3.70	3.55
12	Flower width (cm)	2.96	2.96	3.76	3.10	3.23	3.60	4.95
13	Fruit pedicel length (cm)	3.82	3.22	4.50	4.15	4	4.58	5.48
14	Fruit pedicel thickness (cm)	0.99	1.43	1.13	0.79	1.0	0.88	1.18
15	Fruit calyx length (cm)	3.28	3.3	3.72	2.55	3.48	3.23	5.14
16	Fruit length (cm)	8.86	7.35	7.70	5.12	7.26	7.85	6.30
17	Fruit Diameter (cm)	4.35	4.27	5.49	3.43	5.92	3.10	6.93
18	Fruit weight (g)	57.35	45.78	110.91	30.25	90.81	77.50	112.50
19	Number of fruits per plant	26.64	25.58	24.85	18.75	25,13	32.0	31.5
20	Yield per plant (g)	1411.81	1214.22	2785.00	693.75	2230.89	2607.45	3665.0

minimum between the cluster III and IV while maximum intracluster distance between clusters IV (DBC-46-HA & DBC-104-MH) and VII (DBC-18-AP) followed by between cluster II (DBC-75-KA and DBC-125-KA) and V (DBC-76-KA and DBC-77-KA) indicating the genotypes of these clusters could be used as parents in hybridization programme to get the higher heterotic hybrids or isolate a good variant as genotypes from the seggregant population. Similar views were also expressed by Pramanik *et al.* (1992) and Rajeshkumar *et al.* (1998).

Cluster means for different characters (Table 2) revealed that the cluster values excelled in respect of different characters. Cluster VII was diverse with a good source of yield per plant, fruit weight, fruit width, fruit calyx length, fruit pedicel length, flower width, number of flowers per cluster and leaf area. Cluster III represented with lowest number of fruits per plant, higher fruit calyx length and early maturing genotypes in terms of days to 50 per cent flowering. Thus by involving in the hybridization the genotypes of higher mean performance for required characters under consideration as potential parents, future improvement in brinjal can be achieved (Rajeshkumar *et al.*, 1998).

References

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