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GENETIC DIVERGENCE IN EGGPLANT (*Solanum melongena* L.) GENOTYPES

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Abstract

Multivariate analysis of twenty six genotypes of eggplant were done to estimate the genetic diversity and to select the potential parents for a successful hybridization program. As per PCA, D^2 and cluster analysis, the genotypes were grouped into five clusters. The highest inter-cluster distance was between Cluster II and Cluster III (37.82) and the lowest between Cluster I and Cluster III (4.39). Cluster III showed the maximum intra-cluster distance (1.58), whereas Cluster II showed the lowest intra-cluster distance (0.48). Considering the magnitude of genetic distance and agronomic performance, the genotypes SM 208 and SM 209 from Cluster II and SM 201, SM 218 and SM 227 from Cluster III might be suitable for efficient hybridization program. On the other hand the genotypes of Cluster I (SM 206, SM 210, SM 211, SM 212, SM 213, SM 215, SM 216, SM 217, SM 221, SM 224, SM 225 and SM 226) possess all the superior characters in respect of yield and yield related component. Thus the genotypes SM 206, SM 216, SM 217, SM 224 and SM 225 from this Cluster could be selected to develop high yielding eggplant varieties.

Keywords: Eggplant, D^2, Genetic diversity, Hybridization, Multivariate analysis, PCA.

Introduction

Eggplant (*Solanum melongena* L.) is one of the most important commercial vegetable crops in the world, especially in the tropics and subtropics. Eggplant belongs to the family Solanaceae and is mainly self-pollinated crop (Bose *et al*., 2003).

Various forms, colors and shapes of eggplant are found throughout Southeast Asia, suggesting that this area is an important center of variation and possibly of origin. Vavilov (1928) suggested that its center of origin was in the Indo-Burma region. It originated in India but has a secondary center of variation in China. In China, eggplant has been known for the last 1,500 years. It is extensively grown in Bangladesh, India, Pakistan, Nepal, China, Japan and the Philippines. Batugal (2013) stated genetic diversity as a major factor that determines yield security in future.

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A new variety can be developed from an assembled diverse genetic stock of any crop. The quantification of genetic divergence through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization program (Uddin *et al*., 2014). Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Amin *et al*., 2014).

Multivariate analysis is a useful tool to quantify the degree of divergence between the biological population at genotypic level and to assess the relative contribution of different components to the total divergence both inter and intra cluster levels (Ivy *et al*., 2007; Quamruzzaman *et al*., 2009; Amin *et al*., 2014 and Nalla *et al*., 2014).

Considering the above facts, the present study was under taken to estimate the genetic diversity of selected eggplant genotypes and to select effective parents for future hybridization program.

Materials and Method

The research work was conducted at the Olericulture division of Horticulture Research Centre (HRC), Bangladesh Agricultural Research Institute (BARI), Gazipur during the period from 14 August 2012 to the last week of February 2013. A total of 26 eggplant genotypes were collected by Olericulture division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur, during 2010-2011 which were used in this study. Among 26 genotypes, 22 were collected from abroad (SM 201 from Brazil; SM 202 from Israel; SM 206-210, SM 215-216, SM 220-222, SM 225 and SM 226 from India; SM 211-212, SM 219, SM 223-224 and SM 227 from Thailand; SM 213 from Italy and SM 218 from Netherlands) and 4 (SM 203-204, SM 217 and BARI released Hybrid Tarapuri variety) from local source.

The experiment was laid out in Randomized Complete Block Design with three replications. Each replication contained 26 genotypes and the genotypes were randomly distributed to unit plot within each block. Multivariate analysis was done by computer using GENSTAT 5 (Fifth Edition Beta) and Microsoft Excel Professional Plus 2010 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLA) and Canonical Variate Analysis (CVA).

Results and Discussion

Principal component analysis (PCA)

Principal components were computed from the correlation matrix and genotype scores obtained from first components and succeeding components with latent roots

greater than the unity. Contributions of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal components. The principal component analysis yielded eigen values of each principal component axes with the first axes totally accounting for the variation among the genotypes for days to 50% plant flowering is 48.22, while two of these with eigen values above unity accounted for 63.15% (Table 1).The first three principal axes accounted for 76.59% of the total variation among the 10 characters describing 26 eggplant genotypes. Alam *et al*. (2011) found 78.13% total variation for the first three eigen values for three principal coordination axes from the principal component analysis of 22 lentil genotypes. The minimum acceptable value of cumulative eigen value of the principal component for coconut is 75% (Emannuel, 2002).

Table 1. Eigen values and percent of variation in respect of 10 characters in 26 eggplant genotypes

Principal component Axis	Principal component characters	Eigen values	Percentage of total variation accounted for	Cumulative (%)
I	Days to 50% plant flowering	4.823	48.22	48.22
II	Flower per inflorescence	1.493	14.93	63.15
III	Fruit length (cm)	1.344	13.44	76.59
IV	Fruit breadth (cm)	0.772	7.72	84.31
V	Fruits per infructescence	0.545	5.45	89.76
VI	Fruits per plant	0.544	5.44	95.20
VII	Fruit weight (g)	0. 315	3.15	98.35
VIII	Fruit yield (t/ha)	0.114	1.14	99.49
IX	Seeds per fruit	0.050	0.50	99.99
X	100 seeds weight (g)	0.0005	0.01	100.00

Construction of scatter diagram

Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1 - Z_2) using component score 1 as X-axis and component score 2 as Y-axis was constructed. The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the genotypes (Figure 1).

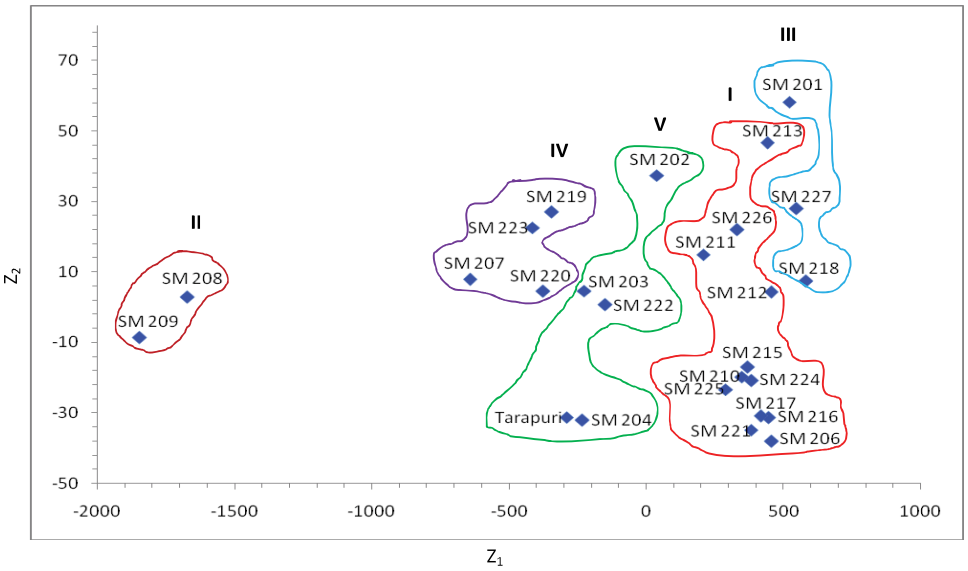

Figure 1. Scatter distribution of 26 eggplant genotypes based on their principal component scores superimposed with clustering.

Cluster analysis (CLA)

Cluster analysis is used to arrange the genotypes into more or less homogeneous groups and it confirmed the clustering pattern of principle component analysis. By using covariance matrix with the application of non- hierarchical clustering, the 26 eggplant genotypes were grouped into 5 (five) clusters. Singh *et al*. (2012) also found five different clusters from the cluster analysis of 36 pecan genotypes on the basis of their genetic distinctness. Compositions of different clusters with their corresponding genotype(s) in each cluster were presented in Table 2.

Table 2. Distribution of 26 eggplant genotypes in five different clusters with their place of collection

Cluster No.	Genotypes	Genotypes including sources of collection
I	12	SM 206, SM 210, SM 211, SM 212, SM 213, SM 215, SM 216, SM 217, SM 221, SM 224, SM 225 and SM 226
II	2	SM 208 and SM 209
III	3	SM 201, SM 218 and SM 227
IV	4	SM 207, SM 219, SM 220 and SM 223
V	5	SM 202, SM 203, SM 204, SM 222 and Tarapuri

Principal coordinate analysis (PCO)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter genotypic distances obtained from Principal Coordinate Analysis

showed that the highest distance (3.931) was observed between the genotypes SM 209 and SM 218 followed by SM 208 and SM 218 (3.930), SM 209 and SM 227 (3.511), SM 208 and SM 227 (3.450) and the lowest distance was observed between the genotypes SM 206 and SM 216 (0.298) followed by SM 217 and SM 221 (0.399), SM 211 and SM 226 (0.454) and SM 215 and SM 224 (0.456) (Table 3). From the principal coordinate analysis of 22 Lentil genotypes Alam *et al*. (2011) observed that the highest distance between two genotypes was 0.9365 where as the lowest distance was 0.0595 which indicate the presence of moderate variability among the genotypes. By using these distances from distance matrix intra and inter-cluster distances were calculated (Table 4).

Table 3. Ten of each higher and lower inter-genotypic distance (D^2) between pair of eggplant genotypes

10 higher D^2 values	Genotypes combination	10 lower D^2 values	Genotypes combination
3.931	SM 209 and SM 218	0.298	SM 206 and SM 216
3.930	SM 208 and SM 218	0.399	SM 217 and SM 221
3.511	SM 209 and SM 227	0.454	SM 211 and SM 226
3.450	SM 208 and SM 227	0.456	SM 215 and SM 224
3.317	SM 207 and SM 218	0.482	SM 208 and SM 209
3.257	SM 201 and SM 209	0.546	SM 206 and SM 221
3.137	SM 218 and SM 223	0.570	SM 206 and SM 217
3.120	SM 218 and SM 219	0.584	SM 210 and SM 215
3.112	SM 201 and SM 208	0.590	SM 216 and SM 221
3.065	SM 206 and SM 208	0.593	SM 216 and SM 217

Canonical variate analysis (CVA)

Canonical variate analysis was used to compute the inter-cluster Mahalanobis' D^2 values. The Table 4 indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances were higher than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 4). Results indicated that the highest inter- cluster distance was observed between Cluster II and Cluster III (37.82) followed by between Cluster I and Cluster II (34.20), Cluster II and Cluster V (26.40) and finally Cluster II and Cluster IV (21.22) (Table 4). The lowest inter-cluster distance was observed between the Cluster I and Cluster III (4.39), followed by Cluster IV and Cluster V (5.51), Cluster I and Cluster V (8.35) and finally Cluster III and Cluster V (11.46) (Table 4). So, genotypes from the Cluster II and Cluster III if involved in hybridization might produce a wide spectrum of segregating population, as genetic variation was very distinct among these groups. According to Singh *et al.* (2012) these

genotypes can also be utilized for transfer of useful traits in the commercial cultivars.

Table 4. Average intra (Bold) and inter cluster distances (D^2) for 26 genotypes of eggplant

Cluster	I	II	III	IV	V
I	**1.08**	34.20	4.39	12.99	8.35
II		**0.48**	37.82	21.22	26.40
III			**1.58**	16.65	11.46
IV				**0.83**	5.51
V					**1.21**

Contribution of characters towards divergence of the genotypes is presented in Table 5. The vector-I (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of the differentiation were 100 seeds weight (g) (3.6482), fruits per infructescence (1.5199), fruit yield (t/ha) (0.1935) and flower per inflorescence (0.1398). In vector-II (Z_2), 100 seeds weight (g) (5.8597), fruits per infructescence (1.8438), fruit yield (t/ha) (0.4458) and days to 50% plant flowering (0.0271) were the important characters responsible for genetic divergence. The role of fruits per infructescence, fruit yield (t/ha) and 100 seeds weight (g) in both the vectors were important components for genetic divergence in these materials. From the canonical variate analysis of 22 Lentil genotypes Alam *et al.* (2011) also noticed three characters such as days to maturity, plant height and pods per plant have positive values in both the vectors which indicate the highest contribution of these characters towards the divergence.

Table 5. Latent vectors for ten characters of 26 eggplant genotypes

Characters	Vector 1	Vector 2
Days to 50% plant flowering	-0.0180	0.0271
Flower per inflorescence	0.1398	-0.5484
Fruit length (cm)	0.0297	-0.0927
Fruit breadth (cm)	-0.1151	-1.0795
Fruits per inflorescence	1.5199	1.8438
Fruits per plant	-0.0054	-0.6222
Fruit weight (g)	-0.1600	-0.1553
Fruit yield (t/ha)	0.1935	0.4458
Seeds per fruit	0.0169	0.0016
100 seeds weight (g)	3.6482	5.8597

Conclusion

Considering the magnitude of genetic distance and agronomic performance, the genotypes SM 208 and SM 209 from Cluster II and SM 201, SM 218 and SM 227 from Cluster III would be suitable for efficient hybridization program.

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