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Genetic Diversity in Exotic Eggplant (*Solanum melongena* L.)

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Abstract: Genetic divergence among 11 eggplant (*Solanum melongena* L.) genotypes was estimated using Mahalanobis D^2 Statistic. The 11 genotypes were grouped into four distinct clusters. Cluster I comprises 4 genotypes, cluster II had 3, Cluster III and IV had 2 genotypes respectively. The highest and the lowest intra cluster distance were observed in cluster II (1.216) and cluster IV (0.047), respectively. The highest inter cluster distance was between clusters I and III (8.757) while it was the lowest between clusters I and II (2.203). Fruit weight, Fruit length, flower petiole length, fruit breadth, plant height and yield per plant had the highest contribution towards total divergence. Cluster III recorded the highest means for number of flowers per inflorescence, north-south plant canopy, leaf petiole length, leaf blade length, number of secondary branches per plant and no. of fruits per plant. Whereas, number of nodes of first flowering, east-west plant canopy, flower pedicel length, leaf petiole diameter, fruit length plant height and yield per plant were in cluster IV with the highest means. Cluster IV also contained the lowest mean for days to first flowering, days to 50% flowering and days to fruit maturity which is desirable for earliness. Cluster I have the highest mean values for flower pedicel diameter, leaf blade width, number of primary branches per plant, fruit weight and fruit breadth. Therefore more emphasis should be given on cluster I, III and IV for selecting genotypes as parents for future breeding program which may produce new recombinants with desired traits. Moderate to high Shannon-Weaver Diversity Index was found among the genotypes for most of the studied characters.

Key words: Genetic diversity % Eggplant (*Solanum melongena* L.) and cluster analysis

INTRODUCTION

Eggplant is a major vegetable crop throughout the tropics and subtropics [1]. Batugal [2] stated genetic diversity as a major factor that determines yield security in future. Information on genetic divergence among parent materials is of vital importance to plant breeder for an efficient choice of parent for hybridization [3]. Precise information on Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Multivariate analysis acts as a useful tool to quantify the degree of divergence between the biological populations at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster levels [4-6]. Exotic germplasm of eggplant may a potential source for improvement of eggplant in concern of desirable characters. Some related results have been reported in eggplant by several researchers [7-10]. These studies did not cover sufficient exotic cultivars or genotypes and were carried out in different agro climate. Haque *et al*. [11] reported with 32 eggplant genotypes, while maximum genotypes were exotic. This is why, in Bangladesh context, information on the selection of exotic eggplant genotypes on the basis of diversity is inadequate. Therefore, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity in some exotic eggplant genotypes in Bangladesh condition. This type of study would be useful for breeding eggplant varieties in the country.

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MATERIALS AND METHODS

The experiment was conducted at the experimental field and laboratory of the department of Genetics and Plant Breeding of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh during the winter season 2008-09 with 11 genotypes of eggplant 9 of which were collected from Netherlands and 2 were from Bangladesh Agricultural Research Institute (BARI). The seeds of these germplasm were sown on the seedbed on 02 November 2008. Forty days old seedlings transplanted in the main field on 12 December 2008. The experiment was laid out in a randomized complete block design (RCBD) with three replications. The unit plot size was 2.3 m × 2.3 m and twelve plants were planted in a plot with a spacing of 60 cm apart in three rows maintaining 45 cm plant to plant distance. Data were recorded from five randomly selected plants from each plot for days to first flowering (DAT), number of nodes of first flower initiation, number of fruits per inflorescence, days to 50% flowering (DAT), flower pedicel length (mm), flower pedicel diameter (mm), east-west plant canopy (cm), north-south plant canopy (cm), leaf petiole length (mm), leaf petiole diameter (mm), leaf blade length (cm), leaf blade width (cm), number of primary branches per plant, no. of secondary branches per plant, fruit weight (gm), fruit length (cm), fruit breadth (mm), days to fruit maturity (DAT), plant height (cm), number of fruits per plant and yield per plant (kg). Plot means over the replications were used for the statistical analysis. Genetic diversity was studied following Mahalonobi's [12] generalized distance (D^2) extended by Rao [13]. Based on the D^2 values, the genotypes were grouped into clusters following the method suggested by Tocher [13]. Intra and inter cluster distances were calculated by the methods of Singh and Chaudhury [14]. Statistical analyses were carried out using Genstat 5.00 software. Shannon-Weaver Diversity index was calculated by using the formula defined by Yu Li *et al.* [15].

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the 11 genotypes for all the 21 characters under study indicating the presence of notable genetic variability among the genotypes. The principal component analysis (PCA) showed that 6 characters had eigen values above unity contribute 92.19% of the total variation among the genotypes (Table 1).

Eleven genotypes were grouped into 4 clusters on the basis of cluster analysis. Maximum 4 genotypes were grouped into cluster I, followed by cluster II (3 genotypes). Cluster III and IV composes only 2 of each (Table 2).

Table 1: Eigen Values and percentage of variation of dispersion matrices of 10 principal components for 21 quantitative characters of 11 eggplant genotypes

Principal component	Latent roots/ Eigen values	Percentage of variance	Cumulative
Variance			
Fruit weight (g)	7.602	36.23	36.23
Fruit length (cm)	4.632	22.06	58.29
Flower petiole length (mm)	2.571	12.24	70.53
Fruit breadth (mm)	1.976	9.41	79.94
Plant height (cm)	1.415	6.74	86.68
Flower pedicel diameter (mm)	*1.157*	5.51	*92.19*
Yield per plant (kg)	0.912	4.34	96.53
Leaf petiole diameter (mm)	0.398	1.90	98.43
Leaf blade width (cm)	0.222	1.06	99.49
No. of primary branches per plant	0.109	0.52	100.00

Table 2: Distributions of 11 Eggplant genotypes in four clusters.

Clusters	No. of genotypes	Name of the genotypes	Fruit characteristics	Place of collection
I	4	Ral 1	Long, soft fruit with black color	Netherlands
		Ral 2	Pear shaped, very soft and black	Netherlands
		Ral 5	Pear, very soft and yellow orange	Netherlands
		Ral 6	Pear shaped, soft and black	Netherlands
II	3	Ral 3	Pear, medium soft and yellow orange	Netherlands
		Ral 4	Pear, medium soft and yellow orange	Netherlands
		Ral 9	Pear, soft and yellow orange	Netherlands
III	2	Ral 7	Pear shaped, very soft and black	Netherlands
		Ral 8	Ovoid, medium soft and green	Netherlands
IV	2	BARI Begun 7	Pear, soft and black	Bangladesh
		BARI begun 8	Pear, slightly hard and yellow orange	Bangladesh

Table 3: Average inter-cluster distance (D^2) and intra-cluster distance (bold/italic) for 11 eggplant genotypes

Clusters	I	II	III	IV
I	1.139			
II	2.203	1.216		
III	8.757	6.818	1.083	
IV	4.227	2.946	8.009	0.047

Table 4: Clusters mean for 21 characters in 11 eggplant genotypes

	Clusters			
Characters	I	II	III	IV
Days to first flowering (DAT)	51.13	5 0.01	61.45	48.11
No. of nodes of first flowering	8.00	7.87	8.27	9.34
No of flowers per inflorescence	2.47	2.53	8.20	5.71
Days to 50% flowering (DAT)	55.99	55.18	65.94	53.28
Flower pedicel length (mm)	24.98	28.19	16.83	31.60
Flower pedicel diameter (mm)	3.60	3.22	2.87	3.23
East-West plant canopy (cm)	56.83	57.67	68.33	77.34
North- South plant canopy (cm)	58.83	55.78	75.34	75.00
Leaf petiole length (mm)	46.08	46.44	76.16	50.84
Leaf petiole diameter (mm)	4.31	4.70	4.32	4.69
Leaf blade length (cm)	15.25	14.69	18.63	14.73
Leaf blade width (cm)	11.89	10.19	11.70	9.63
No. of primary branches per plant	11.04	10.69	11.02	10.22
No of secondary branches per plant	26.83	24.19	28.12	23.74
Fruit weight (g)	131.62	80.72	35.03	103.27
Fruit length (cm)	19.30	17.74	8.38	25.53
Fruit breadth (mm)	40.84	38.72	29.17	26.70
Days to fruit maturity (DAT)	63.60	63.73	67.34	60.50
Plant height (cm)	67.09	58.66	66.45	86.52
No. of fruits per plant	10.67	17.40	30.60	15.74
Yield per plant (kg)	1.40	1.37	0.97	1.62

The maximum inter-cluster distances were recorded between the cluster I and III (8.757) followed by the distance between cluster III and IV (8.009) (Table 3). As the genetic variance is very distinct among the groups, genotypes from these three clusters if used in hybridization may produce a wide spectrum of segregating population. The lowest inter cluster distance was observed between clusters I and II (2.203) followed by the distance between clusters II and IV (2.946) suggesting a close relationship among these three clusters. However, the intra-cluster divergence varied from 0.047 to 1.216, maximum being from cluster II comprised of 3 genotypes of diverse origin, while the minimum distance was observed in cluster IV that comprised of 2 genotypes.

Differences were observed in cluster means for almost all the 21 characters in the 11 genotypes studied (Table 4). Cluster I comprise 4 genotypes and showed maximum mean values for flower pedicel diameter (3.60 mm), leaf blade width (11.89 cm), no. of primary branches per plant (11.04), fruit breadth (40.84 mm) and fruit weight (131.62 gm).

Cluster II constituted of three genotypes and produced lowest mean for no. of nodes of first flowering (7.87) which is desirable.

Cluster III had 2 genotypes and produced highest mean for no. of flowers per inflorescence (8.20), north-south plant canopy (75.34 cm), leaf petiole length (76.16 mm), leaf blade length (18.63 cm), no. of secondary branches per plant (28.12) and no. of fruits per plant (30.60).

Cluster IV also composed of 2 genotypes had highest mean values for flower pedicel length (31.60 mm), east-west plant canopy (77.34 cm), leaf petiole diameter (4.69 mm), fruit length (25.53 cm) and yield per plant (1.62 kg). This cluster produces the lowest mean for days to first flowering (48.11 DAT), days to 50 % flowering (53.28 DAT) and days to fruit maturity (60.50 DAT) which are desirable traits for earliness.

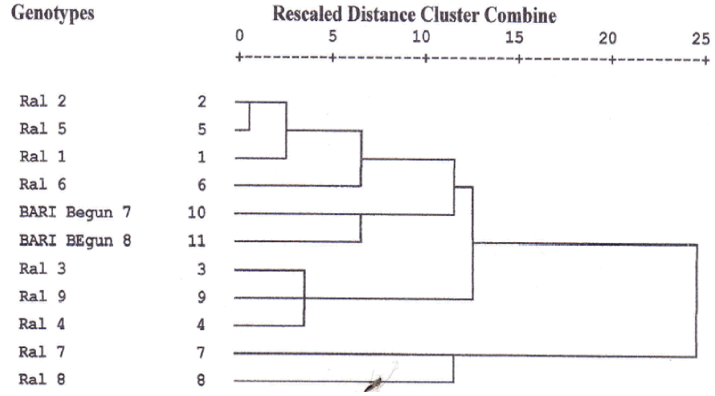

Fig. 1: Dendrogram of different eggplant genotypes constructed using UPGMA hierarchical cluster analysis (Between Groups) based on Squared Euclidean dissimilarity.

Table 5: Shannon-Weaver diversity indices (H') for 21 characters of 11 eggplant genotypes

Characters	Shannon- Weaver diversity indices (H')
Days to first flowering (DAT)	0.60
No. of nodes of first flowering	0.77
No of flowers per inflorescence	0.73
Days to 50% flowering (DAT)	0.77
Flower pedicel length (mm)	0.69
Flower pedicel diameter (mm)	0.38
East-West plant canopy (cm)	0.64
North- South plant canopy (cm)	0.71
Leaf petiole length (mm)	0.71
Leaf petiole diameter (mm)	0.75
Leaf blade length (cm)	0.80
Leaf blade width (cm)	0.73
No. of primary branches per plant	0.80
No of secondary branches per plant	0.80
Fruit weight (g)	0.80
Fruit length (cm)	0.59
Fruit breadth (mm)	0.75
Days to fruit maturity (DAT)	0.80
Plant height (cm)	0.71
No. of fruits per plant	0.63
Yield per plant (kg)	0.71
Average	0.71

Based on principal component axes I and II, a dendrogram was developed reflecting the position of genotypes are presented in Fig. 1. It was revealed that from the dendrogram, there were mainly four clusters. Most distantly located genotypes in cluster were I (Ral 1, Ral 2, Ral 5 and Ral 6) and III (Ral 7 and Ral 8). Distribution pattern of genotypes in the dendrogram also revealed that considerable variability exist in the germplasm studied.

Shannon-Weaver diversity indices (H') are ranged from 0.38 to 0.80 with an average of 0.71 (Table 5), that indicates moderate to high contribution of the characters towards total divergence among the genotypes. Highest value of H' (0.80) found in the characters leaf blade length (cm), no. of primary branches per plant, no. of secondary branches per plant, fruit weight (g) and days to fruit maturity (DAT). Highest value indicates that these characters contribute most towards total divergence and selection of genotypes based on these characters would be effective for future hybridization program. The lowest value of H' (0.38) was found in the character flower pedicel diameter (mm).

Generally crosses involving parents belonging to most divergent clusters are expected to give maximum heterosis and create wide variability in genetic architecture. However, for a practical plant breeder, the objective is not only obtaining high heterosis but also to achieve high level of production with the shortest possible time. In the present study, the maximum distances existed between clusters I and cluster III and between clusters III and IV. Considering group distance and other agronomic performance, the inter-genotypic crosses between the members of cluster I with that of cluster III or between members of clusters III and IV would exhibit high heterosis and is also likely to produce new recombinants with desired traits. Therefore, more emphasis should be given on cluster I, III and IV in selecting inbreds for crossing in eggplant hybridization programmes.

REFERENCES

1. Bose, T.K. and M.G. Som, 1986. Vegetable Crops in India. Nayaprakash, 206, Bidhan Sarani, Calcutta 700006, India, pp: 775.
2. Batugal, P.A., 1999. The Role of International Cooperation in the Development of Biotechnology in Coconut. Current Advances in Coconut Biotechnol., pp: 19-30.
3. Arunachalam, V., 1981. Genetic distance in plant breeding. Indian J. Genet., 41: 226-236.
4. Murty, B.R. and V. Arunachalam, 1966. The nature of genetic divergence in relation to breeding system in crop plants. Indian J. Genet., 26A: 188-198.
5. Sachan, K.S. and J.R. Sharma, 1971. Multivariate analysis of genetic divergence in tomato. Indian J. Genet., 31: 86-93.
6. Jatasra, D.S. and R.S. Paroda, 1978. Genetic divergence in wheat under different environmental conditions. Central Res. Comn., 6: 307-317.
7. Begum, F., 2008. Morphogenetic Diversity in Eggplant (*Solanum melongena* L.). MS thesis. Department of Genetics and Plant Breeding, BSMRAU, Salna, Gazipur, Bangladesh.
8. Rahman, M.M., 2008. Morphological and Genetic Diversity in Brinjal (*Solanum melongena* L.). MS thesis. Department of Genetics and Plant Breeding, SAU, Dhaka, Bangladesh.
9. Uddin, M.S., 2009. Genetic divergence and heterosis in eggplant for heat tolerance. Ph.D thesis. Department of Horticulture, BSMRAU, Salna, Gazipur, Bangladesh.
10. Quamruzzaman, A.K.M., M.A. Rashid, S. Ahmed and M. Moniruzzaman, 2009. Genetic Divergence Analysis in Eggplant. Bangladesh J. Agric. Res., 34(4): 705-712.

11. Haque, M.N., M. Nazim Uddin, M.Z. Hossain, M.A. Rashid and S.M.M. Hossain, 2002. Genetic divergence in brinjal. Bangladesh J. Agril. Res., 27(2): 165-171.
12. Mahalanobis, P.C., 1936. On the generalizeddistance in statistics. Proc. National Inst. Sci. India, 2: 45-55.
13. Rao, C.R., 1952. Advanced Statistical Methods in Biometrical research. John Wiley and Sons. New York.
14. Singh, R.K. and B.D. Choudhury, 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. pp: 102-138.
15. Yu Li, W.K. Shuzhi, Yongsheng Cao and X. Zhang, 1996. A phenotypic diversity analysis of foxtail millet (*Setaria italica* L.P. Beauv) landrace of Chinese origin. Genetic Resources and Crop. Evol., 43: 377-384.