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Research Paper

Study of genetic divergence using mahalanobis D square analysis in brinjal (*Solanum melongena* L.) genotypes

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ABSTRACT

Forty diverse genotypes of brinjal were evaluated for 19 different quantitative and qualitative traits in the experimental field of Division of Vegetable Science, FOH, SKUAST, Kashmir Shalimar during kharif season 2021. The genotypes were grouped into seven diverse clusters on the basis of D^2 statistics. Cluster VI accommodated maximum number of genotypes (9), followed by cluster V and VII (6), cluster III and IV (5), cluster I (4) and cluster II (3). Cluster V had maximum intra cluster distance (40242.92), followed by cluster III (29117.82) and cluster II (22985.97), suggesting considerable genetic divergence among the genotypes of the respective clusters and the genotypes from within the clusters can be chosen as parents for heterotic groupings or mating design based testing. . The inter-cluster distance depicts greater divergence among the clusters and maximum inter-cluster was recorded between cluster II and cluster VI (280335.30) followed by cluster IV and cluster V (252012.10) and cluster I and cluster II (219988.30), suggesting greater diversity between genotypes belonging to respective pairs of clusters. For cluster mean values, the genotypes in cluster IV were having highest values for days to 1st flowering (48.35), days to first fruit set (57.25), number of branches per plant (13.17), phenol content (111.27) and total sugars (2.76). Fruit yield per hectare contributed maximum towards total genetic diversity (50.21), followed by average fruit weight (32.82) and number of fruits per plant (11.41). Rest of the parameters contributed lesser towards total genetic diversity.

Key words: Brinjal, cluster analysis, clustering, D^2 statistics, diversity, percentage contribution.

A frequently cross-pollinated crop, Brinjal (*Solanum melongena* L.), is a member of the angiospermic family "Solanaceae," with cross pollination rates as high as 48% observed (Madhavi, 2015). Brinjal come in a wide variety of sizes, shapes, and colours, indicating that the Indian subcontinent is a significant hub for variation and centre of origin.Brinjal is an important vegetable crop in our nation, and human society has had a social and economic link with it since ancient times. Despite their low yields and susceptibility to diverse pests and diseases, many indigenous cultivars are well-liked in many different places because of their desirable qualities.

Natural genetic variability within crop species has been used since the dawn of agriculture to supply as food for subsistence. However, today plant breeders can create new and improved cultivars with desirable qualities, including traits that are valued by both farmers and breeders, thanks to the diversity of available plant genetic resources. By 2050, there will be more than 9 billion people on the planet (World population prospects, 2017), so we must maintain a supply of cultivated and arable crop species. A long-term boost in food productivity can be achieved by maintaining or investigating genetic diversity, which can produce adaptive and useful genes. Crops must have genetic diversity in order to improve in the future since it gives breeders alternatives for creating new kinds and hybrids. As per reports there is significant genetic variability in Brinjal genotypes for fruit size, shape, colour, growth behaviour, canopy bearing habit and yield (Gazala *et. al.*, 2019). This variability leads to grouping of genotypes into different clusters. However for selection and varietal development programme, complete diversity present in a germplasm must be studied and divided into genotypic, phenotypic, and environmental variability. A crucial prerequisite for genetic improvement in a crop is the availability of genetic diversity. This makes it possible for the breeder to implement an effective breeding plan. Therefore, unpredictability plays a crucial role in determining the quantity of advancement anticipated from selection. Crops have an improvement potential directly correlated with the amount of genetic variability in the germplasm. A high genetic diversity shows greater potential for improvement.

Estimation of genetic divergence helps in reducing the large data of genotypes to manageable proportions. It is assumed that the parents showing wide genetic divergence are best suited for being used in the hybridization programme. In the process of formulating the brinjal improvement programme through hybridization and creating variability for the improvement of yield and other desirable traits, it is essential to understand the nature and degree of genetic divergence present in the available germplasm. Today, a variety of methodologies are available for analyzing divergence. But Mahalanobis generalized distance (Mahalanobis, 1936) stands out among these quantitative trait-based divergence analysis techniques in a big way. This biometric instrument is particularly effective at measuring the degree of biological population divergence. Therefore, this biometric tool will be utilised to measure the extent of biological polulation divergence as well as to evaluate the relative contributions of various components to the overall divergence at both the inter- and intra-cluster levels.

MATERIALS AND METHODS

The experimental field of Division of Vegetable Science is located at the main campus, Shalimar, Srinagar 15 km away from Srinagar city on the foot hills of Mahadev. The altitude of the location is 1685 meter above mean sea level and situated 34º N of latitude and 74.89º E of longitude. The climate is temperate characterized by mild summers .Forty genotypes of Brinjal were evaluated with a spacing of 60x45cm in kharif season 2021 with design of experiement as Randomized Complete Block Design with three replications. The uniform, healthy seedlings were transplanted on ridges maintaining inter and intra row spacing of 60cm x 45cm, respectively. The recommended package of practices for raising a healthy crop was followed. Observations were recorded from five randomly selected plants of each genotype in each replication for various traits. With the aid of Mahalanobis' D^2 analysis, genetic diversity was calculated. Criteria Tocher (Rao, 1952) 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. It is a highly effective method for determining genetic divergence. The distances between and within the clusters were determined using the clusters created using Ward's approach. These findings may shed light on the variety of genotypes within a cluster. The degree of differences between genotypes that belong to various clusters is also provided by cluster means. Additionally, the identification of the selection parameter to be utilised as criteria for the improvement in the yield is aided by the relative contribution of several yield components to overall divergence using Mahalanobis D^2 analysis.

RESULTS AND DISCUSSION

In hybridization programmes, superior genotypes are chosen and employed as parents. However, it can be challenging to choose superior parents from a wide pool of genotypes. In order to identify the genetically diverse parents who are most likely to result in crosses with high levels of heteroticism as well as those who are also likely to produce a wide range of variability during the segregation and recombination of genes at heterozygous polygenic blocks, genetic divergence analysis among genotypes is helpful.

Table 1: Distribution of brinjal (*Solanum melongena* L.) genotypes into clusters based on D^2 Statistics

S. No.	Cluster	No. of genotypes in the cluster	Name of genotypes
1	I	4	SKAU-B-205, SKAU-B-245, SKAU-B-274, SKAU-B-276
2	II	3	IC-354867, SKAU-B-229, SKAU-B-236
3	III	5	IC-089888, IC-090063, SKAU-B-197, SKAU-B-209, SKAU-B-211
4	IV	5	IC-089818, IC-099712, IC-261801, SKAU-B-226, SKAU-B-255
5	V	8	IC-090026, IC-111010, SKAU-B-215, SKAU-B-222, SKAU-B-239, SKAU-B-249, SKAU-B-263, SKAU-B-270
6	VI	9	IC-074207, SKAU-B-193, SKAU-B-219, SKAU-B-224, SKAU-B-234, SKAU-B-241, SKAU-B-247, SKAU-B-251, SKAU-B-255
7	VII	6	IC-074244-1, SKAU-B-231, SKAU-B-259, SKAU-B-266, SKAU-B-268, SKAU-B-279

On the basis of performance of various traits, the clustering pattern of forty genotypes of brinjal has been presented in the Table 1. All the genotypes were grouped into 7 (I-VII) clusters. Maximum numbers of genotypes were accommodated in cluster VI (9) followed by cluster V containing 8 genotypes and VII which contain six genotypes followed by cluster III and IV containing five genotypes each followed by cluster I with four genotypes and cluster II with three genotypes. Group constellation of brinjal genotypes through genetic divergence has been also reported by Singh *et al.* (2006), Polignano *et al.* (2009), Shekar *et al.* (2012), Hassan *et al*. (2015), Kumar *et al.* (2016), Mangi *et al.* (2016) and Nand *et al.* (2018).

Average intra and inter cluster divergence (D^2) values are presented in the Table 2. The diagonal figures in the table represent the intra cluster distances. The intra cluster distance was maximum in cluster V (40242.92) and minimum in cluster VII (10256.34). High intra cluster distance indicated that the genotypes included in VII cluster were genetically heterogeneous to a great extent. The maximum inter cluster distance was recorded between cluster II and VI (280335.30) indicated wide diversity between these two clusters, while lowest (60717.75) was observed between cluster IV and VII indicating their close relationship. Das and Das (2017) studied the genetic divergence in brinjal and grouped 26 genotypes into 11 clusters and also reported maximum and minimum inter and intra cluster distances. Similar kind of work has also been reported by Singh *et al.* (2006), Golani *et al.* (2007), Quamruzzaman *et al*. (2009), Muniappan *et al.* (2010), Shekar *et al.* (2012), Begum *et al.* (2013).

Table 2: Average intra cluster (Diagonal) and inter cluster (Above Diagonal) distance values in brinjal (*Solanum melongena* L.)

S. No.	Cluster	I	II	III	IV	V	VI	VII
1	I	**18386.08**	219988.30	59843.87	195750.30	57274.22	48939.36	189140.90
2	II		**22985.97**	118740.30	118766.20	167083.60	280335.30	76826.20
3	III			**29117.82**	82031.77	96679.68	87508.34	100124.50
4	IV				**22672.85**	252012.10	170511.70	60717.75
5	V					**40242.92**	130345.00	192122.40
6	VI						**11182.95**	156479.90
7	VII							**10256.34**

Further, for getting the reliable conformity on the basis of cluster means, it was calculated for various horticultural traits and has been presented in Table 3a and 3b. The flower appeared at the earliest (days) in cluster VII (44.57) followed by gradual delay as observed in cluster; II (45.87), III (46.04), VI (46.75), I (46.83), V (47.64) and IV (48.35). Similarly, the fruits were earliest (days) set in cluster VI (53.06) followed by cluster II (53.99), VII (54.30), III (54.36), V (55.77), I (56.09) and IV (57.25). The smallest harvest duration (days) was observed in cluster II (62.36), cluster VI (62.83), cluster III (63.11), cluster VII (63.23), cluster V (65.07), cluster IV (65.72) and cluster I (66.60). Maximum number of branches per plant was observed in cluster IV (13.17) followed by cluster VI (13.11), cluster VII (13), cluster III (12.60), cluster I (12.45), cluster V (12.11) and cluster II (11.67). The tallest plants **(**cm) were observed in cluster II (85.13), cluster I (84.02), cluster V (79.86), cluster IV (77.52), cluster III (70.84), cluster VI (70.65) and cluster VII (44.30).The widest plant spread (cm) was seen in cluster V (62.68) followed by cluster I(60.28), cluster II (57.84), cluster III (54.95), cluster IV (53.45), cluster VI (49.97), cluster VII (44.62). Maximum fruit length (cm) was recorded in cluster II (16.55) followed by cluster I (15.92), cluster V (14.47), cluster IV (12.80), cluster III (12.62), cluster VI (11.39) and cluster VII (9.15), while breadth (cm) was highest in cluster VI (4.23) followed by cluster V (4.19), cluster I (4.15), cluster III (4.09), cluster VII (3.97), cluster IV (3.243.89) and cluster II (3.88). Number of fruits per plant was observed highest through cluster III (10.80) followed by cluster I (10.67), cluster IV (10.50), cluster II (10.06), cluster V (9.96), cluster VI (8.95) and cluster VII (8.34). The fruit weight (g) was maximum in cluster II (245.01) followed by cluster V (212.37), cluster I (122.14), cluster III (121.24), cluster VII (187.89), cluster IV (93.89) and cluster VI (82.89). Maximum fruit yield per plant (kg) was obtained in cluster II (1.03) followed by cluster V (0.94), cluster I (0.91), cluster III (0.84), cluster IV (0.84), cluster VII (0.84) and cluster VI (0.81). Highest total soluble solids (°Brix) was estimated in cluster V (4.21), cluster I (4.16), cluster IV (3.92), cluster III (3.81), cluster VII (3.80), cluster II (3.78) and cluster VI (3.35). Similarly, maximum anthocyanin content

Table 3a: Cluster means for various growth, maturity, yield attributing and quality characters in different clusters of brinjal (*Solanum melongena* L.) genotypes

S. No	Cluster	Days to first flowering	Days to first fruit set	Days to first fruit picking	No. of branches / plant	Plant height (cm)	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	No. of fruits per plant	Average fruit weight (g)	Fruit yield/ plant (kg)	Fruit yield/ plot (kg)	Fruit yield/ hectare (q)
1	I	46.83	56.09	66.60	12.45	84.02	60.28	15.92	4.15	10.67	122.14	0.91	69.65	338.05
2	II	45.87	53.99	62.36	11.67	85.13	57.84	16.55	3.88	10.06	245.01	1.03	78.57	381.17
3	III	46.04	54.36	63.11	12.60	70.84	54.95	12.62	4.09	10.80	121.24	0.84	64.21	311.49
4	IV	48.35	57.25	65.72	13.17	77.52	53.45	12.80	3.89	10.50	93.89	0.84	63.75	305.46
5	V	47.64	55.77	65.07	12.11	79.86	62.68	14.47	4.19	9.96	212.37	0.94	72.06	349.75
6	VI	46.75	53.06	62.83	13.11	70.65	49.97	11.39	4.23	8.95	82.89	0.81	62.04	301.08
7	VII	44.57	54.30	63.23	13	44.30	44.62	9.15	3.97	8.34	187.89	0.84	64.11	311.10

(mg/ 100 g) was observed in cluster III (5.74), cluster I (5.13), cluster V (5.04), cluster II (4.69), cluster IV (3.85), cluster VI (1.20) and cluster VII (0.21). Maximum ascorbic acid content (mg/ 100 g) was observed in cluster VI (10.06), cluster VII (9.62), cluster IV (8.95), cluster I (8.06), cluster V (7.04), cluster III (7) and cluster II (5.71). Maximum phenols (mg/ 100 g) were observed in cluster IV (111.27), cluster II (110.09), cluster VII (108.10), cluster III (95.43), cluster VI (83.57), cluster V (83.23) and cluster I (81.67). The total sugars (%) were observed highest in cluster IV (2.76), cluster II (2.72), cluster VI (2.68), cluster I (2.67), cluster V (2.61), cluster III (2.60) and cluster VII (2.08).

The dry matter content (%) was observed highest in cluster VII (10.20), cluster V (6.30), cluster II (6.22), cluster III (5.17), cluster IV (5.15), cluster I (4.93) and cluster VI (4) .Variable cluster mean for different plant growth and fruit yield characters have also been reported by Rahman *et al.* (2014), Vidhya and Kumar (2014), Ullah *et al.* (2014), Uddin *et al.* (2014), Rekha and Celine (2015), Madhavi *et al.* (2015), Prabakaran *et al.* (2015), Sadarunnisa *et al.* (2015), Gupta *et al.* (2015), Karim *et al.* (2016), Kumar *et al.* (2016), Das and Das (2017) and Gupta *et al*. (2017).

Table 3b: Cluster means for various quality characters in different clusters of brinjal (*Solanum melongena* L.) genotypes

S. No.	Cluster	TSS (˚Brix)	Total anthocyanin content (mg/100g)	Ascorbic acid (mg/100g)	Phenols (mg/100g)	Total sugars (%)	Dry matter (%)
1	I	4.16	5.13	8.06	81.67	2.67	4.93
2	II	3.78	4.69	5.71	110.09	2.72	6.22
3	III	3.81	5.74	7.00	95.43	2.60	5.17
4	IV	3.92	3.85	8.95	111.27	2.76	5.15
5	V	4.21	5.04	7.04	83.23	2.61	6.30
6	VI	3.35	1.20	10.06	83.57	2.68	4.00
7	VII	3.80	0.21	9.62	108.10	2.08	10.20

The characters contributing maximum to the divergence are given greater emphasis for deciding on the clusters for the purpose of further selection and choice of parents for hybridization. The highest contributors in this regard were fruit yield per hectare, average fruit weight and number of fruits per plant which were in confirmation to the findings of Sharma *et al*. (2000) for fruit weight; Mohanty and Prusti (2001) for fruit weight and number of fruits per plant; Sharma and Maurya (2004), Singh *et al*. (2006) for number of fruits per plant; and Singh *et al.* (2013) for fruit weight and number of fruits per plant , Arti *et al.* (2018) and Pandey *et al.* (2019) for number of fruits per plant.

Table 4: Percent contribution of individual traits towards total genetic divergence

S. No.	Traits	% contribution towards total divergence
1	Days to first flowering	0.41
2	Days to first fruit set	0.12
3	Days to first fruit picking	0.50
4	No. of branches per plant	1.03
5	Plant height (cm)	0.51
6	Plant spread (cm)	0.50
7	Fruit length(cm)	0.51
8	Fruit diameter (cm)	0.50
9	No. of fruits plant^{-1}	11.41
10	Average fruit weight (g)	32.82
11	Fruit yield plant^{-1} (kg)	0.71
12	Fruit yield per plot (kg)	0.84
13	Fruit yield per hectare (q)	50.21

CONCLUSION

In the present studies, on the basis of genetic divergence, forty diverse genotypes of brinjal were grouped into seven clusters. The resultant seven clusters showed genetic diversity and maximum number of genotypes were accommodated in cluster VI, V and VII. The maximum inter cluster distance was recorded between cluster II and VI, , which suggested that members of these clusters are genetically more diverse to each other and therefore, the hybridization between the genotypes of these two clusters will be more rewarding for getting superior hybrids or recombinants in segregating populations for future breeding programmes. Maximum contribution towards the genetic divergence was shown by fruit yield per hectare, average fruit weight and number of fruits per plant.

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