MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERGENCE IN BRINJAL GENOTYPES (*Solanum melongena* L.)

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CERTIFICATE

This is to certify that thesis entitled, ***"Morphological Characterization and Genetic Divergence in Brinjal Genotypes (Solanum melongena L.)"*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE (M.S.)*** *in* ***GENETICS AND PLANT BREEDING,*** *embodies the results of a piece of bona fide research work carried out by* ***PAPON KUMAR KUNDU,*** *Registration no.* ***14-05817*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

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DEDICATED
TO
MY BELOVED PARENTS

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ABSTRACT

The experiment was conducted at the Sher-e-Bangla Agricultural University (SAU), Dhaka in field condition during the period from September, 2019 to March, 2020 to study the morphological and genetic divergence in brinjal genotypes. Genetic diversity of 15 brinjal genotypes were accomplished based on 14 quantitative traits. Genetic divergence was assessed by Cluster Analysis, Principal Component Analysis, Principal Coordinate Analysis and Canonical Variate Analysis which showed similar results. From ANOVA significant variations were noticed among the brinjal genotypes for all the traits under the current study. Multivariate techniques were applied to classify the genotypes. All the genotypes were grouped into five clusters. Cluster I, II and III each had the minimum one genotype and the cluster III had the maximum of 10 genotypes respectively. The highest inter-cluster distance was observed between II and IV (2585.92), and the lowest inter-cluster distance was observed between the cluster III and IV (705.58) suggesting that existing of wide distance among these clusters. The highest and lowest intra-cluster distance was observed between the cluster IV (941.81) and cluster III (788.83) respectively. Under the correlation coefficient study, it was observed that days to 50% flowering, days to first fruit harvest, weight of single fruit, fruit breadth and fruit number per plant was positively correlated with fruit yield per plant but negatively correlated with percent insect infestation of fruit and plant. The characters such as number of fruits per plant, fruit length, fruit breadth and single fruit weight contributed maximum towards divergence among the genotypes. Considering diversity pattern and other agronomic performance, the genotype G1 from cluster I, Genotype G8 from cluster II, genotype G11 and G14 from cluster III could be considered as better parents for future hybridization program.

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ABBREVIATION	**ELABORATIONS**
AEZ	Agro-Ecological Zone
Anon.	Anonymous
ANOVA	Analysis of Variance
@	at the rate of
a.i	Active ingredient
Adv.	Advanced
Agric.	Agriculture
Agril	Agricultural
B	Boron
BARI	Bangladesh Agricultural Research Institute
SAU	Sher-e-Bangla Agricultural University
BAU	Bangladesh Agricultural University
BBS	Bangladesh Bureau of Statistics
CV	Coefficient of Variation
Cm	Centimeter
cv.	Cultivar
Comms	Communication
DAT	Days After Trasplanting
Df	Degrees of Freedom
et al.	and all
etc.	Etcetera
EC	Emulsifiable Concentrate
FAO	Food and Agricultural Organization
GA_3	Gibberellic Acid
Gm	Gram
Hort.	Horticulture

ABBREVIATION	ELABORATIONS
Mo	Molybdenum
LSD	Least significance difference
RCBD	Randomized Complete Block Design
Ns	Non-Significant
J.	Journal
pp.	Pages
T	Ton
ha^{-1}	Per hectare
$plant^{-1}$	Per plant
%	Percent
Kg	Kilogram
^{0}C	Degree Celsius
Res.	Research
RH	Relative humidity
Sci.	Science
Vol.	Volume

CHAPTER I

INTRODUCTION

Brinjal (*Solanum melongena* L.) is one of the important, popular and extensively cultivated *Solanaceous* vegetable crops. Although, Indo-Burma is the primary center of origin of brinjal, but it is grown all over the world (Vavilov, 1928). It belongs to the genus *Solanum* and subgenus *Leptostemonum*. Over 200 *Solanum* species are found in Africa including 25 indigenous species of Nigeria (Gbile and Adesina, 1988; Burkill, 2000).

Brinjal which is a good source of minerals and vitamins plays important role in vegetable consumption (Islam *et al*., 2018). The unripe fruit is primarily used as a cooked vegetable for the preparation of various dishes in different regions of the world. It has potentiality as raw material in pickle making and in dehydration industries (Singh *et al.*, 1963). Brinjal or eggplants have indigenous medicinal uses, which range from weight reduction to treatment of several ailments including asthma, skin infections and constipation (Gill, 1992; Grubben and Denton, 2004; Okon *et al.*, 2010).

The global brinjal production statistic in 2021 was 52.31 million tons, going up by 2.18% against the previous year. This global brinjal production peaked in 2017, and the growth trend pattern is likely to be on a continuous increase (FAO, 2021). China and India are the top brinjal producing countries in the world followed by Egypt, Turkey, Indonesia, Iran, Philippines, Spain, Mexico, Japan, Italy, and Syria. Brinjal is an important vegetable in South Asia (Bangladesh, India, Nepal and Sri Lanka) and accounts for almost 50% of world area under cultivation (Kumar *et al*., 2016). It is grown on approximately 46,566 hectares of land across the country (Bangladesh) both in winter and summer season, yielding an average of 7.30 ton per hectare and a total production of about 3,39,874 ton (BBS, 2018). The crop is highly diverse for fruit shape, size and colour in Bangladesh due to the Indian gene centre (Hawks, 1983).

Brinjal is popular and cultivated all over the Bangladesh (Rashid, 1995). It plays very significant role to meet the market demand of vegetables of Bangladesh in both summer and winter season. Yield potentiality of the brinjal varieties cultivated in Bangladesh is less and its size, shape, and skin colour varies in different locations of the country. Improvement in fruit yield, colour, size, shape and insect resistances will undoubtedly boost the production and consumption of the brinjal. The broad range of variation was noticed with regard to morphological traits, however till date very few systematic evaluation of genetic diversity on this crop has been carried out. Brinjal productions are impeded due to the infestation of different insects like root and shoot borer, spider mites and diseases like wilt, phomopsis blight, etc. Resistant capacity of the brinjal crop against different diseases and insects is decreased because of selection against various natural defense mechanisms like spines, hairiness etc. Finally, the control approach relying completely on toxic pesticides and chemicals is not effective well in the field. While the chemicals and pesticides incur higher costs of production, environmental pollution, destruction of natural enemies and development of pesticide resistance etc. Identification of natural mechanisms existing in the brinjal land races is essential in order to exploit them in the improvement program.

Identification of variation among accessions plays vital role for the maintenance and utilization of germplasm resources (Mwirigi *et al.,* 2009). Evaluation and systematic study of germplasm is very important for the existing and future agronomic as well as genetic improvement of the crop (Reddy *et al*., 2013). Information on genetic diversity is basic pre-requisite in order to develop high yielding varieties through a systematic breeding programe. The success of any breeding programe depends upon the amount of genetic variability present in the available germplasm of a particular crop (Balas *et al*., 2019). Among different methods, morphological, biochemical and molecular markers are generally used to

identify and estimate the genetic variation of crop plants. Morphological markers are used abundantly to study of genetic variation in plant species. Morphological traits are important diagnostic features for distinguishing genotypes (Osei *et al.*, 2014). Genetic variation in brinjal by morphological characters has been the subject of many studies in many regions of the world (Osei *et al.,* 2014; Yadav *et al*., 2017; Tripathy *et al*., 2020). Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. Assessment of diversity is important to know the source of gene for a particular trait within the available germplasms (Tomooka, 1991). Information on genetic diversity plays very significant role for a systematic breeding program in order to develop high yielding varieties (Rathi *et al*., 2011; Banerjee *et al*., 2018; Balas *et al*., 2019). It usually happens that genetically diverse parents are likely to contribute desirable segregants or to produce high heterotic crosses. More diverse the parents larger are the chances of gaining high heterotic F_1 and wide spectrum of variation in segregating generation through selection (Murty and Arunachalam, 1966; Balas *et al.,* 2019).

Crossing engaging parents selected based on genetic variation may likely produce transgressive segregates. Higher the genetic variation, more are the chances of development through selection (Banerjee *et al*., 2018; Balas *et al*., 2019). Biometrical procedure which helps to quantify genetic diversity (Rao, 1952) could apply to select genetically diverse parents for an effective hybridization program. Many workers established the usefulness of multivariate analysis to compute the degree of divergence and to evaluate the relative contribution of different characters to the total divergence in self-pollinated crops (Das and Gupta, 1984). A good number of genotype having large variation in different traits is being cultivated in Bangladesh and some of the deviation are so localized that their cultivation outside the particular region . Some of these promising genotypes are yet to be known in spite of their restricted distribution. Therefore, evaluation of

performance, variability, diversity and character association study of exotic genotype, local and mutant genotype of brinjal is essential with a view to select proper varieties under the agro-ecological condition of the central plains of Bangladesh during the winter season.

The present study was carried out to assess the nature and magnitude of genetic variation of brinjal and feasibility of exploiting all those information in the improvement of the brinjal variety.

The present investigation was carried out with the following objectives:

1. To categorize the brinjal genotypes based on morphological traits

2. To study the variability and character association in the brinjal genotypes

3. To select the suitable parents in order to utilize in the future hybridization program.

CHAPTER II
REVIEW OF LITERATURE

Studies on different characters of brinjal are very common in the tropical and sub-tropical countries. Although brinjal is mostly cultivated and one of the most popular vegetables grown in Bangladesh, information on its growth habit, productivity and quality of different lines/varieties under different agro-ecological conditions are not enough for its extensive study and improvement. It is an established fact that genetically diverse parents are likely to contribute desirable segregants. It was also observed that the more diverse the parents, greater are the chances of obtaining high heterotic F1 and broad spectrum of variability in the segregating generation. Phenotypic characters and Genetic divergence are most important criteria of parent selection. It is a prerequisite for an efficient plant breeding programme. Therefore, relevant information available in the literature pertaining to the divergence of the brinjal and some other crops of the same family were reviewed in this section. Moreover literatures related to the efficient multivariate techniques for diversity analysis were also reviewed in the following paragraphs.

2.1 Phenotypic Variability of Brinjal Genotypes: A study was conducted by Mohanty *et al*,. (2021) on thirty-eight genotypes including local landraces and public as well as private sector genotypes of brinjal collected from different locality of Odisha, India to assess the value and magnitude of genetic divergence among them using Mahalanobis D^2 statistics. The result revealed existence of wide genetic diversity among the 38 evaluated brinjal genotypes which were grouped into 13 clusters based on 12 important characters. The cluster I was the largest containing 09 genotypes followed by cluster III with 07 genotypes. The diversity among the cluster was measured by inter-cluster distance, highest being observed in between cluster VIII and cluster XIII (D^2 = 1142.59) followed by cluster IX and cluster XIII (D^2 = 941.02) and cluster V and cluster VIII (D^2 = 792.97).

Arti *et al,*. (2018) conducted a study on genetic divergence among 50 eggplant (*Solanum melongena* L.) genotypes and estimated using Mahalanobis D^2 Statistics. The 50 genotypes were grouped into eight distinct clusters. Among the different clusters, cluster II, V and VIII consisted maximum number of genotypes (9) followed by cluster cluster IV (7) and in cluster I, III, VI and VII each were having 4 genotypes. The highest contribution in manifestation of genetic divergence was exhibited by ascorbic acid content (18.53%), number of marketable fruits per plant (17.88%), plant height (14.12%), total soluble solids (12.65%) and number of branches per plant (11.27%). Cluster VIII had highest mean values for plant height, number of branches per plant, fruit breadth and ascorbic acid content. Cluster I showed higher mean values for earliest flowering and harvesting, total harvest duration, fruit yield per plant. Cluster V had highest mean values for number of marketable fruits per plant and total soluble solids whereas, cluster IV had maximum fruit length and cluster VII had maximum fruit weight. Considering the genetic divergence, clustering pattern and mean performance of genotypes for fruit yield and contributing characters 13 genotypes comprising UHF BRL-3, IC-074224-1, DB-144, DB- 181, PBHL-4, Punjab Barsati, PBH-3, UHF BRL-2, DB-143, DBL-139, DB-110, DB-30 and DB-109 may be considered as elite genotypes and hybridization involving these genotypes are likely to give desirable segregants for yield and its components characters.

An investigation was conducted with 21 diverse genotypes of brinjal by Madhavi *et al,*. (2015). The data was recorded for sixteen plant growth and fruit yield related characters viz., days to 50% flowering, plant height at 50% flowering (cm), number of branches per plant, leaf area (cm^2), flowers per cluster, fruits per cluster, fruit setting percentage (%), fruit length (cm), fruit diameter (cm), fruit volume (cm^3) number of fruits per plant, average fruit weight (g). The cultivars viz., Azad T-3, JBGR-1, CH-10-45, Mukta Keshri and Punjab Nagini were found promising as they contained more than one desirable trait. High phenotypic and

genotypic coefficients of variation (PCV and GCV), heritability and genetic advance were observed for number of fruits per plant, average fruit weight, fruit yield per plant, fruit volume, fruits per cluster, number of pickings, flowers per cluster, fruit diameter and dry matter content. Therefore, these characters which may be included in selection criteria for improvement in fruit yield per plant.

Genetic divergence in eighteen eggplant genotypes was studied by Uddin *et al,*. (2014). Eggplant genotypes were evaluated for different quantitative characters. Among the genotypes wide variations were observed for plant, flower and fruit size, shape and color. Out of 18 genotypes only 8 were found to be suitable for summer and summer rainy season cultivation as heat tolerance. The 18 genotypes were grouped into four distinct clusters. Cluster I comprised of 2 genotypes, cluster II had 3, cluster III had 3 and cluster IV had 10 genotypes. Clustering pattern of the genotypes was not correlated with their geographical distribution. The highest inter cluster distance was between cluster I and IV (764.67) while, it was the lowest between cluster II and III (213.30). The highest and lowest intra cluster distance was displayed in cluster II (94.14) and cluster I (28.79) respectively. Yield per plant, number of fruits per plant, plant canopy, fruit weight, fruit length and number of harvest had the highest contribution towards total divergence. Moderate to high Shannon-Weaver Diversity Indices (SWDI) was found among the genotypes for most of the studied qualitative characters. Quantitative vegetative characters had high diversity among the genotypes, while it was moderate to high diversity for both flower and fruit characters.

Nyadanu *et al,*. (2014) condected a stuy with a total of 23 eggplant accessions collected from different agro-ecological zones in Ghana were characterised using morphological descriptors. The accessions varied significantly in days to 50% flowering, days to fruiting, stem girth, fruit weight, number of seeds per fruit, weight of leaves per plant and plant height. Principal components analysis based on the morphological traits showed that PC1 contribute 99% of the total variation

was mainly defined by number of leaves, number of branches, plant height, stem girth and number of leaves per plant. The accessions evaluated were grouped under five clusters. The clustering pattern indicated that intercluster distance was higher than intra-cluster, indicating wide genetic diversity among the accessions. Correlation analyses between morphological traits revealed positive and negative relationships, indicating predictable success for eventual breeding activities.Accessions CAGRICW3, CAGRICW4, CAGRICN2 and CAGRICA4 had more leaves and fruits, and could be used as potential donors for hybridisation programme to develop variety with higher yield potential.

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

Genetic diversity is different forms of genotype and occurs as a result of changes in genetic structure. It may leads to speciation in the long term due to the process of evolution. Divergence in genetic composition is one of the basic feature which increases chance of survival for individuals and populations during natural selection (WEB_2_2007).

Sindhuja *et al,*. (2019) conducted an experiment to estimate the Genetic divergence among fifty six brinjal (*Solanum melongena* L.) genotypes was based on twelve agronomic traits. Significant variations were observed among the brinjal genotypes for all the traits studied. D^2 analysis resolved fifty six genotypes into as many as eight clusters. Maximum genotypes were gathered in cluster V (27 genotypes); followed by cluster IV (11 genotypes); cluster VII (07 genotypes), cluster I (04 genotypes). Cluster II, III and IV each had two genotypes. Cluster VIII was a mono-genotypic one. The intra-cluster distance was maximum with the cluster I. The genotypes grouped in this cluster may also be different genetically. On other hand, the genotypes grouped in the cluster IX may be similar for the traits of interest due to minimum intra-cluster distance. The inter-cluster distance was maximum between the clusters VI and cluster II. The genotypes gathered in these clusters might be different genetically and utilized in crossing programme to get heterotic hybrids and/or superior recombinants segregants.

Patel *et al,*. (2018) conducted a study with 35 germplasm accessions of brinjal to analyze genetic diversity. Principal Component Analysis (PCA) is an important statistical tool through which we can easily access important polygenic characters which are of great importance in a plant breeding programme. The observations were recorded on sixteen different traits. PCA indicated that six components (PC-1 to PC-6) accounted for 70.73% of the total variation among traits in brinjal genotypes. Out of six principal components retained; PC-1, PC-2 and PC-3 explained 21.11%, 13.07% and 11.32% of the total variation respectively. The results of PCA indicated that traits like plant height (PH), leaf area per plant at

50% flowering (LA), transpiration rate at 50% flowering (TR), chlorophyll content at 50% flowering (CC), number of fruits per plant (NF), fruit girth (FG), total phenol content (TPC) and total soluble sugar (TSS) could be used to distinguish the germplasms of brinjal in the heavy rainfall zone of South Gujarat. The result of present study could be utilized in planning and execution of future breeding strategies in brinjal.

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

A study of genetic divergence in 40 brinjal (*Solanum melongena* L.) genotypes for various characters based on qualitative and quantitative characters was done by Yadav *et al,.* (2017). Significant variations were observed among the brinjal lines for all the parameters under study. Based on D^2 values, the accessions were grouped into seven clusters. Average intra- and inter-cluster D^2 values among 40 genotypes revealed that cluster II showed a minimum intra-cluster value of 3.793, indicating that the genotypes within this cluster were similar, while the cluster I showed maximum intra-cluster D^2 value (4.681) revealing the existence of diverse genotypes in these clusters. The inter-cluster D^2 values ranged from 4.657 to

7.174. The minimum inter-cluster D^2 value was observed between cluster III and IV (4.657), indicating the close relationship among the genotypes included in these clusters. The maximum inter-cluster value was observed between cluster V and II (7.174), indicating that the genotypes included in these clusters had maximum divergence. Hence, hybridization between the genotypes included in these different clusters may give high heterotic responses and thus better segregants are greatly suggested for selection and improvement of brinjal crop with good consumer preference and high fruit yield.

Genetic divergence among 50 genotypes of brinjal for 16 characters was estimated using Mahalanobis D^2 statistic by Sadarunnisa *et al,*. (2014). The genotypes were grouped into eight clusters on the basis of relative magnitude of D^2 values. Among the eight clusters, cluster IV was the largest, comprising of 17 genotypes. The maximum and minimum intracluster distances were found in cluster VI and cluster I, respectively. The inter cluster D^2 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.

Ramesh *et al,*. (2013) conducted an experiment on Genetic divergence among 14 eggplant genotypes was estimated using Mahalanobis's D^2 statistic. Altogether six clusters were formed. The maximum number of genotypes (5) was found in cluster III with intra cluster distance of 2597.79. The maximum inter cluster distance was observed between cluster II and cluster V. Hence, genotypes belonging to these clusters may be utilized for involving in hybridization programme for crop improvement. The characters of yield per plant, fruit circumference, little leaf incidence and total phenols content contributed more for genetic divergence.

Mishra *et al,.* (2002) conducted an experiment to determine the genetic diversity among 38 potato genotypes. Based on the mean value for various characters and genetic distance between genotype crosses, namely JP-100 x Kufri Pukhraj, JP-100 x Kufri Ashoka, JP-100 x JX-235, JP-100 x JX-216, and JP-100 x JX-371 were identified as promising with heterotic performance for tuber yield and its components.

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

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

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

Kumar *et al,.* (1993) studied 33 eggplant genotypes using multivariate analysis. The coefficient of variation was high for total phenols content and moderate in fruit yield per plant. Principal component analysis indicated that the first 6

components with an eigen value > 0.61% of total variability. Magnitudes of the total variance attributable to the first 6 principal components were 32.74, 13.87, 5.52 and 4.79%, respectively. Flowering time, fruit circumference, internodal length, leaf area index, fruit yield per plant and average fruit weight were traits contributing the most to the total variability. Fruit yield per plant, the most important economic trait, exhibited significant association with fruit circumference (0.557), fruit width, total phenols content and average fruit weight. Cluster I consist the most genotypes (15) followed by cluster IX (5) and the minimum number of genotypes were in clusters II, V, VII and X.

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

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

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

2.3 Relationship between genetic and geographic diversity in brinjal: An investigation by Akter *et al*,. (2019) with Twenty-two genotypes of eggplant were evaluated to assess the genetic diversity within the genotypes at Bangladesh Agricultural Research Institute (BARI), Jamalpur, Bangladesh during the winter season of 2013-2014. Genetic diversity among 22 eggplant genotypes was estimated using Mahalanobis's D^2 statistic. Altogether five clusters were formed. Cluster II enclosed the highest number of genotypes (6) and cluster IV contained the lowest (1). The inter-cluster distance between I and IV was the highest (26.55) followed by IV-V (25.81), IIIIV (24.37) and II-IV (22.52). Cluster distance between clusters I-IV, IV-V, III-IV, and II-IV were moderate or intermediate. To select cluster for more heterotic genotypes four pairs of clusters I-IV, IV-V, III-IV, and II-IV could be considered. So, hybridization between the genotypes of cluster I, II, III, IV, and V will manifest maximum heterosis and create wide genetic variability for economic characters in eggplant.

Investigation of twelve genotypes of brinjal were evaluated by Saha *et al*,. (2019). Ten quantitative characters of twelve genotypes in a completely randomized design were investigated their research work at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh, from October 2013 to March 2014. They found that PCV slightly higher than the GCV, which suggested the influence of the environment on the variability of these traits. Characters with a lower difference in GCV and PCV value could be improved by following phenotypic selection. Broad-sense heritability, coupled with moderate to low genetic advance was recorded in fruit length, average fruit weight, plant height and days to maturity. These traits were proposing the predominance of additive gene action. Days to first flowering, secondary branches per plant, fruit length and fruit diameter exhibited positive genotypic correlation with fruit yield per plant. In the case of path analysis, secondary branches per plant proposed maximum direct effect on the yield on both genotypic and phenotypic level followed by average fruit weight

and fruit length. To explore interrelations among brinjal genotypes for gaining optimum yield variability, correlation and path coefficient analysis act as prime tools for which this study was conducted.

Solaiman *et al,.* (2014) conducted a study with thirty-five brinjal genotypes in order to screen efficient genotypes for a hybridization program in Bangladesh. The phenotypic coefficient of variation (PCV) was higher than that for the genotypic. The PCV estimates were high for the number of branches, number of fruits per plant, and single fruit weight. Heritability estimates were high for the single fruit weight with high genetic advance. In spite of high heritability values for most traits, the expected genetic advance as a percentage of the mean ranged from 19.92 to 121.51. Multivariate analysis was performed using principal component analysis (PCA), principal coordinate analysis, cluster analysis and canonical variate analysis. With PCA, multivariate analysis of Mahalanobis's distance (D^2), and cluster analysis, the genotypes were grouped into six clusters. The longest inter-cluster distance was between clusters II and III, and the shortest was between clusters V and VI. Cluster VI showed the longest intra-cluster distance but cluster II showed the shortest. Genotypes of cluster I were suitable for the number of branches per plant, cluster II for the fruit length, cluster III for the number of fruits per plant, and cluster IV for the single fruit weight and yield. Considering the performances, genotypes SM-111, SM-84, EGN-27, SM-183, and BARI begun-6 are suitable parents for the hybridization program.

Ramesh *et al,.* (2013) conducted an experiment which consisted of 54 genotypes. Fruit yield was kept as a dependent character and the results were analysed. Analysis of variance revealed that considerable variability among the genotypes for all the characters. High estimates of phenotypic and genotypic co-efficient of variation was observed in the parents and for fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant. The characters viz., fruit length, calyx length, number of fruits per plant, little leaf

incidence, total phenol content and fruit yield per plant also recorded high magnitude of heritability coupled with genetic advance. Therefore, these traits should be kept in mind for better planning of improvement programme in Brinjal. The study further reveals that simple phenotypic selection could be effective for the improvement of aforesaid traits

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

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

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

Information on genetic divergence of sweet potatoes (*Ipomoea batatas*) was reported by Naskar *et al,*. (1996) from

Meghalaya and Bastar, Madhya Pradesh, was derived from data on 8 quantitative characters in 18 genotypes using Mahalanobis's D^2 statistic. The genotypes were grouped into 7 different clusters.

Cluster I had 8 genotypes, clusters II and III had 2 genotypes each, cluster IV had genetic divergence for yield contributing traits in sweet potato (*Ipomoea batatas*).

Yadav *et al,*. (2017) studied genetic divergence in 40 diverse type of brinjal. The genotypes differed significantly for 10 yield contributing characters and were grouped in 6 clusters. They observed no close relation between geographical distribution and genetic divergence.

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

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

(Gurve, 2018) Conducted a study to estimate the genetic divergence in brinjal and to carry out yield component analysis through correlation and path analysis. Twenty genotypes were sown in a randomized block design with two replications, during kharif 2017-2018 at Horticulture Research Scheme, College of agriculture, VNMKV, Parbhani, Maharashtra. The maximum genetic divergence was observed between clusters II and III. The maximum intra cluster distance was shown by cluster II. The characters viz.,fruit yield per hectare,fruit yield per plot, number of fruit per plant, average fruit weight, fruit length, fruit diameter, number of branches per plant, days to 50% flowering and plant spread (N-S) were contributed greatly towards diversity. The clusters showed high genetic divergence

that could be effectively utilized in heterosis breeding programme. If a breeding programme is used at improving nutritional characters, then cluster II showing maximum ascorbic acid that can be utilized in breeding programme. The analysis of variance revealed significant difference for twenty five characters studied suggesting considerable amount of variability exists among the genotypes. Wide range of variability was observed for plant height, plant spread, fruit setting percent, number of fruits per plant, average fruit weight, total phenolic content, fruit yield per plant, fruit yield per plot and fruit yield per hectare indicating the scope for selection of suitable initial breeding material for further improvement. GA as percent of mean, GCV and PCV values are on par with each other for most of the characters that the influence of the environment on the traits. The values observed are not confounding with the environment. It is a true to the reflection of the homeostasis effect or buffer reaction of the gene. Thus, the true reflection of the trait is exhibited. In a true agreement with the GCV and PCV values in the present investigation for the 25 characters was noticed, indicating additive genetic variance governing the high heritability with genetic advance as percent of mean.

An investigation was undertaken to estimate the genetic divergence in brinjal and to carry out yield component analysis through correlation and path analysis by (Gurve, 2018). They fpound that the breeder can employ a simple selection process which will be a rewarding one to improve the characters viz., average fruit weight, fruit length, number of fruit per plant, shoot and fruit borer infestation, ascorbic acid content, fruit yield per plant, fruit yield per plot, fruit yield per hectare, fruit diameter, flavonoid content and number of fruit per cluster. From correlation studies it was observed that fruit yield per plant has exhibited highly significant positive association with plant height, number of branches per plant, plant spread, number of fruit per plant, fruit length, fruit diameter, fruit pedicel length, ascorbic acid and fruit yield per hectare. Path analysis revealed that maximum positive direct effect on fruit yield per plant was exhibited by number of branches per plant, plant spread (N-S), days to 50% flowering, number of fruit per

plant, fruit pedicel length and ascorbic acid. Therefore, it is emphasized to lay attention on these traits like number of fruits per plant and number of branches per plant in crop improvement programme of brinjal in future. On the basis of the mean performance of the genotypes among traits studied, the following were identified as promising lines for further crop improvement in brinjalviz.,VR-2, Aussay, UtkalJyoti, PBNB-6, BH-2, JKGEH-6012, PBNB-5, PBNB-9, KashiTaru, UtkalKeshari and DMU-1.

Through genetic diversity based on multivariate analysis, hundred brinjal accessions were grouped into eight clusters for evaluation by (Rahman *et al,*. 2014). The cluster I contained the highest number of accessions (22) followed by the cluster V (19), III (17), IV (17), VII (10), VIII (7), II (6) and VI (2). The clustering pattern revealed that the accessions collected from the same region did not fall in a same cluster, indicating that there was no relationship between genetic divergence and geographical distribution of the accessions. The results of the PCA revealed that the first four of the principal component axes accounted for 78.07% of the variation among the genotypes considering ten characters. The maximum inter-cluster divergence was found between the cluster II and VI (32.234) and was minimum between V and VII (2.841). The maximum intra-cluster divergence was found between accessions falling in the cluster II. On the basis of the mean performance of different clusters, accessions having acceptable yield were placed in cluster IV, VI and VIII. The superior accessions may be selected from both maximum and minimum divergent clusters for further improvement.

Through genetic diversity based on multivariate analysis, hundred brinjal accessions were grouped into eight clusters by Rabbani *et al,*. (2014). The clustering pattern revealed that the accessions collected from the same region did not fall in a same cluster, indicating that there was no relationship between genetic divergence and geographical distribution of the accessions. The results of the PCA revealed that the first four of the principal component axes accounted for 78.07% of the variation among the genotypes considering ten characters. The maximum

inter-cluster divergence was found between the cluster II and VI (32.234) and was minimum between V and VII (2.841). The maximum intra-cluster divergence was found between accessions falling in the cluster II.

Genetic divergence in eighteen eggplant genotypes was studied by Uddin *et al,*. (2014) using multivariate analysis. The 18 genotypes were grouped into four distinct clusters. Clustering pattern of the genotypes was not correlated with their geographical distribution. The highest inter cluster distance was between cluster I and IV (764.67) while, it was the lowest between cluster II and III (213.30). The highest and lowest intra cluster distance was displayed in cluster II (94.14) and cluster I (28.79) respectively. Yield per plant, number of fruits per plant, plant canopy, fruit weight, fruit length and number of harvest had the highest contribution towards total divergence.

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

There were 36 genotypes of potato were grown in 16 environments were evaluated by Desai *et al,*. (1997) for genetic divergence by Mahalanobis's D^2 statistic. Nine clusters were identified. I was the largest, accommodating 7 genotypes.Cluster I, III, V and VII showed larger genetic divergence. Genotypes in clusters III had the highest tuber yields and other characters like number of stems, maturity, shoot fresh weight, number of tubers, sugar content and harvest index. Cluster I

contained genotypes with high dry matter and cluster IV those with dwarf plant height and early maturity and cluster VI those with high protein content.

An investigation was conducted by (Polignano *et al,*. 2010) to estimate Genetic divergence in 98 accessions of Solanum melongena L. and its allied species S. aethiopicum L. and S. macrocarpon L. for 16 morpho-agronomic and fruit traits revealed the existence of considerable diversity. Such collections were grown in the field during the 5 year EU-EGGNET project for characterization and seed multiplication. Diversity has been observed between the different species as well as within the species. Frequency distributions for fruit pedicel length, bitter flavour, browning, peelability, and cooking test were determined. Besides the qualitative descriptors, 11 quantitative descriptors were described. The relationships among them were analysed by Principal Component Analysis in order to summarize the data and reduce the number of variables for clustering. Plant height, flowering time, flower/inflorescence, fruit length and fruit acidity contributed mostly towards total divergence. Cluster analysis conducted separately for each species, in relation to the genetic status of accession (sub-species, botanical or variety group, cultivar and population), grouped the accessions into three distinct and significant clusters. No relationship was found between genetic divergence and genetic status of sample. In addition, relevant fruit discrete descriptors were used as a classification variable to ascertain whether some of them correspond to certain morpho-agronomic properties. The genotypes included in the diverse clusters could be used as promising parents for hybridization in order to obtain a high heterotic response and thus contribute to eggplant breeding.

The coordinates obtained from the Principal Component Analysis (PCA) are used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al,*. (2009). PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight line between each pair of points.

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

CHAPTER III
MATERIALS AND METHODS

This chapter presents the materials and method used in conducting the experiment. It consists of a short description of location of' the experimental plot, characteristics of soil, climate, material used, treatments, land preparation, manuring, and fertilization, transplanting and gap filling, staking and pruning, after cares, harvesting, and collection of data. These are described below:

3.1 Site of experiment: The study was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during the period from September 2019 to April 2020 The experimental site was at 22" E longitude and 41" N latitude at an altitude of 8.6 meters above the sea level.

3.2 Soil and climate: The soil of the experimental plots was clay loam land was medium high to medium high fertility level. The land belongs to Agro-ecological region of ‘Madhupur Tract’ (AEZ 28) of Nodda soil series. The site was situated in the subtropical climate zone, wet summer and dry winter is the general climatic feature of this region. The Rabi season is generally rainless with moderate temperature and short day length. Meteorological data on rainfall, temperature, relative humidity from September 2019 to April 2020 were obtained from the Department of Meteorological center, Dhaka-1207, Bangladesh. The selected plot was a medium high land. The pH of soil 4.66 to 5.93 while the amount organic carbon content, total N, available P and available K were 0.82%, 0.12%, 21 ppm and 0.27 mg per 100 gm of soil respectively.

3.3 Climatic condition: Climatic condition of the experimental site was located in the subtropical monsoon climatic zone, set aparted by heavy rainfall during the months from April to September (Kharif season) and scant of rainfall during the rest of the year (Rabi season). Plenty of sunshine and moderately low temperature

prevails during October to March (Rabi season) which is generally preferred for vegetable cultivation. Details of the meteorological data during the period of the experiment was collected from the Bangladesh Meteorological Department, Agargaon, Dhaka-1212 and presented in Appendix II.

3.4 Plant materials used in the experiment: A total of fifteen genotypes of brinjal (Table 1) collected from the local market of Joypurhat, Kushtia, Dinajpur, Jamalpur, India, BARI and department of genetics and plant breeding was used in this experiment.

3.5 Design and Layout: The study was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. Each replication contains 75 plants of 15 genotypes. The spacing of plant to plant was 75 cm × 75 cm and the row to row distance was 125 cm × 125 cm. The unit plot size was 13 m × 20 m. The plot distance was 50 cm. The genotypes were randomly distributed to each row within each line.

3.6 Seedbed preparation: Seedbed preparation for raising healthy seedlings was an important task before starting the field research work. In the farm a suitable place was selected for the seedbed and the size of the seedbed was 3 m × 1 m. For making seedbed, the soil was well ploughed and converted into loose friable and dried masses to obtain good tilt. Weeds, stubbles and dead roots were removed from the seedbed. The soil of seedbed was treated by Sevin 50WP @ 5 kg/ha to protect the young plants from the attack of mole crickets, ants and cutworms.

3.7 Treatment of seed: Before sowing seeds in the seedbed Sevin 50WP @ 3g/1kg seeds was applied to treat the seeds to protect some seed borne diseases such as leaf spot, blight, anthracnose, etc.

3.8 Raising of seedlings: Individual seed bed was prepared for different varieties following standard method of bed preparation. Seed were sown in lines in well prepared seed beds in the evening of 6th September, 2019. The seeds were sown at

about 1.25 cm depth and were covered uniformly with light soil for proper germination. Heptachlor was duster over the seedbed to prevent the seedling mainly from ant attack. Adequate measures were taken so as to avoid varietal mixture. The seed bed was watered as and when necessary for proper germination as well for normal growth of the seedling. After germination shading was arranged to protect the young seedling from scorching sunshine and was kept exposed during night, morning and afternoon. Proper nursing was done for developing healthy seedlings. At the attainment of 28 days of age, the seedlings were ready for transplanting.

3.9 Land preparation: The experimental plot was prepared by ploughing with tractor followed by harrowing and laddering by power tiller. Weeds and stubbles were removed. Manures and fertilizers were applied as per the recommended dose before the final land preparation. Irrigation channels were made around each plot. The final land preparation was done on 6th September.

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

3.11 Transplanting of seedlings: Twenty eight days old seedlings were transplanted in well prepared experimental plot on 28th September, 2019. Five plants were planted for each genotype in single row of 7.5 m length in each replication maintaining plant spacing of 75 cm and row to row distance 125 cm.

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 genotype against fruit and shoot borer. Proper shadings were given in the morning at the first stage of transplanting to protect the young seedlings from scorching sunshine during day time. Shadings were removed at the afternoon. Extra soils were added around the root for proper rooting. Sticks were given to protect the plant from falling due to strong wind. Gap filling was done twice, firstly 11 days after transplanting and 2nd time 23 days after transplanting. Weeding was done for the first time 18 days after transplanting. Weeding was also done in several times by two weeks interval. In the early stage of transplanting watering was done twice a daily by water cane. In mature stage, flood irrigation was done to the field.

3.13 Data collection: Three plants were selected for each genotype from every replication and tagged properly at random from each row for recording data. Data on days to first flowering, days to 50% flowering, days to first harvesting, fruit color, fruit shape, plant height, no. of primary branches/plant, no. of secondary branches/plant, fruit length, fruit diameters, fruit per plant, weight per fruit, yield per plant, percent insect infestation were recorded.

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

3.13.2 Hairiness: The presence of hairiness on leaf, stem was recorded.

3.13.3 Plant height (cm): Length of main stem from ground level to the tip of the stem was measured at final harvest.

3.13.4 Days to first flowering: Days from sowing to first flowering of every plant of every genotype was recorded.

3.13.5 Days to 50% flowering: Days from sowing to 50% flowering of every plant of every genotype was recorded according to their flowering performances.

3.13.6 Days to first harvesting: Days from sowing to first harvest of every plant of every genotype was recorded.

3.13.7 Spiny character: The spineness of leaf, stem, and fruit of the brinjal plants was recorded.

3.13.8 Color of fruit: Fruit color of the brinjal genotypes was recorded.

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

3.13.10 Fruit length (cm): Length from the top to the bottom of 5 initially matured fruits per plant was recorded.

3.13.11 Fruit diameter (cm): Measured along the middle part of the harvestable mature fruits.

3.13.12 Number of primary branches per plant: Number of primary branches of each randomly selected plant was recorded.

3.13.13 Number of fruits per plant: Total number of fruits harvested from individual plant was recorded.

3.13.14 Weight of fruit (g): Weight of individual fruit per plant was recorded.

3.13.15 Yield per plant (g): Total fruits harvested from each selected plant in each replication were weighted together and yield per plant was recorded.

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

Plate 1. View of the experimental field.

3.14 Statistical analysis: The analyses of variance (ANOVA) which express the major interaction effects was analyzed using STAR, version 2.0.1 (2014) for all quantitative traits. The Tukey test was performed for mean comparison when varietal differences were found significant.

Multivariate statistical analysis, such as D^2 statistics and principal component analysis (PCA) could be used to assess the genetic diversity of quantitative traits (Melchinger, 1993). Cluster analysis which is a multivariate technique can group individuals or objects on the basis of their characteristics. Individuals having similar descriptions are mathematically congregated into same cluster. Distance, similarity or relatedness of varieties is the foundation of this method. On the basis of distance or model, clustering can be done. There are two groups in distance-based method, such as hierarchical and non-hierarchical. Hierarchical is known as agglomerative hierarchical, where similar varieties are grouped in one cluster

according to their similarities on the other hand dissimilar varieties are grouped in different cluster. The un-weighted pair group method with arithmetic means (UPGMA) is mostly used among different agglomerative hierarchical methods.

The non-hierarchical clustering method is known as K-means clustering, which is based on sequential threshold, parallel threshold, or optimizing. Dendrogram or tree is not constructed in this method. For the analysis of intraspecific genetic diversity in crop plant, non-hierarchical clustering method is hardly used (Mohammadi, 2003). Principal component analysis (PCA) is a method of data reduction in order to clarify the relationship between two or more characters and to divide the total variance of the original characters in to a limited number of uncorrelated new variables (Wiley, 1981). Two or three dimensional scatter plot of individual is found from PCA. Eigen value which defines the amount of total variation is found from PCA calculation and it is displayed on the PC (principal component) axis. The first PC is variability found from the original data relative to all remaining and the second PC is variability not summarized by the first PC and uncorrelated with the first. The ratio of variation due to each PC is revealed as the eigen value (Mohammadi, 2003).

3.14.1 Principal Component Analysis (PCA): Principal component analysis (PCA) is a method of data reduction in order to clarify the relationship between two or more characters and to divide the total variance of the original characters in to a limited number of uncorrelated new variables (Wiley, 1981). Two or three dimensional scatter plot of individual is found from PCA. Eigen value which defines the amount of total variation is found from PCA calculation and it is displayed on the PC (principal component) axis. The first PC is variability found from the original data relative to all remaining and the second PC is variability not summarized by the first PC and uncorrelated with the first. The ratio of variation due to each PC is revealed as the eigen value (Mohammadi, 2003).

3.14.2 Principal Coordinate Analysis (PCO): Genetic diversity was estimated following Mahalanobis's generalized distance (D^2). Selection of parents in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Principal Coordinate Analysis is equivalent to PCA but is used to calculate inter unit distances. Through the use of all dimensions of P it gives the minimum distance between each pair of the N points using similarity matrix (Digby *et al.,* 1989).

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

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

CHAPTER IV
RESULTS AND DISCUSSION

Brinjal (*Solanum melongena*) is an important vegetable crop in Bangladesh cultivated all the year round. It is also grown in tropics and sub-tropics. Brinjal consumers like different types of brinjals which vary from place to place. Wide exploration should be carried out to get good variety including high yield potentiality as well as resistance to insect pests and disease. Genetic diversity plays important role in varietal development of any crop. The success of increasing the productivity of any crop through breeding largely depends on the presence of variability among the breeding materials (Adeyemo and Ojo, 1991). Variation of the parents in a breeding program allows getting transgressive segregants**.** Information regarding the magnitude and nature of genetic variation within a crop species is vital for a successful breeding program. Long term selection gain could be achieved through better knowledge of genetic diversity or genetic similarity. Increase in yield and quality of any crop is normally attained by selecting genotypes with desirable trait combinations existing in nature or by hybridization. Selection of parents identified on the basis of divergence analysis would be more promising for a hybridization program. Information concerning genotypic variation within genotypes with regard to morphology, phenology and yield could help to examine better materials. Therefore, to get information on the degree of divergence in fifteen genotypes of brinjal were raised in the growing season of 2019-2020 at the field of Sher-e-Bangla Agricultural University, Dhaka. The data of days to first flowering, days to 50% flowering**,** fruit number, days to first fruit harvest**, l**eaf area**,** calyx length, fruit yield etc. were collected and analyzed and presented in this chapter.

Table 1. Characteristics of 15 brinjal genotypes

Genotype	Growth Habit	Hairness	Spiny character	Fruit Colour	Fruit Shape
G-1	Erect	Leaf, Stem	No spike	Dark Purple	Semi long
G-2	Semi erect	Leaf, Stem	Stem	Whitish Green	Oval
G-3	Semi erect	Leaf, Stem	No spike	Whitish Green	Round
G-4	Spreading	Leaf, Stem	No spike	Purple	Round
G-5	Semi erect	Leaf, Stem	Stem, leaf lower petiole	Green	Round
G-6	Spreading	Leaf, Stem	Leaf lower petiole	Dark Purple	Round
G-7	Erect	Leaf, Stem	No spike	Green	Round
G-8	Spreading	Leaf, Stem	Leaf lower petiole , Fruit Calyx	Purple	Long Curved
G-9	Spreading	Leaf, Stem	Fruit calyx	Purple	Long Curved
G-10	Spreading	Leaf, Stem	No spike	Purple	Semi Long
G-11	Semi erect	Leaf, Stem	No spike	Purple	Semi Oval
G-12	Erect	Leaf, Stem	No spike	Purple	curved Oval
G-13	Erect	Leaf, Stem	Leaf, Stem	Green	Oval
G-14	Erect	Leaf, Stem	Leaf, Stem, Fruit calyx	Whitish Green	Round
G-15	Semi erect	Leaf, Stem	Leaf, Stem, Fruit calyx	White	Oval

Note:
G1= Brinjal mukta keshi, G2= Kushtia-2 lomba begun, G3= Shabuj sathi, G4=Mental, G5= Gol begun, G6= Brinjal black beauty, G7= Nice ball, G8= Purple king hybrid, G9 = Shingnath, G10= Chumki, G11= Majic ball, G12= Altapon, G13= India-1, G14= Dinajpur katali begun, G15= Aveo round.

Morphological Characterization of brinjal:

4.1.1 Growth habit: Plant breeders emphasized on plant architecture in order to improve plant ideotype for a particular environment. The brinjal genotypes under the current study have been categorized into three different groups based on three separate growth habit. The genotypes G1, G7, G12, G13 and G14 were erect; the genotypes G2, G3, G11 and G15 were semi-erect and rest of the brinjal genotypes were spreading in growth habit (Table 1). The farmers prefer semi-erect brinjal variety to grow more plants in per unit area in order to get higher yield. Moreover, this type of plant is convenient for intercultural operation in the field.

4.1.2 Hairiness: Hairiness which is an important character of brinjal plant plays pivotal role against pest. Densely hairy brinjal plant is highly resistant to pest. All the 15 genotypes were characterized with hairiness in the present study (Table 1). Hairiness was observed generally at leaf and stem.

4.1.3 Shape of fruit: Fruit shape of brinjal is essential trait in case of marketing. Different types of brinjals are found based on shape. Semi-long, long curved, round, oval, semi-oval, curved oval shaped brinjals were found among the genotypes under the study. The genotype G12 merely produced curved oval, genotypes G1 and G10 produced semi long, genotypes G2, G13 and G15 produced oval, genotypes G8 and G9 produced long curved, genotype G11 only produced semi-oval, genotypes G3, G4, G5, G6, G7 and G14 produced round shaped fruits (Table 1).

4.1.4 Color of fruit: Another vital trait of brinjal is fruit colour. It plays good role in brinjal marketing. Usually green and violet color brinjal fruits are commonly seen in the markets. Nevertheless, huge variations in fruit color were observed in the current study and which could be categorized in separate groups: purple, dark purple, green, whitish green and white. The only white color genotype was G15. The genotypes G1 and G6 were dark purple in color; green genotypes were G5,

G7 and G13; whitish green genotypes were G2, G3 and G14; the remaining genotypes G4, G8, G9, G10, G11 and G12 were purple in color (Table 1). The deviation in fruit color provides an excellent possibility for breeding customer favorite characteristics.

4.1.5 Spiny character: Presence or absence of spine is another characteristics found in brinjal plant. Different types of brinjal genotypes are characterized by their spine. This vital trait plays crucial role in defense system particularly in insect resistance. Different genotypes were categorized based on presence of spine in their fruit, stem or leaves. Spine found only in the stem, stem and leaf, stem and leaf lower petiole, in genotypes G2, G13 and G5 respectively. Leaf, stem and fruit calyx of genotypes G14 and G15 were spiny. While spine found only in the leaf lower petiole in case of genotype G6. Spine was seen merely in fruit calyx in genotype G9. Genotype G8 had spine in leaf, lower petiole and in fruit calyx. The rest of the genotypes G1, G3, G4, G7, G10, G11 and G12 had no spine (Table 1).

4.1.6 Days to first flowering: The trait days to first flowering of different genotypes showed variation (Table 4). The genotype G2 took the longest time (74 days) for flowering from seedling on the other hand genotype G7 showed the lowest (60 days) number of days to first flowering (Table 2a). The average number of days to first flowering was 68 days (Table 3). The number of days to flowering recorded in this study is within the range of days reported by Mangi *et al.* (2016). Variation in days to first flowering in different brinjal genotypes are in conformity with Ashwani and Khandelwal (2003), Mahaveer *et al.* (2004). The reason of variation among the genotypes for days to first flowering could be genetic composition along with environmental factor such as temperature or day length. Sambandam (1960) studied the number of days required for flowering in different brinjal genotypes and concluded that the variation was due to the varietal characteristics.

4.1.7 Days to 50% flowering: Days to 50% flowering varied significantly ($P<0.05$) among the different genotypes (Table 3). Genotype G2 had the highest (93.33 days) number of days to 50% flowering on the other hand genotype G13 took the lowest (78.33 days) number of days to 50% flowering (Table 2a). The average number of days to 50% flowering was 88.11 days (Table 3). Deviation with regard to days to 50% flowering in different brinjal genotypes was also reported (Vidhya and Kumar, 2015; Tripathy et al., 2017).

4.1.8 Days to first fruit harvest: Significant differences were observed among all the genotypes for days to first fruit harvest (Table 3). Mean performance of genotypes for days to first fruit harvest ranged from 79.67 days to 103 days with an average of 93.27 days. The earliest fruit harvesting was recorded in genotype G13 (79.67 days) followed by G9 and G10 (87.33 days). However, maximum days to first fruit harvesting were recorded in the genotype G14 (103.01 days) (Table 2). Above findings with regard to variation in first fruit harvesting in different brinjal genotypes are in conformity with. (Begum *et al,*. 2013; Umesh *et al,*. 2018; Gurve *et al,*. 2019).

4.1.9 Leaf area: Leaf area exhibited significant differences among all the genotypes (Table 3). The leaf area ranged in between 44.33 and 83.67 with an average of 58.38. Genotype G3 had the largest (83.67) leaf area while genotype G10 had the lowest (44.33) (Table 2). Variation in leaf area in different brinjal genotypes were also reported. (Javed *et al*., 2011).

4.1.10 Calyx length: Fifteen different brinjal genotypes under the current study revealed variations in their calyx length (Table 3). The average calyx length was 5.95 and it varied significantly (<0.01) from 4.43 to 9. Among the brinjal genotypes under the study, the highest calyx length was observed in genotype G8 (9.01) and the lowest was in G15 (4.43) (Table 2). Dissimilarity in calyx length of

brinjal genotypes was also observed by some scientists (Kumar *et al.,* 2013; Kaushik *et al.,* 2016).

4.1.11 Number of primary branches per plant: Number of primary branches is a vital morphological trait which plays important role to yield and number of fruit per plant. Number of primary branches showed significant differences among all the genotypes (Table 3). Mean performance of genotypes for number of primary branches ranged from 9.43 to 12.88. Average mean for the character was 10.47. The lowest number of primary branches was recorded in genotype G5 (9.43) and the highest was found in genotype G9 (12.88) (Table 2). These results are in conformity with the findings of (Begum, 2014; Tripathy *et al.,* 2017) who reported significant variation among the cultivars of brinjal for the number of primary branches per plant.

4.1.12 Number of secondary branches per plant: The number of secondary branches per plant was found to vary significantly (Table 3) from 18.30 to 31.35 with an average of 24.48. Genotype G6 had the lowest number of secondary branches per plant on the other hand G9 had the highest number of secondary branches per plant (Table 2). These findings were in accordance with Konyak *et al,.* (2020).

Table 2 (a). Mean performance of different characters of fifteen brinjal genotypes

GENOTYPES	DFF	DFIF	DFFH	LA	CL	PBPP	SBPP
G1	64.67ab	83ab	94.33 abc	70.33 bc	4.47 f	9.84 c	23.12ef
G2	74a	93.33a	97.67 ab	76.00 ab	6.90 b	9.53 c	24.13c
G3	67.67ab	92.67 ab	96.00 ab	83.67 a	6.63 bc	10.00 bc	23.6c
G4	68.33ab	91.67 ab	94.00 abc	49.67 de	5.10 def	11.18 abc	24.26def
G5	68.33a	93.33 a	98.00 ab	77.00 ab	5.13def	9.43 c	18.7def
G6	70.67ab	91.67 ab	97.33 ab	56.00 de	5.20 def	10.76 bc	17.23bc
G7	60ab	80.00 ab	88.33 abc	58.67 cd	5.73 cde	9.97 c	21.01ab
G8	70ab	88.00 ab	93.33 abc	69.00 bc	9.00 a	9.67 c	22.07a
G9	62ab	84.00 ab	87.33 bc	53.33 de	8.27 a	12.88 a	31.85a
G10	70.33a	86.33ab	87.33 bc	44.33 e	5.83 cd	10.57 bc	22.82abc
G11	68.67ab	88.33ab	97.00 ab	46.33 e	5.40 def	10.84 bc	31.63ab
G12	73.33ab	91ab	92.67 abc	51.33 de	6.90 b	9.85 c	27.63e
G13	67ab	78.33ab	79.67 c	45.33 e	4.77 ef	10.53 bc	22.31e
G14	71.33a	91ab	103.00 a	45.33 e	5.43 def	12.02 ab	27.15e
G15	63.67ab	89ab	93.00 abc	49.33 de	4.43 f	10.00 bc	22.67e

Note:
G1= Brinjal Mukta Keshi, G2= Kushtia-2 Lomba begun, G3= Shabuj Sathi, G4= Mental, G5= Gol Begun, G6= Brinjal Black Beauty, G7= Nice Ball, G8=Purple King Hybrid, G9= Shingnath, G10=Chumki, G11= Majic Ball (F1), G12=Altapon, G13= India-1, G14= Dinajpur Katali Begun, G15= Aveo Round (F1).DFF= Days to first flowering, DFIF= Days to 50 % flowering, DFFH= Days to first fruit harvest, LA= Leaf area, CL= Calyx length, PBPP= Number of primary branches per plant, SBPP= Number of secondary branches per plant

Table 2 (b). Mean performance of different characters of fifteen brinjal genotypes

GENOTYPES	WSF	FB	FL	FNPP	PIIF	PIIP	FYPP	WSF	FB
G1	328.33 a	7.90 a	20.00 c	23.33a	6.40 i	9.95 ef	7.65 a	328.33 a	7.90 a
G2	154.00 ef	5.77de	18.23 cd	20.00 abc	12.30 fg	21.33 b	3.07 de	154.00 ef	5.77de
G3	170.67 de	7.07 abc	16.00 de	20.67ab	15.60 cde	7.73 f	3.52 d	170.67 de	7.07 abc
G4	126.33 fg	6.40 bcd	14.51ef	20.33 ab	13.37 ef	22.84 ab	2.57 ef	126.33 fg	6.40 bcd
G5	117.00 g	6.30 cd	11.67fg	14.00 ef	18.50 ab	25.33 a	1.64 gh	117.00 g	6.30 cd
G6	111.67 g	7.50 ab	13.30 efg	9.67g	20.82 a	23.62 ab	1.08 h	111.67 g	7.50 ab
G7	188.67 cd	8.03 a	16.07 de	19.00 bc	18.19abc	22.74ab	3.58d	188.67 cd	8.03 a
G8	313.33 ab	4.60 efg	37.93 a	21.33 ab	10.45 gh	12.18de	6.68 b	313.33 ab	4.60 efg
G9	124.67 fg	3.95 g	26.63 b	18.00 bcd	16.25 bcd	21.67 b	2.24 g	124.67 fg	3.95 g
G10	187.00 cde	4.77 efg	20.63 c	13.00 fg	19.75 a	18.12c	2.43 ef	187.00 cde	4.77 efg
G11	287.67 b	5.60def	21.57 c	16.67 cde	12.46 fg	12.95 d	4.79 c	287.67 b	5.60def
G12	97.33 gh	4.47fg	20.68 c	12.00 fg	14.78 def	24.87 a	1.16 h	97.33 gh	4.47fg
G13	76.67 h	4.23 g	10.47 g	15.00 def	13.42 ef	16.24 c	1.15h	76.67 h	4.23 g
G14	217.33 c	7.50 ab	10.73 g	10.33 g	7.97 hi	15.91c	2.24 fg	217.33 c	7.50 ab
G15	183.67 cde	7.17 abc	13.83 efg	14.00 ef	6.87i	9.67 ef	2.56 ef	183.67 cde	7.17 abc

Note:
G1= Brinjal Mukta Keshi, G2= Kushtia-2 Lomba begun, G3= Shabuj Sathi, G4= Mental, G5= Gol Begun, G6= Brinjal Black Beauty, G7= Nice Ball, G8=Purple King Hybrid, G9=Shingnath, G10=Chumki, G11= Majic Ball, G12=Altapon, G13= India-1, G14= Dinajpur Katali Begun, G15= Aveo Round . WSF= Weight of single fruit, FB= Fruit breadth, FL = Fruit length, FNPP= Fruit number per plant, PIIF= Percent insect infestation of fruit, PIIP= Percent insect infestation of plant, FYPP= Fruit yield per plant.

4.1.13 Weight of single fruit: Fifteen different brinjal genotypes under study showed variations in their single fruit weight (Table 3).The genotype G1 was found to have the highest fruit weight (328.33 g) while genotype G13 produced the lowest fruit weight (76.67g). The average fruit weight for this trait was 178.96 g (Table 3). Variation in single fruit weight in different brinjal genotypes was also reported by Akter and Rahman (2019).

4.1.14 Fruit breadth: The trait fruit breadth exhibited significant variation among the brinjal genotypes in this study (Table 3). The highest fruit breadth having genotype was G7 (8.03 cm) on the other hand the lowest fruit breadth having genotype was G9 (3.95 cm) (Table 3). The average mean value for this trait was 6.08 cm. Several other scientists also found variation in fruit breadth among the brinjal genotypes (Akter and Rahman, 2019; Gurve *et. al.*, 2019).

4.1.15 Fruit length: Fruit length was significant among all the brinjal genotypes with an average of 18.15 cm. It ranged from 10.47 to 37.93 cm (Table 3). The highest fruit length was recorded for the genotype G8 and the lowest was for G13. Differences in fruit length among the brinjal genotypes were also reported in many studies (Begum, 2014; Umesh *et al.*, 2018; Gurve *et al.*, 2019).

4.1.16 Fruit number per plant: Wide range of variation was observed in fruit number per plant under the present study (Table 3). Mean performance of genotypes for fruit number per plant varied from 9.67 to 23.33 no with an average mean of 16.49 no. The highest fruit bearing genotype was genotype G1 and the lowest was recorded in genotype G6 (Table 2). These findings regarding to variation in fruit number per plant in different brinjal genotypes are in conformity with, Akter and Rahman, (2019); Mohanty *et al,*. (2021).

Table 3. Analysis of variance for fourteen characters of 15 brinjal genotypes

S.O.V	df	SBPP	WSF	FB	FL	FNPP	PIIF	PIIP
Rep	2	11.31	163.35	0.43	1.95	1.15	2.24	12.89
Genotypes	14	43.19**	18373.42**	6.05**	152.46**	54.61**	61.83**	108.87**
Error	28	1.64	126.97	0.15	1.39	1.36	0.77	0.78
S.O.V	**df**	**FYPP**	**DFF**	**DFIF**	**DFFH**	**LA**	**CL**	**PBPP**
Rep	2	0.04	502.46	30.95	47.40	9.62	0.76	0.05
Genotypes	14	11.38**	47.95ns	69.79*	97.77**	530.08**	5.44**	2.78**
Error	28	0.06	56.56	23.97	26.47	15.43	0.11	0.45

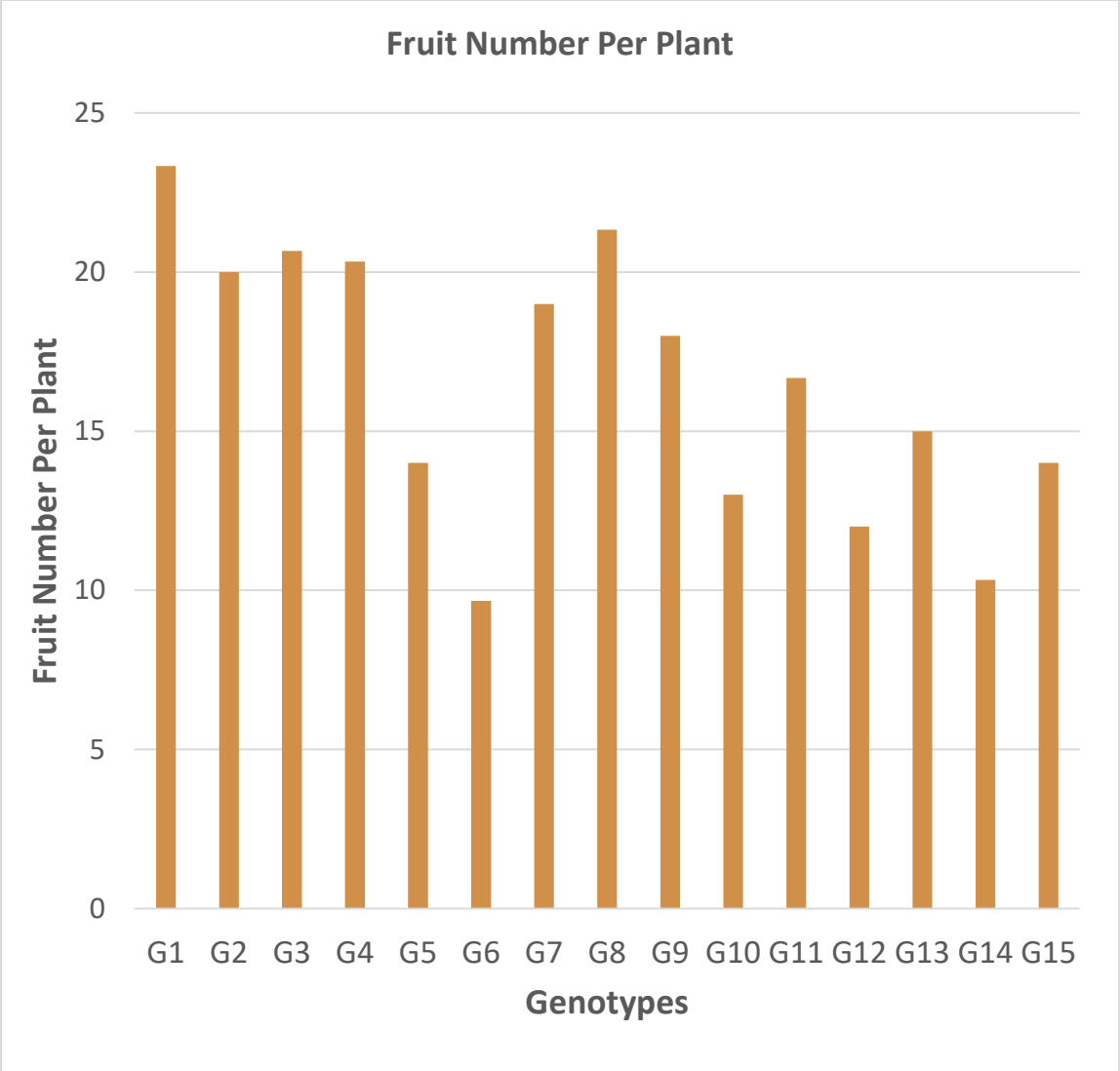
Note:
DFF= Days to first flowering, DFIF= Days to 50 % flowering, DFFH= Days to first fruit Harvest, LA= Leaf Area, CL= Calyx Length, PBPP= Number of primary branches per plant, SBPP= Number of secondary branches per plant, WSF= Weight of single fruit, FB= Fruit breadth, FL= Fruit length, FNPP= Fruit number per plant, PIIF= Percent insect infestation of fruit, PIIP= Percent insect infestation of plant, FYPP= Fruit yield per plant.

4.1.17 Percent insect infestation of fruit: Fruit and shoot borer affect brinjal production and cause significant harm to yield (Table 3). So resistance against insect attack is an efficient trait of brinjal plant. Their rates of attack against different genotypes were significantly different in the current study. In this study, it was revealed that the fruits of genotype G6 (20.82%) was highly affected and the genotype G1 (6.41%) was least affected which mentioned that the genotype G1 was the most resistant and superior to the rest of the variety (Table 3). The average value of this trait was 13.81%. Variation in fruits infestation among different brinjal genotypes was also reported (Vidhya and Kumar, 2015; Akter and Rahman, 2019; Gurve *et al.,* 2019).

4.1.18 Fruit yield per plant (g): The brinjal genotypes under the current study showed significant variation for fruit yield per plant (Table 3). The highest fruit

yielding genotype was G1 (7.65 kg/plant) followed by G8 (6.68 kg/plant) and the lowest genotype for this trait was G6 (1.08 kg/plant) (Table 3).. The average value for this trait was 3.09 kg/plant. These findings regarding to variation in fruit yield per plant in different brinjal genotypes are in conformity with, (Begum, 2014; Gurve *et al*,. 2019; Mohanty *et al*,. 2021).

4.1.19 Percent insect infestation of plant: Percent insect infestation of plant varied significantly among the brinjal genotypes (Table 3). It ranged from 7.73 to 25.33 % indicating variation exists among the genotypes under this study. The average percent insect infestation of plant was 17.68%. Genotype G5 had the highest number of infestation on the contrary genotype G3 had the lowest infestation (Table 3). Begum, (2014) also reported variation in percent insect infestation among different brinjal genotypes.



Note,
G1= Brinjal Mukta Keshi, G2= Kushtia-2 Lomba begun, G3= Shabuj Sathi, G4=Mental, G5= Gol Begun, G6=Brinjal Black Beauty, G7=Nice Ball, G8=Purple King Hybrid, G9= Shingnath, G10=Chumki, G11= Majic Ball, G12= Altapon, G13= India-1, G14= Dinajpur Katali Begun, G15= Aveo Round.
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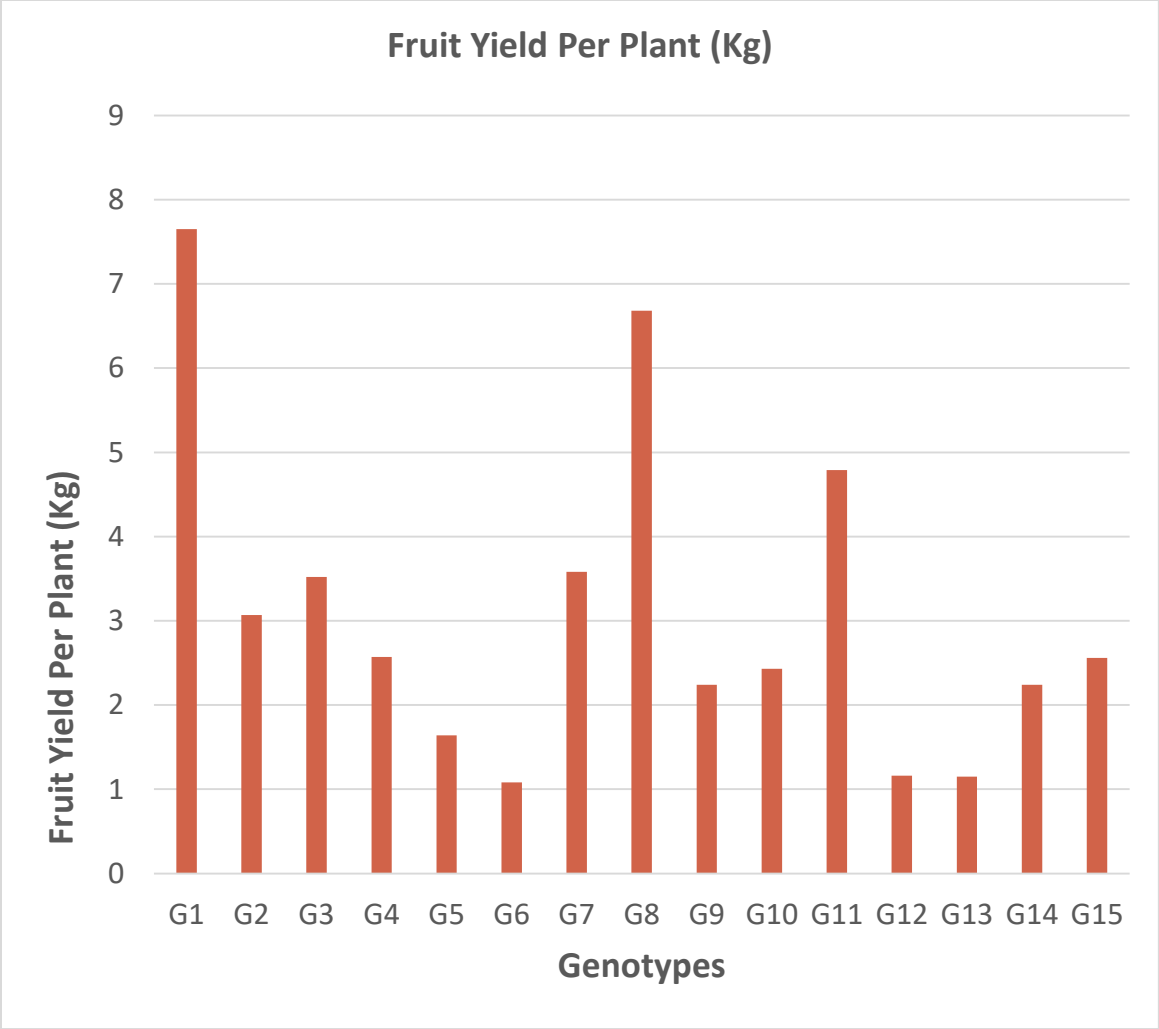
Figure 1. Number of fruit per plant in different brinjal genotypes

4.2 Variability among brinjal genotypes: Analysis of variance exhibited that the brinjal genotypes varied significantly (1% level of probability) with each other (Table 3). Range, mean and co-efficient of variation of 14 characters of brinjal genotypes namely days to first flowering, days to 50% flowering, days to first fruit harvest, leaf area, calyx length, number of primary branches per plant, number of secondary branches per plant, weight of single fruit, fruit breadth, fruit length, fruit number per plant, percent insect infestation of fruit, percent insect infestation of plant, fruit yield per plant have been presented in (Table 2b). The mean values and coefficient of variation of the traits indicated the existence of considerable variation present among the genotypes (Table 4). Among the 15 brinjal genotypes all the traits were significantly varied except days to first flowering. Thus, it implied existence of variation for all the characters among the genotypes. Phenotypic variation among brinjals has been reported by many researchers for different characters in different brinjal genotypes (Nyadanu *et al.,* 2014; Gurve *et al,*. 2019; Akter and Rahman, 2020). Highly significant difference among 22 genotypes of brinjal of Bangladesh with 12 different traits was observed (Akter and Rahman, 2020). Using 10 different traits, Akpan *et al,*. (2016) observed highly significant variation among 10 brinjal genotypes in different study. Previously, high genetic dissimilarity for various quantitative traits in brinjal was also recorded Nyadanu *et al.,* (2014). Similar finding was also reported by some researchers (Begum *et al.,* 2013; Karim *et al*., 2016; Mohanty *et al*., 2021). Highly significant divergence was detected among 50 brinjal genotypes with 12 different traits Arti *et al.,* (2018).



Note,
G1= Brinjal Mukta Keshi, G2= Kushtia-2 Lomba begun, G3= Shabuj Sathi, G4=Mental, G5= Gol Begun, G6=Brinjal Black Beauty, G7=Nice Ball, G8=Purple King Hybrid, G9= Shingnath, G10=Chumki, G11= Majic Ball, G12= Altapon, G13= India-1, G14= Dinajpur Katali Begun, G15= Aveo Round.

Figure 2. Fruit yield per plant in different brinjal genotypes.

Table 4. Range, mean, standard deviation and co-efficient of variation for fourteen characters of 15 brinjal genotypes

Characters	Minimum	Maximum	Mean	Std Error	CV%
DFF	60	74	68	6.14	11.06
DFIF	78.33	93.33	88.11	4.00	5.56
DFFH	79.67	103	93.27	4.20	5.52
LA	44.33	83.67	58.38	3.21	6.73
CL	4.43	9	5.95	0.2785	5.74
PBPP	9.43	12.88	10.47	0.54	6.41
SBPP	18.3	31.35	24.48	1.05	5.24
WSF	76.67	328.33	178.96	9.20	6.3
FB	3.95	8.03	6.08	0.31	6.38
FL	10.47	37.93	18.15	0.96	6.5
FNPP	9.67	23.33	16.49	0.95	7.1
PIIF	6.4	20.82	13.81	0.71	6.36
PIIP	7.73	25.33	17.68	0.72	5.01
FYPP	1.08	7.65	3.09	0.20	8.22

Note:

DFF Days to first flowering, DFIF Days to 50 % flowering, DFFH Days to first fruit harvest, LA Leaf area, CL Calyx length, PBPP Number of primary branches per plant, SBPP Number of secondary branches per plant, WSF Weight of single fruit, FB Fruit breadth, FL Fruit length, FNPP Fruit number per plant, PIIF Percent insect infestation of fruit, PIIP Percent insect infestation of plant, FYPP Fruit yield per plant.

4.2.1 Diversity of the brinjal genotypes: In this experiment, data were analyzed based on Euclidian distance method, using NTSYS-pc software (version 2.1). In order to determine genetic relationships among the brinjal genotypes the UPGMA algorithm and SAHN clustering were applied. The PCA of 15 brinjal genotypes was calculated by EIGEN and PROJ modules of NTSYS-pc and Minitab software (version 17).

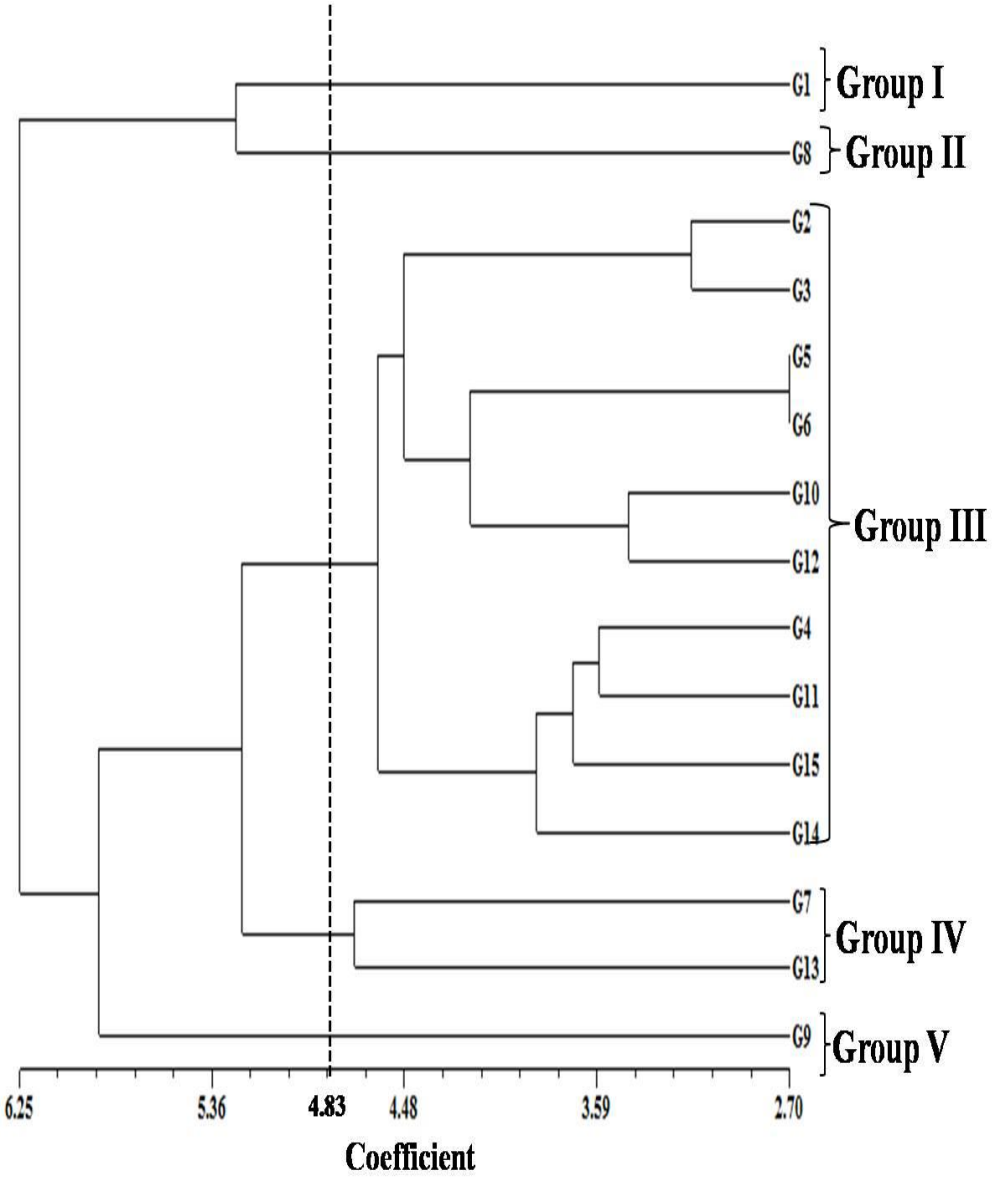
4.2.2 Cluster analysis of different traits: The standardized data were employed to calculate the Euclidean distances among the 15 brinjal genotypes and an UPGMA dendrogram was constructed using these values (Figure 3). In this dendrogram, the 15 brinjal genotypes were grouped into 5 major clusters based on

14 different traits at 4.83 dissimilarity coefficient. In this case, cut off point was set at 4.83 only for the convenience of discussion.

Cluster I, II and V each had one genotype only and cluster III and IV had ten and two genotypes respectively figure 3 and (Table 5). The highest and nearly highest yield and yield component traits such as fruit yield per plant, fruit number per plant, weight of single fruit and less insect infestation were under cluster I followed by cluster II (Table 6).

Cluster III consisted of genotypes with highest and nearly highest average of days to first flowering, days to 50% flowering, days to first fruit harvest, primary branches per plant, secondary branches per plant, fruit breadth, percent insect infestation of fruit, percent insect infestation of plant (Table 6). However, cluster V contained the genotype having lowest and nearly lowest average for most of the traits (Table 6).

The Euclidian clusters analyses grouped 15 brinjal genotypes into five clusters based on different traits at distant coefficient of around 4.83 which implies a high level of diversity in the brinjal genotypes. Result of this assay unveiled the better resolution power of quantitative traits for grouping of brinjal genotypes. On the basis of 12 important characters 50 brinjal genotypes were clustered into eight groups in a study conducted by Arti *et al,*. (2021). In their study, group I, III and VI and VII (each group) consisted of four members. Group II, V and VIII each group had nine members. Group IV contained seven members. Moreover, 22 brinjal genotypes were clustered into five different groups based on 12 different traits. Group II had highest number of genotypes (6) and group IV contained the lowest (I) (Akter and Rahman, 2020). Therefore, classification in this study based on different characters was in agreement with previous report.



Note:

G1= Brinjal Mukta Keshi, G2= Kushtia-2 Lomba begun, G3= Shabuj Sathi, G4=Mental, G5= Gol Begun, G6=Brinjal Black Beauty, G7=Nice Ball, G8=Purple King Hybrid, G9= Shingnath, G10=Chumki, G11= Majic Ball, G12= Altapon, G13= India-1, G14= Dinajpur Katali Begun, G15= Aveo Round.

Figure 3. The dendrogram of 15 brinjal genotypes derived from fourteen different traits using the UPGMA method and dissimilarity coefficient.

Table 5. Distribution of 15 brinjal genotypes in five different cluster

Cluster	Total no. of Genotypes	Name of Genotypes
Cluster I	1	G1
Cluster II	1	G8
Cluster III	10	G2, G3, G4, G5, G6, G10, G11, G12, G14, G15
Cluster IV	2	G7,13
Cluster V	1	G9

Note:

G1= Brinjal Mukta Keshi, G2= Kushtia-2 Lomba begun, G3= Shabuj Sathi, G4=Mental, G5= Gol Begun, G6=Brinjal Black Beauty, G7=Nice Ball, G8=Purple King Hybrid, G9= Shingnath, G10=Chumki, G11= Majic Ball, G12= Altapon, G13= India-1, G14= Dinajpur Katali Begun, G15= Aveo Round.

Table 6. Cluster mean for fourteen characters of 15 genotypes of brinjal

CLUSTER	DFF	DFIF	DFFH	LA	CL	PBPP	SBPP	WSF	FB	FL	FNPP	PIIF	PIIP	FYPP
I	64.67	83.01	94.33	70.33	4.47	9.84	23.51	328.33	7.91	20.01	23.33	6.41	9.95	7.65
II	70.01	88.01	93.33	69.01	9.01	9.67	21.77	313.33	4.61	37.93	21.33	10.45	12.18	6.68
III	69.63	90.84	95.61	57.9	5.7	10.42	24.58	165.27	6.26	16.11	15.07	14.25	18.23	2.51
IV	63.51	79.17	84	52	5.25	10.25	22.4	132.67	6.13	13.27	17.01	15.81	19.49	2.37
V	62.01	84.01	87.33	53.33	8.27	12.88	31.35	124.67	3.95	26.63	18.01	16.25	21.67	2.24

Note:

DFF Days to first flowering, DFIF Days to 50 % flowering, DFFH Days to first fruit harvest, LA Leaf Area, CL Calyx length, PBPP Number of primary branches per plant, SBPP Number of secondary branches per plant, WSF Weight of single fruit, FB Fruit breadth, FL Fruit length, FNPP Fruit number per plant, PIIF Percent insect infestation of fruit, PIIP Percent insect infestation of plant, FYPP Fruit yield per plant.

G1

Plate 2. Fruit of the G1 genotype of the cluster I

G8

Plate 3. Fruit of the G8 genotype of cluster II

G2

G3

G4

G6

Plate 4 (a): Fruit of the G2, G3, G4, G6 genotype of the cluster III

G5

G10

Plate 4 (b): Fruit of the G5, G10 genotype of the cluster III

G11

G12

G14

G15

Plate 4 (c): Fruit of the G11, G12, G14, G15 genotype of the cluster III

G7

G13

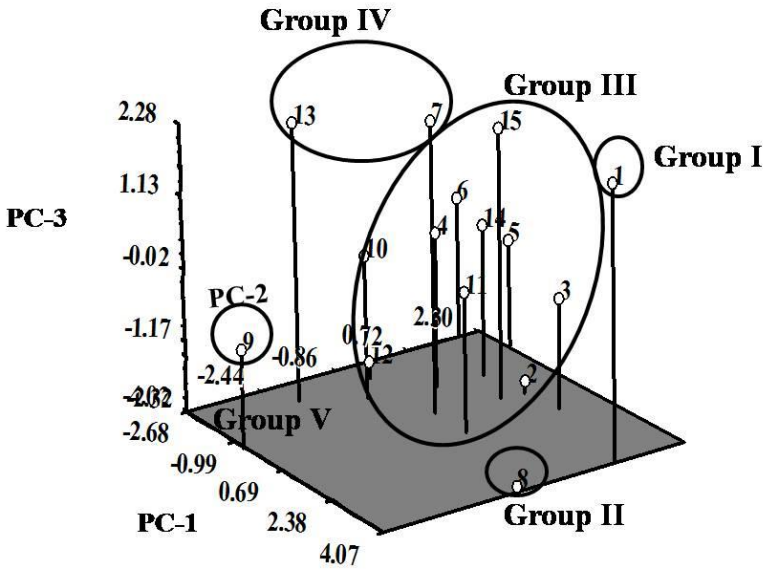
Plate (5): Fruit of the G7, G13 genotype of the cluster IV

G9

Plate (6): Fruit of the G9 genotype of the cluster V

4.2.3 Principal component analysis using different analysis: Generally, a dendrogram helps to understand how the genotypes are grouped. Results of principal component analysis (PCA) help to verify results of cluster analysis. Generally, three dimensional (3D) plots derived from PC analysis which facilitates in understanding the analysis more clearly. These are all multivariate analyses. If one analysis supports the other in the multivariate analysis then the result become more precise. It was found from the principal component analysis that the similar genotypes were grouped together (Figure 4). Cluster analysis was mostly confirmed by PCA and three dimensional (3D) plot (Figure 4) evidences of it. The 15 genotypes clustered or grouped both in dendrogram and PCA following same pattern. In other words, genotypes G1, G8 and G9 were grouped individually both in the PCA and in the dendrogram (Figure 3). The rest of the genotypes also followed the same pattern in grouping both in the PCA and in dendrogram. According to PCA (Table 7), the first four principal components account for about 79% of total variation for all different traits and exhibited high correlation among the characteristics analyzed. It was noticed from the Eigen vectors analysis that 28, 20, 16 and 13% variation of different traits could be explained in respect by the first four principal components (Table 7).

As stated before, PC1 depicted 28% of total variation (Table 7). Among the 14 different traits nine traits were positively and five traits were negatively correlated to PC1. The positively correlated traits were DFFH (days to first fruit harvest) (0.08), LA (leaf area) (0.22), CL (calyx length) (0.12), SBPP (number of secondary branches per plant) (0.02), WSF (weight of single fruit) (0.44), FB (fruit breadth) (0.09), FL (fruit length) (0.29), FNPP (fruit number per plant) (0.38), and FYPP (fruit yield per plant) (0.48). The negatively associated traits were DFF (days to first flowering) (-0.10), DFIF (days to 50% flowering) (-0.07), PBPP (number of primary branches per plant) (-0.14), PIIF (percent insect infestation of fruit) (-0.30), PIIP (percent insect infestation of plant) (-0.35). The first PC increas



Note:
Here in the figure, 15 genotypes are denoted with numerical data.
G1= Brinjal mukta keshi, G2= Kushtia-2 lomba begun, G3= Shabuj sathi, G4=Mental, G5= Gol begun, G6=Brinjal black beauty, G7=Nice ball, G8=Purple king hybrid, G9= Shingnath, G10=Chumki, G11= Majic ball, G12= Altapon, G13= India-1, G14= Dinajpur katali begun, G15= Aveo round.

Figure 4. Three-dimensional plot of PCA indicating relationships among 15 brinjal genotypes based on different traits

with the decrease of negatively correlated traits but with the increase of positively correlated traits. This indicated that the rising in one trait among the positively correlated traits will influence the other to increase. The PC1 could be viewed as a measure of the quality of the positively correlated traits. Moreover, first PC most strongly correlated to FYPP (fruit yield per plant) (0.48) followed by WSF (weight of single fruit) (0.44) and FNPP (fruit number per plant) (0.38). Therefore, based on the value of correlation it could be said that PC1 primarily measures of fruit yield per plant (Table 7).

Similarly, PC2 showed 20% of total variation. Among the 14 traits, eight traits were positively and rests of the traits were negatively correlated in this component. The CL (calyx length) (0.27), PBPP (number of primary branches per plant) (0.29), SBPP (number of secondary branches per plant) (0.27), FL (fruit length) (0.30), FNPP (fruit number per plant) (0.08), PIIF (percent insect infestation of fruit) (0.04), PIIP (percent insect infestation of plant) (0.02), FYPP (0.01) were the positively correlated traits. On the other hand, DFF (days to first flowering) (-0.20), DFIF (days to 50% flowering) (-0.39), DFFH (days to first fruit harvest) (-0.44), LA (leaf area) (-0.27), WSF (weight of single fruit) (-0.03) and FB (fruit breadth) (-0.43) were negatively correlated traits. Thus, the PC2 increases with the increases of negatively correlated traits but the decreases of positively correlated traits. It could be stated from the correlation value that PC2 was mainly a measure of DFFH (days to first fruit harvest) (-0.44) which was most strongly associated to this principal component (Table 7).

The third PC explained 16% of total variation. It was observed that in the third PC, nine traits were positively and five traits were negatively correlated. DFF (days to first flowering) (0.44), DFIF (days to 50% flowering) (0.41), DFFH (days to first fruit harvest) (0.23), LA (leaf area) (0.20), CL (calyx length) (0.49), SBPP (number of secondary branches per plant) (0.15), FL (fruit length) (0.34), PIIF (percent insect infestation of fruit) (0.11), PIIP (percent insect infestation of plant)

(0.17) were positively correlated traits. While, PBPP (number of primary branches per plant) (-0.03), WSF (weight of single fruit) (-0.03), FB (fruit breadth) (-0.31), FNPP (fruit number per plant) (-0.01), FYPP (fruit yield per plant) (-0.03) were the negatively associated traits. This PC rises with the rising of positively correlated traits but with the decline of negatively correlated traits. The PC3 could be said a measure of calyx length on the basis of correlation value (0.49) as it was most strongly correlated to this PC (Table 7).

The fourth PC described 13% of total variation which was the lowest among the 4 PCs. This PC consisted of seven positively as well as seven negatively correlated traits. The negatively correlated traits were LA (leaf area) (-0.36), CL (calyx length) (-0.11), FL (fruit length) (-0.09), FNPP (fruit number per plant) (-0.21), PIIF (percent insect infestation of fruit) (-0.40), PIIP (percent insect infestation of plant) (-0.19), FYPP (fruit yield per plant) (-0.01). On the contrary, the seven positively correlated traits were DFF (days to first flowering) (0.14), DFIF (days to 50% flowering) (0.15), DFFH (days to first fruit harvest) (0.30), PBPP (number of primary branches per plant) (0.41), SBPP (number of secondary branches per plant) (0.50), WSF (weight of single fruit) (0.16) and FB (fruit breadth) (0.05). On the basis of correlation value number of secondary branches per plant most strongly and positively correlated with this PC (Table 7).

The presence of wide difference among the genotypes was further confirmed by principal component analysis, which indicated that the overall diversity observed could be elucidated by a few eigenvectors. The first four principal components analysis from different traits explained 79% of the total variation, with PC1 explaining 28% of the variation, PC2 20%, PC3 16% and PC4 13% of the total variation. The first two principal components cumulatively accounted for 100 percent of the total variance reported by Nyadanu *et al,*. (2014) in their study. This implied a strong correlation among traits which were studied. About 76.59% of

total variation among 26 genotypes was also noticed (Karim *et al.*, 2016) where almost 48.22% variation showed by PC1 and 63.15% by PC2.

Table 7. Eigen vectors and Eigen values of the first four principal components from different traits

Eigenvector				
Variable	**PC1**	**PC2**	**PC3**	**PC4**
Eigenvalue	3.98	2.79	2.36	1.94
Proportion	0.28	0.20	0.16	0.13
Cumulative	0.28	0.48	0.65	0.79
DFF	-0.10	-0.20	0.44	0.14
DFIF	-0.07	-0.39	0.41	0.15
DFFH	0.08	-0.44	0.23	0.30
LA	0.22	-0.27	0.20	-0.36
CL	0.12	0.27	0.49	-0.11
PBPP	-0.14	0.29	-0.03	0.41
SBPP	0.02	0.27	0.15	0.50
WSF	0.44	-0.03	-0.03	0.16
FB	0.09	-0.43	-0.31	0.05
FL	0.29	0.30	0.34	-0.09
FNPP	0.38	0.08	-0.01	-0.21
PIIF	-0.30	0.04	0.11	-0.40
PIIP	-0.35	0.02	0.17	-0.19
FYPP	0.48	0.01	-0.03	-0.01

Note:
DFF Days to first flowering, DFIF Days to 50% flowering, DFFH Days to first fruit harvest, LA Leaf area, CL Calyx length, PBPP Number of primary branches per plant, SBPP Number of secondary branches per plant, WSF Weight of single fruit, FB Fruit breadth, FL Fruit length, FNPP Fruit number per plant, PIIF Percent Insect Infestation of Fruit, PIIP Percent insect infestation of plant, FYPP Fruit yield per plant.

Table 8. Inter-genotypic distance (D^2) of 15 genotypes of brinjal

Between genotypes	Distance (D^2)	Between genotypes	Distance (D^2)
1-8	1285.61	5-7	254.42
1-2	717.83	6-7	436.42
1-3	943.37	2-13	1201.06
1-4	1087.18	3-13	738.83
1-5	1652.95	4-13	605.33
1-6	2264.11	5-13	554.97
1-10	1722.52	6-13	526.66
1-11	584.39	10-13	699.59
1-12	1905.94	11-13	1347.96
1-14	783.32	12-13	828.80
1-15	997.49	13-14	1195.44
1-7	1065.15	13-15	719.79
1-13	2098.88	7-10	289.04
1-9	1778.66	7-11	649.85
2-8	1019.17	7-12	396.94
3-8	2505.31	7-14	1139.40
4-8	1809.11	7-15	1175.76
5-8	2345.78	2-9	485.14
6-8	2847.01	3-9	1450.73
8-10	1800.63	4-9	438.00
8-11	1214.6	5-9	703.07
8-12	1775.03	6-9	831.22
8-14	2357.28	9-10	292.97
8-15	2971.31	9-11	734.41
7-8	1448.78	9-12	203.91
8-13	3723.06	9-14	1538.92
8-9	1193.24	9-15	1764.39
2-7	276.14	7-9	472.10
3-7	890.31	9-13	1282.24
4-7	184.97		

Table 9. Average intra and inter-cluster distances (D^2) of 15 brinjal genotypes

Cluster	I	II	III	IV	V
I	**0.00**	1285.61 (3686)	1265.91 (35.58)	1582.02 (39.77)	1778.66 (42.17)
II		**0.00**	2064.52 (45.44)	2585.92 (50.85)	1193.24 (34.54)
III			**788.83**	705.58 (26.56)	844.28 (29.06)
IV				**941.84**	877.18 (29.62)
V					**0.00**

*Bold figures denotes intra-cluster distance

4.2.4 Principal coordinate analysis: Inter-genotypic distances as obtained by Principal Coordinate analysis for selective combination showed that the highest distance (3723.06) was observed between the genotype 8 and 13, followed by 8 and 15 (2971.31) and the lowest distance was observed between 4 and 7 (184.97) followed by 9 and 12 (203.91) (Table 8).

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 9) as suggested by Singh *et al,*. (1977). Cluster IV which showed the highest intra-cluster distance (941.81) composed of two genotypes and cluster III showed the lowest intra-cluster distance (788.83) composed of 10 genotypes which indicated within group diversity of the genotypes was maximum in cluster IV and minimum in cluster IV. The coordinates obtained from the Principal Component analysis (PCA) are used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al,*. (1989). PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight genotype between each pair of points.

4.2.5 Canonical variate analysis: canonical variate analysis was performed to compute the inter-cluster Mahalanobis's values. Statistical distances represent the index of genetic diversity among the clusters. The average intra and inter-cluster

distance (D^2) values were presented in Table 9. Results indicated that the highest inter-cluster distance was observed between II and IV (2585.92), followed by between II and III (2064.52). The lowest inter-cluster distance was observed between the cluster III and IV (705.58) followed by III and V (844.28), IV and V (877.18) suggesting a close relationship among these clusters (Figure 5). The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 9 and Figure 5). Islam *et al,*. (1995) obtain larger inter-cluster distances than the intra-cluster distances in a multivariate analysis.

However, the maximum inter-cluster distance was recorded was observed between II and IV (2585.92), followed by between II and III (2064.52). Genotypes from these clusters if involved in hybridization might produce a wide range of segregating population, as genetic variation was very distinct among these groups. Results obtained from different multivariate techniques were superimposed in (Figure 1 and 2) from which it might be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one. The clustering pattern of the genotype revealed that varieties/genotypes originating from the same places did not form a single cluster because of direct selection pressure.

4.2.6 Correlation among the traits: Most of the traits under this study showed positive correlation among themselves (Table 10). Out of 91 correlation data (which were derived from quantitative traits through correlation analysis) 56% showed positive and 44% showed negative correlation. Days to first flowering showed positive correlation with the following traits such as days to 50% flowering, days to first fruit harvest, leaf area, calyx length, and number of secondary branches per plant, fruit length, percent insect infestation of fruit and percent insect infestation of plant. However, it had negative correlation with the following traits like number of primary branches per plant, weight of single fruit,

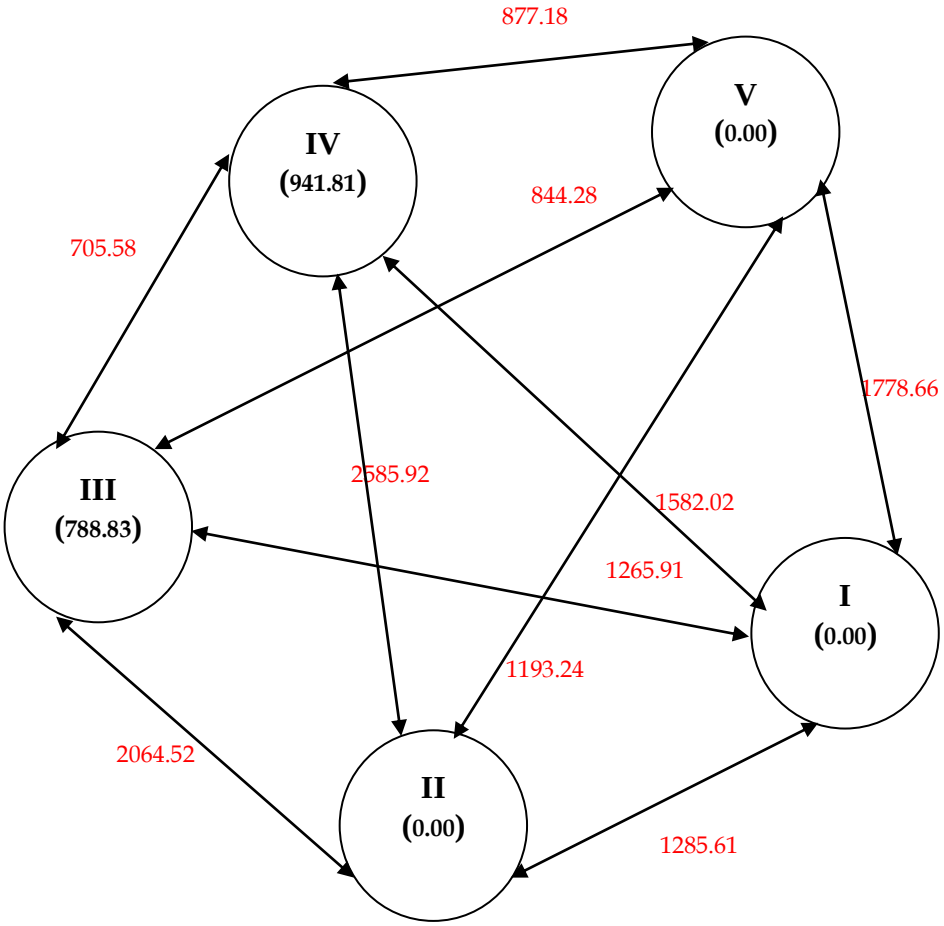


Figure 5. Diagram showing inter-cluster (outside the circle) and intra- cluster (inside the circle) distances of fifteen genotypes of brinjal.

fruit breadth, fruit number per plant and fruit yield per plant. Weight of single fruit exhibited positive correlation with fruit breadth, fruit length, fruit number per plant and fruit yield per plant.

The following traits were found negatively correlated with weight of single fruit such as percent insect infestation of fruit and percent insect infestation of plant. It was observed that days to first fruit harvest was negatively correlated with almost all the traits apart from leaf area, number of secondary branches per plant, weight of single fruit, fruit breadth and fruit yield per plant. Moreover, fruit number per plant was positively correlated with fruit yield per plant but negatively correlated with percent insect infestation of fruit and percent insect infestation of plant.

Yield of genotypes was found positively correlated with five yield traits and two morphological traits in the present study. Among all the traits assessed in the current study, such as fruit length was positively correlated with the fruit yield per plant which in general, was in agreement with Kumar *et al,*. (2016) who also reported positive correlation between fruit length and fruit yield per plant at the phenotypic level. There was positive correlation found between calyx length and fruit yield per plant which was consistent with the findings of Kumar *et al,*. (2016). It was observed that, days to first flowering (0.03), days to first fruit harvest and fruit number per plant negatively correlated with almost all the traits apart from leaf area, number of secondary branches per plant, weight of single fruit, fruit breadth and fruit yield per plant which was similar with (Saha *et al*., 2019 and Das *et al.*, 2018) and in their study, days to first flowering, secondary branches per plant, fruit length and fruit diameter exhibited positive genotypic correlation with fruit yield per plant. Fruit yield per plant was negatively correlated with percent insect infestation of fruit and percent insect infestation of plant which support other related study.

Table 10. Correlation among the traits of Brinjal

	DFF	DFIF	DFFH	LA	CL	PBPP	SBPP	WSF	FB	FL	FNPP	PIIF	PIIP	FYPP
DFF	1**													
DFIF	0.65**	1**												
DFFH	0.44*	0.79**	1**											
LA	0.04ns	0.33*	0.33*	1**										
CL	0.16ns	0.09ns	-0.05ns	0.27	1**									
PBPP	-0.19ns	-0.15ns	-0.07ns	-0.56	0.11ns	1**								
SBPP	0.03ns	0.01ns	0.07ns	-0.31	0.28ns	0.57**	1**							
WSF	-0.10ns	-0.12ns	0.29ns	0.15	0.08ns	-0.15ns	0.04ns	1**						
FB	-0.25ns	0.15ns	0.51**	0.25	-0.56**	-0.18ns	-0.35*	0.25ns	1**					
FL	0.01ns	-0.10ns	-0.11ns	0.15	0.8ns	-0.01ns	0.17ns	0.51**	-0.49**	1**				
FNPP	-0.33*	-0.20ns	-0.11ns	0.54	0.27ns	-0.23ns	0.04ns	0.46*	0.04ns	0.44**	1**			
PIIF	0.03ns	0.04ns	-0.23ns	0.03	0.13ns	0.03ns	-0.35*	-0.55**	-0.17ns	-0.10ns	-0.30*	1**		
PIIP	0.18ns	0.13ns	-0.05ns	-0.14	0.07ns	0.12ns	-.08ns	-0.64**	-0.18ns	-0.18ns	-0.3**	0.63**	1**	
FYPP	-0.20ns	-0.20ns	0.14ns	0.36	0.17ns	-0.26ns	-0.01ns	0.92**	0.2ns	0.58**	0.74**	-0.51**	-0.60**	1**

Note:

DFF= Days to first flowering, DFIF= Days to 50 % flowering, DFFH= Days to first fruit harvest, LA= Leaf area, CL= Calyx length, PBPP= Number of primary branches per plant, SBPP= Number of secondary branches per plant, WSF= Weight of single fruit, FB= Fruit breadth, FL= Fruit length, FNPP= Fruit number per plant, PIIF= Percent insect infestation of fruit, PIIP= Percent insect infestation of plant, FYPP= Fruit yield per plant.

4.3 Selection of genotypes for future hybridization: Selection of genetically distant /diverged parents is a vital task for hybridization program. As a result genotypes would be selected based on specific objectives. Genetically diverged parents are able to produce higher heterosis through crossing (Falconer, 1960; Moll *et al.,* 1962; Ghaderi *et al.,* 1984; Main and Bhal, 1989). Observing agronomic performance, genotype G1 produce higher yield, and maximum number of fruit, highest single fruit weight, and minimum insect infestation of fruit from cluster I than others. Moreover, genotype G8 from cluster II also produce better yield, higher number of fruit, second highest single fruit weight than others except cluster I. However, genotype G11 from cluster III also showed good performance in respect of yield. Genotype G3 from cluster III having large leaf area with the lowest percent insect infestation of plant. Genotype G9 from cluster V produces highest number of primary branch per plant with second highest length of fruit from other cluster. Therefore, considering group distance and other agronomic performance, the intergenotypic crosses between G1 and G3; G8 and G3; G11 and G8; G9 and G1; G8 and G9; G3 and G9; G11 and G1; G11 and G9 could be suggested to utilize for future hybridization program.

CHAPTER V
SUMMARY AND CONCLUSION

A field experiment was carried out in order to evaluate genetic diversity of 15 brinjal genotypes using 14 different quantitative traits in the field of Sher-e-Bangla Agricultural University, Dhaka. The experiment was designed in RCBD with three replications during November, 2019 to April, 2020.

The first four principal components account for about 79% of total variation for all different traits and exhibited high correlation among the characteristics analyzed. As per PCA, D^2 and cluster analysis the genotypes were grouped into five different clusters. Cluster I, II, III, IV and V consist of one, one, ten, two and one genotypes respectively. Results indicated that the highest inter-cluster distance was observed between II and IV (2585.92), followed by between II and III (2064.52) and the lowest inter-cluster distance was observed between the cluster III and IV (705.58) followed by III and V (844.28), IV and V (877.18) suggesting a close relationship among these clusters. The highest and lowest intra-cluster distance were observed between the cluster IV (941.81) and cluster III (788.83) respectively.

Genotypes included in cluster I important for fruit yield per plant, fruit number per plant, fruit breadth and weight of single fruit; cluster II for fruit length, fruit number per plant, weight of single fruit, fruit yield per plant, calyx length, leaf area and days to first fruit harvest; cluster III primary branch per plant, ; cluster IV for days to first flowering, earliness of 50% flowering, earliness of harvesting and cluster V important for earliness of flowering, earliness of harvesting, smaller leaf area and higher primary branch per plant.

On the basis of cluster and PCA analyses and other agronomic performances the genotype G1 from cluster I, Genotype G8 from cluster II, genotype G11 and G14from cluster III could be considered as better parents for future hybridization program. Results from the current studies indicated significant variation among the genotypes for all the

traits studied. Number of fruits per plant, fruit length, fruit breadth and individual fruit weight played very important role towards yield.

In case correlation coefficient, Out of 91 correlation data (which were derived from quantitative traits through correlation analysis) 56% showed positive and 44% showed negative correlation. Days to first flowering showed positive correlation with the following traits such as days to 50% flowering, days to first fruit harvest, leaf area, calyx length, and number of secondary branches per plant, fruit length, percent insect infestation of fruit and percent insect infestation of plant. Days to 50% flowering, days to first fruit harvest, weight of single fruit, fruit breadth and fruit number per plant was positively correlated with fruit yield per plant but negatively correlated with percent insect infestation of fruit and percent insect infestation of plant.

CHAPTER VI
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CHAPTER VII
APPENDICES

Appendix I. Nutrients composition of brinjal per 100 g of edible portion

Nutrients	Amount (100g)
Calories	24.00
Moisture content (%)	92.70
Carbohydrates (%)	4.00
Protein(g)	1.40
Fat (g)	0.30
Fiber (g)	1.30
Oxalic acid (mg)	18.30
Calcium (mg)	16.00
Magnesium	47.00
Phosphorous (mg)	0.90
Iron (mg)	3.00
Sodium (mg)	0.77
Copper (mg)	2.00
Potassium(mg)	44.00
Sulphur (mg)	52.00
Chlorine (mg)	124.00
Vitamin-A (IU)	142.00
Vitamin-B (mg)	0.04
Thiamin	0.11
Riboflavin	0.74
B carotene	0.74
Vitamin –C (mg)	12.00

Source: Anonymous, 1980

Appendix II. Monthly record of air temperature, relative humidity, rainfall and sunshine hour of the experimental site during the period from September 2019 to March 2020

Month	Air temperature (°C)		Relative humidity (%)	Total Rainfall (mm)	Sunshine (hr)
	Maximum	Minimum			
November, 2019	25.8	16.0	76	00	6.8
December, 2019	22.6	13.4	78	05	6.9
January, 2020	24.9	12.2	64	02	5.8
February, 2020	26.7	16.9	69	30	6.7
March, 2020	27.5	19.4	81	22	6.9
April, 2020	28.8	20.8	88	26	6.9

Source: Bangladesh Meteorological Department (Climate & weather division) Agargoan, Dhaka-1212

Appendix III. Soil characteristics of experimental field as analyzed by Soil Resources Development Institute (SRDI), Khamarbari, Farmgate,Dhaka

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Horticulture farm field , SAU, Dhaka
AEZ	Madhupur Tract (28)
General Soil Type	Shallow red brown terrace soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical and chemical properties of the initial soil of the experimental field

Characteristics	Value
% Sand	26
% Silt	43
% clay	31
Textural class	Sandy loam
pH	5.9
Catayan exchange capacity	2.64 meq 100 g/soil
Organic matter (%)	0.78
Total N (%)	0.03
Available P (ppm)	20.00
Exchangeable K (me/100 g soil)	0.10