PHYSIO-MORPHOLOGICAL CHARACTERIZATION GENETIC VARIABILITY AND CORRELATION STUDIES IN BRINJAL GENOTYPES

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This to certify that thesis entitled, **"PHYSIO-MORPHOLOGICAL CHARACTERIZATION, GENETIC VARIABILITY AND CORRELATION STUDIES IN BRINJAL GENOTYPES"** 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 **HORTICULTURE**, embodies the result of a piece of ***bona fide*** research work carried out by **Mahmuda Khatun, Registration No. 05-01628** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2010
Place: Dhaka, Bangladesh

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ABSTRACT

Thirty five genotypes of Brinjal were studied in the experimental field of Bangladesh Agricultural Research Institute, Gazipur, during the period from September 2010 to February 2011. There was significant variation for all the characters within genotypes. The phenotypic coefficient of variation (PCV) was higher than genotypic. The PCV estimates were high for number of branches, number of fruit per plant, single fruit weight. Heritability estimates were high for single fruit weight with high genetic advance. In spite of high heritability values for most traits, the expected genetic advance as percentage of mean ranged from 19.92 to 121.51. Multivariate analysis was performed through principal component analysis (PCA), principal coordinate analysis, cluster analysis and canonical variate analysis. As per PCA, D^2 and cluster analysis, the genotypes were grouped to six clusters. The highest inter-cluster distance was between cluster II and III and lowest between V and VI. Cluster VI showed the maximum intra-cluster distance and II showed the lowest. Genotypes of cluster I were suitable for no. of branches/plant, cluster II for fruit length, cluster III for no. of fruit/plant, cluster IV for single fruit weight and yield. Considering the performances, genotypes SM-111, SM-84, EGN-27, SM-183, BARI begun-6 might be considered as suitable parents for efficient hybridization program.

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LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL WORD
AEZ	Agro-Ecological Zone
et al.	And others
ACC	Accessions
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co-efficient of Variation
etc.	Etcetera
Fig.	Figure
G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
δ^2_g	Genotypic Variance
g	Gram
h^2b	Heritability in broad sense
J.	Journal
Kg	Kilogram
m	Meter
MSS	Mean Sum of Square
mm	Millimeter
MP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
δ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design
R	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate

CHAPTER I

INTRODUCTION

Brinjal or Eggplant or Melongene or Aubergene is one of the most important and popular Solanaceous crops under the botanical name *Solanum melongena* L. (2n = 24) grown in Bangladesh. There are three main botanical varieties under the species melongena (Choudhury, 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.The cultivated brinjal is undoubtedly of Indian origin and has been in cultivation for long time (Thompson and Kelly, 1957). According to Purewal (1957), it is still found growing wild in India. A wide genetic diversity is found here due to the availability of different land races and their wild relatives. 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 throughout 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. Total vegetable growing area in the country is about 885 thousand acres (2.47 acre is equal to a hectare) in 2009-2010 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) 2009-2010 the total area covered by brinjal cultivation was 28.74 thousand hectares with the production of 216 thousand metric tons and in

kharif (summer), the hectares and production was 17.81 thousand and 125 thousand metric tons respectively (BBS 2010).

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 Aruchalam, 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, intracluster and inter-cluster levels, and thus help in the selection of genetically divergent parents for exploitation in hybridization programme. Genetic diversity plays an important role in plant breeding because hybrids between 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 to 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).

Brinjal is grown round the year though bulk of its production is obtained during winter season in Bangladesh. Due to its quality, diversified use, lower market price and year round availability, it has become the widely consumed vegetable in Bangladesh. As it is the major native vegetable of our country, lots of variability is available throughout the country. A number of wild types are also found here and there throughout the country. Among the cultivated types, a wide range of genetic variability exists in this crop. Where there is more variability, more chances of improvements are there either from existing variability or from the segregates of a cross through selection. For effective selection of a superior genotype for their use in any improvement program needs through characterization of the genotypes as well as genetic variability and correlation study. Assessment of genetic resource is the starting point of any crop improvement program. By studying physio-morphological characteristics, genetic variability and correlation of brinjal genotypes we can select the best genotypes.

Considering the above facts, the present study has been under taken to fulfill the following objectives:

- To characterize the genotypes under the study thoroughly.
- To study the genetic variability and correlation between yield and it's component characters.
- To screen out the suitable parents for hybridization

CHAPTER II

REVIEW OF LITERATURE

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. 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

Naik *et al.* (2010) conducted an experiment at Olericulture Unit, Kittur Rani Channmma College of Horticulture, Arabhavi, Gokak, Belgaum, Karnataka during kharif season of 2004-05 to evaluate 61 genotypes using randomized block design. The observations on 24 characters were recorded. High heritability values and high percentages of genetic advance were recorded fruits length, number of fruits per cluster, number of fruits per plant, total yield per plant, yield per plot, yield per hectare which indicated that there were more number of additive factors for these characters and improvement in yield could be brought about by selection, based on phenotypic observations.

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

Lenuta and Nedelea (2010) Most important breeding objectives are complex traits consisting of multiple components. In that direction, in eggplant yield can be decomposed into several yield components as well as branches number/plant, fruit number/plant, fruit weight. The aim of this paper was to evaluate the variability and breeding potential of different eggplant cultivars for some yield traits. A significantly bigger fruit comparing to the control was observed for the following varieties: Baluroi and Long purple, which may be successfully used in plant breeding programs to improve the fruit weight. Given the variability of fruit length and diameter, the choice of the genitors in the eggplant improvement programs the market requirements should be considered. The existing variability within the studied assortment allows the use of considered varieties within eggplant breeding programs taking in

consideration the increased yield that is attainable for certain varieties on the ground of contrasting traits.

Singh *et al.* (2010) carried out an experiment with 99 genotypes (76 F1s, 19 lines and 4 testers) of brinjal to assess the character association and contribution of quantitative trait towards yield. Yield per hectare was positively correlated with number of flowers per plant, number of fruits per plant, fruit length, fruit weight, fruit volume, number of fruit picking, plant height, plant girth, leaf area and plant spread (in both direction) while days to first fruit harvest and per cent of plant wilted showed significant negative association with fruit yield. The path analysis suggested that fruit weight and fruit per plant had high direct effect on fruit yield. However, the indirect contribution of fruit diameter, leaf area and plant spread (in both direction) were appreciable to affect fruit yield in brinjal.

Reena and Mehta (2009) carried out an investigation to study genetic variability in 20 genotypes of brinjal. Phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters. Both phenotypic coefficient of variation as well as genotypic coefficient of variation was high for seed pulp ratio, weight of fruit and number of fruits per plant. High heritability accompanied by high genetic advance was observed for weight of fruit indicating negligible environment effect and this trait will be more amenable to improvement through mass selection progeny selection etc., aiming at exploiting the additive variance. High heritability and moderate genetic advance were observed for plant height, fruiting span and number of fruits per plant suggesting that selection based on phenotypic performance of these traits is possible. Good variation was also observed for the morphological characters investigated. Genotypes PB-64, D-77-19, PB-67 and JB-15 were found least susceptible to discolouration. It is an important character that should be considered in breeding programme for developing variety having good consumer preference.

Correlation and path analysis were studied in 50 F_4 progenies and six parents of brinjal (*Solanum melongena* L.) by Jadhao *et al*. (2009) for eleven yield contributing characters. The phenotypic coefficient of variation was greater than the respective genotypic coefficient of variation for all the characters studied. The yield contributing characters viz., plant height, number of branches per plant, days to last picking, fruit weight and number of fruits per plant showed positive significant correlation with fruit yield per plant. Path coefficient analysis revealed that plant height, number of branches per plant, days to Initiation of flowering, days to first picking, days to last picking, fruit length and fruit weight showed positive direct effect

on fruit yield per plant indicating these characters had direct relation with yield, so while seeking improvement in yield attributes, these characters may get priority.

The phenotypic, genotypic and environmental correlations between six characters of 24 cultivars of eggplant (*Solanum melongena*) were studied in the research centre of Turipana of Corpoica (Cerete Cordoba Colombia 8 degrees 31'N and 75 degrees 58'W, 13 m.a.s.l.) by Aramendiz *et al*. (2009)**.** A completely randomized block design was used with three repetitions and experimental units of 10 m^2. The analyses showed that genetic correlations were of higher or equal magnitude to the phenotypic correlations, while the environmental ones had low effects on the results. The number of fruits and the yield showed a positive and highly significant ($r=0.56$, $P<0.01$) genetic correlation. A negative and highly significant ($r = -0.68$, $P<0.01$) genetic correlation was observed between fruit length and fruit strength. No correlation was detected between yield and fruit weight ($r = 0.04$). Fruit number and fruit weight showed a negative and highly significant genetic correlation ($r = -0.63$, $P<0.01$). It is suggested that the number of fruits per plant could be used as a selection criterium to obtain high yield eggplant cultivars.

Sherly and Shanthi (2008) carried out an investigation with 24 genotypes of brinjal for variability, heritability and genetic advance. The study indicated that high estimates of phenotypic and genotypic coefficients of variation were observed for fruit length, number of fruits per plant, fruit weight and fruit yield per plant. High heritability coupled with high genetic advance was registered for all the characters except total number of harvest and ascorbic acid. These characters can be effectively improved through selection.

Chowdhury *et al*. (2007) conducted an experiment in the Olericulture Division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI) during the winter season 2003-04,**)** to evaluate and compare aubergine genotypes Uttara, BL-081, B-009, BL-SA-02, Nayantara, BL-097, BL-102, BL-113, BL-114, ISD-006, BL-072, EG-195, BL-095, BL-081, BL-099 and Kazla representing samples from the different districts of Bangladesh. Various morphological and yield contributing characters of these aubergine genotypes were observed. Significant variation for most of the morphological characters were observed among the aubergine genotypes. The results revealed that the maximum number of fruits per plant was obtained from the line BL-099 (43.67). The maximum fruit weight (410.9 g), fruit weight per plant (4.79 kg) and fruit breadth (8.71 cm) were recorded from the line ISD-006. The longest fruit was recorded from the line B-009 (30.22 cm).

Naliyadhara *et al.* (2007) carried out an experiment on evaluation of 21 genotypes of brinjal during late kharif season that revealed that PCV was slightly grater than GCV for all the traits. High heritability with moderate to high GCV and genetic gain was observed for all the characters except fruit yield which could be improved by simple selection methods. The genotypic correlation coefficients were higher than corresponding phenotypic one for most characters reflecting predominant role of heritable factors. Fruit yield displayed significant and positive genotypic and phenotypic correlations only with 10-fruits weight. Path coefficient studies explained that fruit length, 10-fruits weight and plant spread exerted higher positive direct effect on fruit yield suggesting to give emphasis on such fruits while imposing selection for fruit yield of brinjal.

Twenty-three genotypes of brinjal [aubergine] were assessed during the late kharif season of 2001/02-2003/04 in Junagadh, Gujarat, India by Golani *et al.* (2007) to determine the nature and magnitude of genetic divergence and genetic variability for fruit yield and its contributing characters: plant height, plant spread, fruit length, fruit girth and 10-fruit weight. The population was grouped into 6 clusters. Cluster I comprised 6 genotypes, followed by clusters II and III, each with 5 genotypes, while cluster VI was a solitary cluster. The clustering pattern indicated that there was no association between the geographical distribution of the genotypes and genetic divergence. However, the shape and colour of fruits and the genotypes played a major role in the grouping of the genotypes into various clusters. The maximum intercluster D2 value was reported between clusters II and III. The genotypic coefficient of variation, heritability and genetic advance as percentage of mean were high for fruit length, fruit girth and 10-fruit weight, indicating additive gene action, which contributed to maximum divergence and played a major role in the improvement of brinjal yield.

Ram *et al*. (2007) carried out an investigation to study the variability and selection parameters was undertaken during kharif 2003-04 in Uttar Pradesh, India using fifteen aubergine lines (KS 219, KS 247, KS 253, KS 262, KS 228, KS 233, KS 250, KS 263, KS 235, KS 227, ACC 5114, ACC 8204, ACC 8206, ACC 8207 and ACC 2623) and four testers (T 3, AB 1, KS 224 and DBR 8). The estimates of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the characters studied. High magnitude of variability was observed in the mean among the parents, F< sub>1</ sub>s and F< sub>2</ sub>s for number of branches per plant, number of fruits per plant, length of fruit, width of fruit and yield per plant. The high genotypic and phenotypic coefficients of variation were observed for yield per plant, plant spread and number of fruits per plant in

parents, F< sub>1</ sub>S and F< sub>2</ sub>S, suggesting the improvement by selection. High heritability coupled with high genetic advance indicating additive gene action was exhibited by characters, plant height, days to marketable maturity, plant spread, days to flowering, yield per plant, fruit weight and number of branches per plant in all the three populations. These characters can be improved by simple selection to get higher yield.

Thirteen diverse genotypes were evaluated by Prabhu and Natarajan (2007) for estimating the range of variability, heritability and genetic advance of growth and yield attributes in aubergine. The high genotypic coefficient of variation expressed by yield contributing traits such as number of fruits per plant, mean fruit weight and fruit borer infestation. Higher values of genetic advance as percent over mean along with higher estimates of heritability was observed for all characters except earliness. This will be useful to get desired improvement in the yield of aubergine genotypes.

Prasad *et al.* (2006) conducted a field experiment in Raipur, Chhattisgarh, India during the kharif season of 2002-03 on genetic variability in 52 aubergine genotypes. Moderate to high estimates of genotypic coefficient of variation, heritability and genetic advance was recorded for average fruit weight, fruit yield, fruit girth, number of fruits per plant and fruit length. Low estimates of genotypic coefficient of variation and genetic advance were recorded for number of days to 50% flowering, fruit set and number of primary branches. Moderate estimates of genotypic coefficient of variation, genetic advance and heritability were recorded for plant height and number of days to first flowering and fruit set.

Combining ability for 9 traits (fruit yield per plant, days to first picking, plant height, plant spread, 1000-seed weight, fruit dry matter, total soluble sugars, total phenols and leaf area per plant) was studied in 10x10 diallel (excluding reciprocals) of aubergine during late summer in Gujarat, India by Suneetha and Kathiria (2006). Analysis of variance for combining ability revealed significant mean squares due to both general (gca) and specific combining ability (sca) for fruit yield, yield components, quality and physiological characters. KS 224, PLR 1, Morvi 4-2 and JBPR 1 appeared to be good general combiners for fruit yield per plant. In addition, KS 224 was a good combiner for total phenols, whereas PLR 1 and Morvi 4-2 were good combiners for total soluble sugars. These parents also recorded high per se performance for the traits. Among the hybrids, 22 crosses exhibited significant and desirable sca effects for fruit yield per plant. Of these, 9 crosses also exhibited high per se performance. KS 224 x PLR 1, involving both good combiner parents, recorded the highest fruit yield per plant and exhibited desirable sca effects and per se performance for most traits. Six other crosses also

recorded significant and desirable sca effects and per se performance for fruit yield and quality traits.

The manifestation of hybrid vigour in 45 aubergine hybrids for yield, yield components, quality and physiological characters was investigated during the summer season in Gujarat, India by Suneetha *et al.* (2006). Hybrids were found to be high yielding, relatively late and tall with greater plant spread and leaf area per plant, compared to their parents. Existence of significant levels of heterobeltiosis and commercial heterosis for all the traits in the material studied was also observed from the significant mean squares recorded for parents vs. hybrids and control vs. hybrids components of variation in the ANOVA. Furthermore, the expression of heterosis was maximum over better parent for total soluble sugars, and for leaf area per plant over the control, GBH 1. Total phenols had also recorded high levels of heterosis (>70%) over both better parent and the control. Heterobeltiosis and standard heterosis more that 20% were also recorded for the number of days to first picking, 100-seed weight and fruit yield per plant. The existence of such high levels of heterosis for fruit yield, yield components, quality and physiological characters in aubergine hybrids during summer indicated the potential of hybrid cultivation during off-season. Among the hybrids, PLR 1 x JBPR 1, a relatively early and dwarf hybrid was identified as a potential hybrid combination for fruit yield per plant, while the hybrid JB 64-1-2 x AB 98-13 was identified as a promising hybrid for both, fruit yield and quality for cultivation during off-season.

Genetic parameters for 13 traits (number of days to first flowering, number of flowers per inflorescence, number of primary branches per plant, plant height, fruit length, fruit diameter, number of marketable and unmarketable fruits per plant, total number of fruits per plant, weight of marketable and unmarketable fruits, total weight of fruits per plant, and early yield per plant) were studied during the winter of 2001-02 and autumn-winter of 2002-03 in 5 round-fruited aubergine cultivars (Pant Rituraj, PB-60, PB-61, PB-62 and T-3) and 10 crosses (produced by diallel crossing between these cultivars) grown in Pantnagar, Uttaranchal, India by Panda *et al*. (2005). Heritability in the narrow sense was highest for number of days to first flowering, whereas the genetic advance was greatest for weight of marketable fruits per plant. The number of flowers per inflorescence, number of marketable fruits per plant, fruit diameter, and total number of fruits per plant were characterized by high genetic advance and high heritability; thus, selection would be suitable for the improvement of these traits. The analysis of the genetic component of variation revealed over dominance for plant height, number of marketable fruits per plant, and total weight of fruits per plant, and partial

dominance for number of days to first flowering, fruit diameter, number of unmarketable fruits per plant, and total number of fruits per plant. Fruit length and number of flowers per inflorescence showed complete dominance. The results suggested that heterosis breeding will be effective for the improvement of plant height, number of marketable fruits per plant, and total weight of fruits per plant, whereas combination breeding will be suitable for the improvement of the other traits.

Variability and correlation analyses for 13 traits (number of days to 50% flowering, number of flowers per cluster, number of fruits per cluster, number of days to first picking, number of pickings, fruit length, fruit diameter, fruit weight, number of fruits per plant, leaf area, number of leaves, plant height, and fruit yield per plant) of aubergine were conducted in Tehri Garhwal, Uttaranchal, India by Kushwah and Bandhyopadhya (2005) during the kharif of 2000. Highly significant variation among the genotypes was recorded for all traits. High phenotypic and genetic coefficients of variation, and high genetic advance were recorded for fruit weight, number of flowers per cluster, and fruit diameter. Except for leaf area and number of leaves, high heritability estimates were recorded, suggesting that selection for the remaining characters would be effective. At the genetic level, the number of fruits per plant, fruit diameter, and number of pickings showed a significant positive correlation with yield per plant. At the phenotypic level, fruit yield was positively correlated with the number of pickings, fruit diameter, and number of fruits per plant, but was negatively correlated with the number of days to first picking. Fruit weight and diameter were negatively correlated with the number of fruits per plant, fruit length, number of fruits per cluster, and number of flowers per cluster.

Prasad *et al.* (2004) conducted an experiment during kharif 2002/03 at Raipur, Chhattisgarh, India, highly significant differences were observed among the 52 aubergine genotypes for all characters except fruit yield. Moderate to high estimates of genotypic coefficient of variation (GCV), heritability and genetic advance were observed for average fruit weight, fruit yield, fruit girth, number of fruits per plant and fruit length, indicating the potential of simple selection for the improvement of these characters. The low estimates of GCV and genetic advance were observed for days to first flowering, fruit set and number of primary branches. Moderate estimates of GCV, genetic advance and heritability were observed plant height, days to first flowering and days to first fruit set, indicating the potential for the improvement of these characters through selection in the germplasm.

Das *et al.* (2002) carried out an investigation 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.

Sharma and Swaroop (2000) conducted a field experiment on 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 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 coefficient of variation estimates was 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. In spite of high heritability values for most traits, the expected genetic advance as percentage of mean ranged from 11.47 to 95.36. Genotypic correlation was higher in magnitude over phenotypic correlation. Most of the characters were positively correlated with yield except for days to 50% flowering. Path coefficient analysis revealed that number of fruits per plant, mean weight of fruits and diameter of fruits had maximum direct effect at genotypic level and hence direct selection could be made for these characters for improving the yield, while maximum direct effect at phenotypic level was showed by number of fruits per cluster, plant height, number of fruits per plant, mean weight of fruits and diameter of fruit. 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.

Mohanty (2001) conducted an experimented on 15 aubergine genotypes during the kharif seasons of 1994, 1995 and 1996 in Orissa, India to determine genotype environment interaction. Genotype environment interaction was significant for average fruit weight, number of fruits/plant, and yield. Phenotypic coefficient of variation was high for number of

fruits/plant (42.0%) and average fruit weight (38.9%), while it was moderate for number of branches/plant, yield and plant height. High magnitude of genotypic coefficient of variation was observed for number of fruits/plant (40.2%) and average fruit weight (36.9%) whereas it was moderate for number of branches/plant (25.6%). The estimates of heritability in the broad sense ranged from 62.9% for plant height to 91.6% for number of fruits/plant. High estimates of genetic gain were obtained for number of fruits/plant (77.26%) and average fruit weight (72.06%) while it was moderate for number of branches/plant (47.43%). The phenotypic and genotypic path coefficient studies showed that average fruit weight had the highest positive direct effect on yield followed by the number of fruits/plant.

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. Evaluation of 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. The genotypic correlation coefficients were higher than corresponding phenotypic one for most character combinations. Yield displayed positive and significant genotypic and phenotypic association with plant height and number of fruits/plant. Path coefficient studies explained that number of fruits/plant and plant height exerted maximum positive direct effect on yield suggesting to give emphasis on such traits while exercising selection to circumvent the yield of aubergine.

Patel *et al.* (1999) estimated genetical parameters of 41 genotypes of brinjal (Solanum melongena) that indicated the highest genetic coefficient of variation for fruit volume followed by seed to pulp ratio. 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.

Information on genetic variance, coefficient of variation, broad-sense heritability and genetic advance for yield and quality characters was derived by Doshi *et al.* (1999) 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 are under the control of additive gene action and can be improved through simple selection procedures.

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.

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) were evaluated by Biswas *et al.* (2005) 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 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 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 was derived from data on 16 characters in 40 diverse cultivars grown during 1993-94 and 1994-95 by Rajesh *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.

Das *et al.* (2002) carried out an experiment 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.

Brinjal or eggplant or aubergine *(Solanum melongena)* is the most popular and widely cultivated vegetable crop in the Central, Southern and in South-east Asia and in some African countries. The cultivated brinjal, *Solanum melongena*, is extremely variable in India. Das *et al.* (2010) conducted an experiment on 40 genotypes of brinjal collected from different places in the country and abroad were evaluated for different morphophysiological characters and genetic diversity was measured among the genotypes through D2 statistics. All the nine characters under study differed significantly among the forty genotypes. The range of D2 values varied from 8.13 to 8015.95 which revealed high variability among the genotypes. Based on the degree of divergence the genotypes were grouped into ten clusters among which cluster ten was the largest having 22 genotypes. The divergence within the cluster showed medium and consistent level of divergence in all the clusters except cluster ten which had highest intra cluster distance. The top two characters which contributed most towards the genetic divergence were fruit yield and fruit weight. Dendrogram among the genotypes also revealed high diversity along with strong intra and inter cluster relationships.

Eggplant is a major crop in Turkey, which produces more of this crop than all of Europe; consequently, germplasm resources are of concern for the country. Molecular characterization of eggplant genotypes collected from different geographical regions of Turkey by Demir *et al*. (2010) carried out using SSR and RAPD markers. With amplification of five SSR loci, the number of alleles per microsatellite locus ranged from 2 to 10, with a total of 24 alleles. The greatest number of alleles was found at the emf21H22 locus (10 alleles); followed by emh11O01 and emf21C11 as five and four alleles, respectively. The average number of alleles per locus was 4.8. Using 11 decamer RAPD primers, 100 bands were amplified, among which 29 were polymorphic. The number of bands per primer ranged from seven (OPH10, OPH19, OPH20, OPH03) to 14 (OPB07). Primer OPB07 was the most

polymorphic, generating 64% polymorphic bands; the rest of the primers gave less than 50% polymorphism. UPGMA dendrograms were used to examine the genetic relatedness of the genotypes.

Diversity is an important criterion in the selection of elite germplasm lines to develop highly heterotic F_1 hybrids. The heterosis and diversity study was conducted by Dharwad *et al.* (2010) on 28 F1 hybrids of brinjal derived from germplasm lines viz., IC-112995, IC-111305, IC-90952, IC-99704, IC-99663, IC-136210, IC-126784 and a local cultivar Manjri Gota at botany garden, UAS Dharwad during summer 2006. Fruit weight (g), number of fruits per plant and fruit yield (g) exhibited considerably high magnitude of heterosis. High heterosis for fruit yield was attributed to increased fruit weight and number of fruits per plant. Thirty six entries comprising 28 F1 hybrids and 8 parents were grouped in six clusters. Based on parental divergence, all 28 hybrids were grouped in 4 divergence classes. The combination of heterosis and diversity analysis indicated the high frequency of hybrids classified under DC2 and DC3 suggesting moderate genetic diversity is most desirable to produce highly heterotic hybrids.

Genetic divergence was studied Singh *et al.* (2006) using 29 aubergine genotypes. From the D^2 statistics and canonical analysis, the genotypes were grouped into 6 clusters, irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. Cluster II topped in having maximum 14 genotypes, while cluster V and VI were solitary clusters. The maximum intercluster distance was observed between cluster I and VI. Among characters contribution study, the number of fruits per plant, plant height, average fruit yield per plant, number of branches per plant contributed maximum divergence and have a major role in improvement**.**

Twenty-three genotypes of brinjal [aubergine] were assessed during the late kharif season of 2001/02-2003/04 in Junagadh, Gujarat, India by Golani *et al.* (2007) to determine the nature and magnitude of genetic divergence and genetic variability for fruit yield and its contributing characters: plant height, plant spread, fruit length, fruit girth and 10-fruit weight. The population was grouped into 6 clusters. Cluster I comprised 6 genotypes, followed by clusters II and III, each with 5 genotypes, while cluster VI was a solitary cluster. The clustering pattern indicated that there was no association between the geographical distribution of the genotypes and genetic divergence. However, the shape and colour of fruits and the genotypes played a major role in the grouping of the genotypes into various clusters. The maximum intercluster D^2 value was reported between clusters II and III. The genotypic

coefficient of variation, heritability and genetic advance as percentage of mean were high for fruit length, fruit girth and 10-fruit weight, indicating additive gene action, which contributed to maximum divergence and played a major role in the improvement of brinjal yield.

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 F1'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).

Genetic diversity for 5 traits, i.e. plant height, branches per plant, fruits per plant, average fruit weight and fruit yield, was evaluated in 15 genotypes of *S. melongena* grown during kharif 1995 in Bhawanipatna, Orissa, India by Mohanty and Prusti (2001). Analysis of variance revealed significant variation among genotypes for all traits studied. 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.

Fourteen genotypes of brinjal [aubergine] were assessed for 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 by Kumar *et al. (*2000**).** Highly significant differences were observed for all the characters under study. Higher values of phenotypic than genotypic coefficient of variation in all the three environments indicated the role of environmental influence in the expression of various characters.

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 HLB24 (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 genotvpes 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 yieldrelated 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) conducted an experiment on Genetic divergence among 20 cultivars of Egg plant (*Solanum melongena*) was estimated using D2 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.

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 was conducted in Pantnagar, Uttar Pradesh, India, during 1999/2000 and 2000/01 rabi season 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.

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 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.

It was revealed by Ushakumiry *et al.* (1991) through the evaluation of fifty four diverse genotypes of brinjal for 10 yield components that phenotypic coefficient 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.

2.3 Relationship between genetic and geographic diversity

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.

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 subtropical 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.

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 inter population 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 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.

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.

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.

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).

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.

An experiment was conducted by Birhman *et al.* (1991) and found that genetic distance was evaluated by applying the ^{D2} 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 11 and VII had high inter-cluster distances. Cross involving parents from these cluster combinations were recommended for an Andigena breeding programme.

CHAPTER III

MATERIALS AND METHODS

The investigation was carried out at the experimental field of the Olericulture division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI) Joydebpur, Gazipur, during the period from September 2010 to February 2011 to study the Physio-morphological characterization, Genetic Variability and Correlation studies in brinjal genotypes. A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc. which are presented as follows:

3.1. Experimental site

The research work was conducted at the Olericulture division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI) Joydebpur, Gazipur during the period from September 2010 to February 2011.

3.2 Geographical Location

The experimental area was situated at 24.00° N latitude and 90.25 E longitude at an altitude of 8.4 meter above the sea level. The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28 (Anon., 1988a). This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as 'islands' surrounded by floodplain (Anon., 1988b).

3.3 Climate

Area has subtropical climate, characterized by scanty rainfall associated with moderately low temperature during the Rabi season (September-February) and high rainfall, high temperature during rest of the year. Meteorological information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented in Appendix I.

3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, Shallow Red Brown. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analysis was done by Soil Resource and Development Institute (SRDI), Dhaka.

Table 1. List of selected 35 genotypes with their place of collection and fruit colour

Sl No.	Name/Accession no.	Place of collection/ Source	Fruit colour
1.	SM-57	Market	Purple black
2.	EGN-17	Nichintopur	Purple black
3.	Uttara	Rajshahi	Purple
4.	EGN-10	Nichintopur	Purple black
5.	Sada begun	Unknown	White
6.	SM-111	Barishal	Purple black
7.	EGN-27	Nichintopur	Purple black
8.	EGN-25	Nichintopur	Green
9.	Chaga	Nichintopur	Green
10.	BARI begun-7	BARI, Gazipur	Black
11.	SM-75	Thakurgaon, Gene Bank, BARI	Purple
12.	BARI begun-9	BARI, Gazipur	Purple black
13.	SM-59(small)	Unknown	Purple black
14.	SM-58	Unknown	Purple black
15.	SM-11	Unknown	Milky white
16.	SM-48	Rangpur	Green
17.	SM-77(long)	Thakurgaon, Gene Bank, BARI	Green
18.	BARI begun-5	Gazipur	Purple black
19.	SM-59(big)	Unknown	Purple black
20.	BARI begun-3	Unknown	Purple black
21.	SM-83	Thakurgaon, Gene Bank, BARI	Green
22.	SM-180	Advanced Line of Netherland seed comp.	Light purple
23.	SM-19	Unknown	Purple
24.	BARI begun-4	Unknown	Purple black
25.	BARI begun-8	Unknown	Light purple
26.	SM-84	Gene Bank, BARI	Light purple
27.	SM-63	Market	Purple black

28.	SM-184	Advanced Line of Netherland seed comp.	Purple
29.	BARI begun-10	BARI, Gazipur	Purple black
30.	SM-185	Advanced Line of Netherland seed comp.	Purple
31.	SM-181	Advanced Line of Netherland seed comp.	Purple black
32.	SM-183	Advanced Line of Netherland seed comp.	Purple
33.	SM-186	Advanced Line of Netherland seed comp.	Purple black
34.	BARI begun-6	Pabna	Green
35.	SM-77(round)	Gene Bank, BARI	Uniform

3.5 Genotypes

A total thirty five genotypes of brinjal (Table 1) representing sample of different districts of the country were collected from Olericulture division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI) Joydebpur, Gazipur.

3.6 Design and layout of the experiment

The experiment was laid out Randomized Complete Block Design (RCBD) with two replications. Each replication contains 35 genotypes having 75cm×60cm spacing. Each plot was 7.5m length and 0.80m breadth. Block to block distance was 0.75m. The genotypes were randomly distributed to unit plot within each block.

3.7 Raising of seedlings

Seeds of selected genotypes were sown in the well prepared seedbed on 16th September 2010. All care and precaution were taken to raise healthy seedlings. When seedlings become 45 days old those were transplanted in the main field.

3.8 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth. Weeds and other stables were removed carefully from the experimental plot and plots were prepared as per layout.

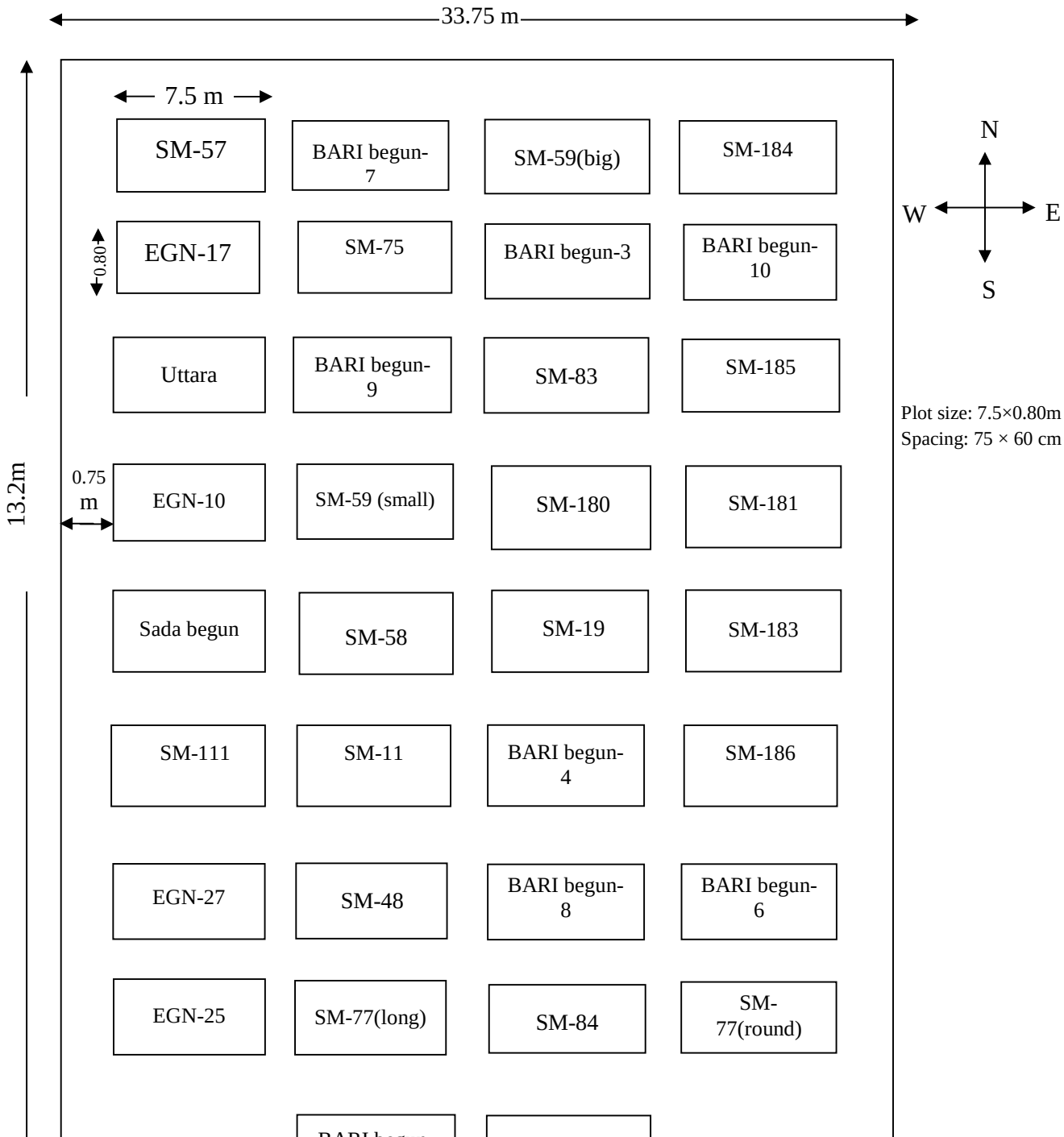
3.9 Manure and fertilizers application

Total cowdung and TSP and MOP were applied in the field during final land preparation. Urea and MOP were applied at two equal installments as top dressing. The first top dressing was done 21

days after transplanting and the 2nd at the flowering. Doses of manure and fertilizers used in the study are shown in table 2.

Table 2. **Doses of manure and fertilizers used in the study**

SL No.	Fertilizer/Manure	Dose
1.	Cowdung	1.5 ton/ha
2.	Urea	375 kg/ha
3.	TSP	150 kg/ha
4.	MOP	250 kg/ha
5.	Gypsum	70 kg/ha
6.	Zinc Oxide	6 kg/ha



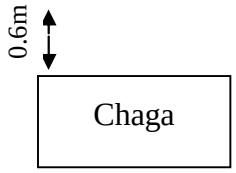


Fig 1. Layout of the experimental field

3.10 Transplanting of seedlings

Forty five days old seedlings were transplanted in well-prepared experimental plot on 31st October 2010.

3.11 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.

3.11.1 Gap filling

Gap filling was done twice. The first gap filling was done on 7th November 2010 just after 7 days of first transplanting and the 2nd one done on 11th November 2010, which was 11 days of first transplanting.

3.11.2 Weeding

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

3.11.3 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.

3.12 Pesticide application

At the seedling stage of brinjal plant, ant attacked tender leaves for this Sevin was sprayed in the field. In mature stage brinjal shoot and fruit borer caused severe damage to the fruit. For a protection from brinjal shoot and fruit borer, Diazinon 50EC @ 2ml/l was applied at 7 days interval along with Ripcord 10EC, Cymbosh 10EC.

3.13 Data Recording

Observations were recorded from five randomly selected plants from each unit plot of each replication for the following physio-morphological parameters as per IBPGR (1990).

3.13.1. Plant characters

- **Plant height (cm):** Measured from the soil surface to the tip of the tallest branch at first harvest and last harvest.
- **Number of branches per plant:** All the primary branches were counted at final harvesting period in each of five selected plants and their average value was taken number of branches per plant.

3.13.2. Leaf & flower characters

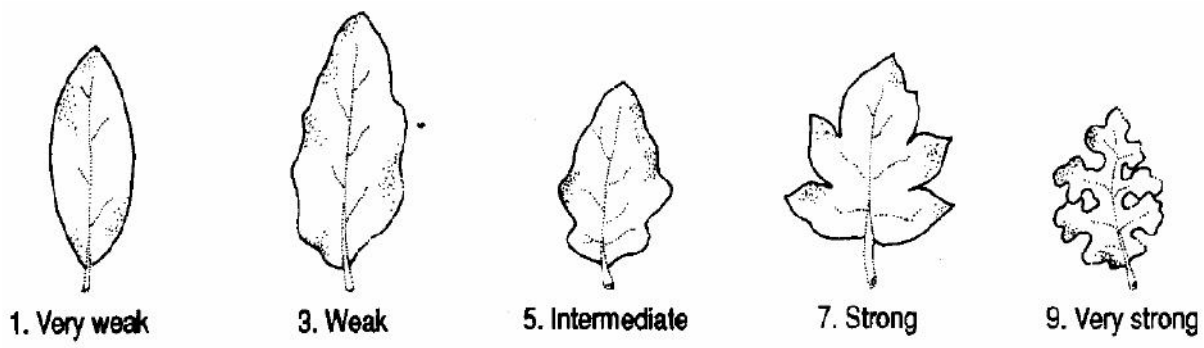
- **Leaf blade length (cm):** Measured from base to the tip of leaf at mature stage and average of randomly selected five leaves of different plants was taken as leaf blade length.

3	Short	~10cm
5	Intermediate	~20cm
7	Long	~30cm

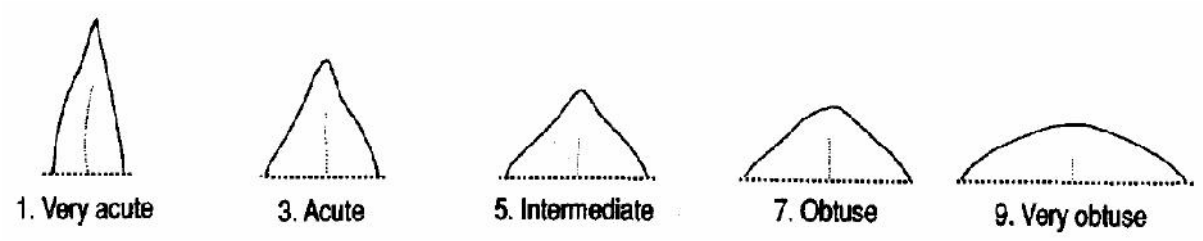
- **Leaf blade width (cm):** Width at the broader portion of the leaf blade was measured and average of five randomly selected leaves was taken as leaf blade width.

3	Naorrow	~5cm
5	Intermediate	~10cm
7	Wide	~15cm

- **Leaf blade lobing:** By visual observation as per the figure below



- **Leaf blade tip angle:** By visual observation as per the figure below



- **Leaf blade color:** Comparing with color chart

1	Light green
2	Green
3	Dark green
4	Greenish violet
5	Violet

- **Petiole length (cm):** Measured by meter scale from junction of the stem to the base of leaf.

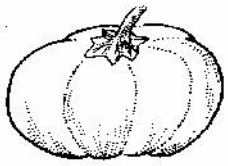
0	None	
1	Very short	<5 cm
3	Short	~10cm
5	Intermediate	~30 cm
7	Long	~50 cm
9	Very long	<100 cm

- **Corolla color:** Comparing with color chart

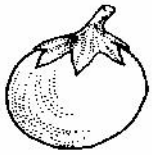
1	Greenish
3	White
5	Pale violet
7	Light violet
9	Bluish violet

3.13.3 Inflorescence and fruit characters

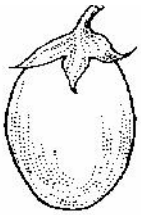
- **Fruit length (cm):** Fruit length was measured with a Vernier caliper from neek of the fruit to the bottom of the same from five representative fruits and their average was taken as length of the fruit
- **Fruit breadth (cm):** Fruit breadth was measured through the equatorial part of same five representative fruits by vernier caliper and their average was taken as fruit breadth.



1. Broader than long



3. As long as broad



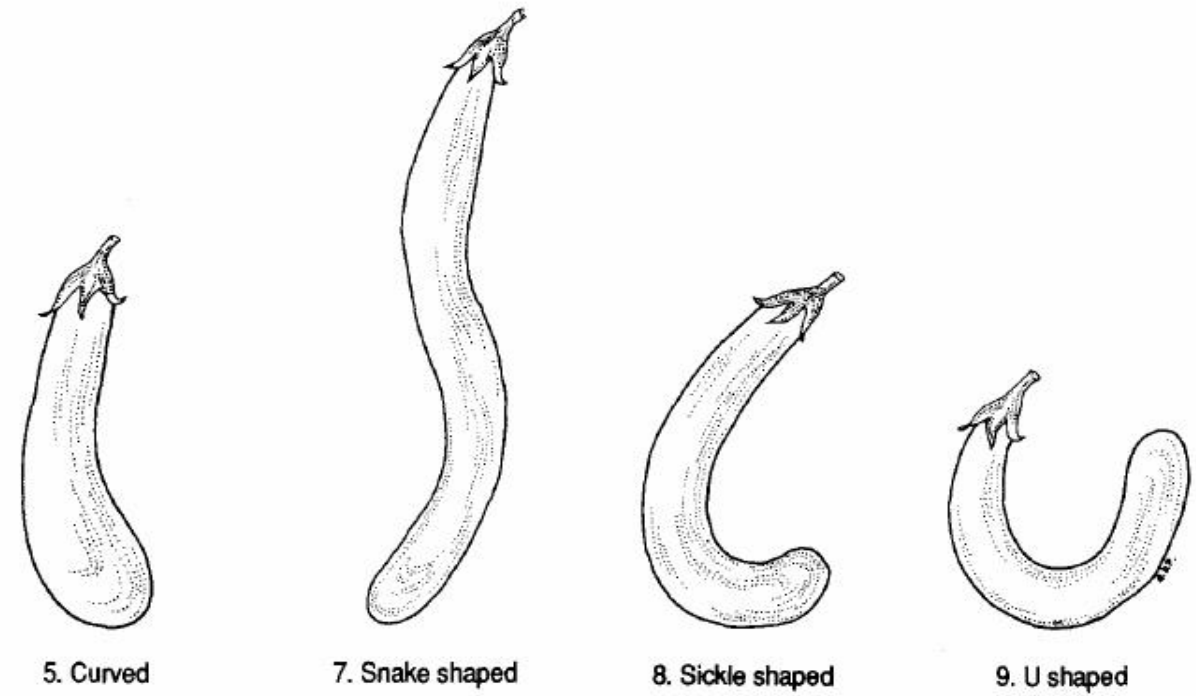
5. Slightly longer than broad

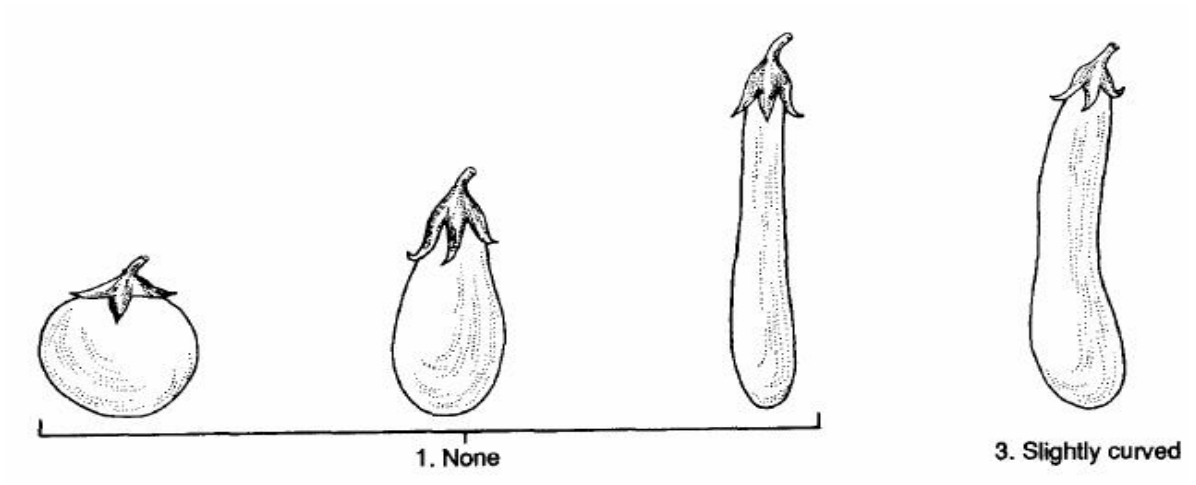
- **Fruit pedicel length (cm):** Measured by meter scale from junction of the stem to the base of fruit.
- **Fruit length/breadth ratio:** Dividing fruit length by fruit breadth.
- **Fruit flesh density :** By visual observation**.**

1	Very loose (sonngy)
3	Loose (crumbly)
5	Average density
7	Dense
9	Very dense

- **100 seed weight (g):** Measured by electric balance.
- **Number of fruits per plant:** Total number of fruits harvested at different dates from the five selected plants was counted.
- **Fruit weight (g):** Average fruit weight in gram was calculated from the five representative fruits.

- **Yield per hectare:** Yield per hectare was calculated from the yield obtained in each of the experimental unit and was expressed in metric tones.
- **Fruit curvature:** By visual observation as per the figure below.





- **Fruit shape:** By visual observation as per as the following shapes :
  - Round
  - Ovate
  - Long
  - Oblong
- **Fruit apex shape:** By visual observation

3	Rounded
5	Protruded
7	Depressed

- **Relative fruit calyx length:** Measured as percentage of total fruit length.

1	Very short	<10%
3	Short	~20%
5	Intermediate	~50%
7	Long	~70%
9	Very long	>75%

- **Fruit color at commercial ripeness:** By visual observation

1	Green
2	Milk white
3	Deep yellow
4	Fire red
5	Scarlet red
6	Lilac grey
7	Purple
8	Purple black
9	Black

- **Fruit color distribution at commercial ripeness:** By visual observation

1	Uniform
3	Mottled
5	Netted
7	Stripped

- **Fruit flesh density:** Observed fruit by punching with hand

1	Very loose (spongy)
3	Loose (crumbly)
5	Average density
7	Dense
9	Very dense

- **Number of seeds per fruit:** Five fully ripened fruit were dried then seeds were separated from the pulp of fruits and the total seeds were counted and average value was considered as number of seeds per fruit.

0	None	
1	Very few	<10
3	Few	~50
5	Intermediate	~100
7	Many	~300
9	Very many	>500

3.14. Statistical analysis

Mean data of the characters were subjected to both univariate and multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.14.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{GMS - EMS}{r}$$

Where,
GMS = Genotypic mean sum of squares
EMS = Error mean sum of square
r = number of replications

$$\text{Phenotypic variance } (\sigma^2 ph) = \sigma^2_g + EMS$$

Where,
σ^2_g = Genotypic variance
EMS = Error mean sum of square

3.14.2 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic covariance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

Genotypic Correlation (*rg*) = $GCOV_{xy} / \sqrt{GV_x . GV_y}$

Where,

$GCOV_{xy}$ = Genotypic co-variance between the traits x and y

GV_x =Genotypic variance of the trait x

GV_y =Genotypic variance of the trait y

Phenotypic Correlation (*rp*) = $PCOV_{xy} / \sqrt{PV_x . PV_y}$

Where,

$PCOV_{xy}$ =Phenotypic covariance between the traits x and y

PV_x =Phenotypic variance of the trait x

PV_y =Phenotypic variance of the trait y

3.14.3 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952).

Genotypic co-efficient of variation (GCV %) = $\sqrt{\frac{\sigma^2_g}{\bar{x}}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) = $\sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$

Where,

σ^2_{ph} = Phenotypic variance

$\bar{x}$ = Population mean

3.14.4 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

$$h^2_b\% = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

Where,

h^2 b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} =Phenotypic variance

3.14.5 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance (GA) = K. h^2 b. σ_{ph}

$$GA = K.\frac{\sigma^2_g}{\sigma^2_{ph}}.\sigma_{ph}$$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

h^2 b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.14.6 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952).

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean } (\bar{x})} \text{ X } 100$$

3.15 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) distance (D^2) general statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing**.** Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.15.1 Principal Component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.15.2 Principal Coordinate analysis (PCO)

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

3.15.3 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In GENSTST, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, 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 can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.15.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.15.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k)^2 \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1to x

x = Number of characters.

3.15.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

Average intra-cluster distance = $\frac{\sum D_i^2}{n}$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster.

n = Number of all possible combinations between the populations in cluster.

3.15.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

Average inter-cluster distance = $\frac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in cluster i and j.

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.15.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.15.9 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

i. Choice of cluster from which genotypes are selected for use as parent(s),
ii. Selection of particular genotype(s) from the selected cluster(s),
iii. Relative contribution of the characters to the total divergence and
iv. Other important characters of the genotypes performance.

CHAPTER IV
RESULTS AND DISCUSSION

Performance of 35 genotypes of brinjal 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 Brinjal genotypes as well as yield and its contributing characters were computed and statistically analyzed and the results thus obtained are discussed below under the following heads:

1. Physio-morphological Characterization Based on Grading
2 Genetic parameters
3. Correlation co-efficient
4. Multivariate analysis

4.1 PHYSIO-MORPHOLOGICAL CHARACTERIZATION

As per the descriptor for Egg plant, IBPGR (1990) the characterization of brinjal genotypes were made.

4.1.1 Leaf blade length

Leaf blade length of different genotypes exhibited moderate variation. Results indicated that leaf blade of the genotypes Sada begun, SM-59(small), BARI begun-5 and SM-59(big) were long (~30cm) while leaf blade of the genotypes SM-84 and SM-181 were short (~10cm). Intermediate (~20cm) leaf blades were produced by rest of the genotypes (Table 3a).

Table 3a. Characterization of 35 brinjal genotypes as per leaf characters

Genotypes	Leaf blade length	Leaf blade width	Leaf blade lobing	Leaf blade tip angle	Leaf blade color
SM-57	Intermediate	Intermediate	Intermediate	Intermediate	Purplish green
EGN-17	Intermediate	Intermediate	Strong	Acute	Purplish green
UTTARA	Intermediate	Wide	Intermediate	Intermediate	Purplish green
EGN-10	Intermediate	Wide	Strong	Acute	Purplish green
Sada begun	Long	Wide	Intermediate	Intermediate	Green
SM-111	Intermediate	Wide	Intermediate	Intermediate	Purplish green
EGN-27	Intermediate	Wide	Intermediate	Intermediate	Purplish green
EGN-25	Intermediate	Wide	Intermediate	Intermediate	Green
Chaga	Intermediate	Wide	Intermediate	Intermediate	Green
BARI begun-7	Intermediate	Wide	Intermediate	Intermediate	Purplish green
SM-75	Intermediate	Wide	Strong	Intermediate	Green
BARI begun-9	Intermediate	Intermediate	Intermediate	Intermediate	Purplish green
SM-59(small)	Long	Wide	Intermediate	Intermediate	Purplish green
SM-58	Intermediate	Wide	Intermediate	Intermediate	Purplish green
SM-11	Intermediate	Wide	Intermediate	Intermediate	Green
SM-48	Intermediate	Wide	Intermediate	Intermediate	Green
SM-77(long)	Intermediate	Wide	Intermediate	Intermediate	Green
BARI begun-5	Long	Wide	Intermediate	Obtuse	Purplish green
SM-59(big)	Long	Wide	Intermediate	Intermediate	Purplish green
BARI begun-3	Intermediate	Wide	Weak	Acute	Purplish green
SM-83	Intermediate	Wide	Intermediate	Acute	Green
SM-180	Intermediate	Intermediate	Intermediate	Acute	Green
SM-19	Intermediate	Intermediate	Intermediate	Intermediate	Purplish green
BARI begun-4	Intermediate	Intermediate	Intermediate	Acute	Purplish green
BARI begun-8	Intermediate	Wide	Intermediate	Acute	Purplish green
SM-84	Short	Narrow	Weak	Intermediate	Green
SM-63	Intermediate	Wide	Intermediate	Acute	Purplish green
SM-184	Intermediate	Intermediate	Intermediate	Intermediate	Green
BARI begun-10	Intermediate	Wide	Strong	Acute	Purplish green
SM-185	Intermediate	Wide	Strong	Acute	Green
SM-181	Short	Intermediate	Intermediate	Intermediate	Purplish green
SM-183	Intermediate	Intermediate	Intermediate	Acute	Purplish green
SM-186	Intermediate	Intermediate	Intermediate	Intermediate	Purplish green
BARI begun-6	Intermediate	Wide	Intermediate	Intermediate	Green
SM-77(round)	Intermediate	Wide	Intermediate	Obtuse	Green

4.1.2 Leaf blade width

The genotypes exhibited moderate variation in leaf blade width (Table 3a). Among the genotypes studied genotypes SM-57, EGN-17, BARI begun-9, SM-11, SM-180, SM-19, BARI begun-4, SM-184, SM-181, SM-183 and SM-186 had intermediate leaf blade (~10cm) while rest of the genotypes produced wide leaf blade (~15cm) but only SM-84 showed narrow leaf blade (~5cm) (Table 3a).

4.1.3 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 greater 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 BARI begun-3 and SM-84 were seen weaker leaf blade; EGN-17, EGN-10, SM-75, BARI begun-10 and SM-185 were strong leaf blade and rest of the genotypes were intermediate habit in their leaf blade lobbing (Table 3a).

4.1.4 Leaf blade tip angle

Among the 35 genotypes EGN-17, EGN-10, BARI begun-3, SM-83, SM-180, BARI begun-4, BARI begun-8, SM-63, BARI begun-10, SM-185 and SM-183 showed acute leaf blade tip angle while the genotypes BARI begun-5 and SM-77 (round) showed obtuse tip angle and rest of the genotypes were intermediate habit in their leaf blade lobbing (Table 3a).

4.1.5 Leaf blade color

Among the genotypes Sada begun, EGN-25, Chaga, SM-75, SM-11, SM-48, SM-77(long), SM-83, SM-180, SM-84, SM-184, SM-185, BARI begun-6 and SM 77(round) produced green leaf and the rest of the genotypes produced purplish green colored leaf (Table 3a).

4.1.6 Petiole length

Petiole length of different genotypes exhibited wide variation. Results indicated that majority of the genotypes,EGN-10, SM-111, EGN-17, BARI begun-7, SM-75, SM-58, SM-11, BARI begun-3, SM-83, BARI begun-8, SM-180, SM-84, SM-63, SM-184, BARI begun-10, SM-185, SM-183 and SM-77(round) produced intermediate petiole length followed by the genotypes SM-57, EGN-17, Sada begun, EGN-25, Chaga, SM-59(small), SM-48, SM-77(long), BARI begun-5, SM-59(big), SM-19, BARI begun-4, SM-181 and BARI begun-6 with long and the genotypes Uttara and SM-186 with short petiole (Table 3b).

4.1.7 Corolla color

Wide variations were observed in corolla color. Of 35 genotypes the genotypes SM-57, EGN-10, Sada begun, SM-111, EGN-27, EGN-25, Chaga, BARI begun-7, SM-75, BARI begun-9, SM-59(small), SM-58, SM-11, SM-48, SM-77(long), BARI begun-5, SM-59(big), BARI begun-3, SM-83, SM-180, SM-19, BARI begun-4, BARI begun-8, SM-84, SM-63, SM-184, BARI begun-10, SM-185, SM-186 and SM-77(round) showed light violet corolla followed by EGN-17, Uttara, SM-181, SM-183 and BARI begun-6 of bluish violet (Table 3b).

Table 3b. Characterization of 35 brinjal genotypes as per flower and fruit characters

Genotype	Petiole length	Corolla color	Fruit calyx color	Fruit calyx prickles	Fruit bearing	Fruit length/breadth ration
SM-57	Long	Light violet	Straw	Few	Solitary	Slightly longer than broad
EGN-17	Long	Bluish violet	Purple	Very few	Cluster	Three times as long as broad
UTTARA	Short	Bluish violet	Green	Few	Cluster	Twice as long as broad
EGN-10	Intermediate	Light violet	Green	Few	Solitary	Twice as long as broad
Sada begun	Long	Light violet	Green	Few	Cluster	Several times as long as broad
SM-111	Intermediate	Light violet	Green	Few	Solitary	Twice as long as broad
EGN-27	Intermediate	Light violet	Green	Few	Solitary	As long as broad
EGN-25	Long	Light violet	Green	Few	Solitary	Three times as long as broad
Chaga	Long	Light violet	Straw	Few	Solitary	Slightly longer than broad
BARI begun-7	Intermediate	Light violet	Straw	Few	Solitary	Several times as long as broad
SM-75	Intermediate	Light violet	Straw	Few	Solitary	Broader than long
BARI begun-9	Intermediate	Light violet	Purple	Very few	Solitary	As long as broad
SM-59(small)	Long	Light violet	Green	Few	Cluster	Twice as long as broad
SM-58	Intermediate	Light violet	Straw	Few	Solitary	Three times as long as broad
SM-11	Intermediate	Light violet	Green	Few	Solitary	Twice as long as broad
SM-48	Long	Light violet	Straw	Very few	Solitary	Twice as long as broad
SM-77(long)	Long	Light violet	Green	Few	Solitary	Three times as long as broad
BARI begun-5	Long	Light violet	Purple	Very few	Solitary	Broader than long
SM-59(big)	Long	Light violet	Green	Few	Solitary	Slightly longer than broad
BARI begun-3	Intermediate	Light violet	Green	Very few	Solitary	Twice as long as broad
SM-83	Intermediate	Light violet	Purple	Very few	Solitary	Several times as long as broad
SM-180	Intermediate	Light violet	Purple	Few	Solitary	Three times as long as broad
SM-19	Long	Light violet	Purple	Very few	Solitary	Several times as long as broad
BARI begun-4	Long	Light violet	Purple	Very few	Solitary	Three times as long as broad
BARI begun-8	Short	Light violet	Straw	Few	Solitary	Several times as long as broad

Genotype	Petiole length	Corolla color	Fruit calyx color	Fruit calyx prickles	Fruit bearing	Fruit length/breadth ration
SM-84	Intermediate	Light violet	Green	Few	Cluster	As long as broad
SM-63	Intermediate	Light violet	Green	Very few	Solitary	Three times as long as broad
SM-184	Intermediate	Light violet	Purple green	Very few	Cluster	Three times as long as broad
BARI begun-10	Intermediate	Light violet	Whitish green	Few	Solitary	Several times as long as broad
SM-185	Intermediate	Light violet	Green	Few	Solitary	Three times as long as broad
SM-181	Long	Bluish violet	Green	Very few	Solitary	Three times as long as broad
SM-183	Intermediate	Bluish violet	Green	Few	Solitary	Several times as long as broad
SM-186	Short	Light violet	Green	Very few	Cluster	Three times as long as broad
BARI begun-6	Long	Bluish violet	Green	Few	Solitary	Broader than long
SM-77(round)	Intermediate	Light violet	Green	Few	Solitary	Twice as long as broad

4.1.8 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, U shape, snake shape and sickle shape. Among 35 genotypes BARI begun-8 and BARI begun-10 were produced sickle shaped; EGN-10, SM-185 and SM-181were produced slightly curved; Sada begun, SM-58, BARI begun-3, SM-180, BARI begun-4, SM-184 were produced curved; SM-19 was produced U shaped; BARI begun-7 and SM-183 were produced snake shaped brinjal and rest of the genotypes had no curvature of their fruits (Table 3c).

4.1.9 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 five genotypes long, oblong and round shaped brinjal were observed. The genotypes EGN-10, Sada begun, SM-111, Chaga, BARIbegun-7, SM-58, SM-48, SM-77(long), BARI begun-3, SM-180, SM-19, BARI begun-4, BARI begun-8, SM-63, SM-184, BARI begun-10, SM185, SM-181, SM-183 and SM-186 produced long fruits, genotypes SM-57, EGN-17, Uttara, EGN-25, BARI begun-9, SM-59(small), SM-11, SM-59(big) and SM-84 produced oblong fruits and genotypes SM-75, BARI begun-5, SM-83, BARI begun-6 and SM-77 (round) produced round fruits (Table 3c).

4.1.10 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. Genotypes SM-184,SM-186 and sm-77(round) produced protruded fruit apex shape, genotypes Sada begun,Chaga,SM-58,SM-63 produced depressed apex shaped fruits while the rest of the genotypes produced round apex shape fruits (Table 3c).

Table 3c. Characterization of 35 brinjal genotypes as per fruit characters

Genotypes	Fruit curvature	Fruit shape	Fruit apex shape	Fruit calyx length
SM-57	None	Oblong	Rounded	Short
EGN-17	None	Oblong	Rounded	Short
UTTARA	None	Oblong	Rounded	Very short
EGN-10	Slightly curved	Long	Rounded	Short
Sada begun	Curved	Long	Depressed	Intermediate
SM-111	None	Long	Rounded	Short
EGN-27	None	Round	Rounded	Short
EGN-25	None	Oblong	Rounded	Short
Chaga	None	Long	Depressed	Short
BARI begun-7	Snake shaped	Long	Rounded	Intermediate
SM-75	None	Round	Rounded	Short
BARI begun-9	None	Oblong	Rounded	Short
SM-59(small)	None	Oblong	Rounded	Short
SM-58	Curved	Long	Depressed	Short
SM-11	None	Oblong	Rounded	Very short
SM-48	None	Long	Rounded	Very short
SM-77(long)	None	Long	Rounded	Short
BARI begun-5	None	Round	Rounded	Short
SM-59(big)	None	Oblong	Rounded	Short
BARI begun-3	Curved	Long	Rounded	Short
SM-83	None	Round	Rounded	Short
SM-180	Curved	Long	Rounded	Short
SM-19	U shaped and curved	Long	Rounded	Short
BARI begun-4	Curved	Long	protruded	Short
BARI begun-8	Sickle shaped	Long	Rounded	Short
SM-84	None	Oblong	Rounded	Very short
SM-63	None	Long	Depressed	Short
SM-184	Curved	Long	protruded	Short
BARI begun-10	Sickle shaped	Long	Rounded	Short
SM-185	Slightly curved	Long	Rounded	Short
SM-181	Slightly curved	Long	Rounded	Short
SM-183	Snake shaped	Long	Rounded	Short
SM-186	Curved	Long	protruded	Short
BARI begun-6	None	Round	Rounded	Short
SM-77(round)	None	Round	protruded	Intermediate

4.1.11 Fruit calyx length

Fruit calyx length of SM-57, EGN-17, EGN-10,SM-111,EGN-27,EGN-25, Chaga, SM-75, BARI begun-9, SM-59(small), SM-58, SM-77(long), BARI begun-5, SM-59(big), BARI Begun-3, SM-83, SM-180, SM-19, BARI begun-4, BARI begun-8, SM-63, SM-184, BARI begun-10, SM-185, SM-181, SM-183, SM-186 and BARI begun-6 were short that of Uttara, SM-11, SM-48, SM-84 were very short and the fruit calyx of Sada begun, BARI begun-7 and SM- 77(round) were intermediate (Table 3c).

4.1.12 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, purple, white, light violet, milky white and blackish purple. The genotype Uttara, SM-75, SM-19, SM-184 and SM-185 produced purple fruit; Milky white fruit was produced in Sada begun; Blackish purple were observed in SM-57, EGN-17, EGN-10, SM-111, EGN-27, BARI begun-7, BARI begun-9,SM-59(small), SM-58, BARIbegun-5, SM-59(big), BARI begun-4, SM-63, SM181, BARI begun-10 and SM-186; Green fruits were observed in EGN-25, Chaga,SM-48, SM-77(long), SM-83, BARI begun-6 and SM-77(round); Light purple fruits were observed in SM-180, BARI begun-8 and SM-84 and light green was observed in SM-11 (Table 3d). This variation offered a good scope for breeding consumer preference attributes.

4.1.13 Fruit distribution at commercial ripeness

In EGN-10, EGN-25, Chaga, SM-11, SM-48, SM-83, SM-84, SM-184, SM-185 and SM-77(round) stripped color distribution was observed at commercial ripeness while rest of all genotypes showed uniform color distribution at commercial ripeness (Table 3d).

Table 3d. Characterization of 35 Brinjal genotypes as per fruit characters

Genotypes	Fruit color	Color distribution at commercial ripeness	Flesh density	No. of seed per fruit
SM-57	Purple black	Uniform	Dense	Very many
EGN-17	Purple black	Uniform	Dense	Very many
UTTARA	Purple	Uniform	Crumbly	Very many
EGN-10	Purple black	Stripped	Dense	Very many
Sada begun	Milky white	Uniform	Dense	Very many
SM-111	Purple black	Uniform	Dense	Many
EGN-27	Purple black	Uniform	Dense	Very many
EGN-25	Green	Stripped	Dense	Very many
Chaga	Green	Stripped	Dense	Very many
BARI begun-7	Black	Uniform	Average density	Very many
SM-75	Purple	Uniform	Dense	Very many
BARI begun-9	Purple black	Uniform	Dense	Very many
SM-59(small)	Purple black	Uniform	Dense	Very many
SM-58	Purple black	Uniform	Dense	Very many
SM-11	Light green	Stripped	Dense	Very many
SM-48	Green	Stripped	Dense	Very many
SM-77(long)	Green	Uniform	Dense	Very many
BARI begun-5	Purple black	Uniform	Dense	Very many
SM-59(big)	Purple black	Uniform	Dense	Very many
BARI begun-3`	Purple black	Uniform	Dense	Very many
SM-83	Green	Stripped	Dense	Very many
SM-180	Light purple	Uniform	Dense	Very many
SM-19	Purple	Uniform	Average density	Very many
BARI begun-4	Purple black	Uniform	Average density	Very many
BARI begun-8	Light purple	Uniform	Average density	Very many
SM-84	Light purple	Stripped	Dense	Many
SM-63	Purple black	Uniform	Dense	Very many
SM-184	Purple	Stripped	Average density	Very many
BARI begun-10	Purple black	Uniform	Dense	Very many
SM-185	Purple	Stripped	Dense	Very many
SM-181	Purple black	Uniform	Dense	Very many

Genotypes	Fruit color	Color distribution at commercial ripeness	Flesh density	No. of seed per fruit
SM-183	Purple	Uniform	Average density	Very many
SM-186	Purple black	Uniform	Average density	Very many
BARI begun-6	Green	Uniform	Average density	Very many
SM-77(round)	Green	Stripped	Average density	Very many

4.1.14 Flesh density

Fruit density of BARI begun-7, SM-19, BARI begun-4, BARI begun-8, SM-84, SM-183, SM-186, BARI begun-6 and SM-77(round) had average dense fruit flesh. Fruit density of Uttara was crumbly and rest of the genotypes was produced dense flesh (Table 3d).

4.1.1.15 No. of seed per fruit

The high amount of seeds present in the fruit had a negative impact on consumer test and preferences for particular lines/varieties. Only genotype SM-111 and SM-84 produced many seeds and rest of the genotypes produced very many seeds (Table 3d).

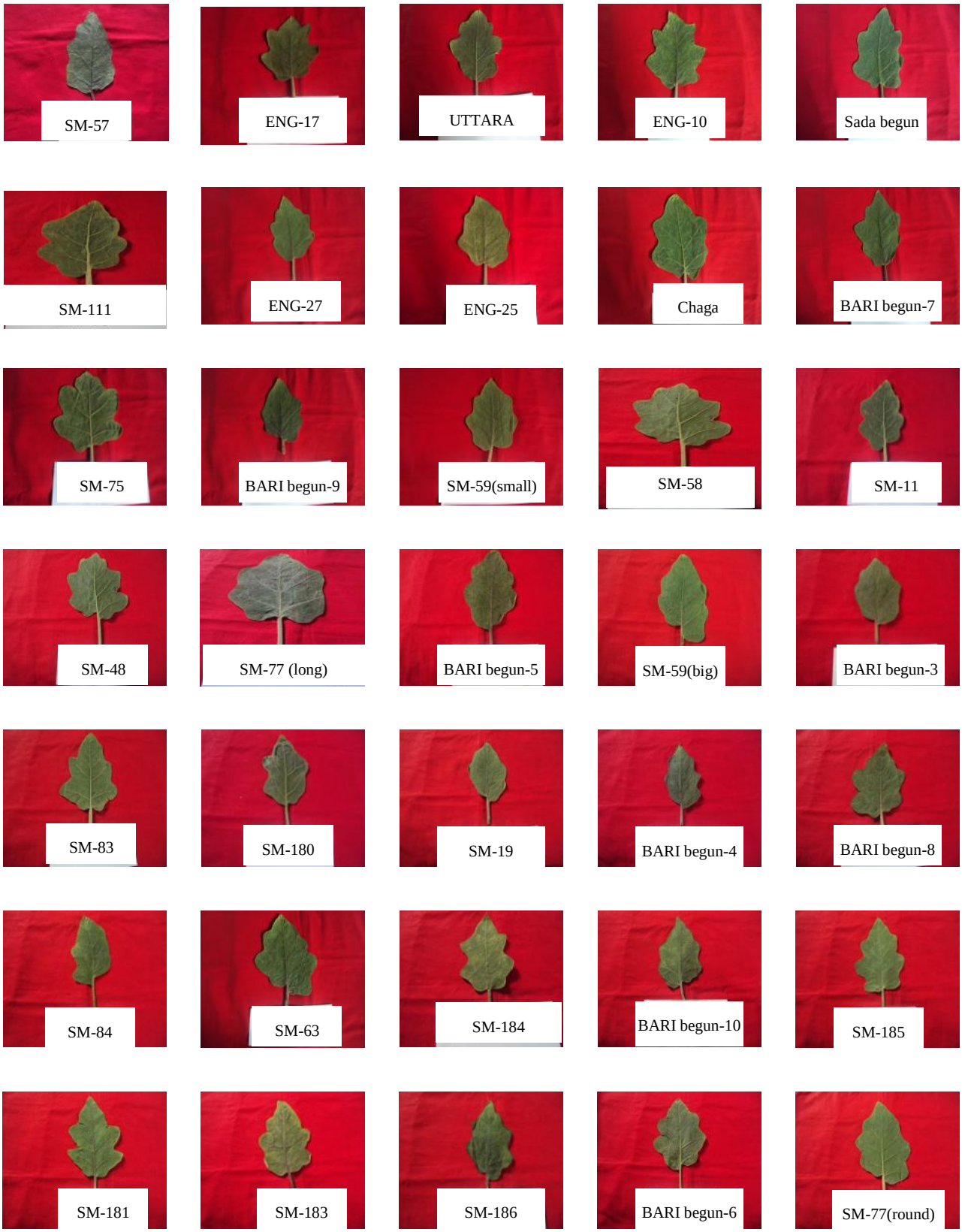


Plate 1. Showing variation in leaf among different brinjal genotypes (Sl. 1-35).

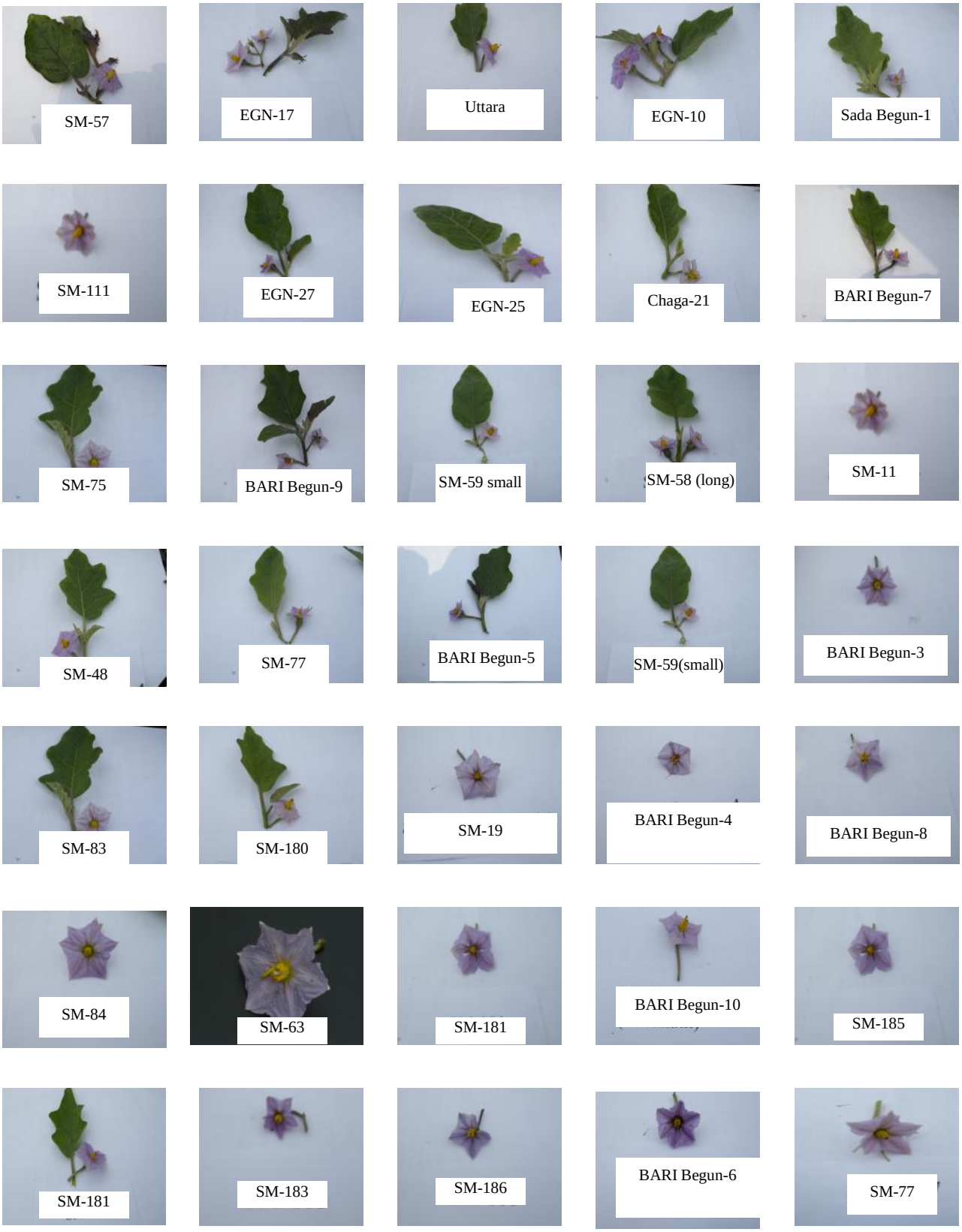


Plate 2. Showing variation in flower among different brinjal genotypes (Sl. 1-35).

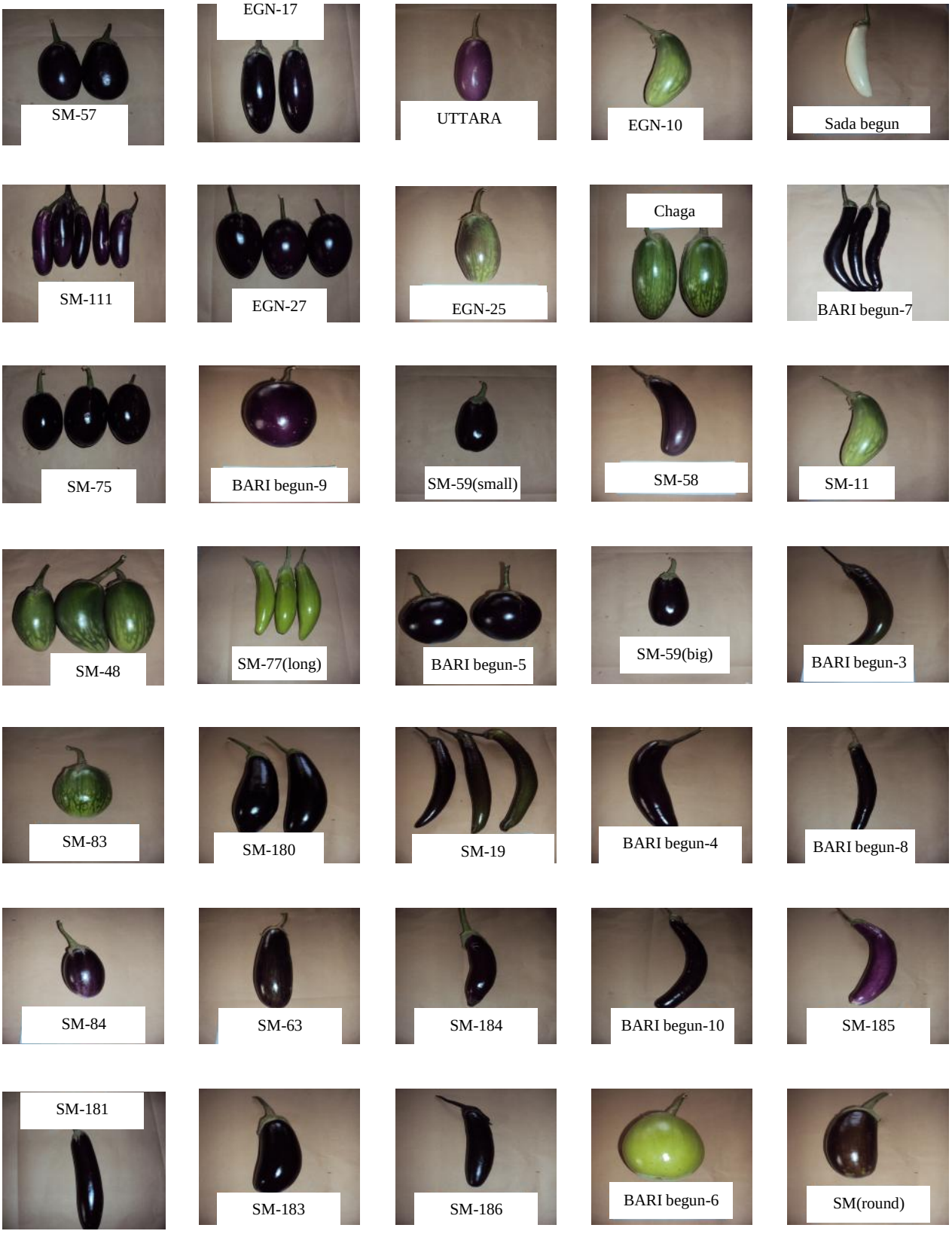


Plate 3. Showing phenotypic variation in fruits among different genotypes of brinjal.

4.2 GENETIC PARAMETERS

The analysis of variances indicated the existence of highly significant variation among the genotypes studied. The mean sum of square, mean, range, variance components, genotypic and phenotypic coefficients of variations, heritability; genetic advance and genetic advance in percent of mean (GAPM) are presented in (Table 4).

The results are discussed character wise as follows:

4.2.1 Days to 50% flowering

Analysis of variance for days to 50% flowering showed highly significant mean sum of square due to genotypic differences (Table 4). The mean value with respect to this trait ranged from 45.00 (SM-84) to 82.00 (BARI Begun-7). The phenotypic variance (108.37) was slightly higher than the genotypic variance (108.17). The difference present among the genotypic and phenotypic variances is indicating that the effect of environment for the expression of the trait is low (Table 4). 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. This estimated heritability was also high (99.82%) with moderate genetic advance in percent of mean (Table 4).

4.2.2 Days to 1st harvest

Highly significant variations were observed for days to first harvesting (Table 4). The early genotype in terms of fruit harvesting was BARI Begun-5(52.50 days) and the late genotype was SM-183,184, 185(127.50 days). The genotypic variance (265.22) was lower than the phenotypic variance (273.87). The considerable differences between phenotypic and genotypic variances indicating the effect of the environment for the expression of the trait (Table 4). The genetic advance was moderate 33.01 and genetic advance in percentage of mean was low (33.05).

Ushakumiry *et al.* (1991) evaluated of fifty four diverse genotypes of Brinjal for 10 yield components and found 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.

4.2.3 Plant height at 1st harvest

Significant mean sum of square for plant height at 1st harvest indicated considerable differences among the genotypes studied (Table 4). The highest and lowest plant heights among the genotypes were 87.35 cm (BARI Begun-7) and 45.60 cm (EGN-17) respectively with the mean value of 63.63cm (Appendix-III).

The phenotypic and genotypic variances for this trait were comparatively high (96.53 and 93.06). The phenotypic variance appeared to be higher than the genotypic variance, suggesting considerable influence of environment on expression of the genes controlling this trait. The phenotypic coefficient of variation (15.44) was higher than the genotypic coefficient of variation (15.16) (Table 4), which suggested that environment, has a little role on the expression of this trait. Heritability estimate was high (96.41) with moderate genetic advance (19.51%) and genetic advance in percent of mean (30.66) was considerable for this trait indicating apparent variation was due to genotypes.

4.2.4 Plant height at last harvest

Highly significant variations were observed for plant height at last harvest (Table 4). The highest and lowest plant heights among the genotypes were 110.43 cm (BARI Begun-7) and 72.33 cm (SM-84) respectively with the mean value of 92.84cm (Appendix-III).

The phenotypic variance (83.29) appeared to be higher than the genotypic variance (81.94), suggesting considerable influence of environment on expression of the genes controlling this trait. The phenotypic coefficient of variation (9.83) was higher than the genotypic coefficient of variation (9.75) (Table 4), which suggested that environment, has a little role on the expression of this trait. Estimated heritability was high (98.38) with moderate genetic advance (18.50%) and genetic advance in percent of mean (19.92) 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).

4.2.5 Number of branches

No. of branches per plant was significant indicating considerable differences among the genotypes studied (Table 4). The maximum and minimum no. of branches per plant among the genotypes were 7.00 (SM-57, SM-181) and 4.00 (SM-84, Uttara and SM-111) respectively with the mean value of 5.27 (Table 5 and Appendix III). The phenotypic and genotypic variances for this trait were comparatively low (0.75 and 0.50). 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 (16.38) was higher than the genotypic coefficient of variation (13.42) (Table 4), which suggested that environment, had a significant role on the expression of this trait. Estimated heritability was high (67.11%) with low genetic advance (1.19%) and genetic advance in percent of mean (22.64) was considerable for this trait indicating apparent variation was due to genotypes (Table 4). Thus, selection based on this trait would be effective.

4.2.6 Leaf blade length (cm)

Mean sum of square for leaf blade length was 16.34 which was highly significant due to genotypes of brinjal (Table 4) indicating existence of considerable difference for this trait. The maximum leaf blade length was found 22.06 in sada begun and the minimum was recorded 7.05 in SM-84 with mean value 16.34 (Appendix III). The phenotypic variance (7.94) appeared to be higher than the genotypic variance (7.28) suggested considerable influence of environment on the expression of the genes controlling this trait. The genotypic co-efficient of variation (16.51) and phenotypic co-efficient of variation (17.24) were close to each other. Heritability (91.75) estimates for this trait was very high, genotypic advance (5.32) and genotypic advance in percent of mean (32.58) were found low. Indicating this trait was governed by the additive gene.

4.2.7 Fruit length (cm)

Different types of genotypes showed wide differences in terms of fruit length. The range of length was from the highest 31.56cm in BARI begun-7 to lowest 7.15 cm. in SM-84 (Table 4). The phenotypic variance (34.09) was little higher than the genotypic variance (33.48). The phenotypic coefficient of variation and the genotypic coefficient of variation were of similar types. The estimated heritability was found very high (98.22%). The genetic advance was low (11.81) with the high genetic advance in percent of mean (74.82).

4.2.8 Fruit width (cm)

Mean sum of square fruit breadth was significant (6.29) due to genotypes in brinjal (Table 4) indicating existence of considerable variation for this trait. The maximum fruit breadth was found 9.01cm in EGN-27 and the minimum was recorded 2.60 in BARI begun-8 with mean value 4.96 (Appendix III). The genotypic variance and phenotypic variance were 3.05 and 3.24 respectively. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 35.22 and 36.25 respectively. Heritability (94.41%) estimates for this trait was high along with low genetic advance (3.50) and genetic advance in percent of mean (70.50) indicated that this character was controlled by non-additive gene.

Table 4. Estimation of genetic parameters in thirteen characters of 35 Brinjal genotypes

Parameters	Range	Mean	MSS	$\pm^0$ p	$\pm^0$g	$\pm^0$ e
Days to 50% flowering	82.00-45	57.186	216.532**	108.37	108.17	0.20
Days to 1st harvest	127.50-45.0	99.88571	539.091	273.87	265.22	8.66
Plant height at 1st harvest	87.35-45.60	63.633	189.587**	96.53	93.06	3.46
Plant height at last harvest	110.43-72.33	92.841	165.235**	83.29	81.94	1.35
Number of branches	7-4	5.271	1.245**	0.75	0.50	0.25
Leaf blade length (cm)	22.06-7.05	16.344	15.22**	7.94	7.28	0.66
Fruit length (cm)	31.56-7.15	15.789	67.574**	34.09	33.48	0.61
Fruit width (cm)	9.01-2.60	4.962	6.29**	3.24	3.05	0.18
Single fruit weight (g)	313.34-35.55	138.907	8511.961**	4257.21	4254.75	2.46
Number of fruit/plant	52.98-7.63	20.898	215.125**	108.09	107.04	1.05
Fruit yield (t/ha)	33.15-3.74	11.714	97.047**	48.79	48.26	0.52
No. of seed/fruit	595.00-197	417.214	11653.508**	5872.08	5781.43	90.65
100 seed weight (g)	0.68-0.16	0.409	0.019**	0.01	0.01	0.00

** Significant at the 0.01 level.

MS = Mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance.

Table 4. Cont'd.

Parameters	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)	CV (%)
Days to 50% flowering	18.20	18.19	0.78	99.82	21.40	37.43	0.78
Days to 1st harvest	16.57	16.30	2.95	96.84	33.01	33.05	2.95
Plant height at 1st harvest	15.44	15.16	2.92	96.41	19.51	30.66	1.25
Plant height at last harvest	9.83	9.75	1.25	98.38	18.50	19.92	2.92
Number of branches	16.38	13.42	9.39	67.11	1.19	22.64	9.4
Leaf blade length (cm)	17.24	16.51	4.95	91.75	5.32	32.58	4.95
Fruit length (cm)	36.98	36.65	4.93	98.22	11.81	74.82	4.93
Fruit width (cm)	36.25	35.22	8.57	94.41	3.50	70.50	8.58
Single fruit weight (gm)	46.97	46.96	1.13	99.94	134.33	96.71	1.13
Number of fruit/plant	49.75	49.51	4.89	99.03	21.21	101.49	4.89
Fruit yield (t/ha)	59.63	59.31	6.17	98.93	14.23	121.51	6.18
No. of seed/fruit	18.37	18.22	2.28	98.46	155.42	37.25	2.28
100 seed weight (gm)	24.45	23.20	7.73	90.00	0.19	45.33	7.52

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation and CV% = Coefficient of variation

4.2.9 Single fruit weight (g)

Mean sum of square for single fruit weight was significant (138.907) indicating existence of considerable difference for this trait (Table 4). The maximum weight per fruit was found 313.34 gm in BARI begun-6 and the minimum was recorded 35.55gm in SM-186 with mean value 138.91 (Appendix III). The differences in magnitudes between genotypic (4254.75) and phenotypic (4257.21) variances was relatively high for this trait. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 46.96 and 46.97 respectively for single fruit weight. Heritability (99.94%) estimates for this trait was high together with considerable high genetic advance (134.33) and genetic advance in percent of mean (96.91) indicated that selection for this character would be effective.

4.2.10 Number of fruit/plant

Genotype mean sum of square for number of fruit per plant was found significant (20.898) as shown in Table 4. The maximum number of fruit per plant was found 52.98 in SM-84 and the minimum was recorded 7.63 in BARI begun-6 with mean value 20.90 (Appendix III). Phenotypic variance (108.09) for this trait was higher than the genotypic variance (107.04) and there is less influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 49.51 and 49.75 respectively which indicated presence of considerable variability among the genotypes. Heritability (99.03.%) estimates for this trait was high, genetic advance (21.21) was found moderately high and genetic advance in percent of mean (101.49) was found moderately high, indicated that the character was controlled by additive gene.

4.2.11 Fruit yield (t/ha)

Significant mean sum of square for yield (97.047) indicated considerable difference among the genotypes studied (Table 4). The maximum yield was found 33.15 t/ha in EGN-27 and the minimum was recorded 3.74 t/ha in BARI-8 with mean value 11.71 t/ha (Appendix III). The differences in magnitudes in between genotypic (48.26) and phenotypic (48.79) variances for this trait indicating environmental influence on this character. The genotypic coefficient of variation and phenotypic co-efficient of variation were 59.31 and 59.63 respectively for yield which indicating that significant variation exists among different genotypes. The heritability value (98.93%) as well as genetic advance (14.23) and genetic advance in percent of mean (121.51) were observed very high. The very high heritability with

moderate genetic advance provided opportunity for selecting high valued genotypes for breeding programme.

4.2.12 No. of seed/fruit

Significant mean sum of square for no. of seed per fruit (417.214) indicated considerable difference among the genotypes studied (Table 4). The maximum seed per fruit was found 595.00 in SM-63 and the minimum was recorded 197.50 in SM-84 with mean value 417.214(Appendix III). The differences in magnitudes in between genotypic (5781.43) and phenotypic (5872.08) variances for this trait indicating environmental influence on this character. The genotypic coefficient of variation and phenotypic co-efficient of variation were 18.22 and 18.37 respectively for no. of seed per fruit which indicating that significant variation exists among different genotypes. The heritability value (98.46%) as well as genetic advance (155.42) and genetic advance in percent of mean (37.25) were observed moderate. The very high heritability with high genetic advance provided opportunity for selecting high valued genotypes for breeding programme.

4.2.13 100 seed weight (gm)

Genotype mean sum of square for number of 100 seed weight was found significant (.019) as shown in Table 5. The maximum seed weight of 100 seed was found .68gm in BARI begun-5 and the minimum was recorded .16gm in SM-57 with mean value .409gm (Appendix III). Phenotypic variance (.01) was equal to genotypic variance (.01) and there is no influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 23.20 and 24.45 respectively which indicated presence of considerable variability among the genotypes. Heritability (90.00.%) estimates for this trait was high, genetic advance (.19) was found very low and genetic advance in percent of mean (45.33) was found moderate indicated that the character was controlled by additive gene.

4.3 Correlation co-efficient

Genotypic and phenotypic correlation was worked out for 13 characters studied to know the nature of association existing among the characters. The results were presented in Table 5. In majority cases, the genotypic correlation co-efficient were higher than corresponding phenotypic correlation co-efficient.

4.3.1 Yield Vs yield components

Fruit yield expressed highly significant and positive correlation with fruit breadth only at phenotypic levels. However, fruit breadth, single fruit weight and number of fruit per plant showed positively significant correlation with yield only at genotypic level (Table 5). Positive association of these yield attributing characters with fruit yield was also reported by Tambe et al., (1992), Narendra Reddy (2003) and Murugavel (2006). Fruit yield expressed highly significant but negative correlation with days to 50% flowering, days to 1st harvest and fruit length at both level.

Table 5. Phenotypic and genotypic correlation between various characters in brinjal genotypes

Characters		DFH	PHFH	PHLH	NBPP	LBL	FL	FB	SFW	NFPP	FY	NSPF	100SW
D50%F	**G**	0.468**	0.045	0.462**	0.148	0.314*	0.488**	-0.084	0.099	-0.336*	-0.497**	0.246	0.088
	P	0.460**	0.040	0.457**	0.124	0.301	0.483**	-0.080	0.099	-0.335*	-0.496**	0.242	0.084
DFH	**G**		-0.268	-0.161	0.078	0.023	0.264	-0.122	-0.023	-0.031	-0.457**	0.006	-0.242
	P		-0.266	-0.165	0.083	0.009	0.263	-0.129	-0.022	-0.030	-0.448**	0.001	-0.231
PHFH	**G**			0.434**	-0.147	0.381*	0.152	-0.092	-0.149	-0.045	-0.049	0.103	0.001
	P			0.427**	-0.166	0.361*	0.150	-0.099	-0.147	-0.420**	-0.043	0.098	-0.009
PHLH	**G**				0.255	0.406**	0.396**	0.023	0.214	-0.460**	-0.068	0.451**	-0.010
	P				0.217	0.377*	0.390*	0.029	0.212	-0.452**	-0.071	0.446**	-0.012
NBPP	**G**					-0.039	0.095	0.161	0.278	-0.488**	-0.163	0.146	-0.133
	P					-0.041	0.072	0.140	0.225	-0.403**	-0.146	0.116	-0.126
LBL	**G**						0.116	0.239	0.255	-0.345*	0.044	0.344*	0.207
	P						0.105	0.222	0.244	-0.331*	0.042	0.326*	0.224
FL	**G**							-0.572**	-0.176	-0.255	-0.453**	0.127	-0.121
	P							-0.554**	-0.174	-0.254	-0.447**	0.126	-0.118
FB	**G**								0.829**	-0.322	0.375*	0.152	0.329*
	P								0.807**	-0.322*	0.583**	0.155	0.291
SFW	**G**									-0.498**	0.336*	0.271	0.223
	P									-0.496	0.334*	0.268	0.212
NFP	**G**										0.338*	-0.638	-0.335*
	P										0.335*	-0.629	-0.317*
FY	**G**											-0.209	-0.052
	P											-0.204	-0.055
NSPF	**G**												0.193
	P												0.188

** Correlation is significant at the 0.01 level. * Correlation is significant at the 0.05 level.

D50%F= Days to 50% flowering, DFH=Days to 1st harvest, PHFH=Plant height at 1st harvest (cm), PHLH= Plant height at last harvest (cm), NBP= Number of branch per plant, LBL= Leaf breath length (cm), FL= Fruit length (cm), FB = Fruit breadth (cm), SFW = Single fruit weight (g), NFP = Number of fruits per plant and FY = Fruit yield (t/ha).

4.3.2 Correlation among yield components

Days to 50% flowering had highly significant positive correlation with days to first harvest, plant height at last harvest and fruit length both at genotypic and phenotypic levels, whereas leaf breadth showed positive significant correlation at genotypic level and no. of fruits per plant showed negative significant correlation with days to 50% flowering at both levels (Table 5).

Plant height 1st harvest showed highly significant correlation with plant height at last harvest in positive direction and the same trait (plant height at 1st harvest) showed significant positive correlation with leaf blade length at both levels, whereas no. of fruits per plant showed negative significant correlation at phenotypic level.

Correlation was highly significant for plant height at last harvest with fruit length and number of seed per fruit at both genotypic and phenotypic levels. Highly significant correlation was also found for fruit breadth with single fruit weight at both levels. Only highly genotypic significant correlation was found for plant height at last harvest with leaf blade length and fruit length. Whereas fruit breadth had positive significant correlation with 100 seed weight only at genotypic level.

Plant height at last harvest and number of branch per plant had highly negative significant correlation with number of fruit per plant at both genotypic and phenotypic levels. Fruit length had highly negative significant correlation with fruit breadth at both levels whereas single fruit weight had highly negative significant correlation with number of fruit per plant only at genotypic level. Leaf blade length had negative significant correlation with number of fruit per plant at both levels whereas fruit breadth had negative significant correlation with number of fruit per plant only at phenotypic level. Number of fruit per plant had negative significant correlation with 100 seed weight at both genotypic and phenotypic levels.

4.4 Multivariate analysis

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.

4.4.1 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 (Appendix III). 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.

4.4.2 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 25.70, while two of these with eigen values above unity accounted for 47.52% (Table 6).The first three principal axes accounted for 61.04% of the total variation among the 13 characters describing 35 brinjal genotypes.

Based on principal component axes I and II (Appendix IV), a two dimensional chart (Z_1 - Z_2) of the cultivars are presented in Figure 1. 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 seven genotypes namely SM-57, EGN-17, Chaga, SM-75, SM-77(long), SM-83, SM-63 (Table 7). From the clustering mean values (Table 9), it was observed that cluster I produced the highest mean values for plant height at last harvest (97.06cm), number of branches per plant (5.50), and the

lowest mean value for number of fruit per plant (14.27) in comparison with other five clusters (Table 8).

Table 6. Eigen values and percent of variation in respect of 13 characters of 35 germplasm of brinjal genotypes.

Principal Component Axis	Principal Component Characters	Eigen Values	% of Total Variation Accounted for	Cumulative Percent
I	Days to 50% flowering	3.341	25.70	25.70
II	Days to 1st harvest	2.837	21.82	47.52
III	Plant height at 1st harvest	1.758	13.52	61.04
IV	Plant height at last harvest	1.159	8.92	69.96
V	Number of branches	1.052	8.09	78.05
VI	Leaf blade length (cm)	0.699	5.37	83.42
VII	Fruit length (cm)	0.641	4.93	88.35
VIII	Fruit width (cm)	0.486	3.74	92.09
IX	Single fruit weight (gm)	0.443	3.41	95.5
X	Number of fruit/plant	0.241	1.85	97.35
XI	Fruit yield/plant (Kg)	0.171	1.31	98.66
XII	No. of seed/fruit	0.120	0.93	99.59
XIII	100 seed weight (gm)	0.052	0.40	100.00

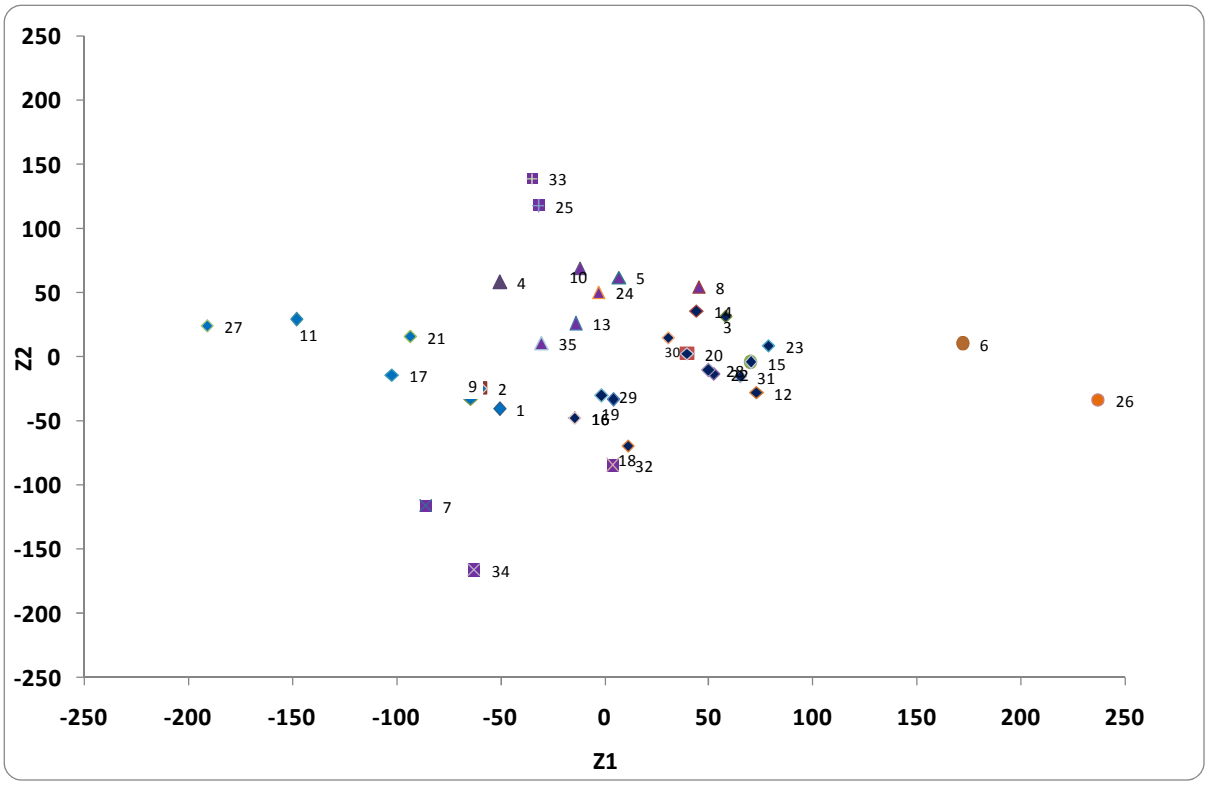


Figure 2. Scatter distribution of 35 brinjal genotypes based on their principal component scores.

Table 7. Distribution of 35 brinjal genotypes in six different clusters with their place of collection

Cluster No.	Number of Genotypes	Genotypes including sources of collation
I	7	SM-57(market), EGN-17(Nichintopur), Chaga, SM-75, SM-77(Long), SM-83 (Thakurgaon), SM-63(market)
II	2	BARI Begun-8, SM-186(Advanced line of Netherland seed company)
III	2	SM-111 (Barisal),SM-84 (Thakurgaon)
IV	3	EGN-27 (Nichintopur), SM-183 (Advanced line of Netherland seed company), BARI Begun-6(Pabna)
V	7	EGN-10, Sada bagun, EGN-25 (Nichintopur), BARI Begun-7, SM-59 (small), BARI Begun-4, SM-77 (Thakurgaon)
VI	14	Uttra (Rajshahi), BARI Begun-9, SM-58, SM-11, SM-48 (Rangpur), BARI Begun-5 (Gazipur), SM-59(big), BARI Begun-3, SM -180(Advanced line of Netherland seed company), SM-19, SM-184(Advanced line of Netherland seed company), BARI Begun-10, SM-185(Advanced line of Netherland seed company), SM-181 (Advanced line of Netherland seed company)

Table 8. Cluster mean for 13 characters of 35 brinjal genotypes

Characters	Cluster					
	I	II	III	IV	V	VI
Days to 50% flowering	57.07	57.75	46.50	57.17	62.21	56.61
Days to 1st harvest	98.64	102	94	107.67	99.36	99.64
Plant height at 1st harvest	63.37	61.64	62.14	55.05	68.20	63.82
Plant height at last harvest	97.06	93	77.74	91.05	95.59	91.88
Number of branches	5.50	5.25	4	5.33	5.29	5.32
Leaf blade length (cm)	16.64	14.33	11.93	17.14	17.83	16.21
Fruit length (cm)	13.17	18.76	8.25	14.54	17.23	17.30
Fruit width (cm)	6.40	2.70	3.50	7.37	4.10	4.69
Single fruit weight (gm)	194.11	44.10	48.31	268.47	101.78	128.59
Number of fruit/plant	14.27	19.97	51.64	18.85	19.03	21.33
Fruit yield (t/ha)	12	3.78	13.53	18.32	8.91	12.43
No. of seed/fruit	501.79	510	236.25	398.33	447.14	376.61
100 seed weight (gm)	0.41	0.44	0.31	0.46	0.39	0.42

Cluster II was associated with two genotypes namely BARI begun-8, SM-186 (Table 8). It was observed that cluster II produced the highest mean values for fruit length (18.76cm), number of seed per fruit (510) and the lowest mean value for fruit width (2.70cm), single fruit weight (44.10gm) and yield (3.78 t/ha).

Among the six clusters, cluster III composed of two genotypes. The genotypes were SM-111, SM-84(Table 7). It was observed that cluster III produced the highest mean values for number of fruit per plant (51.64) and the lowest mean value for days to 50% flowering (46.50days), days to first harvest (94days), plant height at last harvest(77.74cm), leaf blade length (11.93cm), number of branches(4), fruit length (8.24cm), number of seed per fruit(236.25) and 100 seed weight(.31gm)

Cluster IV consisted of three genotypes, namely EGN-27, SM-183, BARI begun-6 (Table 7). From the clustering mean values (Table 8) it was observed that cluster IV produced the highest mean values for days to first harvest (107.67days), fruit width (7.37cm), single fruit weight (268.47gm), yield (18.32t/ha), 100 seed weight (.46gm) and the lowest mean value for plant height at first harvest (55.05cm).

Cluster V constituted only with seven genotypes. The genotypes were EGN-10, Sada begun, EGN-25, BARI begun-7, SM-59 (small), SM-77(Table 7). The genotypes of this cluster were late for both days to first flowering (62.21days) and first fruit harvesting (68.20days).Cluster V produced the highest mean values for leaf blade length (17.83cm)(Table 8).

Cluster VI consisted of fourteen genotypes namely Uttra, BARI Begun-9, SM-58, SM-11, BARI Begun-5, SM-59(big), BARI Begun-3, SM -180, SM-19, SM-184, BARI Begun-10, SM-185, SM-181 (Table 7).

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 days to 50% flowering, days to first harvest, number of fruits per plant, 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 grower's suitability could be considered suitable parents for efficient hybridization in future. The maximum range of variability was observed for single fruit weight and number of fruit per plant. Cluster IV possesses all the superior characters in respect of yield. Thus to develop high yielding varieties genotypes of these group can be selected.

4.3.3 Principal coordinate analysis

By using inter-genotypic distances and intra-cluster genotypic distances were calculated (Table 9) as suggested by Singh *et al.* (1977). Cluster VI which (7.538) composed of fourteen genotypes showed the maximum intra cluster distances and cluster II showed the lowest intra-cluster distance (0.698) 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.

4.3.4 Canonical variate analysis

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. The Table 9 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 II and Cluster III (12.027) followed by between cluster II to cluster IV (11.484), Cluster I to Cluster III (11.107), cluster III to Cluster V (10.169) and Cluster III to Cluster IV (10.169) (Table 9). The lowest inter-cluster distances was observed between the cluster V to Cluster VI (3.115), followed by cluster III to cluster V (4.206), cluster I to cluster V (4.221) and cluster I to cluster VI (4.711) (Table 9). The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 9).

Table 9. Intra (Bold) and inter cluster distances (D^2) for 35 genotypes of brinjal

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**
I	**2.887**	5.919	11.107	6.288	4.221	4.711
II		**0.698**	12.027	11.484	4.206	6.765
III			**0.987**	10.169	10.169	7.855
IV				**1.576**	8.371	6.158
V					**2.773**	3.115
VI						**7.538**

Islam (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 cluster II and Cluster III (12.027) maintaining more distances than other clusters, and the lowest inert-cluster distance found between the cluster V to Cluster VI (3.115) maintaining less distance than other cluster. Genotypes from the cluster II and Cluster III (12.027) 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 2 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. 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 ever, in some cases effect of geographic origin influenced clustering that is geographic distribution was not the sole criterion of genetic diversity. The 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.

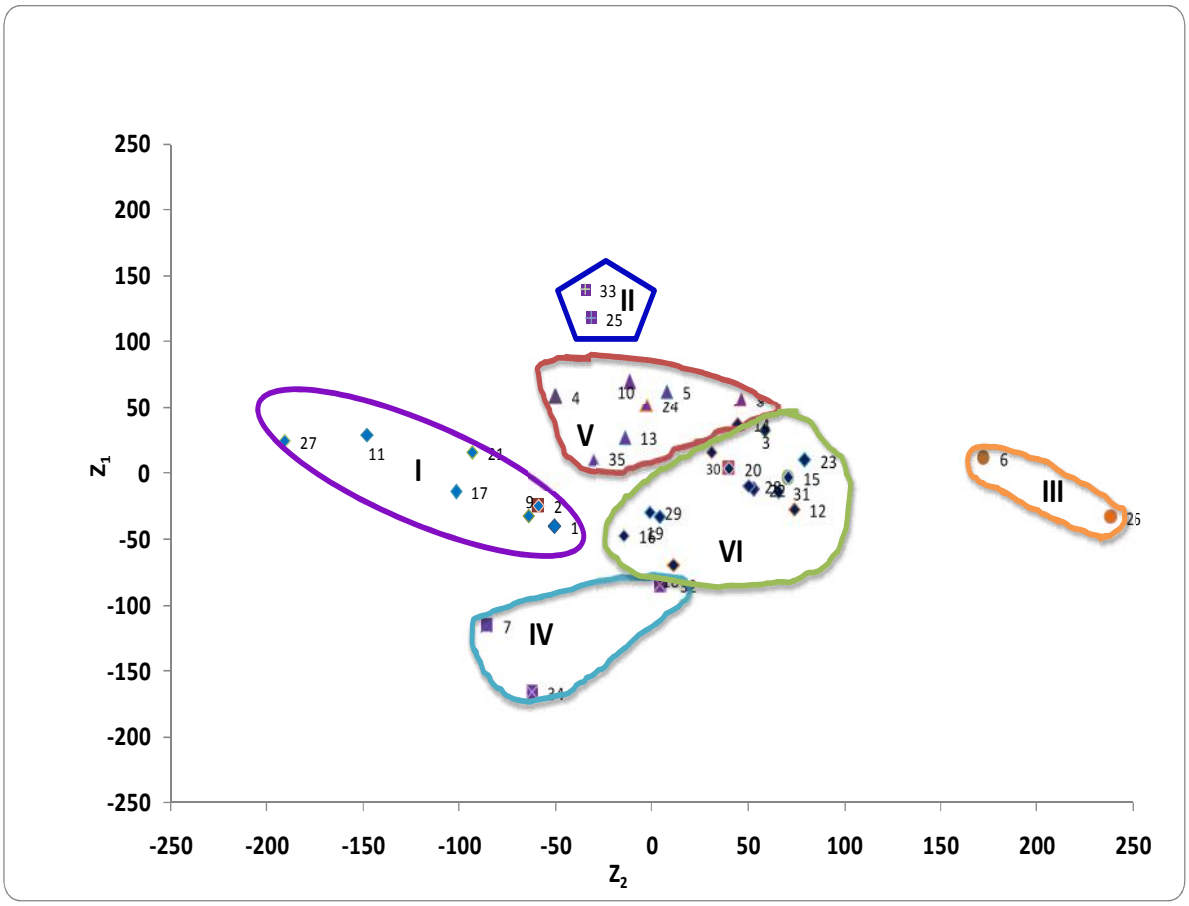


Figure 3. Scatter distribution of 35 brinjal genotypes based on their principal component scores superimposed with clustering

4.3.5 Non- hierarchical Clustering

By using covariance matrix with the application of Non- hierarchical clustering, the 35 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 7. These results confirmed the clustering pattern of the genotypes according to the principal component analysis. So, the results obtained through PCA were confirmed by nonhierarchical clustering.

Joshi *et* a/. (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 seven (7) genotypes (genotypes number) SM-57, EGN-17, Chaga, SM-75, SM-77(long), SM-83, SM-63 (Table 7),collected from Nichintopur, Thakurgaon and market place (Table 1).From the clustering mean values (Table 9), it was observed that cluster I produced the highest mean values for plant height at last harvest (97.06cm), number of branches per plant(5.50), and the lowest mean value for number of fruit per plant (14.27) in comparison with other five clusters (Table 8). These group possessed genotypes with the second highest cluster mean for fruit width (6.40cm), single fruit weight (194.11gm) and number of seed per fruit (501.79).

Mandal and Dada (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.

4.3.5.2 Cluster II

Cluster II was associated with two genotypes namely BARI begun-8, SM-186 (Table 7) that were collected from unknown place and advanced line of Netherland seed company (Table 1). It was observed that cluster II produced the highest mean values for fruit length (18.76cm), number of seed per fruit (510) and the lowest mean value for fruit width (2.70cm), single fruit weight (44.10gm) and yield per plant (3.78kg). These group possessed genotypes with the second highest cluster mean for days to 50% flowering (57.75days), days to first harvest (102 days) On the other hand this group produced lowest mean value for 100 seed weight (.44gm) (Table 8).

4.3.5.3 Cluster III

Cluster III composed of two genotypes. The genotypes were SM-111, SM-84(Table 7) which were collected from Barisal and Thakurgaon. It was observed that cluster III produced the highest mean values for number of fruit per plant

(51.64) and the lowest mean value for days to 50% flowering (46.50 days), days to first harvest (94days), plant height at last harvest(77.74cm), leaf blade length (11.93cm), number of branches(4), fruit length (8.24cm), number of seed per fruit(236.25) and 100 seed weight(.31gm) The genotypes of this cluster produced second lowest mean for yield (13.53 t/ha) (Table 8).

4.3.5.4Cluster IV

Cluster IV consisted of three genotypes, namely EGN-27, SM-183, BARI begun-6 (Table 7) collected from Nichintopur, advanced line of Netherland seed company and Pabna (Table 1). From the clustering mean values (Table 8),it was observed that cluster IV produced the highest mean values for days to first harvest (107.67days), fruit width (7.37cm), single fruit weight (268.47gm), yield (18.32t/ha), 100 seed weight (.46gm) and the lowest mean value for plant height at first harvest (55.05cm). These group possessed genotypes with the second highest cluster mean for leaf blade length (17.14cm) and number of branches (5.33).

4.3.5.5Cluster V

Cluster V constituted only with seven genotypes. The genotypes were EGN-10, Sada begun, EGN-25, BARI begun-7, SM-59 (small), SM-77(Table 7), collected from Nichintopur, Thakorgaon and some unknown places (Table 1). The genotypes of this cluster were late for both days to first flowering (62.21days) and first fruit harvesting (68.20days).Cluster V produced the highest mean values for leaf blade length (17.83cm)(Table 8). The genotypes of this cluster produced second highest mean for plant height at last harvest (95.59 cm) and second lowest mean for yield (13.53 t/ha) (Table 8).

4.3.5.6Cluster VI

Cluster VI consisted of fourteen genotypes namely Uttra, BARI Begun-9, SM-58, SM-11, BARI Begun-5, SM-59(big), BARI Begun-3, SM -180, SM-19, SM-184, BARI Begun-10, SM-185, SM-181(Table 7), collected from Rajshahi, Rangpur,Gazipur, advanced line of Netherland seed company and some unknown places (Table 1). The genotypes of this cluster produced second highest mean for plant height at first harvest (63.82 cm), fruit length (17.30cm) and number of fruit per plant (21.33)

Table 10. Latent vectors for thirteen characters of 35 Brinjal genotypes

Characters	Vector-1	Vector-2
Days to 50% flowering	0.3572	-0.2464
Days to 1st harvest	0.0834	-0.2788
Plant height at 1st harvest	0.1281	-0.0524
Plant height at last harvest	0.3947	-0.0267
Number of branches	0.2039	0.0271
Leaf blade length (cm)	0.3110	0.1002
Fruit length (cm)	0.2323	-0.4075
Fruit width (cm)	0.1254	0.5243
Single fruit weight (gm)	0.2506	0.4159
Number of fruit/plant	-0.4630	-0.0963
Fruit yield (t/ha)	-0.2006	0.4195
No. of seed/fruit	0.3793	0.0622
100 seed weight (gm)	0.1547	0.2102

4.3.6 Comparison of Different Multivariate Techniques

The cluster pattern of D^2 analysis though non-hierarchical 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 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 f characters towards divergence of brinjal.

4.3.7 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 SM-111, SM-84, EGN-27, SM-183, BARI begun-6 from cluster III and cluster IV would be suitable for efficient hybridization programme.

CHAPTER V

SUMMARY AND CONCLUSION

In order to evaluate the performance of yield, yield contributing character, variability and genetic diversity, an experiment was conducted with 35 brinjal genotypes at the experimental field of the Olericulture division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI) Joydebpur, Gazipur, during the period from September 2010 to February 2011 Seeds of the different genotypes were sown in separate seedbeds and fourty days old seedlings were transplanted in the main field in a RCBD with three replications. Data on different morphological and yield contributing characters like leaf blade length, leaf blade width, leaf petiole length 9cm),leaf blade lobbing, fruit shape, fruit colour, colour distribution at commercial ripeness, fruit calyx length, fruit apex shape, fruit bearing habit, days to first fruit harvesting, plant height (cm), no. of branches per plant, fruit length (cm), single fruit weight (gm), no. of fruit per plant, fruit yield , no. of seed per fruit, 100 seed weight (gm) were recorded. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

From the experiment it was observed the highest number of fruit s per plant (52.92) obtained from the line SM-84 followed by SM-111(50.30) and SM-11 (43.17) while other lines bear average number of fruits per plant. Among the cultivar studied the longest fruit (31.56cm) was produced by BARI begun-7 while the smallest fruit (7.15cm) was obtained from SM-84. Fruit breadth was maximum (9.01cm) in EGN-27 and the minimum (2.60cm) was produced by BARI begun-8. The highest single fruit weight (313.34gm) was produced by the line BARI begun-6 while SM-186 produced (35.55gm).

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 16.38 and 13.42 respectively which indicated that the number of branches per plant was mostly depended on the environmental condition.

Amongst the characters the highest genotypic coefficient of variation was recorded for fruit yield (59.31) followed by no. of fruit per plant (49.51), single fruit weight (46.96gm).

The highest estimated heritability amongst thirteen characters of brinjal was 99.94% for single fruit weight and the lowest for 67.11% for number of branches. The highest GA amongst all the characters was found in number of seed per fruit (155.42) and the lowest genetic advance was carried out in 100 seed weight (0.19gm).

The maximum genetic advance in percent of mean was observed for fruit yield (121.51), where as the lowest was for plant height at last harvest (19.92cm).The high heritability (99.94%) with low genetic advance in percent of mean (19.92cm) 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 5.5 software programme. The first three principal component characters with eigen values were greater than unity contributed a total of 61.04% 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 seven, two, two, three, seven and fourteen genotypes respectively. The highest inter cluster distance was observed between cluster II and Cluster III (12.027) followed by between cluster II to cluster IV (11.484), Cluster I to Cluster III (11.107), cluster III to Cluster V (10.169) and Cluster III to Cluster IV (10.169) (Table 9). The lowest inter-cluster distances was observed between the

cluster V to Cluster VI (3.115), followed by cluster III to cluster V (4.206), cluster I to cluster V (4.221) and cluster I to cluster VI (4.711) (Table 9). Cluster VI (7.538) showed the maximum intra cluster distances and cluster II showed the lowest intra-cluster distance (0.698).

Genotypes included in cluster I were suitable for plant height at last harvest (97.06cm), number of branches per plant(5.50),cluster II for fruit length (18.76cm), number of seed per fruit (510), cluster III for number of fruit per plant (51.64) and having lowest mean value for days to 50% flowering (46.50 days), days to first harvest (94days), cluster IV for fruit width (7.37cm), single fruit weight (268.47gm), yield (18.32t/ha), 100 seed weight (0.46gm), cluster V for leaf blade length (17.83cm).

Findings of the present investigation indicated significant difference among the cultivars for all the characters studied. Generally, diversity was influenced by the morphological characters, but not the distribution of genotypes. Which indicated the importance of consumer preference and growers suitability. Considering diversity pattern and other agronomic performances, the genotypes SM-111, SM-84, EGN-27, SM-183, BARI begun-6 from cluster III and cluster IV could be considered as suitable parents for efficient hybridization programme.

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