Genetic diversity of brinjal (*Solanum melongena* Linn.) through multivariate analysis

MO Rahman[1]*, MG Rabbani[1], R Yesmin[2], EJ Garvey[3]

[1]Department of Horticulture, Bangladesh Agricultural University, Mymensingh-2202, Bangladesh
[2]Department of Agricultural Extension, Khamarbari, Dhaka-1215, Bangladesh
[3]USDA/ARS/NGRL, Beltsville, MD-20705, USA

ABSTRACT

Through genetic diversity based on multivariate analysis, hundred brinjal accessions were grouped into eight clusters. The cluster I contained the highest number of accessions (22) followed by the cluster V (19), III (17), IV (17), VII (10), VIII (7), II (6) and VI (2). The clustering pattern revealed that the accessions collected from the same region did not fall in a same cluster, indicating that there was no relationship between genetic divergence and geographical distribution of the accessions. The results of the PCA revealed that the first four of the principal component axes accounted for 78.07% of the variation among the genotypes considering ten characters. The maximum inter-cluster divergence was found between the cluster II and VI (32.234) and was minimum between V and VII (2.841). The maximum intra-cluster divergence was found between accessions falling in the cluster II. On the basis of the mean performance of different clusters, accessions having acceptable yield were placed in cluster IV, VI and VIII. The superior accessions may be selected from both maximum and minimum divergent clusters for further improvement.

Key words: genetic diversity, multivariate analysis, brinjal, accessions and cluster

*Corresponding author. Tel.: + 8801712932860
E-mail address: obaidbau@yahoo.com (MO Rahman)

INTRODUCTION

Brinjal (*Solanum melongena* Linn.) belongs to the family Solanaceae and is normally self-fertilized popular and principal vegetable crop grown in Bangladesh. The origin of brinjal is said to be the Indian subcontinent; the secondary place of origin is China (Zeaven and Zhukovsky, 1975). The Chinese people have been growing it for the last 1500 years (Yawalker, 1969). It is cultivated throughout the entire tropical and subtropical regions of the world and temperate too. It is grown extensively in India, Bangladesh, Pakistan, China and the Philippines. It is also popular in other countries, namely, Japan, Indonesia, Turkey, Italy, France, United States, and in the Mediterranean and Balkan areas (Bose and Som, 1986). Brinjal has high nutritional value in respect of calorie, iron, phosphorus and riboflavin contents (Chowdhury, 1976). The fruits, leaves, stem and

roots of brinjal are widely used in ayurvedic medicine for the patients suffering from diabetes, asthma, otitis, tooth ache, cholera, bronchitis and dysentery. For the development of suitable variety of brinjal, it is essential to evaluate the characters of the available germplasm collected from different parts of the country and conserve those for future use. Genetic diversity is a benchmark to the breeders to breed desired varieties through selection, either from the existing germplasm or from the segregates of different crosses. Hence, the genetic information on yield and yield contributing characters of the crop species need to be properly assessed for its improvement. Moreover, no information on agronomic characters is available that can be used as basis for delineating standardizing different available cultivars. In crop improvement programme, genetic diversity has been considered as an important factor which is also essential pre-

requisite for hybridization programme for obtaining high yielding progenies. If the accessions are identified on the basis of diverse analysis, the resulting recombinants through hybridization would be more promising. The degree of divergence existing in between the parents contributes in generating the desirable segregates. But so far, very few reports are available regarding the genetic diversity of brinjal. Therefore, the present study was under taken to assess the magnitude of genetic divergence in brinjal accessions and to classify them under groups based on genetic divergence.

MATERIALS AND METHODS

The experiment under the present research work was conducted at the field and laboratory of the CVFB project at the Department of Horticulture, Bangladesh Agricultural University, Mymensingh during the period from September 2005 to March, 2006. The study was undertaken to investigate the genetic diversity of brinjal through multivariate analysis. The soil texture was silt loam with a pH 6.7. Hundred brinjal accessions were included in this study that was collected from different regions of Bangladesh. The experiment was laid out in the partial lattice design with three replications. One accession represented one treatment, and 10 plants in an accession represented one replication. The distance between replication, between plants in a row and between rows was 1.0 m and the plot size was 10 m2 (5m x 2m). Seeds were sown in well prepared seedbeds in 16 September 2005. The soil was fertilized with cowdung 4t/ha, Urea 250kg/ha, Triple Super Phosphate (TSP) 100kg/ha and Muriate of Potash (MoP) 150kg/ha. The whole quantity of cowdung, TSP, MoP and half of the quantity of urea were applied during the final land preparation. The rest of the urea was applied in two equal installments at 10 days after transplanting of seedlings. All other cultural practices were carried out uniformly. Mature fruits at the edible stage were harvested at an interval of seven days. Harvesting was started in 2nd week of February and continued up to last week of March. The data on ten different important yield and yield contributing parameters were recorded and included in genetic diversity analysis. Genetic diversity of the collected 100 brinjal accessions

was studied using Mahalanobis (1936) D^2 statistics such as plant height, number of branches per plant, number of flowers per inflorescence, number of fruits per plant, fruit length and breadth and individual fruit weight were recorded and analyzed. Multivariate analyses, viz Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Canonical Vector Analysis (CVA), and Cluster Analysis (CLSA), as developed by Mahalanobis (1936), were performed using the mean data for each character following the widely used GENSTAT[513] program.

RESULTS AND DISCUSSION

Principal component analysis (PCA)

The results of the principal component analysis revealed that the first principal axis largely accounted for the variation among the genotypes which alone contributed (36.41%) to the variation (Table 1). The first four of the principal component axes with eigen values above unity accounted for 78.07% of the total variation among the 10 characters describing 100 brinjal accessions. These results are in close conformity with the findings of Rahman (2005) and Sarker (2000), where they reported that the first five axes in case of pointed gourd and first two axes in case of musk melon accounted for 77.65 and 72.22%, respectively, of the total variation among the selected characters. Based on principal component axes I and II, a two dimensional scatter diagram (Z_1-Z_2) of the accessions using component score I as X-axis and component score II as Y-axis has been constructed and presented in Fig. 1. The distribution of 100 accessions of brinjal in scattered diagram was apparently distributed into 8 groups, which revealed that there exists a considerable diversity among the brinjal accessions.

Non-hierarchical clustering

Non-hierarchical clustering was done by using covariance matrix, where 100 brinjal accessions were grouped into eight different clusters. By the application of this non-hierarchical clustering pattern of the genotypes, the principal component analysis was confirmed. The clustering patterns

obtained through different techniques coincided with the grouping patterns done by PCA, suggesting that the results obtained through PCA were established by non-hierarchical clustering. Based on D^2 analysis, the 100 brinjal accessions were grouped into eight clusters. Kalloo and Sidhu (1982) observed 14 clusters among 45 muskmelon genotypes in D^2 analysis. Ram (2001) carried out component analysis and cluster analysis in 167 pointed gourd accessions, and divided the 167 accessions into 8 groups. Cluster I showed the highest number of accessions (22) followed by cluster V (19), cluster III and IV (17) and VII (10). The lowest number of accessions was observed in cluster VI (2), followed by cluster II (6) and cluster VIII (7). The clustering pattern of the accessions under this study revealed that the accessions collected from the same location were often grouped into different clusters (Table 2), which indicated variation among the accessions irrespective of their site of collection. Banik (2003) also found no variation among the accessions due to geographical distribution; rather genotypes collected from same region were distributed in different clusters randomly. In the present study, it was observed that, 23 accessions of brinjal collected from Mymensingh district were grouped into six different clusters (Table 2). This indicated that factors other than geographical separation are also responsible for divergence, and that the accessions collected from the same place might have different genetic architecture or vice-versa. Mannan *et al*. (1993) and Singh and Singh (1979) which working with pani kachu and okra, respectively, reported that falling of materials of same origin into different clusters was an indication of broad diversity. Upadhya and Murty (1970) opined that genetic drift and natural selection in different environment could cause high diversity among genotypes.

Principal coordinate analysis (PCO):

Principal coordinate analysis was done to get the inter-genotypic distances (D^2) among 100 brinjal accessions. The highest inter-genotypic distance (5.583) was observed between the accessions SM003 and SM096 (Table 3), which was followed by the distance (5.083) observed between the accessions SM016 and SM096. The lowest distance was 0.234, which was observed between the accessions SM069 and SM073, followed by the distance 0.258, observed between the genotypes SM069 and SM076. The difference between the highest and the lowest inter-genotypic distance indicated the presence of variability among the 100 brinjal accessions. Uddin and Chowdhury (1994) reported a range of D^2 values from 0.114 to 1.45 in case of sesame. The intra-cluster distances were computed by using the values of inter-accession distance from distance matrix according to Singh and Chowdhury (1985). It was observed that the number of genotypes in a cluster and the intra-cluster distance did not necessarily always match.

Table 1
Latent roots (eigen values) and percentage of variation for corresponding 10 characters in 100 accessions of brinjal

Principal component axis	Latent roots	Percentage	
		Total variation accounted for	Cumulative
Plant height (I)	3.641	36.41	36.41
Branches per plant (II)	1.672	16.72	53.13
Plant spread (III)	1.422	14.22	67.35
Days to first flowering (IV)	1.072	10.72	78.07
Individual fruit weight (V)	0.720	7.20	85.27
Length of fruit (VI)	0.648	6.48	91.75
Diameter of fruit (VII)	0.439	4.39	96.14
No. of fruits/plant (VIII)	0.159	1.59	97.73
Fruit yield/plant (IX)	0.140	1.40	99.13
No. of seeds/ fruit (X)	0.086	0.86	100.00

Table 2
Distribution of 100 brinjal accessions collected from different location of Bangladesh in 8 clusters

Cluster number	Number of accessions in the cluster	Brinjal accessions	Place of collection (Bangladesh)
I	22	SM008, SM011, SM012, SM021, SM031, SM082, SM 141, SM143	Mymensingh
		SM015, SM016, SM017, SM018, SM019, SM020	Tangail
		SM027,	Pabna
		SM042, SM045, SM050	Rajshahi
		SM055, SM056	Gaibandha
		SM101	Manikgonj
		SM126	Rangamati
II	6	SM003	Jamalpur
		SM005, SM009, SM030, SM095	Mymensingh
		SM026	Pabna
III	17	SM002	Jamalpur
		SM014	Panchagarh
		SM023, SM024, SM028	Pabna
		SM029, SM034, SM036, SM084, SM086	Mymensingh
		SM057	Chapi-Nawabagonj
		SM064, SM068	Comilla
		SM071, SM072, SM074	Chittagong
		SM087	Jessore
IV	17	SM001	Jamalpur
		SM007	Mymensingh
		SM041, SM046, SM047, SM051, SM104	Rajshahi
		SM060, SM069	Comilla
		SM076	Chittagong
		SM077	Dinajpur
		SM088	Jassore
		SM094	Khagrachori
		SM106, SM109	Chapai-Nawabagonj
		SM119, SM123	Rangpur
V	19	SM010, SM032, SM033, SM083	Mymensingh
		SM013	Panchagarh
		SM052	Rajshahi
		SM059	ChapaiNawababgonj
		SM062, SM063, SM065, SM067, SM070	Comilla
		SM075	Chittagong
		SM080, SM081, SM097, SM105	Dinajpur
		SM091	Satkhira
		SM103	Rajshahi
VI	2	SM037	Rajshahi
		SM096	Satkhira
VII	10	SM006	Mymensingh
		SM053, SM054	Gaibandha
		SM058	Chapai Nawababgonj
		SM073, SM107	Chittagong
		SM090	Jessore
		SM093	Khagrachori
		SM098	Dinajpur
		SM121	Rangpur

VIII	7	SM025	Pabna
		SM038	Rajshahi
		SM092	Jessore
		SM102	Manikgonj
		SM108, SM110	Chapai-Nawabagonj
		SM138	Gajipur

Table 3
Ten of each lower and higher inter accessions distance between pairs of 100 brinjal accessions

10 lower D^2 values	Accessions Combination	10 higher D^2 values	Accessions Combination
0.234	SM 069× SM 073	5.583	SM 003×SM 096
0.258	SM 069× SM 076	5.083	SM 016× SM 096
0.299	SM 069× SM 088	4.917	SM 095× SM 096
0.301	SM 062× SM 069	4.856	SM 005× SM 096
0.317	SM 067× SM 105	4.833	SM 019× SM 096
0.324	SM 024× SM 027	4.71	SM 018× SM 096
0.329	SM 051× SM 052	4.698	SM 012× SM 096
0.341	SM 064× SM 081	4.61	SM 003× SM 025
0.348	SM 073× SM 076	4.609	SM010×SM096
0.375	SM 051× SM 054	4.492	SM 017× SM 096

Table 4
Inter and intra group distance of 100 brinjal accessions

Clusters	I	II	III	IV	V	VI	VII	VIII
I (22)*	**1.142**	4.889	3.141	12.425	6.321	27.858	9.134	17.052
II (6)		**1.327**	8.023	17.138	11.152	32.234	13.918	21.692
III (17)			**0.8156**	9.394	3.223	25.013	6.062	14.055
IV (17)				**0.8524**	6.183	15.804	3.351	4.675
V (19)					**0.9954**	21.887	2.841	10.855
VI (2)						**1.297**	19.119	11.212
VII (10)							**1.035**	8.026
VIII (7)								**0.8431**

Intra (bold) and inter cluster D^2 values for nine characters
* Number of accessions in the cluster

The magnitudes of the intra-cluster distances were not always proportional to the number of accessions in the clusters (Table 4). In the present study, it was noticed that although the cluster I composed of the highest number of accessions 22, its intra cluster distance was not necessarily the highest. The highest intra cluster distance was observed in cluster II (1.327) which was composed of only 6 accessions followed by cluster VI (1.297) containing only 2 accessions, cluster I (1.142) with 22 accessions and cluster VII (1.035) having 10 accessions.

Canonical Vector analysis (CVA)

Canonical vector analysis was performed to compute the cluster distance (Mahalanobis' D^2 value). The intra- and inter-cluster distance or D^2 values are presented in Table 3 and Fig. 1- 2. The highest inter cluster distance was observed between cluster II and cluster VI (32.234), indicating a wide range of genetic diversity between these two clusters; which was followed by inter cluster distances between cluster I and cluster VI (27.858) and cluster III and cluster VI (25.013). Intermediate or moderate inter cluster distance was observed between Cluster VI and VII (19.119), cluster II and IV (17.138) and cluster I and VIII (17.052). The lowest inter cluster distance was observed between cluster V and VII
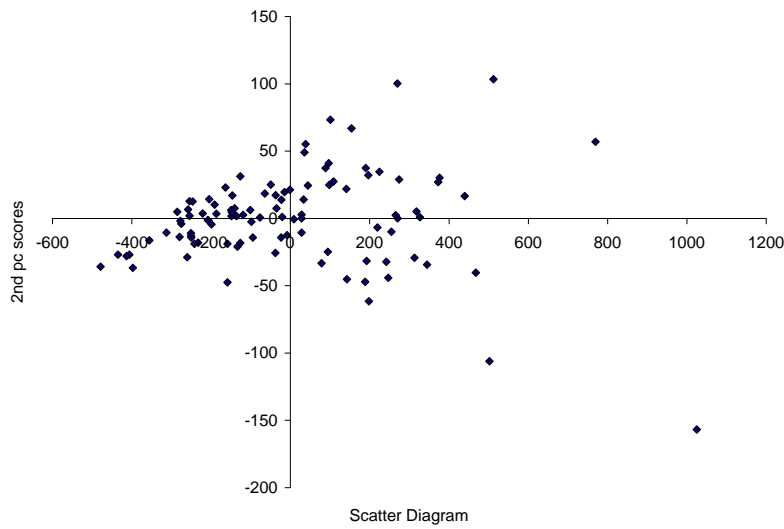
Figure 1

Scattered diagrams of 100 brinjal accessions based on their principal component scores
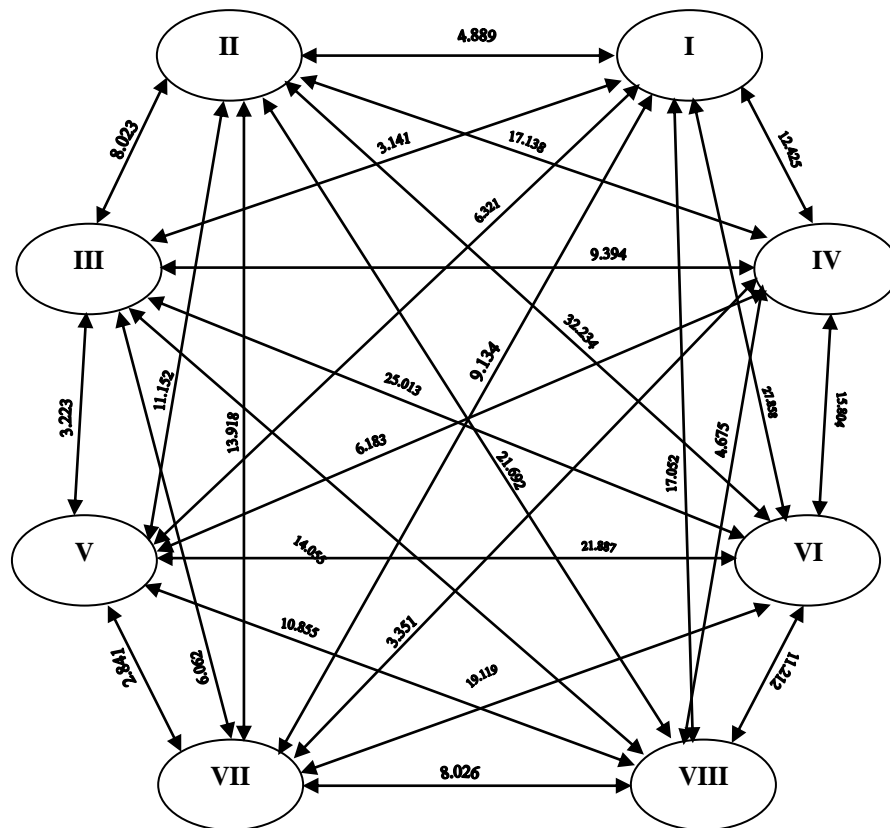

Figure 2

Cluster diagram showing the average intra and inter cluster distances (D = $\sqrt{D^2}$) of 100 brinjal accessions (The values along the lines indicate inter cluster distances and the values within the circle indicate intra cluster distances)

(2.841), which was followed by cluster I and III (3.141), cluster III and V (3.223) and cluster IV and VII (3.351), suggesting a close relationship between the accessions of these clusters, and the accessions were genetically close. The lowest inter cluster distance was also reported by Prasad (1995) in bush bean. These relationships were also reflected in the scatter diagram (Fig. 1) and the intra and inter cluster distances diagrammatically presented in Fig 2. The brinjal accessions among the clusters separated by high D^2 values could be used in hybridization program for obtaining a wide spectrum of variation among the segregates (Seetharaman *et al.* 1988; Masud *et al.*, 1995; Sarker, 2000).

Cluster means

The cluster means, in respect of 10 different characters, of 100 brinjal accessions are shown in the Table 5. Cluster I was comprised 22 accessions, had the second highest mean value for number of fruits per plant (68.4), number of branches per plant (7.0). The cluster had moderate mean values in rest of the characters. The cluster II had 6 accessions, which had the highest mean value for number of branches (8.3) and fruits (108.6) per plant. This cluster had the minimum mean value for days to first flowering (88.3), individual fruit weight (23.7 g) and fruit breadth (8.4 cm). The cluster III, having 17 accessions had

the lowest mean value for yield per plant (1.8kg)). Cluster III, did not have highest mean value for any character. Cluster IV comprising of 17 accessions, had the second highest mean values for yield per plant (2.6 kg) per plant and plant height (54.6 cm) with the lowest mean values for number of branches per plant (5.4), plant spread (52.3 cm) and number of fruits per plant (18.3). Cluster V, having 19 accessions, had the highest mean value for fruit length (13.5 cm), second highest for plant height (54.6 cm), and low yield per plant (2.0 kg). Cluster VI, consisting of 2 accessions, had the highest mean values for plant height (56.3 cm), plant spread (59.5 cm), days to first flowering (100.6), individual fruit weight (334g), fruit breadth (32.4 cm) and number of seeds per fruit (15.19) and the lowest mean values for number of branches (5.1) and number of fruits (9.5) per plant. Cluster VII, consisted of 10 accessions, and the mean values for all the yield contributing characters and yield were moderate. Cluster VIII, having 7 accessions, had the highest mean value for yield per plant (3.2 kg) and the second highest mean values for individual fruit weight (183.2 g) and fruit breadth (25.0 cm). The mean values of all 8 clusters of brinjal indicated that cluster VIII was the highest yielder of fruits per plant, cluster II was the produce of highest number of fruits per plant, cluster VI was the produce of highest individual fruit weight, and cluster II was the earliest to produce the first flower.

Table 5
Cluster mean values of 100 accessions of brinjal

Characters	Clusters							
	I (22)*	II(6)	III (17)	IV (17)	V (19)	VI (2)	VII (10)	VIII (7)
Plant height	53.4	49.9	53.7	54.6	54.6	56.3	53.8	54.1
No. of branch/plant	7.0	8.3	6.0	5.4	5.8	5.1	5.4	5.4
Plant spreading	53.5	54.0	55.3	52.3	54.5	59.5	52.8	58.5
Days to first flowering	93.3	88.3	93.5	97.5	93.2	100.6	97.3	95.6
Individual fruit weight	37.2	23.7	60.5	143.5	76.8	334.0	94.0	183.2
Length of fruit	9.6	7.2	11.7	12.9	13.5	13.1	12.5	12.3
Breadth of fruit	11.3	8.4	13.0	20.3	14.0	32.4	15.9	25.0
No. of fruit /plant	68.4	108.6	30.4	18.3	25.4	9.5	22.7	18.5
Yield/plant(g)	2.2	2.3	1.8	2.6	2.0	2.6	2.2	3.2
No. of seeds /fruit	418.4	248.6	525.3	893.7	652.1	1519.0	765.4	1074.1

* Number of accessions in the cluster

Contribution of different characters towards divergence

The results of contribution responsible for genetic divergence on the accessions are presented in Table 6. Vector I (Z_1) obtained from PCA expressed that the important characters responsible for genetic divergence in the major axis were, yield per plant, number of fruits per plant, fruit breadth and number of seeds per fruit. Hence, considerable emphasis should be given on these characters to increase fruit yield in brinjal. Other characters had minor contribution in determining genetic divergence. Vector II (Z_2), which was the second axis of differentiation, expressed that the important characters were, the number of branches per plant, plant spread, length and breadth of fruit, number of fruits per plant and fruit yield per plant play to a major role in determining genetic divergence. The number of fruits per plant, fruit yield per plant and fruit breadth in both the vectors was positive across two axes indicating as the important components of genetic divergence among these characters. The negative values in both the vectors for plant height, days to first flowering and individual fruit weight were indicated as the lowest contributor towards the total divergence of brinjal. Masud *et al*. (1995) found that the number of fruits per plant, average fruit weight and yield per plant played a major role in determining genetic divergence of pumpkin.

Table 6
Relative contributions of 10 characters towards genetic divergence in 100 accessions of brinjal

Characters	Vector 1	Vector 2
Plant height	-0.01986	-0.00201
No. of branches/plant	-0.07429	0.01496
Days to first flowering	-000607	-0.04260
Canopy volume	-0.02445	0.00661
Individual fruit weight	-0.00125	-0.02861
Length of fruit	-0.00492	0.07743
Breadth	0.01365	0.09325
No. of fruits /plant	0.01313	0.04375
Fruit yield/plant	0.33447	0.87484
No. of seeds/fruit	0.02448	-0.00015

The D^2 and Principal component analysis were found to be alternative methods on giving information regarding the clustering pattern and the contribution of characters towards divergence on brinjal accessions. It was concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of the other.

REFERENCES

Banik VR (2003). Inheritance pattern in snake gourd (*Trichosanthes anguina* L.). Ph.D. thesis. Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur. pp. 40-60.

Bose TK and Som MG (1986). Vegetable Crops in India. Mitra Naya Prokash, 206, Bidhan Sarani, Calcutta, India. pp.4-293.

Chowdhury B (1976). Vegetables (4th ed.). National Book Trust, New Delhi, pp. 50-58.

Kalloo G and Sidhu AS (1982). Genetic divergence in muskmelon (*Cucumis melo* L.). Genetica Agaria, 36:1-8.

Mahalanobis P C (1936). On the generalized distance in statistics. Proceedings of the Indian National Science Academy, 2: 49-55.

Mannan MA, Ahmed MS, Rashid MM, Bhuiuan MKR and Gomes R (1993). Genetic diversity of *Colocassia esculenta* (L. Schtt.). Root Crops, 19(2): 95-99.

Masud MAT, Chowdhury MAZ, Hossain MA and Hossain SMM (1995). Multivariate analysis in pumpkin (*Cucurbita moschata* Duch ex Poir). Bangladesh Journal of Plant Breeding and Genetics, 8 (1&2): 45-50.

Rahman ASM M (2005). Studies on genetic diversity and production technology of pointed gourd. PhD thesis, Department of Horticulture, Bangladesh Agricultural University, Mymensingh. pp. 30-85.

Ram D (2001). Non-hierarchical Euclidean cluster analysis in pointed gourd. Indian Journal of Horticlture, 58(3) : 264-268.

Sarker MBA (2000). Characterization, evaluation and improvement of muskmelon (*Cucumis melo*). PhD thesis, Department of Horticulture, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur, Bangladesh. 180 p.

Seetharaman R, De N, Sinha RMK and Banerjee SP (1988). Genetic divergence in rice. Indian Journal of Genetics, 48: 189-194.

Singh RK and Chowdhury BD (1985). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi. pp. 225-252.

Singh SP and Singh HN (1979). Genetic divergence in okra (*Abelmoschus esculentus* L. Moerch). Indian Journal of Horticulture, 36(2): 166-170.

Uddin MJ and Chowdhury MAQ (1994). Multivariate analysis in sesame (*Sesamum indicum* L.). Bangladesh Journal of Plant Breeding and Genetics, 7(1): 37-41.

Upadhya MR and Murty BR (1970). Genetic diversity in relation to geographical distribution in pear millet. Journal of Plant Breeding and Genetics, 75 (3 & 4): 233-238.

Yawalkar KS (1969). Vegetable Crops in India. Agri-Horticulture Publishing House, Nagpur, India. 94p.

Zeaven AC and Zhukovsky PM (1975). Dictionary of Cultivated Plants and their Centre of Diversity. Wageningen, the Netherlands. 219p.