

GENETIC DIVERSITY IN EGGPLANT GENOTYPES FOR HEAT TOLERANCE

M. S. Uddin^{*1}, M. M. Rahman², M. M. Hossain² and M. A. K. Mian³

Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman
Agricultural University, Gazipur-1703, Bangladesh

ABSTRACT

Genetic divergence in eighteen eggplant genotypes was studied at Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur, Bangladesh during February 2007 to December 2008 using multivariate analysis. Eggplant genotypes were evaluated for different quantitative characters. Among the genotypes wide variations were observed for plant, flower and fruit size, shape and color. Out of 18 genotypes only 8 were found to be suitable for summer and summer rainy season cultivation as heat tolerance. The 18 genotypes were grouped into four distinct clusters. Cluster I comprised of 2 genotypes, cluster II had 3, cluster III had 3 and cluster IV had 10 genotypes. Clustering pattern of the genotypes was not correlated with their geographical distribution. The highest inter cluster distance was between cluster I and IV (764.67) while, it was the lowest between cluster II and III (213.30). The highest and lowest intra cluster distance was displayed in cluster II (94.14) and cluster I (28.79) respectively. Yield per plant, number of fruits per plant, plant canopy, fruit weight, fruit length and number of harvest had the highest contribution towards total divergence. Moderate to high Shannon-Weaver Diversity Indices (SWDI) was found among the genotypes for most of the studied qualitative characters. Quantitative vegetative characters had high diversity among the genotypes, while it was moderate to high diversity for both flower and fruit characters. Eight eggplant genotypes were selected as heat tolerance based on genetic diversity of morphological characters in eggplant.

Key words: Eggplant, Genetic diversity, Genotype, Heat tolerance, Qualitative character.

* Corresponding author email: mdsharafuddin@yahoo.com

¹ Associate Professor, Dept. of Agro-forestry and Environmental Science, Sylhet Agricultural University, Sylhet-3100, Bangladesh;

² Professor, Dept. of Horticulture, BSMRAU, Gazipur-1703, Bangladesh

³ Professor, Dept. of Genetics and Plant Breeding, BSMRAU, Gazipur-1703, Bangladesh

INTRODUCTION

Eggplant (*Solanum melongena* L) is an important and popular vegetable crop of Bangladesh. There is an increasing demand of its varieties throughout the year for different culinary purposes. It is imperative to assess the relative magnitude of genetic variability, nature and extent of character association with yield and its related characters for a sound breeding program. A new variety can be developed from an assembled diverse genetic stock of any crop. Hence the success of any breeding program depends much on the genetic variability available to the breeders and the judicious selection of the parents (Islam, 2008). The quantification of genetic divergence through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization program. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). The utility of multivariate analysis for measuring the degree of genetic divergence and for assessing the relative contribution of different characters to the total divergence in self and cross pollinated crops has been established by several workers (Kete, 2001; Thuy, 2002; Emmanuel, 2002 and Uddin, 2003 and 2005). Mahalanobis's generalized distance has been used as an efficient tool in the quantitative estimation of genetic diversity and a rational choice of potential parents for a successful hybridization program. Such study permits to choose genetically diverse parents for obtaining desirable recombinant in segregating generations. Since information on genetic divergence of eggplant during summer and summer rainy season is not available in Bangladesh, the present study was undertaken to find out genetic diversity of collected eggplant genotypes, to identify the most diverged genotypes in relation to yield and yield contributing characters and to find out the characters, which contribute towards divergence of the genotype.

MATERIALS AND METHODS

A study on genetic diversity in eggplant genotypes was conducted at Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh during February 2007 to September 2009. A total of eighteen eggplant genotypes viz., SM001, SM002, SM003, SM004, SM005, SM006, SM024, SM034, SM057, SM058, SM061, SM062, SM064, SM065, SM066, SM067, SM068 and SM069, were collected from different parts of the country including Jessore, Tangail, East-West Seed Co. Ltd, Bangladesh, Horticulture Research Center and Plant Genetic Resources Center of Bangladesh Agriculture Research Institute, Gazipur during 2006-2007. Eighteen eggplant genotypes were evaluated during summer and summer rainy season 2008 and 2009 for diversity study against hot humid condition of Bangladesh. The experiment was laid out in randomized complete block design with three replications. The minimum and maximum temperature during the study period was 26.8°C and 33.49°C, respectively. The fruits were harvested at marketable stage starting from June to September every year. Data on 34 quantitative characters (plant, leaf, flower and fruit characters) were recorded following the descriptor of eggplant (IBPGR, 1988).

Multivariate analysis including Principal Component Analysis, Principal Coordinate Analysis, Canonical vector analysis/ Euclidean D^2 values (Singh and Choudhury., 1985) and Shannon-Weaver Diversity Index (Yu Li et al., 1996) were performed with the data for each character using MS Excel, MSTATC and SPSS program for genetic diversity study.

RESULTS AND DISCUSSION

Genetic diversity of 18 eggplant genotypes were determined by using the multivariate analysis and the results are presented in table 1 to 10 and discussed under the following headings:

Principal Component Analysis (PCA)

Eigen values and eigen vectors of corresponding ten principal component axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in table 1 and 2 respectively. Table 1 represents that the cumulative eigen values of first four principal components accounted for 99.15 per cent of the total variation among the genotypes. The first principal component accounted for 93.32 per cent of the total variation; the second, third and fourth components accounted for 2.83%, 1.58% and 1.42% of the total variation respectively. The rest of the components accounted for only 0.85% of the total variation. The minimum acceptable value of cumulative eigen value of the principal component for coconut is 75% (Emanuel, 2002).

Latent vectors presented in table 2 revealed that for principal component 1 (PRIN 1), yield per plant contributed the highest loading (0.998) for the variation among the genotypes followed by fruit per plant, east-west canopy (cm), north-south canopy (cm), individual fruit weight (g), fruit length (mm) and number of harvest contributing loads of 0.030, 0.026, 0.020, 0.018, 0.011 and 0.011 respectively. For principal component 2, fruit length (mm) contributed the highest loading (0.912) followed by plant height (0.138). For principal component 3, N-S canopy of the plant contributed the highest loading (0.715) followed by E-W canopy (0.603). For principal component 4, individual fruit weight (g) contributed the highest loading (0.846) followed by plant height (cm) (0.168). From the observation of principal component 1 to 4 it was clear that yield and yield contributing characters contributed to diversity of the genotypes. The first principal component accounts for as much of the variability in the data as possible and each succeeding component accounts as much of the remaining variability as possible ([http:// www.fon.hum.uva. nl/ praat manual/ Principal component analysis, 2003](http://www.fon.hum.uva.nl/praat/manual/Principal%20component%20analysis))

The principal component analysis revealed that among the significant descriptors contributing to the first principal component, yield per plant contributed mostly to the total variation (loading-0.998). The findings of the present study corroborated to Rahman (1999) who found that the yield per plant contributed the highest for total variation of eggplant genotypes. The author further noted that fruit

weight, fruit length, number of fruit per plant and days to 50% flowering were also important to some extent for the variation. Similar observations were noted by Kete (2001), Thuy (2002) and Uddin (2003, 2005) in coconut and Rajput et al. (1996) in eggplant. Rajput et al. (1996) found that plant height, fruit/plant, fruit weight, fruit length and percent fruit set were the main characters contributed to yield in eggplant.

Intra cluster distance

The magnitudes of the intra cluster distances were not always proportional to the number of genotypes in the clusters (Table 4). Statistical distances represent the extent of genetic diversity among the clusters. The highest intra cluster distance was obtained from cluster II (94.14) composed of 3 genotypes followed by cluster IV (83.43) and cluster III (72.67), composed of 10 and 3 genotypes respectively. The lowest intra cluster distance was noted in cluster I (28.79) composed of 2 genotypes. The lowest intra cluster distance indicated the close relationship between the genotypes of this cluster. The higher intra cluster distances indicated that the genotypes in the same cluster were more heterogeneous than the genotypes consisting on the other clusters.

Inter cluster distance

Inter cluster distances presented in table 4 revealed that the inter cluster distance was highest between cluster I and IV (764.67) followed by cluster I and III (493.85), cluster II and IV (482.81) and the lowest inter cluster distance was noted between cluster II and III (213.30). The higher value of inter cluster distances indicated that the genotypes belonging to all the clusters were far diverged. Again it was observed that the inter cluster distances were larger than the intra cluster distances suggested wider genetic diversity among the genotypes of different clusters/groups. Rahman (1999) and Chowdhury (2005), Islam (2008) also obtained larger inter cluster distance than the intra cluster distances in eggplant and hyacinth bean respectively.

The genotypes of distant clusters could be used in hybridization program for obtaining a wide range of variation among the segregants. Similar reports were also made by Islam (2008) in hyacinth bean. Wenxing et al. (1994) reported the beneficial effect of crossing carried out between sesame genotypes belonging to different groups having genetic distance (D^2) greater than 12.5. In the present study, the intra cluster distances of all the clusters and inter cluster distances among all the clusters were higher than 12.5 suggesting suitability of crossing between the desirable genotypes of any of the clusters for getting greater heterotic effect.

Cluster mean

Cluster means of 34 quantitative characters are presented in table 5. Although cluster IV composed of the largest number of genotypes (Table 3), yield and yield contributing characters earned the lower mean values. Most of the yield contributing characters earned maximum mean values in cluster III, cluster I and cluster II. There

was significant difference among the clusters for yield and yield contributing characters. Cluster means presented in table 5 revealed that cluster I composed of 3 genotypes (Table 3) earned the maximum mean value for yield per plant (847.16 g), number of fruit per plant (32.05) and number of harvest (11.10) followed by cluster II (566.41g, 10.10 and 9.67 respectively) and cluster III (362.46g, 5.22 and 7.00 respectively). On the other hand cluster IV earned the lowest value for these characters (85.75g, 2.68 and 2.65 respectively). Cluster II earned maximum values for individual fruit weight (79.60g) followed by cluster III (79.54g). On the other hand, cluster I earned the lowest value in this respect (26.20g). Among the clusters, cluster I showed the earliness (61.90 days for first flowering). The second early genotypes comprising in the cluster II (79.40 days) and the genotypes of other clusters were late in flowering. Fruit length was the highest in genotypes of cluster III (121.98mm) followed by cluster I (91.34 mm). The shortest fruit was exhibited by genotypes under cluster II (76.00 mm). The highest fruit breadth was found in the genotypes under cluster (II) (55.67 mm) followed by cluster III (52.54 mm). Pulp thickness was the highest in cluster I (8.01mm) followed by cluster III and II (7.65 mm and 7.60 mm respectively).

From the findings of the present study it was clear that cluster I, II and III showed the higher cluster mean values for yield and yield contributing characters (Table 5). Considering the highest and foremost contribution of yield per plant for diversity among the genotypes, the genotypes of cluster I, II and III could be selected for future hybridization program to get the higher heterotic effect.

D² statistics (Euclidean Distance)

Considering the similarity of the genotypes it was clear that the genotypes SM001 and SM002 were closely related to each other and the distance was only 57.70 (Table 6). These two genotypes are far distant from others. The genotypes SM004, SM006 and SM024 were more closely related to each other than the other genotypes. The distance between SM004 and SM024 was only 69.26 and the distance between SM006 and SM024 was 127.02 and between SM002 and SM006 was 161.13. The genotypes SM057, SM067 and SM034 were more closely related to each other. Among these three genotypes, the distance was lower between SM057 and SM067 (106.03). The distance between SM034 and SM057 was 183.89 and between SM034 and SM067 were 186.88. The genotypes SM003, SM005, SM061, SM062, Sm064, SM065, SM066, SM058, SM068 and SM069 were more or less closely related to each other. The distance between SM003 and SM061 was 84.08; between SM003 and SM062 were 81.25; between SM003 and SM065 was 56.97 and between SM003 and SM066 was 83.54. The similarity or dissimilarity of the genotypes was mainly based on yield parameter of the genotypes that could be confronted from Table 2. The highest distance was noticed between SM002 and SM066 (836.41) followed by the distance between SM002 and SM064 (835.84), between SM002 and

SM061 (831.38) and between SM002 and SM062 (827.31). This indicated that SM001 and SM002 were far distance from SM066, SM0064, SM0061, and SM062.

Shannon-Weaver Diversity Index (H')

Shannon-Weaver Diversity Indices (H') were calculated by using twenty three qualitative and 34 quantitative characters related to vegetative (plant and leaf), flower and fruit characters to determine the diversity among the eggplant genotypes.

SWDI (H') for qualitative characters

Low to high diversity was found among the studied genotypes for qualitative characters. The SWDI (H') values for qualitative characters among the eggplant genotypes ranged from 0 to 0.85. Most of the qualitative characters had moderate to high diversity among the genotypes with a mean of 0.48 for plant and leaf characters and 0.62 for flower and fruit characters which also indicated the low to moderate diversity. The highest diversity among the genotypes was observed for fruit apex shape ($H'=0.85$) followed by plant growth habit, plant stem color, flower pedicel color ($H'= 0.82$ for each character). Low diversity ($H'= 0.20-0.47$) was found for nine qualitative characters of eggplant. Among these nine characters, the lowest diversity was found among the genotypes for the presence of prickles on stem (0.20), while there was no diversity among the genotypes for presence of prickles on upper surface of leaf (Table 7a).

Jamago (2000) classified the diversity of mungbean based on morphological characters as high ($H'= >0.750$), moderate ($H'= 0.50-0.75$) and low ($H'= <0.50$) diversity. The same classification was followed by Kete (2001), Thuy (2002), Emmanuel (2002) and Uddin (2003 and 2005) in coconuts. Thuy (2002) found low diversity for qualitative vegetative characters while Uddin (2003 and 2005) found moderate to high diversity for those in coconut. The current findings corroborates with Uddin (2003 and 2005).

SWDI (H') for quantitative characters

Quantitative vegetative characters

High diversity ($H' =0.76-0.86$) was found among the studied genotypes for all the vegetative characters except number of branches per plant. Moderate diversity ($H' =0.70$) was observed for number of branch per plant. The SWDI (H') values for quantitative vegetative characters among the eggplant genotypes ranged from 0.70 to 0.86 with a mean of 0.81 which also indicated the high diversity. The highest diversity among the genotypes was observed for north-south canopy, leaf petiole length and leaf blade width ($H'=0.86$) followed by leaf petiole diameter, leaf blade length ($H'= 0.82$ for each character) and plant height ($H'=0.81$) (Table 8).

Thuy (2002) and Emmanuel (2002) found moderate diversity for quantitative vegetative characters while for those characters Uddin (2003) found high diversity except bunch per palm and number of leaves per palm in coconut. The current findings corroborates with Uddin (2003).

Quantitative flower characters

High diversity ($H' = 0.76-0.82$) was found among the studied genotypes for fifty per cent of the flower characters and for the rest fifty per cent had moderate diversity ($H' = 0.59-0.72$). The SWDI (H') values for quantitative flower characters among the eggplant genotypes ranged from 0.59 to 0.82 with a mean of 0.71 which also indicated the moderate diversity. The highest diversity among the genotypes was observed for stamen length ($H' = 0.82$) followed by style length and flower calyx length ($H' = 0.79$ and 0.77 respectively) (Table 9). Thuy (2002) and Emmanuel (2002) found moderate diversity for quantitative flower characters, while for those characters Uddin (2003 and 2005) found high diversity in coconut. The current findings corroborates with Uddin (2003 and 2005).

SWDI (H') for quantitative fruit characters

The SWDI (H') values among the eggplant genotypes for quantitative fruit characters ranged from 0.52 to 0.84 with a mean of 0.71 which indicated the moderate diversity. Among the studied characters fifty per cent of the fruit characters had high diversity ($H' = 0.76-0.84$) and the rest fifty per cent had moderate diversity ($H' = 0.52-0.73$). The highest diversity among the genotypes was observed for pedicel length ($H' = 0.84$) followed by core diameter (0.80) and fruit calyx length ($H' = 0.79$) and fruit pulp thickness ($H' = 0.78$) (Table 10). Kete (2001) and Emmanuel (2002) found low to moderate diversity for quantitative fruit characters, while for those, Uddin (2003) found high diversity in coconut.

CONCLUSION

It was concluded that moderate to high diversity was present among the genotypes for quantitative characters. Yield and yield contributing characters contributed more towards diversity among the genotypes. All the genotypes were grouped in to 4 clusters. Eight genotypes viz., SM001, SM002, SM004, SM006, SM024, SM034, SM057 and SM067 were selected as heat tolerance based on genetic diversity of morphological characters in future hybridization program for heterotic effects.

REFERENCES

- Chowdhury, M.S.I. 2005. Study of genetic diversity and characterization of some cultivars of eggplant (*Solanum melongena* L.). MS Thesis. Dept. of Horticulture, BSMRAU, Gazipur, Bangladesh
- Emmanuel, E.E. 2002. Morphometric traits and DNA profiles of three generations of selected coconut genotypes. M.S. Thesis. Plant Genetic Resources Conservation and Management, University of Philippines (UPLB), Los Baños, Laguna, Philippines. p. 89
- http://www.fon.hum.uva.nl/praat/manual/Principal_component_analysis.html. 2003. Google search. Principal Component Analysis
- Islam, M.S. 2008. Genetic Diversity, combining ability and heterosis in hyacinth bean (*Lablab purpureus* (L.) Sweet). PhD. Dissertation. Dept of Horticulture. BSMRAU, Gazipur, Bangladesh. p. 190

- Jamago, J.M. 2000. Morpho-agronomic and molecular diversity of the Philippines mungbean germplasm. M.S. Thesis. Plant Genetic Resources Conservation and Management, University of Philippines (UPLB), Los Baños, Laguna, Philippines. p. 141
- Kete, T.N. 2001. GIS-aided morphological diversity assessment of coconut (*Cocos nucifera* L.) in three southern Tagalog Provinces, Philippines. M.S. Thesis. Plant Genetic Resources Conservation and Management, University of Philippines (UPLB), Los Baños, Laguna, Philippines. p. 115
- Rahman, A.B.M. 1999. Genetic divergence in brinjal. MS Thesis. Dept. of Genetics and Plant Breeding, BSMRAU, Gazipur, Bangladesh
- Rajput, J.C., S.S. Pandit, S.L. Patil and V.H. Patil. 1996. Variability, heritability and inter-relationship of important quantitative characters in eggplant. *Annals of Agricultural Research*, 17(3): 235-240
- Singh, R.K. and B.D. Choudhury. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. pp. 102-138
- Tomooka, N. 1991. Genetic diversity and landrace differentiation of mungbean, *Vigna radiata* (L) Wilcsek and evaluation of its wild relatives as breeding materials. tech. p. 1. Bull. Tropical Research Centre, Japan. No. 28. Ministry of Agriculture. Forestry and Fisheries. Japan
- Thuy, N.T. L. 2002. Morphological diversity, genetic erosion and indicators of in situ conservation of coconut (*Cocos nucifera* L.) in Vietnam. M.S. Thesis. Plant Genetic Resources Conservation and Management, University of Philippines (UPLB), Los Baños, Laguna, Philippines
- Uddin, M. Sharaf. 2003. Diversity and on-farm conservation of coconut (*Cocos nucifera* L.) in northern Luzon, Philippines. M.S. Thesis. Plant Genetic Resources Conservation and Management, University of Philippines (UPLB), Los Baños, Laguna, Philippines
- Uddin, M. S., J.B. Sangalang and T.H. Borromeo. 2005. Study on Diversity of Selected Coconut populations in Northern Luzon, the Philippines. *Bangladesh Journal of Agricultural Research*, 31 (1):139-152
- Wenxing, W, Z. Hong, Y.L. Feng, W. Shuang Ling, W.X. Wei, H. Zhang, F.Y. Lu and S.L. Wei. 1994. Principal components analysis and genetic distance estimation and their application in sesame breeding program. *Acta Agriculture Boreali Sinica*, 9(3): 29-33.
- 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 Evolution*, 43:377-384

Table 1: Eigen values and percentage of variation of dispersion matrices of principal components for 34 quantitative characters of eggplant genotypes

| Principal component | Latent roots/ Eigen values | Percentage of variance | Cumulative variance |
|---------------------|----------------------------|------------------------|---------------------|
| PRIN 1 | 1337264.652 | 93.315 | 93.315 |
| PRIN 2 | 40599.378 | 2.833 | 96.148 |
| PRIN 3 | 22659.272 | 1.581 | 97.729 |
| PRIN 4 | 20396.295 | 1.423 | 99.152 |
| PRIN 5 | 5467.447 | 0.382 | 99.534 |
| PRIN 6 | 3085.153 | 0.215 | 99.749 |
| PRIN 7 | 1540.678 | 0.108 | 99.857 |
| PRIN 8 | 866.352 | 0.060 | 99.917 |
| PRIN 9 | 524.160 | 0.037 | 99.954 |
| PRIN10 | 298.490 | 0.021 | 99.974 |

Table 2: Latent vectors/eigen vectors of 34 quantitative characters of eggplant in the first four principal components

| Characters | Latent vectors in descending orders | | | |
|--------------------------------|-------------------------------------|--------|--------|--------|
| | PRIN 1 | PRIN 2 | PRIN 3 | PRIN 4 |
| Yield/plant (g) | 0.998 | -0.004 | -0.028 | -0.006 |
| Fruits/plant | 0.030 | 0.001 | 0.026 | -0.114 |
| East-west plant canopy (cm) | 0.026 | -0.155 | 0.604 | 0.037 |
| North-south plant canopy (cm) | 0.020 | -0.148 | 0.715 | 0.017 |
| Fruit weight (g) | 0.018 | -0.072 | -0.127 | 0.846 |
| Fruit length (mm) | 0.011 | 0.912 | 0.132 | 0.116 |
| Harvest number | 0.011 | 0.009 | -0.004 | 0.001 |
| Plant height (cm) | 0.005 | 0.138 | 0.195 | 0.168 |
| Branches/plant | 0.003 | 0.001 | -0.011 | 0.001 |
| Pulp thickness (mm) | 0.003 | -0.009 | 0.007 | 0.016 |
| Fruit pedicel length (mm) | 0.002 | 0.098 | 0.114 | 0.194 |
| Flowers/inflorescence | 0.001 | 0.007 | -0.007 | -0.007 |
| Fruits/inflorescence | 0.001 | -0.001 | -0.004 | -0.006 |
| Bisexual flowers/inflorescence | 0.001 | 0.002 | -0.006 | -0.004 |
| Stamen length (mm) | 0.000 | -0.002 | 0.002 | 0.013 |

| Characters | Latent vectors in descending orders | | | |
|-----------------------------------|-------------------------------------|--------|--------|--------|
| | PRIN 1 | PRIN 2 | PRIN 3 | PRIN 4 |
| Fruit length/breadth ratio | 0.000 | 0.039 | 0.003 | -0.004 |
| Fruit pedicel. diameter (mm) | 0.000 | -0.007 | -0.004 | 0.036 |
| Style length (mm) | 0.000 | -0.004 | 0.002 | -0.002 |
| Leaf petiole. thickness (mm) | -0.000 | 0.004 | 0.009 | 0.012 |
| Stamen length (mm) | -0.000 | -0.001 | 0.001 | -0.004 |
| Leaf petiole diameter. (mm) | -0.000 | 0.004 | 0.010 | 0.011 |
| Flower calyx length (mm) | -0.001 | 0.035 | 0.002 | 0.096 |
| Flower pedicel diameter (mm) | -0.001 | -0.004 | 0.001 | 0.007 |
| Corolla length (mm) | -0.002 | 0.005 | -0.008 | 0.036 |
| Leaf blade length (cm) | -0.002 | -0.000 | 0.016 | 0.004 |
| Flower pedicel length. (mm) | -0.002 | 0.000 | 0.007 | 0.023 |
| Leaf petiole length. (mm) | -0.003 | -0.017 | 0.027 | -0.006 |
| Flower calyx length. (mm) | -0.003 | 0.023 | -0.007 | 0.039 |
| Leaf blade width. (cm) | -0.004 | -0.003 | 0.030 | 0.023 |
| Core diameter (mm) | -0.004 | -0.146 | -0.070 | 0.246 |
| Fruit breadth (mm) | -0.005 | -0.178 | -0.031 | 0.244 |
| Relative fruit calyx length. | -0.010 | -0.167 | -0.038 | 0.099 |
| Days to 50% flowering | -0.018 | 0.050 | 0.163 | 0.167 |
| Days to 1 st flowering | -0.019 | 0.040 | 0.045 | 0.132 |

Table 3: Cluster Membership/Distribution and place of collection of 18 eggplant genotypes in four clusters

| Cluster | Number of genotypes | Genotypes | Source/Place of collection |
|---------|---------------------|-----------|----------------------------|
| I | 2 | SM001 | HRC, BARI |
| | | SM002 | Tangail |
| II | 3 | SM034, | PGRC, BARI |
| | | SM057 | PGRC, BARI |
| | | SM067 | Jessore |
| III | 3 | SM004 | HRC, BARI |
| | | SM006 | HRC, BARI |
| | | SM024 | PGRC, BARI |
| IV | 10 | SM003 | HRC, BARI |
| | | SM005 | East-West Seed Co. |
| | | SM058 | PGRC, BARI |
| | | SM061 | Jessore |
| | | SM062 | Jessore |
| | | SM064 | Jessore |
| | | SM065 | Jessore |
| | | SM066 | Jessore |
| | | SM068 | Tangail |
| SM069 | Tangail | | |

Table 4: Intra (bold) and inter cluster distances between final cluster centers of 18 eggplant genotypes

| Cluster | I | II | III | IV |
|---------|--------------|--------------|--------------|--------------|
| I | 28.79 | 295.28 | 493.85 | 764.67 |
| II | | 94.14 | 213.30 | 482.81 |
| III | | | 72.67 | 285.59 |
| IV | | | | 83.43 |

Table 7a: Shannon-Weaver diversity indices (H') for qualitative plant and leaf characters of different eggplant genotypes

| Characters | SWDI (H') |
|---|-------------|
| Plant growth habit | 0.82 |
| Stem color at flowering stage | 0.82 |
| Fruit position on the plant | 0.42 |
| Presence of prickles on stem | 0.20 |
| Presence of prickles on upper surface of leaf | 0.00 |
| Presence of prickles on lower surface of leaf | 0.25 |
| Leaf petiole color | 0.68 |
| Leaf blade color (upper surface) | 0.43 |
| Mid rib color | 0.64 |
| Leaf blade lobing | 0.41 |
| Leaf blade tip angle | 0.60 |
| Mean | 0.48 |

Table 7b: Shannon-Weaver diversity indices (H') for qualitative flower and fruit characters of different eggplant genotypes

| | |
|---|-------------|
| Corolla color | 0.42 |
| Flower pedicel color | 0.82 |
| Extent of pollen production | 0.79 |
| Fruit color at commercial ripeness | 0.47 |
| Fruit color distribution at commercial ripeness | 0.68 |
| Fruit color at physiological ripeness | 0.67 |
| Fruit flavor at commercial ripeness | 0.63 |
| Fruit curvature | 0.43 |
| Fruit apex shape | 0.85 |
| Position of widest part from base to tip | 0.78 |
| Fruit cross section | 0.28 |
| Fruit flesh density | 0.63 |
| Mean | 0.62 |

Table 8: Shannon- Weaver diversity indices (H') for quantitative plant and leaf characters of different eggplant genotypes

| Characters | SWDI (H') |
|-------------------------------|-------------|
| Plant height (cm) | 0.81 |
| East-west plant canopy (cm) | 0.76 |
| North-south plant canopy (cm) | 0.86 |
| Number of branches/plant | 0.70 |
| Leaf petiole length (cm) | 0.86 |
| Leaf petiole diameter (mm) | 0.84 |
| Leaf petiole thickness (mm) | 0.81 |
| Leaf blade length (cm) | 0.83 |
| Leaf blade width (cm) | 0.86 |
| Average | 0.81 |

Table 9: Shannon- Weaver diversity indices (H') for quantitative flowering characters of different eggplant genotypes

| Characters | SWDI (H') |
|--|-------------|
| Days to first flowering | 0.59 |
| Days to 50% flowering | 0.72 |
| Number of flowers/inflorescence | 0.60 |
| Number of bisexual flowers/inflorescence | 0.59 |
| Flower pedicel length (mm) | 0.76 |
| Flower calyx length (mm) | 0.77 |
| Stamen length (mm) | 0.82 |
| Style length (mm) | 0.79 |
| Relative style length (longer than stamen) | 0.71 |
| Corolla length (mm) | 0.80 |
| Average | 0.71 |

Table 10: Shannon- Weaver diversity indices (H') for quantitative fruit characters of different eggplant genotypes

| Characters | SWDI (H') |
|-------------------------------|-------------|
| Fruit length (mm) | 0.62 |
| Fruit breadth (mm) | 0.77 |
| Fruit length breadth ratio | 0.61 |
| Fruit calyx length (mm) | 0.79 |
| Relative fruit calyx length | 0.76 |
| Fruit pedicel length (mm) | 0.84 |
| Fruit pedicel diameter (mm) | 0.78 |
| Number of fruit/inflorescence | 0.52 |
| Fruit pulp thickness (mm) | 0.78 |
| Fruit core diameter (mm) | 0.80 |
| Number of harvest | 0.73 |
| Fruit weight (g) | 0.62 |
| Fruits/plant | 0.59 |
| Yield/plant (g) | 0.71 |
| Average | 0.71 |