CHARACTERIZATION, GENETIC DIVERSITY AND TRAITS ASSOCIATION OF EGGPLANT GERMPLASM

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CHARACTERIZATION, GENETIC DIVERSITY AND TRAITS ASSOCIATION OF EGGPLANT GERMPLASM

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I further certify that such help or source of information, as has been availed during the course of this investigation has been duly acknowledged and style of this thesis have been approved and recommended for submission.

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ABSTRACT

Fourty (40) genotypes of Brinjal were studied in the experimental field of Olericulture division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute, Gazipur, during September 2018 to March 2019. There was significant variation observed for all the characters within genotypes. Multivariate analysis was performed through principal component analysis(PCA), principal coordinate analysis (PCO), canonical variate analysis(CVA) and cluster analysis(CLSA). As per PCA, D^2 and cluster analysis, the genotypes were grouped to five clusters. The highest inter-cluster distance was between cluster I and IV and lowest between II and III. Cluster IV showed the maximum intra-cluster distance and I showed the lowest. Regarding agronomic performance, different characters contribute increasing the higher yield of brinjal. The height cluster yield mean observe from cluster I which include genotype SM 359, SM 362, SM 364, SM 367, SM 378 used as advance line. This advance line further used for development of high yielding OP (Open pollinated) variety in future. Due to the higher inter cluster distance, the genotypes BARI Begun-6 from cluster I, SM 359, SM 362, SM 364, SM 367, SM 378 from cluster II and SM 323, SM 351, SM 365, SM 373, SM 387, SM 393, SM 398, SM 399, BARI Begun-7, BARI Begun -8 from cluster IV would be suitable for efficient hybridization programme.

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ABBREVIATION	WORD MEANING
AEZ	Agro-Ecological Zone
et al.	And others
ACC	Accessions
Av.	Average
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
CV	Co-efficient of Variation
etc.	Etcetera
Fig.	Figure
HRC	Horticulture Research Centre
MSS	Mean Sum of Square
MOP	Muriate of Potash
%	Percent
OP	Open pollination
RCBD	Randomized Complete Block Design
R	Analysis Software
Res.	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
TSP	Triple Super Phosphate

CHAPTER I

INTRODUCTION

Solanum melongena L. (Melongene or Aubergene or Eggplant also known as brinjal in Bangladesh) is one of the most important and popular Solanaceous crops 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 second important, inexpensive, popular and nutritious vegetables in Bangladesh which is a cheaper and economically feasible source of vitamin A, B, C and iron. The consumption of fruits and vegetables is important from the nutritional point of view and many consumers are now conscious about the health benefits of foods. The current nutritional condition of third world and some emerging countries like Bangladesh is a matter of concern as many people are suffering from malnutrition (Begum et al., 2017). Brinjal can play a significant role in this case and can mitigate the nutritional shortage to some extent. 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.

It is grown both winter and summer season in Bangladesh. In winter season, its grown on nearly 80,195hectares of land across the country and produce 347541 metric tons(MT) and in summer season, its grown on nearly 27833 hectares of land across the country and produce103900 metric tons(MT) (BBS, 2017).Its production provides an important source of cash income for small resource-poor Bangladeshi farmers. The biggest constraints to eggplant production are chronic and widespread infestations by the eggplant fruit and shoot borer. Caterpillars damage eggplant shoots and flowers, but the most serious damage is caused by their boring into the fruit and rendering it unmarketable. Farmers routinely spray broad-spectrum insecticides, often two to three times per week and in some cases twice a day. Consequently, over 100 sprays per season may be applied, resulting in high residues on the fruit. Farmers lose anywhere from 30 to 60% of the crop yield to EFSB despite the high use of insecticides. The cost of insecticide treatments accounts for 35 to

40% of the total cost of cultivation of brinjal. Such an insecticide-dependent strategy poses both environmental and health concerns.

The crop is highly diverse for fruit shape, size and colour in Bangladesh due to the Indian gene centre. BARI released 20 varieties of brinjal including two hybrid and four transgenic varieties for cultivation in Bangladesh. The fruit and shoot borer resistant, trangeneic varieties are 'BARI Bt Bagun-1', 'BARI Bt Bagun-2', 'BARI Bt Bagun-3' and 'BARI Bt Bagun-4' (Azad et al., 2017). Bangladesh Considering the potentiality of this crop, there is a need for improvement and to develop varieties for specific agro- ecological conditions and also for specific end use. PGRC of BARI conserved 282 accessions in the genebank. Systematic research such as collection, conservation, characterization and evaluation, and utilization of brinjal germplasm has been done at PGRC of BARI. Characterization and evaluation of plant germplasm is imperative for categorization of germplasm and identification of desirable genotypes carried out in precision fields under sufficient growth and plant protection conditions for utilization in breeding programs. Before these resources can be exploited, they should be systematically evaluated to assess genetic diversity. Until a collection has been properly evaluated and its attributes become known to breeders, it has little practical use (Thomas and Mathur, 1991). Such a situation is just like a library where none of the books are catalogued. Therefore, the current piece of research will help to identify suitable germplasm of brinjal which can be used to develop desirable varieties. The specific purpose of this study was to characterize and to study the genetic diversity and identify the potential accessions for varietal improvement of brinjal in Bangladesh. 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). 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. This selection technique measure the forces of differentiation thus help in the selection of genetically divergent parents for exploitation in hybridization programme. 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. 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 and genetic variability and. Assessment of genetic resource is the starting point of any crop improvement program. By studying morphological characteristics and genetic variability of brinjal genotypes, we can select the best genotypes. Considering availability of genetic diversity, there is bright scope of fruit yield improvement in eggplant in the country. Therefore, the present investigation is undertaken to fulfill the following objectives**:**

- To characterize the eggplant germplasm.
- To develope good quality high yielding OP (open pollinated) variety.
- To access the potential genetic diversity among eggplant genotypes for selection of parents in hybridization programme to obtain better sergeant's in advanced generation.

2.1 Characterization and Variability of Brinjal Genotypes

Jayalakshmi and Praneetha (2018) Fifty local types of brinjal were collected from several districts of Tamil Nadu and various other sources were evaluated during September 2016 and February 2017 to assess the mean performance.For yield and its quality characters. Among the genotypes, Sevanthampatty Local (123.23 cm) recorded highest plant height. Pachai Round (8.80) had the highest number of branches per plant. Karur Local and Udumalai Samba recorded earliest to first flowering (47.65 and 47.73 days), 50% flowering (55.20 and 55.31 days) and days to first harvest (66.81 and 67.03 days). Highest marketable yield per plant was recorded by Karur local (2.97 kg) followed by Udumalai Samba (2.86 kg). Similarly Karur Local (19.82 per cent) had lowest fruit borer infestation followed by Udumalai Samba (20.57 percent).

Arindam Das *et al.* (2017) A total of forty seven characters viz. growth, yield and morphological, were studied and significant variation observed among the brinjal genotypes collected across the country. This variation may be due to the effect of genotype, environment or their interaction. A randomized block design with three replication has been used for this experiment. Mean data pooled over the years has been furnished and statistically analyzed for all the characters except number of fruits per plant, weight of fruits, number of seeds per fruit, yield per plant and yield per hectare. Though genotype BCB-27 followed by BCB-8, is the highest yielder/plant for two seasons, BCB-8 is superior to any other genotypes in total fruiting period, fruit length and number of fruits per plant.

CAKIR *et al.* (2017) Turkey is one of the most important countries in the world for plant genetic resources and genetic diversity. Genetic resources are characterized by morphological and agronomical traits. There is a need to collect, characterize and evaluate remnants of local populations before they disappear. Morphological characterization is the first stage of the identification and classification of genetic resources. In this study, the aim was to determine the similarities and differences in the morphological variations of the eggplant populations collected from different eco geographical regions of Turkey. Seventy five populations of eggplant were characterized using standard morphological descriptors

specified by the IBPGR. The phenotypic diversity in their fruit characters was also assessed.

Tiwari *et al.* (2016) analyzed the extent of morphological diversity among 96 accessions of brinjal. The results could clearly distinguish prickly and non-prickly types of accessions and further classified on the basis of growth habit, fruit characterslike shape and color. Most of genotypes showed upright to intermediate growth habit, oblong to long fruit shape and green color fruit.

Khan and Singh (2014) studied the 192 accessions of eggplant and characterized for ten quantitative and eleven qualitative characters. Most of genotypes showed spreading and semi-spreading growth habit with non spiny stem. The fruit shape was observed round (39.06%), oblong (38.02%), and long (22.92%). The genotypes fell into five fruit color groups namely purple (46.35%), green (32.81%), purple black (11.98%), light purple (6.77%) and milky white (2.08%).

Chandrasekhar *et al.* (2013) studied 31 eggplant genotypes and characterized based on response for 7 qualitative and 14 quantitative characters. The dominant characters were found to be upright habit, intermediate lobbing, no prickles, pale violet-colored leaves, no fruit curvature, protruded fruit apices, and purple black fruit color.

Shinde *et al.* (2012) recorded that most of the genotypes showed spreading and semi-spreading growth habit and 72.31% of the genotypes had spreading, 18.46%had semi-spreading and 9.23% had erect growth habit. Fruiting habit was also solitary in most of genotypes (90.77%). Most of genotypes were non spiny (78.46%) while the remaining were spiny (21.54%). Out of 65 genotypes, 64 were having purple color flowers while one genotype had white color flowers. Maximum genotypes had either oval or round fruits. The fruit shape was observed to variable and oblong (20.00%), oval (36.92%), round (32.31%), medium long (9.23%) and long (1.54%). The genotypes fell into five fruit color groups namely purple (47.69%), green (21.54%), white (4.62%), purple with white stripes (16.92%) and green with purple and white strips (9.23%).

Chattopadhyay *et al.* (2011) characterized the thirty five diverse genotypes of brinjal collected from different parts of Eastern India as per the documenteddescriptors and were evaluated for their morphological and yield componentcharacters during autumn-winter season. The predominant growth habit was semi-erect growth habit (71.43%) followed by spreading growth habit (17.14%). In the case of leaf spineness, the percentage of spiny leaves was 11.43% and the rest genotypeshad spine less leaves. The pre-dominant corolla

color was purple. The pre-dominant flowering and fruiting pattern was mixed type (45.71%) followed by cluster type(42.86%). The fruit shape was mostly oblong type (37.14%) followed by long andslender type (17.14%).

Tumbilen et al. (2011) studied the genetic variability of sixty seven Turkish eggplant accessions from the national germplasm collection was assessed with 30 morphological traits and AFLP markers. Morphological analysis indicated considerable variability especially for semi-long and round types.

Naujeer (2009) studied the morphological characterization of twenty seven S.melongena, two S. macrocarpon, one S. nigrum, three S. violaceum and one S.torvum accessions. Nine quantitative and fourteen qualitative traits were characterized based on (IBPGR 1988) eggplant descriptor list.

Pathmarajah et al. (2005) analysied the potential use of electrophoretically detectedisozymic variability complement to the morphological characteristics inbrinjal cultivar to examined nine morphological characters (growth habit, leaf bladecolour, leaf blade lobing, fruit curvature, fruit colour distribution, % of type of flower sper plant, number of fruits per infruitescence and days to first harvest). Three cultivars and six accessions (53%) could be differentiated by combining qualitative morphological characters and rest could be categorized into four groups.

Hazra et al. (2003) studied seventy enteries of brinjal embracing elite varieties, stable breeding lines and indigenous cultivars were evaluated for 33 morphological, growth, floral and fruit characters. Most of the genotypes showed semi-erect growth habit and shallow lobed leaf margin. Pigment production was a common feature, however, its expression in different plant prarts was not same. Propensity of pigment expression was highest in stem and petiole followed by the fruits, veins, calyx and lamina. Development of prickles in different plant parts was a predominant feature. Flowering was extra-axillary and borne in three pattern: solitary, cyme and mixed(both solitary and cyme). Fruits developed from solitary and basal flowers of the cymewere bigger in size compared to those from additional flowers in the cyme. Maximum genotypes had either oval or oblong fruits.

Germplasm is the basic raw material for any crop improvement programme. Conservation and use of genetic resources have a great significance. It may either be introduced from other sources or may be developed by concerned breeder from hisown material. For maintaining adequate variability, the germplasm should include and races, obsolete

varieties, varieties and parents of hybrids, breeding lines with genetic markers, other morphological variants, wild forms and their relatives. Hence, collection, evaluation, maintenance, categorization and utilization of germplasm have special significance. The precise evaluation of genetic stock and dissemination of findings is important for their utilization in breeding programme. The systematically evaluated genetic resources of crops play prominent role in crop improvement.

2.2 Genetic divergence

Banerjee et al. (2018) Brinjal (Solanummelongena L.) is an important solanaceous vegetable crop cultivated throughout the world. Thirty eight genotypes were evaluated in RBD with 3replications in GBPUA&T, Pantnagar for the analysis of genetic divergence. The present study evaluated genetic diversity of accessions through genetic components analyses, and genetic divergence by multivariate and principal component analysis (PCA). Thirty eight genotypes were meaningfully grouped into seven clusters. Cluster III was the largest having fourteen genotypes followed by cluster I, cluster II, cluster IV, cluster V, cluster VI and cluster VII had minimum genotypes. There is no direct relationship between geographical distribution and genetic distance. Among the seven clusters, cluster III showed maximum intra-cluster distance followed by cluster II. Based on inter-cluster distances, the maximum divergence was observed between cluster IV and cluster VII indicating that the genotypes in these clusters could be utilized as parents in hybridization programme to develop high heterotic hybrids and to identify transgressive segregant in F2 generation. Among the studied characters number fruit per plants showed maximum contribution towards the diversity. On the basis of principal component analysis and average values, genotypes 'PusaKaushal', 'PB-70' and 'Niranjan' possessed optimum combinations of all variables and could be utilized as donor parents in breeding of eggplant. enetic divergence among 35 genotypes of brinjal for 19 characters was evaluated in a breeding programme aimed at improving yield potential by using Mahalanobis D2 statistics.

Ravali , Reddy, Saidaiah and Shivraj (2017)The genotypes were grouped into ten clusters suggesting considerable amount of genetic diversity in the material. The cluster V had maximum 10 genotypes followed by II and IV having 6 and 4 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity. The intra-cluster D2 value ranged from 21.71 to 52.61 while, inter-cluster D2 value ranged from 39.09 to 103.59. The maximum intra cluster distance was exhibited by cluster II followed by cluster V and cluster X. The maximum inter-cluster D2 value was observed

between VIII and IX. Maximum contribution towards the total divergence was exhibited by fruit yield per plant (30.57%) followed by average fruit weight (29.90%) and ascorbic acid content (15.51%). Noteworthy is that cluster VIII and X reflected high cluster means for fruit yield per plant, average fruit weight, number of fruits per plant and these clusters can be successfully utilized in hybridization programmes to get desirable transgressive segregant. Multivariate analysis of twenty six genotypes of eggplant were done to estimate the genetic diversity and to select the potential parents for a successful hybridization program.

Karim, Rahman and Quamruzzaman (2016) as per PCA, D2 and cluster analysis, the genotypes were grouped into five clusters. The highest inter-cluster distance was between Cluster II and Cluster III (37.82) and the lowest between Cluster I and Cluster III (4.39). Cluster III showed the maximum intra-cluster distance (1.58), whereas Cluster II showed the lowest intra-cluster distance (0.48). Considering the magnitude of genetic distance and agronomic performance, the genotypes SM 208 and SM 209 from Cluster II and SM 201, SM 218 and SM 227 from Cluster III might be suitable for efficient hybridization program. On the other hand the genotypes of Cluster I (SM 206, SM 210, SM 211, SM 212, SM 213, SM 215, SM 216, SM 217, SM 221, SM 224, SM 225 and SM 226) possess all the superior characters in respect of yield and yield related component. Thus the genotypes SM 206, SM 216, SM 217, SM 224 and SM 225 from this Cluster could be selected to develop high yielding eggplant varieties.

Kumar et al. (2016) grouped of 33 brinjal genotypes from different geographical locations into 10 clusters. Cluster I contained the most genotypes (15) followed by cluster IX (5) and the minimum number of genotypes were in clusters II,V, VII and X. Intermating between genotypes of clusters I and IX would produce more desirable transgressive segregants for breeding. Singh and Singh (2016) observed high intra-clusters distances in cluster IV, while the inter-cluster distances was highest between cluster III and cluster V, thus signifying their role in exploitation of heterosis.

Sadarunnisa et al. (2015) studied genetic divergence among 50 genotypes of brinjal for 16 characters and grouped into eight clusters. The maximum and minimum intra-cluster distances were found in cluster VI and cluster I, respectively. The inter cluster values was maximum between the cluster VI and VII while the minimum inter cluster distance was observed between cluster I and II. The mean value for most of the traits was highest in cluster VII. The characters like average fruit weight, days to last harvest and bacterial wilt

incidence contributed maximum to genetic divergence and hence played a major role in improvement of brinjal.

Chaitanya (2015) grouped fifty one genotypes in to eight clusters. The pattern of distribution of genotypes into various clusters revealed that there was no relationship between geographical distribution and genetic diversity. The traits ascorbic acid content, average fruit weight and total number of fruits per plant were the major contributors towards divergence.

Khan and Singh (2015) grouped 192 genotypes into five different clusters. The maximum intra-cluster distance was found in cluster I and minimum in cluster V whereas, the maximum inter-cluster value (18.031) was obtained between cluster II and V and minimum between cluster I and III (2.869).

Rahman*et al.* (2014) grouped hundred brinjal accessions into eight clusters. The maximum inter-cluster divergence was found between the cluster II and VI (32.234) and was minimum between V and VII (2.841). The maximum intra-cluster divergence was found between accessions falling in the cluster II. On the basis of the mean performance of different clusters, accessions having acceptable yield were placed in cluster IV, VI and VIII. The superior accessions may be selected from both maximum and minimum divergent clusters for further improvement.

Ahmed *et al.* (2014) revealed the first principal component largely accounted for the variation among the brinjal genotypes (29.90%) followed by second principal component (20.35%) and third (20.08%). The maximum inter-cluster distances were recorded between the cluster I and II (278.26) followed by the distance between I and V (245.32) may be uses for hybridization. The lowest inter-cluster distance was observed between cluster II and V (35.26) followed by III and V (45.75) suggesting a close relationship among these three clusters. Based on the cluster means the important cluster was Cluster I for fruit weight, fruit length, fruit width and yield per plant. Cluster II for plant height, plant spread, and number of primary branches. Cluster III for number of fruit per plant.

Patel *et al.* (2014) studied thirty five genotypes of brinjal and grouped into six clusters, where, cluster I was very comprising of 30 genotypes and others were solitary clusters. The maximum inter-cluster distance was obtained between cluster V and VI followed by cluster III and VI as well as Cluster II and VI which may serve as potential genotypes for hybridization programme. Fruit length, fruit diameter, number of branches per plant and plant height an important role in divergence between the population.

Begum *et al.* (2013) studied 92 genotypes and observed highest inter-cluster distance between cluster II and VIII (30.86) indicated the genotypes in these clusters were more diverged than those of other clusters. The lowest inter-cluster distance was observed between the clusters V and X (3.72) suggesting a close relationship among the genotypes included within these clusters. Cluster II constitute three genotypes and produced the highest mean value for number of flowers per inflorescence (4.67) and yield per plant (812.33) and the lowest mean value days to 1st flowering (108.22).Cluster IV constitute three genotypes namely EP-080, EP-081, EP-089 and produced fruits for longer duration (82.33). Cluster VIII constitute seven genotypes and showed the lowest mean value for number of infected shoots per plant (1.57). Therefore, more emphasis should be given on cluster II, IV and VIII for selecting genotypes as parents for crossing which may produce new recombinants with desired traits.

Rathi *et al.* (2011) revealed minimum intra cluster distance in cluster IV and maximum in cluster II. The maximum distance at inter cluster level was between clusters I and clusters IV followed by II and IV which may serve as a potential genotypes for hybridization programme. On the basis of mean performance of different clusters, genotypes having high yield along with fruit diameter, fruit index and average fruit weight were observed in cluster V having genotypes like DBR-31 (Delhi), Green Long (Kalyani), KS-335 (Kalayanpur), G-190 (IARI, Delhi), DBR-8 (IARI, Delhi), SL-91-2 (Pantnagar), SL-190-10-12 (Panipat), Swarna Shree (Ranchi) and ABR-1 (Anand) . Arunkumar*et al.* (2013) observed minimum inter cluster distance between cluster II and V (13635.14) indicating close relationship among the genotypes and maximum inter cluster distance was found between clusters II and VII (65237.45) followed by clusters VI and VII (56306.80) which indicated that genotypes included in these clusters were genetically diverse.

Muniappan et al. (2010) studied thirty four genotypes of eggplant and grouped into seven clusters. Cluster II showed minimum intra-cluster distance (49.18) and maximum intra-cluster distance was exhibited by cluster III (144.95) followed by cluster V (144.14). Maximum inter cluster distance was found between clusters II and VII (255.42). This was followed by clusters VI and VII (237.29). Minimum inter cluster distance was observed between clusters II and V (116.77)

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 UniversidadeEstadual 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 inbreeds 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 i 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.

CHAPTER III
MATERIALS AND METHODS

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 2018 to March2019.

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 smallhillocks of red soils as 'islands' surrounded by floodplain (Anon, 1988).

3.3 Climate

Area has subtropical climate, characterized by scanty rainfall associated with moderately low temperature during the Rabi season (September-March) 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 Science discipline lab, BARI, Joydebpur, Gazipur.

3.5 Planting materials

Fourty (40) germplasm of brinjal were included in this study. Therty four (34) germplasm were collected from different parts of Bangladesh and different foreign country. Six(6) germplasm were collected from HRC, BARI, Joydebpur, Gazipur. The name of the germplasm with the source have presented in Table 1.

Table1. List of selected 40 brinjal germplasm with their Source of collection and fruit colour

Sl.No.	Accession name	Commercial name	Company	Souce Collection	Fruit shape
1	SM 323	Kranti OP	Bankim	HRC,BARI,Gazipur	Elongate
2	SM 343	BE 706	Manik	HRC,BARI,Gazipur	Elongate
3	SM 351	Green Ball	Manik	HRC,BARI,Gazipur	Oval
4	SM 358	SM358	Vangor	HRC,BARI,Gazipur	Oblong
5	SM 359	Rakhain Begun	Patuakhali	HRC,BARI,Gazipur	Elongate
6	SM 361	SM 217A	Patuakhali	HRC,BARI,Gazipur	Oblong
7	SM 362	Islampuri	Patuakhali	HRC,BARI,Gazipur	Oval
8	SM 363	PM House-Gol	Dr. A.G	HRC,BARI,Gazipur	Cylindrical
9	SM 364	PM House-Lomba	Dr. A.G	HRC,BARI,Gazipur	Round
10	SM 365	Black Beauty	Australia	HRC,BARI,Gazipur	Elongate
11	SM 366	Madhubala	Ocen seed	HRC,BARI,Gazipur	Oval
12	SM 367	Tal	Manik	HRC,BARI,Gazipur	Oval
13	SM 369	Tal Begun	Alamgir	HRC,BARI,Gazipur	Oval
14	SM 370	Pintoo	Nufield	HRC,BARI,Gazipur	Oval
15	SM 371	Black round	Nufield	HRC,BARI,Gazipur	Round
16	SM 373	Purple King	LalTeer	HRC,BARI,Gazipur	Cylindrical
17	SM 375	Menka	Nufield	HRC,BARI,Gazipur	Elongate
18	SM 376	Menka	Nufield	HRC,BARI,Gazipur	Elongate
19	SM 377	DebjhuriHazari	Debgiri	HRC,BARI,Gazipur	Elongate
20	SM 378	706	Manik	HRC,BARI,Gazipur	Elongate
21	SM 380	SonaJhuiri	NSC Nirman	HRC,BARI,Gazipur	Oblong
22	SM 381	Black long	Masud	HRC,BARI,Gazipur	Elongate
23	SM 382	Long Black	Chia Tai	HRC,BARI,Gazipur	Cylindrical
24	SM 383	Chomok	Chia Tai	HRC,BARI,Gazipur	Cylindrical
25	SM 385	Gol begun	Alamgir	HRC,BARI,Gazipur	Oval
26	SM 386	Gol Begun	Manik	HRC,BARI,Gazipur	Elongate
27	SM 387	Green ball	Malik	HRC,BARI,Gazipur	Oval
28	SM 388	Green super	Chia tai	HRC,BARI,Gazipur	Oval
29	SM 391	Sadagol Begun	Local	HRC,BARI,Gazipur	Round
30	SM 393	China Begun	Rajshahi	HRC,BARI,Gazipur	Oval
31	SM 394	Kallany	United Seed	HRC,BARI,Gazipur	Cylindrical
32	SM 395	Luna	United Seed	HRC,BARI,Gazipur	Oval
33	SM 398	Local-Gol	Local	HRC,BARI,Gazipur	Round
34	SM 399	Local-Lombasada	Local	HRC,BARI,Gazipur	Elongate
35	BARI Begun-1	BARI Begun-1	BARI release	HRC,BARI,Gazipur	Elongate
36	BARI Begun-4	BARI Begun-4	BARI release	HRC,BARI,Gazipur	Elongate
37	BARI Begun-5	BARI Begun-5	BARI release	HRC,BARI,Gazipur	Round
38	BARI Begun-6	BARI Begun-6	BARI release	HRC,BARI,Gazipur	Oval
39	BARI Begun-7	BARI Begun-7	BARI release	HRC,BARI,Gazipur	Cylindrical
40	BARI Begun -8	BARI Begun -8	BARI release	HRC,BARI,Gazipur	Cylindrical

3.6 Germplasm

Total fourty germplasm of brinjal (Table 1) representing sample of different districts of the country and many parts of other foreign country were collected from Olericulture division of Horticulture Research Centre (HRC) of Bangladesh Agricultural Research Institute (BARI) Joydebpur, Gazipur.

3.7 Design and Pictorial view of experimental field

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. Each replication contains 40 germplasm having 75cm×60cm spacing. Each plo twas 7.5m length and 0.80m breadth. Block to block distance was 0.75m. The germplasm were randomly distributed to unit plot within each block. Pictorial view of some germplasm in the field are shown in plate.

Plate1. Pictorial view of brinjal genotype line on experimental field

3.8 Raising of seedlings

Seeds of selected germplasm were sown in the well prepared seedbed on 16[th]September2018. All care and precaution were taken to raise healthy seedlings. When seedlings become45 days old those were transplanted in the main field.

3.9 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.

3.10 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 days after transplanting and the 2nd at the flowering. Doses of manure and fertilizers used in the study are followed by fertilizer recommendation guide 2012 (Appendix II).

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

SL No.	Fertilizer/Manure	Dose
1.	Cowdung	10 ton/ha
2.	Urea	300 kg/ha
3.	TSP	300 kg/ha
4.	MOP	250 kg/ha
5.	Gypsum	100 kg/ha
6.	Boric acid	5 kg/ha
7.	Magnesium Sulphate	5 kg/ha
8.	Zinc Oxide	5 kg/ha

Source: Fertilizer Recommedation Guide (2012)

3.11 Transplanting of seedlings

Forty five days old seedlings were transplanted in well-prepared experimental plot on 31st October 2018.

3.12 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 germplasm 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.

3.12.1 Gap filling

Gap filling was done twice. The first gap filling was done on 7th November 2018 just after 7 days of first transplanting and the 2nd one done on 11th November 2018, which was 11 days of first transplanting.

3.12.2 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.

3.12.3 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.

3.13 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.

3.14 Data Recording

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

3.14.1 Days to 50% flowering: Number of days required from 50% flowering shown in the plant.

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3.14.2 Plant height at 1ˢᵗharvest (cm): Measured from the soil surface to the tip of the tallest branch at first.

3.14.3 Primary branch no. at 1ˢᵗ harvest: All the primary branch were counted at first harvesting period in each of five selected plants and their average value was taken number of branches per plant.

3.14.4 Secondary branch no. at 1ˢᵗharvest: All the secondary branches were counted at first harvesting period in each of five selected plants and their average value was taken number of branches per plant.

3.14.5 Plant height at last harvest (cm): Measured from the soil surface to the tip of the tallest branch at last harvest.

3.14.6 Primary branch no. at last harvest: All the primary and secondary branches were counted at final harvesting period in each of five selected plants and their average value was taken number of branches per plant.

3.14.7 Secondary branch no. at last harvest: All the primary and secondary branches were counted at final harvesting period in each of five selected plants and their average value was taken number of branches per plant.

3.14.8 Leaf 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

3.14.9 Leaf breadth (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.

3.14.10 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.

3.14.11 Fruit diameter (cm): Fruit breadth was measured through the equatorial part of same five representative fruits by caliper and their average was taken as fruit breadth.

3.14.12 No. of fruits: Total number of fruits harvested at different dates from five selected plants was counted.

3.14.13 Weight of fruits (kg): Fruit weight in gram was calculated from the five representative fruits.

3.14.14 Av. fruit weight (gm): Average fruit weight in gram was calculated from the five representative fruits.

3.14.15 Yield (t/ha): Yield per hectare was calculated from the yield obtained in each of the experimental unit and was expressed in tones.

3.14.16 No. of infected fruits: Total number of infected fruits harvested at different dates from the five selected plants was counted.

3.14.17 Weight of infected fruits (kg): Infected fruit weight in gram was calculated from the five representative fruits.

3.15 Statistical analysis

Mean data for each character was subjected to multivariate analysis methods viz. principal component analysis (PCA), principal coordinate analysis (PCO), canonical veriate analysis (CVA) and cluster analysis (CLSA) using "R" software and Microsoft Excel 2000 computer software.

3.15.1 Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores obtained for the first component and succeeding component with latent roots greater than unity (Jager*et al.*, 1983).

3.15.2 Principal co-ordinate analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Though the use of all dimensions of P it gives the minimum distances between each pair of the N points using similarity matrix (Digby*et al.*, 1989). Inter distances between germplasm were measured by Principal coordinate analysis

3.15.3 Canonical variate analysis (CVA)

The CVA complementary to D^2-statistic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively are derived. Canonical vector analysis finds linear combination of original variability that maximize the ratio of between groups to within groups 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 maximize the ratio of among groups to within group variations.

3.15.4 Cluster analysis (CLSA)

Cluster analysis was performed by D^2 analysis (originally outlined by Mahalanobis, 1928; 1936 and extended by Rao, 1952), which divides the germplasm based on the data set into more or less homogeneous groups. D^2 is the sum of squares of differences between any two populations for each of the uncorrelated variables (obtained by transforming correlated variables through Pivotal condensation method). Clustering was done using non-hierarchical and hierarchical classification. D^2 statistic is defined by

$$D^2 x = \Sigma\Sigma \ (\psi^{ij}) \ d_i \ d_j$$
$$\qquad ii$$

Where,

X = Number of metric traits in point

P = Number of populations or germplasm

ψ^{ij} = the matrix reciprocal to the common dispersion matrix

$d_i d_j$ = the differences between the mean values of the two germplasm for the ith and j^{th} characters respectively.

In simpler form D^2 statistic is defined by the formula

$$D^2 = \overset{x}{\underset{i}{\Sigma}} \ d^2 I = \underset{i}{\Sigma} \ (y^j i - y^k j) \qquad (j \neq k)$$

Where,

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

X = number of characters

Superscripts j and k to y = a pair of any two germplasm

3.15.5 Computation of average intra-cluster distances

The average intra cluster distance for each cluster was calculated by taking all possible D^2 values within the members of a cluster obtained from PCO. The formula used to measure the average intra cluster distance was:

Intra-cluster distance = $\Sigma D^2/n$

Where,

$\Sigma D^2/n$ is the sum of distances between all possible combinations (n) of the germplasm included in a cluster.

3.15.6 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 = $\quad \dfrac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

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.

3.15.7 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse germplasm for hybridization purposes. The germplasm grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by the largest statistical distance (D^2) express the maximum divergence among the germplasm included into these different clusters.

Singh and Chaudhury (1985) stated the following points should be considered while selecting germplasm for hybridization

Choice of cluster from which germplasm are selected for use as parent(s)
Selection of particular genotype(s) from the selected cluster(s)
Relative contribution of the characters to the total divergence
Other important characters of the germplasm (*Per Se* performance)

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CHAPTER IV

RESULTS AND DISCUSSION

Performance of 40 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 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. Morphological character 2. Genetic parameter 3. Multivariate analysis.

MORPHOLOGICAL CHARACTER

4.1.1 Spine present in leaf

The genotypes exhibited high, low and no Spine present in leaf (Table 3). Among the genotypes studied genotypes SM 399, SM 391showed high spine, SM 399 low spine and rest of all genotype showed no spine present on leaf (Table 3).

Table 3. Characterization of 40 brinjal genotypes as per leaf characters

Genotype	Leaf spine	Leaf Stalk spine	Leaf blade color	Leaf Stalk color	Midrib color
SM 323	None	None	Purple green	Purple green	Purple
SM 343	None	None	Light green	Purple green	Purple green
SM 351	None	None	Green	Green	Green
SM 358	None	None	Green	Green	Green
SM 359	High	High	Purple green	Purple green	Deep purple
SM 361	None	None	Purple green	Purple green	Deep purple green
SM 362	None	None	Light green	Purple green	Deep purple
SM 363	None	None	Purple green	Purple green	Purple
SM 364	None	None	Deep green	Light purple green	Purple green
SM 365	None	None	Deep green	Deep green	Light green
SM 366	None	None	Light purple green	Light purple green	Deep purple
SM 367	None	None	Purple green	Purple green	Deep purple
SM 369	None	None	Green	Purple green	Purple green
SM 370	None	None	Deep green	Deep green	Green
SM 371	None	None	Green	Purple green	Light purple green
SM 373	None	None	Purple green	Deep purple green	Deep purple
SM 375	None	None	Purple green	Green	Purple
SM 376	None	None	Purple green	Purple green	Purple
SM 377	None	None	Purple green	Purple green	Purple
SM 378	None	None	Light green	Purple green	Deep green
SM 380	None	None	Purple green	Purple green	Purple
SM 381	None	None	Purple green	Purple green	Light purple
SM 382	None	None	Green	Light green	Light purple
SM 383	None	None	Green	Purple green	Light purple

SM 385	None	None	Deep green	Purple green	Light purple
SM 386	None	None	Green	Purple green	Light green
SM 387	None	None	Green	Purple green	Green
SM 388	None	None	Green	Purple green	Green
SM 391	High	High	Green	Light green	Deep green
SM 393	None	None	Purple green	Purple green	Light green
SM 394	None	None	Purple green	Purple green	Light purple
SM 395	None	Medium	Purple green	Green	Light green
SM 398	None	Low	Green	Green	Purple
SM 399	Low	High	Purple green	Green	Deep green
BARI Begun-1	None	None	Green	Light purple green	Purple
BARI Begun-4	None	None	Green	Deep green	Light purple
BARI Begun-5	None	None	Deep green	Purple	Deep purple
BARI Begun-6	None	None	Green	Purple green	Purple green
BARI Begun-7	None	None	Green	Purple green	Purple
BARI Begun -8	None	None	Green	Green	Purple

4.1.2 Spine present in leaf stalk

The genotypes exhibited high, medium, low and no Spine present in leafstalk (Table 3). Among the genotypes studied genotypes SM 359 and SM 391 showed high spine SM395 medium spine SM 398 low spine and rest of all genotype showed no spine present on leafstalk (Table 3).

4.1.3 Leaf blade color

Among the genotypes SM 323, SM 359, SM 361, SM 363, SM 367, SM 373, SM 375, SM 376, SM 377, SM 380, SM 381, SM 393, SM 394, SM 395, SM 399 produced purple green SM 343, SM 362 produce light green SM 366 produce light purple SM 364, SM 365, SM 370, SM 385 and BARI Begun-5 produce deep green and the rest of the genotypes produced purple green colored leaf (Table 3).

4.1.4 Leaf stalk color

Among the genotypes SM 351, SM 358, SM 375, SM 395, SM 398, SM 399 produced green SM 366, SM 364 produce light purple green SM-366, SM-370, BARI Begun-4produce deep green SM 378 produce deep purple green SM 382, SM 391 produce light green BARI begun-5 and the rest of the genotypes produced purple green colored leaf (Table 3).

4.1.5 Midrib color of leaf

Among the genotypes SM 343, SM 364, SM 369, BARI Begun-6 produced purple green, SM 351, SM 358, SM 370, SM-387, SM-388 produce green, SM-365 produce light green,SM371produce light purple green, SM 361 produce deep purple green, SM 359, SM 362, SM 366, SM 367, SM 373, BARI Begun-5produce deep purple, SM 381, SM 382,SM 383, SM 385, SM 386, SM394, BARI Begun-5produce light purple and the rest of the genotypes produced purple colored midrib presented on leaf (Table 3)

Table 4. Characterization of 40 brinjal genotypes as per stem character

Genotype	Spine in stem	Stem color	Spine in calyx
SM323	Low	Purple green	None
SM 343	None	Light green	Medium
SM 351	Low	Green	Low
SM 358	Low	Green	Low
SM 359	High	Green purple	High
SM 361	None	Purple green	Low
SM 362	Low	Light green	Medium
SM 363	Medium	Purple green	Low
SM 364	Low	Deep green	None
SM 365	Low	Green	Low
SM 366	Low	Green purple	Low
SM 367	None	Light purple	Low
SM 369	Low	Green	Low
SM 370	None	Green	None
SM 371	Low	Green	Medium
SM 373	None	Light green	Medium
SM 375	Low	Green purple	Low
SM 376	None	Green	Low
SM 377	Medium	Green	Low
SM 378	None	Deep green	None
SM 380	Medium	Green	Medium
SM 381	None	Green	Low
SM 382	Low	Purple green	Medium
SM 383	Low	Light purple green	None
SM 385	Low	Green	Low
SM 386	Low	Green	None
SM 387	Medium	Green	Medium
SM 388	None	Purple green	Medium
SM 391	High	Green	High
SM 393	Low	Green	Low
SM 394	Medium	Green	Medium
SM 395	Low	Green	Medium
SM 398	Low	Purple green	Low
SM 399	High	Green	High
BARI Begun-1	Medium	Purple	Medium
BARI Begun-4	None	Purple green	None
BARI Begun-5	Medium	Purple	Medium
BARI Begun-6	Low	Green	Medium
BARI Begun-7	Low	Purple green	None
BARI Begun -8	None	Light green	Low

4.1.6 Spine present in stem

The genotypes exhibited high, low and no Spine present on stem (Table 4). Among the genotypes studied genotypes SM 359, SM 391, SM 399 showed high spine SM 343, SM 363, SM 377, SM 380, SM 387, SM 394,BARI Begun-1,BARI Begun-5 produce medium

spine SM 361, SM 367, SM 370, SM 373, SM 376, SM 378, SM 381, SM 388, BARI Begun-4, BARI Begun-8 showed no spine and rest of all genotype showed low spine present on stem (Table 4).

4.1.7 Stem color

Among the genotypes SM 323, SM 359, SM 361, SM 363, SM 366, SM 375, SM 382, SM 388, SM 398,BARI Begun-4,BARI Begun-7produced purple green SM 343, SM 362, SM 373,BARI Begun-8 produce light green SM 364, SM 378 produce deep green SM 364 light purple SM 383 light purple green BARI Begun-1, BARI Begun-5 produce purple and the rest of the genotypes produced green colored stem (Table 4).

4.1.8 Spine present in calyx

The genotypes exhibited high, low,medium and no Spine present in calyx of brinjal fruit (Table 4). Among the genotypes studied genotypes SM 323, SM 378, SM 383, SM 386, BARI Begun-4,BARI Begun-7 showed no spine SM343, SM 362, SM 371, SM 373, SM 380, SM 382, SM 387, SM 388, SM 394, SM 395, BARI Begun-1,BARI Begun-5andBARI Begun-6 produce medium spine SM 359, SM 391, SM-399produce high spine and rest of all genotype showed low spine present in calyx of brinjal fruit (Table 4).

Table 5.Characterization of 40 brinjal genotypes as per fruit character

Genotype	Color	Shape
SM323	Deep purple	Elongate
SM 343	Deep purple	Elongate
SM 351	Deep green with white stripe	Oval
SM 358	Light purple	Oblong
SM 359	Purple	Elongate
SM 361	Deep purple	Oblong
SM 362	Deep purple	Oval
SM 363	Deep purple	Cylindrical
SM 364	Purple	Round
SM 365	Purple	Elongate
SM 366	Deep purple	Oval
SM 367	Deep purple	Oval
SM 369	Light green	Oval
SM 370	Purple	Oval
SM 371	Blackish purple	Round
SM 373	Deep purple	Cylindrical
SM 375	Purple	Elongate
SM 376	Purple	Elongate
SM 377	Purple	Elongate
SM 378	Deep purple	Elongate
SM 380	Purple	Oblong
SM 381	Purple	Elongate
SM 382	Deep purple	Cylindrical
SM 383	Deep purple	Cylindrical

SM 385	Light green	Oval
SM 386	Light green	Elongate
SM 387	Light green with white spot	Oval
SM 388	Light green with white spot	Oval
SM 391	White	Round
SM 393	Light green with white spot	Oval
SM 394	Blackish purple	Cylindrical
SM 395	Deep purple	Oval
SM 398	Light green	Round
SM 399	White	Elongate
BARI Begun-1	Majenta purple	Elongate
BARI Begun-4	Black purple	Elongate
BARI Begun-5	Black purple	Round
BARI Begun-6	Light green	Oval
BARI Begun-7	Black purple	Cylindrical
BARI Begun -8	Purple	Cylindrical

4.1.9 Fruits color

Fruit color is one of the important traits for consumer preference in brinjal marketing. Generally a lot of variations in fruit color were found in the present study and that could be classified in distinct groups: deep green with white stripe, white, deep green with white spot, purple, light purple, light green, blackish purple, majenta purple, black purple, deep purple. The genotype SM 351 produce deep green with white stripe,SM391, SM 399 produce white, SM 387, SM 388, SM 393 produce deep green with white spot SM 358producelight purple SM 359, SM 364, SM 365, SM 370, SM 375, SM 376, SM 377, SM 380, SM 381, BARI Begun -8, produce purple SM 369, SM 385, SM 386 and BARI Begun -6producelight green, SM 371, BARI Begun -7 blackish purple BARI Begun -1 produce majenta purple BARI Begun -4,BARI Begun -5 produce black purple and rest of the genotype produce deep purple color fruit (Table 5). This variation offered a good scope for breeding consumer preference attributes.

4.1.10 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 fourty genotypes elongated, oval, cylindrical, round and oblong shaped brinjal were observed. The genotypes SM 351, SM 362, SM 366, SM 367, SM 369, SM 370, SM 385, SM 387, SM 388, SM 393, BARI Begun -6 produce oval SM 363, SM 373, SM 382, SM383 produce cylindrical SM 364, SM 371, BARI Begun -5 produce round SM358, SM 361, SM 380, BARI Begun -7, BARI Begun -8 produce oblong and rest of the genotype produce elongated shaped fruits (Table 5).

Table 6.Characterization of 40 brinjal genotypes as per flower and plant character

Genotype	Flower size	Growth at later stage
SM323	Medium	Medium
SM 343	Small	Small
SM 351	Medium	Medium
SM 358	Medium	Medium
SM 359	Medium	Medium
SM 361	Large	Large
SM 362	Large	Large
SM 363	Medium	Medium
SM 364	Medium	Medium
SM 365	Small	Small
SM 366	Medium	Medium
SM 367	Medium	Medium
SM 369	Medium	Medium
SM 370	Small	Small
SM 371	Large	Large
SM 373	Medium	Medium
SM 375	Medium	Medium
SM 376	Medium	Medium
SM 377	Small	Small
SM 378	Large	Large
SM 380	Small	Small
SM 381	Medium	Medium
SM 382	Small	Small
SM 383	Medium	Medium
SM 385	Medium	Medium
SM 386	Small	Small
SM 387	Medium	Medium
SM 388	Large	Large
SM 391	Small	Small
SM 393	Medium	Medium
SM 394	Small	Small
SM 395	Medium	Medium
SM 398	Large	Large
SM 399	Small	Small
BARI Begun-1	Small	Small
BARI Begun-4	Small	Small
BARI Begun-5	Medium	Medium
BARI Begun-6	Medium	Medium
BARI Begun-7	Small	Small
BARI Begun -8	Medium	Medium

4.1.11 Flower size

Various types of brinjal flower were found from the fourty genotypes small, medium and large brinjal flower were observed. The genotypes SM 361, SM 362, SM 371, SM 378, SM 388, SM 398producelargeSM 351, SM 343, SM 365, SM 370, SM 377, SM 380, SM

382, SM 386, SM 391, SM 394, SM 399, BARI Begun -1, BARI Begun -4, BARI Begun - 7 produce small and rest of the genotype produce medium sized flower (Table 6).

4.1.12 Growth at later stage

From the fourty genotypes good, medium and weak brinjal plant size were observed on growth at later stage. The genotypes SM 356, SM 359, SM 361, SM362, SM363, SM 371, SM 375, SM 387, SM 393, SM 394 produce good SM 364, SM 367, SM 377, SM 382, SM 386, SM 388, SM 391 produce weak and rest of the genotype produce medium size brinjal plant growth at later stage (Table 6).

4.2 GENETIC PARAMETERS

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

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 7). Significant variation was observed among the genotypes for days to 50% flowering of brinjal (Table 7). It ranged from 92.00 to 107.33 days. Minimum days required in genotypes SM 367 (92.00 days) and SM 367 (92.00 days) followed by SM 366 (96.00 days), SM 369 (96.00 days), SM 375 (97.00 days) while the maximum days required by SM 365 (115.33 days). As per frequency distribution 9 (22.5%) genotypes had early flowering (92.00-97.67days), 23 (57.5%) genotypes had medium (98.00-103.33 days) and 8 (20.0%) genotypes had late (107.33-115.33 days) days to 50% flowering (Table 8).

Table 7. Quantitative characteristics of 40 brinjal genotypes as per days to 50% flowering

Genotype	Days to 50% flowering
SM323	100.67 a
SM 343	100.33 b
SM 351	102.00 b
SM 358	102.67 b
SM 359	97.33 b
SM 361	101.67 b
SM 362	103.33 b
SM 363	102.33 b
SM 364	98.00 c
SM 365	115.33 c
SM 366	96.00 cd
SM 367	92.00 cd
SM 369	96.00 c-e
SM 370	97.00 c-e
SM 371	98.33 c-e
SM 373	102.00 c-e
SM 375	97.00 c-e

SM 376	99.33 c-f
SM 377	100.00 c-f
SM 378	92.00 c-g
SM 380	102.33 c-g
SM 381	103.00 c-h
SM 382	97.67 c-h
SM 383	103.33 c-h
SM 385	101.33 c-i
SM 386	100.67 c-i
SM 387	97.00 d-f
SM 388	101.67 e-j
SM 391	100.33 f-k
SM 393	110.00 g-k
SM 394	101.33 h-k
SM 395	108.00 h-k
SM 398	110.00 i-k
SM 399	108.33 jk
BARI Begun-4	110.00 jk
BARI Begun-1	108.33 jk
BARI Begun-5	107.33 k
BARI Begun-6	98.67 k
BARI Begun-7	102.00 l
BARI Begun-8	100.67 l
C.V. (%)	1.89
Level of significance	**

Means in a column followed by the same letters are not significantly different at 1 % level by DMRT

Table 8 Frequency distribution of quantitative characteristics of 40 brinjal genotypes as per days to 50% flowering

Characters	Class	Number of accession	Frequency (%)	Range
Days to 50% flowering	Early flowering= < 98days	9	22.5	92.00-97.67days
	Medium flowering= 98-105 days	23	57.5	98.00-103.33 days
	Late flowering= >105days	8	20.0	107.33-115.33 days

4.2.2 Plant height at 1st harvest

Significant variation was observed among the genotypes for plant height at 1st harvestofbrinjal (Table 9). It ranged from 49.33 to 71.33 cm. Minimum height showed in genotypes SM 323 (49.33 cm) and SM 343 (52.33cm) followed by SM 351 (52.67 cm), SM 358 (54.33cm), SM 359 (54.33cm) while the maximum days required by BARI Begun-8(71.33 cm). As per frequency distribution 9 (22.5%) genotypes had small height (49.33-56.67cm), 20 (50.0%) genotypes had medium height (57.00-64.33cm) and 11 (27.5%) genotypes had long height (66.00-71.33cm) at first harvest (Table 10).

4.2.3 Primary branch no. at 1st harvest: Significant variation was observed among the genotypes for primary branch no. at 1st harvest of brinjal (Table 9). It ranged from 2.00 to 3.67. Minimum primary branch observed in genotypes BARI Begun-1 (2.00 no.) and BARI Begun-8 (2.00 no.) followed BARI Begun-7 (2.00 no.), BARI Begun-6 (2.33 no.), BARI Begun-5 (2.33 no.) while the maximum no. of primary branch produce by SM 323(3.67 no.). As per frequency distribution 0 (00.00%) genotypes had lower no. of primary branch (0.00-0.00 no.), 31 (77.50%) genotypes had moderate no. of primary branch (2.00-3.00 no.) and 9(22.50%) genotypes had higher no. primary of branch (3.33-3.67 no.) at first harvest (Table 10).

4.2.4 Secondary branch no. at 1st harvest: Significant variation was observed among the genotypes for secondary branch at 1st harvest of brinjal (Table 9). It ranged from 4.33 to 6.33. Minimum Secondary branch no. observed in genotypes and SM 323 (4.33 no.) followed by SM 376 (4.33 no.) while the maximum secondary branch no. at 1st harvest produce by SM 343 and BARI Begun-1 (6.33 no.). As per frequency distribution 11 (18.18%) genotypes had produce (4.33-4.67 no.), 25(40.90%) genotypes had moderate (5.00-6.00 no.) and 4(40.90%) genotypes had produce highest no. of secondary branch(6.33-6.33 no.) to first harvest (Table 10).

Table 9. Quantitative characteristics of 40 brinjal genotypes as per plant height and branch no.

Genotype	Plant height at 1st harvest	Primary branch at 1st harvest	Secondary branch at 1st harvest
SM323	54.33 i-k	3.67 a	4.33 d
SM 343	58.67 f-j	3.67 a	6.33 a
SM 351	57.67 f-j	3.67 a	5.00 b-d
SM 358	60.00 e-i	3.67 a	5.67 a-c
SM 359	60.33 d-i	3.67 a	4.67 cd
SM 361	71.33 a	3.33 ab	6.00 ab
SM 362	52.33 jk	3.33 ab	5.00 b-d
SM 363	67.33 a-d	3.33 ab	6.00 ab
SM 364	60.00 e-i	3.33 ab	6.00 ab
SM 365	56.67 g-j	3.00 a-c	6.33 a
SM 366	61.00 c-i	3.00 a-c	5.67 a-c
SM 367	61.33 c-i	3.00 a-c	4.33 d
SM 369	62.67 b-h	3.00 a-c	5.33 a-d
SM 370	56.67 g-j	3.00 a-c	5.67 a-c
SM 371	66.00 a-e	2.67 b-d	5.00 b-d
SM 373	55.67 h-k	2.67 b-d	4.67 cd
SM 375	66.00 a-e	2.67 b-d	5.33 a-d
SM 376	59.33 e-j	2.67 b-d	4.33 d
SM 377	60.00 e-i	2.67 b-d	5.33 a-d

SM 378	52.67 jk	2.67 b-d	5.00 b-d
SM 380	71.00 a	2.67 b-d	5.33 a-d
SM 381	57.67 f-j	2.67 b-d	6 .00ab
SM 382	71.33 a	2.67 b-d	5.33 a-d
SM 383	57.00 g-j	2.33 cd	4.33 d
SM 385	60.33 d-i	2.33 cd	5.33 a-d
SM 386	55.67 h-k	2.33 cd	4.67 cd
SM 387	67.67 a-c	2.33 cd	4.67 cd
SM 388	60.00 e-i	2.33 cd	4.33 d
SM 391	66.33 a-e	2.33 cd	4.67 cd
SM 393	57.00 g-j	2.33 cd	5.33 a-d
SM 394	58.67 f-j	2.33 cd	5.67 a-c
SM 395	54.33 i-k	2.33 cd	4.67 cd
SM 398	64.33 a-f	2.33 cd	6.33 a
SM 399	49.33 k	2.33 cd	5.33 a-d
BARI Begun-1	63.00 b-g	2.33 cd	6.33 a
BARI Begun-4	57.67 f-j	2.33 cd	6.00 ab
BARI Begun-5	59.33 e-j	2.33 cd	5.67 a-c
BARI Begun-6	67.67 a-c	2.00 d	5.67 a-c
BARI Begun-7	70.33 a	2.00 d	5.33 a-d
BARI Begun -8	69.00 ab	2.00 d	5 b-d
C.V. (%)	7.11	19.78	11.96
Level of significance	**	**	**

Means in a column followed by the same letters are not significantly different at 1 % level   by DMRT

Table 10. Frequency distribution of quantitative characteristics of 40 brinjal genotypes as per plant height and branch no. at 1st harvest

Characters	Class	Number of accession	Frequency (%)	Range
Plant height at 1st harvest	Small height= < 57 cm	9	22.5	49.33-56.67cm
	Medium height = 57-65 cm	20	50.0	57.00-64.33cm
	Long height = >65 cm	11	27.5	66.00-71.33cm
Primary branch no. at 1st harvest	Lowest no. = <2 no.	0	00.00	0.00-0.00 no.
	Moderateno.= 2-3 no.	31	77.50	2.00-3.00 no.
	Higher no.= >3 no.	9	22.50	3.33-3.67 no.
secondary branch no. at 1st harvest	Lowest no. = <5 no.	11	18.18	4.33-4.67 no.
	Moderate no.= 5-6 no.	25	40.90	5.00-6.00 no.
	Higher no= >6 no.	4	40.90	6.33-6.33 no.

4.2.5 Plant height at last harvest (cm)

Significant variation was observed among the genotypes for Plant height at last harvest of brinjal (Table 11). It ranged from 59.33 to 120.67 cm. Minimum height showed in genotypes BARI Begun-8 (59.33 cm) and BARI Begun-6 (70.00) followed by BARI Begun-5(78.00 cm), BARI Begun-1(80.00cm) while the maximum height required by SM

361 (120.67). As per frequency distribution 13(32.5%) genotypes had small height (59.33-84.33 cm), 19 (47.50%) genotypes had medium height (85.00-94.67 cm) and 8(20.00%) genotypes had tall height (96.00-120.67 cm) at last harvest (Table 12).

4.2.6 Primary branch no. at last harvest

Significant variation was observed among the genotypes for Primary branch no. at last harvest of brinjal (Table 11). It ranged from 2.00 to 3.67. Minimum primary branch observed in genotypes BARI Begun-7(2.00 no.) and BARI Begun-8 (2.00 no.) followed by BARI Begun-6(2.00 no.), BARI Begun-1(2.00 cm) while the maximum no. of primary branch produce by SM 323, SM 343, SM 351, SM 358, SM 359.As per frequency distribution 0 (00.00%) genotypes had lower no. of Primary branch (0.00-0.00 no.), 31 (77.50%) genotypes had moderate no. of primary branch (2.00-3.00 no.) and 9 (22.50%) genotypes had height no. of primary branch (3.33-3.67 no.) at last harvest (Table 12).

4.2.7 Secondary branch no. at last harvest

Significant variation was observed among the genotypes for secondary branch no.at last harvest of brinjal (Table 11). It ranged from 4.33 to 6.33. Minimum secondary branch no. produce in genotypes BARI Begun-7 (4.67 no.) and BARI Begun-8 (4.67no.) followed by BARI Begun-5 (5.00no.), BARI Begun-4(5.00 no.), BARI Begun-1 (5.00 no.) while the maximum no. of secondary branch by SM 323 (8.00 no.). As per frequency distribution 11 (27.50%) genotypes had lower no. of Primary branch (4.60-5.67 no.), 27(67.50%) genotypes had medium no. of Primary branch (6.00-7.00 no.) and 2(5.00%) genotypes had produce no. of primary branch (7.33-8.00 no.) to last harvest (Table 12)

Table 11.Quantitative characteristics of 40 brinjal genotypes as per plant height and branch no.

Genotype	Plant height at last harvest	Primary branch at last harvest	Secondary branch at last harvest
SM323	120.00 a	3.67 a	8.00 a
SM 343	116.67 a	3.67 a	7.33 ab
SM 351	109.67 ab	3.67 a	7.00 a-c
SM 358	109.33 b	3.67 a	7.00 a
SM 359	100.33 b	3.67 a	7.00 a
SM 361	120.67 c	3.33 ab	7.00 a
SM 362	97.67 cd	3.33 ab	7.00 a
SM 363	96.00 cde	3.33 ab	7.00 a
SM 364	94.67 c-f	3.33 ab	7.00 a
SM 365	92.00 d-g	3.00 a-c	6.67 b-d
SM 366	92.00 d-g	3.00 a-c	6.67 b-d
SM 367	92.00 d-g	3.00 a-c	6.67 b-d
SM 369	91.33 d-h	2.67 b-d	6.33 b-e
SM 370	91.00 d-i	2.67 b-d	6.33 b-e

SM 371	91.00 d-i	2.67 b-d	6.33 b-e
SM 373	90.67 d-i	2.67 b-d	6.00 c-f
SM 375	90.00 e-i	2.67 b-d	6.00 c
SM 376	89.33 e-i	2.67 b-d	6.00 c
SM 377	87.67 f-j	2.67 b-d	6.00 c
SM 378	87.00 g-k	2.67 b-d	6.00 c
SM 380	86.67 g-k	2.67 b-d	6.00 c
SM 381	86.00 g-k	2.67 b-d	6.00 c
SM 382	85.67 g-k	2.67 b-d	6.00 c
SM 383	85.33 g-l	2.33 cd	6.00 c
SM 385	85.33 g-l	2.33 cd	6.00 c
SM 386	85.00 g-l	2.33 cd	6.00 c
SM 387	85.00 g-l	2.33 cd	6.00 c
SM 388	84.33 h-l	2.33 cd	6.00 c
SM 391	83.67 i-l	2.33 cd	6.00 c
SM 393	81.67 j-l	2.33 cd	5.67 d-g
SM 394	81.00 j-l	2.33 cd	5.67 d-g
SM 395	81.00 j	2.33 cd	5.67 d-g
SM 398	81.00 j	2.33 cd	5.33 e-g
SM 399	81.00 j	2.33 cd	5.33 e-g
BARI Begun-1	80.00 kl	2.00d	5.33 eg-
BARI Begun-4	80.00 kl	2.33cd	5.00 fg
BARI Begun-5	78.00 l	2.33cd	5.00 fg
BARI Begun-6	70.00 m	2.00 d	5.00 fg
BARI Begun-7	68.67 m	2.00 d	4.67 g
BARI Begun -8	59.33 n	2.00 d	4.67 g
C.V. (%)	5.25	19.26	12.54
Level of significance	**	**	**

Means in a column followed by the same letters are not significantly different at 1 % level by DMRT

Table 12.Frequency distribution of quantitative characteristics of 40 brinjal genotypes as per plant height and branch no. at last harvest

Characters	Class	Number of accession	Frequency (%)	Range
Plant height at last harvest	Small height= < 85 cm	13	32.5	59.33-84.33cm
	Medium height = 85-95 cm	19	47.5	85.00-94.67cm
	Long height = >95 cm	08	20.0	96.00-120.67cm
Primary branch no. at last harvest	Lower no. = <2 no.	0	00.00	0.00-0.00 no.
	Moderate no.= 2-3 no.	31	77.50	2.00-3.00 no.
	Higher no= >3 no.	9	22.50	3.33-3.67 no.
Secondary branch no. at last harvest	Lower no. = <6	11	27.50	4.60-5.67 no.
	Moderate no.= 6-7	27	67.50	6.00-7.00 no.
	Higher no= >7	2	5.00	7.33-8.00 no.

4.2.8 Leaf length (cm)

Significant variation was observed among the genotypes for leaf length of brinjal (Table 13). It ranged from 8.30 to 22.16. Minimum leaf length observed in genotypes SM 323 (8.30 cm) and SM 343 (11.46 cm) followed by SM 351(11.96 cm), SM 358(12.16 cm) while the maximum leaf length observed in BARI Begun-7(22.16). As per frequency distribution 7 (17.50%) genotypes had shorter length (8.36-12.63 cm.), 18 (45.00%) genotypes had medium length (13.03-14.96 cm.) and 15 (37.50%) genotypes had longer length (15.20-22.16cm)of leaf (Table 14).

4.2.9 Leaf breadth (cm)

Significant variation was observed among the genotypes for leaf breadth of brinjal (Table 13). It ranged from 5.7 to 13.4. Minimum leaf breadth observed in genotypes SM 365 (5.17 cm) and SM 399 (6.47 cm) followed by SM 391 (7.13 cm), SM 371 (7.27 cm) , SM 323 (7.23 cm) while the leaf breadth observed by SM 398 (13.4 cm). As per frequency distribution 13 (32.50%) genotypes hadhighleaf breadth (5.16-7.87 cm.), 20 (50.00%) genotypes had mediumleaf breadth (8.00-9.80 cm.) and 7 (17.50%) genotypes had longleaf breadth (10.06-13.40 cm) of leaf (Table 14).

Table 13. Quantitative characteristics of 40 brinjal genotypes as per leaf length and breadth

Genotype	Leaf length	Leaf breadth
SM323	14.3 h-k	7.37 o-r
SM 343	12.2 m-o	7.4 o-r
SM 351	15.93 c-g	8 i-q
SM 358	15.2 d-i	10.6 b-d
SM 359	13.37 j-n	7.8 k-r
SM 361	14.97 e-j	8.6 f-p
SM 362	22.17 a	13.1 a
SM 363	18.73 b	11.47 b
SM 364	11.47 o	7.53 n-r
SM 365	8.37 p	5.17 s
SM 366	14.53 f-k	9.1 e-k
SM 367	13.57 j-n	9 e-l
SM 369	13.47 j-n	8.57 f-p
SM 370	12.57 l-o	8.9 e-n
SM 371	11.97 no	7.27 p-r
SM 373	16.37 c-e	10.07 c-e
SM 375	15.2 d-i	8.67 f-o
SM 376	15.67 d-h	9.27 d-i
SM 377	12.63 l-o	7.87 j-q
SM 378	13.03 k-o	7.6 m-r
SM 380	16.77 cd	9.53 d-g
SM 381	13.27 k-n	7.63 l-r
SM 382	18.6 b	11.27 bc
SM 383	15.53 d-h	9.67 d-f
SM 385	16.1 c-f	9.5 d-h
SM 386	14.43 g-k	9.2 e-j
SM 387	17.53 bc	10.27 b-e
SM 388	14.4 g-k	9.8 d-f
SM 391	14.3 h-k	7.13 qr
SM 393	16.33 c-e	9.03 e-k
SM 394	13.43 j-n	7.63 l-r
SM 395	15.33 d-h	8.97 e-m
SM 398	21.87 a	13.4 a
SM 399	12.17 m-o	6.47 rs
BARI Begun-1	14.53 f-k	8.67
BARI Begun-4	13.47 j-n	9.33 d-i
BARI Begun-5	14.27 h-k	8.13 h-q
BARI Begun-6	13.67 i-m	7.87 j-q
BARI Begun-7	14.4 g-k	9.03 e-k
BARI Begun -8	14.13 h-l	8.23 g-q
C.V. (%)	14.75	9.60
Level of significance	**	**

Table14. Frequency distribution Quantitative characteristics of 40 brinjal genotypes as per leaf length and breadth

Characters	Class	Number of accession	Frequency (%)	Range
Leaf length (cm)	Shorterlength = <13 cm	7	17.50	8.36-12.63 cm
	Medium length =13-15 cm	18	45.00	13.03-14.96 cm
	Longerlength = >15 cm	15	37.50	15.20-22.16cm
Leaf breadth(cm)	Shorter breadth= <8	13	32.50	5.16-7.87 cm
	Medium breadth=8-10 cm	20	50.00	8.00-9.80 cm
	Longer breadth = >10 cm	7	17.50	10.06-13.40 cm

4.2.10 Fruit length (cm)

Significant variation was observed among the genotypes for fruit length of brinjal (Table 15). It ranged from 9.00 to 28.00. Minimum fruit length of brinjal observed in genotypes SM 393 (9.00 cm) and BARI Begun-8 (9.00 cm) followed by SM 370 (10.00 cm) SM 398 (11.00cm) while the maximum fruit length observed by SM 359 (28.00). As per frequency distribution 14 (35.00%) genotypes had lowest fruit length (9.00-14.00 cm.), 17 (42.50%) genotypes had moderate fruit length (15.33-24.00 cm.) and 9 (22.50%) genotypes had lowest fruit length (24.33-28.00cm) (Table 16).

4.2.11 Fruit diameter(cm)

Significant variation was observed among the genotypes for fruit diameter of brinjal (Table 15). It ranged from 2.50 to 10.67. Minimum fruit diameter observed in genotypes BARI Begun-8 (2.50 cm) and SM 380 (2.57 cm) followed by SM 381 (2.57 cm) , SM 363 (2.83 cm) , BARI Begun-7(3.20 cm) while the maximum fruit diameter observed in BARI Begun-1(10.67cm). As per frequency distribution 15 (37.50%) genotypes had shorter breadth (2.5-4.47 cm), 15 (37.50%) genotypes had moderate breadth (4.50-6.53 cm.) and 10 (25.00%) genotypes had longer breadth (7.1-10.66 cm) (Table 16).

Table 15. Quantitative characteristics of 40 brinjal genotypes as per fruit length and diameter

Genotype	Fruit length	Fruit diameter
SM323	16.33 l	3.5 fg
SM 343	19 j	3.5 fg
SM 351	16 lm	6.17 b-g
SM 358	24.33 d	4.33 e-g
SM 359	28 a	6.33 b-g
SM 361	23.33 e	9.07 ab
SM 362	12 q	6.5 a-g
SM 363	27 b	2.83 g
SM 364	14 o	8.7 a-c
SM 365	25.67 c	7.1 a-f
SM 366	11.67 qr	7.2 a-f
SM 367	12 q	5.4 b-g

SM 369	19.67 i	6.5 a-g
SM 370	10 t	4.83 c-g
SM 371	11.33 rs	5.5 b-g
SM 373	12 q	4.47 d-g
SM 375	23.33 e	3.73 fg
SM 376	20.67 g	6.2 b-g
SM 377	17.33 k	3.87 fg
SM 378	24 d	3.4 fg
SM 380	21.67 f	2.57 g
SM 381	20.33 gh	2.57 g
SM 382	26.67 b	4.17 efg
SM 383	27.67 a	6.53 a-g
SM 385	26 c	7.2 a-f
SM 386	15.33 n	6.37 b-g
SM 387	13 p	7.2 a-f
SM 388	10 t	4.5 c-g
SM 391	12.67 p	6.33 b-g
SM 393	9 u	4.5 c-g
SM 394	24 d	4.33 efg
SM 395	20.67 g	6.11 b-g
SM 398	10 t	4.73 c-g
SM 399	11 s	7.33 a-f
BARI Begun-1	25.67 c	10.67a
BARI Begun-4	24.33 d	4.47 d-g
BARI Begun-5	20 hi	8.33 a-e
BARI Begun-6	16 lm	8.67 a-d
BARI Begun-7	15.67 mn	3.2 fg
BARI Begun -8	9 u	2.5 g
C.V. (%)	2.21	5.53
Level of significance	**	**

Means in a column followed by the same letters are not significantly different at 1 % level by DMRT

Table 16. Frequency distribution of quantitative characteristics of 40 brinjalgenotypeas per fruit length and breadth

Characters	Class	Number of accession	Frequency (%)	Range
Fruit length (cm)	Shorter length = <15	14	35.00	9.00-14.00cm
	Moderate length=15-24	17	42.50	15.33-24.00 cm
	Longer length = >24	9	22.50	24.33-28.00cm
Fruit breadth(cm)	Shorter breadth= <4.5	15	37.50	2.5-4.47cm
	Moderate breadth=4.5-7.0	15	37.50	4.50-6.53cm
	Longer breadth = >7.00	10	25.00	7.1-10.66 cm

4.2.12 No. of fruit

Significant variation was observed among the genotypes for no. of fruits of brinjal (Table 17). It ranged from 17.00 to 44.00. Minimum no. of fruit of brinjal obtain from genotypes BARI Begun-6 (17.00 no.) and SM 393 (20.67 no.) followed by BARI Begun-5 (24.00no.) SM 367 (29.33 no.), SM 339 (29.33 no.) while the maximum no. of fruit obtain from BARI begun-4(69.67 no.).As per frequency distribution 12 (30.00%) genotypes had

highest no. of fruits(17.00-31.33 no.), 18 (45.00%) genotypes had medium no. of fruits (32.00-39.33 no.)and10 (25.00%) genotypes had lowest no. of fruits (40.67-4.00 no.) to harvest (Table 18).

4.2.13 Weight of fruits (kg)

Significant variation was observed among the genotypes for weight of fruits of brinjal (Table 17). It ranged from 2.90 to 7.38. Minimum weight of fruits of brinjal obtain from genotypes SM 377 (2.90 kg) and SM 386(3.11 kg) followed by SM 375 (3.38 kg) SM 376 (3.39 kg) SM370 (3.42 kg) while the maximum weight of fruits of brinjal obtain from genotypes SM362 (7.38 kg).As per frequency distribution 15 (37.50%) genotypes had minimum fruit weight (2.58-3.92 kg), 11(27.50%) genotypes had moderate fruit weight (4.23-4.98 kg) and 14 (35.00%) genotypes had maximum fruit weight (5.12-7.38 kg) (Table 18).

4.2.14 Average fruit weight (gm)

Significant variation was observed among the genotypes for Av. fruit weight of brinjal (Table 17). It ranged from 74.67to305.33. Minimum Av. fruit weight obtain from genotypes SM 370 (74.67 g) and SM 375(77.00gm) followed by BARI Begun-1(77.67 g) SM377 (82.67) BARI Begun-4(83.33gm) while the maximum Av. fruit weight obtain from BARI Begun-6 (305.33gm).As per frequency distribution 7 (17.50%) genotypes Minimum Av. fruit weight (74.67-86.7 g), 23(57.50%) genotypes had medium (92.00-167.00 gm) and 10 (25.50%) genotypes have maximum Av. fruit weight (173.67-305.33 gm) (Table 18).

Table 17. Quantitative characteristics of 40 brinjal genotypes as per no. of fruits, Av. fruit weight and wt. of fruits

Genotype	No. of fruit	Av. fruit weight (gm)	Weight of fruits/Pant(kg)
SM323	37.67 f-j	126.33 kl	4.74 jk
SM 343	34.33 j-p	94.67 o-r	3.24 qr
SM 351	41 d-g	133.67 i-l	5.4 f
SM 358	32.67 l-q	176.67 d-f	5.75 cd
SM 359	32 m-q	193.67 c-e	6.16 b
SM 361	32 m-q	154.33 f-i	4.9 ij
SM 362	33 k-q	224.33 b	7.38 a
SM 363	34.67 j-o	102 m-p	3.53 op
SM 364	30.67 o-r	205.67 bc	6.24 b
SM 365	42 c-e	112 l-o	4.64 kl
SM 366	32 m-q	176.33 d-f	5.62 de
SM 367	29.33 qr	198 cd	5.7 cd
SM 369	29.33 qr	176.67 d-f	5.17 g
SM 370	46 c	74.67 r	3.42 p
SM 371	33 k-q	173.67 e-g	5.73 cd
SM 373	43.33 c-e	127.33 kl	5.51 ef

SM 375	44 cd	77 qr	3.38 pq
SM 376	43 c-e	79.33 p-r	3.39 pq
SM 377	35 j-n	82.67 p-r	2.9 t
SM 378	39.33 e-i	147.67 h-k	5.8 c
SM 380	40.67 d-h	96.67 n-r	3.92 n
SM 381	37 g-k	98.67 n-q	3.64 o
SM 382	41.67 d-f	92 o-r	3.83 n
SM 383	36.67 h-l	92.67 o-r	3.39 pq
SM 385	30.33 p-r	164 f-h	4.97 hi
SM 386	36 i-m	86.67 p-r	3.11 rs
SM 387	37 g-k	122.67 lm	4.53 l
SM 388	33 k-q	167 f-h	5.5 ef
SM 391	32.33 m-q	146.33 h-k	4.74 jk
SM 393	20.67 tu	125.33 kl	2.58 u
SM 394	31.33 n-q	151.33 g-j	4.74 jk
SM 395	31.33 n-q	156.33 f-i	4.87 ij
SM 398	27 rs	111.67 l-o	3.01 st
SM 399	26.67 rs	118.33 l-n	3.15 rs
BARI Begun-1	63 b	77.67 qr	4.87 ij
BARI Begun-4	69.67 a	83.33 p-r	5.79 cd
BARI Begun-5	24 st	305.33 a	4.23 m
BARI Begun-6	17 u	176.67 d-f	5.12 gh
BARI Begun-7	30.33 p-r	127.67 kl	3.85 n
BARI Begun -8	36 i-m	130.33 j-l	4.68 kl
C.V. (%)	7.25	10.34	2.36
Level of significance	**	**	**

Means in a column followed by the same letters are not significantly different at 1 % level by DMRT

Table 18. Frequency distribution of quantitative characteristics of 40 brinjal genotypes as per no. of fruits, Av. fruit weight and wt.of fruits

Characters	Class	Number of accession	Frequency (%)	Range
No. of fruits	Small height = < 32 cm	12	30.00	17.00-31..33cm
	Medium height = 32-40	18	45.00	32.00-39.33cm
	cm	10	25.00	40.67-69.67cm
	Late height = >40 cm			
Av. fruit weight (gm)	Lower no. = <92gm	7	17.50	74.67-86.7gm
	Medium no.= 92-170gm	23	57.50	92.00-167.00gm
	Higher no= >170gm	10	25.50	173.67-305.33gm
Weight of fruits (kg)	Lower no. = <4 kg	15	37.50	2.58-3.92 kg
	Medium no. = 4-5 kg	11	27.50	4.23-4.98 kg
	Higher no = >5 kg	14	35.00	5.12-7.38 kg

4.2.15 Yield (t/ha)

Significant variation was observed among the genotypes for yield(t/ha) of brinjal (Table 19). It ranged from 33.58 to70.62 kg. Minimum yield obtain from genotypes SM 393 (33.58 ton) and SM 377(36.34 ton) followed by SM 398 (37.56 ton) SM 386 (37.27 ton) SM399(38.49 ton) while the maximum yield obtain from genotypes SM 362 (70.62 ton).As per frequency distribution 9 (22.50%) genotypes gave minimum yield (33.58-39.94 ton), 17(42.50%) genotypes gave moderate (40.32-53.45 ton) and 14(35.00%) genotypes gave highest yield (55.86-70.62 ton) (Table 20)

Table 19.Quantitative characteristics of 40 brinjal genotypes as per yield

Genotype	Yield (t/ha)
SM323	50.95jk
SM 343	38.78qr
SM 351	56.65 f
SM 358	61.97 cd
SM 359	64.02 b
SM 361	52.72ij
SM 362	70.62 a
SM 363	40.76 op
SM 364	64.13 b
SM 365	50.12 kl
SM 366	58.64 de
SM 367	61.07 cd
SM 369	56.01g
SM 370	40.32 p
SM 371	61.07 cd
SM 373	58.15ef
SM 375	39.15pq
SM 376	39.94pq
SM 377	36.34 t
SM 378	62.18 c
SM 380	43.63n
SM 381	41.50 o
SM 382	43.00n
SM 383	39.63pq
SM 385	53.45hi
SM 386	38.27rs
SM 387	53.39 l
SM 388	57.82ef
SM 391	51.57jk
SM 393	33.58 u
SM 394	51.23jk
SM 395	52.43ij
SM 398	37.56st
SM 399	38.49rs
BARI Begun-1	52.21ij
BARI Begun-4	43.35 n
BARI Begun-5	45.02 m

BARI Begun-6	55.86gh
BARI Begun-7	50.53 kl
BARI Begun -8	61.45 cd
C.V. (%)	2.37
Level of significance	**

Means in a column followed by the same letters are not significantly different at 1 % level by DMRT

Table 20.Frequency distribution of quantitative characteristics of 40 brinjal genotypes as per fruit yield character

Characters	Class	Number of accession	Frequency (%)	Range
Yield (t/ha)	Lower fruit yield = <40	9	22.50	33.58-39.94 kg
	Medium fruit yield = 40-55	17	42.50	40.32-53.45 kg
	Higher fruit yield => 55	14	35.00	55.86-70.62kg

4.2.16 No. of infected fruits: Significant variation was observed among the genotypes for No. of infected fruit of brinjal (Table 21). It ranged from 2.67 to 6.00. Minimum No. of infected fruit observed in genotypes SM 377 (2.67 no.) and SM 380 (3.00 no.) followed by SM 385 (3.00 no.) SM 343 (3.33 no.) SM358 (3.33 no.) while the maximum No. of infected fruit in BARI Begun-6 (6.00 no.).As per frequency distribution 8 (20.00%) genotypes had lowest no. of infected fruit (2.67-3.67 no.), 24(60.00%) genotypes had medium no. of infected fruit (4.00-5.00 no.) and 8 (20.00%) genotypes had highest no. of infected fruit (5.33-6.00 no.) (Table 22)

4.2.17 Weight of infected fruits (kg): Significant variation was observed among the genotypes for Wt. of infected fruit of brinjal (Table 21). It ranged from 0.25 to 0.95 kg. Minimum Wt. of infected fruit observed in genotypes SM 377 (0.25 kg) and SM 386 (0.34 kg) followed by SM 363 (.34 kg) SM 399 (0.34 kg) SM 343 (.35 kg) while the maximum Wt. of infected fruit by SM 362 (0.95 kg). As per frequency distribution11 (27.50%) genotypes had lowest amount of infected fruit (0.25-0.39 kg), 14(35.00%) genotypes had medium (0.40-0.59 kg) and 15(37.50%) genotypes had highest amount of infected fruit (0.61-0.95 kg) (Table 22)

Table 21. Quantitative characteristics of 40 brinjal genotypes as per No. of infected fruit and Wt. of infected fruit

Genotype	No. of infected fruit	Wt. of infected fruit (kg)
SM323	4.33 ab	0.95 a
SM 343	3.33 ab	0.62 ab
SM 351	4.67 ab	0.35 a-c
SM 358	3.33 ab	0.47 b-d

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SM 359	5.33 a-c	0.64 b-e
SM 361	5 a-c	0.62 c-f
SM 362	4 a-d	0.71 d-g
SM 363	4.67 a-d	0.34 d-h
SM 364	5 b-e	0.66 e-i
SM 365	4 b-e	0.56 f-j
SM 366	4.33 b-e	0.68 f-k
SM 367	6 b-e	0.8 f-k
SM 369	5 b-e	0.82 g-l
SM 370	5 b-e	0.39 g-l
SM 371	3.67 b-f	0.53 h-l
SM 373	4.33 b-f	0.43 h-m
SM 375	4.67 b-f	0.43 i-n
SM 376	4 b-f	0.36 j-o
SM 377	2.67 b-f	0.25 k-p
SM 378	4.33 b-g	0.87 l-p
SM 380	3 b-g	0.47 m-q
SM 381	5.67 b-g	0.48 m-r
SM 382	5 b-g	0.39 m-s
SM 383	6 b-g	0.49 n-t
SM 385	3 b-g	0.32 n-t
SM 386	3.67 c-g	0.27 o-u
SM 387	4 c-g	0.62 o-u
SM 388	4.67 c-g	0.48 o-u
SM 391	5 c-g	0.54 p-u
SM 393	4 c-g	0.36 q-u
SM 394	5.67 c-g	0.64 q-v
SM 395	4.67 d-g	0.52 r-w
SM 398	3.33 d-g	0.35 s-w
SM 399	4.33 e-g	0.34 t-w
BARI Begun-1	6 ab	0.91 t-w
BARI Begun-4	6 ab	0.76 u-w
BARI Begun-5	4.33 b-fg	0.74 u-w
BARI Begun-6	7 a	0.6 u-w
BARI Begun-7	5.33 a-d	0.44 vw
BARI Begun -8	4 c-g	0.41 w
C.V. (%)	19.7	13.74
Level of significance	**	**

Means in a column followed by the same letters are not significantly different at 1 % level by DMRT

Table 22. Frequency distribution of quantitative characteristics of 40 brinjal genotypes as per No. of infected fruit and Wt. of infected fruit

Characters	Class	Number of accession	Frequency (%)	Range
No. of infected fruit	Small height= < 4cm	8	20.00	2.67-3.67cm
	Medium height =4-5 cm	24	60.00	4.00-5.00cm
	Late height = >5cm	8	20.00	5.33-6.00cm
Wt. of infected fruit	Lower no. = <0.4 kg	11	27.50	0.25-0.39 kg
	Medium no.= 0.4-0.6 kg	14	35.00	0.40-0.59 kg.
	Higher no= >0.6 kg	15	37.50	0.61-0.95 kg

4.3 Multivariate analysis

Genetic divergence in Brinjal was analyzed by using open source "R" software programme. Genetic diversity analysis involved estimation of distance between the clusters and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001; Juned *et al.* 1988 and Ario,1987). In the analysis of genetic diversity in brinjal multivariate techniques were used.

4.3.1 Principal component analysis

Seventeen characters were considered for genetic diversity analysis. Eigen values of seventeen principal axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in Table 23. The results revealed that the first principal axis largely accounted for the variation among the genotypes which alone contributed 25.56% of the variations followed by the 2nd axis (15.50%) while the first five Eigen values for the principal component axes of genotype accounted for 74.62% of the total variation among 17 characters describing 40 genotypes while the former two accounted for 41.06%.

Table 23. Latent roots (Eigen values) and percent of variation in respect of 17 characters in brinjal

Sl. No.	Principal component axis	Latent roots	% of total variation accounted for	Cumulative percent
1	Days to 50% flowering	2.08	25.56	25.56
2	Plant height at 1st harvest (cm)	1.62	15.50	41.06
3	Primary branch number at 1st harvest	1.48	12.93	53.99
4	Secondary branch number at 1st harvest	1.41	11.85	65.84
5	Plant height at last harvest (cm)	1.22	8.77	74.62
6	Primary branch number at last harvest	1.06	6.67	81.29
7	Secondary branch number at last harvest	0.96	5.48	86.78
8	Leaf Length (cm)	0.85	4.30	91.09
9	Leaf breadth (cm)	0.71	2.97	94.06
10	Fruit length (cm)	0.65	2.52	96.58
11	Fruit diameter (cm)	0.47	1.35	97.93
12	No. of fruits/ plant	0.41	1.01	98.95
13	Av. Fruit wt. (g)	0.28	0.47	99.43
14	Wt. of fruits/ plant (kg)	0.24	0.36	99.79
15	Yield (t/ha)	0.18	0.20	100.00
16	No. of infected fruits/ plant	0.00	0.00	100.00
17	Wt.of infected fruit	0.00	0.00	100.00
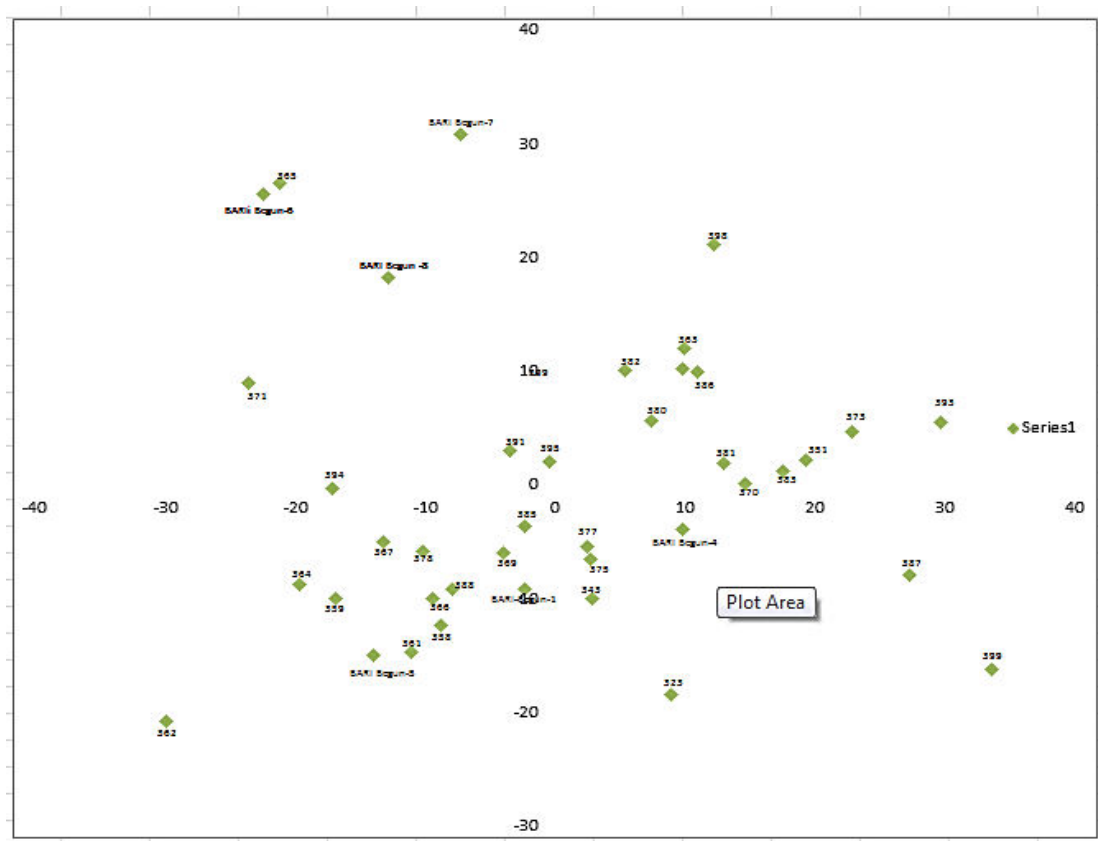
Figure 1. Scatter distribution of 40 brinjal genotypes based on their principal component scores

4.3.2 Principal Coordinate analysis (PCO)

Principal Coordinate analysis (PCO) was done to get inter genotypic distances. The lowest distance was observed between the genotypes SM366 and SM369 (0.40) followed by the genotypes SM 366 and SM 388 (0.42) and genotypes SM 373& SM 351(0.43) (Table 24). The highest inter genotypic distance (2.12) was observed between the genotypes BARI Begun-1 and BARI Begun-6followed by the genotypes SM 343 and SM 393(2.11) and genotypes SM 343 and BARI Begun-6 (2.90) (Table 24). The difference between the highest and the lowest inter genotypic distance indicated the existence of variability among the 40 genotypes of brinjal. Sukhija*et al*. (1982) while analyzing 46 lines of water melon found that the D^2 values ranged from 3.84 to 308.43 showing high divergence among different lines. Hasan*et al*. (2000) and Rahman*et al.* (2000) obtained a range of 2.001 to 7.72 and 4.87 to 19.989 D^2 values in Yam and Chili.

Table 24. Ten of each lower and higher inter-genotypic distance between pair of 40 genotypes of brinjal

10 lower D² values	Genotype combination	10 higher D² values	Genotype combination
0.40	SM 366 & SM 369	2.12	BARI Begun-1 & BARI Begun-6
0.42	SM 366 & SM 388	2.11	SM 343 & SM 393
0.43	SM 373 & SM 351	1.90	SM 343 & BARI Begun-6
0.44	SM 394 &SM 395	1.89	SM 376 & BARI Begun-6
0.46	SM 375 &SM 376	1.87	BARI Begun-4 & BARI Begun-6
0.46	SM 343 & SM 3 77	1.85	SM 375 & BARI Begun-6
0.47	SM 343 &SM 381	1.85	SM 399 & BARI Begun-6
0.47	SM 343 &SM 374	1.84	SM 383 & BARI Begun-6
0.48	SM 343& SM 377	1.82	SM 386 & BARI Begun-6
0.49	SM 380 & SM 382	1.81	SM 370 & BARI Begun-6

The intra-cluster distances were calculated from these inter-genotypic distances as suggested by Singh and Chowdhury (1985). The magnitude of the intra-cluster distances was not always proportional to the number of genotypes in the clusters (Table 24). Quamruzzaman et al. (2008a, 2008b, 2008c) concluded same result in bottle gourd, bitter gourd and ridge gourd.

In the present study it was found that although the cluster III composed of largest number of genotypes 13 (Table 25) but intra-cluster distance was not necessarily the highest (Table 26).The highest intra-cluster distance was recorded in cluster IV 1.073 (Table 26) containing 10 genotypes SM 323, SM 351, SM 365,3 SM 73, SM 387, SM 393, SM 398, SM 399,BARI Begun-7, BARI Begun -8 (Table 25) followed by cluster II was 0. 939 (Table 26) also containing 5 genotypes SM 359, SM 362, SM 364, SM 367, SM 378 (Table 25). The intra-cluster distances of cluster III was 0.905 (Table 26)and composed of 13 genotypes SM 343, SM 363, SM 370, SM 375, SM 376, SM 377, SM 380, SM 381, SM 382, SM 383, SM 386, BARI Begun-1, BARI Begun-4 (Table 25). The least intra-cluster distance was observed in cluster I 0.000 (Table 26) consisting of 1 genotypes BARI Begun-6 (Table 25). This least intra-cluster distance indicated that the genotype in this cluster was more homogenous than the genotypes consisting on the other clusters. The lower intra-cluster and higher intra-cluster values suggested that the population grouped were homogenous within and heterogeneous between clusters. The intra-cluster distances in all the clusters were less than inter-cluster distances which revealed that the genotypes within the same cluster were closely related.

Table 25. Distribution of 40 genotypes of brinjal genotypes in 5 clusters

Cluster	No. of genotypes	Genotypes
I	1	BARI Begun-6
II	5	SM 359, SM 362, SM 364, SM 367, SM 378
III	13	SM 343, SM 363, SM 370, SM 375, SM 376, SM 377, SM 380, SM 381, SM 382, SM 383, SM 386, BARI Begun-1, BARI Begun-4
IV	10	SM 323, SM 351, SM 365, SM 373, SM 387, SM 393,SM 398, SM 399, BARI Begun-7, BARI Begun -8
V	11	SM 358, SM 361, SM 366, SM 369, SM 371, SM 385, SM 388, SM 391, SM 394, SM 395, BARI Begun-5

4.3.3 Canonical variate analysis

The CVA was done to obtain the inter-cluster distances (Mahalanobis D² values). The values of inter cluster distance (D²) are presented in following table (Table 26). Statistical distances represent the index of genetic diversity among the clusters. The inter cluster distances were larger than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 26). Quamruzzaman et al. (2008a, 2008b, 2008c) obtained larger inter cluster distances than the intra cluster distances in a multivariate analysis in bottle gourd, bitter gourd and ridge gourd while Masud*et al.* (1995, 2001) reported similar findings in pumpkin and sponge gourd.

The results indicated that the maximum inter cluster distance was observed between cluster cluster I to cluster IV (13.128) followed by between cluster II to cluster IV (11.825), cluster IV to cluster IV (11.533), cluster Ito cluster V (9.361) and cluster III to Cluster IV (8.549) (Table 25). The lowest inter-cluster distances was observed between the cluster III to cluster II (3.524), followed by cluster III to cluster V (3.822), cluster II to cluster V (4.306) and cluster I to cluster II (4.711) (Table 25). The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 25).

Table 26.Intra (Bold) and inter cluster distances (D^2) for 35 genotypes of brinjal

Custer	I	II	III	IV	V
I	**0.000**	5.101	7.175	13.128	9.361
II		**0. 939**	3.524	11.825	4.306
III			**0. 905**	8.549	3.822
IV				**1.073**	11.533
V					**0.763**

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

However the maximum inter-cluster distance was observed betweenclusterI to cluster IV (13.128).Similarly the higher inter cluster values between cluster II to cluster IV (11.825) Cluster IV to Cluster V (11.533) indicated the genotypes belonging to each pair of cluster were far diverged. The lowest inert-cluster distance found between the cluster III to Cluster II (3.524)maintaining less distance than other clustersuggesting a close relationship between the genotypes of these those clusters. Genotypes from the cluster I to cluster IV (13.128)if involved in hybridization might produce a wide spectrum of segregating population, as genetic variation was very distinct among these groups. From the present study it was observed that the cluster I and IV were highly diverged followed by cluster II to cluster IV. It is expected that the crosses between the genotypes of cluster I and IV would exhibit high heterosis and also likely to produce new recombinants with desired traits.

The genotypes of distant clusters could be used in hybridization programme for obtaining a wide range of variation among the segregates. Similar reports were also made by Swain and Dikshit (1997) and Uddin*et al*. (1994) in sesame. Wenxing*et al*. (1994) reported that the beneficial effect of crossing carried out between genotypes belonging to different groups having genetic distance (D^2) greater than 12.5. Thus it could be suggested that crosses should be made between genotypes belonging to the distant clusters for higher heterotic response. In the present study the inter-cluster distance between III and IV, II and IV were the highest in suggesting crossing between the desirable genotypes of these three clusters for getting greater heterotic effect. Mian and Bahl (1989) reported that parental clusters separated by medium D^2 values exhibited significant positive heterosis. Thus heterosis could also be exploited by crossing between genotypes belonging to clusters with moderate diversity like between genotypes of cluster I and IV, cluster IV and V and cluster I and V.

4.3.4 Non- hierarchical Clustering

By using covariance matrix with the application of Non- hierarchical clustering, the 40brinjal genotypes were grouped into 5 (Five) 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 27.

These results confirmed the clustering pattern of the genotypes according to the principal component analysis. So, the results obtained through PCA were confirmed by non hierarchical clustering.

Joshi *et.al*. (2003) assessed the nature and magnitude of genetic divergence using non hierarchical Euclidean cluster analysis in 73 tomato *(Lycopersiconesculentum)* genotypes of diverse origin for different quantitative and qualitative traits. Maximum value of coefficient of variability (53.208) was recorded for shelf lifeof 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

Table 27. Distribution and place of collection of 40 brinjal genotypes in 5 clusters

| Cluster	No. of genotypes	Genotypes	Source of collection	
			Company	Collection
I	1	BARI Begun-6	BARI release Vriety	HRC, BARI, Gazipur
II	5	SM359	Patuakhali	HRC, BARI, Gazipur
		SM 362	Patuakhali	HRC, BARI, Gazipur
		SM 364	Dr. A.G	HRC, BARI, Gazipur
		SM 367	Manik	HRC, BARI, Gazipur
		SM 378	Manik	HRC, BARI, Gazipur
III	13	SM 343	Manik	HRC, BARI, Gazipur
		SM 363	Dr. A.G	HRC, BARI, Gazipur
		SM 370	Nufield	HRC, BARI, Gazipur
		SM 375	Nufield	HRC, BARI, Gazipur
		SM 376	Nufield	HRC, BARI, Gazipur
		SM 377	Manik	HRC, BARI, Gazipur
		SM 380	NSC Nirman	HRC, BARI, Gazipur
		SM 381	Masud	HRC, BARI, Gazipur
		SM 382	Chia Tai	HRC, BARI, Gazipur
		SM 383	Chia Tai	HRC, BARI, Gazipur
		SM 386,	Manik	HRC, BARI, Gazipur
		BARI Begun-1	BARI release Vriety	HRC,BARI,Gazipur
		BARI Begun-4	BARI release Vriety	HRC,BARI,Gazipur
IV	10	SM 323	Manik	HRC, BARI, Gazipur
		SM 351	Manik	HRC, BARI, Gazipur
		SM 365	Australia	HRC, BARI, Gazipur
		SM 373	LalTeer	HRC, BARI, Gazipur
		SM 387	Manik	HRC, BARI, Gazipur
		SM 393	Rajshahi	HRC, BARI, Gazipur
		SM 398	Local	HRC, BARI, Gazipur
		SM 399	Local	HRC, BARI, Gazipur
		BARI Begun-7	BARIreleaseVriety	HRC, BARI, Gazipur
		BARI Begun -8	BARIreleaseVriety	HRC, BARI, Gazipur
V	11	SM 358	Vangor	HRC, BARI, Gazipur
		SM 361	Patuakhali	HRC, BARI, Gazipur
		SM 366	Ocen seed	HRC, BARI, Gazipur
		SM 369	Alamgir	HRC, BARI, Gazipur
		SM 371	Nufield	HRC, BARI, Gazipur
		SM 385	Alamgir	HRC, BARI, Gazipur
		SM 388	Chia Tai	HRC, BARI, Gazipur
		SM 391	Local	HRC,BARI,Gazipur
		SM 394	United Seed	HRC, BARI, Gazipur
		SM 395	United Seed	HRC, BARI, Gazipur
		BARI Begun-5	BARI release Vriety	HRC, BARI, Gazipur
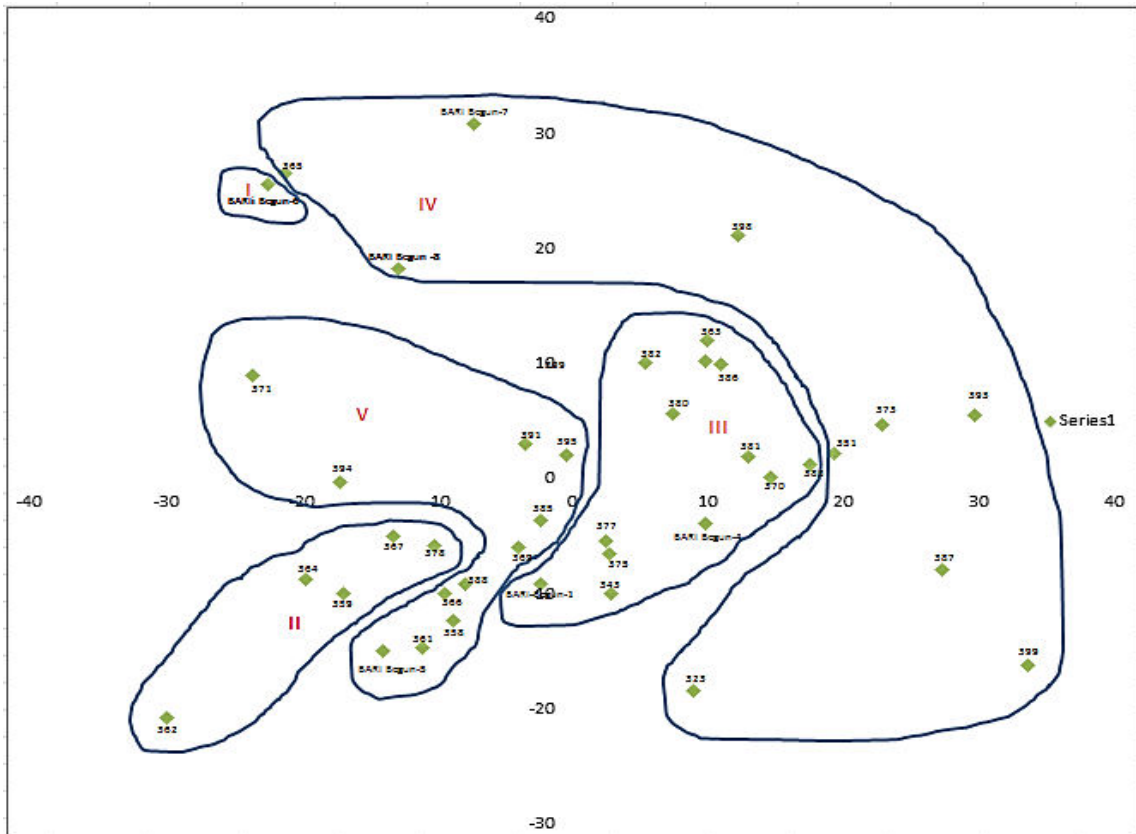
Figure 2. Scatter distribution of 40brinjal genotypes based on their principal component scores superimposed with clustering.

4.3.4.1 Cluster I

Cluster I had one (1) genotypes BARI Begun-6 collected from HRC, BARI,Gazipur (Table 27). From the clustering mean values (Table 28), it was observed that cluster I produced the highest mean values for av. fruit wt. (305.36 gm), Plant height at last harvest (120 cm), and the lowest mean value for Wt. of infected fruits (.74 kg) in comparison with other five clusters (Table 28). 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.

4.3.4.2 Cluster II

Cluster II was associated with five genotypes namely SM 359, SM 362, SM 364, SM 367, SM 378 (Table 27) thats were collected from different place and advanced line of seed company by HRC, BARI, Gazipur (Table 27). It was observed that cluster II produced the highest mean values for leaf length (15.14 cm), number of fruit yield (64.40 t/h) and the lowest mean value for primary branch number at 1st harvest (2.83

50

cm), primary branch number at last harvest (2.83 cm). These group possessed genotypes with the second highest cluster mean for Av. Fruit wt. (205.35gm), days to 50% flowering (97.66 days) .On the other hand this group produced lowest mean value wt. of infected fruits (.74 kg) (Table 28).

4.3.4.3 Cluster III

Cluster III composed of therteen genotypes. The genotypes were SM 343, SM 363, SM 370, SM 375, SM 376, SM 377, SM 380, SM 381, SM 382, SM 383, SM 386,BARI Begun-1, BARI Begun-4 (Table 27) that were collected from different place and advanced line of seed company by HRC, BARI, Gazipur that were collected from different place and advanced line of seed company by HRC, BARI, Gazipur (Table 27). It was observed that cluster III produced the highest mean values for days to 50% flowering (101.64 days) and the lowest mean value for wt. of infected fruits (.74 kg) (Table 10). The genotypes of this cluster produced second lowest mean for Primary branch number at last harvest (2.83 cm) (Table 28).

4.3.4.4 Cluster IV

Cluster IV consisted of ten genotypes namely SM 323, SM 351, SM 365, SM 373, SM 387, SM 393, SM 398, SM 399, BARI Begun-7, BARI Begun -8 that were collected from different place and advanced line of seed company by HRC, BARI, Gazipur (Table 27). From the clustering mean values,it was observed that cluster IV produced the highest mean values for av. Fruit wt. (123.51gm) and the lowest mean value for Wt. of infected fruits (.39 kg). These group possessed genotypes with the second highest cluster mean for days to 50% flowering (104.80 days) (Table 28).

4.3.4.5 Cluster V

Cluster V constituted only with eleven genotypes. The genotypes were SM 358, SM 361, SM 366, SM 369, SM 371, SM 385, SM 388, SM 391, SM 394, SM 395,BARI Begun-5 (Table 27), that were collected from different place and advanced line of seed company by HRC, BARI, Gazipur that were collected from different place and advanced line of seed company by HRC, BARI, Gazipur (Table 27). Cluster V produced the highest mean values for av. fruit wt. (123.51gm) The genotypes of this cluster produced second highest mean for days to 50% flowering (104.80 days) and the lowest mean value for wt. of infected fruits (.63 kg) (Table 28)

Table 28.Cluster mean values for different characters of 40 brinjal genotypes

Characters	Cluster				
	I	II	III	IV	V
Days to 50% flowering	98.67	97.66	101.64	104.80	100.55
Plant height at 1st harvest (cm)	67.67	58.49	61.64	60.20	61.05
Primary branch number at 1st har	3.67	2.83	2.59	2.56	2.91
Secondary branch number at 1st harvest	6.67	6.00	5.97	6.10	6.27
Plant height at last harvest (cm)	120	87.83	85.71	89.70	90.41
Primary branch number at last harvest	3.67	2.83	2.61	2.53	2.83
Secondary branch number at last harvest	6.67	6.00	5.97	6.10	6.27
Leaf Length (cm)	13.67	15.14	14.89	15.14	14.25
Leaf breadth (cm)	8.13	9.35	9.08	8.66	8.65
Fruit length (cm)	15.67	16.5	20.38	16.30	18.05
Fruit diameter (cm)	10.67	6.73	4.63	5.07	6.06
No. of fruits/ plant	17.00	31.25	43.20	34.16	31.72
Av. Fruit wt. (g)	305.36	205.35	87.42	123.51	163.97
Wt. of fruits/ plant (kg)	5.12	6.37	3.72	4.20	5.16
Yield (t/ha)	55.86	64.40	41.27	49.09	54.27
No. of infected fruits/ plant	4.00	5.08	4.59	4.53	4.41
Wt. of infected fruits	0.74	0.69	0.39	0.54	0.63

4.3.5 Contribution of characters towards divergence of the genotypes

The characters contributing maximum to the divergence might be given greater emphasis for selection and the choice of parents for hybridization (Jagadeb*et al.*, 1991).

Contribution of characters towards divergence obtained from latent vector presented in Table 29. The values of vector I and vector II revealed that both the vectors had positive values for days to 50% flowering, plant height at 1[st]harvest, primary branch number at last harvest, leaf breadth, fruit diameter, no. of fruits/ plant, av. fruit wt., no. of infected fruits/ plant. These results indicated that these seven characters had highest contribution towards the divergence among 40 genotypes of brinjal.

In vector I, the other important characters responsible for genetic divergence in the major axis of differentiation were secondary branch number at 1[st]harvest (1.4083) and leaf breadth (0.5592) having positive vector values. While in vector II (the second axis of differentiation) leaf length (0.0154) wt. of fruits/ plant (0.0644), yield (0.0052), wt. of

infected fruits (2.0192) positive vector values were important. Negative values in both the vectors were absent indicated that no characters had lowest contribution to the total divergence. Quamruzzaman*et al.* (2008b) reported that days to 1st male flower open, days to 1st female flower open, fruit diameter, single fruit weight and fruits per plant contributing major portion of the total genetic diversity in ridge gourd. In other study Quamruzzaman*et al.* (2008a) reported fruits per plant and fruit yield per plant contribute towards divergence in bitter gourd. Alam *et al.* (2006) reported that days to heading, 1000 grain weight, yield per plant were the major contributors towards divergence in hull-less barley. Masud *et al.* (1995) found that number of fruits per plant and yield per plant was one of the important contributors to genetic divergence in pumpkin. Moreover Habib *et al.* (2007) in rice reported more or less similar result for grain per panicle, grain length and harvest index.

Table 29. Latent vectors for 17 principal component characters of 40 brinjal genotypes

Characters	Vector-I	Vector-II
Days to 50% flowering	0.0579	0.0699
Plant height at 1st harvest	0.0834	0.0849
Primary branch number at 1st harvest	-1.7944	-1.4346
Secondary branch number at 1st harvest	1.4083	-0.2192
Plant height at last harvest (cm)	-0.1292	0.1118
Primary branch number at last harvest	0.6767	0.7217
secondary branch number at last harvest	2.0561	2.1952
Leaf Length (cm)	-0.0836	0.0154
Leaf breadth (cm)	0.5592	-0.0661
Fruit length (cm)	-0.0233	-0.0029
Fruit diameter (cm)	0.3571	0.1457
No. of fruits/ plant	0.1107	0.0658
Av. Fruit wt. (g)	0.3312	0.1969
wt. of fruits/ plant (kg)	-0.3545	0.0644
Yield (t/ha)	-0.0266	0.0052
No. of infected fruits/ plant	0.1966	0.623
Wt. of infected fruits9kg)	-0.8327	2.0192

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 principal component score 1(Z1) and principal component score 2 (Z2) vector of the principal component analysis were found to be alternative methods in giving the

information regarding the clustering pattern of genotypes. However, the principal component analysis provides the information regarding the contribution of characters towards divergence of brinjal.

4.3.7 Selection of advance line for high yielding OP variety development:

Regarding agronomic performance, different characters contribute increasing the higher yield of brinjal. The height cluster yield mean observe from cluster II (Table 28) which include genotype SM 359, SM 362, SM 364, SM 367, SM 378 used as advance line. This advance line further used for development of high yielding OP variety in future. Therefore, cluster yield mean observe from cluster I and IV (Table 28) is optimum which include genotype BARI Begun-6andSM 323, SM 351, SM 365,3 SM 73, SM 387,SM 393, SM 398, SM 399,BARI Begun-7, BARI Begun -8 respectively. This genotype also use in advance line for selection of good quality high yielding OP variety.

4.3.8 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 yield performance, the genotypes BARI Begun-6from cluster-I SM359, SM 362, SM 364, SM 367, SM 378from cluster-II and SM 323, SM 351, SM 365,3 SM 73, SM 387,SM 393, SM 398, SM 399,BARI Begun-7,BARI Begun -8from cluster-IV would be suitable for efficient hybridization programme.

C H A P T E R V

S U M M A R Y A N D C O N C L U S I O N

In order to evaluate the performance of yield, yield contributing character and genetic diversity an experiment was conducted with 40brinjal 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 2018 to March 2019. 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 Days to 50% flowering, lant height at 1st harvest(cm), Primary branch no. at 1st harvest, Secondary branch no. at 1st harvest, plant height at last harvest (cm), primary branch no. at last harvest, secondary branch no. at last harvest, leaf length (cm), leaf breadth(cm), fruit length (cm), fruit diameter (cm), no. of fruit, weight of fruits (kg), av. fruit weight (gm), yield(t/ha), no. of infected fruit, wt. of infected fruit(kg) 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 fruits per plant obtained from the line BARI begun-4(69.67 cm)followed by BARI begun-1 (63.00 cm) and SM-370 (46.00 cm) while other lines bear average number of fruits per plant. Fruit length was maximum (27.67 cm) in SM 383 and the minimum (9.00cm) was produced by BARI begun-8.Fruit breadth was maximum (9.07cm) in SM 361and the minimum (2.50cm) was produced by BARI begun-8. The highest single fruit weight (305.33gm) was produced by the line BARI begun-5 while SM-370 produced (74.67gm).

The significant variations among the genotypes for seventeen characters of brinjal were observed. Multivariate analysis was performed through principal component analysis, principal coordinate analysis, canonical variate analysis and cluster analysis using **"R"** software programme. The first three principal component characters with eigen values were greater than unity contributed a total of 74.62% variation towards divergence. As per as principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into five 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, IVand V composed of one, five, thirteen, ten and eleven genotypes respectively. the maximum inter cluster

distance was observed between cluster cluster I to cluster IV (13.128) followed by between cluster II to cluster IV (11.825), cluster IV to cluster IV (11.533), cluster I to cluster V (9.361) and cluster III to cluster IV (8.549) (Table 26). 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 26).

However the maximum inter-cluster distance was observed between cluster I to cluster IV (13.128).Similarly the higher inter cluster values between cluster II to cluster IV (11.825) Cluster IV to Cluster IV (11.533) indicated the genotypes belonging to each pair of cluster were far diverged. The lowest inert-cluster distance found between the cluster III to Cluster II (3.524) maintaining less distance than other cluster suggesting a close relationship between the genotypes of these those clusters. Genotypes from the cluster I to cluster IV (13.128) if involved in hybridization might produce a wide spectrum of segregating population, as genetic variation was very distinct among these groups. From the present study it was observed that the cluster I and IV were highly diverged. It is expected that the crosses between the genotypes of cluster I and IV would exhibit high heterosis and also likely to produce new recombinants with desired traits.

Regarding agronomic performance, different characters contribute increasing the higher yield of brinjal. The height cluster yield mean observe from cluster II (Table 28) which include genotype SM 359, SM 362, SM 364, SM 367, SM 378 used as advance line. This advance line further used for development of high yielding OP variety in future. Therefore, cluster yield mean observe from cluster I and IV (Table 28) is optimum which include genotype BARI Begun-6 and SM 323, SM 351, SM 365, SM 373, SM 387,SM 393, SM 398, SM 399,BARI Begun-7, BARI Begun -8 respectively. This genotype also use in advance line for selection of good quality high yielding OP variety.

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 the genotypes BARI Begun-6 from cluster I, SM359, SM 362, SM 364, SM 367, SM 378 from cluster II and SM 323, SM 351, SM 365,3 SM 73, SM 387,SM 393, SM 398, SM 399, BARI Begun-7, BARI Begun -8 from cluster IV would be suitable for efficient hybridization programme.

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Appendix I. Monthly average temperature, total rainfall, relative humidity and sunshine of the experimental site during the period from September 2018 to April 2019

Month	Temperature(^{0}c)	Rainfall (mm)	Relative Humidity (%)	Sunshine(hours)
September	28.8	271	71	12.3
October	27.5	164	65	11.6
November	23.7	31	53	11.0
December	20.0	5	50	10.7
January	18.8	8	46	10.9
February	21.5	21	37	11.4
March	25.7	55	38	12.0

Source: Bangladesh Metrological Department (www.bmd.gov.bd)

Appendix II. Doses of manure and fertilizers used in the study

SL No.	Fertilizer/Manure	Dose
1.	Cowdung	10 ton/ha
2.	Urea	300 kg/ha
3.	TSP	300 kg/ha
4.	MOP	250 kg/ha
5.	Gypsum	100 kg/ha
6.	Boric acid	5 kg/ha
7.	Magnesium Sulphate	5 kg/ha
8.	Zinc Oxide	5 kg/ha

Source: Fertilizer Recommedation Guide (2012)

Appendix III. Analysis of variance of the data on yield contributing character of brinjal

Source of variation	Degree of freedom	Mean Square						
		Days to 50% flowering	Plant height at 1st harvest (cm)	Primary branch number at 1st harvest	Secondary branch number at 1st harvest	Plant height at last harvest (cm)	Primary branch number at last harvest	Secondary branch number at last harvest
Replication	2	0.758	196.66	0.2583	3.325	38.9	0.1583	5.033
Treatment	39	74.27**	95.43**	0.7726*	1.159**	483.5**	0.7895*	1.702**
Error	78	3.664	18.81	0.2925	0.402	22	0.278	0.589

**Significent at 0.01 level of profitability   * Significent at 0.05 level of profitability

Appendix IV. Analysis of variance of the data on yield contributing character of brinjal

Source of variation	Degree of freedom	Mean Square			
		Leaf Length (cm)	Leaf breadth (cm)	Fruit length (cm)	Fruit diameter (cm)
Replication	2	42.62	13.908	1.03	0.211
Treatment	39	19.74**	7.791**	112.99**	11.943**
Error	78	0.99	0.724	2.61	0.162

**Significent at 0.01 level of profitability   * Significent at 0.05 level of profitability

Appendix V. Analysis of variance of the data on yield contributing character of brinjal

Source of variation	Degree of freedom	Mean Square					
		No. of fruits/ plant	Av. Fruit wt. (g)	wt. of fruits/ plant (kg)	Yield (t/ha)	No. of infected fruits/ plant	wt. of infected fruits/ plant (kg)
Replication	2	11.58	126	0.029	4.9	2.233	0.01153
Treatment	39	268.77**	71.57**	3.782**	63.91**	2.759**	0.09926**
Error	78	6.69	200	0.012	2	1.097	0.00552

**Significant at 0.01 level of profitability   * Significent at 0.05 level of profitability