

BREEDING POTENTIAL OF COMMON EGGPLANT (*SOLANUM MELONGENA* L.) USING DIVERGENCE ANALYSIS

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Abstract

Genetic divergence among 21 eggplant genotypes was assessed for a number of agro-morphological traits. Based on D^2 statistics these genotypes were grouped into 5 distinct clusters. Scatter diagram represented pattern of genotypic distribution in different clusters through principal component scores. Genotype belongs to cluster I and cluster V can be selected in crop improvement program because of their highest inter-cluster distance (72.15). Genotypes of cluster V possessed heterogeneous nature and showed highest intra-cluster distance (4.97). Highest cluster mean for different yield and yield contributing traits was observed in cluster I which contains a solitary genotype (Sada Begun) followed by cluster IV. As important contributor towards genetic divergence the character yield/plant (g) (48.10%), fruit stalk length (cm) (11.90%), fruit length (cm) (11.43%), harvesting period (10.95%), fruit circumference (cm) (10.00%), fresh weight/fruit (g) (4.76%) and fruits/plant (2.86 %), can be considered as authentic as well as desirable traits for selecting parents in improving eggplant.

Introduction

In Bangladesh eggplant *Solanum melongena* L. is the second most important vegetable next to potato in terms of total production area under cultivation (Khalil *et al.* 2013) and possessing 3.68 lac metric tons in both rabi and kharif season during 2012-2013 (BBS 2013) as against in China 288 lac metric tons, India 122 lac metric tons and Iran 13 lac metric tons (Faostat 2014).

Almost 60 eggplant cultivars are available in Bangladesh which are mainly cultivated on commercially and home garden for essential nutrition source and cash income (Meah *et al.* 2007). Average yield performance of eggplant both local and hybrid varieties in Bangladesh is poor regarding to size, shape, skin color and locally sustainable cultivars. Recently genetic modification of the eggplant has flourished in our country though its adverse effects on soil eco-system, environment, human and animal health. To avoid recent concern in consumption of genetically modified crops this type of study would be effective for producing high yield and sustainability which will certainly enhance the production and consumption of this crop. D^2 statistics is an important tool which represents nature and extent of genetic divergence in selecting sustainable genotypes for better yield. In Bangladesh selection of parents on the basis of divergence analysis has been reported in eggplant by Quamruzzaman *et al.* 2009, Begum *et al.* 2013, Rahman *et al.* 2014, Solaimana *et al.* 2015. Therefore, the present investigation was carried out to choose the suitable eggplant genotypes for further breeding programs.

Materials and Methods

Eggplant (*Solanum melongena* L.) belonging to Solanaceae is widely cultivated vegetable in both temperate and tropical areas, specially in Asian countries like India, Bangladesh, Pakistan,

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China, Japan, Indonesia and Philippines (Rahman *et al.* 2014). It is a diploid species $2n = 24$ with a basic chromosome number 12 (Ray and Das 2010).

The present investigation was conducted at experimental field in Botanical Garden of Jahangirnagar University during Rabi season (November - March, 2013 - 2014) and Kharif season (April - July, 2014). The experiment was laid out in RCBD with three replications using 21 common eggplant genotypes which were collected from different sources (Table 1). The unit pits was 3 feet \times 3 feet with 0.5 feet \times 0.5 feet spacing. The fertilizer and manure were applied as per recommended dose for the commercial cultivation of eggplant and the cultural practice were done as and when required. Observations were recorded randomly for each genotype in each replication for different quantitative traits, namely plant height (cm), no. of primary branches/plant, no. of secondary branches/plant, stem diameter (cm), days to first flowering, days to first fruiting, harvesting period, no. of fruits in inflorescence/plant, no. of fruits in solitary/plant, fruit length (cm), fruit stalk length (cm), fruit circumference (cm), fresh weight/fruit (g), fruits/plant and yield/plant (g).

Table 1. Eggplant genotypes used in the experiment.

Designation	Genotypes	Source of collection
1	Kata Begun	Jessore
2	Green Beauty	Maherpur
3	Islampuri Tal Begun	Goforgaon
4	Debjhuri Hajari	India
5	Begun Singhnat	Narsingdi
6	BARI-6	Bangladesh Agriculture Research Institute
7	BARI-7	"
8	BARI-8	"
9	BARI-9	"
10	BARI-10	"
11	Banani	Lal teer Seed Industry Limited
12	Kajla	"
13	Sraboni	"
14	Sada Begun	Savar
15	Fata Begun	"
16	Parthib	Lal teer Seed Industry Limited
17	BNB-478	India
18	Nandini	"
19	Singhnat 60	Narshingdi
20	Tal Begun	Tangail
21	Singhnat HYV Brinjal	Narshingdi

The collected data were assembled and formulated in proper forms of statistical analysis. Analysis of variance was performed with the help of a MSTAT-C program (Freed 1986). D^2 statistics (Mahalanobis 1936) were used to assess genetic divergence among the entries genotypes in which distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhary (1979). Mean value for each character was subjected to evaluate Cluster Analysis (CLSA), Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO) and Canonical Variate Analysis (CVA) using GENSTAT 5.5

software. Character contribution was calculated through using Indostat 9.1 software. Three dimensional scattered diagrams and biplot analysis for different principal component axis were done by R software.

Results and Discussion

By applying non-hierarchical clustering using co-variance matrix based on 15 quantitative characters, 21 genotypes were grouped into five distinct clusters (Table 3). Highest numbers of genotypes were found in cluster V containing eight genotypes and cluster I had solitary genotype. Cluster II and cluster III both of each contained five genotypes while cluster IV consisted of two genotypes. Clustering pattern in the present study showed significant variability among the concerned genotypes. Based on 15 characters Kumar *et al.* (2013) found 6 clusters for 14 eggplant genotypes whereas Mishra *et al.* (2013) found 6 clusters using 30 genotypes of eggplant.

Table 2. ANOVA for different quantitative traits in eggplant.

Character	Genotypes (df = f20)	Error (df = f20)	CV%
Plant height (cm)	1112.161**	274.533	10.3
No. of primary branches/plant	21.699*	7.967	17.71
No. of secondary branches/plant	128.233**	34.654	17.04
Stem diameter (cm)	0.832**	0.107	6
Days to first flowering	115.857**	22.495	4.26
Days to first fruiting	144.131**	24.631	4.08
Harvesting period	1086.681**	20.481	6.14
No. of fruits in inflorescence/plant	142.021**	11.649	43.05
No. of fruits in solitary/plant	14.175*	4.961	52.02
Fruit length (cm)	36.648**	1.678	8.14
Fruit stalk length (cm)	2.419**	0.338	8.82
Fruit circumference (cm)	116.966**	3.998	11.2
Fresh weight/fruit (g)	18001.846**	527.747	14.38
Fruits/plant	145.039**	10.481	26.5
Yield/plant (g)	2447424.176**	221159.238	27.08

** = Significant at 1% level. * = Significant at 5% level. CV% = Coefficient of variance.

Table 3. Distribution of different eggplant genotypes into cluster based on D² statistics.

Cluster	No. of genotypes	Genotypes name
I	1	Sada Begun
II	5	Kata Begun, BARI-6, BARI-7, Parthib, Singhnat HYV brinjal
III	5	Islampuri Tal Begun, BARI-9, Banani, Kajla, Sraboni
IV	2	Debjhuri Hajari, Begun Singhnat
V	8	Green Beauty, BARI-8, BARI-10, Fata Begun, BNB-478, Nandini, Singhnat 60, Tal Begun

The principal component analysis yielded Eigen values and per cent contribution for each principal component axis where variation among genotypes accounted through the per cent contribution of these axes. A three dimensional scatter diagram was constructed using first three principal component axes PCA1 (31.32%), PCA2 (23.45%) and PCA3 (17.51%) which

cumulatively accounted for 72.28% of the total variation among 15 principal component axes for all the genotypes (Fig.1). Scatter diagram represented the distribution pattern of genotype into clusters which revealed substantial variability among the existed genotypes (Fig.1). Based on PCA scores distribution pattern among 35 genotypes was observed by Solaimana *et al.* (2015) and 100 genotypes by Rahman *et al.* (2014).

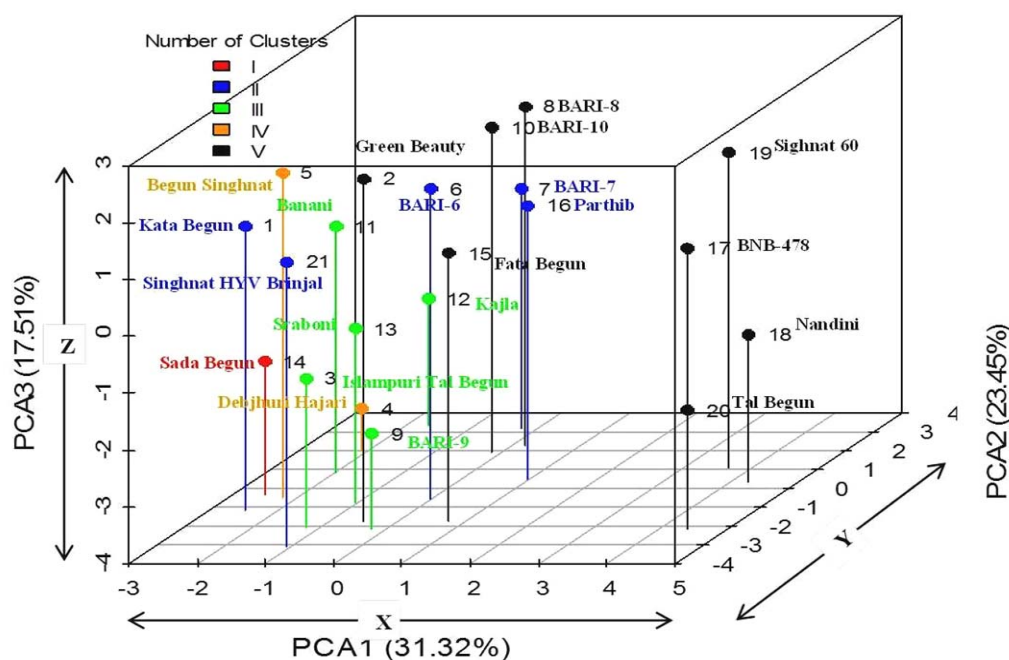


Fig. 1. Three dimensional scattered diagram of different eggplant genotypes based on principal component scores.

Intra-cluster distance was calculated from inter-genotypic distances obtained through principle coordinate analysis (PCO). Genotypes within cluster V were very diverse because of highest intra-cluster distance (4.97) followed by cluster II (3.7), III (2.96) and IV (1.41) (Table 4). Lowest intra-cluster distance was observed in cluster I (0.0) due to having only one genotype. Highest inter-cluster distance observed between cluster I and cluster V (72.15) followed by cluster I and cluster II (62.61), cluster IV and cluster V (49.29), cluster I and cluster III (44.82), cluster I and cluster IV (42.18) indicated that heterogeneous nature existed between these clusters (Table 4). This is indicative of the fact that the genotypes included in these cluster would give heterotic hybrids in advanced generations as suggested by Ahmed *et al.* (2014). Lowest inter-cluster distance observed in cluster III and cluster IV (14.84) indicated that homogenous nature of germplasm lines between these clusters. Shinde *et al.* (2012) emphasized that selection of superior eggplant genotypes belonging to clusters should be based on high inter-cluster distance along high cluster mean for yield and its related traits. Difference between intra- and inter-cluster distances revealed that genotypes within the same cluster were closely related and genotypes between different clusters exposed wide range of genetic diversity as concluded by Begum *et al.* (2013) and Sadarunnisa *et al.* (2015).

The cluster mean for yield and yield related traits indicated considerable differences among the clusters (Table 5). The genotype of cluster I produced highest mean for yield/plant (g) (4587.9), fresh weight/fruit (g) (247.5) and fruit circumference (cm) (23.9) which resemble superior over other clusters and also genotypes of cluster IV for producing highest mean in fruits/plant (22.9), fruit length (cm) (18.6) and no. of fruits in inflorescence/plant (19.8). The performance of cluster II and cluster III was moderate. Considering yield and other contributing traits genotypes of cluster I and cluster IV would be effective in obtaining higher heterosis because of their highest mean value. Similar conclusions in eggplant were reported by Rath *et al.* (2011) and Uddin *et al.* (2014) based on highest cluster mean for yield and its related traits.

Table 4. Average intra- (bold) and inter-cluster distance for eggplant genotypes.

	I	II	III	IV	V
I	0				
II	62.61	3.7			
III	44.82	19.54	2.96		
IV	42.18	32.24	14.84	1.41	
V	72.15	18.42	35.03	49.29	4.97

Table 5. Cluster mean for different characters in eggplant genotypes.

Character	I	II	III	IV	V
Plant height (cm)	159	169.4*	148.6	166.1	162
No. of primary branches/plant	16.5	17.9*	16.1	17.5	14.2
No. of secondary branches/plant	39	36.6	39.2*	39.1	28.6
Stem diameter (cm)	4.8	5.6	5.3	5.7*	5.4
Days to first flowering	105	109.8	106.1	108.5	117.1*
Days to first fruiting	112.5	122	114.6	117	128.4*
Harvesting period	70	64.6	82.3*	69	75.7
No. of fruits in inflorescence/plant	13.9	5	10.4	19.8*	4.6
No. of fruits in solitary/plant	5	4.7	6.9*	3.2	2.6
Fruit length (cm)	17.2	16.4	15.1	18.6*	15.3
Fruit stalk length (cm)	6.3	6.7*	6.6	6.3	6.6
Fruit circumference (cm)	23.9*	20.7	18.9	20.8	13.9
Fresh weight/fruit (g)	247.5*	192.9	153.8	245.7	110.4
Fruits/plant	18.9	9.7	17.3	22.9*	7.1
Yield/plant (g)	4587.9*	1534.3	2405.8	3243.8	711.5

* = Highest value.

Contribution towards genetic divergence for a certain trait would be greater when the concerned trait performs maximum number of times for its rank. In the present study the character yield/plant (g) showed the maximum contribution (48.10%) towards genetic divergence followed by fruit stalk length (cm) (11.90%), fruit length (cm) (11.43%), harvesting period (10.95%), fruit circumference (cm) (10.00%), fresh weight/fruit (g) (4.76%) and fruits/plant (2.86%) (Fig. 2). The relative contribution of other characters for divergence among the genotypes was found nil. Kumar *et al.* (2013) found that yield/plant as the maximum contributor towards genetic divergence followed by other characters and gave emphasis on selecting parents based on high contributing

characters. Therefore, selection of parents should be emphasized on yield/plant (g), fruit stalk length (cm), fruit length (cm), harvesting period, fruit circumference (cm) because of their maximum contribution towards genetic divergence in eggplant, similar investigation was reported by Dutta *et al.* (2009).

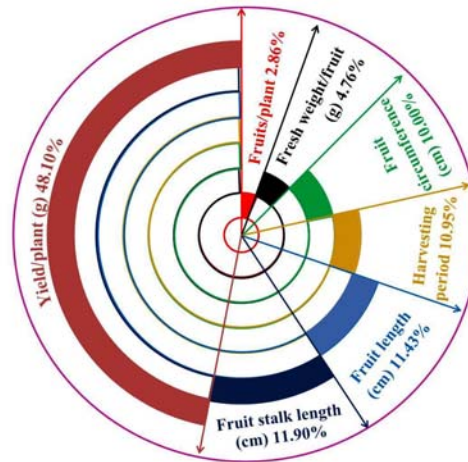


Fig. 2. Relative contribution of different characters towards genetic diversity in eggplant.

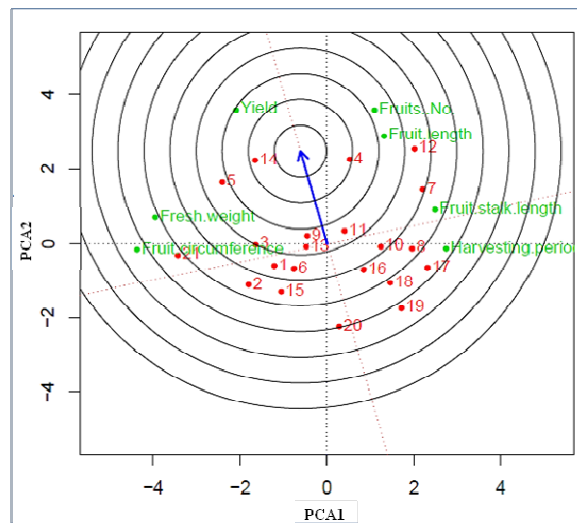


Fig. 3. Ranking of different eggplant genotypes using bilpot analysis.

All the genotypes along with most divergent contributing traits particularly yield/plant, fruit stalk length, fruit length, harvesting period, fruit circumference, fresh weight/fruit, fruits/plant were considered under biplot analysis to obtain best genotype. Genotypes located at the center of concentric circle are Sada Begun followed by Debjhuri Hajari, Begun Singhnat and close to the indicator of superiority (blue arrow line) are regarded as superior genotypes (Fig. 3). Thus in recombinant breeding program genotype Sada Begun, Debjhuri Hajari and Begun Singhnat would be effective in selecting parents in order to produce new recombinants with desired traits. Biplot analysis in eggplant also reported by Ullah *et al.* (2014).

Considering most divergent contributing characters, higher inter-cluster distance and above all mean performances it can be concluded that Sada Begun of cluster I and Debjhuri Hajari, Begun Singhnat of cluster IV would be effective parents for future breeding program.

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