The Pharma Innovation Journal 2021; 10(12): 996-999

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277- 7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2021; 10(12): 996-999

www.thepharmajournal.com
Received: 15-09-2021
Accepted: 30-11-2021

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Genetic divergence study in brinjal (*Solanum melongena* L.)

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Abstract

A study on genetic divergence was carried out in sixty genotypes of aubergine at Main Vegetable Research Station, Anand Agricultural University located at Anand district of Gujarat during crop season *kharif- rabi* 2017-18. The sixty genotypes were grouped into six clusters through Mahalanobis D^2 statistics. Total soluble sugars, total phenol, fruit weight, total soluble solids, fruit length, plant height, number of fruits per plant, number of branches per plant, fruit girth and days to 50 per cent flowering contributed maximum to the total genetic divergence. The maximum genetic divergence was observed between cluster III and cluster V, followed by cluster I and VI. The maximum average fruit yield value found for cluster V followed by cluster I, cluster II, cluster III, cluster IV and cluster VI.

Keywords: Genetic divergence

Introduction

Brinjal or eggplant (*Solanum melongena* L.) is an important solanaceous crop of sub-tropics and tropics. The name brinjal is popular in Indian subcontinents and was derived from Arabic and Sanskrit. Whereas, the name eggplant has been derived from the shape of the fruit of some varieties, which are white and resemble in shape to chicken eggs. It is also called aubergine (French word) in Europe. The brinjal is of much importance in the warm areas of Far East, being grown extensively in India, Bangladesh, Pakistan, China and Philippines. It is also popular in Egypt, France, Italy and United States. In India, it is one of the most common, popular and principal vegetable crops grown throughout the country except higher altitudes. It is a versatile crop adapted to different agro-climatic regions and can be grown throughout the year. It is perennial in nature, but grown commercially as an annual crop. A number of cultivars are grown in India, consumer preference being dependent upon fruit color, size and shape. A great extent of divinity present in various qualitative and quantitative traits among the genotypes of brinjal suggested good scope for improvement in economic traits through conventional breeding. In any crop improvement programme, 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. Genetic diversity can be worked out with the help of D^2 analysis which was given by Mahalanobis (1936) [5]. For the first time use of this technique for assessing the genetic variability in plants was suggested by Rao (1952) [8]. It is a very potent technique of measuring genetic divergence. Now it is reliably and extensively used in plants for measuring genetic divergence. The aim of forming clusters and finding the intra and inter cluster divergence is to provide the base of selecting parents for a planned breeding programme. Keeping in view the above facts present investigation was undertaken to work out genetic divergence among 60 genotypes based on twelve important traits of brinjal, to help the breeders in selecting promising and genetically diverse parents for desired improvement.

Materials and Methods

The experiment comprising of sixty diverse genotypes was carried out in randomized block design with three replications during *kharif-rabi* season of the year 2017-18 at Main Vegetable Research Station, Anand Agricultural University, Anand. Each plot had eight plants of single genotype with inter and intra row spacing of 90 cm × 75 cm. The genotypes were randomly allotted to the plots in each replication. The package of practices was followed as per the recommendations for raising good and healthy crop. Three plants were selected in each plot in each replication excluding border plants for recording and observation.

Data were recorded on twelve characters as indicated in Table 3. Genetic diversity between groups was estimated using D^2 statistics given by Mahalanobis PC [5]. All the twelve traits were correlated and transformed into uncorrelated linear combinations through computer. The mean values of the uncorrelated linear combination where computed to calculate D^2 values between all possible pairs of genotypes. The grouping of genotypes was done by using Tocher's method as described by Rao CR [8]. The criterion used in clustering by this method is that varieties belonging to same cluster should show a smaller D^2 value than those belonging to different clusters.

Table 1: Distribution of 60 genotypes of brinjal to different clusters on the basis of D^2-statistics

Sr. No.	Cluster	Number of genotypes	Name of the genotypes	Source
1	I	25	GPBRJ 4, GPBRJ 5, GPBRJ 11, GPBRJ 24, GPBRJ 28, GPBRJ 39, GPBRJ 40, GPBRJ 50, GPBRJ 63, GPBRJ 65, GPBRJ 66, GPBRJ 68, GPBRJ 70, GPBRJ 99, GPBRJ 103, GPBR 108J, GPBRJ 110, GPBRJ 111, GPBRJ 114, GPBRJ 116, GPBRJ 176, GPBRJ 184,	AAU, Anand (Gujarat)
			GPBRJ 141	NCR (Delhi)
			GPBRJ 195	Shimala (HP)
			Kashi Taru	IIVR, Varanasi (UP)
2	II	19	GPBRJ 12, GPBRJ 31, GPBRJ 38, GPBRJ 72, GPBRJ 73, GPBRJ 75, GPBRJ 78, GPBRJ 100, GPBRJ 112, GPBRJ 121, GPBRJ 126, GPBRJ 198, GAOB 2, GOB 1, Doli 5	AAU, Anand (Gujarat)
			GPBRJ 149	Virpura, (Gujarat)
			GPBRJ 158	Tamilnadu
			GPBRJ 200	Dholka, (Gujarat)
			Punjab Sadabhar	PAU, Ludhiana (Punjab)
3	III	7	GPBRJ 187, ABSR 2	AAU, Anand, (Gujarat)
			JBL 10-08-08	JAU, (Gujarat)
			NSP 1	NAU, (Gujarat)
			Swarna Mani	CHES, Bhubaneswar (Orrissa)
			KS 224	Kalyanpur (West Bengal)
			JBGR 1	JAU, (Gujarat)
4	IV	6	GPBRJ 97, GPBRJ 119,	AAU, Anand, (Gujarat)
			GPBRJ 133	Namchi (Sikkim)
			GPBRJ 148	Kotdapitha, (Gujarat)
			GPBRJ 153	Rudtal, (Gujarat)
			Arka Kesav	IIHR,Bengaluru (Karnataka)
5	V	2	GPBRJ 127	AAU, Anand, (Gujarat)
			GPBRJ 137	Sabar katha (Gujarat)
6	VI	1	GPBRJ 117	AAU, Anand, (Gujarat)

Result and Discussion

Group constellation: The D^2 values between all pairs ranged from 44.36 (between GPBRJ 111 and GPBRJ 184 genotypes) to 1307.16 (between GPBRJ 117 and Arka Kesav genotypes), which indicated the presence of high genetic diversity among the genotypes for all the characters. On the basis of D^2 statistics six clusters were formed from sixty genotypes of brinjal. The composition of clusters is given in the Table 1. The cluster I was the largest having 25 genotypes followed by cluster II (19 genotypes), cluster III (7 genotypes) and cluster IV (6 genotypes). The cluster V contain only two genotypes. While, cluster VI found monogenotypic. The clustering pattern indicated that the genetic diversity was not fully associated with geographical diversity, hence, there was no formal relationship between geographical diversity and genetic diversity. Similarly fifty seven diverse genotypes of brinjal were grouped into eight different clusters by Kumar *et al.* (2007) [4]. Twenty four diverse genotypes of brinjal were grouped into four clusters by Sherly and Shanthi (2007) [9]. Mehta and Sahu (2009) [6] carried out a similar type of genetic divergence study in fourteen genotypes of brinjal and grouped them into five clusters using Tocher's method.

Inter-cluster and Intra-cluster Distances: The perusal of intra-cluster and inter-cluster distance (Table 2) revealed that inter-cluster values were greater than intra-cluster distance values. The maximum inter-cluster distance (D^2=8362.80) was found between cluster III and cluster V, followed by cluster I and cluster VI (D^2=7446.40), cluster V and cluster VI (D^2=7197.50), cluster II and cluster VI (D^2=6310.90), cluster I and cluster V (D^2=4866.80) and cluster II and cluster III (D^2=4682.96). The minimum inter-cluster distance was observed between cluster II and cluster IV (D^2=1387.00). The maximum intra-cluster distance (D^2) contributed by cluster III (D^2=786.15) followed by cluster V (D^2=523.72), cluster IV (D^2=507.06), cluster I (D^2=454.31) and the minimum intra cluster distance was contributed by cluster II (D^2=440.76). Selection of parents from highly diverse genotypes for hybridization work gives a range of useful combination and result into highly heterotic hybrids.

Cluster Means of Different Characters: The mean values of 12 characters for six clusters are summarized in Table 3. The maximum average fruit yield value found for cluster V (1.27 kg per plant) followed by cluster I (1.24 kg/plant), cluster II (1.22 kg/plant), cluster III (1.22 kg/plant), cluster IV (1.21 kg/plant) and cluster VI (0.92 kg/plant). For days to 50 per cent flowering cluster VI (42.8), cluster V (44.2) and cluster II (46.3) found early than average value for the trait. The highest and the lowest mean values for plant height was recorded by cluster VI (114.70 cm) and cluster I (75.80 cm), respectively. While, number of branches per plant recorded significantly the highest mean for cluster VI (4.77). Cluster IV manifested higher value for number of fruits per plant

(15.8) and fruit length (17 cm). The cluster III recorded significantly higher cluster mean value for fruit weight. Important qualitative character *viz.*, total phenol and moisture content found higher for cluster III (20.94) and cluster II (81.71) respectively. The cluster V depicted higher cluster mean value for the trait total soluble sugar (4.62) and total soluble solids (5.5). There were different characters which showed superiority with respective clusters, therefore, breeder should select genotypes from particular clusters according to need of crop improvement programme.

Characters Contribution towards Genetic Divergence: The analysis of variance for each character was carried out using mean of the sixty genotypes. Estimation of inter-cluster and intra-cluster variances, along with ratio (R^2) of inter-cluster variance to the total variance for the twelve characters were worked out and presented in Table 3. The maximum value of R^2 was observed for total soluble sugars (0.94) and total phenol (0.93) followed by days to 50 per cent flowering (0.77), total soluble solids (0.61), fruit weight (0.41), fruit length (0.39), plant height (0.34), number of fruits per plant (0.19), number of branches per plant (0.18) and fruit girth (0.097). These traits had more contribution in genetic divergence. The R^2 value of moisture content (0.07) was the least among all the characters under study depicting the minimum contribution of the trait for the divergence.

Inter-cluster coefficient of variance (CV_b) was the maximum for total soluble sugar (147.22) followed by total phenol (121.79), fruit weight (28.79), total soluble solids (20.79), fruit length (18.56), plant height (17.39), number of fruits per plant (16.75), number of branches per plant (11.37), fruit girth (7.16) and days to 50 per cent flowering (3.54). These traits manifested higher CV_b values demonstrating an important role in the genetic discrimination of the genotypes included under study. The minimum CV_b (2.39) was observed for moisture content. Based on the high inter-cluster value crossing of genotypes of cluster III and V could be useful to get maximum hybrid vigour and desirable segregants. Also based on mean performance and genetic distance, hybridization involving GPBRJ 187, ABSR 2, JBL 10-08-08, NSP 1, Swarna Mani, KS 24 and JBGR 1 (cluster III) and GPBRJ 127 and GPBRJ 137 (cluster V) should result in desirable recombinants leading to the development of useful genetic stocks.

Estimates of inter-cluster and intra-cluster variances, along with the ratio (R^2) of inter-cluster variance to the total variance and the inter-cluster coefficient of variation (CV_b) for 12 characters were worked out. The maximum value of R^2 was observed for total soluble sugars (0.94) and total phenol (0.93), followed by days to 50 per cent flowering (0.77), total soluble solids (0.61), fruit weight (0.41), fruit length (0.39), plant height (0.34), number of fruits per plant (0.19), number of branches per plant (0.18) and fruit girth (0.097). These traits had more contribution in genetic divergence. Similar result reported regarding fruit weight and fruit length by Kumar *et al.* (2007) [4] and Devmore *et al.* (2015) [1], for plant height, days to 50 per cent flowering and fruit length by Polignano *et al.* (2009) [7], for fruit girth by Islam *et al*. (2011) [2] and for total phenol by Kumar *et al.* (2013) [3] for the maximum contribution towards genetic divergence. Hence, selection of divergent parents based on these characters will be useful for selection in heterosis breeding in brinjal. The R^2 value of moisture content was the least among all the characters under study depicting the minimum contribution of the trait for the divergence.

Table 2: Average intra-cluster and inter-cluster value for 60 genotypes of brinjal

Clusters	I	II	III	IV	V	VI
I	454.31	1622.61	2954.40	2602.71	4866.80	7446.40
II		440.76	4682.96	1387.00	1475.10	6310.90
III			786.15	2673.40	8362.80	2968.70
IV				507.06	2347.80	2497.60
V					523.72	7197.50
VI						0

Table 3: Clusters means of different characters in brinjal

Cluster	FYP	DFF	PH	NBP	NFP	FL	FG	FW	TP	MC	TSS_1	TSS_2
I	1.24	47.8	75.8	3.48	13.6	12.44	17.62	100.4	6.09	78.67	0.55	5.03
II	1.22	46.3	87.1	3.65	15.4	13.98	17.07	101.7	6.59	81.71	2.59	4.66
III	1.22	48.8	89.1	3.72	11.6	12.58	18.37	151.9	20.94	78.60	0.37	3.53
IV	1.21	49.3	92.3	3.48	15.8	17.0	15.14	96.1	16.24	78.61	2.87	4.08
V	1.27	44.2	81.9	2.61	14.7	12.50	17.10	90.8	7.40	78.34	4.62	5.50
VI	0.92	42.8	114.7	4.77	8.57	13.77	20.22	113.8	30.83	77.35	3.16	5.00
Mean	1.22	47.40	83.46	3.56	14.17	13.42	17.31	106.30	9.45	79.58	1.59	4.66
SEm	8.67	1.88	6.52	0.27	1.59	0.99	1.22	11.85	1.01	2.10	0.17	0.24
CD(0.05)	NS	NS	18.08	0.77	4.41	2.76	NS	32.85	2.81	NS	0.48	0.69
CV %	21.70	12.24	24.04	24.04	34.57	22.82	21.82	34.29	32.99	8.13	33.87	16.49
R^2	-	0.77	0.34	0.18	0.19	0.39	0.09	0.41	0.93	0.07	0.94	0.61
CV_b %	-	3.54	17.39	11.37	16.75	18.56	7.16	28.79	121.79	2.39	147.22	20.79

FYP: Fruit yield per plant, DFF: Days to 50% flowering, PH- Plant height, NBP: Number of branches per plant, NFP: Number of fruits per plant, FL: Fruit length, FG-Fruit girth, FW: Fruit weight, TP: Total phenol content, MC: Moisture content, TSS_1: Total soluble solids, TSS_2: Total soluble sugars, R^2: Ratio of the inter-cluster variance to the total variance, NS: Non significant, - : Not estimated due to –ve variance, CV_b: Inter-cluster coefficient of variation.

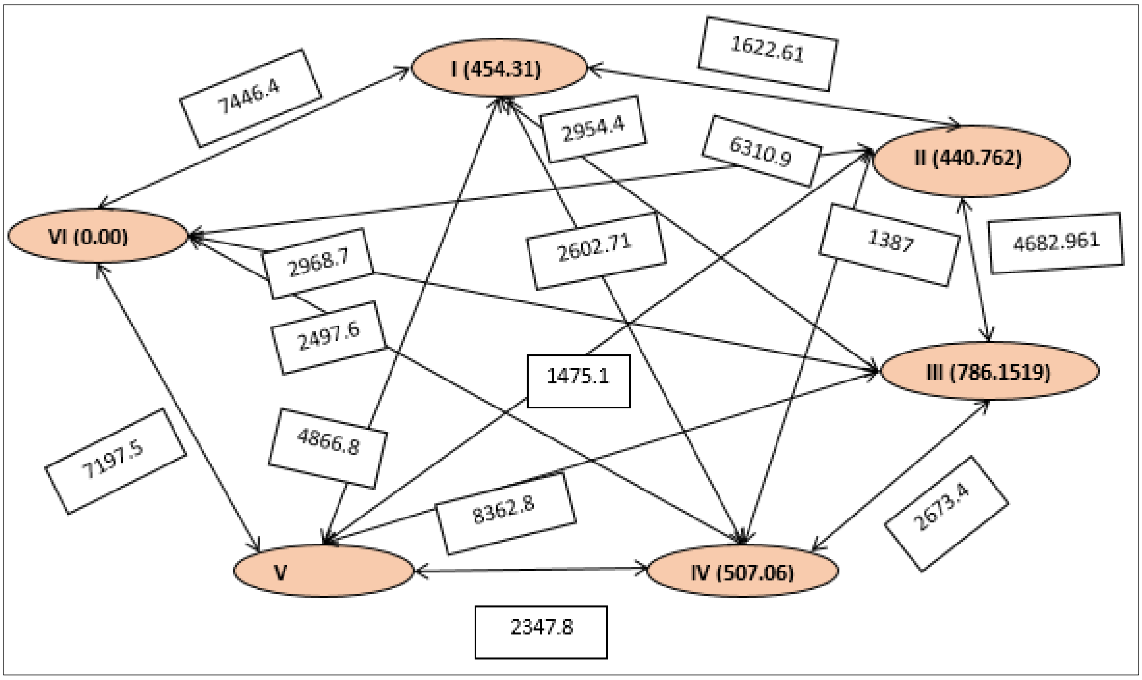

Fig 1: Clustering pattern of different group with inter cluster and intra cluster distance among the brinjal genotypes

Conclusion

Maximum inter cluster distance between clusters III and V and maximum contribution of total soluble sugars, total phenol, fruit weight, total soluble solids, fruit length, plant height, number of fruits per plant, number of branches per plant, fruit girth and days to 50 per cent flowering suggested that selection of one or two elite genotypes from such divergent clusters based on the above characters and crossing would result in more heterosis and throw useful transgresssive segregants.

The most productive hybrids and diverse segregating materials may come from high yielding parents with high genetic diversity. Therefore, from D^2 analysis of genetic diversity, based upon high yielding genotypes and large inter-cluster distance, it is advisable to attempt crossing of the genotypes from cluster III with cluster V, which may lead to a broad spectrum of favorable genetic variability for yield improvement in brinjal.

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