Studies on Genetic Divergence in Brinjal (*Solanum melongena* L.) Genotypes under *Tarai* Conditions of Uttarakhand

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A B S T R A C T

The present experiment was carried out using 51 genotypes at Vegetable Research Centre of G. B. P. U. A & T., Pantnagar, during *kharif* season of 2019. Mahalanobis D^2 statistics was worked out using 11 quantitative characters to assess the degree of genetic divergence. On the basis of D^2 value generated using Tocher's method, 51 genotypes were grouped into six clusters. Cluster I is largest with 42 genotypes followed by clusterII and III with 3 genotypes and cluster IV, V and VI containing 1 genotype in each. Cluster IV exhibited highest cluster mean value for the fruit diameter (8.46), average fruit weight (82.27), yield per plant (1.03), marketable yield per plant (0.84) and total yield per hectare (22.67). Highest inter cluster distance was found between cluster II and V (D^2 =1139.496) suggesting the genotypes belong to these clusters would produce the best heterosis effect and have more chances of generating the best recombinants. Cluster III having only 3 genotypes showed highest intra cluster distance (D^2 = 215.253) indicating the genotypes under the group possess higher degree of genetic variability. Percent contribution of characters towards the divergence showed that out of eleven characters, 60.79 % contribution came from the single character i.e. number of fruits per plant followed by fruit length (16.52 %).

Introduction

Brinjal (*Solanum melongena* L., 2n = 2x = 24) known by different names such as eggplant, aubergine and Guinea squash one among the few cultivated species of solanaceae originating from the old world and moved to the new world while rest of the commercial species (tomato, chillies, potato and tobacco) hails from the new world (Daunay *et al.,* 2001). It is one of the principal vegetable crop widely cultivated in India. Presently its

cultivation undertaken in an area of 0.73 million hectare with 12.80 million tonnes of production and productivity of 17.5 tonnes/ha (NHB, 2018-2019). Despite of the spectacular achievements in crop improvement in recent past, due its irreplaceable position in Indian cuisine and popularity among different sections of the societies, there is constantly changing demands by consumers for the new and novel varieties of brinjal with strong local preference (Das and Das, 2017). It can be met with initiating the crop improvement program

with suitable breeding methods and ample germplasm in hand. Breeding of any crop is such that it cannot proceed without having enough variation in the crop to be improved. Easy way to create variation is through collection of different germplasm. Mere collection of germplasm would not help to breeder, thus its need to be systematically evaluated and characterized. It is well established fact that parental lines originating from the different source population or population possessing higher genetic diversity gives the best heterosis effect than the lines having narrow genetic base or hails from the same source of population. It is also a fact that Genetic distance between the parental lines indicates how far apart and how diverse are germplasm (more the genetic distance between the germplasm, better will be chance of getting hybrids). It is thus, necessary to know the nature of genetic divergence and distinctiveness of the gathered germplasm in order to determine which parental lines could be used in heterosis or for isolating better segregants in segregating generations (Singh and Narayanan, 2015). Morphological similarities and eco geographical diversity were the few methods used to discriminate diverse gathered populations in earlier days which were now replaced by more scientific and advanced biometrical techniques like multivariate analysis based on D^2 statistics (Rao, 1952; Saxesena*et al.,* 2013). The concept of D^2 statistics originally developed by P. C. Mahalanobis (Dubbed as father of modern statistics in India) in 1928 and Rao (1952) suggested this technique for assessment of genetic divergence in plant breeding. D^2 analysis classify the genotypes into different clusters and identifies the genotypically diverse and desirable genotypes. The present experiment was carried out to reveal the kind of genetic divergence exists among the 51 genotypes based on 11 yield and yield contributing characters.

Materials and Methods

The experiment was carried out during the *kharif* season of 2019 at Vegetable Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar. Region comes under the agro-climatic zone-I i.e. Humid Western Himalayan region (Jammu and Kashmir, Himachal Pradesh, Uttarakhand) of the 8 agro climatic zones recognised under the All India Coordinated Vegetable Improvement Project (AICRP) (Ram, 1998). Experimental material having 51 genotypes (including two checks i. e. Pant Samrat and Pant Rituraj) were arranged in randomized block design with three replications. Observations recorded for 11 characters viz, days to 50 % flowering, days to first harvest, average fruit weight (g), fruit length (cm), fruit diameter (cm), number of primary branches per plant, plant height (cm), number of fruits per plant, yield per plant (kg), marketable yield perp plant (kg) and total yield per hectare (quintal). All necessary measures and practices were followed for raising healthy seedlings. Five weeks old seedlings were transplanted at spacing 75 cm between the rows and 60 cm between the plants. One treatment consist of ten plants in a plot and five randomly selected plants from each plot were tagged for the recording the observations and average of five tagged plants was worked out and used for analysis. Mahalanobis D^2 statistics was worked out for 51 genotypes to assess the degree of genetic divergence. Grouping and clustering was done according to Tocher's methods as suggested by Rao (1952). The intra and inter cluster distances were worked out by using the procedure elaborated by Singh and Chaudhary (1985).

Results and Discussion

Based on the D^2 value generated using Tocher's method, 51 genotypes were grouped

into six clusters by treating estimated D^2 values as the square of the generalized distance. Distribution of brinjal genotypes into different clusters based on Mahalanobis D^2 value represented in Table 1. Genotypes were constellated in such way that genotypes within the group had lower D^2 value than those between the groups. Among six clusters generated, cluster I is largest with 42

genotypes followed by cluster II and III with 3 genotypes and cluster IV, cluster V and cluster VI containing 1 genotype in each group. Based on the grouping of genotypes, it is observed that clustering was not in accordance with geographical distribution and has no direct relationship with the genetic distance.

Table.1 Distribution of brinjal genotypes into different clusters based on Mahalanobis D^2 value

Clusters	Number of genotypes	Genotypes
Cluster I	42	Pant Rituraj (check),Pant Samrat (check),Pusa Bindu,Pusa Ankur,Pusa Uttam,Tara BWX,White Sel – 154,KS-331,BARI,Swarna Abhinav,PHP-1,PB-6,PB-105,PB-109,PB-110,PB-111,PB-112,PB-113,PB-114,GBL-1,WB-1,DBI-02,Selection-32,Selection-31,PB- 3,PB-72,PB-70,PB-71,Muktakeshi,Sel-1,Pusa Ankur –Sel,PB-104-Sel-2,PB-104-Sel-3,PB-104 -Sel-1,White Selection 26,PS-Se-1,PB-114 Sel,PB-16,PB-110 Sel-1,PB-110 Sel-2, BARI-Sel,New Sel.
Cluster II	3	Pusa Kaushal – Sel,PB-85,PB-101.
Cluster III	3	Pusa purple cluster,Pusa Anupam,SMB-115.
Cluster IV	1	PS-Sel-2
Cluster V	1	PPL-1
Cluster VI	1	*S. gilo*

Table.2 Inter and intra cluster distances of six clusters

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**94.299** **(9.71)**	985.456 (31.39)	384.931 (19.61)	274.112 (15.71)	269.068 (16.40)	432.752 (20.80)
Cluster II		**114.934** **(10.72)**	344.047 (18.54)	689.200 (26.25)	1139.496 (33.75)	1123.767 (33.52)
Cluster III			**215.253** **(14.67)**	348.373 (18.66)	420.802 (20.51)	687.338 (26.21)
Cluster IV				**0.000**	664.245 (25.77)	432.549 (20.79)
Cluster V					**0.000**	960.499 (30.99)
Cluster VI						**0.000**

Note: Bold and diagonal values indicate intra cluster distances. The values in parenthesis are square roots of D^2 values

Table.3 Cluster means of different characters of brinjal genotypes

Clusters	Days to 50% flowering	Days to first harvesting	Average fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	No of primary Branches	Plant height (cm)	No of fruits per plant	Yield per plant (Kg)	Marketable yield per plant(kg)	Total yield per ha(quintal)
I	50.362	71.754	71.314	11.742	5.113	5.714	82.260	7.586	0.528	0.310	11.598
II	46.222	67.000	36.681	11.617	4.755	5.908	87.648	24.996	0.930	0.694	20.554
III	49.000	71.333	47.084	15.354	4.050	6.254	81.290	16.763	0.790	0.627	17.533
IV	52.667	74.000	82.273	8.943	8.463	5.467	83.210	12.210	1.030	0.843	22.367
V	44.333	65.333	62.067	22.813	3.327	5.853	68.977	8.603	0.527	0.330	11.967
VI	74.000	90.000	25.000	4.767	4.033	11.600	102.000	7.667	0.280	0.300	9.000

Table.4 Contribution of different characters towards the divergence

Character		Contribution (%)
	Days to 50% flowering	2.513
1.	**Days to first harvest**	0.013
2.	**Average fruit weight**	1.701
3.	**Fruit length**	16.521
4.	**Fruit diameter**	4.017
5.	**Number of fruits per plant**	60.798
6.	**Number Primary branches per plant**	3.533
7.	**Plant height**	0.591
8.	**Yield per plant**	0.001
9.	**Marketable yield per plant**	7.309
10.	**Total yield per hectare**	3.005

The genotypes that are hailed from one region had been grouped into different clusters, signifying that genotypes from the same geographic place underwent structural and genetical changes over the period of time due to selection pressure put forth by humans. Apart from this, genetic drift also took part in the process. Influence of these two factors culminating into creation of wide genetic diversity rather genetic distance.

Cluster mean values of 11 quantitative characters of 51 genotypes for six clusters given in the Table 2. The cluster mean values generated by varying number of genotypes in each cluster, though, cannot be used for statistical comparison, but in order to get a comparative idea of diversity and divergence among the clusters they are compared. Based on the range of means for each character, it became possible to know the characters influencing the divergence. Cluster II recorded highest mean value 24.99 for the character number of fruits per plant. Cluster IV exhibited highest cluster mean values for the fruit diameter (8.46), average fruit weight (82.27), yield per plant (1.03), marketable yield per plant (0.84) and total yield per hectare (22.67). Cluster V recorded the highest mean value for fruit length (22.81), days to 50 % flowering (44.33) and days to first harvesting (65.33). Cluster VI recorded highest cluster mean for the characters number of primary branches per plant (11.60) and plant height (102)

Distance between the two groups specifies the degree of divergence or diversification among the clusters. Higher the distance between the two groups higher the genetic divergence and *vice versa*. As it stated earlier, genotypes with higher genetic divergence produces best heterosis effect and have more chances of generating the best recombinants. Higher distance was found between cluster II and cluster V (D^2 =1139.496) followed bycluster

II and cluster VI (D^2 =1123.767) and cluster I and cluster II (D^2 =985.456).Thus, genotypes belong to cluster II and cluster V can be recommended for the utilisation in hybridisation program. Cluster distance between the cluster I and cluster V (D^2 =269.068) was lowest among all the groups due to close relationship among genotypes of these groups.

Intra cluster distance was recorded for only 3 cluster out of 6 clusters formed. Cluster III having only 3 genotypes showed highest intra cluster distance (D^2 = 215.253) indicating the genotypes under the group possess considerable degree of genetic variability compare to the genotypes clustered in other groups and can be recommended for the utilisation in further breeding program. Cluster I, though contains 42 genotypes recorded the lowest intra cluster distance (D^2 = 94.299). It is believed that genotypes belong to this cluster more or less similar to each other due to considerably lower intra cluster distance. Cluster II containing 3 genotypes still recorded intra cluster distance (D^2 = 114.934) higher than cluster I indicating genotypes under the group possess some degree of genetic variability compare to genotypes belong to cluster I. Cluster IV, cluster V and cluster VI fail to generate intra cluster value due to the presence of only one genotype in each group. It is stated that cluster showing higher intra cluster distance indicates the presence of sizeable genetic variability in the genotypes. It is thus, advisable that breeder can chose the genotypes from cluster III due presence of sizeable degree genetic variability over the other clusters. Inter and intra cluster distances of 6 cluster given in the Table 3.

Percent Contribution of characters towards the divergence showed that Out of eleven characters, 60.79 % contribution came from

the single character i.e. number of fruits per plant. Fruit length contributed 16.52 % which is next to the number of fruits per plant. Rest of the characters contributed to a very limited extent. Table 4 depicts the relative contribution of the characters to the genetic divergence. Outcomes of the present experiment are in consonance with the results reported by Singh *et al.,* (2008), Gupta *et al.,* (2017) Bhushan *et al.,* (2018) and Silambarasan *et al.,* (2020). The findings are of paramount importance for brinjal researchers particularly information about genetic diversity between cluster II and V (D^2=1139.496) and cluster III which showed highest intra cluster distance ($D^2 = 215.253$) possessing high variability for future breeding programme.

Acknowledgement

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