Morphological characterization and genetic diversity studies of promising brinjal genotypes for hybridization program in Bangladesh

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ABSTRACT

In this Morphological variation of thirty-five brinjal genotypes was investigated in order to screen efficient genotypes for a hybridization program in Bangladesh. The phenotypic coefficient of variation (PCV) was higher than that for the genotypic. The PCV estimates were high for the number of branches, number of fruits per plant, and single fruit weight. Heritability estimates were high for the single fruit weight with high genetic advance. In spite of high heritability values for most traits, the expected genetic advance as a percentage of the mean ranged from 19.92 to 121.51. Multivariate analysis was performed using principal component analysis (PCA), principal coordinate analysis, cluster analysis and canonical variate analysis. With PCA, multivariate analysis of Mahalanobis's distance (D^2), and cluster analysis, the genotypes were grouped into six clusters. The longest inter-cluster distance was between clusters II and III, and the shortest was between clusters V and VI. Cluster VI showed the longest intra-cluster distance but cluster II showed the shortest. Genotypes of cluster I were suitable for the number of branches per plant, cluster II for the fruit length, cluster III for the number of fruits per plant, and cluster IV for the single fruit weight and yield. Considering the performances, genotypes SM-111, SM-84, EGN-27, SM-183, and BARI begun-6 are suitable parents for the hybridization program.

Indexing terms/Keywords

brinjal genotypes, genetic diversity, hybridization, morphological characters

Academic Discipline And Sub-Disciplines

Agriculture; Horticulture

SUBJECT CLASSIFICATION

Horticulture; morphological screening (MS), genetic diversity

TYPE (METHOD/APPROACH)

Original research work, morphological screening for hybridization programme.

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INTRODUCTION

Brinjal (Solanum melongena L.) is one of the most important and popular Solanaceous crops in Bangladesh and three main botanical varieties of the species melongena; esculentum, serpentintum, and depressum, have been grown commercially mainly during the dry season (October to March) [1] For example, the total production area and fruit yield of brinjal during the dry season of 2010-2011 were 28.7 thousand ha and 216 thousand metric t, respectively, while in the rainy season (June to September), they were 17.8 thousand ha and 125 thousand metric t, respectively [2]. However, because of the limited number of promising varieties, the breeding of new varieties using native and imported germplasms is required [3].

Precise information on the nature and degree of genetic divergence of brinjal land races is a prerequisite for future breeding program [4-6].

Genetic diversity arises due to either geographical separation or genetic barriers to crossing [3]. Hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains [7]. Therefore, evaluation of genetic diversity is used as a major tool in hybridization program for selecting efficient parents [8]. One of the effective techniques multivariate analysis of Mahalanobis's distance (D^2) [9] and D^2 cluster and factor analyses, such as principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CA), and canonical vector analysis (CVA), have also been used successfully for assessing the genetic diversity of different cops [10]. This technique measures the forces of differentiation at two levels; intra-cluster and inter-cluster levels, and thus helps in the selection of genetically divergent parents for exploitation in hybridization program.

A number of brinjal cultivars including land races have been cultivated in Bangladesh, and they show a wide range of genetic variations [11-12], but the study of their genotypes remains a challenge [13], because of species' large genomes, overlapping eco-geographical distributions [14] and morphological plasticity [15]. Therefore, it is necessary to characterize individual accessions and cultivars as a general guide in the selection of parents for hybridization [16]. The advancement of knowledge on genetic diversity or similarity would be helpful for the sustainable long-term selection [17].

In addition to aiding in the selection of divergent parents for hybridization, the Mahalanobis D2 statistic measures the degree of diversification and determines each component character as a relative proportion of the total divergence [18-19].

Therefore, our main aim was to identify better genotypes for the breeding of brinjal in Bangladesh. Considering the above facts, the present study was undertaken with the following objectives: 1. to characterize the genotypes morphologically. 2. to assess the genetic variability and correlation between the yield and its component characters, and 3. to screen suitable parents for hybridization.

MATERIALS AND METHODS

Experimental site

The study was conducted at Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh. The experimental area was situated at 24.00° N latitude and 90°25´ E longitude at an altitude of 8.4 m. The area has a subtropical climate, characterized by limited rain along with a slightly low temperature during the winter (September-April), and high rainfall, and a high temperature during the rest of the year. Soil of the experimental site is comprised of sand: silt: clay = 37: 27: 37%. The soil pH ranges from 6.0- 6.6, and contains organic matter at a rate of 0.84%.

Genotype, design of the experiment, and plant cultivation

A total of thirty-five cultivated genotypes of brinjal were collected from different places/districts/markets of Bangladesh (Table 1). The experiment followed a randomized complete block design with two replications. A plot was 7.5 x 0.80 m (L x W) with a block to block distance of 0.75 m. Cow manure, urea, Triple super phosphate (TSP), Muriate of potash (MOP), and gypsum were applied at 1500, 375, 150, 250, and 100 kg ha-1, respectively, according to the recommendations of BARI [20]. Seeds of selected genotypes were sown in a seedbed on 16 September, 2013 and the seedlings were transplanted into the plot on day 45.

Data recording

All plants were grown for 130 days in the plot and 5 plants from each plot per genotype were chosen randomly. The morphological characters: plant height (cm) at the first (PHFH) and last harvest (PHLH), number of branches per plant (NBPP), leaf blade length (LBL, cm), fruit length and breadth (FL and FB, respectively, cm), fruit curvature (FC), single fruit weight (SFW, g), number of fruits per plant (NFP), number of seeds per fruit (NSPF), days to 50% flowering (D50%F) , fruit yield (FY, t ha-1), and 100-seed weight (100-SW), were measured according to the IBPGR eggplant descriptor tool [21].

Statistical analysis

Mean data for each character were subjected to both uni- and multivariate analyses. Multivariate analysis was performed using GENSTAT 5.13 (11th edn.) (VSN International Ltd, Hemel Hempstead, UK) with four techniques: principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CA) and canonical vector analysis (CVA). Multivariate analyses (MVA) [9, 22] were also modified [23-25]. Genotypes were grouped into clusters [22], and inter- and intra-cluster distances were calculated according to [26].

RESULTS AND DISCUSSION

Morphological characterization

Most of the genotypes showed a solitary fruit-bearing habit but EGN-17, Uttara, Sada begun, SM-84, and SM-186 bore fruit in clusters (Table 1). Among the genotypes, BARI begun-8, and BARI begun-10 were sickle-shaped; Sada begun, SM-58, BARI begun-3, SM-180, BARI begun-4, SM-184 were curved; SM-19 was U-shaped, and curved; BARI begun-7 and SM-183 were snake-like and the rest of the genotypes had no curvature. Most genotypes produced oblong or long fruits, while SM-75, BARI begun-5, SM-83, BARI begun-6, and SM-77 produced round fruits. Among the genotypes, 7 showed a striped fruit color, while the rest of them showed a uniform color distribution at the time of commercial harvest. Only SM-111 and SM-84 produced limited number of seeds, while the rest of the genotypes produced many seeds.

Brinjal fruits with a round (6 genotypes) or curved shaped (7) with a uniform (25) purple black colour (16), and many seeds (33 genotypes) are preferred by consumers and breeders [3, 12]. From the viewpoint of fruit characteristics, SM-111, SM-84, BARI begun-8, BARI begun-6, SM-183, EGN-27, and SM-57 are promising for future hybridization program.

Genetic diversity

Genetic diversity analysis involved several steps: estimation of the distance between genotypes, clusters, and analysis of the inter-cluster distance and, therefore, more than two multivariate techniques were required to represent the results more clearly [27-30].

Analysis of variance showed significant variations among all genotypes for the 13 characters studied. Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z1 - Z2) using component score 1 as the X-axis and component score 2 as the Y-axis was constructed (Fig. 1). The positions of the genotypes in the scatter diagram were distributed into six groups, indicating marked diversity among the genotypes. Mahmud et al. [31] also investigated 58 new Brassica lines with this technique, and identified diversity among the genotypes. However, the distribution of genotypes in different clusters of the D2 analysis showed a similar trend of the Z1 and Z2 vectors of the principal component analysis, which was found to be an alternative method for providing information on the clustering pattern of genotypes. PCA provides information regarding the contribution of characters towards the divergence of brinjal. The six clusters obtained with the scatter diagram were located at a distance from each other.

PCA yielded Eigenvalues of each PC axis with the first axis of 25.70%, while two of these with Eigenvalues above unity accounted for 47.52% (Table 2). The first three PC axes accounted for 61.04% of the total variation among the 13 characters describing the 35 brinjal genotypes (Table 2).

Cluster VI involved the maximum number of genotypes (14) followed by I, V, IV, and, II and III (Fig.1). This grouping pattern was similar to that of the collection site (origin) of the genotypes (Table 3), indicating that the genetic diversity of the materials was also influenced by the geographic variations, as reported by [32-33].

From the mean cluster values (Table 4), it was revealed that cluster IV mostly showed the highest mean values for DFH (107.67), FW (7.37), SFW (268.47), fruit yield (18.32), and 100-SW (0.46), but the lowest (55.05) for PHFH (Table 4). Cluster I showed highest PHLH (97.06), NBPP (5.5), and NSPF (501.79), and cluster V showed highest mean values for D50%F (62.21), PHFH (68.2), and LBW (17.83). On the contrary, cluster III showed the lowest mean values for most of the parameters. Joshi et al. [34] assessed the quantitative and qualitative traits of 73 tomato genotypes using non-hierarchical Euclidean cluster analysis, and they were grouped into 15 clusters. Dharmatti et al. [35] grouped 402 tomato lines into 4 clusters based on the similarities of D2 values, and revealed that the mean cluster values for D50%F, DFH, and NFPP, were similar. Naskar [36] grouped 22 sweet potatoes genotypes into 7 different clusters. Desai et al. [37] evaluated the genetic divergence of thirty-six potato genotypes by D2 statistic, and revealed that cluster IV exhibited the maximum yield.

Inter-cluster and intra-cluster genotypic distances were calculated according to the method of Singh et al. [38]. The inter cluster distance was greater than the intra cluster distance, indicating wider genetic diversity among the genotypes (Table 5). As shown in the Table 5, the longest inter-cluster distance was observed between clusters II and III (12.027), followed by between II and IV (11.484), and II and III (11.107), while the shortest inter-cluster distance was observed between V and VI (3.115), followed by between II and V (4.206). Therefore, combined hybridization should be chosen between clusters II (BARI begun-8 and SM-186) and III (SM-111 and SM-84) for producing a wide spectrum of segregating generations [39].

To calculate the inter-cluster Mahalanobis's D2 values, CVA was used. The inter-cluster distances were longer than the intra-cluster distance shown in Table 5, suggesting wider genetic diversity among the genotypes of different groups as shown in the multivariate analysis of eggplants [40]. The results obtained from different multivariate techniques are superimposed in Fig. 1, showing that all techniques yielded similar results, and each technique supplemented and confirmed the results of another.

The contribution of characters towards divergence of the genotypes obtained from CVA is presented in Table 6. Vector-1 obtained from PCA showed that PHLH, D50%F, DFH, PHFH, LBL, FL, FW, SFW, NSF, and 100-SW were important characters for genetic diversity in the first axis of differentiation while, vector-2 showed, NBPP, FL, FW, SFW, FY, NSF, and 100-SW were important (Table 6). Murty and Arunachalam [6] reported that genetic drift and selection in different environments could cause greater diversity than the geographic distance. Furthermore, there is a free exchange of seed material among different regions of Bangladesh; as a consequence, the characters might be associated with particular

regions in nature but may lose their individuality through human interference. In some cases, the geographic distribution was not the sole criterion of genetic diversity. The clusters of the lines suggest that the maximum yield in different regions depends on directional selection.

CONCLUSION

The present findings indicated that the characters studied in this experiment exhibited significant differences among the genotypes. Generally, diversity was influenced by the morphological characters, but not the distribution of genotypes, which indicated the importance of consumer preference, and suitability of growing conditions. Considering the diversity pattern and other agronomic performances, the genotypes SM-111, SM-84, EGN-27, SM-183, and BARI begun-6 from clusters III and IV were considered as suitable parents for an efficient hybridization program. The results of this investigation also suggested that crossing of the genotypes with a high mean yield and long inter-cluster distance would lead to greater heterotic expression and a broad spectrum of favorable genetic traits in segregating generations for improvement of the fruit yield of brinjal.

Table 1: List of 35 selected brinjal genotypes and their fruit characteristics

Sl. No.	Name/Accession No.	Botanical variety	Place of collection/ Source	Fruit bearing	fruit curvature (FC)	Fruit shape	Fruit colour	No. of seed per fruitz	Colour distribution at harvest
1.	SM-57	esculentum	Local market	Solitary	None	Oblong	Purple black	Many	Uniform
2.	EGN-17	esculentum	Nichintopur	Cluster	None	Oblong	Purple black	Many	Uniform
3.	Uttara	esculentum	Rajshahi	Cluster	None	Oblong	Purple	Many	Uniform
4.	EGN-10	esculentum	Nichintopur	Solitary	Slightly curved	Long	Purple black	Many	Stripped
5.	Sada begun	serpentintum	Unknown	Cluster	Curved	Long	White	Many	Uniform
6.	SM-111	esculentum	Barishal	Solitary	None	Long	Purple black	Few	Uniform
7.	EGN-27	esculentum	Nichintopur	Solitary	None	Round	Purple black	Many	Uniform
8.	EGN-25	esculentum	Nichintopur	Solitary	None	Oblong	Green	Many	Stripped
9.	Chaga	esculentum	Nichintopur	Solitary	None	Long	Green	Many	Stripped
10.	BARI begun-7	serpentintum	Gazipur	Solitary	Snake shaped	Long	Black	Many	Uniform
11.	SM-75	esculentum	Thakurgaon	Solitary	None	Round	Purple	Many	Uniform
12.	BARI begun-9	esculentum	Gazipur	Solitary	None	Oblong	Purple black	Many	Uniform
13.	SM-59 (small)	depressum	Unknown	Cluster	None	Oblong	Purple black	Many	Uniform
14.	SM-58	serpentintum	Unknown	Solitary	Curved	Long	Purple black	Many	Uniform
15.	SM-11	esculentum	Unknown	Solitary	None	Oblong	Milky white	Many	Stripped
16.	SM-48	esculentum	Rangpur	Solitary	None	Long	Green	Many	Stripped
17.	SM-77 (long)	esculentum	Thakurgaon	Solitary	None	Long	Green	Many	Uniform
18.	BARI begun-5	esculentum	Gazipur	Solitary	None	Round	Purple black	Many	Uniform
19.	SM-59 (big)	esculentum	Unknown	Solitary	None	Oblong	Purple black	Many	Uniform
20.	BARI begun-3	serpentintum	Unknown	Solitary	Curved	Long	Purple black	Many	Uniform
21.	SM-83	esculentum	Thakurgaon	Solitary	None	Round	Green	Many	Stripped
22.	SM-180	serpentintum	Advanced Line of Netherland seed comp.	Solitary	Curved	Long	Light purple	Many	Uniform
23.	SM-19	serpentintum	Unknown	Solitary	U shaped and curved	Long	Purple	Many	Uniform
24.	BARI begun-4	serpentintum	Unknown	Solitary	Curved	Long	Purple black	Many	Uniform
25.	BARI begun-8	serpentintum	Unknown	Solitary	Sickle shaped	Long	Light purple	Many	Uniform
26.	SM-84	esculentum	Gazipur	Cluster	None	Oblong	Light purple	Many	Stripped
27.	SM-63	esculentum	local market	Solitary	None	Long	Purple black	Many	Uniform
28.	SM-184	serpentintum	Advanced Line of Netherland seed comp.	Cluster	Curved	Long	Purple	Many	Stripped
29.	BARI begun-10	serpentintum	Gazipur	Solitary	Sickle shaped	Long	Purple black	Many	Uniform

30.	SM-185	serpentintum	Advanced Line of Netherland seed comp.	Solitary	Slightly curved	Long	Purple	Many	Stripped
31.	SM-181	serpentintum	Advanced Line of Netherland seed comp.	Solitary	Slightly curved	Long	Purple black	Many	Uniform
32.	SM-183	esculentum	Advanced Line of Netherland seed comp.	Solitary	Snake shaped	Long	Purple	Many	Uniform
33.	SM-186	esculentum	Advanced Line of Netherland seed comp.	Cluster	Curved	Long	Purple black	Many	Uniform
34.	BARI begun-6	esculentum	Pabna	Solitary	None	Round	Green	Many	Uniform
35.	SM-77 (round)	esculentum	Gazipur	Solitary	None	Round	Uniform	Many	Stripped

[z] <100: very few, 101-300: few and > 300: many.

Table 2: Eigenvalues and percent variation in respect to 13 characters of 35 germplasms of brinjal genotypes

Principal component axis	Principal component characters	Eigen values	Total variation (%)	Cumulative percentage
I	Days to 50% flowering (D50%F)	3.341	25.70	25.70
II	Days to first harvest (DFH)	2.837	21.82	47.52
III	Plant height at first harvest (PHFH)	1.758	13.52	61.04
IV	Plant height at last harvest (PHLH)	1.159	8.92	69.96
V	Number of branches (NB)	1.052	8.09	78.05
VI	Leaf blade length (LBL, cm)	0.699	5.37	83.42
VII	Fruit length (FL, cm)	0.641	4.93	88.35
VIII	Fruit width (FW, cm)	0.486	3.74	92.09
IX	Single fruit weight (SFW, gm)	0.443	3.41	95.5
X	Number of fruit plant^{-1} (NFPP)	0.241	1.85	97.35
XI	Fruit yield plant^{-1} (FY, Kg)	0.171	1.31	98.66
XII	No. of seedfruit^{-1} (NSPF)	0.120	0.93	99.59
XIII	100 seed weight (100-SW, gm)	0.052	0.40	100.00

Table 3: Distribution of 35 brinjal genotypes in six different clusters with their collection site

Cluster No.	Number of genotypes	Genotypes including sources of collation
I	7	SM-57(market), EGN-17 (Nichintopur), Chaga, SM-75, SM-77 (Long), SM-83 (Thakurgaon), SM-63 (local market)
II	2	BARI Begun-8, SM-186(Advanced line of Netherland seed company)
III	2	SM-111 (Barisal),SM-84 (Thakurgaon)
IV	3	EGN-27 (Nichintopur), SM-183 (Advanced line of Netherland seed company), BARI Begun-6 (Pabna)
V	7	EGN-10, Sada bagun, EGN-25 (Nichintopur), BARI Begun-7, SM-59 (small), BARI Begun-4, SM-77 (Thakurgaon)
VI	14	Uttara (Rajshahi), BARI Begun-9, SM-58, SM-11, SM-48 (Rangpur), BARI Begun-5 (Gazipur), SM-59 (big), BARI Begun-3, SM -180 (Advanced line of Netherland seed company), SM-19, SM-184 (Advanced line of Netherland seed company), BARI Begun-10, SM-185 (Advanced line of Netherland seed company), SM-181 (Advanced line of Netherland seed company)

Table 4: Mean intra- (bold) and inter-cluster distances (D^2) for 35 genotypes of brinjal obtained on the basis of morphological characters

Cluster	I	II	III	IV	V	VI
I	**2.887**	5.919	11.107	6.288	4.221	4.711
II		**0.698**	12.027	11.484	4.206	6.765
III			**0.987**	10.169	10.169	7.855
IV				**1.576**	8.371	6.158
V					**2.773**	3.115
VI						**7.538**

Table 5: Cluster means of 35 brinjal genotypes obtained on the basis of morphological characters

Character	Cluster					
	I	II	III	IV	V	VI
D50%F[z]	57.07	57.75	46.50	57.17	62.21	56.61
DFH[y]	98.64	102	94	107.67	99.36	99.64
PHFH[x]	63.37	61.64	62.14	55.05	68.20	63.82
PHLH[w]	97.06	93	77.74	91.05	95.59	91.88
NB[v]	5.50	5.25	4	5.33	5.29	5.32
LBL (cm)[u]	16.64	14.33	11.93	17.14	17.83	16.21
FL (cm)[t]	13.17	18.76	8.25	14.54	17.23	17.30
FW (cm)[s]	6.40	2.70	3.50	7.37	4.10	4.69
SFW (g)[r]	194.11	44.10	48.31	268.47	101.78	128.59
NFPP[q]	14.27	19.97	51.64	18.85	19.03	21.33
FY (t ha^{-1})[p]	12	3.78	13.53	18.32	8.91	12.43
NSPF[o]	501.79	510	236.25	398.33	447.14	376.61
100-SW (g)[n]	0.41	0.44	0.31	0.46	0.39	0.42

[z] - Days to 50% flowering, [y]- Days to first harvest, [x] - Plant height at first harvest, [w] - Plant height at last harvest, [v]-number of branches, [u] -Leaf blade length, [t] - Fruit length [s]- Fruit width, [r] -Single fruit weight, [q] - Number of fruit plant^{-1}, [p]- Fruit yield plant^{-1}, [o] - No. of seedfruit^{-1} , [n] - 100-seed weight

Table 6: Latent vectors of 35 brinjal genotypes on the basis of morphological characters

Character	Vector-1	Vector-2	Character	Vector-1	Vector-2
D50%F[z]	0.3572	-0.2464	FW (cm)[s]	0.1254	0.5243
DFH[y]	0.0834	-0.2788	SFW (g)[r]	0.2506	0.4159
PHFH[x]	0.1281	-0.0524	NFPP[q]	-0.4630	-0.0963
PHLH[w]	0.3947	-0.0267	FY (t ha^{-1})[p]	-0.2006	0.4195
NB[v]	0.2039	0.0271	NSPF[o]	0.3793	0.0622
LBL (cm)[u]	0.3110	0.1002	100-SW (g)[n]	0.1547	0.2102
FL (cm)[t]	0.2323	-0.4075			

[z] - Days to 50% flowering, [y]- Days to first harvest, [x] -Plant height at first harvest, [w] - Plant height at last harvest, [v]-number of branches, [u]-Leaf blade length, [t] - Fruit length [s] - Fruit width, [r] -Single fruit weight, [q] - Number of fruit plant^{-1}, [p]- Fruit yield plant^{-1}, [o]- No. of seedfruit^{-1} ,[n]- 100-seed weight
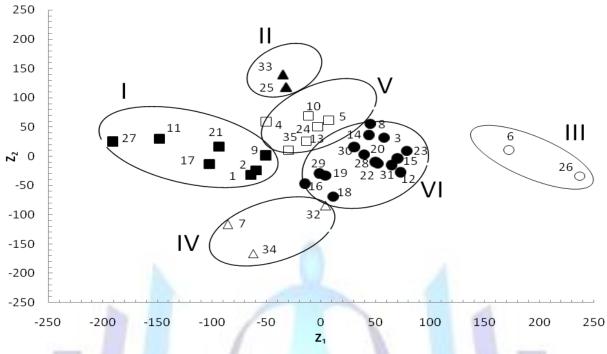
Fig1: Scatter distribution of 35 brinjal genotypes based on their principal component scores superimposed with clustering.

Here, Z_1– Principal component score- 1, Z_2- Principal component score- 2.

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