GENETIC DIVERSITY IN BRINJAL (*Solanum melongena* L.) GENOTYPES OF BANGLADESH

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By

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CERTIFICATE

This is to certify that thesis entitled, "GENETIC DIVERSITY IN BRINJAL (Solanum melongena L.) GENOTYPES OF BANGLADESH" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of ***MASTER OF SCIENCE*** *in* ***GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by MOST. NUR SHAHI BEGUM, Registration No: 08-3148 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated:

(Dr. Md. Ashaduzzaman Siddikee)
Supervisor

Place: Dhaka, Bangladesh

LIST OF ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro Ecological Zone	AEZ
Bangladesh Agricultural Research Institute	BARI
Centimeter	cm
Degree Centigrade	0^c
Gram(s)	gm
Muriate of Potash	MP
Number	No.
Randomized Complete Block Design	RCBD
Triple Super Phosphate	TSP
ton/hectare	t/ha
Percent	%
Hour	hr
Degree of freedom	df
Co-efficient of Variance	CV
Standard Error	SE
Meter	M
Milligram	mg
Concentrate of H^+	pH
Kilogram	Kg

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Study on genetic diversity based on qualitative and quantitative character among 15 genotypes of brinjal were done on 15 brinjal genotypes at the farm of Sher-e- Bangla Agricultural University, Dhaka during November, 2013 to April, 2014 .Diversity was estimated by cluster distance. Significant variations were observed among the brinjal genotypes for all the parameters under study. Multivariate techniques were used to classify the genotypes. All the genotypes were grouped into five clusters. Principal Component Analysis, Principal Coordinate Analysis and Canonical Variate Analysis had exhibited similar results. Cluster I had the maximum of saven and the cluster III and IV had the minimum of 1 genotype respectively. The highest intra-cluster distance was observed in cluster II followed by I. The highest inter-cluster distance was observed between cluster III and IV and the lowest between the cluster I and II. The characters such as number of fruits per plant, fruit length, fruit diameter and fruit weight contributed maximum towards divergence among the genotypes. Genetic divergence was not found to be related to geographical diversity. Analyzing diversity pattern and other agronomic performance, the genotype 6 from cluster II, genotype 13 from cluster IV, genotype 14 from cluster I and 15 from cluster V were selected as better parents for future hybridization program.

CHAPTER I

INTRODUCTION

Eggplant (*Solanum melongena* L), also known as aubergine or brinjal, is a member of the family Solanaceae. It is one of the few cultivated solanaceous species originating from the old world and an important vegetable in central, southern and south-east Asia, and in a number of African countries (Kalloo, 1993). Brinjal eggplant belongs to the very large genus *Solanum*, as well as its largest subgenus, *Leptostemonum*, which includes many wild relatives, as well as other cultivated species, such as the Gboma eggplant (*Solanum macrocarpon* L.) and the scarlet eggplant (*Solanum aethiopicum* L.) grown mostly in Africa for their fruits and leaves. More than 200 *Solanum* species are known in Africa, with about 25 species indigenous in Nigeria (Gbile and Adesina, 1988; Burkill, 2000).

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). Contrary to the common belief, it is quite rich in nutritive value and can be compared with tomato (Choudhury, 1976). The unripe fruit is primarily used as a cooked vegetable for the preparation of various dishes in different regions of the world. It has potentiality as raw material in pickle making and in dehydration industries (Singh *et al.,* 1963). Fried brinjal in sesame oil has same medical value to cure liver problem (Chauhan, 1981).

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 (1.3Mt), Indonesia (0.7 Mt), Iraq (0.6 Mt) Japan (0.6Mt) 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.

Brinjal (*Solanum melongena*) is one of the important vegetable crops grown in all parts of Bangladesh (Rashid, 1995). It has a positive role in both summer and winter to fulfill the market demand of vegetables of Bangladesh. Yield potentiality of the varieties cultivated in Bangladesh is less and brinjal size, shape, and skin colour varies in different locations. Improvement in fruit yield, colour, and insect resistances will certainly enhance the production and consumption of the crop. The actual area under brinjal cultivation is not available due to its seasonal nature of cultivation. In Bangladesh total cultivated area of kharif and rabi brinjal reported to be 22,221 hectares and 42,836 hectares of land respectively (BBS, 2000) and total production was 3,78,000 metric tons (BBS, 2002). The wide range of variability was observed in respect of morphological traits, but till date very few systematic assessment of genetic diversity on this crop has been done. But their productions are hampered due to the infestation of different insects like root and shoot borer, spider mites and diseases like wilt, phomopsis blight, etc. Selection against various natural defense mechanisms like spines, hairiness etc. reduced the resistant capacity of the crop against diseases and insects. Ultimately the control approach based entirely on toxic pesticides and chemicals is not working properly in the field. On the other hand, the chemicals and pesticides led to higher costs of production, environmental pollution, destruction of natural enemies, development of pesticide resistance etc. It is important to identify the natural mechanisms prevailing in the brinjal land races to utilize them in the improvement program.

The identification of variability among accessions is pivotal to the maintenance and utilization of germplasm resources (Mwirigi *et al.,* 2009). Systematic study and evaluation of germplasm is of great importance for current and future agronomic and genetic improvement of the crop (Reddy *et al*., 2013). To identify and estimate the genetic diversity of plants, various methods can be used including morphological, biochemical and molecular markers. Morphological markers are used abundantly to study of genetic variation in plant species. Morphological traits are important diagnostic features for distinguishing genotypes (Osei *et al.*, 2014). Genetic variation in eggplant by morphological characters has been the subject of many studies in regions of the world (Mazzucato *et al.*, 2008, Osei *et al.*, 2014).

Variability is the basic requirement for any crop improvement. Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. It usually happens that genetically diverse parents are likely to contribute desirable segregants or to produce high heterotic crosses. More diverse the parents greater are the chances of obtaining high heterotic F_1 and broad spectrum of variability in segregating generation (Murty and Arunachalam, 1966). Evaluation of diversity is important to know the source of gene for a particular trait within the available germplasms (Tomooka, 1991).

The importance of genetic diversity for the improvement of crop has been stressed in both self and cross-pollinated crops (Griffin and Lindstorm, 1954; Murty and Anand, 1966; Gaur *et al.,* 1998). Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). The quantification of genetic diversity through biometrical procedure (Anderson, 1957; Rao, 1952) has made it possible to choose genetically diverse parents for a successful hybridization program. The utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution of different characters to the total divergence in self-pollinated crops has been established by several workers (Golakia and Makne, 1992; Natarajan *et al*., 1988; Das and Gupta, 1984; Sindhu *et al*., 1989).

A large number of genotype having wide variability in different characters are being cultivated in Bangladesh and some of the variations are so localized that their cultivation beyond the particular zone is completely unknown. Due to their restricted distribution, some of these promising genotype are yet to be known. So it is necessary to evaluate the performance and characteristics of local, mutant and exotic genotype of brinjal for finding out suitable variety under the agro-ecological condition of the central plains of Bangladesh during the winter season.

The present study was undertaken to estimate the nature and magnitude of genetic diversity of brinjal and to study the feasibility of utilizing all those information for the varietal improvement of the brinjal.

The present investigation was undertaken with the following objectives:

1. To study the genetic diversity among the genotypes.
2. To categories the brinjal materials on the basis of morphological and yield contributing characters.
3. To select the genetically divergent parents to use them in the future hybridization programme.

CHAPTER II

REVIEW OF LITERATURE

Information on genetic divergence among the available germplasm is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants. It was also observed that the more diverse the parents, greater are the chances of obtaining high heterotic F_1 and broad spectrum of variability in the segregating generation (Arunachalam, 1981). Improvement in yield and quality is normally 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 programme..Studies on quantitative and qualitative characters of brinjal are receiving much attention in the tropical and sub-tropical countries. Although brinjal is a common and one of the most popular vegetables occupying a wider acreage under its cultivation in Bangladesh, information on its growth habit and productivity of different genotype under varied agro-ecological conditions are very much lacking. In Bangladesh and elsewhere in the world, research effort on diversity analysis of brinjal seems to be negligible. Thinking about magnitude of diversity for yield and its component characters, considerable interest to the plant breeders for planning and execution of genetic improvement program; a large number of such investigations have been carried out in different crops. All these studies were on the basis of simple analysis of variance which enabled to compute genetic variance for different characters. But total genetic diversity among different natural populations could not obtain which was important to evolutionary and breeding point of view. Under these circumstances, statistical analysis such as Mahalanobis's D^2, multivariate analysis was of great importance. Therefore, relevant information available in the literature pertaining to the diversity of the brinjal and some other crops of the same family were reviewed in this section. Moreover literatures related to the efficient multivariate techniques for diversity analysis were also reviewed in the following paragraphs

2.1 Genetic diversity

Genetic diversity arises due to geographical separation or due to genetic barriers to crossability. Variability differs from diversity is the sense that the former has observable phenotypic differences, whereas the latter may or may not have such an expression. One of the potent techniques of assessing genetic divergence is the D^2 static proposed by Mahalanobis in 1936. This technique measure the forces of differentiation of two levels, namely, intracluster and inter-cluster levels, and thus help in the selection of genetically divergent parents for exploitation in hybridization programme. Genetic diversity plays an important role in plant breeding because hybrids between genotypes of diverse origin generally display a greater heterosis than those between closely related strains. In addition to aiding in the selection of divergent parents for hybridization, D^2 statistic measures the degree of diversification and determines the relative proportion of each component character to the total divergence. The genotypes grouped together are less divergent than the one, which are placed in different clusters. The clusters, which are separated by the greatest statistical distance, show the maximum divergence. Three important points should be taken into consideration while selecting parents on the basis of D^2 statistic. These points are: the relative contribution of each character to the total divergence; the choice of clusters with the maximum statistical distance and the selection of one or two genotypes from Such clusters.

Genetic diversity is different forms of genotype and occurs as a result of changes in genetic structure (WEB_2 2007). It potentially leads to speciation in the long term due to the process of evolution (Raven *et al.* 1999a and WEB_2 2007). Diversity in genetic composition is the basic feature which increases chance of survival for individuals and populations during natural selection (WEB_2 2007).

Morphological similarity, eco-geographic diversity were the few easier methods used to discriminate divergent populations which were reinstated by more scientific and advanced biometrical techniques viz. multivariate analysis based on Mahalanobis's D^2 statistics. Nair and Mukherjee (1960) estimated degree of divergence between biological populations and relevant contribution of different components to the total divergence by D^2 statistic as a measure of genetic divergence in the field of plant breeding. Comparative analysis of complex developmental pathway depends on our ability to resolve the function of members of gene families across taxonomic groups studied by Fridman *et al.* (2003). LINS 5 which belongs to a small gene family of apoplastic invertases (beta-fructofuranosidase) in tomato (*Lycopersicon esculentum*), is a quantitative trait locus that modifies fruit sugar composition. Rapid regulatory divergence is characteristic of the invertase family. The observation that functional orthology cannot be identified through analysis of expression, similarity highlights the caution that needs to be exercised in extrapolating development networks from a model organism.

Mishra *et al.* (2002) conducted an experiment in Pantnagar, Uttar Pradesh, India, during 1999/2000 and 2000/01 rabi season to determine the genetic diversity among 38 potato genotypes. Based on the mean performance for various characters and genetic distance between genotype crosses, namely JP-100 x Kufri Pukhraj, JP-100 x JW-96, JP-100 x JX-23, JP-100 x Kufri Ashoka, JP-100 x JX-235, JP-100 x JX-216, and JP-100 x JX-371 were identified as promising and were likely to result in progenies with heterotic performance for tuber yield and its components.

Three hundred accessions of andigena group of potato germplasms were evaluated by Sandhu *et al.* (2001) for genetic divergence based on 8 distinct traits, namely plant height, number of stems, number of nodes, inter node length, leaflet index, tuber yield, tuber number and average tuber weight. Principal component analysis based on adjusted mean values yielded 8 each Eigen vectors and Eigen roots. Eight genetically diverse and agronomically promising genetic stocks were identified which may be involved in crossing programme.

Genetic divergence among 20 cultivars of brinjal (*Solanum melogena* L.) was estimated by Mishra *et al.* (1998) using D^2 statistics for eleven yield traits. The cultivars were grouped into 7 clusters. Maximum genetic distance was found between clusters IV and VI followed by that between clusters I and IV, suggesting wide diversity among these groups. Considering cluster means and the genetic distances, the crosses of the cultivar of cluster VI (A-I) with the cultivars of clusters I and IV were likely to recombine the genes for high yield.

Ramesh *et al.* (2013) conducted an experiment on Genetic divergence among 14 eggplant genotypes was estimated using Mahalanobis's D^2 statistic. Altogether six clusters were formed. The maximum number of genotypes (5) was found in cluster III with intra cluster distance of 2 597.79. The maximum inter cluster distance was observed between cluster II and cluster V. Hence, genotypes belonging to these clusters may be utilized for involving in hybridization programme for crop improvement. The characters of yield per plant, fruit circumference, little leaf incidence and total phenols content contributed more for genetic divergence.

Amaral *et al.* (1997) observed that the efficiency in predicting the behavior of tomato hybrids based on the parents, genetic divergence was evaluated via D^2 analysis of data on 15 characteristics in 5 parents and their hybrids. Almost all correlations between D^2 and hybrid population means, heterosis and combining abilities were positive, indicating that genetic divergence was a high efficiency parameter for hybrid behavior predication.

An experiment was conducted by Gopal *et al*. (1997) to study the effectiveness of genetic divergence for cross prediction in potato, progeny means, heterosis and specific combining ability effects were correlated with parental genetic distances (D^2 values) estimated under six in vitro and four in vivo conditions for tuber yield in 72 crosses. Genetic distances under in vitro conditions had no relationship with the progeny means for tuber yield. The magnitudes of the significant correlation coefficients showed that genetic divergence could be used as an indirect parameter of moderate effectiveness in selecting parents to produce heterotic high yielding progenies.

Fifty two potato genotypes comprising *Solanum tuberosum* (35) were observed by Pandey *et al*. (1995). Indigena (4) and inter sub specific crosses (13) were compared for genetic divergence on the basis of 11 plant and tuber characters. The genotypes were grouped into 11 clusters. The genotypes with wild species in their pedigree had high genetic diversity and were distributed in almost all clusters. However genotypes with common species in their pedigree showed a low diversity. Genotypes developed from the same parentage at those or involving one common parent also had low genetic diversity.

Information on genetic variation, heritability and genetic advance was derived from data on 10 yield components in 16 tomato lines grown during the winter season of 1986 at Bhubaneswar reported by Sahu *et al.* (1994). There were significant differences among the lines for all the characters studied. Yield per plant, number of fruits per plant, number of flower trusses per plant and fruit weight had high genotypic coefficient of variation with values for heritability and genetic advance.

Randhawa *et al.* (1993) studied 22 genotypes of brinjal on 24 quantitative characters for deriving information on yield co-relation and observed that fruits/plant and number of branches/plant had the highest direct effect on yield.

Hybrids from a diallel set of crosses between 11 varieties of tomato were evaluated by Sidhu *et al.* (1993) for field heterosis over the better parent in relation to the genetic distance between the parents. The genetic divergence between the parents was not clearly related to the performance of the hybrids with the highest heterosis were listed.

Mandal and Dana (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that fruits/plant; secondary branches/plant and plant height were important traits for the selection of superior genotypes.

Vedivel and Bapu (1990) studied nineteen genotypes of eggplant including 7 from foreign sources, which were grown in a Randomized Block Design for observation on growth and yield related traits. Plant height, fruit weight and fruit/plant exhibited high genotypic variance. High heritability coupled with high genetic gain from fruit yield/plant, fruit/plant and length indicated the predominance of additive gene effects.

It was revealed by Ushakumiry *et al.* (1991) through the evaluation of fifty four diverse genotypes of brinjal for 10 yield components that phenotypic co-efficient of variation was higher than genotype co-efficient of variation for all the characters since they showed high heritability values. They concluded that there was enough scope for improvement of quantitative characters in brinjal by selection.

Singh *et al.* (1963) studied genetic divergence through D^2 statistics with 40 potato genotypes growing in 12 environments based on 13 characters. They searched the clustering pattern and their inter and intra-cluster distances taking 30 clusters using D^2 statistics. On the basis of stability, high yield and divergence among the genotypes, nine crosses were recommended as suitable for using in breeding program.

Gopimony *et al.* (1984) studied the analysis of data on total fruit yield/plant and 11 related traits from 27 *Solanum melongena* verities/ lines revealed that the phenotypic coefficient of variation ranged being highest for yield and single fruit weight, heritability and genetic advance being highest for single fruit weight and over all mean. The association of high heritability and genetic advance shown by yield, single fruit weight and fruit diameter was taken as an indication of additive gene effects.

Sidhu *et al*. (1981) evaluated 81 genotypes of potato for genetic divergence by using Mahalanobis's D^2 statistics. The 81 genotypes were grouped into six clusters of which cluster I was the largest accommodating 48 genotypes. The cluster VI had large genetic distance from the remaining clusters.

Bhutani *et al*. (1977) studied genetic variability in 17 brinjal genotype of diverse origin. The number of marketable fruits per plant and the total number of fruits per plant both had high genetic coefficient of variation and high estimates of heritability and genetic advance.

By the investigation of 29 genotypes of brinjal for the varietal variation in flower type Chadha and Saimbhi (1977) showed that all the genotypes bear flower cluster along with a solitary flower and the fruiting habit in a variety was not directly related to the occurrence of different flower types in cluster.

Mehrotra and Dixit (1973) observed a wide range of phenotypic variation for fruit yield, fruit length and plant height in 45 genotype of eggplant. High heritability accompanied by high estimates of genetic advance expressed as a percentage of the mean was observed for plant height and bottom girth of the fruit.

Genetic characters were studied in 36 different genotypes of brinjal by Mili *et al.* (2014) The genotypes showed significant differences for all the characters under study. High genetic coefficient of variation was observed for single fruit weight, fruit diameter, seed yield/ fruit, pulp seed ratio, total fruit yield/ plot, fruits/ plant, fruit yield/ plant and fruit length. Heritability estimates were high for fruit yield/ plant, pulp seed ratio, plant height, seed yield/ fruit, single fruit weight, fruits/ plant and fruit diameter.

Bhukya Ravi Nayak and P. K. Nagre. (2014) conduct a experiment comprised of 20 genotypes along with one check of brinjal and the experimental was laid out in randomized block design with three replications. Variability studies revealed that highly significant differences were recorded among the varieties for all characters. Correlation and path analysis revealed that fruit length, diameter, weight influenced the fruit yield in plant with high direct effect and significant positive correlation. Therefore, fruit length, diameter, weight are an important characters which may be included in selection criteria for improvement in fruit yield per plant.

2.2 Relationship between genetic and geographic diversity in brinjal

Genetic divergence is not always related to geographical diversity. The genotypic divergences among different genotypes for several characters were studied by plant breeders using Mahalanobis's D^2 statistic. They observed the characters namely yield contributed toward genetic divergence. They demonstrated that geographical isolation might not be the only factor causing genetic diversity; plant height, mature fruit, days to maturity contributed much to the total divergence.

The nature and magnitude of genetic divergence was assessed by Joshi *et al.* (2003) using nonhierarchical Euclidean cluster analysis in 73 tomato (*Lycopersicon esculentum* L.) genotypes of diverse origin for different quantitative and qualitative traits. Maximum value of coefficient of variability (53.208) was recorded for shelf life of fruits while it was minimum (69.208) for days to first picking. The grouping of the genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity.

Thirty four genotypes of brinjal (*Solanum melongena*) of diverse origin were evaluated by Sarma *et al.* (2000) in plots at Jorhat. Analysis of data on yield and its components grouped the genotypes into 10 clusters using Mahalanobis's D^2 statistic. Fruit circumference and average fruit weight were the main characters affecting grouping of genotypes. Eco-geographic diversity of the genotypes was not related to genetic diversity.

Investigation of twenty two potato genotypes (2 of subsp. andigena and the rest of subsp. tuberosum) were evaluated by Gopal *et al.* (1999) for ten morphological characters under four in vivo seasons (2 springs and 2 autumns) in the field. Mahalanobis's generalized intra and inter-group genetic distance and the distribution of genotypes into different clusters, led to the same conclusions under both in vitro and in vivo conditions. It appeared that genetic diversity was not related to geographic diversity while genetic distances were higher between tuberosum and andigena subspecies than within either tuberosum and andigena.

Information on genetic divergence of sweet potatoes (*Ipomoea batatas*) was reported by Naskar *et al.* (1996) from Meghalaya and Bastar, Madhya Pradesh, was derived from data on 8 quantitative characters in 18 genotypes using Mahalanobis's D^2 statistic. The genotypes were grouped into 7 different clusters. Cluster I had 8 genotypes, clusters II and III had 2 genotypes each, cluster IV had genetic divergence for yield contributing traits in sweet potato (*Ipomoea batatas*).

Yadav *et al.* (1996) studied genetic divergence using Mahalanobis's D^2 statistic in 40 diverse type of brinjal. The genotypes differed significantly for 10 yield contributing characters and were grouped in 9 clusters. They observed that there was no close correspondence between geographical distribution and genetic divergence.

Tambe *et al.* (1993) studied the diversity using D^2 analysis among 25 diverse genotypes of brinjal. The 25 genotypes were grouped into 5 clusters with substantial genetic divergence between them. They reported that geographical distribution did not necessarily follow clustering pattern.

Investigation on genetic diversity in 22 accessions of wild potato was done by Juned *et al.* (1988) from Paraguay and Argentina. They observed a close relationship between the geographical groups using Principal Component Analysis (PCA), Cluster Analysis and genetic diversity.

Genetic divergence using Mahalanobis's D^2 statistics and Canonical Analysis among 25 genotypes of tomatoes was studied by Petter and Rai (1976) found that genetic and geographical divergence was not related.

Several authors (Moll *et al.*, 1962; Timothy, 1963; Murty and Arunachalam,1966; Katiyar and Sing, 1990) could not find any direct relationship between geographic distribution and genetic divergence.

Muniappan *et al.* (2010) study on the genetic divergence was carried out to assess the variability, association, direct and indirect effects of eight morphological characters in thirty four eggplant (*Solanum melongena* L.) genotypes. High PCV and GCV were recorded different characters like as, number of branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight, and fruit yield per plant. All the characters were accompanied by high heritability and high genetic advance excepting days of 50 per cent flowering. The characters were mostly controlled by additive gene action, hence it could be inferred that simple selection will be effective for these characters

Ramesh *et al.* (2013) conducted an experiment which consisted of 54 genotypes. Fruit yield was kept as a dependent character and the results were analysed. Analysis of variance revealed that considerable variability among the genotypes for all the characters. High estimates of phenotypic and genotypic co-efficient of variation was observed in the parents and for fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant. The characters viz., fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant also recorded high magnitude of heritability coupled with genetic advance. Therefore, these traits should be kept in mind for better planning of improvement programme in Brinjal. The study further reveals that simple phenotypic selection could be effective for the improvement of aforesaid traits

2.3 Technique of multivariate analysis:

Genetic diversity analysis is mainly based on different multivariate techniques. During last decade different multivariate techniques have been developed which may be due to the improvement of computer. However, literature related to efficient multivariate techniques for genetic diversity analysis are reviewed in the following paragraphs:

It was reported by Dharmatti *et al*. (2001) that genetic diversity in a population of 402 tomato genotypes was assessed using multivariate analysis, in a field experiment carried out in Dharwad, Karnataka, India, during 1994-95. Observations were recorded for plant height, number of branches/plant, number of fruits per plant, yield per plant, incidence of tomato leaf curl virus (TLCV), and number of whiteflies per plant. The 402 genotypes were grouped into 4 clusters based on the similarities of D^2 values. Considerable diversity within and between the clusters was noted, and it was observed that the characters TLCV resistance, fruit yield per plant and number of whiteflies per plant contributed maximum to the divergence. Therefore, selection of divergent parents based on these characters may be useful for heterosis breeding in summer tomato.

Thirty six genotypes of potato were grown in 16 environments during 1991- 93, and were evaluated by Desai *et al.* (1997) for genetic divergence by Mahalanobis's D^2 statistic. Nine clusters were identified; I being the largest, accommodating 7 genotypes.

Cluster I, III, V, VI and VII showed larger genetic divergence. Genotypes in clusters III had the highest tuber yields and other characters like number of stems, number of leaves, maturity, shoot fresh weight, number of tubers, average tuber weight, sugar content and harvest index. Cluster I contained genotypes with high dry matter and starch contents, cluster IV those with dwarf plant height and early maturity and cluster VI those with high protein content. The genotypes differed significantly for all characters, suggesting a good scope of selection.

Estevez *et al.* (1994) reported that analysis of data on yield and its components from tests of 15 varieties enabled the varieties to be classified into 7 groups on the basis of genetic divergence (measured by values for the Mahalanobis's D^2 statistics). A group comprising Lipsi and Allrad and another comprising Simcoe showed the greatest divergence between themselves and from other types which suggested that they would be suitable for use as parents in breeding.

The influence of four types of genetic divergence on the vigour and variability of the progenies was studied in two field experiments at Fredericton, Brunswick, Canada reported by Loiselle *et al.* (1991). The measures of genetic divergence were (1) the progenies inbreeding coefficients; (2) the Mahalanobis's distances between the parents obtained from their agronomic traits. These measures of divergence were not significantly related. Canonical correlation analysis between the divergence parameters and vigour related traits produced significant relationships in one experiment only. The methods of estimating genetic divergence appeared to be a good predictor of either the mean on the variability of a progeny.

Birhman *et al.* (1991) found that genetic distance was evaluated by applying the D^2 statistic to data on 9 yield components in 26 potato genotypes comprising 9 elite varieties and 17 advanced breeding genotypes. Genotypes were grouped into 8 clusters, cluster I having 12 genotypes and the others between 1 and 4. Intercrossing of genotypes in clusters III, VI and VIII was thought the most advantageous in terms of tuber yield gain.

Peyne *et al.* (1989) reported that the hierarchical nature of the grouping into various number of classes could impose undue constrains and the statistical properties of the resulting groups were not at all clear. Therefore, they have suggested non-hierarchical classification as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. They also reported that the squared distance between means were Mahalanobis's D^2 statistics when all the dimensions were used, could be computed using Principal Coordinate Analysis (PCO). They also commended the Canonical Variate Analysis (CVA) for discriminatory purpose.

An experiment was conducted by Naskar *et al.* (1985) and reported that cluster analysis was applied to 9 characters in 22 diverse. Indian genotypes in 1981 and 1982, all genotypes were grouped into 9 clusters in both years although the clustering pattern was not consistent over the years. Genetically diverse (as estimated by Mahalanobis's D^2 statistic) use in crosses to give promising sergeants. High heterosis, it was suggested, could be achieved by crosses between members of distant clusters.

The use and the comparison of different multivariate techniques in classifying some important number of tomato genotype were reported by Balasch *et al*. (1984). Principal Component Analysis, as a simple multivariate technique, was compared with factorial analysis and Mahalanobis's D^2 distance. It was marked that three methods gave similar results. But factorial discriminate and Mahalanobis's D2 distance methods required collecting data plant by plant, while the PCA method required taking data by plots.

The coordinates obtained from the Principal Component Analysis (PCA) are used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al*. (1989). PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight line between each pair of points.

Genetic divergence among 19 eggplant genotypes was estimated by Quamruzzaman *et al*. (2009) using Mahalanobis's D^2 statistic. Altogether five clusters were formed. The highest intra-cluster distance was observed for cluster V (1.067) and the lowest for cluster III (0.916). The highest inter-cluster distance was observed between cluster IV and V (10.748). Cluster V recorded the highest mean for plant height at last harvest (cm), leaf blade length (cm), leaf blade diameter (cm), leaf pedicel length (cm), fruit pedicel length (cm), prickle on calyx. Whereas, number of branches per plant, fruit diameter (cm), individual fruit weight (g), fruit yield (t/ha) and prickle on fruit pedicel were in cluster II with the highest means.

An experiment was conducted by Saurabh *et al. (*2011) with 50 brinjal genotypes . The intra-cluster distance was minimum for cluster IV and maximum in cluster II. The maximum distance at inter-cluster level was between clusters I and clusters IV followed by II and IV which may serve as a potential genotypes for hybridization programme. On the basis of mean performance of different clusters, genotypes having high yield along with fruit diameter, fruit index and average fruit weight were observed in cluster V having genotypes like DBR-31 (Delhi), Green Long (Kalyani), KS-335 (Kalayanpur), G-190 (IARI, Delhi), DBR-8 (IARI, Delhi), SL-91-2 (Pantnagar), SL-190-10-12 (Panipat), Swarna Shree (Ranchi), ABR-1 (Anand) .

Genetic divergence in eighteen eggplant genotypes was studied by Uddin *et al*. (2014) using multivariate analysis. The 18 genotypes were grouped into four distinct clusters. 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 .

Through genetic diversity based on multivariate analysis, hundred brinjal accessions were grouped into eight clusters by Rabbani *et al.* (2014). 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.

Caguiat and Hautea (2014) conducted an experiment for genetic diversity sessment of 64 Philippine eggplant germplasm. The morphological trait and SSR data were analyzed as separate and combined data sets using principal component analysis PCA) and unweighted pair-group method with arithmetic averages (UPGMA) cluster analysis. This study provided significant information for the need to increase the present eggplant collection and to widen the genetic diversity of currently cultivated eggplant varieties in the Philippines.

Prokash *et al* (2008) reported high heritability (in broad sense) with high genetic advance in percentage of mean for number of fruits per plant, individual. fruit weight and plant height by conducting an experiment with 50 brinjal genotypes . However, yield per plant showed moderate heritability and low genetic advance but highest genetic advance as percentage of mean under selection

CHAPTER III

MATERIALS AND METHODS

3.1 Site of experiment

The study was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during the period from November, 2013 to April, 2014. The experimental site was at 900^0 22" E longitude and 230^0 41" N latitude at an altitude of 8.6 meters above the sea level.

3.2 Materials

A total of fifteen genotypes (15) of brinjal (Table 1) collected from local market and BARI was used in this experiment.

3.3 Soil and climate

The soil of the experimental plots was clay loam, land was medium high to medium high fertility level. The site was situated in the subtropical climate zone, wet summer and dry winter is the general climatic feature of this region. The robi season is generally rainless with moderate temperature and short day length. Meteorological data on rainfall, temperature, relative humidity from December 2013 to February 2014 were obtained from the Department of Meteorological centre, Dhaka-1207, Bangladesh. The selected plot was a medium high land. The pH of soil 4.66 to 5.93 while the amount organic carbon content, total N, available P and available K were 0.82%, 0.12%, 21 ppm and 0.27 mg per 100 gm of soil respectively

3.4 Design and Lay out

The experiment was laid out in Randomized Complete Block Design (RCBD) further sub divided into 15 genotypess where genotypes were randomly assigned. The plot size was 3m with single line. Row to row distance were 50 cm. The genotypes were distributed to each line with each block randomly

Table 1. Characterization of 15 brinjal genotypes

Geno type No.	**Name of the genotypes**	**Growth Habit**	**Hairiness**	**Fruit shape**	**Fruit color**	**Spiny character**
G1	Bolaka green	Erect	Leaf, Stem	Round	Whitish green	Fruit stock
G2	BD-2698	Semi erect	Leaf, Stem	Ovate	Whitish green	Stem, Fruit stock
G3	BD-2754	Semi erect	Leaf, Stem	Round	Whitish green	Stem, Fruit stock
G4	BD-2705	Spreading	Leaf, Stem	Ovate	Purplish green	Stem, Fruit stock
G5	BD-2775	Semi erect	Leaf, Stem	Round	Purplish green	Stem, Fruit stock
G6	BD-2791	Spreading	Leaf, Stem	Ovate	Whitish green	Stem
G7	BD-2796	Erect	Leaf, Stem	Round	Whitish green	Stem, Fruit stock
G8	Uttora hajari	Spreading	Leaf, Stem	Ovate	Violet	Fruit stock
G9	BD-2750	Spreading	Leaf, Stem	Round	Whitish green	Stem, Sepal
G10	BD-2662	Spreading	Leaf, Stem	Round	Violet	Fruit stock
G11	Plastid black beauty	Semi erect	Leaf, Stem	Round	violet	Stem, Fruit stock
G12	BD-2704	Erect	Leaf, Stem	ovate	purple	Fruit stock
G13	Sada begun	Erect	Leaf, Stem	ovate	White	Stem
G14	BD-2653	Erect	Leaf, Stem	long	Whitish purple	Fruit stock
G15	BD-2724	Semi erect	Leaf, Stem	Round	Whitish purple	Fruit stock

3.5 Land preparation

The experimental plot was prepared by ploughing with tractor followed by harrowing and laddering by cows. Weeds and stubbles were removed. Manures and fertilizers were applied as per the recommended dose before the final land preparation. Irrigation channels were made around each plot. The final land preparation was done on 30th November.

3.6 Manure and fertilizer

The crop was fertilized at the rate of 11 ton cowdung, 380 kg urea, 155 kg Triple Super Phosphate (TSP) and 260 kg Muriate of Potash (MP) per hectare. At this recommended rate 1.0 ton cowdung, 31 kg urea, 12 kg TSP and 19 kg MP were applied into the experimental plots. The half amount of cowdung was applied during final land preparation. The rest amount of cowdung, entire TSP and 1/3 Urea and 1/2 of MP were applied before transplanting the seedling. The rest of the urea and MP were applied at three equal installments- the first top dressing was done at 21 days after transplanting and second and the third was done respectively at 35 and 55 days after transplanting.

3.7 Raising of seedling

Individual seed bed was prepared for different varieties following standard method of bed preparation. Seed were sown in lines in well prepared seed beds in the evening of 1st November, 2013. The seeds were sown at about 1.25 cm depth and were covered uniformly with light soil for proper germination. Heptachlor was duster over the seedbed to prevent the seedling mainly from ant attack. Adequate measures were taken so as to avoid varietal mixture. The seed bed was watered as and when necessary for proper germination as well for normal growth of the seedling. After germination shading was arranged to protect the young seedling from scorching sunshine and was kept exposed during night, morning and afternoon. Proper nursing was done for developing healthy seedlings. At the attainment of 45 days of sowing the seedlings were ready for transplanting.

3.8 Transplanting of seedlings

Twenty eight days old seedlings were transplanted in well prepared experimental plot on 15th January, 2014. 3 plants were planted for each genotype in single row of 3 m length in each replication maintaining plant spacing of 50 cm and row to row distance 80 cm. Field view of the experiment was shown in Plate 1.

3.9 Intercultural operations

Intercultural operations such as weeding, mulching, irrigation etc. were done when necessary for proper growth and development of the plants. But no insecticide was used to study the resistance capacity of the genotype against fruit and shoot borer. Proper shadings were given in the morning at the first stage of transplanting to protect the young seedlings from scorching sunshine during day time. Shadings were removed at the afternoon. Extra soils were added around the root for proper rooting. Sticks were given to protect the plant from falling due to strong wind. Gap filling was done twice, firstly 11 days after transplanting and 2nd time 23 days after transplanting. Weeding was done for the first time 18 days after transplanting. Weeding was also done in several times by two weeks interval. In the early stage of transplanting watering was done twice a daily by water cane. In mature stage, flood irrigation was done to the field.

3.10 Data collection

Three plants were selected for each genotype from every replication and tagged properly at random from each row for recording data. Data on days to first flowering,, fruit color, fruit shape, plant height, no. of primary branches/plant, fruit length, fruit diameters, fruit per plant, weight per fruit, yield per plant, percent insect infestation were recorded.

Plate 1. Field view of the experiment

3.10.1 Growth habit

Plant growth characters were recorded according to their canopy, branches, dwarf ness and erect habit.

3.10.2 Hairiness

The presence of hairiness on leaf, stem was recorded.

3.10.3 Plant height (cm)

Length of main stem from ground level to the tip of the stem was measured at final harvest.

3.10.4 Days to first flowering

Days from sowing to first flowering of every plant of every genotypes was recorded.

3.10.5 Spiny character

The spinyness of leaf, stem, and fruit of the brinjal plants was recorded.

3.10.6 Color of fruit

Fruit color of the 15 brinjal genotypes was recorded.

3.10.7 Shape of fruit

The fruit of different genotypes showed differences in shape. The shape of fruit was recorded.

3.10.8 Fruit length (cm)

Length from the top to the bottom of 5 initially matured fruits per plant was recorded.

3.10.9 Fruit diameter (cm)

Measured along the middle part of the harvestable mature fruits.

3.10.10 Number of primary branches per plant

Number of primary branches of each randomly selected plant was recorded.

3.10.11 Number of fruits per plant

Total number of fruits harvested from individual plant was recorded.

3.10.12 Weight of fruit (g)

Weight of individual fruit per plant was recorded.

3.10.13 Yield per plant (g)

Total fruits harvested from each selected plant in each replication were weighted together and yield per plant was recorded.

3.10.14 Insect infestation

Brinjal genotypes were affected by shoot and fruit borers. Numbers of infected fruits were counted. The rate of insect infestation against different genotypes was calculated in percentage.

3.11 Statistical analysis

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Selection of parents in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are efficient method of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. For univariate analysis of variance, analysis was done individually and least of significance was done by F- Test (Pense and Shukhatme, 1978). Mean, range, co-efficient of variation (CV) and correlation was estimated using MSTAT computer program. Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT program.

Peyne *et al.* (1989) reported that the hierarchical nature of the grouping into various number of classes could impose undue constrains and the statistical properties of the resulting groups were not at all clear. Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. They also reported that the squared distance between means were Mahalanobis's D^2 statistics when all the dimensions were used, could be computed using Principal Coordinate Analysis (PCO). They also commended the Canonical Variate Analysis (CVA) for discriminatory purpose.

3.11.1 Principal Component Analysis (PCA)

Principal Component Analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters. It can be done from the sum of squares and products matrix for the characters. Principal components were computed from the correlation matrix and genotype scores obtained for the first components and succeeding components with latent roots greater than unity (Jeger *et al.,* 1983). Contributions of different morphological characters towards divergence were discussed from the latent vectors of the first two principal components.

3.11.2 Principal Coordinate Analysis (PCO)

Principal Coordinate Analysis is equivalent to PCA but is used to calculate inter unit distances. Through the use of all dimensions of P it gives the minimum distance between each pair of the N points using similarity matrix (Digby *et al.,* 1989).

3.11.3 Clustering

To divide the genotypes of a data set into some number of mutually exclusive groups clustering was done using non- hierarchical classification. In GENSTAT, algorithm was used to search for optimal values of chosen criteria which proceed as follows:

Starting from some initial classification of the genotypes in required number of group, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion when no further transfer could be found to improve the criterion. The algorithm switched to a second stage, which examined the effect of swapping two genotypes of different classes and so on.

3.11.4 Canonical Variate Analysis (CVA)

Canonical Variate Analysis complementary to D^2 statistic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical Variate Analysis computed linear combination of original variability that maximized the ratio between ground and within group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation sequentially maximized the ratio of the groups to within group variations.

3.11.5 Cluster diagram

A cluster diagram was drawn using the values (D^2) of intra and inter- cluster distance. The diagram represented the brief idea of the pattern diversity among the genotypes and relationships between different genotypes included in the cluster.

CHAPTER IV

RESULTS AND DISCUSSION

The availability of transgressive segregants in breeding program depends upon the divergence of the parents. So, the accurate information on the nature and degree of diversity of the parents is the pre-requisite of an effective breeding program. The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to screen better materials. Therefore, to generate information in the degree of diversity fifteen genotypes of brinjal were raised in the growing season of 2013-2014 at the field of Sher-e-Bangla Agricultural University, Dhaka. The data in respect of plant height, days to first flowering, fruit shape, fruit color, fruit size etc. were recorded and analyzed and presented in this chapter.

4.1 Morphological characterization of brinjal

4.1.1 Growth habit

Plant architecture is an important character to the breeders for improvement of plant ideotype under given environment. The genotypes studied have been grouped into three distinct characteristics. The genotype 4,6,8,9 and 10 were spreading; genotype 1, 7,12,13 and 14 were erect in plant growth habit and rest of the genotypes were semi erect in growth habit (Table 1). Generally farmers are looking for semi erect plant type to accommodate more plants per unit area to obtain higher yield. These types of materials are suitable for intercultural operation in the field.

4.1.2 Hairiness

Hairiness is an important character of brinjal plant. This character is related to its resistance against pest. The more densely hairy plant is more resistance against pest. All the genotypes under study were characterized with hairiness (Table 1). Hairiness was observed mostly at leaf and stem.

4.1.3 Shape of fruit

It is also an important consumer preference trait in brinjal marketing. Various types of brinjal were found according to their shape. From the 15 genotypes long, ovate, round shaped brinjal was observed. The genotype 14 only produced long fruits, genotype 2,4,6,8,12,13, produced ovate fruits, the rest of the genotypes produced more or less round fruits (Table 1).

4.1.4 Color of fruit

Fruit color is an important consumer preference trait in brinjal marketing. Generally green and violet color fruits are common in the market. However, a lot of variations in fruit color were found in the present study and that could be classified in distinct groups: violet, white, whitish green, purplish green ,whitish purple ,violet, purple. The violet genotypes were 8,10 and 11; purple genotypes was 12; whitish purple were 14 and 15; purplish green ware 4,5; white genotype was 13 and the rest of the genotypes were whitish green (Table 1). This variation offered a good scope for breeding consumer preference attributes.

4.1.5 Spiny character

Various types of brinjal genotypes are characterized by their spinyness. It is an important character which is related to insect resistance. Different genotypes were classified having spine in their fruit, stem or leaves. The genotype 6, 13 had spine in stem, the genotypes 1,8,10,12 having in fruit stock. The genotype 9 having spine in stem and sepal. But the fruit stock and stem of the rest of the genotypes were spiny (Table1).

4.1.6 Plant height

The plant height of different genotypes exhibited wide variation (Table 2). The plant height was maximum in genotype 13 (71.33 cm), which was identical to 1 (71.00 cm), 5 (70.33 cm). The genotype 4 (47.33 cm) produced the shortest plant type which was more or less identical to genotype 6 (53.00 cm) and 15 (55.33) The remaining genotypes were intermediate in this regard (Table 2)Statistically genotype 13 produce the tallest plant then rest of the genotype (Table-4).

Mandal and Dana (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that fruits/plant, secondary branches/plant and plant height are important traits for the selection of superior genotypes

4.1.7 Days to first flowering

Wide range of variability was observed in respect of flowering time among the genotypes. The genotype 13 took the shortest time (52 days) which is identical to genotype 12,8,15 for flowering from seedling while the genotype 8 took the longest time (82 days) to flower which is identical to genotype 14 (71.33 days) (Table 2). The difference among the genotypes might be related to the genetically characteristics of the genotypes, influence of day length and temperature. The genotype 13 took the shortest time (52 days) and the genotype 8 took the longest genotype (82 days) to flower (Table 4).

Sambandam (1960) studied the number of days required for flowering in different brinjal genotypes and concluded that the variation was due to the varietal characteristics.

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4.1.8 Number of primary branches per plant

Number of primary branches is an important morphological character which is related to yield and number of fruit per plant. The number of primary branches each plant was recorded and their average mean was calculated. It was observed that the maximum numbers of primary branches were produced by the genotype 8 (8) and genotype 10 (8) which was more or less identical to genotype 3 (6.33) and genotype 15 (6.67). The genotype 7 (2.67) produced the least number of primary branches which was more or less identical to genotype 2 (3.33), 4 (3.33) and genotype 9 (4.00) (Table 2).). Genotype 8 and genotype 10 was statistically better from the rest of the genotype. (Table-4)

Randhawa *et al.* (1993) studied 22 genotypes of brinjal on 24 quantitative characters for deriving information on yield co-relation and observed that fruits/plant and number of branches/plant had the highest direct effect on yield.

4.1.9 Fruit length (cm)

The average marked difference among the genotypes was observed. The fruits of the genotype 4 (11.oo cm) and genotype 14 (11.00) were found to be the longest followed by the genotype, 7(8.33) 3 (8.17 cm) and 2 (8.3 cm) . The genotype 10 produced the shortest fruit (4.67 cm) (Table 2). The differences in the average length of fruits of different genotypes of brinjal were statistically significant (Table 3). The genotype 4 and 14 produced the longest fruit while the smollest fruit was produced by the genotype 10.The co-efficient of variation of this trait was 11.75 % (Table -4).

4.1.10. Fruit diameter (cm)

The average diameter of fruit showed marked difference among themselves. In respect of diameter, the experimental data showed that the fruit of 13 was round to be widest (20.3cm) followed by 8 (19.20),2 (18.70), 1 (16.67 cm).The lowest diameter was observed in genotype 12 (10.77 cm) which was more or less identical with genotype 6 (11.33) and genotype 14 (11.10) (Table 2). The differences in the average diameter of fruits of different genotypes of brinjal were statistically significant (Table 3). The co-efficient of variation of this trait was 7.76% (table-4)

4.1.11. Fruit weight (g)

Fifteen different brinjal genotypes under study showed variations in their fruit weight. The genotype 15 was found to have the highest fruit weight (111.80 g) which was statistically superior to the rest of the genotypes while genotype 8 produced the second highest fruit weight (102.20 g) (Table 2) which was also statistically significant from the rest of the genotypes (Table 3). The least individual fruit weight was produced by 14 (15.57 g) while the other genotypes took intermediate positions though there were statistical differences among themselves.

Table 3. Analysis of variance for nine characters of brinjal

Sorces of variation	**Df**	**Mean sum of square**								
		Plant height (cm)	**DFF**	**BPB**	**FPP**	**FD (cm)**	**FL (cm)**	**WPF (g)**	**YPP (kg)**	**PII**
Replication	2	1.089	18.156	0.067	6.959	0.691	0.471	4.851	0.001	1.087
Genotypes	14	159.079**	169.317**	7.752**	280.698**	28.752**	9.825**	2358.383**	1.400**	111.188**
Error	28	4.994	3.989	0.590	4.956	1.449	0.815	2.902	0.0004	5.461

*= Significant at 1 % level of probability, **= Significant at 5 % level of probability, df = Degree of freedom, DFF = Days to first flowering, PH= Plant height, NPB =No. of primary branches, FL =Fruit length, FD =Fruit diameter, DFH =Days to first harvesting, WPF =Fruit weight, FPP =fruit per plant, YPP =Yield per plant, PII =% Insect infestation

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4.1.12. Number of fruit per plant

The number of fruits produced by different brinjal genotypes were recorded and presented in Table 2. It was revealed that the maximum number of fruits were produced by the genotype 6 (45.67) which were statistically superior to the rest of the genotypes. The genotype 10 produced second highest number of fruit per plant (28.00), which was also statistically different from the rest of the genotypes. The genotype 8 produced the least number of fruits(3.00) while the other genotype took intermediate positions and they were statistically different among themselves.

Sarma *et al.* (2000) evaluated thirty four genotypes of brinjal (*Solanum melongena*) of diverse origin were in plots at Jorhat and reported that fruit circumference and average fruit weight were the main characters affecting grouping of genotypes.

The differences in respect of number of fruits produced per plant might be due to genetical characteristics of the genotypes. Sambandam (1960) recorded the number of fruit per plant of different genotype of brinjal and reported that the number varied from variety to variety due to the difference in their yield potential.

In brinjal, it has been reported that there is a strong association between the number of fruits per plant and yield per plant (Srivastava and Sachan, 1973 and Hiremath and Gururaja, 1974). Similarly path analysis in brinjal was conducted by Srivastava and Sachan (1973) and Vijoy *et al.* (1978) showed that the number of fruits per plant exhibited maximum direct effects on yield. It is therefore to be considered useful to select the best variety of brinjal on the basis of number of fruits per plant for effective improvement of this crop.

4.1.13 Yield per plant (g)

Fifteen different brinjal genotypes under study showed wide variation in their fruit yield per plant. The genotype 6 was found to give the highest yield per plant. This genotype produced fruits 2.78 kg/plant on the average, followed by 15 (2.42 kg/plant), 1 (1.52 kg/plant), while the lowest yield was recorded in variety 13 (0.23 kg/plant) (Table 2). This trait was also statistically significant from the rest of the genotypes (Table 3). The co-efficient of variation of this trait was 1.71% (Table-4).

Ahmad (1968) and Siddique (1968) obtained similar results while carrying out experiments with different varieties/genotypes in Bangladesh. Ahmad (1968) reported that the variety Nayankazal tended to out yield all other varieties/genotypes including Islampur and D.R.C. while Siddique (1968) obtained superiority of Singnath over Islampuri.The result obtained in the experiment under review tended to differ to some extent with there as referred above. These differences might be due to environmental factors and for the use of different germplasms. Experimental data showed that no. of fruit per plant was influenced by the individual fruit weight. The genotype 6 produced maximum number of fruits (45.6) per plant but its individual seed weight is low (60.93) (Table 2). Yield was influenced by both the no. of fruit per plant and individual fruit weight. The individual seed weight of genotype 14 was highest (111.80 g) and fruit per plant was low (21.67) and it produced highest yield. Sambandam (1960) and Siddique (1968) also obtained similar results.

Siddique and Husain (1971) obtained the highest yield (280 t/ha) from the variety Singnath followed by khotkhotia and Islampuri in Mymensingh areas. Sarker and Haque (1980) recorded the highest yield from Japani (29.0 t/h) followed by Khotkhotia (22.3 t/ha) in Ishuridhi area and Ahmed *et al.* (1983) reported Singnath as the highest yielder (38.5 t/ha) followed Japani (30 t/h), D. R. Chowdhury (25.5 t/ha) and Khotkhotia (22.9 t/ha) at Jamalpur areas. The yield difference within the cultivars observed in different investigations was possibly due to agro-climatic variations and effect of different germplasm.

4.1.14. Insect infestations

Brinjal is mostly affected by shoot and fruit borer. It caused great harm to yield and reduced production of brinjal. So resistance is an efficient character of brinjal plant. Their rates of attack against different genotypes were significantly different. The attack of insect of brinjal depend on its morphological i.e. spinyness, hairiness, hardiness of fruit coat; physiological and genetical characteristics of plant. The different genotypes are genetically different from each other. From under study it was revealed that the genotype 8 (36.63%) was highly affected and the genotype 13 (12.93) was least affected which mentioned that the genotype 13 was the most resistant and superior to the rest of the variety (Table 2).

Dharmatti *et al.* (2001) reported that genetic diversity in a population of 402 tomato genotypes was assessed using multivariate analysis. Observations were recorded for plant height, number of branches/plant, number of fruits per plant, yield per plant, incidence of tomato leaf curl virus (TLCV), and number of white flies per plant. Considerable diversity within and between the clusters was noted and it was observed that the characters TLCV resistance, fruit yield per plant and number of whiteflies per plant contributed maximum to the divergence. Therefore, selection of divergent parents based on these characters may be useful for heterosis breeding in summer tomato.

4.2 Variability among brinjal genotypes

Analysis of variance showed that the brinjal genotypes varied significantly (1 % level of probability) with each other (Table 3). Range, mean and co-efficient of variation of nine characters of brinjal genotypes namely days to first flowering, plant height (cm), no. of primary branches/plant, no, fruit length, fruit diameter, individual fruit weight, number of fruit per plant, yield per plant, present of insect infestation have been presented in Table 4. The mean values of above parameters were 62.89 days, 62.55 cm, 5.13, 7.69 cm, 15.51 cm, 68.71 g, 19.89, 1.25 kg , 20.98 respectively and the co-efficient of variation of the above parameters were 3.57, 3.18, 14.97, 11.75, 7.76, 2.48, 11.19, 1.71, and 11.14 % respectively which indicated the existence of considerable variation existing among the genotypes.

Table 4. Range, mean, standard error and co-efficient of variation for nine characters of brinjal

Characters	Minimum	Maximum	Mean ± SE	CV%
Plant height (cm)	47.33	71.33	62.55±7.28	3.57
Days of 1st flowering	52.67	82.33	62.89±7.51	3.18
Number of primary branch	2.67	8.00	5.13±1.61	14.97
Number of fruits per plant	3.00	45.67	19.89±9.67	11.19
Fruit diameter (cm)	10.77	20.03	15.51±3.10	7.76
Fruit length (cm)	4.67	11.00	7.69±1.81	11.75
Fruit weight (g)	15.57	111.80	68.71±28.03	2.48
% insect infestation	12.93	36.63	20.98±6.09	11.14
Yield per plant (kg)	0.23	2.78	1.25±0.68	1.71

4.3 Diversity of the brinjal genotypes

Genetic diversity was analyzed using GENSTAT software program. Genetic diversity analysis involves several steps, i.e., estimation of distance between the varieties, clustering and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001; Juned *et at.*, 1988 and Ario, 1987). In the analysis of genetic diversity in brinjal multivariate techniques were used.

4.3.1 Construction of scatter diagram

Based 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, which has been presented in Figure1. 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.

4.3.2 Principal Component Analysis

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 contribution of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal component. The Principal Component Analysis yielded Eigen values of each Principal Component axes with the first axes totally accounting for the variation among the genotypes, while four of these with Eigen values above unity accounted for 80.94%. The first three Principal axes accounted for 67.54% of the total variation among the 9 characters describing 15 genotypes (Table 5). Based on Principal Component axes I and II, a two dimensional chart (Z_1-Z_2) of the cultivars are presented in (Figure 1). The scattered diagram revealed that apparently there were mainly five clusters

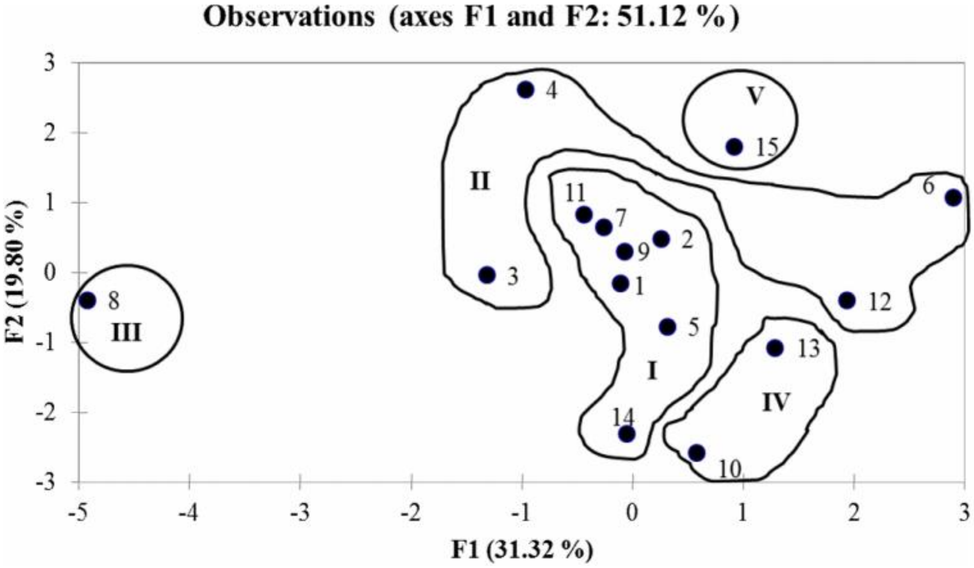

Figure 1. Scattered distribution of fifteen brinjal genotypes on principal component score superimposed with clustering

Table 5. Eigen values and percentage of variation in respect of nine characters in brinjal

Principal component axis	Eigenvalues	% of total variation accounted for	Cumulative %
I	2.82	31.32	31.32
II	1.78	19.80	51.12
III	1.48	16.42	67.54
IV	1.21	13.40	80.94
V	0.54	6.03	86.97
VI	0.48	5.35	92.33
VII	0.44	4.87	97.20
VIII	0.24	2.70	99.90
IX	0.01	0.10	100.00

Balasch *et al.* (1984) reported the use and the comparison of different multivariate techniques in classifying some important number of tomato varieties/genotypes. It was marked that three methods gave similar results. But factorial discriminate and Mahalanobis's D^2 distance methods required collecting data plant by plant, while the PCA method required taking data by plots.

Among five clusters, cluster I was composed of seven genotypes: 1,2,5,7,9,11 and 14. From the clustering mean value (Table 9), it was observed that cluster I produced the highest mean for plant hight (65.57 cm), second highest mean of fruit length (7.73 cm), insect infestation (20.86 %) and the second lowest value for days of first flowering (62.95 days), . Cluster II was composed of four genotypes; 3,4,6,12. These genotypes produced the highest mean of length of fruit (8.63 cm), 2nd highest mean for fruits per plant (22.75), yield per plant (1.60 kg), and their 2nd lowest mean values for primary branch per plant (4.67), plant height (57.67 cm) and their lowest mean values for fruit diameter (13.57 cm). Cluster III was constituted of genotype 8. The genotype of this cluster produced the highest mean for branch per plant (8.00), fruit diameter (19.20 cm), days of first flowering (82.33 days),present of insect infestation (36.63 %) and second highest value for fruit weight (102.20 g) and also lowest value for fruit per plant (3.00), length of fruit (6.33 cm). Cluster IV constituted of two genotype, genotype 13 and 10. The genotype produced the highest mean for fruit per plant (27.83), second highest mean for plant height (64.50 cm),fruit diameter (16.45 cm), and the lowest mean values for length of fruit (6.33 cm),days to first flower (57.50 days),fruit weight (30.08 g), present of insect infestation (15.83 %) and second lowest mean for yield per plant (0.83 kg). Cluster V constituted of one genotypes; genotype 15. The genotype of this cluster produced the highest mean values for fruit weight (111.83 g), yield per plant (2.42 kg), second highest mean value for length of fruit (7.67 am), and lowest mean values for plant height (55.33 cm), days to first flower (55.57 days).

Joshi *et al*. (2003) assessed the nature and magnitude of genetic divergence using non hierarchical Euclidean cluster analysis in 73 tomato genotypes of diverse origin for different quantitative and qualitative traits. Maximum value of coefficient of variability (53.208) was recorded for shelf life of fruits while it was minimum (69.208) for days to first picking. The grouping of the genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity.

Dharmatti *et al.* (2001) reported that genetic diversity in a population of 402 tomato genotypes was assessed using multivariate analysis. The 402 genotypes were grouped into 4 clusters based on the similarities of D^2 values. Considerable diversity within and between the clusters was noted, and it was observed that the characters TLCV resistance, fruit yield per plant and number of whiteflies per plant contributed maximum to the divergence. Therefore, selection of divergent parents based on these characters may be useful for heterosis breeding in summer tomato.

It was observed that all the cluster mean values for plant height, days to first flower, days to first harvest, fruit length, fruit diameter, number of fruits per plant, individual fruit weight were more or less similar. Information on genetic divergence of sweet potatoes was reported by Naskar *et al.* (1996). The genotypes were grouped into 7 different clusters. Cluster I had 8 genotypes, clusters II and III had 2 genotypes each, cluster IV had genetic divergence for yield contributing traits in sweet potato. Cluster IV and V included mainly early flowering and early maturing genotypes with high yield. The maximum ranges of variability were observed for yield (398.61 g to 1416.23 g) among all the characters in five clusters. Genetic divergence among 20 cultivars of brinjal (*Solanum melogena*) was estimated by Mishra *et al.* (1998) using D^2 statistics for eleven yield traits. The cultivars were grouped into 7 clusters. Maximum genetic distance was found between clusters IV and VI followed by that between clusters I and IV, suggesting wide diversity among these groups. Considering cluster means and the genetic distances, the crosses of the cultivar of cluster VI (A-I) with the cultivars of clusters I and IV were likely to recombine the genes for high yield. So, to develop high yielding varieties/genotypes, genotypes cluster IV and V can be used in hybridization program. Number of fruits per plant, fruit length, fruit diameter and individual fruit weight contributed maximum towards yield improvement.

Desai *et al.* (1997) evaluated thirty six genotypes of potato for genetic divergence by Mahalanobis's D^2 statistic. Nine clusters were identified; I being the largest, accommodating 7 genotypes. Cluster I, III, V, VI and VII showed larger genetic divergence. Genotypes in clusters III had the highest tuber yields and other characters like number of stems, number of leaves, maturity, shoot fresh weight, number of tubers, average tuber weight, sugar content and harvest index. Cluster I contained genotypes with high dry matter and starch contents, cluster IV those with dwarf plant height and early maturity and cluster VI those with high protein content. The genotypes differed significantly for all characters, suggesting a good scope of selection. Generally, diversity was influenced by the morphological characters which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performance genotypes 6, 13, 14 and 15 may be considered suitable parents for efficient hybridization in future.

4.3.3 Principal Coordinate Analysis

Inter-genotypic distances as obtained by Principal Coordinate analysis for selective combination showed that the highest distance (5.13) was observed between the genotype 6 and 14, followed by 8 and 12 (5.11) and the lowest distance was observed between 3 and 6 (4.51) followed by 4 and 8 (4.54), 6 and 7 (4.59) (Table 6).

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 7) as suggested by Singh *et al.* (1977). Cluster II which showed the highest intra-cluster distance (22.82) composed of seven genotypes and cluster IV showed the lowest intra-cluster distance (13.83) composed of 1 genotypes which indicated within group diversity of the genotypes was maximum in cluster II and minimum in cluster Iv. The coordinates obtained from the Principal Component analysis (PCA) are used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al*. (1989). PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight genotype between each pair of points.

Table 6. Inter-genotypic distance (D^2) of some genotypes of different clusters

Between genotypes	**Distance (D^2)**	**Between genotypes**	**Distance (D^2)**
1-4	4.72	6-15	4.91
1-10	4.74	7-8	4.58
2-10	4.91	7-12	4.61
3-6	4.51	7-15	4.67
4-5	4.97	8-9	4.85
4-8	4.54	8-10	4.63
4-10	4.89	8-12	5.11
4-13	4.75	8-13	4.87
4-14	4.93	8-14	5.02
4-15	4.94	8-15	5.08
5-13	4.77	9-14	4.72
5-14	4.54	9-15	4.80
5-15	4.67	10-14	4.77
6-7	4.59	10-15	5.06
6-8	5.01	11-14	4.76
6-9	4.94	12-14	4.66
6-10	4.73	12-15	4.76
6-12	4.60	13-14	5.01
6-13	4.97	13-15	4.82
6-14	5.13	14-15	4.93

Table 7. Average intra and inter-cluster distances (D^2) for 15 brinjal genotypes

	I	II	III	IV	V
I	**18.29**				
II	19.22	**22.82**			
III	49.11	41.20	**0.00**		
IV	35.33	49.99	82.92	**13.83**	
V	50.59	34.04	39.72	82.62	**0.00**

*Bold figures denotes intra-cluster distance

4.3.4 Canonical Variate Analysis

Canonical Variate Analysis was performed to compute the inter-cluster Mahalanobis's values. Statistical distances represent the index of genetic diversity among the clusters. The average intra and inter-cluster distance (D^2) values were presented in Table 7. Results indicated that the highest inter-cluster distance was observed between III and IV (82.92), followed by between IV and V (82.62), I and V (50.59). The lowest inter-cluster distance was observed between the cluster I and II (19.22) followed by II and V (34.04), I and IV (35.33) suggesting a close relationship among these clusters (Figure 2). The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 6 and Figure 2). Islam *et al*, (1995) obtain larger inter-cluster distances than the intra-cluster distances in a multivariate analysis.

However, the maximum inter-cluster distance was recorded between cluster III and IV (82.92) followed by between V and IV (82.62). Genotypes from these clusters if involved in hybridization might produce a wide range of segregating population, as genetic variation was very distinct among these groups. The inter-cluster divergence varied from 22.82 to 13.83 maximum being from cluster II which comprised of four cultivars of diverse origin, while the minimum distance was observed in cluster IV which comprised only two genotypes.

Results obtained from different multivariate techniques were superimposed in Figure 1 from which it might be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one. The clustering pattern of the genotype revealed that varieties/genotypes originating from the same places did not form a single cluster because of direct selection pressure.

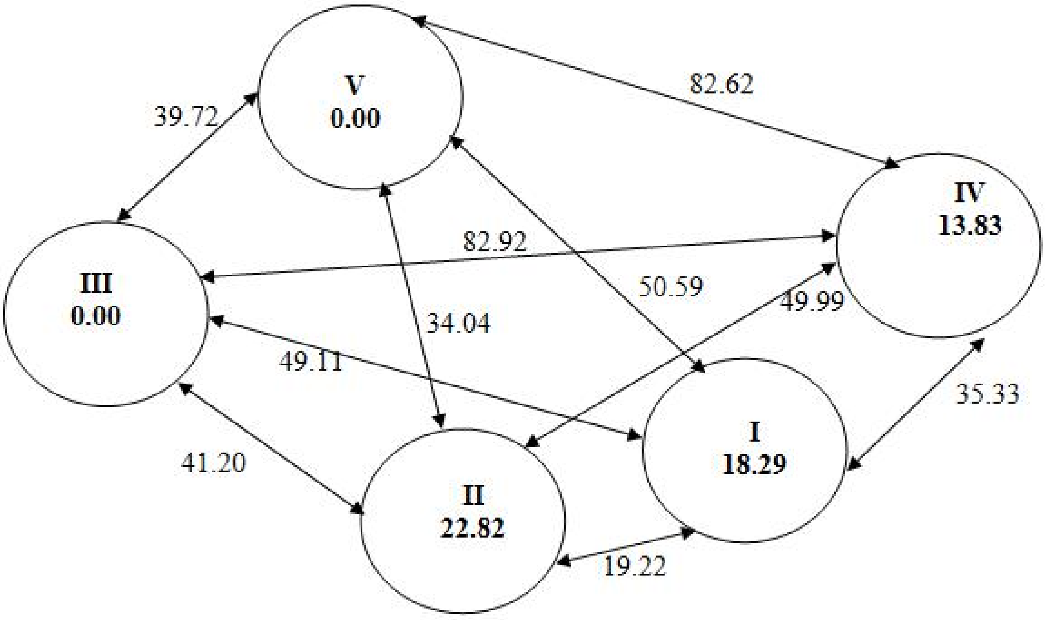

Figure 2. Diagram showing inter-cluster (outside the circle) and intra-cluster (inside the circle) distances of fifteen genotypes of brinjal

It has been observed that geographic diversity is not always related to genetic diversity and therefore, it is not adequate as an index of genetic diversity. Murty and Arunachalam (1966) studied that genetic drift and selection in different environment could cause greater diversity than geographic distance.

Furthermore, there is a free exchange of seed material among different region as a consequence, the characters constellation that might be associated with particular region in nature loose their individuality under human interference and however, in some cases effect of geographic origin influenced clustering that is why geographic distribution was not the sole criterion of genetic diversity. The free cluster of the genotypes suggested dependence upon directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices would favour constancy of the associated characters. This would suggest that it was not necessary to choose diverse parents for diverse geographic regions for hybridization.

4.3.5 Non – hierarchical clustering

The computation from co-variance matrix gave non-hierarchical clustering among 15 genotypes. By application of non- hierarchical clustering using covariance matrix, the 15 brinjal genotypes were grouped into five different clusters. These results confirmed the clustering pattern of the genotypes according to the Principal Component Analysis. So, the results obtained through PCA were confirmed by non-hierarchical clustering. Compositions of different clusters with their corresponding genotypes included in cluster were presented in Table 8. Cluster I had maximum seven genotypes followed by cluster II, and IV, which had four and two genotype and cluster III and V had single genotype respectively.

Joshi *et al.* (2003) assessed the nature and magnitude of genetic divergence using non hierarchical Euclidean cluster analysis in 73 tomato (*Lycopersicon esculentum*) genotypes of diverse origin for different quantitative and qualitative traits. Maximum value of coefficient of variability (53.208) was recorded for shelf life of fruits while it was minimum (69.208) for days to first picking. The grouping of the genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity.

cluster I was composed of seven genotypes: 1,2,5,7,9,11 and 14. From the clustering mean value (Table 9), it was observed that cluster I produced the highest mean for plant hight (65.57 cm), second highest mean of fruit length (7.73 cm), insect infestation (20.86 %) and the second lowest value for days of first flowering (62.95 days) . Fruit type of the different genotypes of this cluster has been presented in Plate 2.

Mandal and Dana (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that fruits/plant, secondary branches/plant and plant height are important traits for the selection of superior genotypes.

Cluster II was composed of four genotypes; 3,4,6,12. These genotypes produced the highest mean of length of fruit (8.63 cm), 2nd highest mean for fruits per plant (22.75), yield per plant (1.60 kg), and their 2nd lowest mean values for primary branch per plant (4.67), plant height (57.67 cm) and their lowest mean values for fruit diameter (13.57 cm). Fruit type of this cluster has been presented in Plate 3.

Table 8. Distribution of 15 brinjal genotypes in five different clusters

Cluster	Total no. of genotype	Name of genotypes
I	7	1,2,5,7,9,11, 14
II	4	3,4,6,12
III	1	8
IV	2	10,13
V	1	15

Table 9: Cluster mean for 9 characters of 15 genotypes of eggplant

Cluster	Plant height (cm)	Branch per plant (no.)	Fruits per plant (no.)	Fruit diameter (cm)	Fruit length (cm)	Days to 1st flower	Yield per plant (kg)	Fruit weight (g)	% insect infes-tation
I	65.57	4.29	18.14	15.98	7.73	62.95	1.14	63.09	20.86
II	57.67	4.67	22.75	13.57	8.63	62.42	1.60	78.70	20.38
III	64.33	8.00	3.00	19.20	6.33	82.33	0.31	102.20	36.63
IV	64.50	6.83	27.83	16.45	6.33	57.50	0.83	30.08	15.83
V	55.33	6.67	21.67	14.50	7.67	55.67	2.42	111.83	18.90

G 1

G 2

G 5

G 7

G 9

G 11

G 14

Plate 2. Fruit type of the different genotypes of cluster I

G 3

G 4

G 6

G 12

Plate 3. Fruit type of the different genotypes of cluster II

G -8

Plate 4. Fruit type of the different genotypes of cluster III

Cluster III was constituted of genotype 8. The genotype of this cluster produced the highest mean for branch per plant (8.00), fruit diameter (19.20 cm), days of first flowering (82.33 days), present of insect infestation (36.63 %) and second highest value for fruit waight (102.20 g) . Fruit type of the genotype of this cluster has been presented in Plate 4.

Cluster IV constituted of two genotype, genotype 13 and 10. The genotype produced the highest mean for fruit per plant (27.83), second highest mean for plant height (64.50 cm),fruit diameter (16.45 cm). Its fruit type has been presented in Plate 5.

Cluster V constituted of one genotypes; genotype 15. The genotype of this cluster produced the highest mean values for fruit weight (111.83 g), yield per plant (2.42 kg), second highest mean value for length of fruit (7.67 am). Its fruit type has been presented in Plate 6 .

Observing the class mean value it was observed that all the cluster mean values for plant height, days to first flower, fruit length, fruit diameter, number of fruits per plant, individual fruit weight were more or less similar. The maximum range of variability was observed for yield (o.31 kg to 1.60 kg) among all the characters in five clusters. Cluster IV and V included mainly early flowering and early maturing genotypes with high yield. To develop high yielding varieties/genotypes, genotypes of this group could be used in hybridization program.

G-10

G-13

Plate 5. Fruit type of the different genotypes of cluster IV

G- 15

Plate 6. Fruit type of the different genotypes of cluster V

4.4 Contribution of characters towards divergence of the genotypes

The character contributing maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization (Jagadev *et al.,* 1991). The PCA revealed that in vector I (Z_1) the important characters responsible for genetic divergence in the major axis of differentiation were number of fruit per plant (0.510), length of the fruit (0.022 cm) yield per plant (0.380 kg) (Table 10).

In vector II (Z_2) that was the second axis of differentiation, fruit diameter (0.228 cm), length of fruit (0.231 cm), fruit weight (0.591 g), present of insect infestation (0.137) and yield per plant (0.447 kg) was important.

The role of length of fruits per plant and yield per plant for both the vectors was positive across two axes indicating the important components of genetic divergence in these materials.

Table10. Latent vectors for 9 characters of brinjal

Parameter	Vector 1	Vector 2
Plant height (cm)	-0.032	-0.428
Branch per plant (no.)	-0.199	-0.357
Fruits per plant (no.)	0.510	-0.060
Fruit diameter (cm)	-0.299	0.228
Length of fruit (cm)	0.022	0.231
Days to 1st flower	-0.417	-0.111
Yield per plant (kg)	0.380	0.447
Fruit weight (g)	-0.238	0.591
% insect infestation	-0.483	0.137

4.5 Selection of genotypes for future hybridization

Selection of genotypically distant parents are an important step for hybridization programme. as a result genotypes would be selected on the basis of specific objectives. Crosses between genetically distant parents able to produce higher heterosis (Falconer, 1960; Moll *et al*.; 1962; Ramanujam *et al.;* 1974; Ghaderi *et al.;* 1984; Main and Bhal, 1989).

Considering the agronomic performance, genotype 6 produce higher yield, maximum number of fruit, maximum present of insect infestation from cluster II than others. genotype 13 from cluster IV having earliness in days of first flowering with larger diameter of fruits .genotypes 14 produce higher length of fruit from cluster I. genotype 15 produce high yield with the highest fruit weight from cluster V.

Therefore, considering group distance and other agronomic performance, the inter-genotypic crosses between 6 and 15; 14 and 15; 13 and 6; 13 and 6 may be suggested to use for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

An experiment with 15 brinjal genotypes was conducted in the field of Sher-e-Bangla Agricultural University, Dhaka in RCBD with three replications to study diversity pattern based on 9 characters during November, 2013 to April, 2014.

Significant differences among the clusters were observed. The first four components with eigen value were greater than unity contributed a total of 80.94% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into five different clusters. Cluster I, II, III, IV and V composed of seven, four, one, two and one genotypes respectively. Results indicated that the highest inter-cluster distance was observed between III and IV (82.92), followed by between IV and V (82.62), I and V (50.59). The lowest inter-cluster distance was observed between the cluster I and II (19.22) followed by II and V (34.04), I and IV (35.33) .The highest and lowest intra-cluster distances were observed in II (22.82) and in cluster IV (13.83), respectively. Genotypes included in cluster I important for plant height ; cluster II for fruit length and yield per plant ; cluster III for present of insect infestation, and fruit diameter ; cluster IV also fruit per plant and cluster V important for fruit weight and earliness of flowering. The clustering pattern of the genotypes revealed that genotypes collected from the same places did not form a single cluster.

Considering cluster distance and other agronomic performances the genotype 6 from cluster II, genotype 13 from cluster IV, genotypes 14 from cluster I and genotype 15 from cluster V could be considered as better parents for future hybridization program.

Results of the present studies indicated significant variation among the genotypes for all the characters studied. Number of fruits per plant, fruit length, fruit diameter and individual fruit weight contributed maximum towards yield.

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APPENDICES

Appendix I. Composition of brinjal per 100 g of edible portion

Nutrients	Amount
Calories	24.00
Moisture content (%)	92.70
Carbohydrates (%)	4.00
Protein(g)	1.40
Fat (g)	0.30
Fiber (g)	1.30
Oxalic acid (mg)	18.30
Calcium (mg)	16.00
Magnesium	47.00
Phosphorous (mg)	0.90
Iron (mg)	3.00
Sodium (mg)	0.77
Copper (mg)	2.00
Potassium(mg)	44.00
Sulphur (mg)	52.00
Chlorine (mg)	124.00
Vitamin-A (IU)	142.00
Vitamin-B (mg)	0.04
Thiamin	0.11
Riboflavin	0.74
B carotene	0.74
Vitamin –C (mg)	12.00

Source: Anonymous, 1980

Appendix II. physical and chemical characteristics of initial soil (0-15 cm depth)

A. Physical composition of the soil

Soil separates	**%**	**Methods employed**
Sand	36.90	Hydrometer method (Day,1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No	**Soil characteristics**	**Analytical Data**	**Methods employed**
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1 : 2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Appendix III. Monthly average of Temperature, Relative humidity, Total Rainfall and sunshine hour of the experiment site during the period from November , 2013 to April, 2014

Year	**Month**	**Air temperature**			**Relative Humidity (%)**	**Rainfall (mm)**	**Sunshins (hr)**
		Maximun	**Minimum**	**Mean**			
2013	Novembor	30.4	19.4	24.9	70	0	184.43
	Decembor	29.1	14.3	21.7	65	215	214.54
2014	January	24.2	14.5	19.35	73	0	165.34
	February	21.2	13.1	17.5	71	0	161.47
	March	26.5	15.7	21.1	69	Trace	187.23
	April	30.3	15.2	22.75	67	75	225.76

Source: Bangladesh Metrological Department (Climate division),

Agargaon. Dhaka-1207

Table 2. Mean performance of nine characters of fifteen brinjal genotypes

Line	Genotypes	PH	DFF	NB	FPP	DF	FPL	WPF	YPP	PII
1	Bolaka green	71.00 a	61.00 e	5.00 cde	24.00 cd	16.67 c	7.90 bc	63.37 h	1.52 c	27.23 b
2	BD-2698	69.67 ab	62.00 de	3.33 fg	17.67 fg	18.70 abc	8.03 b	78.93 e	1.39 d	15.47 ef
3	BD-2754	64.33 c	64.67 cd	6.33 bc	10.67 i	14.50 d	8.17 b	88.97 d	0.95 g	24.73 bc
4	BD-2705	47.33 f	65.00 cd	3.33 fg	12.00 hi	17.67 bc	11.00 a	98.37 c	1.17 e	23.80 bc
5	BD-2775	70.33 a	65.67 cd	4.33def	20.00 def	13.33 de	5.00 ef	69.97 f	1.39 d	19.23 de
6	BD-2791	53.00 e	65.00 cd	4.67def	**45.67 a**	11.33 ef	8.17 b	60.93 h	**2.78 a**	**19.37 de**
7	BD-2796	58.33 d	66.33 c	2.67g	15.33 gh	17.93 abc	8.33 b	61.63 h	0.94 g	18.60 de
8	Uttora hajari	64.33 c	82.33 a	8.00 a	3.00 j	19.20 ab	6.33 cde	102.20 b	0.31 i	36.63 a
9	BD-2750	65.67 bc	54.00 f	4.00 efg	17.67 efg	17.33 bc	8.17 b	62.37 h	1.11 f	25.73 bc
10	BD-2662	57.67 d	62.33 de	8.00 a	28.00 b	12.87 def	4.67 f	20.30 j	0.56 h	18.73 de
11	Plastid black beauty	57.67 d	60.33 e	5.00 cde	15.67 gh	16.77 c	5.67 def	89.80 d	1.40 d	22.83 cd
12	BD-2704	66.00 bc	55.00 f	4.33 def	22.67 d	10.77 f	7.17 bcd	66.51 g	1.50 c	13.60 f
13	Sada begun	71.33 a	52.67 f	5.67 bcd	27.67 bc	20.03 a	8.00 bc	39.87 i	1.10 f	12.93 f
14	BD-2653	66.33 bc	71.33 b	5.67 bcd	16.67 fg	11.10 f	11.00 a	15.57 k	0.23 j	16.93 ef
15	BD-2724	55.33 de	55.67 f	6.67 ab	21.67 de	14.50 d	7.67 bc	**111.80 a**	**2.42 b**	18.90 de

PH= Plant height (cm), DFF= Days to 1st flowering, NB=Number of branch, FPP= Number of fruits per plant, DF= Diameter of the fruit (cm), FPL= Length/fruit (cm), WF=Fruit weight (g), YPP= Yield per plant (kg), PII= % insect infestation

Table 3. Analysis of variance for nine characters of brinjal

Sorces of variation	**Df**	**Mean sum of square**								
		Plant height (cm)	**DFF**	**BPB**	**FPP**	**FD (cm)**	**FL (cm)**	**WPF (g)**	**YPP (kg)**	**PII**
Replication	2	1.089	18.156	0.067	6.959	0.691	0.471	4.851	0.001	1.087
Genotypes	14	159.079**	169.317**	7.752**	280.698**	28.752**	9.825**	2358.383**	1.400**	111.188**
Error	28	4.994	3.989	0.590	4.956	1.449	0.815	2.902	0.0004	5.461

*= Significant at 1 % level of probability, **= Significant at 5 % level of probability, df = Degree of freedom, DFF = Days to first flowering, PH= Plant height, NPB =No. of primary branches, FL =Fruit length, FD =Fruit diameter, DFH =Days to first harvesting, WPF =Fruit weight, FPP =fruit per plant, YPP =Yield per plant, PII =% Insect infestation

PH= Plant height (cm), DFF= Days of 1st flowering, NB=Number of branch, FPP= Number of fruits per plant, DF= Diameter of the fruit (cm), FPL= Length/fruit (cm), WF=Weight/fruit (g), YPP= Yield per plant (kg), PII= % insect infestation