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Morphological diversity of eggplant (*Solanum melongena*) in Bangladesh

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Abstract

Morphological diversity in 92 eggplant genotypes based on twenty one characters was estimated using Mahalanobis's D^2 statistics. The highest intra-cluster distance was observed in cluster VIII (2.13), containing seven genotypes and the lowest intra-cluster distance (1.18) was observed in cluster IV having four genotypes. Ninety two eggplant genotypes were grouped into ten different clusters by non-hierarchical clustering. The cluster X had the maximum number (17) of genotypes and cluster II and III had minimum number (3) of genotypes. The highest inter-cluster distance was observed between cluster II and VIII (30.86) indicated the genotypes in these clusters were more diverged than those of other clusters. The lowest inter-cluster distance was observed between the clusters V and X (3.72) suggesting a close relationship among the genotypes included within these clusters. Cluster II constitute three genotypes and produced the highest mean value for number of flowers per inflorescence (4.67) and yield per plant (812.33) and the lowest mean value days to 1st flowering (108.22). Cluster IV constitute three genotypes namely EP-080, EP-081, EP-089 and produced fruits for longer duration (82.33). Cluster VIII constitute seven genotypes and showed the lowest mean value for number of infected shoots per plant (1.57). Cluster X established with 17 genotypes produced the lowest mean value for number of infected fruit per plant (8.26). Therefore, more emphasis should be given on cluster II, IV and VIII for selecting genotypes as parents for crossing which may produce new recombinants with desired traits.

Key words: Eggplant, Genotypes, Genetic divergence, Multivariate, Cluster analysis, D^2 statistics

Introduction

Brinjal or eggplant or aubergine (*Solanum melongena* L.) is indigenous to a vast area stretching from northeast India and Burma, to Northern Thailand, Laos, Vietnam and Southwest China and wild plants can still be found in these locations (Daunay and Janick, 2007). Eggplant was domesticated from wild forms in the Indo-Burma region with indications that it was cultivated in antiquity. Several Sanskrit documents, dated from as early as 300 BCE, mention this plant with various descriptive words, which suggest its wide popularity as food and medicine (Nadkarni, 1927). In the *Ayurvedic*, a Hindi system of medicine, white types were recommended for diabetic patients, and roots for the treatment of asthma (Khan, 1979). Eggplant is widely cultivated as vegetable in both temperate and tropical areas, especially in Asia. Eggplant is a major fruit vegetable with world production exceeding 32 million tonnes (Mt). The world leading eggplant producers are China (18.2 Mt), India (15.6 Mt), Egypt (2.0 Mt), Turkey (1.3 Mt), Indonesia (0.7 Mt), Iraq (0.6 Mt) Japan (0.6 Mt) and Italy (0.5 Mt each) (FAO, 2008). Eggplant is particularly favoured in Asia where it has been cultivated for millennia, and in India it is considered King of Vegetables.

For an effective breeding program, information concerning the extent and nature of genetic diversity within a crop species is essential. It is particularly useful for characterizing individual accessions and cultivars and as a general guide in the selection of the parents for hybridization (Furini and Wunder, 2004). Better knowledge on genetic diversity or genetic similarity could help to sustain long term selection gain (Chowdhury et al., 2002). Improvement in yield and quality is normally

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achieved by selecting genotypes with desirable character combinations existing in the nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization program. Some related results have been reported in eggplant (Tambe et al., 1993; Chaudhary and Pathania, 1998; Singh and Gapalakrishnan, 1999; Kumar et al., 2000). A previous knowledge of the structure of the genetic diversity within a large collection of germplasm may be of great help to make decisions on management procedures, as well as on breeding strategies to use in current and future breeding programs. According to Sharma and Jana (2002), assessment of genetic variation in a species is a prerequisite for initiating an efficient breeding program, as it provides a basis for tailoring desirable genotypes. Genetically diverse parents are likely to segregates and or to produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic F_1s and broad spectrum of variability in segregating generations (Arunachalam, 1981). Genetic diversity study also permits to select the genetically divergent parents to obtain the desirable recombinant in the segregating generations of eggplants. The aim of the present study was to characterize eggplant genotypes collected from different regions of Bangladesh and exotic sources to assess the genetic diversity within the germplasm. Assessment of genetic diversity is important for selecting breeding strategies.

Materials and Methods

Ninety two genotypes of indigenous and exotic eggplants collected from the Plant Genetic Resources Centre (PGRC) and Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI) were studied to measure the diversity among the genotypes at the Field Laboratory, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur. Genotypes of eggplant representing samples from different origins (local and exotic from AVRDC). The seeds of these germplasm were sown on the seedbed and thirty five days old seedlings were transplanted in the main field. The experiment was laid out in a randomized complete block design with three replications. The unit plot size was 7.5 × 0.70m and 10 plants were accommodated in a plot with a plant spacing of 75cm maintaining a row distance of 70cm. Data were recorded from five randomly selected plants from each plot for leaf blade length (cm), leaf blade width (cm), leaf blade lobing, leaf blade tip angle, leaf prickles, leaf blade color, petiol color, days to 1st flowering, number of flowers per inflorescence, plant height at flowering stage (cm), plant breadth at flowering stage (cm), number of primary branches per plant, days to 1st fruit setting, fruit length (cm), fruit breath (cm), fruit length / breath ratio, days to 1st fruit harvest, duration of fruiting (days), number of healthy shoots per plant, number of infected shoots per plant, yield per plant (g). The selection of morphological characters was made by applying the IBPGR eggplant descriptor (IBPGR 1990). Plot means over the replications were used for the statistical analysis. Genetic diversity was studied following Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Based on the D^2 values, the genotypes were grouped into clusters following the method suggested by Tocher (Rao, 1952; Jager et al., 1983; Digby et al., 1989). Intra and inter cluster distances were calculated by the methods of Singh and Chaudhury (1985). Statistical analyses were carried out using GENSTAT 5 software.

Results and Discussion

D^2 Statistics

Analysis of variance exhibited significant differences among the genotypes under study. Thus, it indicated notable genetic variability among the 92 genotypes.

Principal component analysis (PCA)

Analysis yielded eigen values of each principle component axes of coordination of genotype with the first axes totally accounted for 20.07% variation among the genotype, while eight of these eigen values above unity accounted for 73.87% of the total variation among the 21 principal component axes describing 92 genotypes of eggplant (Table 1).

Principal coordinate analysis (PCO)

The inter genotypic distances (D^2) as obtained by principle coordinate analysis (PCO) for all possible combinations between the pairs of genotypes. Inter genotypic distances as obtained from principle coordinate analysis showed that the highest distance was observed between the genotype EP-047 and EP-039 followed by the genotype E-074 and EP-047 (Table 2). The lowest distance was observed between genotype EP-026 and EP-025. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 92 genotypes of eggplant studied.

Intra-cluster distance were calculated from these inter genotypic distances (Singh and Chaudhury, 1985). The highest intra-cluster distance was observed in cluster VIII (2.13), containing seven genotypes, followed by cluster III (2.05) containing

11 genotypes. The lowest intra-cluster distance (1.18) was observed in cluster IV having four genotypes. The intra-cluster distances in all the ten clusters were lower than the inter-cluster distances and which indicated that genotypes within the same cluster were closely related.

Non-hierarchical clustering

With the application of co-variance matrix for non-hierarchical clustering, 92 eggplant genotypes were grouped into ten different clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 3 represents the clusters occupied by 92 genotypes of eggplant. The cluster X had the maximum (17) number of genotypes, followed by cluster VI (15 genotypes). The cluster I and cluster III had 11 genotypes, cluster IX had 10 genotypes, cluster V had eight genotypes, cluster VII and cluster VIII had 7 genotypes, c luster II and III had 3 genotypes.

These results confirmed the clustering pattern of the genotype according to the principle component analysis. Composition of different cluster with their corresponding genotypes and collection site included in each cluster are presented in table. The cluster pattern obtained from the nonhierarchical clustering is coincidence with the apparent grouping pattern perform by PCA. For the reason it can be said that the results obtained through PCA were established by non-hierarchical clustering.

Table 1. Eigen values and percentage of variation for corresponding 21 component characters in 92 genotypes of eggplant.

Principle component axes	Eigen values	Percentage of total variation	Percentage of cumulative
A	4.21	20.07	20.07
B	3.03	14.43	34.5
C	2.00	9.54	44.04
D	1.49	7.12	51.16
E	1.41	6.75	57.91
F	1.28	6.11	64.02
G	1.06	5.06	69.08
H	1.00	4.79	73.87
I	0.82	3.94	77.81
J	0.69	3.30	81.11
K	0.68	3.25	84.36
L	0.60	2.90	87.26
M	0.52	2.48	89.74
N	0.48	2.30	92.04
O	0.39	1.86	93.9
P	0.33	1.61	95.51
Q	0.26	1.27	96.78
R	0.24	1.18	97.96
S	0.19	0.93	98.89
T	0.14	0.69	99.58
U	0.09	0.44	100.00

Table 2. Five highest and five lowest inter genotypic distances of eggplant genotypes.

Genotype	Distance	Genotype	Distance
Highest value		Lowest value	
EP-047 – EP-039	4.058	EP-026 – EP-025	0.598
EP-074 – EP-047	3.965	EP-089 – EP-034	0.646
EP-079 – EP-047	9.904	EP-064 – EP-034	0.669
EP-086 – EP-030	3.875	EP-089 – EP-087	0.689
EP-047 – EP-008	3.820	EP-003– EP-002	0.696

Table 3. Distribution of 92 genotypes of eggplant in different cluster.

Cluster number	Number of genotypes	Genotypes
I	11	EP-019, EP-024, EP-033, EP-037, EP-043, EP-049, EP-051, EP-053, EP-074, EP-087, EP-088
II	3	EP-017, EP-039, EP-079
III	11	EP 12, EP 13, EP 15, EP 20, EP 23, EP 27, EP 46, EP 50, EP 57, EP 86, EP 90
IV	3	EP 80, EP 81, EP 89
V	8	EP3, EP8, EP18, EP31, EP59, EP68, EP77, EP 91
VI	15	EP14, EP16, EP29, EP35, EP41, EP45, EP56, EP 61, EP65, EP66, EP67, EP69, EP73, EP75, EP 92
VII	7	EP 22, EP 30, EP 34, EP 36, EP 44, EP 64, EP 70
VIII	7	EP 11, EP 21, EP 47, EP 48, EP 54, EP 62, EP 76
IX	10	EP 1, EP 2, EP 6, EP 25, EP 38, EP 42, EP 52, EP 60, EP 71, EP 84
X	17	EP-004, EP-005, EP-007, EP-009, EP-010, EP-026, EP-028, EP-032, EP-040, EP-055, EP-058, EP-063, EP-072, EP-078, EP-082, EP-083, EP-085

Table 4. Intra and inter cluster distances among 92 genotypes of eggplant.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	1.74	8.107	16.293	11.446	7.881	19.048	10.069	23.356	13.395	4.801
II		1.64	23.829	19.205	15.605	26.498	17.673	30.876	20.940	12.474
III			2.05	5.867	9.114	3.914	6.821	7.366	3.844	11.688
IV				1.18	4.978	8.696	3.909	12.668	4.027	7.058
V					1.97	12.004	4.261	16.011	6.088	3.727
VI						1.96	9.374	5.379	6.606	14.505
VII							1.90	13.706	4.605	5.631
VIII								2.13	10.430	18.775
IX									1.99	8.853
X										2.00

Canonical variate analysis

Canonical variate analysis was done to compute the inter-cluster Mahalanobis's D^2 values. The intra and inter cluster distance (D^2) value are presented in Table 4. Result indicated that the highest inter-cluster distance was observed between cluster II and VIII (30.86) followed by cluster II and VI (26.49) and cluster II and III (23.82). The maximum inter-cluster distances between these clusters indicate wide spectrum of variability of population. However, the highest inter-cluster distance was observed between cluster II and VIII indicated the genotypes in these clusters were more diverged than those of other clusters. The lowest inter-cluster distance was observed between the clusters V and X (3.72), suggesting a close relationship among the genotypes included within these clusters. The intra-cluster distance varied from 1.13 to 2.13, the maximum for cluster VIII that was composed seven genotypes of diverse origin, while the minimum distance was found in cluster IV that was composed three genotypes. Statistical distances represent the index of genetic diversity among the cluster. The inter-cluster distances were larger than the intra-cluster distances that indicated wider genetic diversity among the genotypes of different groups.

Cluster mean value

The individual genotype was characterized in respect of their mean values for different character with a view to get idea that weather genotypes having similar characteristics could be disseminated. The mean values for all the 21 characters along with the marking of the highest (H) and the lowest (L) for each of the cluster are presented in Table 5. Cluster II constitute three genotypes and produced the highest mean value for number of flowers per inflorescence (4.67), number of infected shoot per plant (8.67), yield per plant (812.33). But the lowest mean value leaf blade width (4.33), leaf blade lobbing (4.33), leaf blade color (3.00), days to 1st flowering (108.22). Cluster III constitute 11 genotypes namely EP-012, EP-013, EP-015, EP-020, EP-023, EP-027, EP-046, EP-050, EP-057, EP-086, EP-090 produce the

highest mean value for fruit length breath ratio (5.82). Cluster IV constitute three genotypes namely EP-080, EP-081, EP-089 and produced the highest plant height at flowering stage (35.47), plant breath at flowering stage (56.86), fruit length (14.50), duration of fruiting (82.33). Cluster V constitute eight genotypes namely EP-003, EP-008, EP-018, EP-031, EP-059, EP-068, EP-077, EP-091 produce the highest mean value for leaf blade length (5.50), leaf blade width (6.00), fruit breadth (6.53). Cluster VIII constitute seven genotypes namely EP-011, EP-021, EP-047, EP-048, EP-054, EP-062, EP-076 produce the highest mean value for days to 1st flowering (129.12), number of primary branches per plant (6.29) But the lowest mean value duration of fruiting (54.98), number of infected shoot per plant (1.57),yield per plant (121.00). Cluster X established with 17 genotypes namely EP-004, EP-005, EP-007, EP-009, EP-010, EP-026, EP-028, EP-032, EP-040, EP-055, EP-058, EP-063, EP-072, EP-078, EP-082, EP-083, EP-085 produced the lowest mean value for number of infected fruit per plant (8.26).

Table 5. Cluster mean values of 21 characters of 92 genotypes in brinjal.

Character	Cluster									
	I	II	III	IV	V	VI	VII	VIII	IX	X
Leaf blade length	5.18	4.33(L)	5.00	5.00	5.50(H)	4.87	5.29	5.00	5.40	4.88
Leaf blade width	5.36	4.33(L)	5.18	5.67	6.00(H)	5.53	5.57	5.29	5.60	5.47
Leaf blade lobing	4.73	4.33(L)	5.18	5.00	5.00	5.40	5.29	4.43	5.20	5.24(H)
Leaf blade tip angle	4.64	4.33	4.45	5.00(H)	4.75	4.87	4.43	4.43	4.40	4.29(L)
Leaf prickles	0.55	0.33	0.64	0.00	1.37	1.07	1.00	1.43	1.40	1.53
Leaf blade color	6.27	3.00	5.36	7.00	6.00	5.00	5.00	5.57	5.40	4.88
Petiol color	2.55	2.00	1.91	2.67	2.87	2.07	2.00	1.86	3.60	2.06
Days to 1st flowering	117.05	108.22	124.26	126.00	123.04	126.43	128.59	129.12	120.35	122.31
No. of flowers per inflorescence	3.45	4.67	3.37	2.00	3.62	3.36	2.86	3.14	3.80	3.00
Plant height at flowering stage	30.47	29.77	27.03	35.47	28.80	38.85	33.43	28.78	31.25	31.04
Plant breadth at flowering stage	47.79	41.70	47.72	56.86	48.58	50.60	52.85	50.89	47.48	48.80
No. of primary branches per plant	5.82	5.33	5.82	4.67	5.50	5.67	5.86	6.29	5.50	5.41
Days to 1st fruit setting	133.42	121.11	136.11	134.68	139.60	138.46	144.59	143.34	133.71	136.54
Fruit length	10.33	9.68	13.31	14.50	9.95	12.33	10.09	11.76	10.07	9.74
Fruit breath	4.23	3.14	3.29	3.02	6.53	3.90	4.27	3.71	3.98	4.55
Fruit length / breath ratio	3.03	3.00	5.82	5.07	2.01	4.45	2.99	4.74	2.38	2.86
Days to 1st fruit harvest	187.14	182.22	187.73	182.11	182.17	203.94	200.40	195.36	182.17	187.86
Duration of fruiting	76.91	80.83	72.03	82.33	75.71	57.51	63.76	54.98	76.03	74.53
No of healthy shoot per plant	8.59	9.56	9.61	8.67	6.67	9.45	10.21	8.67	9.33	8.26
No of infected shoot per plant	5.76	8.67	3.36	2.89	3.87	1.93	2.81	1.57	2.93	4.00
Yield per plant	643.51	812.33	288.39	395.67	476.17	229.39	426.55	121.00	354.92	540.08

Table 6. Latent vectors for 21 component characters of 92 genotype of eggplant.

Characters	Vector 1	Vector 2	Characters	Vector 1	Vector 2
Leaf blade length	0.03	-0.12	No. of primary branches per plant	0.08	0.14
Leaf blade width	0.24	-0.24	Days to 1st fruit setting	0.38	0.07
Leaf blade lobing	0.14	-0.07	Fruit length	-0.01	0.41
Leaf blade tip angle	0.08	-0.08	Fruit breadth	0.18	-0.35
Leaf prickles	0.12	-0.26	Fruit length / breath ratio	-0.05	0.47
Leaf blade color	-0.13	0.28	Days to 1st fruit harvest	0.31	0.18
Petiole color	-0.12	0.11	Duration of fruiting	-0.34	-0.22
Days to 1st flowering	0.36	0.13	No of healthy shoots per plant	-0.02	0.07
No. of flowers per inflorescence	-0.20	0.18	No of infected shoot per plant	-0.36	-0.02
Plant height at flowering stage	0.11	0.08	Yield per plant	-0.24	-0.23
Plant breadth at flowering stage	0.24	0.01			

Contribution of characters toward divergence of the genotypes

Contribution of characters towards the divergence obtained from canonical variate analysis is presented in Table 6. In this method vectors was calculated to represent the varieties in the graphical form (Rao, 1952). This is helpful in cluster analysis as it facilitates the study of group constellations and also serves as a pictorial representation of the configuration of various groups. The absolute magnitude of the coefficients in the first two canonical vectors also reflects to a great extent, the importance of the characters for primary and secondary differentiation. The character, which gives high absolute magnitude for vector 1, is considered to be responsible for primary differentiation. Likewise, the characters, which give higher absolute magnitude for vector 2 is considered to be responsible for secondary differentiation. If the same character gives equal magnitude for both the vectors then the character is considered responsible for primary as well as secondary differentiation. The PCA revealed that the important characters responsible for genetic divergence in the major axis of differentiation (Vector 1) were leaf blade width, days to 1st flowering, plant breath at flowering stage, days to 1st fruit setting, fruit breadth, and days to 1st fruit harvest (Table 6). It was the reflection of first axis of differentiation. In vector 2, leaf blade color, days to 1st flowering, plant breath at flowering stage, plant height at flowering stage, no of flower per inflorescence, number of primary branches per plant, fruit length, days to 1st fruit harvest showed their important role towards genetic divergence. Other characters played a minor role in determining genetic divergence. The role of days to 1st fruit harvest, days to 1st flowering for both the vectors was positive across two axes indicating the important components of genetic divergence in these materials.

Selection of genotypes as parent for hybridization program

The inter cluster distance between II and VIII was the highest followed by II- VI (26.498), II- III (23.829) and I- VIII (23.356). Cluster distance between cluster I- III, I- VI, II- IV, II- V, II- VII, II- IX, V- VIII, VI- X and VIII- X were moderate or intermediate. Intermediate diverse parents have the more chance to contribute heterosis in the subsequent generations. Arunachalan *et al*. (1984) suggested in groundnut that the magnitude of heterosis for yield and its components were found higher in crosses between inter mediate divergences than extreme ones. Ramanujam *et al*. (1974) suggested in mung bean that there was a fair agreement between the extent of heterosis and the genetic divergence between parents. To select cluster for more heterotic genotypes four pairs of clusters II & VIII, II & VI, II & III and I & VIII could be considered.

Cluster II had the highest cluster mean for number of flowers per inflorescence, yield per plant and the lowest for days to first flowering. The cluster IV had the highest cluster mean for Plant breadth at first flowering, fruit length and duration of flowering. Cluster V had the highest cluster mean for fruit breadth and the lowest for number of infested shoots per plant. Cluster VIII had the highest cluster mean for number of primary branches per plant and the lowest for number of infested fruits per plant. So, hybridization between the genotypes of cluster II, IV, V and VIII will manifest maximum heterosis and create wide genetic variability for economic characters in eggplant. Considering cluster distance and cluster mean, the genotypes EP- 017 and EP- 039 from cluster II, genotypes EP- 089 from cluster IV,

genotypes EP- 003 and EP- 091 from cluster V, genotypes EP- 011, EP- 021, EP- 047 and EP- 054 from cluster VIII may be considered as parents for future hybridization program.

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