## International Journal of Chemical Studies

P-ISSN: 2349–8528 E-ISSN: 2321–4902 IJCS 2019; 7(4): 1456-1459 © 2019 IJCS Received: 04-05-2019 Accepted: 06-06-2019

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### Genetic divergence studies in brinjal (Solanum melongena L.) under Tarai conditions of Uttarakhand

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### Abstract

Forty One genotypes of two groups (long purple and round purple) including two checks (Pant Rituraj and Pant Samrat) at executed at Vegetable Research Centre, Department of Vegetable Science, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, U.S. Nagar, during winter season 2017-2018 to estimate genetic divergence in brinjal genotypes. Observations were recorded on 13 quantitative characters namely as, Days to 50% flowering, days to first harvest, total marketable fruit yield (q/ha), plant height(cm), fruit length(cm), fruit diameter(cm), number of primary branches per plant, number of secondary branches per plant, number of fruits per plant, average fruit weight(g), fruit yield per plant(kg), harvest-wise yield kg/plot and reaction to fruit and shoot borer. In the present investigation, D<sup>2</sup> analysis revealed the presence of considerable diversity in the set of 41 genotypes of brinjal. The genotypes were observed to be distributed in ten different clusters. Cluster I had highest number of genotypes (30) followed by cluster IV (3) and Cluster II, III, V, VI, VII, VIII, IX and X having one genotype each. Maximum intra-cluster distance was found in cluster IV showing existence of wide genetic divergence. Maximum inter-cluster D<sup>2</sup> values were observed between the clusters IX and X indicating that the genotypes in these clusters can be used as parents in hybridization programme. Among the characters, reaction to fruit and shoot borer showed maximum contribution towards the diversity followed by average fruit weight, number of fruits per plant, fruit length, days to first harvest and fruit diameter Among the characters, reaction to major biotic stress like fruit and shoot borer showed maximum contribution towards the diversity followed by average fruit weight, number of fruits per plant, fruit length, days to first harvest and fruit diameter. The genotypes PB-301, PB-306 and PB-307 as round fruit shape genotypes, PB-321, PB-310 and PB-319 for long fruit shape genotypes are higher yielder and the infestation of fruit and shoot borer was found minimum for PB-304 and PB-330. Based on these observations, above genotype can be recommended for cultivation under tarai region of Uttarakhand.

Keywords: Genetic divergence studies, brinjal (Solanum melongena L.), Tarai conditions

### Introduction

Brinjal or eggplant (Solanum melongena L., 2n=2x=24) is one of the most popular and principal Solanaceous vegetable crops. It is worldwide known as aubergine or guinea squash which is one of the most popular and major vegetable crop in India and other parts of the world. It Southern Europe, brinjal is a staple vegetable and it is a favourite dish in South East of France. Brinjal has got much potential as raw material in pickle making and dehydration industries. It is highly productive and usually finds its place as the poorman's vegetable. In India, it is being consumed as a cooked vegetable in many ways and is liked by both poor and rich. Year round availability, easy culture, moderate to high yield and consumption in varieties of ways like salad, bhaji, stuffed brinjal, bhartha, chatni, pickles etc., has made brinjal the king of vegetables in India. Further, in recent years brinjal is being exported in the form of products like baingan bhartha, chatni, pickles etc. Solanum incanum, a wild species and having wide distribution in atleast 10 habitats in India is the progenitor of the cultivated species, Solanum melongena. Brinjal crop is under constant assault by biotic agents including various pathogens and insect herbivores, with enormous economic and ecological impact and the most extensive damage to brinjal fruit yield is caused by fruit & shoot borer and diseases like phomopsis blight and little leaf which reduces the yield and inflicts colossal loss in production. There is an utmost need for development of high yielding varieties and hybrids for specific environments (Vaddoria et al., 2009).

Genetic divergence plays a pivotal role in assessment of diversity and establishing relationships among cultivated species and thus facilitates the establishment of conservation strategies, the use of genetic resources in breeding programmes, and the study of crop evolution (Mishra *et al.*, 2013)<sup>[8]</sup>. Therefore, brinjal having a greater variation with regard to fruit yield and its component traits, genetic divergence based on Mabalanobis D<sup>2</sup> technique as described by Rao (1952)<sup>[11]</sup> appears to be a fruitful approach which is based on multivariate analysis and serves to be a good index of genetic diversity. Existence of large variability among the genotypes necessitates further analysis of genetic divergence (Mehta *et al.*, 2004)<sup>[7]</sup>.

### **Materials and Methods**

The field experiment under present investigation was conducted during winter season 2017-2018, at the Vegetable Research Centre, Department of Vegetable Science, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, U S. Nagar (U.K.). The experimental field had sandy loam soil, low in organic carbon, nitrogen, medium in phosphorus, potash, and slightly alkaline in nature with pH 7.2. The experimental material for the present investigation comprised of 41 genotypes of brinjal collected from different places in India and being maintained at Vegetable Research Centre, Department of Vegetable Science, Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, U. S. Nagar (U.K.). The experiment was conducted in Randomized Complete Block Design with three replications during winter season in 2017-2018 to assess the performance of 41 genotypes. Transplanting was done at a spacing of 75 cm between row to row and 60 cm plant to plant. All the recommended package of practices for raising a healthy crop were followed. Observations were recorded on five randomly selected plants of each genotype in each replication for various traits. The data thus obtained was analyzed as per method given by Mahalanobis, 1936. Criteria Toucher (Rao, 1952)<sup>[11]</sup> was used for determining the groups and clustering was done accordingly. Average inter and intra cluster distances were estimated as per method given by Singh and Chaudhary, 1985.

### **Results and Discussion**

Fourty One genotypes of two groups (long purple and round purple) including two checks (Pant Rituraj and Pant Samrat) were grouped into six clusters on the basis of  $D^2$  values, suggesting adequate genetic diversity for selecting superior and diverse parents which can be suitable exploited for any brinjal improvement programme.

On the basis of  $D^2$  values forty one genotypes including two checks were grouped into ten clusters by treating estimated  $D^2$ values as the square of the generalized distance. The distribution of entries into various clusters is given in Table 1

Table 1:	Classification of	of brinial ge	notypes into	different clus	ters based on $D^2$ value
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Cluster number	Number of genotypes	Name of the genotype				
Ι	30	PB-302, PB-305, PB-309, PB-310, PB-311, PB-313, KashiTaru, Punjab Sadabahar, PB-314, PB-316, PB-318, PB-319, PB-320, PB-321, PB-322, PB-323, PB-324, PB-325, PB-326, PB-327, PB-328, PB-328, PB-329, P				
		329, PB-331, PB-332, PB-333, PB-334, PB-335, PB-336, Pant Rituraj and Pant Samrat				
II	1	PB-330				
III	1	PB-308				
IV	3	PB-307, PB-312 and PB-315				
V	1	PB-303				
VI	1	PB-301				
VII	1	PB-304				
VIII	1	PB-317				
IX	1	PB-306				
Х	1	PB-337				

Cluster I was the largest having 30 genotypes followed by cluster IV with 3 genotypes, cluster III, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX and cluster X having one genotype each. Genotypes usually did not cluster according to geographical distributions. Singh and Nandpuri (1974)<sup>[12]</sup>, Pramanick et al. (1992)<sup>[10]</sup>, Doshi et al. (1998)<sup>[1]</sup>, Kumar et al. (1998)<sup>[4]</sup>, Mohanty and Prusti (2000)<sup>[9]</sup> also reported similar results in brinjal. In present study also no direct relationship was noticed between geographical distribution and genetic distance. Intra-cluster and Intercluster average D<sup>2</sup>values are presented in Table 2. Among the ten clusters, cluster IV with 3 genotypes showed maximum intra-cluster diversity (D<sup>2</sup>=22.01) followed by cluster I (D<sup>2</sup>=18.57) and cluster II, cluster III, V, VI, VII, VIII, IX and X had no intra-cluster distance (D<sup>2</sup>=0.00) as they possessed single genotype. Maximum intra-cluster distance in cluster IV (22.01) showed existence of wide genetic divergence when compared to other clusters. High degree of divergence among the genotypes within a cluster could produce more segregating breeding material and selection within such cluster can be performed based on maximum mean value for the desirable characters.

Based on distances between clusters, *i.e.*, inter-cluster distances, the maximum divergence was observed between clusters IX and cluster X (D<sup>2</sup>=76.41) followed by clusters VIII and IX (D<sup>2</sup>=70.60), cluster IV and X (D<sup>2</sup>=65.34), cluster V and IX (D<sup>2</sup>=60.94), cluster VI and IX (D<sup>2</sup>=60.53), cluster VIII and IX (D<sup>2</sup>=57.15), cluster III and IX (D<sup>2</sup>=54.78), and cluster II and X (D<sup>2</sup>=54.70), cluster III and X (D<sup>2</sup>=52.02), cluster VIII and X (D<sup>2</sup>=50.98), cluster IV and VII (D<sup>2</sup>=50.22). The minimum inter-cluster D2 values were recorded in case of cluster VI and cluster VII (D<sup>2</sup>=23.55), cluster VI and cluster X (D<sup>2</sup>=23.55), cluster V and VI (D<sup>2</sup>=24.48), cluster I and cluster III (D<sup>2</sup>=24.58), cluster I and cluster II (D<sup>2</sup>=24.60), cluster III and cluster VIII (D<sup>2</sup>=25.72), cluster V and cluster VIII (D<sup>2</sup>=26.19), cluster I and cluster V (D<sup>2</sup>=26.98) in Table 2.

The higher inter- cluster distance indicated greater genetic divergence between the genotypes of these clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. Hence these genotypes can be used in singly as well as multiple crossing programmes for the development of promising hybrids.

 Table 2: Inter and Intra cluster distances of ten clusters of brinjal genotypes

Clusters	Cluster- I	Cluster- II	Cluster- III	Cluster- IV	Cluster- V	Cluster- VI	Cluster- VII	Cluster- VIII	Cluster- IX	Cluster- X
Cluster-I	18.57	24.60	24.58	32.67	26.98	30.28	30.83	30.66	48.16	47.19
Cluster-II		0.00	37.77	29.96	38.83	40.03	31.36	47.86	31.81	54.70
Cluster-III			0.00	33.06	25.72	31.92	43.17	23.55	54.78	52.02
Cluster-IV				22.01	42.12	46.68	50.22	47.51	31.57	65.34
Cluster-V					0.00	24.48	31.71	26.19	60.94	41.05
Cluster-VI						0.00	22.97	35.85	60.53	23.55
Cluster-VII							0.00	44.34	57.15	28.77
Cluster-VIII								0.00	70.60	50.98
Cluster-IX									0.00	76.41
Cluster-X										0.00

Table 3: Cluster mean of different characters of brinjal genotypes

Cluster Traits	Days To 50 % Flowering	Days To First Harvest	Total Marketable Fruit yield (q/ha)	Plant Height (cm.)	Fruit Length (cm.)	Fruit Diameter (cm)	No. of Primary Branches Per plant	No. of Secondary Branches Per Plant	No. of Fruits Per Plant	Average Fruit Weight (g)	Fruit Yield Per Plant (kg)	Harvest Wise- Yield Kg/ Plot	Reaction To Fruit And Shoot Borer
Cluster-I	121.93	147.13	129.68	63.19	11.34	5.75	5.73	15.31	9.63	61.00	0.58	5.84	25.66
Cluster-II	121.33	149.33	141.92	64.11	7.24	6.98	7.08	15.53	7.47	85.46	0.64	6.39	16.61
Cluster-III	122.00	139.33	108.21	63.37	8.56	7.32	5.33	18.37	8.75	55.65	0.48	4.87	40.60
Cluster-IV	123.33	156.00	151.59	71.24	12.07	4.82	5.72	16.16	6.64	104.53	0.68	6.82	32.75
Cluster-V	121.33	177.33	119.33	67.82	7.60	7.17	5.01	12.60	12.96	41.42	0.54	5.37	33.48
Cluster-VI	120.67	142.00	224.01	56.63	9.69	7.37	4.65	10.52	22.27	45.25	1.01	10.08	29.20
Cluster-VII	128.33	148.33	192.18	70.18	7.39	8.17	4.43	12.40	18.75	46.12	0.87	8.65	14.10
Cluster-VIII	143.00	148.33	47.96	61.92	14.34	3.84	4.33	14.85	7.54	28.64	0.22	2.16	35.97
Cluster-IX	125.33	148.00	204.31	68.70	7.95	8.49	5.63	12.57	6.58	140.25	0.92	9.20	23.11
Cluster-X	119.67	138.00	155.27	72.66	7.59	6.01	5.29	12.60	25.25	27.64	0.70	6.99	19.82

### **Cluster means**

The mean values of thirteen characters for ten clusters are summarized in Table 3. The highest cluster mean for the character days to 50% flowering was found in the cluster number VIII (143.00) followed by cluster VII (128.33), cluster IX (125.33), cluster IV (123.33) and cluster III (122.00). The lowest cluster mean was found in cluster X (119.67). The highest cluster mean for days to first harvest was found in cluster V (177.33) followed by cluster IV (156.00), cluster II (149.33), cluster VII (148.33), cluster VIII (148.33) and cluster IX (148.00). The lowest cluster mean was found in cluster X (138.00). The highest cluster mean for total marketable fruit yield (q/ha) was found in cluster VI(224.01) followed by cluster IX (204.31), cluster VII (192.18), cluster X (155.27) and cluster IV(151.59). The lowest cluster mean was found in cluster VIII (47.96). The highest cluster mean for plant height (cm) was found in cluster X (72.66) followed by cluster IV (71.24), cluster VII (70.18), cluster IX (68.70) and cluster V (67.82). The lowest cluster mean was found in cluster VI (56.63). The highest cluster mean for fruit length (cm) was found in cluster VIII (14.34) followed by cluster IV (12.07), cluster I (11.34), cluster VI (9.69) and cluster III (8.56). The lowest cluster mean was found in cluster II (7.24). The highest cluster mean for fruit diameter (cm) was found in cluster IX (8.49) followed by cluster VII (8.17), cluster VI (7.37), cluster III (7.32) and cluster II (6.98). The lowest cluster mean was found in cluster IV (4.82). The highest cluster mean for no. of primary branches per plant was found in cluster II (7.08) followed by cluster I (5.73), cluster IV (5.72), cluster IX

(5.63) and cluster III (5.33). The lowest cluster mean was found in cluster VIII (4.33). The highest cluster mean for no. of secondary branches per plant was found in cluster III (18.37) followed by cluster IV (16.16), cluster II (15.53), cluster I (15.31) and cluster VIII (14.85). The lowest cluster mean was found in cluster VI (10.52). The highest cluster mean for no. of fruits per plant was found in cluster IX (25.25) followed by cluster VI (22.27), cluster VII (18.75), cluster V (12.96) and cluster I (9.63). The lowest cluster mean was found in cluster IX (6.58). The highest cluster mean for average fruit weight (g) was found in cluster IX (140.25) followed by cluster IV (104.53), cluster II (85.46), cluster I (61.00) and cluster III (55.65). The lowest cluster mean was found in cluster X (27.64). The highest cluster mean for fruit yield per plant was found in cluster VI (1.01) followed by cluster IX (0.92), cluster VII (0.87), cluster X (0.70) and cluster IV (0.68). The lowest cluster mean was found in cluster VIII (0.22). The highest cluster mean for harvest-wise yield kg/plot was found in cluster VI (10.08) followed by cluster IX (9.20), cluster VII (8.65), cluster X (6.99) and cluster IV (6.82). The lowest cluster mean was found in cluster VIII (2.16). The highest cluster mean for reaction to fruit and shoot borer was found in cluster III (40.60) followed by cluster VIII (35.97), cluster V (33.48), cluster IV (32.75) and cluster VI (29.20). The lowest cluster mean was found in cluster VII (14.10).

The contribution of different character was different towards the divergence as mentioned in Table 4. These clusters have been formed on the basis of contribution of different character towards divergence. Among the characters reaction to major biotic stress like fruit and shoot borer (30%) showed maximum contribution towards the diversity followed by average fruit weight (29.27%), no. of fruits per plant (21.10%), fruit length (9.27%), days to first harvest (5.98%), fruit diameter (3.05%), days to 50% flowering (0.61%), total marketable fruit yield q/ha (0.24%), plant height (0.12%), no.

of secondary branches per plant (0.12%). Other character shows negligible contribution towards the divergence. The contribution of characters like fruit weight, fruit diameter, number of fruits per plant towards the diversity was also reported by Golani *et al.* (2007) <sup>[2]</sup>, Hazara *et al.* (2010) and Madhavi *et al.* (2015) <sup>[5]</sup>.

Table 4: Per cent contribution of thirteen characters towards total genetic divergence in brinjal

S.N.	Source	<b>Contribution %</b>	Times Ranked Ist
1	Days to 50% flowering	0.61	5.000
2	Days to first harvest	5.98	49.000
3	Total marketable fruit yield (q/ha)	0.24	2.000
4	Plant height (cm)	0.12	1.000
5	Fruit length (cm)	9.27	76.000
6	Fruit diameter (cm)	3.05	25.000
7	Number of primary branches per plant	0.00	0.000
8	Number of secondary branches per plant	0.12	1.000
9	Number of fruits per plant	21.10	173.000
10	Average fruit weight (g)	29.27	240.000
11	Fruit yield per plant(kg)	0.00	0.000
12	Harvest-wise yield kg/plot	0.00	0.000
13	Reaction to major biotic stress like fruit and shoot borer	30.24	248.000

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