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Multivariate Genetic Divergence Studies in Brinjal (*Solanum melongena* L.)

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Abstract: ***The present experiment was conducted during July-December, 2017 in RBD with two replication to study genetic diversity for nine quantitative traits in brinjal at APHC College farm, APHC, Kalavai using Mahalanobis D^2 statistics method. The 35 genotypes were grouped into nineteen clusters, indicating the presence of diversity for different traits. The cluster I had the highest number containing six genotypes followed by cluster II and III containing four genotypes each while the clusters IV,V,VI,XVII and XIX consisted two genotypes each. However, the cluster VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI and XVIII were solitary. There is no relationship between geographical distribution and genetic distance. The maximum intra-cluster distance was recorded within cluster III (604.33) and the maximum inter-cluster distance between cluster IX and XIII (6070.31), indicating the existence of wide genetic variability and the genotypes in these clusters could be utilized as parents in hybridization programme to develop high heterotic hybrids and to identify trangressive segregants in F_2 generation. Among the characters studied total fruit yield per plant, fruit length, days to first flower, number of branches per plant showed maximum contribution towards the diversity. The genetic divergent offered by these characters will offer scope for improving yield through rational selection.***

Keywords: genetic diversity, multivariate analysis, brinjal, accessions and cluster.

1. Introduction

Brinjal (*Solanum melongena* L.) a member of Solanaceae family, is one of the most important vegetable crops grown widely all over the world. The origin of brinjal is said to be the Indian subcontinent; the secondary place of origin is China (Zeaven and Zhukovsky, 1975). The Chinese people have been growing it for the last 1500 years (Yawalker, 1969). It is cultivated throughout the entire tropical and subtropical regions of the world and temperate too. It is grown extensively in India, Bangladesh, Pakistan, China and the Philippines. It is also popular in other countries, namely, Japan, Indonesia, Turkey, Italy, France, United States, and in the Mediterranean and Balkan areas (Bose and Som, 1986). Brinjal has high nutritional value in respect of calorie, iron, phosphorus and riboflavin contents (Chowdhury, 1976). The fruits, leaves, stem and roots of brinjal are widely used in ayurvedic medicine for the patients suffering from diabetes, asthma, aotitis, tooth ache, cholera, bronchitis and dysentery.

For the development of suitable variety of brinjal, it is essential to evaluate the characters of the available germplasm collected from different parts of the country and conserve those for future use. Genetic diversity is a benchmark to the breeders to breed desired varieties through selection, either from the existing germplasm or from the segregates of different crosses. Hence, the genetic information on yield and yield contributing characters of the crop species need to be properly assessed for its improvement. Furthermore, if an

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improvement program is to be carried out, evaluation of germplasm is imperative, in order to understand the genetic background and breeding value of the available germplasm (Singh *et al.*, 2002). Reshuffling the genes through recombination is the principal way of developing
Improved genotypes in breeding programs.

Evaluation of germplasm is of immense important in genetic improvement of the crop. Genetic diversity analysis assists in interpreting the genetic background and breeding value of the germplasm. It was also said that plant breeders use a much less diverse genetic pool than the overall available genetic diversity within the crop (Joshi *et al.*, 2012). Heterogeneous local population of the genus forms an important source of genetic variation (Zeven, 1998). For the selection of parents in hybridization, diversity among parents for the character of interest, estimation of genetic distance is most important as diverse plants are supposed to give high hybrid vigour (Harrington, 1940). Estimation of genetic divergence also allows breeders to eliminate some parents in downsizing the gene pool available and concentrate their efforts in a smaller number of hybrid combinations

Among the various methods identified/developed to study the genetic divergence in the genotypes, the Mahalanobis D^2 (Mahalanobis, 1936) is reliable and most frequently used. D^2 analysis is a useful tool in quantifying the degree of divergence (between biological population at genotypic level and to assess relative contribution of different components to the total divergence, both at the inter- and intra-cluster levels. Keeping these points in mind, the present study, the genetic divergence was estimated by using D^2 statistics suggested by Mahanlanobis (1936), which is based on multivariate analysis of quantitative traits. It is one of the very potential tools for measuring genetic divergence within a set of population using the concept of statistical distance employing multivariate measurements. The grouping of genotypes into different clusters is done by following Tocher's method as described by Rao (1952). Improvement in self-pollinated crops like brinjal is normally achieved by selecting the genotypes with desirable character combinations existing in nature or by hybridization (Meena *et al.*, 2013). Such studies are also useful in the selection of parents for hybridization to recover superior transgressive segregates. Considering the above facts, the research has been planned with the following objective to assess the extent of genetic diversity in the available germplasm based on nine traits comprising of qualitative and quantitative traits.

2. Materials and Methods

The present investigation was carried out at APHC College Farm APHC, Department of Vegetable Science, Affiliated to Tamil Nadu Agricultural University, Kalavai, Tamil Nadu. The experimental materials comprised of thirty-five genotypes (Table-1) of brinjal collected from different sources. The experiment was laid out in a randomized block design with two replications accommodating 20 plants in each genotype. The study was done during July-December, 2017. Thirty day old seedlings were transplanted at a spacing of 60 x 75 cm. All the recommended cultural practices were adopted for raising the crop successfully. The observation were recorded on five randomly selected plants per replication for each genotype on nine characters: i) plant height (cm), ii) number of branches per plant, iii) plant spread (cm^2), iv) days to first flowering (days), v) number of fruits per plant, vi) total fruit yield per plant(g) , vii) fruit weight (g), viii) fruit length (cm), ix) fruit girth (cm). Mean across two replications were calculated for each traits and the analysis of variation was carried out. Multivariate analysis was done utilizing Mahalanobis D^2 statistic which are cited below (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher's method. The inter and intra cluster distances were worked out as per method suggested by Murty and Arunachalam (1967) to find actual divergence within and between the clusters.

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2.1. Clustering of genotypes using D^2 values

All the genotypes used were clustered into different groups by following Tocher's method (Rao, 1952). The intra and inter cluster distance were also computed. The criterion used in clustering by this method was that any two varieties belonging to the same cluster at least on an average show a smaller D^2 values than those belonging to two different clusters.

The device suggested by Tocher (Rao, 1952) was started with two closely associated populations and find a third population which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average of D^2 value from the first three and so on. If at any stage increase in average D^2 value exceeded the average of already included, because of addition of new genotypes, then the genotype was deleted. The genotypes those are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those, that were already included in former cluster and grouping them in to different clusters.

2.2. Mahalanobis D^2 analysis

Mahalanobis (1936) D^2 analysis was used for assessing the genetic divergence among the test entries involving quantitative characters. The generalized distance between any two populations is given by the formula.

a) D^2 Analysis

$D^2 = \Sigma\Sigma\_ij\ \sigma ai\ \sigma aj$ (1)

Where,

D^2 = Square of generalized distance

_ij = Reciprocal of the common dispersal matrix

σ ai = (μi1-μi2)

σaj =(μj1-μj2)

μ=General mean

Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated un-standardized character mean (Xs) to standardized uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between pairs of corresponding uncorrelated (s) values of any two uncorrelated genotypes (Rao, 1952).

b) Cluster of D2 values

All n (n-1)/2 D^2 values were clustered using Tocher's method described by Rao (1952). (2)

c) Intra cluster distance

Square of the intra cluster distance = $\Sigma D^2 i / n$ (3)

Where, $\Sigma D^2 i$ is the sum of distance between all possible combinations of the entries included in a cluster.

n = Number of all possible combinations

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d) Inter cluster distance

Square of the inter cluster distance = ΣD2i / ninj (4)

Where,

ΣD2i is the sum of distances between all possible combinations (ninj) of the entries included in the clusters study.

ni = Number of entries in cluster i

nj =Number of entries in cluster j

2.2 Contribution of Individual characters

The character contribution towards genetic divergence was computed by using the method given by **Singh and Chaudhary (1985)**. In all the combination, each character is ranked on the basis of

di = yij – yik **(5)**

Where,

di = mean deviation

yij = mean value of jth genotype for the ith character

yik = mean value of kth genotype for the ith character

Rank 'I' is given to the highest mean difference and rank 'p' is given to the lowest

Mean difference

Where,

P is the total number of characters.

Finally, number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

3. Results and Discussion

3.1. Clustering

Clustering of genotypes under study is presented in Table-1. Based on the D2 values all the genotypes were grouped into nineteen clusters, signaling the presence of diversity for different traits. The cluster I had the highest number containing six genotypes followed by the clusters II and III containing four genotypes each while the clusters IV,V,VI,XVII and XIX consisted two genotypes each. However, the clusters VII, VIII, IX, X, XI, XII, XIII, XIV, XV, XVI and XVIII were monogenotypic. The clustering pattern of these genotypes under the study suggested that geographic diversity may not be necessarily related with genetic diversity. Many cultivars collected from the same place have been scattered into different clusters and also cultivars collected from various places grouped into same cluster. Therefore, geographical diversity could not be related to genetic diversity in the material investigated. This is an agreement with results of Rathi *et al.* (2011), Swadeshbanarjee *et al.* (2018). So selection of genotypes for hybridization to generate diverse new gene combinations should be based on genetic diversity rather than geographic diversity (Pawar *et al.*, 2013). It is very difficult to establish the actual location of origin of a genotype. The diverse use of genetic material among the crop improvement programmes in the country makes it unmanageable to conserve the real identity of the genotypes. Mostly, breeding progenies incorporate genes from motleyed sources, resulting in casting off the basic geographical identity of the genotype (Meena *et al.*, 2013)

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In perusal of the Table number.2 the intra-cluster distances indicates the divergence among the genotypes within the clusters and inter-cluster indicates diversity between clusters. The maximum intra-cluster distance was recorded within cluster III (604.33) followed by cluster II (524.50) and cluster XIX (468.61). The maximum inter-cluster distance was recorded between the clusters IX and XIII (6070.31) followed by the clusters VII and XV (5824.97) and VII and XIII (5745.01). These results suggest maximum divergence between genotypes of these clusters indicating the fact that the genotypes when used in hybridisation programme produce superior seggregants. The information obtained from inter-cluster distances may be used to select genetically diverse and superior genotypes. The genotypes possessing maximum genetic divergence is expected that more heterotic F_1 and most promising segregant in segregating generations. Intercrossing of divergent groups would lead to greater opportunity for crossing over, which may release hidden variability. Kumar *et al.*, 2013, Rahman et al.2014). The minimum inter-cluster distance was observed between cluster II and XII (394.00) followed by cluster VII and XIX (534.57). In general, less intra-cluster distance than inter cluster distance suggested homogenous and heterogeneous nature of the genotypes within and between the clusters, respectively. These results are conformity with the findings by Kumar *et al.* (2013), Rathi et al. (2011). Ravali *et al.*,(2017)

3.2 Contribution of characters towards divergence

The diversity among 35 genotypes was measured by employing D2 statistic. The contribution of each character towards total genetic diversity is presented in Table 3. It is evident from the table and figure that the character, fruit yield per plant contributed the maximum to the level of 31.93 per cent followed by fruit length (21.34%), days to first flower (21.18 %), number of branches per plant (15.80 %) and plant height (7.73 %) while other traits contributed less than one per cent. Thus, the first five characters may be given high emphasis while selecting the lines for hybridization programme to generate large variability and will provide immense scope for the improvement of yield through selection.(Figure:1)

3.3 Cluster mean analysis

The Table number.4 demonstrates the mean values for nine characters in nineteen clusters, which vary in their value differently from each other. The plant height was high for cluster XV (100.25 cm). The genotype Sm-2 included in cluster VI is recorded minimum days to 50% flowering (57.45 days). Numbers of branches per plant were highest for cluster XIII (14.61). The number of fruits per plants and average fruit weight, which directly correlates with yield per plant, was high for the cluster V (32.57) and VII (98.45 g) respectively. The highest value for fruit length and fruit girth are recorded for the clusters VI (10.48 cm) and IV (16.37 cm). The economically important character high fruit yield per plant was supreme for the cluster XIII (1639.19 g) which indicates that the genotypes included in these clusters could effectively be used for the crop improvement programme for increasing yield-contributing characteristics. Choice of parents is the most important aspect of crop improvement programme and highly diversified parents were selected based on the yielding ability of the respective parents. It is suggested that hybridization among the genotypes of above said clusters would produce seggregants for more than one economic character. The potential lines are picked out from different clusters and used as parents in a hybridization programme. The choice should be based on genetic distance and depending upon the objective of the breeding programme.

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4. Conclusion

Many workers have observed that more diverse the parents within its overall limits of fitness, the greater are the chances of heterotic expression in F_1's and a broad spectrum of variability in segregating generations. In choosing parents for hybridisation programme, the clustering pattern could be employed that would likely to render the maximum possible variability for various economic characters. Moreover, it will be effective to intercross genotypes belonging to more diverse clusters like cluster II, III, VII, XIII and XIV to create wide spectrum of variability and to produce transgressive segregates for brinjal.

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Table 1: Composition of D^2 Clusters

Clusters	Genotypes	Number of Genotypes
I	Sm- 1,Sm- 9,Sm- 12,Sm- 14,Sm- 28,Sm-31	6
II	Sm-10, Sm- 21,Sm- 23,Sm-24	4
III	Sm-15, Sm- 16,Sm- 22,Sm-30	4
IV	Sm- 5,Sm-6	2
V	Sm- 11,Sm-20	2
VI	Sm- 2,Sm-7	2
VII	Sm-4	1
VIII	Sm-34	1
IX	Sm-3	1
X	Sm-25	1
XI	Sm-8	1
XII	Sm-13	1
XIII	Sm-17	1
XIV	Sm-35	1
XV	Sm-18	1
XVI	Sm-26	1
XVII	Sm-19, Sm-27	2
XVIII	Sm-29	1
XIX	Sm-32, Sm-33	2

Table 2: Intra and inter cluster distance for various clusters in brinjal

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	462.93	1307.21	935.17	1012.17	2526.41	1493.25	51116.00	2191.67	1193.33	796.00	1712.16	1984.16	5005.5	2254.67	1629.67	911.50	2012.50	911.67	3353.50
II		524.50	1515.94	1541.38	3014.63	1405.63	4443.75	2145.50	3674.50	2682.25	1134.25	393.00	3283.00	2670.00	2215.00	1302.00	1435.88	1294.67	3262.75
III			604.33	563.23	1464.00	1842.25	4840.25	958.00	1153.00	1645.50	864.50	1710.00	3424.50	1199.00	2777.00	1348.75	1126.88	891.00	1620.38
IV				225.00	1016.00	1428.25	3422.00	830.50	1425.00	1143.50	1158.00	1617.50	2485.00	755.50	2160.50	1231.50	1751.50	1086.50	1231.00
V					373.00	2630.50	5949.50	2426.00	2998.50	3186.00	2829.00	2869.00	3158.00	1139.00	4592.00	2671.50	2763.00	3426.00	1688.50
VI						321.00	3463.50	2922.00	2997.50	2769.75	2044.50	1119.50	5603.50	3699.50	3044.50	2296.50	1703.25	2331.50	4069.25
VII								2930.90	5018.77	4701.34	3370.92	3370.32	5745.01	5257.13	5801.98	5824.97	4950.50	4695.52	3898.00

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VIII									1564.99	2369.19	611.09	2150.61	2492.49	1244.54	3644.89	2593.37	1766.00	1236.02	534.57
IX										1546.19	1738.29	3822.02	6070.31	2420.92	3879.58	2600.10	2327.50	1708.48	2327.65
X											2683.70	3039.18	4213.38	1863.05	793.41	776.92	3922.50	1091.44	3414.00
XI												1114.15	3611.11	2206.88	3493.87	2121.33	585.00	800.73	1544.45
XII													3398.98	2844.27	2824.67	1561.51	1219.00	1528.51	3723.50
XIII														1154.60	4222.88	3157.56	5305.00	3441.68	1934.50
XIV															3028.00	1616.00	3292.00	1891.00	925.50
XV																667.54	4937.00	1210.72	2106.50
XVI																	2938.87	675.13	3489.50
XVII																	284.11	1319.00	2709.25
XVIII																			2516.50
XIX																			468.61

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Figure :1Contibution of Charectars towards divergence

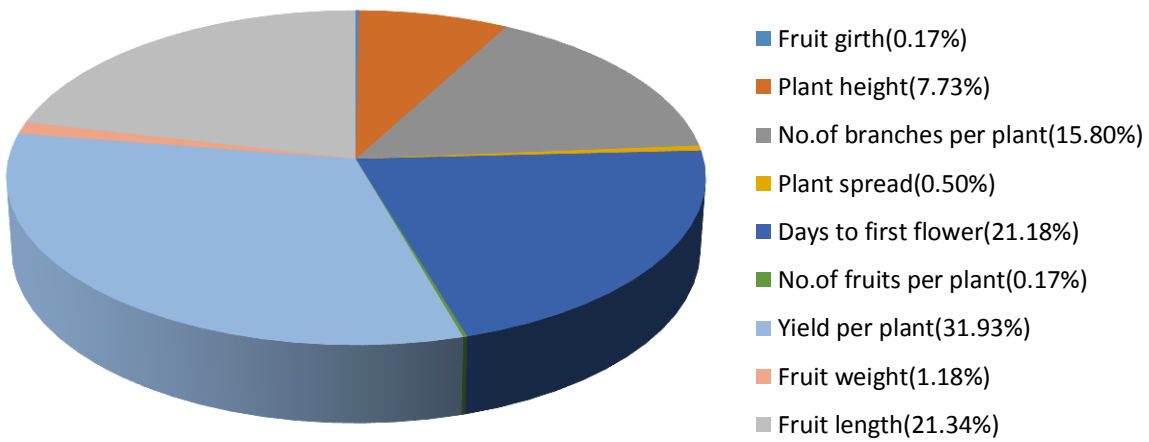

Table: 3 Relative contribution of fruit yield and yield attributing morphological characters to genetic divergence in brinjal

S.no	Characters	Number of appearances in first ranking	Contribution of each characters (%)
1	Plant height(cm)	46	7.73
2	Number of branches per plant	94	15.80
3	Plant spread(cm2)	3	0.50
4	Days to first flowering(days)	126	21.18
5	Number of fruits per plant	1	0.17
6	Total fruit yield per plant(g)	190	31.93
7	Fruit weight(g)	7	1.18
8	Fruit length(cm)	127	21.34
9	Fruit girth(cm)	1	0.17

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Table: 4 Cluster mean for yield attributing characters in brinjal

Clusters	Plant height(cm)	Number of branches per plant	Plant spread(cm)	Days to first flower(days)	Number of fruits per plant	Total fruit yield per plant(g)	Fruit weight(g)	Fruit length (cm)	Fruit girth(cm)
I	72.85	11.60	3491.00	70.50	15.54	524.02	34.77	5.95	12.35
II	87.86	13.48	6736.08	72.05	16.66	754.10	45.14	7.55	13.73
III	71.62	13.77	4848.90	75.41	20.69	731.90	35.90	7.01	14.26
IV	71.47	12.30	4432.17	69.3	20.32	978.32	48.20	9.09	16.18
V	63.03	9.83	4372.83	71.85	32.57	1319.00	40.57	8.84	12.35
VI	66.85	12.59	5364.44	58.95	15.82	716.72	45.32	10.48	11.72
VII	68.25	9.80	4982.30	60.37	12.56	1236.53	98.45	9.10	15.17
VIII	72.87	14.52	5008.85	78.33	16.27	931.18	57.23	8.97	14.71
IX	55.80	9.70	3330.50	73.25	12.80	529.30	41.20	6.90	15.21
X	80.23	11.25	3212.02	70.78	14.97	687.87	45.95	5.41	13.13
XI	73.58	10.87	6210.30	77.20	14.02	734.23	52.37	7.02	14.15
XII	81.25	10.71	6982.26	68.15	17.02	899.51	52.85	6.02	15.06
XIII	93.17	14.61	5732.13	80.25	24.75	1639.19	66.23	6.23	15.27
XIV	76.46	12.17	4225.52	77.54	25.81	1284.05	49.75	6.27	16.02
XV	100.25	12.78	4321.61	71.37	13.82	604.20	43.72	8.27	12.45
XVI	89.21	9.97	4855.74	72.50	18.91	746.57	39.40	5.37	16.05
XVII	65.00	12.14	6620.72	74.08	16.42	623.15	38.52	6.86	13.59
XVIII	87.35	12.35	5321.12	78.08	12.74	534.70	41.97	7.15	13.83
XIX	66.64	11.75	4848.83	79.41	21.02	1296.01	61.87	8.90	14.50

