GENETIC DIVERGENCE IN BRINJAL
(*Solanum melongena* L.)

BY

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CERTIFICATE

This is to certify that the thesis entitled, ***"GENETIC DIVERGENCE IN BRINJAL (Solanum melongena L.)"*** *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* ***Mohammad Mizanur Rahaman, Registration No.: 06-02154,*** *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 sources of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: June, 2007

Place: Dhaka, Bangladesh

(Prof. Dr. Md. Shahidur Rashid Bhuiyan)

Supervisor

Dedicated to

My

Late Grandmothers and Grandfathers

LIST OF ABBREVIATIONS AND SYMBOLS

Full Word	Abbreviations
Agro-Ecological Zone	AEZ
And Others	*et al.*
Bangladesh Bureau of Statistics	BBS
Bangladesh Agricultural Research Institute	BARI
Bangladesh Rice Research Institute	BRRI
Centimeter	cm
Days to First Fruit Harvesting	DFH
Coefficient of Variations	CV
Days to First Flowering	DFF
Days to First Fruit Harvesting	DFH
Days after Transplanting	DAT
Degree Celsius	^0C
Degrees of freedom	d.f
East-West Seed (Bangladesh) Ltd.	EWSL
Etcetera	Etc.
Food and Agricultural Organization	FAO
Figure	Fig.
Genetic Advance	GA
Gram	gm
Genotypic Coefficient of Variation	GCV
Genotypic Variance	σ^2_g
Hectare	ha.
Heritability in broad sense	h^2b
Journal	*J.*
Kilogram	Kg
Mean Sum of Squire	MSS
Meter	m
Momen Seed Ghar	MSG
Muriate of Potash	MoP
Nadim Seed Company	NSC
Number	no.
Percent	%
Phenotypic Coefficient of Variation	PCV
Phenotypic Variance	σ^2_p
Randomized Complete Block Design	RCBD
Relative Humidity	RH
Sher-e-Bangla Agricultural University	SAU
Squire meter	m^2
Triple Super Phosphate	TSP

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The Author

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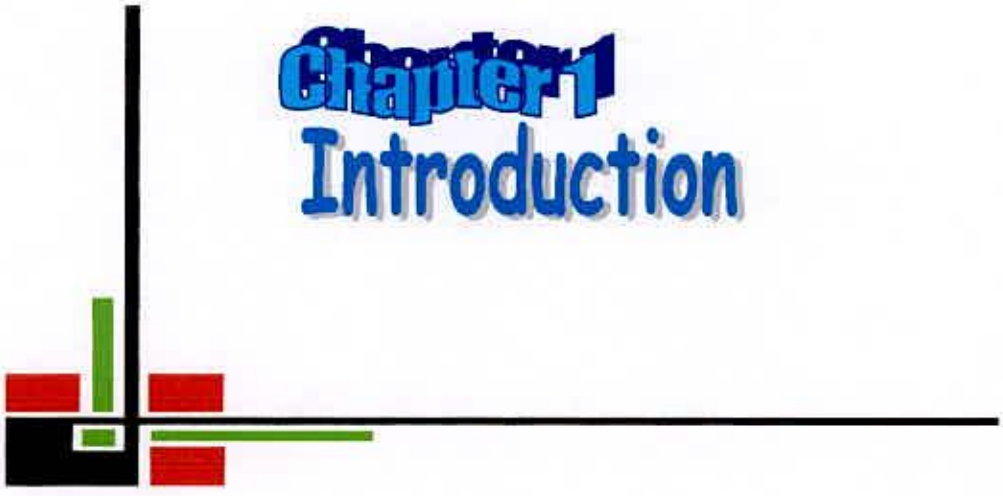
ABSTRACT

The genetic diversity, genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean were studied for 34 genotypes of brinjal were determined in a field experiment conducted at the farm of Sher-e-Bangla Agricultural University, Dhaka during October, 2006 to April, 2007. Significant genotypic differences were observed for all the characters studied. The phenotypic coefficient of variation was higher than genotypic coefficient of variation in all the characters. The phenotypic coefficient of variation (PCV) estimates were high for no. of flower per inflorescence, no. of fruit per plant, % insect infestation of plants and individual fruit weight, whereas days to first fruit harvesting showed very low PCV. Heritability estimates were high for fruit weight with high genetic advance, yield per plant, fruit length and plant height. In spite of high heritability values for most traits, the expected genetic advance as percentage of mean ranged from 19.10 to 98.91. Multivariate analysis was performed through principal component analysis (PCA); principal coordinate analysis, cluster analysis and canonical variate analysis were used to classify 34 brinjal genotypes. As per as PCA, D^2 and cluster analysis, the genotypes were grouped into six different clusters. Cluster III and cluster V had the maximum of nine and minimum of two genotypes respectively. The highest inter-genotypic distance was found between G17 and G26 and the lowest distance between G09 and G10. The maximum inter-cluster distance was observed between the clusters I and cluster V, whereas the lowest-inter cluster distance was found between the cluster II and cluster III. The highest intra-cluster distance was identified in cluster III and the lowest intra cluster distance was found in cluster V. Genotypes included in cluster I suitable for no. of secondary branches per plant, fruit circumference, individual fruit weight and yield per plant, cluster IV for having the highest mean value for fruit length, tallest plant and the percent insect infestation of fruits was lowest, cluster V for early in both first flowering, first fruit harvesting, produced maximum number of fruits per plant and the percent insect infestation of plants was also very low in this cluster and cluster VI for no. of primary branches and number of flowers per Inflorescence. Considering diversity pattern and other agronomic performances the genotypes G03, G16, G25, G26, G32 and G34 from cluster I and genotypes G17 and G33 from cluster V could be considered suitable parent for future hybridization programme.

Chapter 1
Introduction



CHAPTER I
INTRODUCTION

Brinjal or Eggplant or Melongene or Aubergene is one of the major *Solanaceous* crops under the botanical name *Solanum melongena* L. (2n = 24) grown in Bangladesh. There are **3** main botanical varieties under the species *melongena* (Chowdhury, 1976). The round or egg-shaped cultivars are grouped under var. *esculentum*, the long slender types are included under var. *serpentintum* and the dwarf brinjal plants are put under var. *depressum*. Brinjal is a native crop of Indian sub-continent. A wide genetic diversity is found here due to the availability of different land races and their wild relatives. Brinjal is not as rich nutritionally as other *solanaceous* vegetables, but it has high demand among the consumers due to its diversified uses.

The brinjal or eggplant is a crop of uncertain origin. The cultivated brinjal is undoubtedly of Indian origin and has been in cultivation for long time (Thompson and Killy, 1957). According to Purewal (1957), it is still found growing wild in India. Different forms, colors, sizes and shapes of brinjal are found throughout the Southeast Asia suggesting that this area is an important centre of diversity and possibly of origin. Now, the brinjal is of great importance in the warm areas of Far East, being grown more extensively in India, Bangladesh, Pakistan, China and Philippines. For the intensive cultivation and increased production of brinjal, improved varieties/ lines with desirable traits need to be identified.

Brinjal is grown commonly in almost all parts of the country and liked both poor and rich. It is a main vegetable to the plains and is available more or less through out the year. Country to the common belief, it is quite high in nutritive value and can be compared with tomato (Choudhury, 1976). It is rich in protein, calorie, riboflavin calcium and iron, vitamin A, B and C. The unripe fruit is primarily used as a cooked vegetable for the preparation of various dishes in different regions of the world. It has potentially as raw material in pickle making

and in dehydration industries (Singh *et al.* 1963). It is supposed to contain certain medicinal properties in Ayurvadic medicines and white brinjal is said to be good for diabetic patients (Choudhury, 1976). Fried brinjal in till has some medicinal value to cure liver problem (Chauhan, 1981).

In Bangladesh, more than 60 different types of vegetables of indigenous and exotic origin are grown. At present, total vegetable growing area in the country is about 268.83 thousand hectares (2.47 acre is equal to a hectare), of which 60% are cultivated during winter. Depending on yield, size, shape as well as consumer's preference a number of brinjal genotypes are being cultivated throughout the country. The actual area under brinjal cultivation in Bangladesh is not available due to its seasonal nature of cultivation. However, in rabi (winter) 2003-2004 the total area covered by brinjal cultivation was 37.65 thousand hectares with the production of 240 thousand metric tons and in kharip (summer), the hectares and production was 22.67 thousand and 118 thousand metric tons respectively (Appendix IV). So, as single vegetables crop in the year 2003-04 brinjal were cultivated 22.44% of total area under vegetables cultivation, and the production was 20.59% of the total vegetables production (Appendix III).

However, brinjal production are greatly 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 prickliness, pubescence 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 and health hazard etc. It is important to identify the natural mechanisms prevailing in the brinjal land races to utilize them in the future breeding programme.

Precise information on the nature and degree of genetic divergence of the parents is the prerequisite of variety development program. The importance of

genetic diversity in the improvement of a crop has been stressed in both self and cross pollinated crop (Griffing and Lindstrom, 1954; Murty and Anand 1966; Gaur *et al.* 1977). The quantification of genetic diversity through biometrical procedures (Anderson, 1957; Rao, 1952) has made it possible to choose genetically diverse parents for a successful hybridization program. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991).The utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution of different character 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).

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, intra-cluster 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 lines 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. Other characters, like disease

resistance earliness quality etc. should also be considered. Crossing of the selected genotypes in a dialed fashion may generate some useful segregants. In order top increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed: Variability and genetic diversity are the fundamental law of plant breeding which is a major tool being used in parent selection for efficient hybridization programme (Bhatt, 1973).

As it is the major native vegetables in our country, a large number of genotypes 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. Because of their restricted distribution, the promising genotypes are yet to be known. Besides this such investigation would go a long way in helping the scientists as well as the farmers for effective selection of a superior genotype to use in any improvement programme through characterization of the genotypes as well as genetic diversity study.

The present investigation was therefore, undertaken with local, mutant and exotic varieties/lines of brinjal to evaluate their performance and characteristics for finding out suitable genotypes under the agro-ecological condition of the central plains of Bangladesh during the winter season. The present investigation was undertaken with the following objectives:

- To study the genetic variability for different quantative characters involved among brinjal genotypes,
- To study the genetic diversity among the materials,
- To characterize the genotypes on the basis of different morphological and yield contributing characters,
- To select the genetically diverged parents to involve them in the future hybridization programme.

Chapter 2

Review of Literature

CHAPTER II
REVIEW OF LITERATURE

Genetic diversity is one of the criteria of parent selection. It is a prerequisite for an efficient plant breeding programme. The qualification of grnetic diversity through biometrical procedures such as Mahalanobis's D^2- statistic and Canonical Variate Analysis (CAV) has possible to choose genetically diversed parents. Recent work indicates that the Mahalanobis generalized distance (D^2 statistic) may be an efficient tool in the quantitative estimation of genetic diversity. The divergence analysis has a definite role to play in an efficient choice of divergence parents for hybridization to exploit maximum heterosis. Genetic diversity is essential tool to meet the diverse goals such as producing cultivars with increased yields, wider adoption, desirable quality, and pest and disease resistance. Inclusion of more diverse parents (within a limit) in hybridization is supposed to increase the chance of obtaining maximum heterosis and give broad spectrum of variability in segregating generations.

In order to increase desired genotypes in breeding progenies, superior parents with high breeding values are needed. Variability and genetic diversity are the fundamental law of plant breeding which is a major tool being used in parent selection for efficient hybridization progarmme (Bhatt, 1973).

Therefore, relevant information available in the literature pertaining to the characterization, variability and 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 headings.

2.1 Characterization and variability of brinjal genotypes

2.2 Genetic diversity

2.3 Relationship between genetic and geographic diversity in brinjal (*Solanum melongena* L.)

2.4 Technique of multivariate analysis

2.1 Characterization and Variability of Brinjal Genotypes

Sharma *et al.* (2000) conducted an experiment on genetic variability and character association in brinjal (*Solanum melongena* L.) and observed genetic variability in terms of mean, genotypic and phenotypic coefficient of variances, heritability, expected genetic advance and expected genetic advance as per cent of mean, correlation and path coefficient were studied for yield per plant and its attributing traits in 27 genotypes. Considerable variation was observed in all the characters. The phenotypic coefficient of variation was higher than genotypic coefficient of variance in all the characters. The genotypic coefficients of variation estimates were high for number of fruits per plant, mean fruit weight and yield per plant. Heritability estimates were high for length of fruits, number of fruits per plant, mean fruit weight and yield per plant. The number of fruits per cluster showed maximum indirect positive effect on yield. Number of flowers per cluster, number of branches per plant, plant height and length of fruit had positive indirect effect towards yield per plant via number of fruits per plant and hence simultaneous selection for these characters can be made for the improvement of yield.

Genetic variability, heritability and genetic advance of fruit yield and nine other characters were studied in eight genotypes of aubergine by Chaudhary and Pathania (1999). Sufficient variability was exhibited for fruit diameter, fruit length, fruit weight, number of fruits per plant and total soluble solids. These traits also showed high heritability estimates coupled with moderate to high genetic advance expressed as percentage of mean. High heritability values along with low genetic advance were observed for number of branches per plant, plant height, yield per plant, days to 50 per cent flowering and days to first picking.

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.

Vedivel and Bapu (1990) studied nineteen genotypes of eggplant 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.

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.

Bhutani *et al.* (1977) studied genetic variability in 17 brinjal varieties/lines 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.

Genetic variability for eight quantitative traits (plant height, number of leaves, number of branches, tuber number and weight at 60 and 90 days after planting (DAP) and plant weight) Biswas *et al.* (2005) were evaluated in seven parents during 2001 in Bangladesh. In general, high component of variation and coefficient of variability were observed for most of the traits. The highest

component of variation, coefficient of variability and heritability were observed for plant weight, tuber weight at 60 DAP and tuber number at 60 DAP. Traits with high genetic variability and genetic advance were considered to be important for selecting the desirable parents.

Mehrotra and Dixit (1973) observed a wide range of phenotypic variation for fruit yield, fruit length and plant height in 45 varieties/lines 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.

Singh *et al.* (2005) conducted an experiment on 15 advance generation breeding lines of tomato, including 4 control cultivars, to study the variation and heritability of quality characteristics in tomato raised under normal and high temperature conditions. Data were recorded for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene content and dry matter content. There were significant differences among the genotypes under normal conditions, whereas differences were not significant under high temperature conditions. In general, the phenotypic coefficients of variation were higher than genotypic coefficients of variation indicating that the genotypic effect is lessened under the influence of the given environment. Heritability estimates (in the broad sense) were high for all the characters for November planting except for lycopene content.

Estimates of genetic variability were analyzed in seventy-two germplasm lines and three commercial cultivars by Shirshat, Giritammannavar and Patil (2007). The analysis of variance and other genetic parameters indicated considerable genetic variability for different characters among the genotypes. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all characters indicating the influence of environment on these characters. Fruit attributes viz., fruit length, fruit surface area, weight of dry fruit, pericarp weight of fruit, number of seeds per fruit, weight of seeds per fruit, stalk length, ascorbic acid and sugar content showed very narrow differences between phenotypic and genotypic coefficient of variation, indicating lesser sensitivity to environmental influence. Heritability estimates in

respect of fruit length, fruit surface area, number of seeds per fruit, weight of seeds per fruit, weight of dry fruit, pericarp weight of fruit, ascorbic acid content and sugar content were high ranging from 74.00 percent to 99.40 percent. Moderate genetic advance was observed for the characters like number of fruits per plant, number of seeds per fruit and sugar content of the fruit. Heritability was high in these characters except for number of fruits per plant. In case of attributes like fruit length, fruit surface area, weight of dry fruit, pericarp weight of fruit, number of seeds per fruit and weight of seeds per fruit, the genetic advance was low to moderate coupled with high heritability. Yield per plant, the complex trait, which is dependent on several component characters showed moderate heritability with low genetic advance.

Genetic variability, heritability, genetic advance and genetic advance as a percent over mean for twelve characters were assessed by field evaluation of eighty chilli accessions by Krishna *et al.* (2007) at Kittur Rani Channamma of Horticulture, Arabhavi (Kama taka) during 2002. High degree of variation was observed for all characters. The difference between phenotypic coefficient of variation and genotypic coefficient of variation were found to be narrow for most of the traits except primary and secondary branches, tertiary branches, fifty per cent flowering, early and late fruit yield per plant. Most of these characters also had moderate to high estimates of genetic advances as a percent over mean except days to first flowering.

Forty diverse chilli genotypes were evaluated by Smitha and Basvaraja (2007) to study the extent of variability present in the genotype for 32 characters studied which was confirmed by analysis of variance as indicated by high GCV and PCV values. Selection strategy for yield improvement should rely on number of fruits per plant, fruit weight, number of primary branches, fruit length, fruit diameter, plant height and number of primary branches during selection process, because these characters are going to contribute directly towards the yield.

Mohanty, (1999) evaluated 15 genotypes of aubergine over two years (1994 and 1995) in Orissa, India revealed considerable genotype environment

interaction for expression of yield, average fruit weight, number of fruits and branches/plant. Phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the traits. High heritability accompanied by moderate to high genetic gain and GCV were recorded for average fruit weight, number of fruits and branches/plant, which could be improved by simple selection methods. Plant height, days to first harvest and yield exhibited high heritability with low GCV and genetic gain which required heterosis breeding for their amelioration.

Doshi *et al.* (1999) studied on variance, coefficient of variation, broad-sense heritability and genetic advance for yield and quality characters was derived using data from 41 genotypes of brinjal *(Solanum melongena)*. The highest genetic coefficient of variation was observed for anthocyanin content followed by glycoalkaloid content. High heritability was observed for all the characters studied for brinjal. Further, anthocyanin content, total phenols, polyphenol oxidase activity, total soluble sugars and reducing sugars had high genetic advance coupled with high heritability, which suggested that these traits were under the control of additive gene action and could be improved through simple selection procedures.

Information on heritability and genetic variance is derived from data on 16 characters in 40 diverse cultivars grown during 1993-94 and 1994-95 by Rajesh, Kumar and Verma *et al.* (1998). Plant spread, days to 1st flowering, flowers/plant, fruits/plant and fruit yield/plant gave comparatively lower values of heritability indicating environmental influence of these characters. The highest estimate for genetic advance was noted for fruit weight.

The variability and heritability of 17 traits were estimated in 78 accessions of *S. melongena* in Kerala, India by Singh and Gopalakrishnan (1999). Significant variation was observed for both the qualitative and quantitative traits. The highest yield was obtained from the accession Annapoorna (2.28 kg/plant). The genotypic and phenotypic coefficient of variation was highest in number of fruits per plant (54.8 and 60.90%, respectively) and yield per plant (52.67 and 57.12%, respectively). The highest heritability estimate (0.94) was observed in plant spread, average fruit weight, and days to 50% harvest,

while number of fruits per plant (101.65%) and yield per plant (106.09%) gave the highest genetic advance.

Information based on 41 genotypes of brinjal (*Solanum melongena*) has revealed that the highest genetic coefficient of variation was observed for fruit volume followed by seed to pulp ratio Patel *et al.* (1999). High heritability was observed for most of the characters studied. Further, characters like fruit weight, fruit volume, plant height and seed to pulp ratio had high heritability coupled with high genetic advance as a percentage of mean which suggested that these traits are under the control of additive gene action and would be improved through simple selection.

An investigation was carried out by Varalakashmi *et al.* (1991) on Genetic divergence; heritability and genetic advance for 10 characters in 32 genotypes of chilli (*Capsicum annuum* L.) were studied. Based on D^2 values, the genotypes were clustered in 11 gene constellations. Groupings of genotypes in different clusters were not related to their geographical origin. Considerable amount of genotypic and phenotypic coefficients of variation was observed for leaf area index, fruits/plant, fruit weight, and total yield, indicating existence of greater diversity for these characters. High heritability coupled with high genetic advance as percentage of mean and genetic coefficients of variation was observed in respect of leaf area index, fruits/plant, fruit weight, seeds, fruit, plant height and fruit length, indicating that these characters are under control of additive gene or no environmental effects and could be dependable for yield improvement in chilies.

Das *et al.* (2002) was carried out with 11 genotypes of aubergine under three fertility levels. The pooled data revealed that characters like average fruit weight, wilt incidence, fruits per plant, plant height, fruit yield per plant, leaf width, leaves per plant, leaf length and stem girth showed high heritability values. Considering the three genetic parameters namely genotypic coefficient of variability, heritability and genetic advance together, it was evident that phenotypic selection would be more effective for characteristics

like average fruit weight, fruit yield per plant, fruits per plant and wild incidence than other characteristics.

The genetic diversity, heritability and genetic advance in 39 genotypes of aubergine were determined in a field experiment conducted in Hisar, Haryana, India during 1997 by Baswana *et al.* (2002). Significant genotypic differences were observed for all the characters studied. Among the genotypes, Arka Sirish recorded the highest number of fruits per plant, whereas CHBR-1 recorded the highest fruit weight. H-17 recorded the lowest number of days before 50% flowering. Fruit yield was highest in AB-1. High genotypic and phenotypic coefficients of variation were observed for number of fruits per plant, yield per plant and fruit weight. High heritability and genetic advance were observed for number of fruits per plant, fruit weight and fruit yield per plant.

2.2 Genetic Diversity

Eggplant is one of the most important vegetable crops grown in all parts of Bangladesh. In Bangladesh research effort on characterization, diversity and comparative studies of eggplant seem to be poor. Therefore, relevant information available in the literatures is reviewed in this section.

Singh *et al.* (2005) carried out research on thirty five genotypes of brinjal for genetic diversity in the rainy season of 2003 in the Punjab Agricultural University, Ludhiana. The genotypes were grouped into eleven clusters. The clustering was irrespective of geographic divergence. Therefore, for management of diversity in germplasm, the pattern obtained with cluster analysis may be the single most effective one. Three genotypes, viz. Punjab Sadabahar, Punjab Jamunigola and HP-14 exhibited maximum diversity from other genotypes and thus could effectively be used as one of the parent in hybrid breeding programme to exploit heterotic expressions for yield and other economic characters.

An evaluation of 42 F_1's and 13 parents of eggplant were conducted during winter season at the farm of Olericulture Division, HRC, Bangladesh

Agricultural Research Institute, Gazipur by Al-Faruque *et al.* (2004). BL-114 and 4 X5 produced the maximum number of fruits per plant (61.3) and individual fruit weight was highest (299gm) in ISD-006 and lower in EG-195 (60gm). ISD-006 gave significantly higher yield (4.79 kg/pl.) followed by the 4 X 5 (4.55 kg/pl).

Mohanty *et al.* (2001) studied genetic diversity for 5 traits, i.e. plant height, branches per plant, fruits per plant, average fruit weight and fruit yield in 15 genotypes of *S. melongena* grown during kharif 1995 in Bhawanipatna, Orissa, India. The genotypes were grouped into 5 clusters. The highest intercluster distance was obtained between cluster IV (KT 4 and BB4) and cluster V (Pusa Kranti and Bhawanipatna local). Based on the pattern of clustering among genotypes, it was observed that genetic diversity was not correlated with the geographical distribution of the genotypes, indicating that other forces, such as genetic drift, free and frequent exchange of breeding material, natural and artificial selection, and incorporation of breeding progenies are responsible for the creation of genetic diversity. Intercrossing among genotypes belonging to cluster III, IV and V was suggested to develop high-yielding genotypes with other desirable traits.

Kumar *et al.* (2000a) evaluated fourteen genotypes of eggplant for assessing genetic diversity for 10 yield components in three different environments created by manipulating the dates of sowing (20 February, 10 March and 30 March 1996). The experiment was conducted in Hisar, Haryana, India. Highly significant differences were observed for all the characters under study. Higher values of phenotypic than genotypic coefficient of variation in all three environments indicated the role of environmental influence in the expression of various characters.

Basar (1999) conducted an experiment with 30 eggplant genotypes at the field of Genetic Resource' Centre in Bangladesh Agricultural Research Institute (BARI), Joydevpur, Gazipur to study their diversity based on qualitative and quantative characters was observed for during November 1998 to March 1999. Significant variation in the characters number of flowers

per inflorescence, number of fruits per plant, fruit length, fruit breadth, fruit weight among the eggplant genotypes.

An experiment in Haryana, India during 1996 was conducted by Kumar *et al.* (2000 b) to evaluate the performance of eleven advance lines along with three standard control cultivars of eggplant *(Solanum melongea)* under spring summer season. HLB-25 genotype recorded the highest fruit yield (980.38 gm/pl) followed by HLB-18 (863.76 gm/pl), HLB-106 (858.28 gm/pl) and HLB-24 (824.23gm/pl). Hisar Jamuni genotype exhibited the highest number of seeds/fruit (540.93) followed by HOB-108 (487.42)

Forty-one genotypes of aubergine were used to study the genetic diversity for 9 yield and agronomic characters in a field experiment conducted in Anand, Gujarat, India during the rabi season of 1995-96 by Doshi *et al.* (1999). The genotypes were grouped in six clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. Characters like reducing sugar content, polyphenol oxidase activity, glycoalkloid content and total soluble sugars played an important role in divergence between the populations. A breeding programme based on the study has been suggested.

Thirumurugan *et al.* (1999) studied genetic divergence using D^2 statistic of 43 eggplant *(Solanum melongena)* genotypes of different geographic origins revealed the existence of considerable diversity. The genotypes were grouped into 13 clusters. The cluster I was the largest containing 12 genotypes followed by cluster III with 6 genotypes. Cluster IX, X, XI, XII and XIII were unique and had only one genotype each. The diversity among the genotypes as estimated by inter-cluster distance was adequate for improvement of eggplant by hybridization and selection. The genotypes included in the diverse clusters can be used as promising parents for hybridization to obtain high heterotic response and thus better segregants in eggplant.

Thirty-four genotypes of brinjal *(Solanum melongena)* of diverse origin were evaluated in plots by Sarma *et al.* (2000) at Jorhat. Analysis of data on yield and its components grouped the genotypes into 10 clusters using

Mahalanobis' D^2 statistic. Fruit circumference and average fruit weight were the main characters affecting grouping of genotypes. Ecogeographic diversity of the genotypes was not related to genetic diversity.

Genetic divergence in 40 accessions of *Solanum melongena* for 17 yield-related traits was studied by Kumar *et al.* (1998) at Ranchi. Multivariate analysis of the results grouped the accessions into 6 distinct clusters. No relationship was found between genetic divergence and geographical distribution. Fruit width (58.72%), fruit length (18.08%) and yield per plot (12.12%) contributed most towards total divergence.

Mishra *et al.* (1998) was conducted an experiment on Genetic divergence among 20 cultivars of Egg plant *(Solanum melongena)* was estimated 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 mean and the genetic distance, 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.

Thirty five (35) genotypes of brinjal were studied for genetic diversity in 1996 by Sarnaik *et al.* (1998). Genotypes were clustered into 5 groups. The maximum inter cluster distance was observed between cluster III and IV (20.38) while minimum distance was recorded between cluster I and II (11.80). The cluster mean for yield was the highest in cluster IV (2.74 kg/plant) and the lowest in cluster V (1.36 kg/plant). A suitable hybridization programme has been suggested on the basis of these results.

Information on genetic diversity as estimated using Mahalanobis' D^2 statistic is derived from data on 10 yield-related characters in 65 genotypes grown at Patharchatta, India by Singh *et al.* (1995). Fourteen clusters were formed, with no relationship between clustering pattern and ecogeographical distribution of the genotypes.

Yadav *et al.* (1996) conducted an experiment, using Mahalanobis' D^2 statistic with 10 quantitative characters including yield per plant in a collection of 40 diverse types of brinjal *(Solanum melongena)*. The genotypes differed significantly for the 10 characters and were grouped in 9 clusters on the basis of relative magnitude of D^2 values during both years. The maximum genetic distance was observed between clusters VI and IX during 1987-88 and II and IX during 1988-89. There was no close correspondence between geographical distribution and genetic divergence. The study also revealed that clustering behaviour, entries and mean yield performance of genotypes of individual clusters were not consistent over environments because of genotype X environment interaction.

An experiment in Pantnagar, Uttar Pradesh, India, during 1999/2000 and 2000/01 rabi season was by Mishra *et al.* (2002) 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.

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 coefficient 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.

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.

D^2 analysis revealed no relationship between genetic and geographic diversity in 50 varieties of *C. frutescens* Linn. The number of branches and number of fruits per plant were the chief contributors towards genetic divergence Sundaram *et al.* (1980).

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

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.

An investigation carried out by Singh and Singh (1980) to study genetic divergence on *Lycopersicon esculentum* for yield and its components, i.e., days to flower, number of fruits, fruit size, number of locules/fruit, days to maturity, number of fruits/bunch, primary branches/plant and plant length, in 30 varieties of tomato (*L. esculentum* Mill.). The maximum divergence was contributed by the number of fruits/bunch, followed by fruit size and number of primary branches/plant. The 30 varieties were grouped in 8 clusters. The clustering pattern showed that genetic divergence was not parallel to geographical distribution.

By the investigation of 29 genotypes of brinjal for the varietal variation in flower type Chadha and Saimbhi (1977) showed that all the varieties/lines

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.

Forty genotypes of Indigenous and Exotic origin of chilli *(Capsicum annuum L.)*, collected from NBPGR, New Delhi were evaluated by Karad *et al.* (2002) to study the variability and genetic divergence. Diversity analysis revealed good amount of variation among the genotypes studied. D^2 values ranged between 0.1032 and 8.7702. Forty genotypes were grouped into eight clusters. The clusters I was the largest containing 23 genotypes, followed by cluster II (4), cluster III (3), cluster IV (3), cluster VII (3) and cluster VI with 2 genotypes. The clusters V and VIII were monogenotypic. Inter-cluster distance (D^2) ranged between 7.45 (cluster II and V) and 1.15 (cluster III and VII). The variance of cluster means revealed that fresh fruit weight and fruits plant-1 had maximum contribution towards divergence.

Birhman and Kaul (1991) conducted an experiment by using D^2 statistics, genetic divergence was studied for 26 genotypes comprising 9 elite varieties and 17 advanced breeding lines of cultivated potato *Solanum tuberosum* L. These genotypes got grouped into 8 clusters of which cluster I was the largest having 12 genotypes, others had 1-4 genotypes each. Maximum inter-cluster distance with 6 clusters other than cluster II was exhibited by cluster III. Based on genetic heterozygosity, inter-crossings of certain genotypes from cluster III, VI and VIII is desirable to ensure maximal tuber yield-gain and heterozygote-advantage in the cultivated potato.

2.3 Relationship between genetic and geographic diversity in Brinjal (*Solanum melongena* L.)

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.

Chen and Nelson (2005) conducted an experiment on soyabean (*Glycine max* L.) was domesticated in China. Information about the amount and distribution of genetic diversity in China is critical to effective soyabean germplasm management. Information is currently available from only a few provinces in China. The objectives of this research are to estimate the genetic variation within and among four geographically diverse provinces (Zhejiang, Sichuan, Gansu, and Hebei) in China and to determine the relationship between geographical origin and genetic diversity. Genetic distances were calculated by means of Jaccard's coefficient and expressed as dissimilarity coefficients. Unweighted paired group method using arithmetic averages (UPGMA), Ward's minimum-variance method, VARCLUS, and multidimensional scaling (MDS) were applied to define the genetic relationships. AMOVA identified significant genetic differences between all pairs of provinces except between Zhejiang and Sichuan. The greatest difference was observed between Hebei and Zhejiang. There was disagreement among the clustering methods, but each procedure identified clusters of accessions that originated from the same province. Based on data from all clustering procedures, six major clusters containing a total of 32 accessions were defined with each cluster dominated by accessions from a single province. These data provide additional evidence that primitive cultivars of China were generally genetically isolated in relatively small geographical areas.

Seventeen potato genotypes were studied separately both in the sub-tropical plains and the temperate hills for estimation of genetic divergence using Mahalanobis's D^2 statistic by Joseph *et al.* (1999). The clustering pattern was different under the sub-tropical and the temperate conditions where the 17 genotypes were grouped into 8 and 6 clusters, respectively. There was very little common with regard to distribution of different genotypes into different clusters under the two conditions. Cluster I was the largest in both the growing conditions. The maximum genetic distance was between cluster II and V and the minimum genetic distance was between cluster VI and VII under sub-

tropical conditions, whereas, the maximum genetic distance was between cluster II and VI and the minimum genetic distance was between cluster II and IV under temperate conditions. Intra-cluster distances were lower than the inter-cluster distances and the major contributor to genetic divergence was tuber yield under both the conditions. The genetic diversity was not related to geographic diversity as genotypes originating in different countries were grouped together in the same cluster.

Genetic divergence among 42 bottle gourd (*Lagenaria siceraria* Mol. Standl.) accessions was estimated by Islam, Md. Tariqul (2004) using D^2 and canonical analysis. The accessions were grouped into five clusters. No clear relationship was observed between geographic origin and genetic diversity. The maximum inter-cluster distances were between cluster I and cluster II, and the minimum was between cluster III and cluster IV. Primary branches per plant, fruit length and weight, number of fruits and yield per plant contributed maximum to the total genetic divergence. The results obtained by D^2 analysis were also confirmed by canonical analysis. The accessions included in the most divergent clusters I and II, are promising parents for a hybridization programme for obtaining high heterosis and thus better segregants in bottle gourd.

An investigation was conducted by Rio and Bamberg (2002) and collecting germplasm to broaden breeding resources is an essential activity of genebanks. Research to understand how genetic diversity is partitioned in nature might help to identify collections rich in diversity. Previous studies among wild populations of *Solanum fendleri* (a disomic polyploid selfer) and *S. jamesii* (a diploid outcrosser) revealed no significant associations between genetic and ecogeographic variation. Even physical separation did not predict genetic differences. In this study, 28 populations of *S. sucrense* Hawkes (2n=4x=48), a Bolivian species with another breeding system (polysomic polyploid oucrosser), were evaluated. The objective was to assess whether genetic differences between populations are predicted by differences in geographic parameters at the natural site of origin. Genetic differentiation was

estimated by using 216 RAPD markers. The average genetic distance (GD) found between pairs of populations was 31% (ranging from 8% to 44%). Correlations of GD with latitude, longitude, altitude and distance were not significant. Multiple regression analysis also confirmed that GD was not explained by the geographic parameters used. We conclude that geographic origin data is not very useful in gauging interpopulation genetic diversity in the genebank.

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. The 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.

Sarma *et al.* (2000) was carried out an investigation of thirty-four genotypes of brinjal *(Solanum melongena* L.) from diverse sources were grouped into 10 clusters. Perimeter of fruit and average weight of fruit had great impact on grouping. Eco-geographic diversity of the genotypes was not found to be clearly related to genetic diversity.

Investigation of twenty two potato genotypes (2 of subsp. andigena and the rest of sub sp. *tuberosum*) were evaluated by Gopal (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*).

Genetic divergence using Mahalanobis's D^2 statistic in 40 diverse types of brinjal studied by Yadav *et al.* (1996). 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.

An experiment was conducted by Tambe *et al.* (1993) studied the diversity using D^2 analysis among 25 diverse varieties/lines 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 varieties/ lines of tomatoes was studied by Petter and Rai (1976) found that genetic and geographical divergence was not related.

Twenty-six varieties of potato were subjected to multivariate analysis by Sidhu and Pandita (1980) to study divergence among them. Out of the 5 characters studied, number of stems and tuber weight were the major contributors towards divergence in the material under study. On the basis of

Mahalanobis's D^2 values, the 26 varieties were grouped in 6 clusters. Generally, geographic diversity was not related to genetic diversity.

An investigation was conducted by Gaur *et al.* (1977) with sixty-seven potato varieties/hybrids were grouped in 15 clusters on the basis of D^2 values. The clustering pattern was not influenced by the geographic diversity of the varieties. However, segregation between varieties of the *Tuberosum* and *Andigena* type varieties was observed. The exotic potato varieties and also the Indian varieties bred from Tuberosums showed a poor divergence. In contrast, the divergence in the varieties developed from *Tuberosum-Andigena* crosses was much greater. The inter-cluster distance of such varieties, with respect to *Tuberosum and Andigena* clusters, appeared to be influenced by the cytoplasm they carried. The varieties with *Tuberosum* cytoplasm were closer to clusters having *Tuberosum* varieties and those with *Andigena* cytoplasm were closer to clusters having *Andigena* type varieties. The characters least influenced by the selection during the course of evolution of the present day varieties were found to be mainly responsible for adding divergence to the population. A breeding plan involving varieties from different clusters has been outlined.

2.4 Technique of Multivariate Analysis

Multivariate statistics or multivariate statistical analysis in statistics describes a collection of procedures which involve observation and analysis of more than one statistical variable at a time. Sometimes a distinction is made between univariate (e.g., ANOVA, t-tests) and multivariate statistics (K.V. Mardia *et al.* (1979).

Multivariate techniques were used to evaluate the genetic divergence among 56 accessions of chilli and sweet pepper (*Capsicum* spp.) by Amaral (2005) from the germplasm collection of Universidade Estadual do Norte Fluminense. Eleven quantitative descriptors proposed by International Plant Genetic Resources Institute were utilized in a field experiment carried out in Campos dos Goytacazes, Rio de Janeiro State, Brazil. Generalized Mahalanobis

distance (D^2) was used as dissimilarity measure. Canonical variate analysis, cluster analysis using Tocher's optimization method and distances in the plan were applied. The variables: fruit length, fruit diameter, number of seeds per fruit, fruit average weight, plant height, plant canopy width, 1000-seed weight, days to flowering, days to fruiting, fruit number per plant and fruit weight per plant were evaluated. There were significant differences among accessions for all descriptors evaluated. General agreement among all multivariate techniques used was observed and it was possible to separate the accessions in eight distinct groups, indicating that there is genetic variability for the evaluated traits.

An investigation was taken up by Rama Subrahmanyam *et al.* (2003) at the Directorate of Oilseeds Research, Hyderabad, India, to determine the extent of genetic divergence with respect to eleven characters in 85 sunflower genotypes consisting of 80 inbreds and five check cultivars. Univariate and multivariate analysis of variance revealed the presence of significant differences among the genotypes. Mahalanobis' D^2 statistic indicated the presence of substantial genetic diversity. The genotypes were grouped into fifteen clusters. Based on the inter-cluster distance and cluster mean for various characters, potential lines were identified from clusters III, IV, VI, VIII, XI, XII and XIV for crossing program. Among the investigated characteristics, the number of filled seeds per head, test weight, kernel to hull ratio and seed yield per plant exhibited high contribution towards genetic divergence.

The phenetic divergence among 19 clones of cactus forage was evaluated in *Caruaru, Pernambuco*, Brazil using multivariate techniques by Ferreira *et al.* (2003). The experimental design was a complete block design, with three blocks. The length, width, thickness, number and weight of the green matter, presence of thorns, number of cladodios for order and total, total height, infestation of cochineal and weight of the green matter were measured. Analyses of variance (ANOVA) and multivariate (MANOVA), the canonical variables (CV), and cluster analysis (CA) were used. In ANOVA, differences were verified among the clones. Differences among vectors of averages of clones were detected by means of MANOVA. It was possible to reduce the

original dimension for two dimensions, which explained 85.03% of the total variation, by applying VC. The infestation percentage by cochineal was considered a characteristic of susceptible plants. In CA, nine groups were identified. In the studied conditions, the characteristic infestation percentage for cochineal should not be included in the study of the genetic diversity; the characteristics of importance were thickness average for cladodio primary, secondary and tertiary, number of primary cladodio and medium weights of green matter for secondary and tertiary cladodio. In breeding for cactus forage, the group of clones and the clone performance must be considered.

It was reported by Dharmatti *et al.* (2001) that genetic diversity in a population of 402 tomato lines 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 lines 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 might be useful for heterosis breeding in summer tomato.

Selection of parents based on genetic divergence is a prerequisite in a heterosis breeding program. The parents need to be selected from diverse groups so as to generate genetic variability. Since hybrid vigor essentially depends on genetic divergence of parents, it is necessary to identify diverse parents for hybridization. Multivariate analysis by means of Mahalanobis' D^2 statistic has been widely used for assessing the genetic divergence in several crops. It is a powerful tool in quantifying the degree of genetic divergence among parents (Joshi and Singh, 1979; Muppidathi *et al.* 1995).

In study of genetic diversity with thirty-nine accessions of Panikachu or aquatic taro through multivariate analysis, Mannan *et al.* (1994) observed that

plant height, number of stolons per plant and length of stolons contributed maximum towards total divergence.

Balasch *et al.* (1984) conducted an experiment and measured twenty characters on 60 tomato varieties cultivated in the open-air and in polyethylene plastic-house. Data were analyzed by means of principal components, factorial discriminant methods, Mahalanobis D^2 distances and principal coordinate techniques. Factorial discriminant and Mahalanobis D^2 distances methods, both of which require collecting data plant by plant, lead to similar conclusions as the principal components method that only requires taking data by plots. Characters that make up the principal components in both environments studied are the same, although the relative importance of each one of them varies within the principal components. By combining information supplied by multivariate analysis with the inheritance mode of characters, crossings among cultivars can be experimented with that will produce heterotic hybrids showing characters within previously established limits.

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.

The analysis of data was done by Estevez *et al.* (1994) 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.

An experiment was conducted by Birhman *et al.* (1991) and 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 lines. 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.

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, Peyne *et al.* (1989). 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.

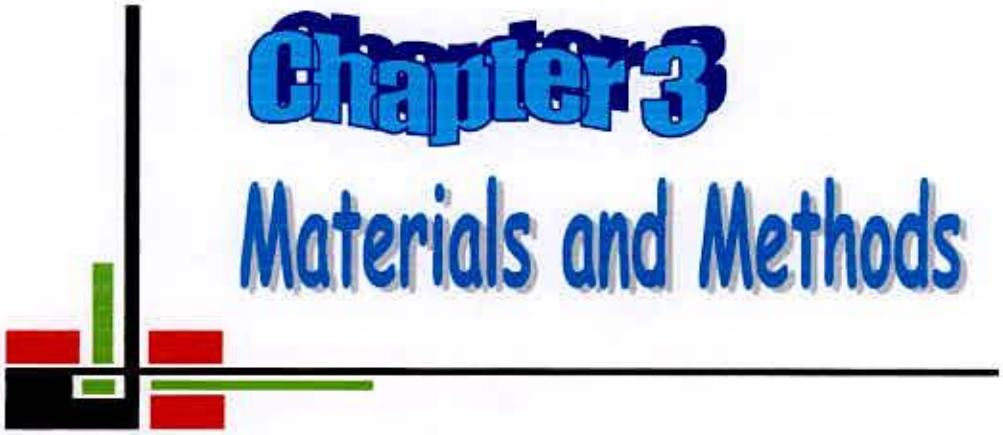
Naskar *et al.* (1985) reported from his experiment that cluster analysis was applied to 9 characters in 22 diverse. Indian genotypes in 1981 and 1982, all

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 varieties/lines were reported by Balasch (1986). 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 D^2 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.

Kumar and Kang (1998) conducted an investigation by using Multivariate analysis for genetic divergence among thirty *Andigena* accessions by D^2 statistics led to their grouping into seven clusters. D^2 estimates were based on eleven characters. The clustering pattern in pooled analysis was used for selecting diverse parents. Cluster VII and IV, VII and V, VII and VI, IV and I, IV and III, and II and VII had high inter-cluster distances. Cross involving parents from these cluster combinations were recommended for an Andigena breeding programme.



Chapter 3

Materials and Methods

CHAPTER III
MATERIALS AND METHODS

3.1 Experimental Site

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during October, 2006 to April, 2007. The location of the experimental site was situated at $23^0$41' N latitude and $90^0$22' E longitude with an elevation of 8.6 meter from the sea level (Figure 1). The physical and chemical characteristics of the soil have been presented in Appendix I.

3.2 Climate and Soil

The experimental site was situated in the subtropical zone. The soil of the experimental site lies in Agroecological region of "Madhupur Tract" (AEZ No. 28) of Norda soil series. The soil is sandy loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 5.47 to 5.63 and organic carbon content is 0.82% (Appendix I).The mean temperature during the research period was 24.21^0C with average maximum and minimum being 29.4^0C and 19.03^0C respectively. The record of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix II).

3.3 Genotypes

A total number of 34 (thirty four) genotypes were used in this experiment. The seeds of the eighteen genotypes was collected from Chittagong, three F_1 (Hybrid) were collected from the Department of Genetics and Pant Breeding, SAU, nine genotypes including five released varieties were collected from Bangladesh Agricultural Research Institute (BARI) and rest of the four

genotypes were collected from four Non- Governments Seeds Companies like East-West Seed (Bangladesh) Ltd. (Lal Tere), Nadim Seed Company, Momin Seed Ghar and Metal Agro Limited.

3.4 Design and Layout

The experiment was laid out in Randomized complete Block Design (RCBD) with three replications. The total area of the experiment was 31.7m X 27.10 m = 859.07 m^2. The unit size was 29.7 m X 7.70 m, and the distance between two units was 1 m. Each replication contains 408 plants of thirty four genotypes with the spacing of 0.90 m X 0.70 m. The thirty four genotypes were distributed to each plot within each unit randomly (Figure 2).

3.5 Raising of Seedling

Individual seed bed was prepared for different varieties following standard method of bed preparation. Seeds were sown in lines in well prepared seed beds on 17th October 2006. The seeds were sown at about 1.25 cm depth and were covered uniformly with light soil for proper germination. Heptachlor was dusted over the seedbed to prevent the seedling mainly from ant attack. 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 30 days of age the seedlings were transplanted to the Experimental Plot.

3.6 Land Preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with power tiller and country plough to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on15 November 2006.

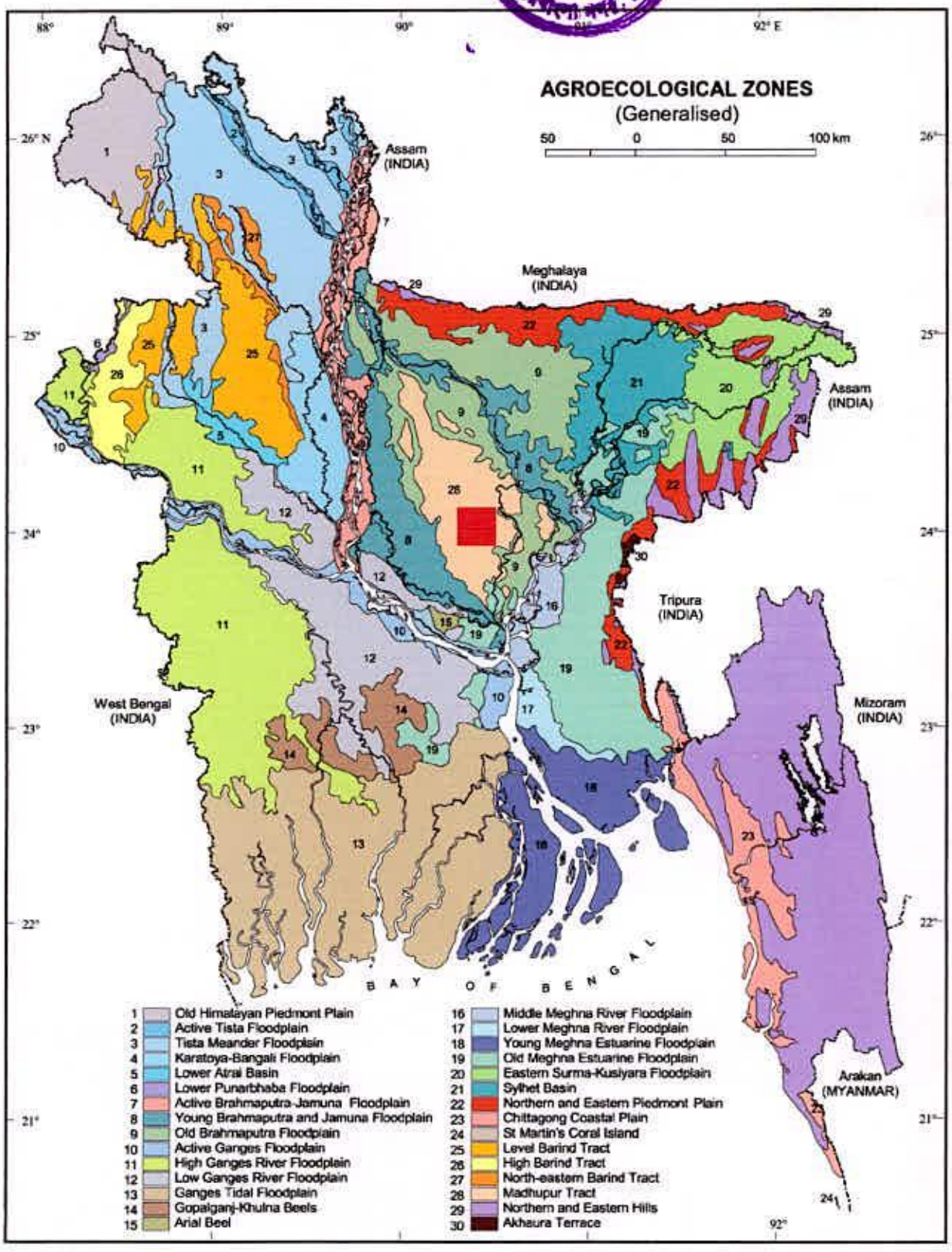


Figure 1. Location of the experimental field

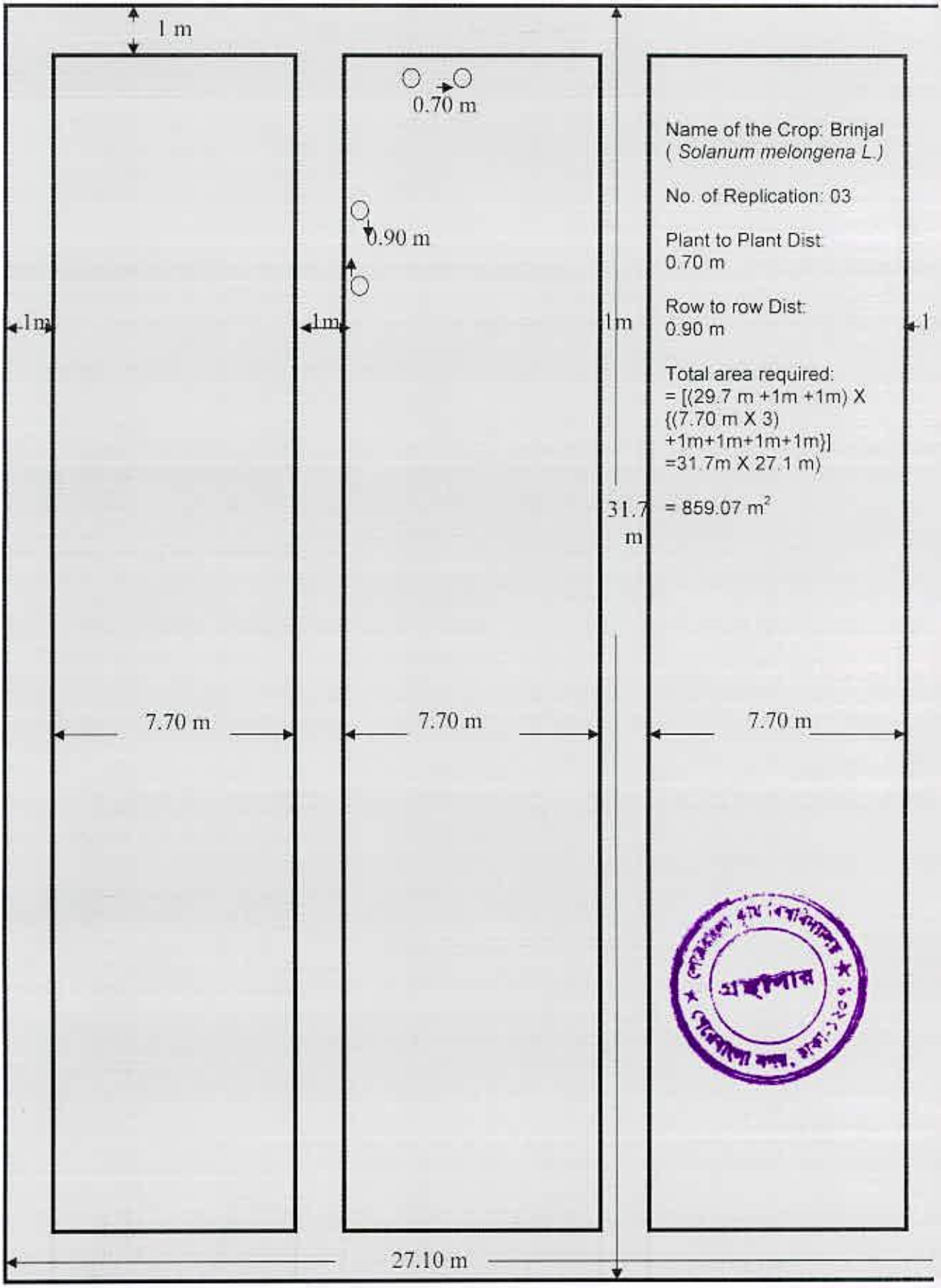


Figure 2. Layout of the experimental plot

Table 1. Sources of 34 brinjal genotypes

Sl. No.	Designation	Genotypes	Name of the Lines	Sources
01	G-01	Line-03	Ac. No. 03	BARI Chitg
02	G-02	Line-04	Ac. No. 04	BARI Chitg
03	G-03	Line-08	Ac. No. 08	BARI Chitg
04	G-04	Line-09	Ac. No. 09	BARI Chitg
05	G-05	Line-10	Ac. No. 10	BARI Chitg
06	G-06	Line-11	Ac. No. 11	BARI Chitg
07	G-07	Line-13	Ac. No. 12	BARI Chitg
08	G-08	Line-14	Ac. No. 14	BARI Chitg
09	G-09	Line-15	Ac. No. 15	BARI Chitg
10	G-10	Line-16	Ac. No. 16	BARI Chitg
11	G-11	Line-17	Ac. No. 17	BARI Chitg
12	G-12	Line-18	Ac. No. 18	BARI Chitg
13	G-13	Line-19	Ac. No. 19	BARI Chitg
14	G-14	Line-20	Ac. No. 20	BARI Chitg
15	G-15	Line-21	Ac. No. 21	BARI Chitg
16	G-16	Line-22	Ac. No. 22	BARI Chitg
17	G-17	Line-23	Ac. No. 23	BARI Chitg
18	G-18	Line-27	Ac. No. 27	BARI Chitg
19	G-19	Line-30	BL -117	BARI Gazi
20	G-20	Line-31	B -009	BARI Gazi
21	G-21	Line-33	BK -18	BARI Gazi
22	G-22	Line-34	BL- 114	BARI Gazi
23	G-23	BARI-1	Uttara	BARI Gazi
24	G-24	BARI-4	Kajla	BARI Gazi
25	G-25	BARI-5	Nayontara	BARI Gazi
26	G-26	BARI-6	BARI-6	BARI Gazi
27	G-27	BARI- 8	BARI-8	BARI Gazi
28	G-28	Volanath Begun	Volanath Begun	MSG
29	G-29	Shinhnath-60	Shinhnath-60	MAL
30	G-30	Shainnath-666	Shainnath-666	EWSL
31	G-31	NSC Shingnath	NSC Shingnath	NSC
32	G-32	Line-01 X Line-25	F_1	SAU
33	G-33	Line-23 X Line-24	F_1	SAU
34	G-34	Line-27 X Line-14	F_1	SAU

SAU – Sher-e-Bangla Agricultural University, NSC – Nadim Seed Company
BARI – Bangladesh Agricultural Research Institute, Chitg - Chittagong
MAL – Metal Agro. Limited, EWSL- East West Seed (Bangladesh) Ltd.
F_1 - First Filial Generation, MSG – Momin Seed Ghar, Gazi - Gazipur

3.7 Application of Manure and Fertilizer

The crop was fertilized at the rate of 10 tons of Cowdung, 380 kg urea, 155 kg Triple Super Phosphate (TSP) and 255 kg Muriate of Potash (MoP) per hectare. At this recommended rate 910 Kg Cowdung, 35 kg Urea, 14 kg TSP and 24 kg MoP were applied into the experimental plots. The half amount of Cowdung was applied during final land preparation. The rest amount of Cowdung and TSP, and 1/3 Urea and 1/3 of MoP were applied during the time of pit preparation. This was done before transplanting the seedlings into the experimental field. The rest of the urea and MoP 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 60 days after transplanting.

3.8 Transplanting of Seedling

Thirty days old seedlings were transplanted in well prepared experimental plot on 17th November, 2006. Twelve plants were planted for each genotype in single row in each replication maintaining plant spacing of 70 cm and row to row distance 90 cm. Shades were provided to increase seedling survivality just after transplanting. Field view of the experiment was shown in Plate 1a. and Plate 1b.

Plate 1a. Field view of the experimental site

Plate 1b. Field view of the experimental field

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 genotypes against fruit and shoot borer. Proper shading was given in the morning at the first stage of transplanting to protect the young seedlings from scorching sunshine during the day time.

3.9.1 Gap filling

Gap filling was done twice. The first gap filling was done on 23 November 2006 just after 7 days of first transplanting and the 2nd one done on 27 November 2006, which was 11 days of first transplanting.

3.9.2 Weeding

The first weeding was done after 20 days of transplanting to keep the crop free from weeds. Weeding was also done in several times when it was needed.

3.9.3 Irrigation

In the early stage of transplanting, watering was done twice daily by water cane. In mature stage, flood irrigation was done to the field when it was necessary for the crop.

3.10 Data Collection

The data were recorded on ten plants for each genotype by avoiding the two boarder plants from every replication. Data on days to first flowering, no. of flowers/ inflorescence, days to first fruit harvesting, fruit color, fruit shape, fruit curvature, amount of seed in the fruit, leaf blade lobbing, plant prickliness, plant pubescence, plant growth habit, plant height, no. of primary branches/plant, no. of secondary branches/plant, fruit length, fruit circumference, no. of fruit per plant, weight per fruit, yield per plant, percent insect infestation of plants, % insect infestation of fruits were recorded.

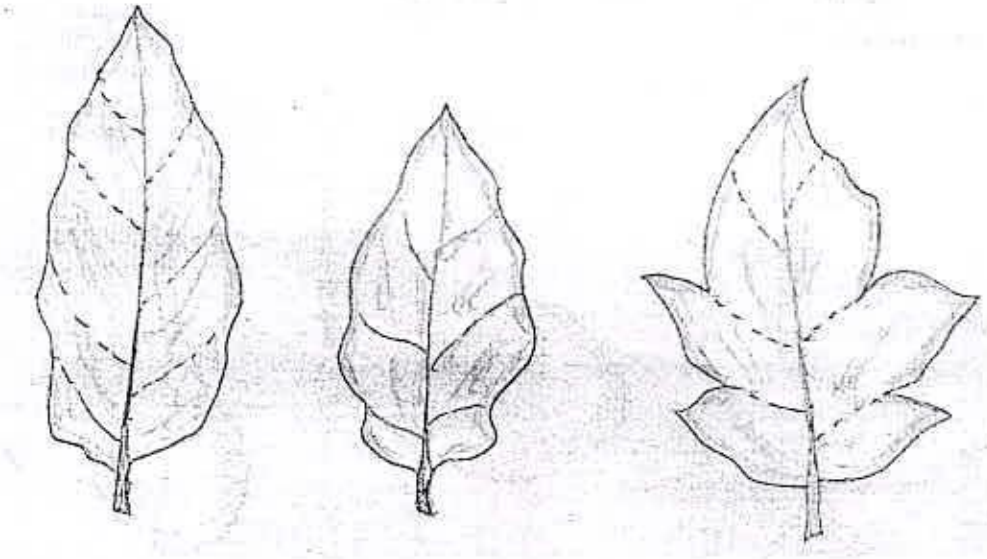
3.10.1 Growth habit

Plant growth characters were recorded according to the performance of canopy and branches. The performance of canopy and branches were observed under the following habits:

- Erect
- Semi-erect
- Spreading

3.10.2 Leaf blade lobbing

The data were recorded by observing leaf structure phenotypically as per as the following structure:



Weak **Intermediate** **Strong**

3.10.3 Shape of fruit

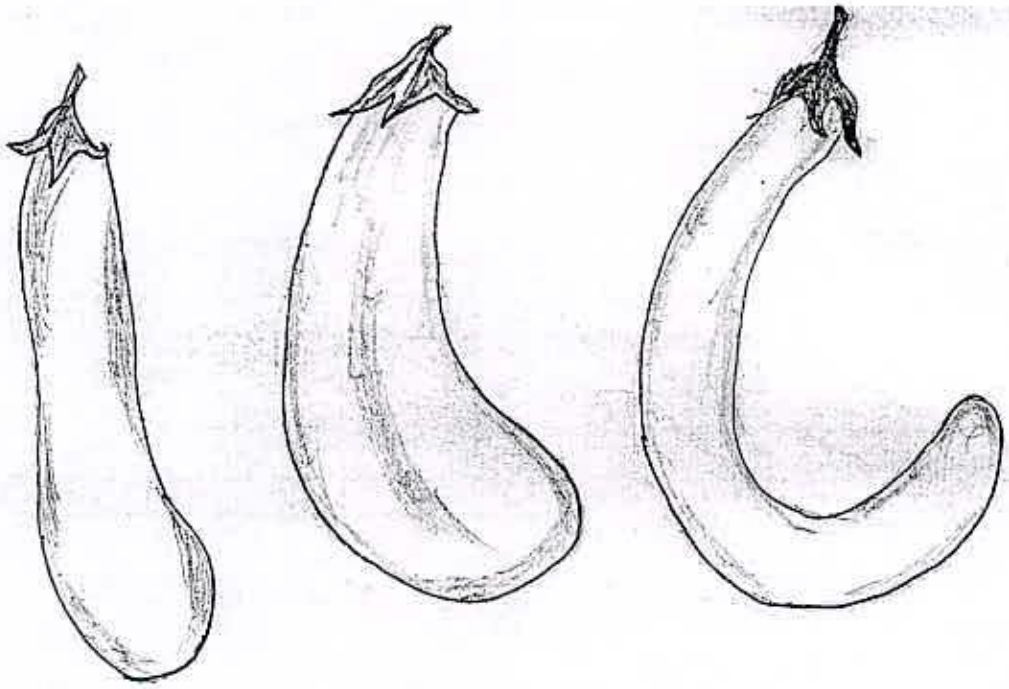
The fruit of different genotypes showed differences in their shape. The fruit of every genotype was recorded as per as the following shapes:

- Round
- Ovate
- Long
- Oblong

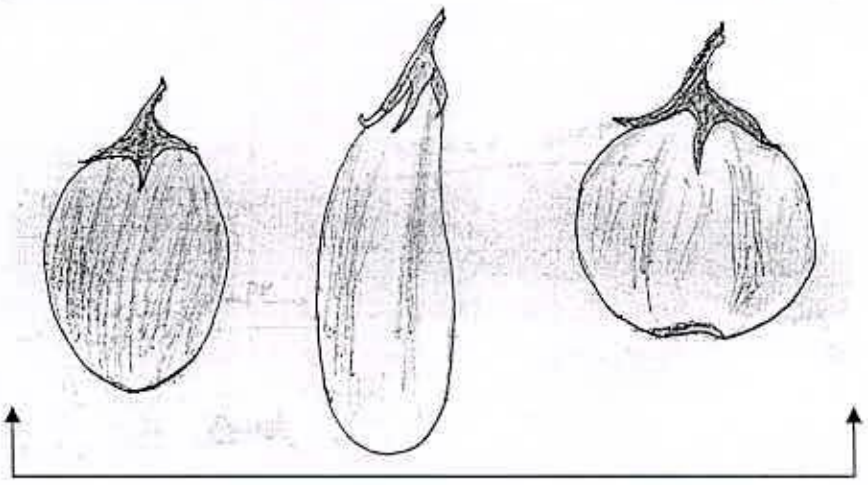
3.10.4 Fruit curvature

The data were recorded by observing the following structure of the fruits of different genotypes. Fruit curvature was divided into:

- None
- Slightly Curved
- Curved
- Sickle Shaped



Slightly Curved **Curved** **Sickle Shaped**



None

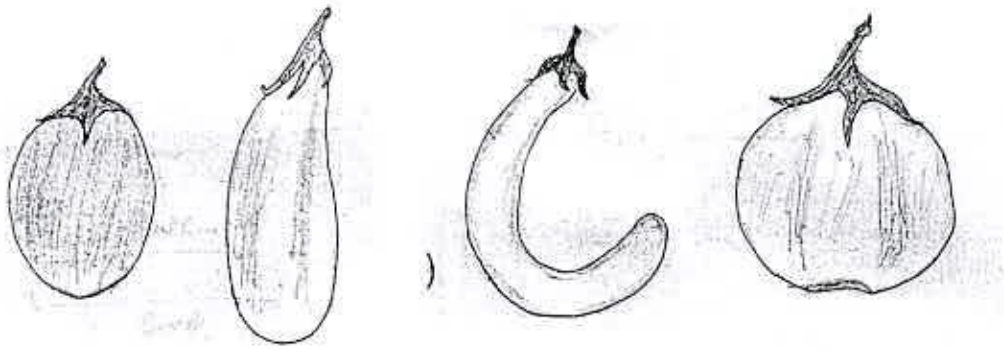
3.10.5 Color of fruit

The fruit colour of 34 (thirty four) brinjal genotypes were recorded.

3.10.6 Fruit apex shape

Fruit apex shape was recorded by watching under the following structure of the fruits.

- Protruded
- Rounded
- Depressed



Round Protruded Depressed

3.10.7 Amount of seed in the fruit

Amount of seed was observing by cutting five fruits of every genotype. By observing amount of seed in the fruit the data were recorded into three different groups ie., high, medium and low .

3.10.8 Prickliness character

The prickliness character of brinjal was recorded at mature stage of the plant. The presence of prickle in the leaf, stem, and calyx of the fruit was recorded.

3.10.9 Plant pubescence

The presence of pubescence on leaf, stem and calyx was recorded during the mature stage of the plant by touching the stem and branch of the plant.

3.10.10 Plant pigmentation

Leaf blade and stem colours were recorded by observing different brinjal genotypes phenotypically as per as the following colours:

- Green
- Greenish Violet
- Light Violet
- Violet
- Deepest Violet

3.10.11 Plant height

Length of main stem from ground level to the longest tip of the stem was measured at middle stage of harvesting period. The data were measured in centimeter (cm).

3.10.12 Number of primary branches per plant

Number of primary branches of each plant under each genotype recorded at the mature stage of the plant.

3.10.13 Number of secondary branches per plant

The total number of secondary branches of each plant present in each genotype were counted and recorded.

3.10.14 Days to first flowering

Days to first flowering were recorded from transplanting date to the date of first flowering of every plant of every genotype.

3.10.15 Number of flowers/inflorescence

The total number of flowers present in an inflorescence of an individual plant of each genotype was recorded.

3.10.16 Days to first fruit harvest

The data were recorded from the date of transplanting to the date to first fruit harvest of every single plant of every genotype.

3.10.17 Fruit length

Length from the top to the bottom of 5 initially matured fruits per plant was measured in centimeter (cm) and recorded.

3.10.18 Fruit circumference

The fruit circumference of every genotype measured along the middle part of the harvestable mature fruits. The data were measured in centimeter.

3.10.19 Weight per fruit

After harvesting each of fruit of an individual plant weighing in gram (gm) and the weight of the fruit of every genotype was recorded.

3.10.20 Number of fruits per plant

The number of fruits harvested from each plant of each genotype was recorded.

3.10.21 Yield per plant

The total number of fruits harvested in different times from each selected plant in each replication of each genotype was weighted in kilogram (Kg) and yield per plant was recorded.

3.10.22 Percent insect infestation of fruits

Five fruits of each plant were cutting and infected fruits were counted. The rate of insect infestation against different genotypes was calculated in percentage.

3.10.23 Percent insect infestation of plants

Brinjal lines were intensively observed phenotypically and the total number of infected plants was counted. The percentage of insect infestation was calculated under different genotypes.

3.11 Statistical Analysis

Genetic divergence is one of the most important parameters evaluated by plant breeders in starting a breeding program. This is a necessary, but not sufficient, condition for the occurrence of heterosis and the generation of a population with broad genetic variability. Subsequently, heterosis is directly proportional to genetic divergence and to dominance squared (Falconer, 1981; Cruz, 1990; Ferreira, 1993) and is also associated with adaptation. A second approach is to use multivariate methods to estimate genetic divergence and then predict hybrid performance. In this case, it is not necessary to make crosses. Furthermore, a large number of materials may be successfully evaluated (Hallauer and Miranda Filho, 1981).

In the latter approach, a large number of traits must be measured. A canonical variate technique is often used to reduce the number of these traits, through a linear combination of them, without a significant loss of the total variation. Additionally, this technique takes into account the structure of residual covariances. Thus, it allows plant breeders to obtain information about traits that are important for genetic divergence among varieties.

The concept of D^2 statistics was originally developed by P.C. Mahalanobis in 1928. He used this technique in the study of Antropomatry and Psychometry. Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. Now this technique is extensively used in plant breeding and genetics for the study of genetic divergence in the various breeding materials. This is one of the potent techniques of measuring genetic divergence. In plant breeding, Genetic diversity plays an important because hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related parents. This has been observed in fescue, maize, alfalfa, cotton and several other crops. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability.

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.

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 Peyne *et al.* (1989). Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. Peyne *et al.* (1989) 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 Variability of Brinjal Genotypes

3.11.1.1 Estimation of Phenotypic and Genotypic Variance

Genotypic and phenotypic variances were estimated by Johnson *et al.* (1955). Genotypic variance (σ^2_g) was obtained by subtracting genotype mean sum of squire to error mean sum of squire and dividing by the number of replication as given below:

$$\text{Genotypic Variance } (\sigma^2_g) = \frac{\text{GMS - EMS}}{\text{Number of replication (r)}}$$

Where, GMS = Genotypic mean sum of squire

EMS = Error mean sum of squire

The phenotypic variances (σ^2_p) were come from by adding genotypic variances (σ^2_g) with error variance (σ^2_e) as shown by the given formula:

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

3.11.1.2 Estimation of Genotypic and Phenotypic Coefficient of Variation

According to the Johnson *et al.* (1955) genotypic and phenotypic coefficient of variation were estimated

$$\textbf{Genotypic Coefficient of Variation (GCV)} = \frac{\sigma_g}{\textbf{Grand Mean}}$$

Where,

σ_g = Genotypic standard deviations

$$\textbf{Phenotypic Coefficient of Variation (PCV)} = \frac{\sigma_p}{\textbf{Grand Mean}}$$

Where,

σ_p = Phenotypic standard deviations

3.11.1.3 Estimation of Heritability

Johnson *et al.* (1955) was suggesting a formula for estimating broad sense heritability.

$$\% \, h^2b = \frac{\sigma^2_g}{\sigma^2_p} \quad X\ 100$$

Where,

h^2b = Heritability in broad sense
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

3.11.1.4 Estimation of Genetic Advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Johnson *et al.* (1955)

$$\text{Genetic Advance (GA)} = \frac{\sigma^2_g}{\sigma^2_p} \times K \times \sigma_p$$

Where,

K = Selection intensity, the value of which is 2.06 at 5 % selection intensity
σ_p = Phenotypic standard deviation
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

3.11.1.5 Estimation of Genetic Advance in Percentage of Mean

Genetic advance in percentage of mean was calculated from the formula given by Comstock and Robinson (1952).

$$\text{Genetic Advance in Percentage of Mean} = \frac{\text{Genetic Advance}}{\text{Grand Mean}} \times 100$$

3.11.2 Genetic Diversity Analysis

3.11.2.1 Principal Component Analysis (PCA)

It is a way of identifying patterns in data, and expressing the data in such a way as to highlight their similarities and differences. Since patterns in data can be hard to find in data of high dimension, where the luxury of graphical representation is not available, PCA is a powerful tool for analyzing data. The purpose of principal component analysis is to derive a small number of linear combinations (principal components) of a set of variables that retain as much of the information in the original variables as possible.

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.

3.11.2.2 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).

3.11.2.3 Clustering

The term *cluster analysis* (first used by Tryon, 1939) encompasses a number of different algorithms and methods for grouping objects of similar kind into respective categories.

In multivariate analysis, cluster analysis refers to methods used to divide up objects into similar groups, or, more precisely, groups whose members are all close to one another on various dimensions being measured. In cluster analysis, one does not start with any apriori notion of group characteristics. The definition of clusters emerges entirely from the cluster analysis - i.e. from the process of identifying "clumps" of objects.

Cluster analysis is an exploratory data analysis tool for solving classification problems. Its object is to sort cases (people, plant, things, events, etc) into groups, or clusters, so that the degree of association is strong between members of the same cluster and weak between members of different clusters. Each cluster thus describes, in terms of the data collected, the class to which its members belong; and this description may be abstracted through use from the particular to the general class or type.

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, he algorithm switched to a second stage, which examined the effect of swapping two genotypes of different classes and so on.

3.11.2.4 Canonical Variate Analysis (CVA)

Discriminant function or canonical variate analysis attempt to establish whether a set of variables can be used to distinguish between two or more groups.

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.

Several techniques that seek to illuminate the ways in which sets of variables are related one another. The term refers to regression analysis, MANOVA, discriminant analysis, and, most often, to canonical correlation analysis.

3.11.2.5 Cluster Diagram

In D^2 analysis a line diagram is constructed with the help of D^2 values which is known as cluster diagram. The squires roots of average intra and inter cluster D^2 value are used in the construction of cluster diagram. This diagram provides information on the following aspects:

- The depicts the genetic diversity in an easily understandable manner.
- The number of cluster represents the number of groups in which a population can be classified on the basis of D^2 analysis.

- The distance between two clusters in the measure of the degree of diversification. The greater the distance between two cluster the greater the divergence and vice versa.
- The genotypes filling in the same cluster are more closely related then those belonging to another cluster. In other words, the genotypes grouped together in one cluster are less divergent than those which are placed in different cluster.
- It provides information about relationship between various clusters.

A cluster diagram was drawn using the values ($\sqrt{D^2}$) 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.

3.11.2.6 Selection of Genotypes for Future Hybridization Programme

Genotypes were selected from the study for future hybridization programme considering genetic variability and other performances related to yield (kg), number of fruit per plant, color of fruit and presence and absence of prickle, number of primary branches, number of secondary branches, no. of flower per inflorescence, days to first flowering, weight per fruit (gm), percent insect infestation of fruits, percent insect infestation of plants, curvature of the fruit, fruit length (cm) and fruit circumference (cm).

Chapter 4

Results and Discussion

CHAPTER IV
RESULTS AND DISCUSSION

The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to screen better genotypes. Therefore, to generate information in the degree of diversity thirty four lines of brinjal were raised in the growing season of 2006-2007 at the field of Sher-e-Bangla Agricultural University, Dhaka. The data in respect of plant height, days to first flowering, no. of flowers per inflorescence, no. of primary branches per plant, no. of secondary branches per plant, fruit length, fruit circumference, individual fruit weight, no. of fruit per plant, yield per plant, plant prickliness, plant pigmentation, fruit shape, fruit color, fruit curvature etc. were recorded, analyzed and presented in this chapter.

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. Performance of 34 genotypes of eggplant was investigated in winter season and the findings of present study have been discussed under different morphological characters. The result of the study showed marked variation in different characters and the variation of different characters are presented in the following Tables, Figures and Plates.

The data pertaining to ten characters were computed and statistically analyzed and the results obtained are described below:

4.1 Characterization of brinjal

4.1.1 Morphological characterization based on grading

4.1.2 Characterization of brinjal genotypes on the basis of yield and yield contributing characters

4.2 Variability of brinjal genotypes on the basis of yield and yield contributing characters

4.3 Genetic diversity presents among the brinjal genotypes

4.1 Characterization of Brinjal

4.1.1 Morphological Characterization Based on Grading

4.1.1.1 Plant growth habit

Plant architecture is an important character to the breeders for improvement of plant ideotype under given environment. The lines studied have been grouped into three distinct characteristics viz. erect, semi-erect and spreading. The genotypes G21, G22, G23, G24 and G25 were spreading type; genotypes G02, G04, G12 G13, G14, G17, G19, G28, G29, G30, G31 and G33 were erect in growth habit while the rest of the lines were semi erect in growth habit (Table 2 A).

4.1.1.2 Leaf blade lobbing

Leaf blade lobbing is an important traits to choice a brinjal genotypes for future breeding programme. Leaf blade lobbing can help to a breeder to know the information on photosynthesis rate. Strong leaves can have a grater opportunity to get maximum sunlight than the weaker leaves. The strong leaves holder genotypes were shown better growth than the intermediate and weaker leaves holder genotypes. The genotypes G01, G03, G17, G22, G23 and G24 were seen weaker leaf blade; G19, G26, G27 and G32 were strong leaf blade and rest of the genotypes were intermediate habit in their leaf blade lobbing (Table 2 A).

4.1.1.3 Fruit shape

Fruit shape is an important consumer preference trait in brinjal marketing. Various types of brinjal were found according to their different shape. From the thirty four genotypes long, ovate, oblong and round shaped brinjal were observed. The genotypes G19, G20, G23, G27, G28, G29, G30 and G31, produced long fruits, genotypes G03, G13, G14, G17, G18, G21, G22, G32, G33 and G34 produced ovate fruits and genotypes G24 produced oblong fruits. The rest of the genotypes produced more or less round fruits (Table 2 A).

Table 2. A. Characterization of 34 of brinjal genotypes

G. No.	Name of Genotypes	Plant Growth Habit	Leaf Blade Lobbing	Fruit Shape	Fruit Curvature	Fruit Color	Fruit Apex Shape	Amount of Seed in the Fruit
01	Line-03	Semi Erect	Week	Round	None	Green	Rounded	Medium
02	Line-04	Erect	Intermediate	Round	None	Green	Rounded	Medium
03	Line-08	Semi Erect	Week	Ovate	None	Green	Rounded	Low
04	Line-09	Erect	Intermediate	Round	None	Whitish Green	Rounded	Medium
05	Line-10	Semi Erect	Intermediate	Round	None	Whitish Green	Protruded	Many
06	Line-11	Semi Erect	Intermediate	Round	None	Whitish Green	Rounded	Many
07	Line-13	Semi Erect	Intermediate	Round	None	Whitish Green	Depressed	Medium
08	Line-14	Semi Erect	Intermediate	Round	None	Green	Rounded	Medium
09	Line-15	Semi Erect	Intermediate	Round	None	Green	Depressed	High
10	Line-16	Semi Erect	Intermediate	Round	None	Green	Rounded	Low
11	Line-17	Semi Erect	Intermediate	Round	None	Whitish Violet	Depressed	Low
12	Line-18	Erect	Intermediate	Round	None	Greenish Violet	Depressed	Medium
13	Line-19	Erect	Intermediate	Ovate	None	Greenish Violet	Protruded	Medium
14	Line-20	Erect	Intermediate	Ovate	None	Whitish Violet	Depressed	Medium
15	Line-21	Semi Erect	Intermediate	Round	None	Green	Depressed	Medium
16	Line-22	Semi Erect	Intermediate	Round	None	Violet	Depressed	Medium
17	Line-23	Erect	Weak	Ovate	None	Green	Rounded	Many
18	Line-27	Semi Erect	Intermediate	Ovate	None	Whitish violet	Rounded	Medium
19	Line-30	Erect	Strong	Long	Curved	Whitish violet	Protruded	Medium
20	Line-31	Semi Erect	Intermediate	Long	Curved	Green	Protruded	Low
21	Line-33	Spreading	Intermediate	Ovate	None	Purple	Depressed	Medium
22	Line-34	Spreading	Weak	Ovate	None	Purple	Depressed	Low
23	BARI-1	Spreading	Intermediate	Long	Slightly Curved	Light Violet	Protruded	Medium
24	BARI-4	Spreading	Intermediate	Oblong	Slightly Curved	Blackish Purple	Protruded	Medium
25	BARI-5	Spreading	Intermediate	Round	None	Deep Purple	Depressed	Low

Table 2 A. (Cont'd.)

G. No.	Name of Genotypes	Plant Growth Habit	Leaf Blade Lobbing	Fruit Shape	Fruit Curvature	Fruit Color	Fruit Apex Shape	Amount of Seed in the Fruit
26	BARI-6	Semi Erect	Strong	Round	None	Light Green	Rounded	Medium
27	BARI-8	Semi Erect	Strong	Long	Slightly Curved	Purple	Rounded	Medium
28	Volanath Begun	Erect	Intermediate	Long	Slightly Curved	Purple	Rounded	Low
29	Shinhnath-60	Erect	Intermediate	Long	Curved	Purple	Rounded	Many
30	Shainnath-666	Erect	Intermediate	Long	Sickle Shaped	Blackish Violet	Protruded	Low
31	NSC Shingnath	Erect	Strong	Long	Slightly Curved	Red Violet	Protruded	Low
32	Line-01 X Line-25	Semi Erect	Strong	Ovate	None	Greenish Violet	Rounded	Medium
33	Line-23 X Line-24	Erect	Intermediate	Ovate	None	Whitish green	Rounded	Many
34	Line-27 X Line-14	Semi Erect	Intermediate	Ovate	None	Whitish green	Depressed	Medium

4.1.1.4 Fruits curvature

Fruit Curvature is a one of the important morphological traits that has a direct effect on consumer preference and marketing value of brinjal. Fruit curvatures were recorded under the following categories: none, slightly curved, curved and sickle shape. Genotypes 30 produced sickle shape, G19, G20 and G29 produced curved shaped; G23, G24, G27, G28 and G31 was produced slightly curved brinjal and rest of the genotypes had no curvature of their fruits (Table 2 A).

4.1.1.5 Fruits colour

Fruit color is one of the important traits for consumer preference 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, whitish green, whitish violet, purple, light green, greenish violet, light violet, red violet and blackish purple. The genotype G16 produced violet fruit; purple fruits were produced in G21, G22, G27, G28 and G29; blackish purple were observed in G24 and G25; whitish violet fruits were G11, G14, G18 and G19; red violet fruits were G31; greenish violet fruits were G12, G13 and G32; and light violet fruit was observed in G23; light green was G26 and the rest of the genotypes were produced green and whitish green fruit (Table 2 A). This variation offered a good scope for breeding consumer preference attributes.

4.1.1.6 Fruit apex shape

Fruit apex shape is another important character for brinjal purchaser, because it plays a critical impact on consumer preference. Fruit apex shape was divided into three groups: protruded, depressed, and round. Genotype 13, G20, G23, G30 and G31 produced protruded fruit apex shape, genotype 07, G09, G11, G12, G14, G15, G16, G21, G22, G25 and G34 produced depressed apex shaped fruits while the rest of the genotypes produced round apex shape fruits (Table 2 A).

4.1.1.7 Amount of seed in the fruits

The high amount of seeds present in the fruit had a negative impact on consumer test and preferences for particular lines/varieties. The genotype 03, G10, G11, G20, G22, G25, G28 and G30 produced lower number of seeds, G05, G06, G09, G17, G29 and G33 was produced many seeds and rest of the genotypes produced medium number of seeds (Table 2 A). Relative amount of seeds in different brinjal genotypes is presented in Plate 2.

4.1.1.8 Plant prickliness

Various types of brinjal lines are characterized by their prickliness habit. It is an important character which is related to insect resistance. Different genotypes were classified having prickle in their fruit/calyx, stem and leaves. The data were recorded according to presence of none, low, medium and high prickle in different genotypes. The genotypes 32 had high or maximum prickle and genotype G03 had medium prickle and G05, G13, G15, G23, G27 and G28 had low prickle in leaves, stem and calyx/fruit respectively. The genotypes G06, G14, G18, G20 and G22 had medium prickle on their stem and calyx/fruits and low or none prickle presence on their leaves (Table 2 B).

4.1.1.9 Plant pubescence

Plant pubescence is an important character of brinjal plant. This character is related to its resistance against pest. The more densely pubescence plant is more resistance against pest. All the genotypes under study were characterized by the presence of pubescences. Pubescence was observed by touching leaf, stem and calyx/fruit. Out of thirty four brinjal genotypes some genotypes had low pubescence and some have intermediate pubescence in their leaves stems and calyx/fruits.

The genotypes G01, G03, G04, G05, G07, G08, G10, G15, G18, G20, G29 and G30 had intermediate pubescence on their leaves, stems and calyx/fruits while the genotypes G06, G11, G12, G14, G16, G17, G23, G24, G25, G26, G27, G28, G31, G32 and G33 had low pubescence on their leaves, stems and fruits/calyx (Table2 B).

Table 2 B. Characterization of 34 brinjal genotypes

G. No.	Name of Genotypes	Plant Prickliness			Pubescence of the Plant			Plant Pigmentation	
		Leaf	Stem	Calyx/ Fruit	Leaf	Stem	Fruit/ Calyx	Leaf	Stem
01	Line-03	None	Low	Low	Intermediate	Intermediate	Intermediate	Green	Green
02	Line-04	None	Low	Low	Intermediate	Low	Low	Green	Light Violet
03	Line-08	Medium	Medium	Medium	Intermediate	Intermediate	Intermediate	Green	Green
04	Line-09	None	Low	Low	Intermediate	Intermediate	Intermediate	Green	Light Violet
05	Line-10	Low	Low	Low	Intermediate	Intermediate	Intermediate	Greenish Violet	Violet
06	Line-11	Low	Medium	Medium	Low	Low	Low	Green	Light Violet
07	Line-13	Low	Low	Medium	Intermediate	Intermediate	Intermediate	Green	Green
08	Line-14	None	Low	Low	Intermediate	Intermediate	Intermediate	Green	Light Violet
09	Line-15	Medium	Low	Low	Low	Low	Low	Green	Light Violet
10	Line-16	None	Low	None	Intermediate	Intermediate	Intermediate	Green	Green
11	Line-17	None	None	None	Low	Low	Low	Green	Light Violet
12	Line-18	Low	Low	Medium	Low	Low	Low	Light Violet	Light Violet
13	Line-19	Low	Low	Low	Intermediate	Low	Low	Greenish Violet	Light Violet
14	Line-20	Low	Medium	Medium	Low	Low	Low	Light Violet	Light Violet
15	Line-21	Low	Low	Low	Intermediate	Intermediate	Intermediate	Green	Green
16	Line-22	None	Medium	None	Low	Low	Low	Green	Green
17	Line-23	None	None	None	Low	Low	Low	Green	Green
18	Line-27	Low	Medium	Medium	Intermediate	Intermediate	Intermediate	Green	Light Violet
19	Line-30	None	Low	Medium	Intermediate	Low	Intermediate	Greenish Violet	Violet
20	Line-31	None	Medium	Medium	Intermediate	Intermediate	Intermediate	Greenish Violet	Violet
21	Line-33	Low	Low	Medium	Intermediate	Intermediate	Low	Green	Light Violet
22	Line-34	None	Medium	Medium	Intermediate	Low	Low	Green	Green
23	BARI-1	Low	Low	Low	Low	Low	Low	Green	Light Violet
24	BARI-4	None	Low	None	Low	Low	Low	Greenish Violet	Violet
25	BARI-5	None	Low	None	Low	Low	Low	Greenish Violet	Violet
26	BARI-6	None	Low	Medium	Low	Low	Low	Green	Green

Table 2 B. (Cont'd.)

G. No.	Name of Genotypes	Plant Prickliness			Pubescence of the Plant			Plant Pigmentation	
		Leaf	Stem	Calyx/ Fruit	Leaf	Stem	Fruit/ Calyx	Leaf	Stem
27	BARI-8	Low	Low	Low	Low	Low	Low	Green	Light Violet
28	Volanath Begun	Low	Low	Low	Low	Low	Low	Greenish Violet	Deepest Violet
29	Shinhnath-60	None	Low	Low	Intermediate	Intermediate	Intermediate	Light violet	Violet
30	Shainnath-666	Low	Low	None	Intermediate	Intermediate	Intermediate	Green	Light Violet
31	NSC Shingnath	None	Low	Low	Low	Low	Low	Green	Light Violet
32	Line-01 X Line-25	High	High	High	Low	Low	Low	Greenish violet	Violet
33	Line-23 X Line-24	None	Low	Low	Low	Low	Low	Green	Green
34	Line-27 X Line-14	Low	Medium	Low	Intermediate	Intermediate	Low	Green	Light Violet

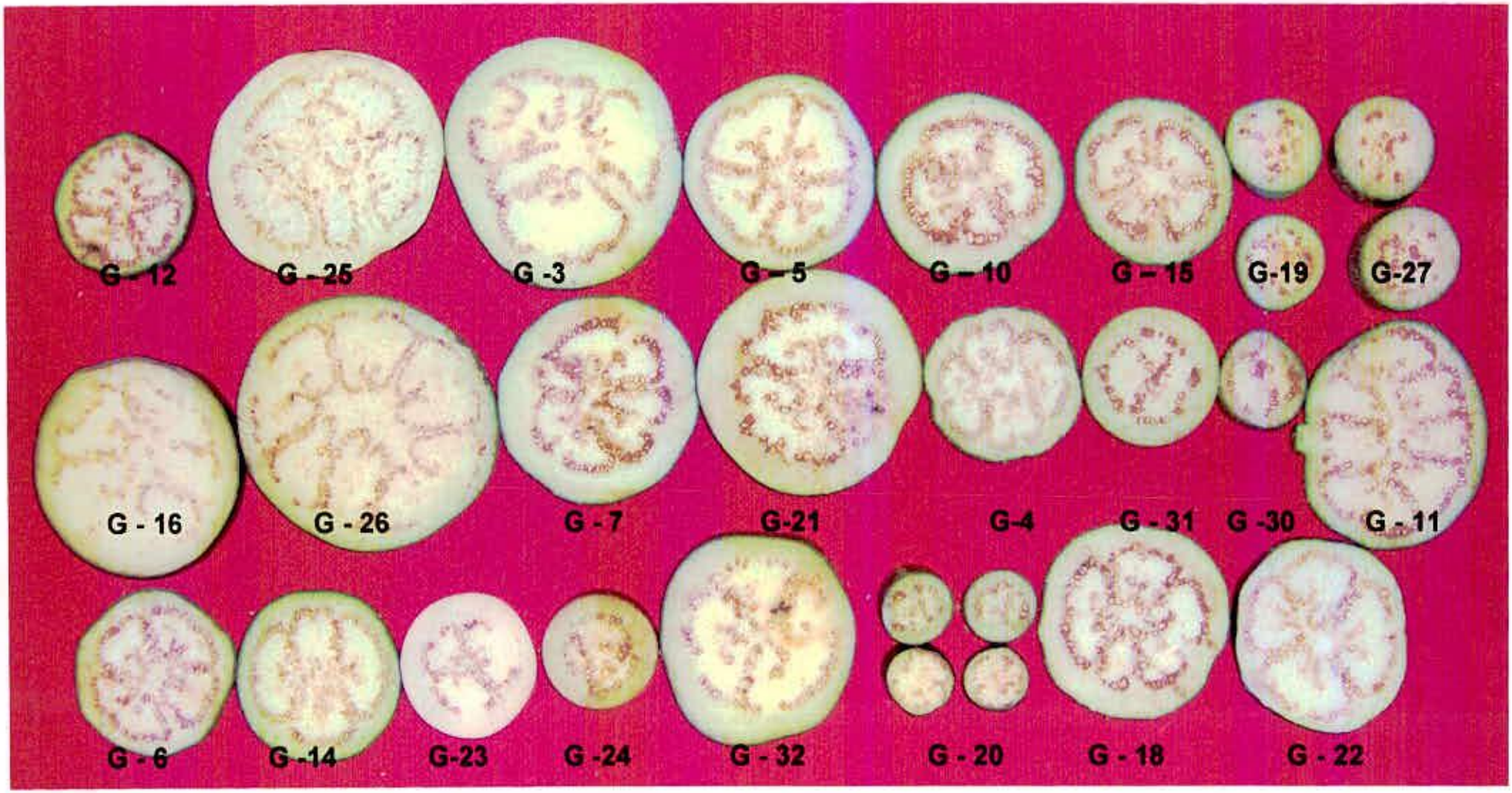


Plate 2. Amount of seed in different brinjal genotypes

4.1.1.10 Plant Pigmentation

Plant pigmentation data were recorded by observing the pigment of leaves and stems of different brinjal genotypes. Among the 34 genotypes studied leaf pigmentation of genotypes G05, G13, G19, G20, G24, G25, G28 and G32 were greenish violet, genotypes G12, G14 and G29 were light violet while the rest of the genotypes were green. In case of stem pigmentation the genotypes G05, G19, G20, G24, G25, G29 and G32 were violet; G28 were deepest violet; G01, G03, G07, G10, G15, G16, G17, G22 G23, G26, G27 G30, G31, G33 and G34 were green and rest of the genotypes were light violet (Table 2 B).

4.1.2 Characterization on the Basis of Yield and Yield Contributing Characters

4.1.2.1 Plant height (PH)

The plant height of different lines exhibited wide variation (Table 3). The plant height was maximum in genotype G29 (86.80 cm), which was more or less identical to G19, G20, G32 and G30. The genotype G17 was the shortest plant (52.33 cm). The remaining genotypes were intermediate in this regard (Table 3). Statistically the G29 produced tallest plants than rest of the genotypes.

4.1.2.2 Number of primary branches (NPB) per plant

Number of primary branches is an important morphological character which is number of fruit per plant and yield as well. It was observed that the maximum number of primary branches was produced by the genotype G32 (13.33) which were statistically superior from the rest of the genotypes. The genotype G12 produced the least number (6.67) of primary branches per plant (Table 3).

4.1.2.3 Number of secondary branches (NSB) per plant

The number of secondary branches of each plant was recorded and their average mean was calculated. It was found that the genotype G32 produced the highest number of secondary branches (31.85) which was statistically

Table 3. Mean performances of thirteen characters of thirty four brinjal genotypes

G. No.	PH (cm)	NPB	NSB	DFF	NFI	DFH	FL(cm)	FC (cm)	FW (gm)	FPP	YPP (kg)	%IIF	%IIP
G01	65.23	9.20	21.30	43.92	1.47	56.56	8.54	18.15	74.21	12.94	0.969	17.64	33.33
G02	76.57	10.20	27.00	42.90	1.50	57.95	9.33	19.85	69.88	14.87	1.019	18.65	40.00
G03	71.47	7.90	16.94	40.90	1.21	50.48	13.17	27.94	141.62	9.37	1.328	18.13	36.67
G04	65.74	9.57	22.63	41.09	1.80	58.41	9.08	23.20	87.89	12.23	1.081	13.06	10.00
G05	74.70	10.53	23.13	40.54	1.37	57.41	9.90	21.73	86.84	11.84	1.003	21.54	36.67
G06	64.62	8.53	19.71	49.78	1.47	62.14	8.10	22.47	78.47	15.67	1.176	18.97	33.33
G07	81.23	9.20	25.63	46.33	2.33	63.21	8.58	19.94	65.97	14.48	0.903	12.96	16.67
G08	63.26	9.47	18.97	52.52	1.43	61.25	9.16	20.18	94.68	12.97	1.194	22.44	30.00
G09	71.78	8.33	23.46	41.79	1.33	59.94	10.83	24.37	107.19	12.64	1.317	26.17	43.33
G10	75.57	9.07	27.03	44.22	1.40	59.05	9.27	23.29	98.81	13.20	1.263	22.51	40.00
G11	65.40	11.27	31.47	41.12	1.30	55.93	9.29	23.95	92.10	12.59	1.117	18.38	20.00
G12	64.97	6.67	18.37	39.40	1.83	46.75	7.30	19.94	95.38	11.73	1.086	31.44	30.00
G13	71.13	8.73	19.23	52.28	1.47	67.54	10.40	22.63	79.22	11.50	0.889	19.74	46.67
G14	68.16	7.37	15.77	49.43	2.43	61.48	12.34	20.30	83.10	13.46	1.079	12.94	23.33
G15	70.73	9.23	18.15	50.35	1.00	63.38	8.24	22.33	97.74	11.42	1.051	26.06	40.00
G16	69.54	10.80	18.93	44.05	1.63	52.65	8.43	25.19	118.35	10.18	1.135	30.08	40.00
G17	52.33	7.17	19.33	27.97	2.57	42.93	6.20	13.46	23.64	36.43	0.819	15.74	16.67
G18	62.58	10.90	21.57	44.54	1.50	54.29	9.57	20.85	88.84	13.87	1.206	15.30	16.67
G19	85.11	9.03	20.41	51.68	3.50	55.67	19.77	12.16	79.08	10.92	0.807	14.71	13.33
G20	85.67	10.47	22.77	40.95	3.77	62.55	19.08	13.40	48.27	15.27	0.710	12.21	13.33
G21	60.26	9.40	26.80	40.17	3.13	54.98	11.80	22.11	70.39	13.62	0.965	14.83	16.67
G22	55.13	9.87	27.98	43.45	1.37	55.85	8.63	19.45	62.22	12.90	0.762	19.34	33.33

Table 3. (Cont'd.)

G. No.	PH (cm)	NPB	NSB	DFF	NFI	DFH	FL (cm)	FC (cm)	FW (gm)	FPP	YPP (kg)	%IIF	%IIP
G23	68.15	12.13	27.83	42.82	5.80	56.56	11.26	11.97	56.68	23.40	1.247	13.46	23.33
G24	61.73	10.23	23.12	48.06	2.83	57.95	13.30	13.36	58.31	24.04	1.330	8.90	13.33
G25	62.90	9.67	24.13	41.39	2.73	50.48	9.17	20.72	126.95	10.26	1.274	13.65	20.00
G26	69.27	10.37	23.60	52.17	1.53	58.41	11.51	26.14	143.45	7.80	1.091	16.04	33.33
G27	74.60	11.45	24.26	46.16	4.20	57.41	24.42	12.33	68.92	12.30	0.775	12.31	16.67
G28	75.26	9.63	18.70	44.22	4.63	62.14	12.91	12.47	63.19	12.88	0.752	22.29	30.00
G29	86.80	11.37	17.23	48.36	4.23	63.21	20.31	8.43	50.55	14.00	0.649	23.06	33.33
G30	82.86	9.90	21.01	53.35	3.87	68.05	22.42	10.71	70.66	13.47	0.902	17.28	26.67
G31	75.87	9.20	22.07	52.15	2.73	59.94	20.94	10.92	66.02	13.70	0.880	16.98	16.67
G32	84.47	13.33	31.85	50.08	2.10	59.05	13.29	23.19	126.52	14.84	1.706	15.86	20.00
G33	57.63	10.07	22.82	39.11	2.47	55.93	6.42	13.66	25.58	42.01	1.019	19.87	16.67
G34	69.78	10.43	30.63	40.41	1.00	46.75	13.32	24.83	123.97	13.78	1.654	22.21	23.33

PH= Plant height (cm), NPB= No. of primary branches/plant, NSB= No. of secondary branches/plant, DFF= Days to first flowering, NFI= No. of flower/Inflorescence, DFH= Days to first fruit harvesting, FL= Fruit length (cm), FC= Fruit circumference (cm), WPF= Weight/Fruit (g), FPP= Fruit/plant, YPP= Yield/plant (g), PIIF= Percent insect infestation of fruits, PIIP= Percent insect infestation of plants

better from the rest of the genotypes. The lowest numbers of secondary branches were produced by the G14 (15.77) (Table 3).

Mandal and Dana (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that secondary branches/plant was an important trait for the selection of superior genotypes.

4.1.2.4 Days to first flowering

A wide range of variability was observed in respect of flowering time among the genotypes. The genotype G17 took the shortest time (28 days) for first flowering from transplanting while the G30 took the longest time (53 days) to first flower (Table 3). Sambandam (1960) studied the number of days required for flowering in different brinjal lines and concluded that the variation was due to the varietal characteristics.

4.1.2.5 No. of flower per inflorescence

The average no. of flower per inflorescence showed difference among the 34 brinjal genotypes. In respect of no. of flower per inflorescence the genotype G23 produced maximum no. of flowers/inflorescence (5.80) followed by G28 (4.63). The lowest no. of flower per inflorescence (1.00) was produced by G15 (Table 4). The differences in the average no. of flower per inflorescence of different genotypes of brinjal were statistically significant with coefficient of variation of 16.85 % (Table 4).

4.1.2.6 Days to first fruit harvest

Variability was observed in respect of first harvesting time among the genotypes. The G17 took only 43 days for first fruit harvesting from the date of transplanting, while the G30 took the longest time of 68 days (Table 3).

4.1.2.7 Fruit length (cm)

The genotype G27 produced the longest fruit which was 24.42 cm followed by G30 (22.42 cm). It is also found that the genotype 17 produced shortest fruit (6.20 cm), which was identical to G33 (6.42 cm) and G12 (7.30 cm) (Table 3). The differences in the average length of fruits of different genotypes of brinjal were statistically significant (Table 5). The G27 produced the longest fruit while the shortest fruit was produced by the genotype G17 (Table 3).

Table 4. Grand mean, range and coefficient of variation

Characters	Minimum	Maximum	Grand Mean	CV%
Plant height (cm)	52.33	86.80	70.31	3.36
No. of primary branches	6.670	13.330	9.73	7.46
No. of secondary branches	15.77	31.85	22.76	13.54
Days to first flowering	27.97	53.35	44.93	3.55
No. of flower per inflorescence	1.00	5.80	2.32	16.85
Days to first fruit harvesting	42.92	68.05	57.84	3.39
Fruit length (cm)	6.20	24.42	11.95	8.42
Fruit circumference (cm)	8.43	27.94	18.99	7.96
Fruit weight (gm)	23.64	143.45	83.08	5.62
No. of fruits per plant	7.80	42.01	14.90	11.78
Yields per plant (kg)	0.649	1.706	1.063	4.36
Percent insects infestation of fruits	8.90	31.44	18.37	11.87
Percent Insects infestation of plants	10.00	46.67	26.57	31.09

Table 5. Mean sum squires from the ANOVA of 34 brinjal genotypes in respect of thirteen characters

Characters	d.f			Mean Sum of Square		
	Replication	Genotype	Error	Replication	Genotype	Error
Plant height (cm)	2	33	66	57.702**	233.146**	5.572
No. of primary branches	2	33	66	00.211^{NS}	5.760**	0.527
No. of secondary branches	2	33	66	74.33**	53.206**	9.501
Days to first flowering	2	33	66	02.639^{NS}	88.108**	2.538
No. of flower per inflorescence	2	33	66	00.571*	4.295**	0.153
Days to first fruit harvesting	2	33	66	02.453^{NS}	100.466**	3.846
Fruit length (cm)	2	33	66	30.163**	68.673**	1.011
Fruit circumference (cm)	2	33	66	46.118**	84.347**	2.284
Fruit weight (gm)	2	33	66	04.706^{NS}	2539.633**	21.796
No. of fruits per plant	2	33	66	05.665^{NS}	144.729**	3.081
Yields per plant (kg)	2	33	66	00.002^{NS}	0.18**	0.002
Percent insects infestation of fruits	2	33	66	02.796^{NS}	80.426**	4.757
Percent Insects infestation of plants	2	33	66	15.686^{NS}	320.172**	68.212

* Significant at 1% level of probability
** Significant at 5% level of probability
^{NS} Non-significant

4.1.2.8 Fruit circumference (cm)

The average circumference of fruit of different genotypes showed marked difference among themselves. The fruit of genotype G03 was round but widest (27.94 cm) followed by G16 (25.19 cm), and G26 (26.14 cm). The lowest circumference was observed in genotype 29 (8.43 cm) (Table 3). The differences in the average circumference of fruits of different genotypes of brinjal were statistically significant with coefficient of variation of 7.96 % (Table 4 and 5).

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.

4.1.2.9 Weight of fruit (gm)

The heaviest fruit of 143.45 gm was produced by the genotype G26 followed by G03 (141.62 gm), G25 (126.95 gm) and G32 (126.52 gm) (Table 3). The lowest fruit weight was observed from the genotype G17 (23.64 gm) followed by the genotype G33 (25.58 gm), while the other genotypes took intermediate positions though there were statistical differences among themselves. The coefficient of variation of this trait was 5.62% (Table 4).

4.1.2.10 Number of fruit per plant

The total no. fruit per plant varied from 42.01 to 7.80. The genotype G33 (42.01) had the highest no. of fruits per plant, which was more or less similar with G17 (36.43) and G24 (24.04). The lowest fruit per plant was obtained from G26 (7.80) which were statistically similar with G03 (9.37), G25 (10.26) and G19 (10.92) (Table 3) while the other lines took intermediate positions and they were statistically different among themselves (Table 5).

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 lines 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.

4.1.2.11 Yield per plant (Kg)

The genotypes showed a difference in producing yield per plant (Table 3). The data indicated that genotype G32 produced the highest yield of 1.706 kg, which was significantly different from others and followed by G34 (1.654 kg) and G03 (1.328 kg). Though the genotype G29 had the lowest yield per plant 0.649 kg, which was more or less identical with G28 (0.752 kg) and G27 (0.775 kg).

The result obtained in the experiment tended to differ to some extent 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 G33 produced maximum number of fruits per plant (42.01) but its fruit weight was 25.58 gm, which was second lowest fruit weight. Yield was influenced by both the no. of fruit per plant and individual fruit weight. The heaviest individual fruit weight was found in G26 (143.45 gm) with lowest no. fruits per plant (7.80) where as the total yield per plant was more or less similar in both cases.

Ahmad (1968) and Siddique (1968) obtained carried out an experiments with different varieties/lines of Bangladesh. Ahmad (1968) reported that the variety Nayankazal tended to out yield all other varieties/lines including Islampur and D.R.C. while Siddique (1968) obtained superiority of Singnath over Islampuri.

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.

4.1.2.12 Percent insect infestations of fruits

Brinjal is mostly affected by shoot and fruit borer. It causes great harm to yield and reduce the production of brinjal. So, resistance to this insect is an important character of brinjal plant. The rate of insect attack against different genotypes was significantly different. The attacks of insect of brinjal depend on its morphological, physiological and genetical characteristics of plant. The different genotypes are genetically different from each other. From this investigation it was revealed that the genotype G12 (31.44%) was highly affected and the genotype G24 (8.90%) was least affected, which meant that the G24 (8.90%) was the most resistant and superior to the rest of the genotypes (Table 3).

4.1.2.13 Percent insect infestations of plants

By observing overall plant view of different brinjal genotypes, it was observed that the percentage of insect infestation was significantly different from each other. It was revealed that the genotype G13 (46.67%) was highly affected and the genotype G04 (10.00 %) was least affected, which meant that the G04 (10.00%) was the most resistant and superior to the rest of the genotypes (Table 3).

4.2. Variability of Brinjal genotypes on the Basis of Yield and Yield Contributing Characters

Analysis of variance showed that the brinjal genotypes varied significantly with each other (Table 5). Range, mean and co-efficient of variation of thirteen characters of brinjal genotypes namely days to first flowering, no. of flower per inflorescence, days to first fruit harvesting, plant height (cm), no. of primary branches/plant, no. of secondary branches/plant, fruit length, fruit circumference, individual fruit weight, number of fruit per plant, yield per plant, % insect infestation of fruits and % insect infestation of plants have been presented in Table 4. The mean values of above parameters were 44 days, 2.32, 58 days, 70.31 cm, 9.73, 22.76, 11.95 cm, 18.99 cm, 83.98 days, 83.08 gm, 14.90, 1.063 kg, 18.37% and 26.57%, respectively and the co-efficient of variation of the above parameters were 3.55, 16.85, 3.39, 3.36, 7.46, 13.54, 8.42, 7.96, 5.62, 11.78, 4.36, 11.87 and 31.09%, respectively which indicted considerable variation existing among the genotypes.

4.2.1 Genetic variability, heritability and genetic advance in brinjal genotypes

The genotypes varied significantly for all the characters (Table 5). The extent of variation among the genotypes in respect of 13 characters were studied mean value, MSS, EMSS, genotypic variance (σ^2_g), phenotypic variances (σ^2_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2b), genetic advance (GA) and genetic advance in percent of mean have been presented in Table 6 . The mean value of all genotypes for each character is also given in Table 4. Performances of the genotypes are described below for each character.

4.2.1.1 Plant height (PH)

Significant mean sum of squire for plant height indicated considerable differences among the genotypes studied (Table 5). The highest and lowest plant heights among the genotypes were 86.80 cm (G29) and 52.33 cm (G17) respectively with the mean value of 70.31cm (Table 3).

Table 6. Variability, genetic parameter, heritability (h^2b), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA), genetic advance in percent of mean for 13 yield and yield contributing characters of brinjal

Characters	GM	MSS	Error	σ^2_g	σ^2_p	GCV	PCV	h^2b	GA (%)	GA in % of mean (1%)
Plant height (cm)	70.309	233.146**	5.572	75.86	81.43	12.39	12.83	93.16	17.32	24.63
No. of primary branches	9.729	5.760**	0.527	1.74	2.27	14.22	16.22	76.80	2.38	25.66
No. of secondary branches	22.76	53.206**	9.501	14.57	24.07	16.77	21.56	60.53	6.12	26.88
Days to first flowering	44.932	88.108**	2.538	28.52	31.06	11.89	12.40	91.83	10.54	23.46
No. of flower per inflorescence	2.322	4.295**	0.153	1.38	1.53	50.60	53.33	90.02	2.30	98.91
Days to first fruit harvesting	57.84	100.466**	3.846	32.21	36.05	9.81	10.38	89.33	11.05	19.10
Fruit length (cm)	11.949	68.673**	1.011	22.55	23.57	39.74	40.63	95.71	9.57	80.10
Fruit circumference (cm)	18.988	84.347**	2.284	27.35	29.64	27.54	28.67	92.29	10.35	54.51
Fruit weight (gm)	83.08	2539.633**	21.796	839.28	861.08	34.87	35.32	97.47	58.92	70.92
No. of fruits per plant	14.899	144.729**	3.081	47.22	50.30	46.12	47.60	93.87	13.71	92.05
Yields per plant (kg)	1.063	0.18**	0.002	0.06	0.06	22.91	23.30	96.74	0.49	46.43
Percent insects infestation of fruits	18.374	80.426**	4.757	25.22	29.98	27.33	29.80	84.13	9.49	51.65
Percent Insects infestation of plants	26.569	320.172**	68.212	83.99	152.20	34.49	46.43	55.18	14.02	52.78

The phenotypic and genotypic variances for this trait were comparatively high (81.43 and 75.86). The phenotypic variance appeared to be higher than the genotypic variance, suggesting considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (12.83) was higher than the genotypic coefficient of variation (12.39) (Table 6), which suggested that environment, has a little role on the expression of this trait. Heritability estimate was high (93.16%) with moderate genetic advance (17.32%) and genetic advance in percent of mean (24.63) was considerable for this trait indicating apparent variation was due to genotypes. So, selection based on this trait would be effective. This result also has the agreement with the findings of Singh *et al.* (2005).

4.2.1.2 No. of primary branches per plant (NPB)

No. of primary branches per plant was significant indicating considerable differences among the genotypes studied (Table 2). The maximum no. of primary branches and minimum no. of primary branches per plant among the genotypes were 6.67 (G12) and 13.330 (G32) respectively with the mean value of 9.73 (Table 3). The phenotypic and genotypic variances for this trait were comparatively low (2.27 and 1.74). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (16.22) was higher than the genotypic coefficient of variation (14.22) (Table 6), which suggested that environment had a significant role on the expression of this trait. Estimated heritability was high (76.80%) with low genetic advance (2.38%) and genetic advance in percent of mean (25.66) was considerable for this trait indicating apparent variation was due to genotypes (Table 6). Thus, selection based on this trait would be effective.

4.2.1.3 No. of secondary branches per plant (NSB)

The total no. of secondary branches per plant highly significant as shown in Table 5. This trait varied from 15.77 (G14) to 31.85 (G32) with the mean value of 22.76. The phenotypic variance (24.07) is higher than the genotypic

variance (14.57) as presented in Table 6. This feature indicated higher influences of environment on the expression of the trait. This character showed high genotypic and phenotypic coefficient of variation (16.77 to 21.56) respectively. In this regard, the phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicating the apparent variation not only due to genotypes but also due to the influence of environment. Estimated heritability of trait was moderate with high genetic advance in percent of mean (26.88).

4.2.1.4 Days to first flowering (DFF)

Analysis of variance for days to first flowering showed highly significant mean sum of squire due to genotypic differences (Table 5). The mean value with respect this trait ranged from 27.97 (G17) to 53.35 (G30). The phenotypic variance (31.06) was slightly higher than the genotypic variance (28.52). The difference present among the genotypic and phenotypic variances is indicating the effect of environment for the expression of the trait is low (Table 6). The phenotypic coefficient of variation was little higher than the genotypic coefficient of variation indicating the apparent variation not only due to genotypes but also due to the influence of environment. A heritability estimate was also high (91.83%) with moderate genetic advance in percent of mean (Table 6).

4.2.1.5 No. of flower per inflorescence (NFI)

The analysis of variance (ANOVA) presented in Table 5 showed highly significant value for no. of flower per inflorescence. The highly significant genotypic differences indicated that there was a wide range of variation among the genotypes. The mean values ranged from 1.00 (G15) to 5.80 (G23). The genotypic and phenotypic variances for this character were comparatively low 1.38 and 1.53 respectively. The phenotypic variance appear to be higher than the genotypic variance suggesting little influence of environment on the expression of the genes controlling this trait. The difference between phenotypic coefficient of variation (53.33) and genotypic coefficient of variation (50.60) was minimum (Table 6). Estimating of

heritability for this trait was high (90.02%) with low genetic advance (2.30%) and low genetic advance in percent of mean (98.91) (Table 6).

4.2.1.6 Days to first fruit harvesting (DFH)

Highly significant variations were observed for days to first fruit harvesting (Table 5). The early genotype in terms of fruit harvesting was G17 (42.93 days) and the late genotype was G30 (68.05 days). The genotypic variance (32.21) was lower than the phenotypic variance (36.05).The considerable differences between phenotypic and genotypic variances indicating effect of the environment for the expression of the trait (Table 6). The genetic advance was moderate 11.05 and genetic advance in percentage of mean was low (19.10).

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.

4.2.1.7 Fruit length (FL)

Different types of genotypes showed wide differences in terms of fruit length. The range of length was from the highest 24.42 cm to lowest 6.20 cm. (Table 3). The phenotypic variance (23.57) was little higher than the genotypic variance (22.55). The phenotypic coefficient of variation and the genotypic coefficient of variation were of similar types. The estimated heritability was found very high (95.71%). The genetic advance was low (9.57) with the high genetic advance in percent of mean (80.10).

4.2.1.8 Fruit circumference (FC)

Fruits of different plants were of different types not in size but also in shape. The highest fruit circumference was observed in G03 (27.94 cm) and the lowest fruit length was G17 (8.43 cm) with the mean value of 18.99 cm (Table 3). The phenotypic variance (29.64) was slightly higher than the genotypic variance (27.35). There was small difference between GCV and PCV. The estimated heritability was found very high (92.29%). The genetic advance was

moderate (10.35) with the moderate genetic advance in percent of mean (54.51) (Table 3). A comparative fruit appearance of different brinjal genotypes is presented in Plate 3.

4.2.1.9 Fruit weight (FW)

As fruit size and shape were of different types, there were significant differences for fruit weight among the different genotypes (Table 5). The highest fruit weight was found in G26 which was 143.45 gm and the lowest fruit weight were found in genotype G17 (23.64 gm) with the mean value of 83.08. The phenotypic variance (861.08) was higher than the genotypic variance (839.28). The difference present among the genotypic and phenotypic variances is indicating the effect of environment for the expression of the trait (Table 6). The PCV (35.32) was little higher than the GCV (34.87) indicating the apparent variation not only due to genotypes but also due to the influence of environment. A highest heritability among the thirteen characters was estimated 97.47%, with high genetic advance in percent of mean (70.92) (Table 6).

4.2.1.10 No. of fruits per plant (FPP)

A highly significant mean sum of squire was found in Table 2, which indicated considerable differences among the genotypes studied. The highest no. of fruit per plant and lowest no. of fruit per plant among the 34 brinjal genotypes found in G33 (42.01) and G26 (7.80) respectively with the mean value of 14.90 (Table 6). The phenotypic and genotypic variances for this trait were 50.30 and 47.22 respectively. The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The PCV (47.60) was higher than the GCV (46.12) (Table3), which suggested that environment, has a significant role on the expression of this trait. Heritability estimated was high (93.87%) with moderate genetic advance (13.71) and high genetic advance in percent of mean (92.05) was considerable for this trait indicating apparent variation was due to genotypes. So, selection based on this trait would be effective.

Plate 3. Fruit appearance of different brinjal genotypes

4.2.1.11 Yield per plant (YPP)

As there were variations in sized shape of the brinjal; in the no. of fruits and weight as well. Thus the yield of the different genotypes showed variations among the genotypes. The yield per plant was maximum in G32 (1.706 kg) and the minimum yield per plant was found in genotypes G29 (0.649 kg) with the mean value of 1.063 kg (Table 6). The phenotypic variance (0.06) and genotypic variance (0.062) was almost equal. The genotypic coefficient of variation was (22.91) and the phenotypic coefficient of variation was (23.30). That means PCV was little higher than GCV. The estimated heritability was found very high (96.74%) with low genetic advance (0.49) and genetic advance in percent of mean (52.78) (Table 3).

4.2.1.12 Percent Insect infestation of fruits

The genotypes showed significant differences for percent insect infestation of fruits. The mean value of this trait ranges from 31.44 (G12) to 8.90 (G24) with grand mean 18.37. The component of variation for insect infestation percentage showed considerable phenotypic variation (29.98 in comparison to genotypic variation (25.22) suggesting the influence of environment to a great extent for this characters (Table 6). The phenotypic coefficient of variation and genotypic coefficient of variation were moderate, which were 29.80 and 27.33, respectively. The estimated heritability was high (84.13%) with low genetic advance (Table 6).

4.2.1.13 Percent Insect infestation of plants

Percentage insect infestation of plants showed significant differences among the genotypes. The mean value of percent insect infestation of plants ranges from 46.67 (G13) to 10.00 (G04) with the grand mean of 26.57. The phenotypic and genotypic variances for this trait were 152.20 and 83.99 respectively. The phenotypic coefficient of variation (46.43) was higher than the genotypic coefficient of variation (34.49) indicating the apparent variation not only due to genotypes but also due to the influence of environment. A heritability estimated was also moderate (55.18%), with high genetic advance in percent of mean (Table 6).

4.3 Diversity of the Brinjal Genotypes

Genetic divergence in Brinjal was analyzed by using GENSTAT software programme. Genetic diversity analysis involved several steps i.e., estimation of distance between the genotypes, clusters, 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 al.* 1988 and Ario, 1987). In the analysis of genetic diversity in brinjal multivariate techniques were used.

4.3.1 Construction of scatter diagram

In multivariate analysis, cluster analysis refers to methods used to divide up objects into similar groups, or, more precisely, groups whose members are all close to one another on various dimensions being measured. Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1 - Z_2) using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Figure 3. The position of the genotypes in the scatter diagram was apparently distributed into six 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. Contributions of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal components. The principal component analysis yielded eigen values of each principal component axes with the first axes totally accounting for the variation among the genotypes is 29.82, while two of these with eigen values above unity accounted for 54.48% (Table 7). The first three principal axes accounted for 70.77% of the total variation among the 13 characters describing 34 brinjal genotypes.

Table 7. Eigen values and percentage of variation in respect of 13 characters in 34 brinjal genotypes

Principle Component Axis	Principal Component Characters	Eigen Values	% of Total Variation Accounted for	Cumulative Percent
I	Plant height (cm)	3.876	29.82	29.82
II	No. of primary branches	3.205	24.66	54.48
III	No. of secondary branches	2.117	16.29	70.77
IV	Days to first flowering	1.025	7.88	78.65
V	No. of flower per inflorescence	0.798	6.14	84.79
Vi	Days to first fruit harvesting	0.602	4.63	89.42
VII	Fruit length (cm)	0.396	3.05	92.47
VIII	Fruit circumference (cm)	0.291	2.24	94.71
IX	Fruit weight (gm)	0.260	2.00	96.71
X	No. of fruits per plant	0.199	1.53	98.24
XI	Yields per plant (kg)	0.115	0.89	99.13
XII	Percent insects infestation of fruits	0.074	0.57	99.70
XIII	Percent Insects infestation of plants	0.041	0.31	100.00

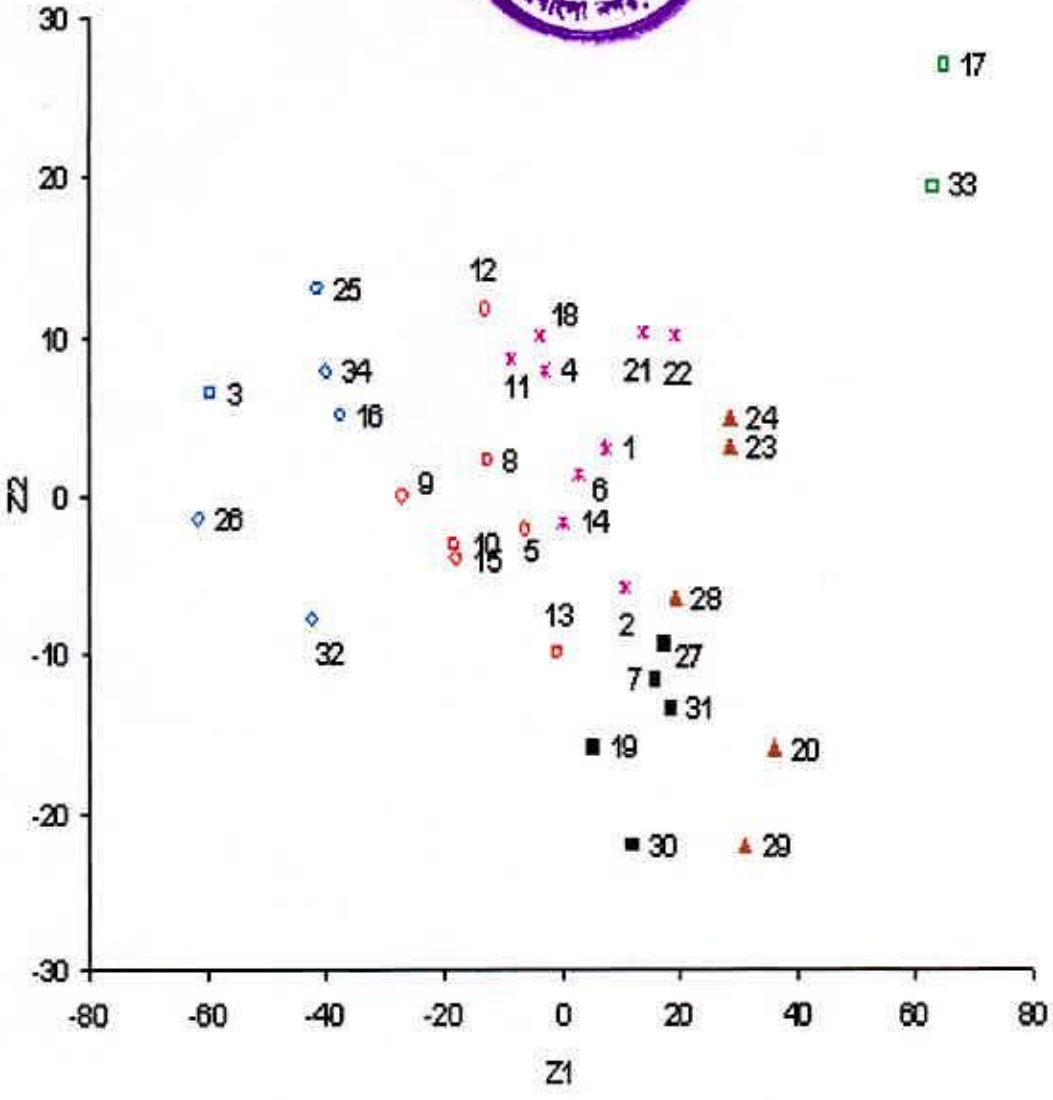


Figure 3. Scatter distribution of 34 brinjal genotypes based on their principle component scores.

Based on principal component axes I and II (Appendix VI), a two dimensional chart (Z_1 - Z_2) of the cultivars are presented in Figure 3. The scatter diagram revealed that apparently there were mainly six clusters. The genotypes were distantly located from each other.

Balasch *et al.* (1984) reported the use and the comparison of different multivariate techniques in classifying some important number of tomato varieties/lines. 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.

Out of six clusters, cluster I was associated with five genotypes namely G03, G16, G25, G26, G32 and G34 (Table 8). From the clustering mean values (Table 8), it was observed that cluster I produced the highest mean values for no. of secondary branches (24.35), fruit weight (130.14 gm), fruit circumference (24.67 cm) and yield per plant (1.360 kg) and the lowest mean value for no. of fruit per plant (11.04) in comparison with other five clusters (Table 9).

Cluster II was associated with seven genotypes namely G05, G08, G09, G10, G12, G13 and G15 (Table 8). These genotypes produced the lowest flowers per inflorescence (1.10) and percent insect infestations in both the cases (fruits and plants) were very high (24.27% and 38.10%) and rank the top position (Table 9).

Among the six clusters, cluster III composed of nine genotypes, which was the biggest cluster. The genotypes were G01, G02, G04, G06, G11, G14, G18, G21 and G22 (Table 8). These genotypes produced second highest no. of secondary branches per plant (23.80).

Cluster IV consists of five genotypes, namely G07, G19, G27, G30 and G31 (Table 8). From the clustering mean values (Table 9), it was observed that cluster IV produced the highest mean values for plant height (79.93 cm), fruit length (19.23 cm) and having very low yield (0.850 kg) and for first fruit harvesting it took 63 days.

Table 8. Distribution of 34 brinjal genotypes in six different clusters

Cluster No.	*Number of Genotypes*	*Types of Genotype*	*Genotypes Designation*
I	06	Line-8, Line-22, BARI-5, BARI-6, Line-01 X Line-25, Line-27 X Line-14	G3, G16, G25, G26, G32, G34
II	07	Line-10, Line-14, Line-15, Line-16, Line-18, Line-19, Line-21	G5, G8, G9, G10, G12, G13, G15
III	09	Line-3, Line-4, Line-9, Line-11, Line-17, Line-20, Line-27, Line-33, Line-34	G1, G2, G4, G6, G11, G14, G18, G21, G22,
IV	05	Line-13, Line-30, BARI-8, Shinhnath-666, NSC- Shingnath	G7, G19, G27, G30, G31
V	02	Line-23, Line23 X Line24	G17, G33
VI	05	Line-31, BARI-1, BARI-4, Volanath Begun, Shingnath-60	G20, G23, G24, G28, G29

Table 9. Cluster mean for 13 characters of 34 brinjal genotypes

Sl. No.	Characters	Cluster					
		I	II	III	IV	V	VI
01	Plant height (cm)	71.24	70.31	64.85	79.93	54.98	75.52
02	No. of primary branches	10.42	08.87	09.59	09.76	08.62	10.77
03	No. of secondary branches	24.35	21.19	23.80	22.68	21.08	21.93
04	Days to first flowering	44.83	45.87	44.04	49.94	33.54	44.88
05	No. of flower per inflorescence	01.70	01.10	01.77	03.33	02.52	04.25
06	Days to first fruit harvesting	56.48	59.33	57.51	62.82	45.45	57.99
07	Fruit length (cm)	11.48	09.30	09.63	19.23	06.31	15.37
08	Fruit circumference (cm)	24.67	22.07	21.15	13.21	13.56	11.93
09	Fruit weight (gm)	130.14	94.27	78.57	70.13	24.61	55.40
10	No. of fruits per plant	11.04	12.19	13.57	12.97	39.22	17.91
11	Yields per plant (kg)	1.360	1.110	1.040	0.850	0.920	0.940
12	Percent insects infestation of fruits	19.33	24.27	16.57	14.85	17.81	15.98
13	Percent Insects infestation of plants	28.89	38.10	24.81	18.67	16.67	22.66

The percent insect infestation of fruits (14.85%) was very low, while the highly infested (24.27%) genotypes presented in cluster II.

Cluster V constituted only with two genotypes. The genotypes were G17 and G33 (Table 8). The genotypes of this cluster were early for both days to first flowering and first fruit harvesting. It took 33 days fro producing first flower and 45 days for first fruit harvesting. On the other hand these genotypes produced fruit having lowest fruit length (6.31 cm) and lowest individual fruit weight (24.61 gm) in comparison with other clusters. However, this cluster produced maximum no. of fruits per plant (39.22) (Table 9).

The genotypes 20, G23, G24, G28 and G29 were included in cluster VI (Table 8). These genotypes produced highest no. of primary branches per plant (10.77) and second tallest plant (75.52 cm). This cluster also produced fruit with lowest circumference (11.93 cm) in comparison with other clusters (Table 9).

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 of 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.

Dharmatti *et al.* (2001) in a population of 402 tomato lines was observed 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.

It was observed that all the cluster mean values for plant height, days to first flower, days to first harvest, fruit length, fruit circumference, 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.

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.

Generally, diversity was influenced by the morphological characters which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performances of G03, G16, G25, G26, G32, G33 and G34 could 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 (2.698) was observed between the G17 and G26, followed by G26 and G33 (2.615) and G03 and G17 (2.613) and the lowest distance was observed between G09 and G10 (0.299) followed by G05 and G10 (0.326), G01 and G06 (0.357) (Table 10).

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 11) as suggested by Singh *et al.* (1977). Cluster III which (1.835) composed of nine genotypes showed the maximum intra cluster distances and cluster V showed the lowest intra-cluster distance (0.537) which composed of 2 genotypes. The coordinates obtained from the Principal Component analysis (PCA) were used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al.* (1989). PCA was used for the graphical representation of the points while PCO was used to calculate the minimum distance straight line between each pair of points.

Table 10. Inter genotypic distances (D^2) of 20 higher and lower values of different cluster

Sl. No.	20 higher D^2 values of different clusters genotypes		Sl. No.	20 lower D^2 values of different clusters genotypes	
	Between Genotypes	Distance (D^2)		Between Genotypes	Distance (D^2)
01	G 17 – G 26	2.698	01	G 09 – G 10	0.299
02	G 26 – G 33	2.615	02	G 05 – G 10	0.326
03	G 03 – G 17	2.613	03	G 01 – G 06	0.357
04	G 03 – G 33	2.590	04	G 06 – G 08	0.372
05	G 16 – G 17	2.456	05	G 01 – G 02	0.394
06	G 17 – G 32	2.365	06	G 02 – G 22	0.396
07	G 17 – G 34	2.361	07	G 01 – G 05	0.412
08	G 09 – G 17	2.345	08	G 19 – G 31	0.424
09	G 09 – G 33	2.243	09	G 08 – G 15	0.438
10	G 33 – G 34	2.218	10	G 01 – G 08	0.444
11	G 13 – G 17	2.215	11	G 02 – G 22	0.445
12	G 10 – G 17	2.213	12	G 02 – G 10	0.460
13	G 05 – G 17	2.111	13	G 15 – G 16	0.479
14	G 17 – G 25	2.208	14	G 19 – G 27	0.490
15	G 15 – G 33	2.200	15	G 13 – G 15	0.493
16	G 32 – G 33	2.177	16	G 02 – G 06	0.504
17	G 25 – G 33	2.172	17	G 10 – G 15	0.514
18	G 17 – G 27	2.164	18	G 01 – G 13	0.540
19	G 17 – G 19	2.141	19	G 30 – G 31	0.549
20	G 13 – G 33	2.132	20	G 20 – G 13	0.551

Table 11. Average intra and inter-cluster distances ($\sqrt{D^2}$) for 34 Brinjal genotypes

Clusters	I	II	III	IV	V	VI
I	1.519					
II	1.825	1.401				
III	2.335	1.456	1.835			
IV	3.130	2.563	2.149	1.253		
V	5.863	5.740	5.679	5.399	0.537	
VI	3.444	2.980	2.691	1.744	5.117	1.484

- Highest and lowest intra cluster distances

- Highest and lowest inter cluster distances

4.3.4 Canonical variate analysis

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. The Table 10 indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances were higher than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups. Results indicated that the highest inter cluster distance was observed between cluster I and Cluster V (5.863) followed by between cluster II to cluster V (5.740), Cluster III to Cluster V (5.679), cluster IV to Cluster V (5.399) and Cluster V to Cluster VI (5.117) (Figure 4). The lowest inter-cluster distances was observed between the cluster II to Cluster III (1.456), followed by cluster IV to cluster VI (1.744), cluster I to cluster II (1.825) and cluster III to cluster IV (2.149) (Figure 4). The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 11 and Figure 4).

Islam *et al*, (1995) was carried out an experiment on groundnut (*Arachis hypogaea* L.) and obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis.

However the maximum inter-cluster distance was observed between the cluster I and cluster V (5.863) maintaining more distances than other clusters, and the lowest inert-cluster distance found between cluster II to cluster III (1.456), maintaining less distance than other cluster. Genotypes from the cluster I and cluster V (distances 5.863), if involved in hybridization might produce a wide spectrum of segregating population, as genetic variation was very distinct among these groups.

Results obtained from different multivariate techniques were superimposed in Figure 5 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 lines revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure. 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.

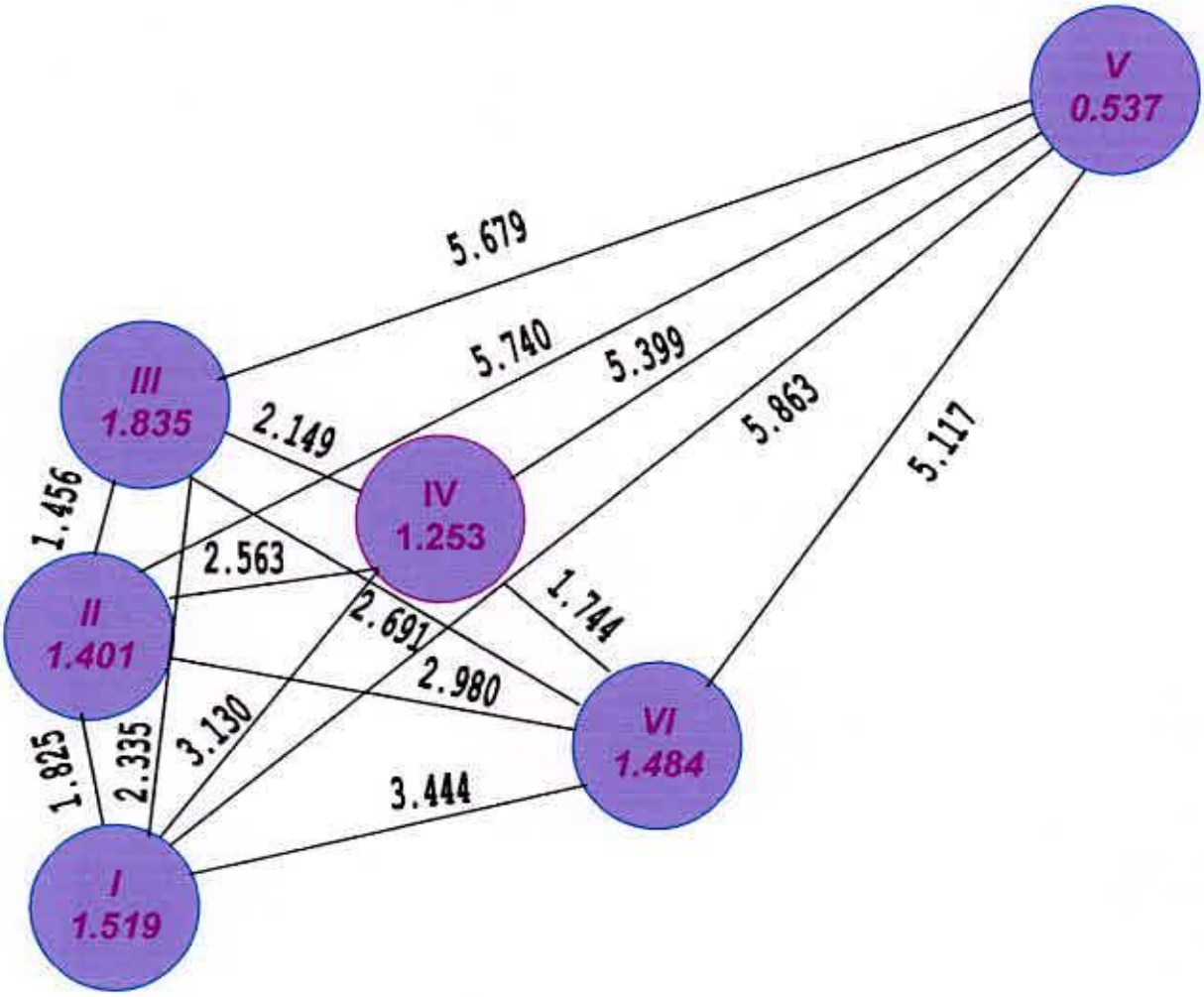


Figure 4. Diagram showing inter-cluster (outside the circle) and intra-cluster (inside the circle) distances of thirty four genotypes of brinjal.

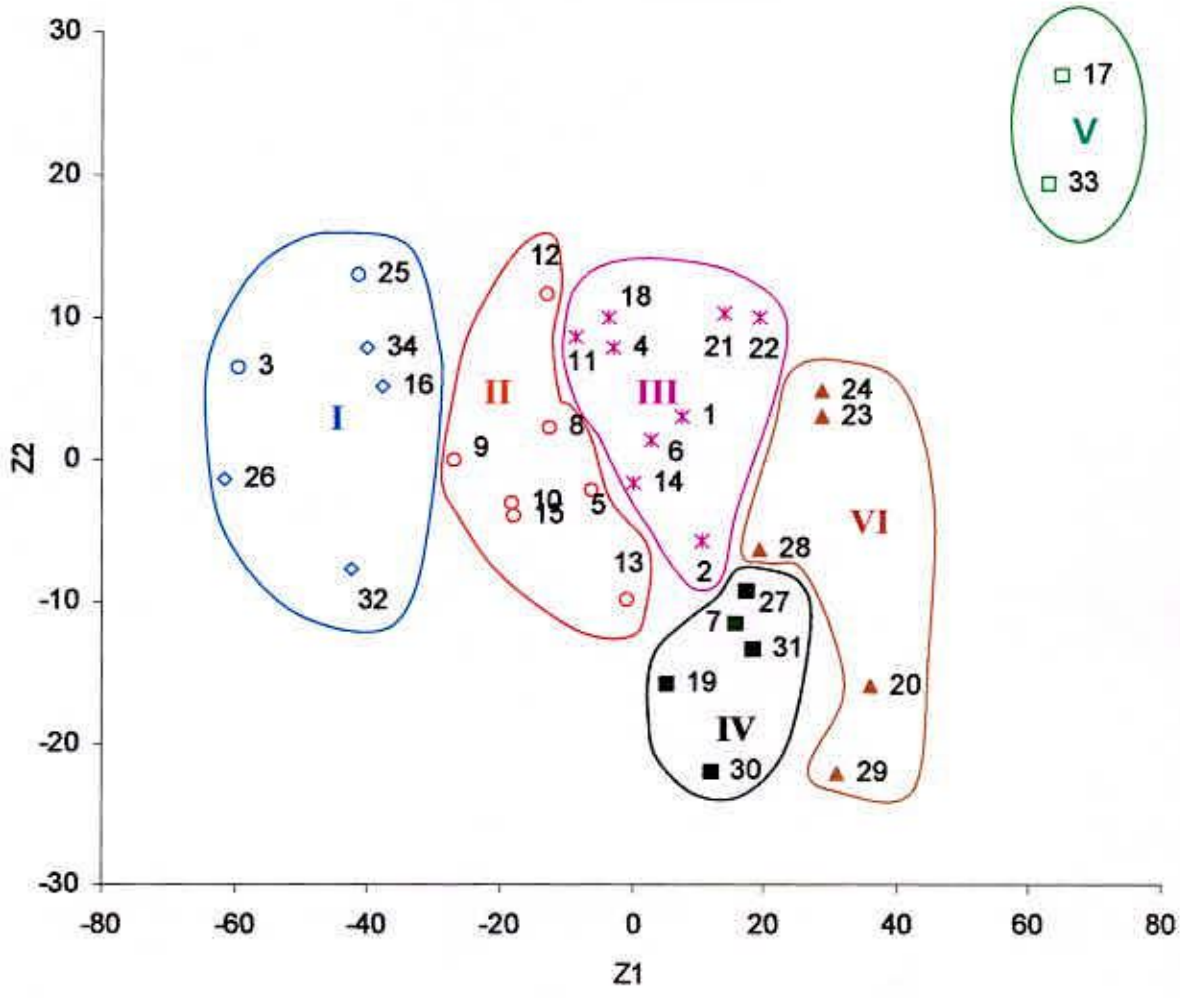


Figure 5. Scatter distribution of 34 brinjal genotypes based on their principle component scores superimposed with clustering.

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 lines 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

By using covariance matrix with the application of Non- hierarchical clustering, the 34 brinjal genotypes were grouped into 6 (six) clusters. These results confined the clustering pattern of the genotype according to the principle component analysis. Khan, (2006) reported five clustering, Islam (2005) reported four clusters, and Kumar *et al.* (1998) reported six distinct clusters in brinjal. Compositions of different clusters with their corresponding genotypes in each cluster were presented in Table 8. 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.

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

4.3.5.1 Cluster I

Cluster I had six (6) genotypes (genotypes number) G03, G16, G25, G32 and G34 (Table10) collected from SAU, BARI Gazipur and Chittagong (Table 1). From the clustering mean values (Table 9), it was observed that cluster I produced the highest number of mean values for the characters no. of secondary branches per plant (24.35), fruit circumference (24.67 cm), fruit weight (130.14 gm) and yield per plant (1.360 Kg). It had also the lowest value of number of fruit per plant (11.04). Cluster I also had the second highest number of cluster mean values for number of secondary branches per plant (10.42) and percent insects infestation of plants (28.89%) (Table 9).

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. Fruit type of the different genotypes of this cluster has been presented in Plate 4.

4.3.5.2 Cluster II

Cluster II was composed of seven genotypes viz. G05, G08, G09, G10, G12, G13, and G15 (Table 8) and collected from BARI Chittagong (Table 1). These genotypes produced the highest mean values for percent insect infestation of plants (38.10 %) and percent insect infestation of fruits (24.27%).

These group possessed genotypes with the second highest cluster mean for days to first flowering (45.87 days), days to first fruit harvesting (59.33 days), fruit circumference (22.07 cm), individual fruit weight per plant (94.27 gm) and yield per plant (1.110 kg). On the other hand this group produced lowest mean value for no. of flowers per inflorescence (1.10) and second lowest mean values for no. of secondary branches per plant (21.19), days to first fruit harvesting (Table 9). Fruit type and fruit with plant of this cluster has been presented in Plate 5.

4.3.5.3 Cluster III

From the clustering mean value (Table 11) it was observed that Cluster III had the maximum number of 9 genotypes and consisted of genotypes G01, G02, G04, G06, G11, G14, G18, G21 and G22 (Table 8) and are collected from BARI Chittagong and Gazipur (Table 1). The genotypes of this cluster produced second lowest number of days to first flowering (44.04), on the other hand it also produced second highest cluster mean values for no. of secondary branches (23.80) and no. of fruits per plant (13.57). Plant view with fruits of different genotypes of this cluster has been presented in Plate 6.

Cluster - I. G - 03

Cluster- I. G - 16

Cluster – I, G - 25

Plate 4. Fruit view and plant view of different brinjal genotypes of Cluster I

Cluster I. G - 26

Cluster –I. G - 32

Cluster –I. G - 34

Plate 4. (Cont'd.)

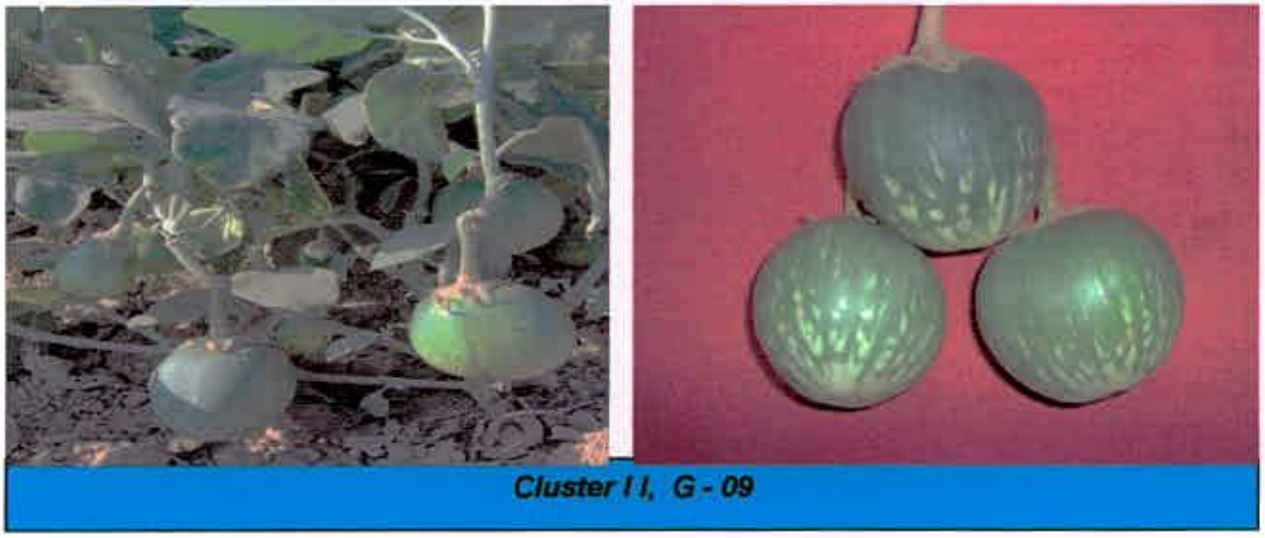


Plate 5. Fruit view and plant view of different brinjal genotypes of Cluster II.

Cluster I I, G -10

Cluster II. G - 12

Plate 5. (Cont'd.)

Cluster II. G - 13

Cluster II. G - 15

Plate 5. (Cont'd.)

Cluster III, G - 01

Cluster III. G - 02

Cluster III. G - 04

Plate 6. Plant view and fruit type of the different brinjal genotypes of cluster II

Cluster III, G - 6

Cluster III. G - 11

Cluster III. G - 14

Plate 6. (Cont'd.)

Cluster IIII, G - 18

Cluster III, G - 21

Cluster III, G - 22

Plate 6. (Cont'd.)

4.3.5.4 Cluster IV

Five genotypes constituted the cluster IV. The genotypes are G07, G19, G27, G30 and G31 (Table 10) collected from BARI Chittagong and Gazipur, Nadim Seed Company, Metal Agro. Limited (Table 1). These genotypes were late in both first flowering (79.33) and first fruit harvesting (62.82) and percent of insect infestation of fruits was lowest (14.85%). It also produced the fruit having the highest mean value for fruit length (19.23 cm). Cluster IV produced the tallest plant (79.33 cm) among the different clusters. On the other hand cluster IV produced the lowest yield 0.850 Kg (Table 9). Plant view with fruits and fruit view of different genotypes of this cluster has been presented in Plate 7.

4.3.5.5 Cluster V

Cluster V constituted only two genotypes viz. genotype 17 and genotype G33 (Table 8), collected from BARI Chittagong and SAU (Table 1). These genotypes were early in both first flowering (34 days), first fruit harvesting (46 days) and produced maximum number of fruits per plant (39.22). It also produced the fruit having the lowest mean value for fruit length (6.31cm), fruit weight (24.61 gm) and lowest mean value for plant height (54.98 cm), number of primary branches (8.62), number of secondary branches (21.08) per plant (Table 9). Plant fruit view of different genotypes of this cluster has been presented in Plate 8.

4.3.5.6 Cluster VI

This cluster had five genotypes namely G20, G23, G24, G28 and G29 (Table 10), collected from BARI Gazipur, Momen Seed Ghar, East – West Seed (Bangladesh) Ltd. (Table 1). These genotypes were produced the highest mean values for no. of primary branches (10.77) and number of flowers per Inflorescence (4.25) and produced the second highest number of mean values for number of fruits per plant (17.91). On the other hand it also produced lowest mean values for fruit circumference (11.93 cm) and percent of insect infestation of fruits (11.93%) (Table 9). Plant view with fruits and fruit view of different genotypes of this cluster has been presented in Plate 9.

Cluster IV. G - 07

Cluster IV. G - 19

Cluster IV. G - 27

Plate 7. Fruit view and plant view of different brinjal genotypes of Cluster IV

Cluster IV. G - 31

Cluster IV. G - 30

Plate 7. (Cont'd.)

Cluster V. G - 17

Cluster V. G - 33

Plate 8. Fruit view and plant view of different brinjal genotypes of Cluster V

Cluster VI. G - 20

Cluster VI, G - 23

Cluster VI, G - 24

Plate 9. Fruit view and plant view of different brinjal genotypes of Cluster VI

Cluster VI. G - 28

Cluster VI. G - 29

Plate 9. (Cont'd.)

It was observed that all the cluster mean values for plant height (cm), no. of primary branches, no. of secondary branches, % insect infestation of fruits and % insect infestation of plants more or less similar. The maximum range of variability was observed for yield (0.920 to 1.360 kg), fruit weight (24.61 gm to 130.11 gm) and fruit circumference (11.93 cm to 24.67 cm) in cluster I among in five clusters. Cluster II and VI included mainly no. of flowers per inflorescence (1.10 to 4.25). Cluster IV and Cluster V included mainly early flowering (33.54 days to 49.94 days) and early days to first fruit harvesting (45.45 days to 62.82 days). However, to develop high yielding varieties/lines, of cluster I genotypes G03, G16, G25, G26, G32 and G34 could be selected for future hybridization programme.

4.4 Contribution of Characters towards Divergence of the Genotypes

Contribution of the characters towards divergence is presented in Table 9.The character contributing maximum to the divergence were 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 vector-1 (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the major axis of differentiation were plant height (0.1769), no. of primary branches (0.1409), days to first flowering (0.0731), no. of flowers per inflorescence (0.4341) days to first fruit harvesting (0.0904) and fruit length (0.03469), no. of fruit per plant (0.1670) (Table 12).

In vector II (Z_2) that was the second axis of differentiation for genetic divergence were plant height (0.4058), no. of primary branches (0.0.1774), no. of secondary branches (0.0114), days to first flowering (0.4500), days to first fruit harvesting (0.4572), fruit length (0.3058), fruit circumference (0.0763), fruit weight per plant (0.2794) yields per plant (0.0407), % insect infestation of fruits (0.0165) and % of insect infestation of plants (0.1713) (Table12).

The role of plant height, no. of primary branches, days to first flowering, days to first flowering and fruit length for both the vectors was positive across two axes indicating the important components of genetic divergence in these materials.

Table 12. Latent vectors for thirteen characters of 34 Brinjal genotypes

Sl. No.	Characters	Vector-I	Vector-II
01	Plant height (cm)	0.1769	0.4058
02	No. of primary branches	0.1409	0.1774
03	No. of secondary branches	-0.0266	0.0114
04	Days to first flowering	0.0731	0.4500
05	No. of flower per inflorescence	0.4341	-0.0060
06	Days to first fruit harvesting	0.0904	0.4572
07	Fruit length (cm)	0.3469	0.3058
08	Fruit circumference (cm)	-0.4656	0.0763
09	Fruit weight (gm)	-0.3635	0.2794
10	No. of fruits per plant	0.1670	-0.4283
11	Yields per plant (kg)	-0.2984	0.0407
12	Percent insects infestation of fruits	-0.2805	0.0165
13	Percent Insects infestation of plants	-0.2851	0.1713

4.5 Comparison of Different Multivariate Techniques

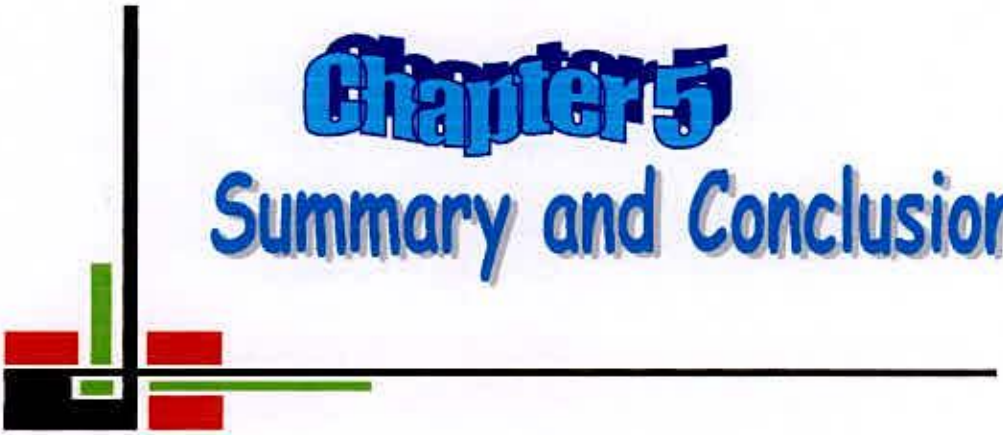
The cluster pattern of D^2 analysis though non-hierchical clustering has taken care of simultaneous variation in all the characters under study. However, the distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the Z_1 and Z_2 vector of the principal component analysis were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However, the principal component analysis provides the information regarding the contribution of characters towards divergence of brinjal

4.6 Selection of Genotypes for Future Hybridization Programme

Selection of genetically divergent genotypes is an important step for hybridization programme. So, the genotypes were to be selected on the basis of specific objectives. A higher heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.* 1974; Ghaderi *et al.* 1989; Main and Bhal, 1989).

Considering the magnitude of genetic distance and agronomic performance, the genotypes G03, G16, G25, G26, G32 and G34 from cluster I would be suitable for highest yield per plant, maximum fruit circumference (cm) and higher fruit length (cm); the genotypes G17 and G33 from cluster V produced maximum number of fruits and having earliness in both days both first flowering and days to first fruit harvesting. The genotypes of cluster V produced shortest plants in comparison with other clusters.

Therefore, considering group distance and other agronomic performance, the inter-genotypic crosses between G03 and G33; G16 and G33; G32 and G33; G34 and G33; G25 and G33; G26 and G33, G17 and G33, might be used for future hybridization programme.



Chapter 5

Summary and Conclusion

CHAPTER V
SUMMARY AND CONCLUSION

In order to evaluate the variability and genetic diversity, an experiment was conducted with 34 brinjal genotypes at the experimental farm of Sher-e-Bangla Agricultural University, during October, 2006 to April, 2007. Seeds of the different genotypes were sown in separate seedbeds and thirty days old seedlings were transplanted in the main field in a RCBD with three replications. Data on different morphological and yield contributing characters like plant growth habit, leaf blade lobbing, fruit shape, fruit colour, fruit apex shape, amount of seed in the fruit, prickliness of the plant, pubescence of the plant, plant pigmentation, days to first flowering, no. of flowers per plant, days to first fruit harvesting, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, fruit length (cm), fruit circumference (cm), fruit weight (gm), no. of fruit per plant, yield per plant, percent insect infestation of fruits and percent insect infestation of plants were recorded. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

The phenotypic variance was higher than the corresponding genotypic variance for all the characters indicating greater influence of environment for the expression of these characters. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the characters. The maximum differences between phenotypic and genotypic coefficient of variation were 46.43 and 34.49 respectively which indicated that the rate of insect infestation was mostly depended on the environmental condition.

Amongst the characters the highest genotypic coefficient of variation was recorded for no. of flower per inflorescence (50.60) followed by no. of fruit per plant (46.12), fruit length (39.74 cm) and individual fruit weight (34.87 gm).

The maximum genotypic and phenotypic variations were 83.99 and 152.20 respectively in percent insect infestation of plants percent.

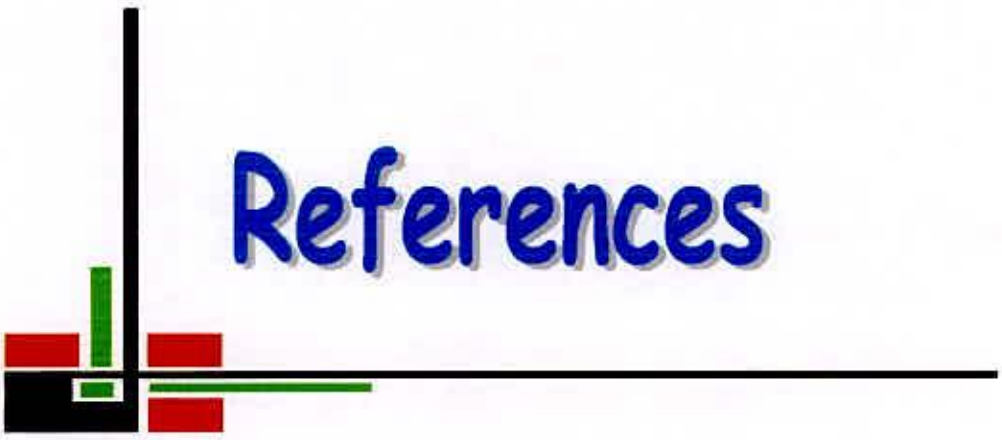
The highest estimated heritability amongst thirteen characters of brinjal was 97.47% for fruit weight and the lowest for 55.18 for percent insect infestation of plants. The highest GA amongst all the characters was found in individual fruit weight 58.92 gm and the lowest genetic advance was carried out in yield per plant (0.49).

The maximum genetic advance in percent of mean was observed for no .of flower per inflorescence (98.91), followed by no. of fruit per plant (92.05) and fruit length (80.10 cm), where as the lowest was for days to first fruit harvesting (19.10) and followed by days to first flowering (23.46) and plant height (24.63 cm). The high heritability (89.33%) with low genetic advance in percent of mean (19.10) indicated non- additive gene action for expression of the characters.

The significant variations among the genotypes for thirteen characters of brinjal were observed. Multivariate analysis was performed through principal component analysis, principal coordinate analysis, cluster analysis and canonical variate analysis using GENSTAT 513 software programme. The first three principal component characters with egen values were greater than unity contributed a total of 70.77% variation towards divergence. As per as principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into six different clusters. These clusters were found from a scatter diagram formed by Z_1 and Z_2 values obtained from PCA. Cluster I, II, III, IV, V and VI composed of six, seven, nine, five, two and five genotypes respectively. The highest inter-genotypic distance was found between genotypes G17 and G26 (2.698) and the lowest distance between G09 and G10 (0.299). The maximum intra-cluster distance was observed between the clusters I and V (5.863), followed by cluster II and cluster V (5.740). The lowest-inter cluster distance was found between the cluster II and cluster III (1.456), followed by cluster IV and cluster VI (1.744).

The highest intra-cluster distance was identified in cluster III (1.835) and the lowest intra cluster distance was found in cluster V (0.537). Genotypes included in cluster I were suitable for no. of secondary branches per plant (24.35), fruit circumference (24.67 cm), individual fruit weight and yield per plant (1.360 kg), cluster IV for having the highest mean value for fruit length (19.23 cm), tallest plant (79.33 cm) and the percent insect infestation of fruits was lowest (14.85%), cluster V for early in both first flowering (34 days), first fruit harvesting (46 days), produced maximum number of fruits per plant (39.22) and the percentage insect infestation of plants was also very low (16.67%) in this cluster and cluster VI for no. of primary branches (10.77) and number of flowers per Inflorescence (4.25).

Findings of the present investigation indicated significant differences among the cultivars for all the characters studied. Generally, diversity was influenced by the morphological characters, but not by the distribution of genotypes, which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performances, the genotypes G03, G16, G25, G26, G32 and G34 from cluster I and genotypes G17 and G33 from cluster V could be considered as suitable parents for efficient hybridization in future hybridization programme. Inter-genotypic crosses between the diverse genotypes, *viz.* G03 and G33; G16 and G33; G32 and G33; G34 and G33; G25 and G33; G26 and G33, G17 and G33, might be able to produce desirable segregants.



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Appendices

Appendix I. Morphological, physical and chemical characteristics of initial soil (0 – 15 cm depth)

A. Physical Composition of the Soil

Sl. No.	*Soil Separates*	*%*	*Methods Employed*
01	Sans	36.90	Hydrometer Methods (Day, 1915)
02	Silt	26.40	Same
03	Clay	36.66	Same
04	Texture Class	Clay Loam	Same

B. Chemical Composition of the Soil

Sl. No.	*Soil Characteristics*	*Analytical data*	*Methods Employed*
01	Organic Carbon (%)	0.82	Walkley and Black, 1947
02	Total Notrozen (Kg/ha)	1790.0	Bremner and Mulvaney, 1965
03	Total S (ppm)	225.00	Bardsley and Lanester, 1965
04	Total Phosphorus (ppm)	840.0	Olsen and Sommers, 1982
05	Available Nitrozen (kg/ha)	54.0	Bremner, 1965
06	Available Phosphorus (kg/ha)	69.00	Olsen and Dean, 1965
07	Exchangeable K (Kg/ha)	89.50	Pratt, 1965
08	Available S (kg/ha)	16.00	Hunter, 1984
09	pH (1:2.5 Soil to Water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Appendix II. Monthly average temperature, no. of rainy days, relative humidity and total rainfall of the experiment site during the period from October, 2006 to April, 2007

Year	Months	*Air Temperature (^{0}C)			Number of Rainy Days**	Relative Humidity (%)	**Rainfall (mm)
		Maximum	Minimum	Mean			
2006	October	32.3	24.7	28.50	07	72	88
	November	29.7	20.1	24.90	04	65	05
	December	26.9	15.8	21.35	00	68	00
2007	January	24.6	12.5	18.55	00	66	00
	February	27.1	16.8	21.95	00	64	00
	March	31.5	19.6	25.55	10	47	160
	April	33.7	23.7	28.70	12	65	87
Total		*205.80*	*133.2*	*169.50*	*33*	--	--

*Monthly Average
**Monthly Total
Source: Bangladesh Meteorological Department (Climate Division), Agargaon, Dhaka – 1212.

Appendix III. Total Production and yields of vegetables crops of Bangladesh from 2001-2002 to 2003-2004

Name of Crops	Name of Season	2001-2002			2002-2003			2003-2004		
		Area '000' Ha.	Per Ha. Yield (Kg)	Production '000' M. Tons	Area '000' Ha.	Per Ha. Yield (Kg)	Production '000' M. Tons	Area '000' Ha.	Per Ha. Yield (Kg)	Production '000' M. Tons
Total Vegetables Production	Rabi (Winter)	153.44	7002.45	1073	155.06	6876.48	1064	159.92	7066.67	1131
	Kharif (Summer)	104.86	5063.50	534	108.91	5014.10	541	114.57	5346.08	608
Total		**255.30**	**6221.93**	**1607**	**263.97**	**6081.14**	**1605**	**268.83**	**6335.55**	**1739**

Source: BBS, (2004)

Appendix IV. Area, Production and yields of brinjal in Bangladesh from 2001-2002 to 2003-2004.

Name of Crops	Name of Season	2001-2002			2002-2003			2003-2004		
		Area '000' Ha.	Per Ha. Yield (Kg)	Production '000' M. Tons	Area '000' Ha.	Per Ha. Yield (Kg)	Production '000' M. Tons	Area '000' Ha.	Per Ha. Yield (Kg)	Production '000' M. Tons
Brinjal	Rabi (Winter)	40.89	6476.34	264	40.49	6305.91	256	37.65	6397.30	240
	Kharif (Summer)	22.27	5137.60	114	22.27	5174.65	114	22.67	5248.75	118
Total		**63.16**	--	**378**	**62.75**	--	**370**	**60.32**	--	**358**

Source: BBS, (2004)

Appendix V. Area and production percentage of Brinjal in Bangladesh from 2001-2002 to 2003-2004

Name Of Crops	Name of Season	2001-2002		2002-2003		2003-2004	
		Area (Ha.) %	Production(MT) %	Area (Ha.) %	Production (MT) %	Area (Ha.) %	Production (MT) %
Brinjal	Rabi (Winter)	26.65	24.60	26.11	24.06	23.54	21.22
	Kharif (Summer)	21.24	21.35	20.45	21.07	19.78	19.41

Source: BBS, (2004)

Appendix VI. Principle Component Scores for 34 (thirty four) Brinjal genotypes

Genotypes Number	Z_1	Z_2
01	7.68	3.00
02	10.48	-5.71
03	-59.45	6.59
04	-2.85	7.84
05	-6.06	-2.18
06	2.96	1.32
07	17.18	-9.26
08	-12.53	2.20
09	-27.06	-0.04
10	-18.40	-2.98
11	-8.63	8.65
12	-12.87	11.62
13	-0.80	-9.91
14	0.17	-1.64
15	-17.84	-3.99
16	-37.83	5.12
17	64.84	26.98
18	-3.63	10.00
19	5.11	-15.78
20	36.10	-15.89
21	13.77	10.35
22	19.29	9.99
23	28.75	3.07
24	28.57	4.91
25	-41.59	12.96
26	-61.70	-1.32
27	15.65	-11.55
28	19.13	-6.39
29	30.93	-22.16
30	12.00	-22.04
31	18.25	-13.30
32	-42.40	-7.71
33	62.73	19.44
34	-39.95	7.82

Appendix VII. Nutritive value per 100 gums edible portion of brinjal (*Solanum melongena* L.)

Nutrients	*Value*	*Nutrients*	*Value*
Moisture	92.7 gms	Protein	1.4 gms
Fat	0.3 gms	Minerals	0.3 gms
Fibre	1.3 gms	Carbohydrate	4 gms
Energy	24 kcal	Calcium	18 mgs
Phosphorous	47 mgs	Vitamin C	12 mgs
Sodium	3 mgs	Potassium	200 mgs
Vitamin A	142.0 IU	Vitamin B	0.04 mgs

(Ismail, 2005)