MORPHOLOGICAL CHARACTERIZATION, GENETIC VARIABILITY AND PHENOTYPIC DIVERSITY ANALYSIS IN BRINJAL (*Solanum melongena* L.) GENOTYPES

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CERTIFICATE

This is to certify that the thesis entitled ***'Morphological characterization, genetic variability and phenotypic diversity analysis in brinjal (Solanum melongena* L.*) genotypes'*** submitted to the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **Master of Science in Genetics and Plant Breeding**, embodies the result of a piece of bona fide research work carried out by **Sumaiya Afroz**, Registration number: **19-10174** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2021

Dhaka, Bangladesh

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DEDICATED

TO

MY BELOVED PARENTS

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LIST OF CONTENTS

LIST OF CONTENTS (Cont.)

LIST OF CONTENTS (Cont.)

LIST OF CONTENTS (Cont.)

LIST OF CONTENTS (Cont.)

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

LISTS OF COMMONLY USED ABBREVIATIONS

Full word	Abbreviation
Agro Ecological Zone	AEZ
Analysis of variance	Anova
And others	et al.
At the rate	@
Bangladesh	BD
Bangladesh Agricultural Research Institute	BARI
Bangladesh Agricultural University	BAU
Bangladesh Institute of Nuclear Agriculture	BINA
Centimeter	Cm
Degree	^{0}C
Co-efficient of variation	CV
Days after sowing	DAS
Degrees of Freedom	Df
Environmental variance	σ_e^2
Et cetera	etc.
Food and Agricultural Organization	FAO
Genetic Advance	GA
Genotypic Coefficient of variation	GCV
Genotypic correlation	r_g
Genotypic variance	σ_g^2
Gram	G
Heritability in broad sense	h^2b
Kilogram	Kg
Meter	M
Milliliter	mL
Mean sum of square	MS
Metric ton	MT
Muriate of Potash	MOP
Number	No.
Percent	(%)
Percentage of Coefficient of Variation	CV%
Phenotypic varience	σ_p^2
Phenotypic Coefficient of variation	PCV
Phenotypic correlation	r_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Species	*sp.*
Square meter	m^2
Standard error	SE
Triple Super Phosphate	TSP

MORPHOLOGICAL CHARACTERIZATION, GENETIC VARIABILITY AND PHENOTYPIC DIVERSITY ANALYSIS IN BRINJAL (*Solanum melongena* L.) GENOTYPES

ABSTRACT

A field experiment was conducted to evaluate twenty brinjal genotypes by calculate the significance of variation, heritability, genetic advance, correlation, path coefficient and genetic diversity for thirteen yield contributing characters. The experiment was executed following Randomized Complete Block Design (RCBD) with three replications at Sher-e-Bangla Agricultural University, Dhaka, from August 2019 to March 2020. In this experiment, significant differences were exhibited among the existing genotypes for all characters. Higher Phenotypic Co-efficient of Variation (PCV) than the Genotypic Co-efficient of Variation (GCV) were observed for all characters. Highest PCV (59.24) and GCV (58.58) were observed for % of infested fruit. High heritability associated with high genetic advance in percentage of mean were found with all the character except days to 1st flowering, days to 1st fruiting, and days to 1st harvesting which indicating selection on the basis of phenotype would be effective. At genotypic level, number of primary brunches per plant (0.355), number of secondary brunches per plant (0.356), and fruit diameter (0.494) exhibited highly significant and positive correlation with yield per plant. Path analysis revealed that the number of flowers per plant (2.616) had the maximum positive and direct effect on yield per plant. Through genetic diversity, 20 brinjal genotypes were grouped into four cluster. The cluster I containing the maximum number of genotypes (7) followed by Cluster II (6), IV (4), and III (3). Maximum intra-cluster distance was exhibited by cluster I (1.74), whereas the highest value for inter-cluster distance was observed between Cluster I and Cluster III (32.04). Mean performance of cluster showed the highest yield per plant (1.62) value in cluster IV. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean performance and agronomic performance the genotype G8 (Ventura), G15 (Bt), and G17 (Kustia 2) from cluster I, G12 (Pirgonj) from cluster III, and G16 (Avo round) along with G18 (Altapon) from cluster IV would be considered as better parents for future hybridization programs.

CHAPTER I

INTRODUCTION

Solanum melongena L. (eggplant, aubergine or guinea squash and also known as brinjal) in Bangladesh belonging to the family Solanaceae, it is one of the most common, inexpensive and popular vegetable grown in Bangladesh (Ahmed *et al.,* 2019). It is the second most important and popular vegetable grown in Bangladesh (Shelton *et al.,* 2020). In 2019, it is grown on 18,47,787 ha with a total production of 5,51,97,878 tons in the world (FAO, 2021). Asia is the largest eggplant production continent, including more than 90% production area with over 87% eggplant production in the world (Ahmed *et al.,* 2019). In Bangladesh, it is grown and available all throughout the year. In 2018-2019, it was annually produced in 52,374 hectares areas and the total production was 5,30,610 metric tons (BBS, 2019). It is grown in almost all agro-climatic zones with over 100 different varieties having fruits of different color, size, shape, and taste (Shelton *et al.,* 2020) and also providing an important source of cash income for small resourced-poor Bangladeshi farmers.

Brinjal is a warm-weather crop mostly cultivated in tropical and subtropical regions of the World (Taher *et al.,* 2017). Brinjal is probably originated in India and exhibited secondary diversity in South East Asia. It is being extensively grown in India, Bangladesh, Pakistan, China, Japan, Philippines, France, Italy, and U.S.A. (Vaishya *et al.,* 2017). Vavilov (1951) considered brinjal as being native to the "Indo-Chinese center of origin." However, recent evidence shows that brinjal had a multiple independent domestication, which was naturally distributed in tropical Asia from Madagascar to the Philippines (Knapp *et al.,* 2013). Brinjal in both India and China is equally old, though evidence suggests that utilization of wild eggplants may have started earlier in India than China, with center of domestication in the Philippines (Meyer *et al.,* 2012). Brinjal spread eastward to Japan and then westward along the Silk Road into Western Asia, Europe, and Africa by Arab traders during the fourteenth century. Then it was introduced into America soon after Europeans arrived there and later expanded into other parts of world (Taher *et al.,* 2017).

Brinjal is very popular vegetable with high nutrient value; it has a very low caloric value and is considered among the healthiest vegetables for its high content of vitamins,

minerals and bioactive compounds for human health (Taher *et al.*, 2017). It can provide at least 5% of a person's daily requirement of fiber, copper, manganese, vitamin B-6 and thiamine (Ware, 2019) (Appendix V). It is highly beneficial for the regulation of blood sugar levels which helps to control the absorption of glucose (Saha *et al.*, 2019) and its fruits are mainly used to cure diabetes (Verma *et al.*, 2018). Brinjal is source of phenolic compounds (Ware, 2019) and that's why it is one of the vegetables with highest antioxidant activity (Saha *et al.*, 2019). In the peel of brinjal fruits phenolics, glycoalkaloids, amide and anthocyanine are present. It is also rich with vitamin A, B1 trace amount of micro nutrient like Cu, Mn, Mg, and K (Verma *et al.*, 2018). The fruit contain high percentage (65%) of polyunsaturated fatty acid, magnesium, and potassium so that, it acts as a cholesterol-reducing agent and is used as a medicine for controlling high blood cholesterol and liver problems (Daunay and Hazra, 2012). The extracts of brinjal root and leaves can cure problems such as skin diseases, cough, toothache, piles, inflammation, throat problems, and stomach problems (Barik *et al.*, 2020).

Farmers need improved brinjal varieties for sustainable production and adaptation to climate change challenges as it has a relatively long growth period and it is more exposed to a wide range of plant diseases, pests, nematodes, and weeds than the other vegetables (Taher *et al.*, 2017). Production of brinjal is highly affected by insect pests, they play a pivotal role for lowering the yield of brinjal, by attacking them right from the nursery stage to till harvesting (Borkakati, 2019). More than 70 number insect species attack the brinjal (Subbarathnam and Butani, 1982), of which Brinjal Shoot and Fruit Borer (BSFB), leafhopper, aphid, stem borer, epilachna beetle, white fly, lacewing bug with non-insect pest red spider mite were the major pests (Borkakati, 2019). Brinjal is also prone to massive attacks by several species of fungi and bacteria that cause wilt, soft rot and root rot (Singh *et al.*, 2014). Most common diseases for brinjal include bacterial wilt, verticillium wilt, fusarium wilt, anthracnose fruit rot, alternaria rot, damping off, phytophthora blight, phomopsis blight, fruit rot, leaf spot, little leaf of brinjal, and mosaic (Taher *et al.*, 2017). Fruit rot and leaf blight disease caused by *Diaporthe vexans* are of major concern in brinjal producing areas of as it reduces yield and marketable value (Mahadevakumar & Janardhana 2016).

Being most important to growers and consumer and to fulfill the increasing demands, it is needed to increase its productivity and mass cultivation of brinjal, improved varieties with desirable traits need to be identified for better performance. Evaluation of germplasm is the basic tool for identification of important genotypes. The great extent of natural variation present among the different genotypes suggests good scope of improvement in economic traits. Large variability ensures better chance of producing new types. Variability parameters like genotypic and phenotypic coefficient of variations, heritability and genetic advance, degree of association between the various characters and direct effect of yield contributing characters on total yield, is of paramount significance in formulating a proper breeding strategy, aimed at exploiting the inherent variability of the original population. Phenotypic variability changes under different environmental conditions but genetic variability always remains unchanged which is useful for exploitation in selection or hybridization.

Yield of crops is controlled by several yield contributing traits which are highly influenced by environmental factors, consequently estimates of heritability and genetic advance are useful for selection (Vaishya *et al.*, 2017). Genetic diversity analysis is fundamental for any breeding program. It is also necessary to understand the relationship on brinjal with its wild relatives and with the domestication of cultivated variety, as well as the relationships among wild, semi-domesticated, and cultivated eggplant are intricate, and the origin, evolution, and migration are also need to be understood (Levin *et al.*, 2006; Meyer *et al.*, 2012; Taher *et al.*, 2017). Variability and genetic diversity are the fundamental laws of plant breeding which are largely used in selection of parents for efficient hybridization program (Bhatt, 1973).

Brinjal is grown all year round in Bangladesh. It is highly consumed by all types of people in our country due to its high quality, taste, lower market price and year-round availability as well as it becomes one of the major crops. There are lots of variability is available throughout the country of brinjal, also a number of wild varieties are found here. A wide range of genetic variability exists in brinjals, which creates more chances of improvements either from existing variability or from the segregates of a cross through selection. For effective selection of a superior and desirable genotype for use in any improvement program characterization of the genotypes as well as genetic variability, correlation study and diversity analysis are needed.

Considering the above facts, the experiment has been under taken with the following objectives -

- To study the genetic variability and correlation between yield and yield contributing traits of twenty brinjal genotypes;
- To study the genetic diversity among the twenty brinjal genotypes;
- To identify the high yielding genotype of brinjal and recommend the best genotypes for breeding program in future and
- To study the morphological characteristics of twenty brinjal genotypes against brinjal shoot and fruit borer;

CHAPTER II

REVIEW OF LITERATURE

Studies on quantitative and qualitative traits of brinjal are receiving much attention in the tropical and sub-tropical countries, although brinjal is a one of the most popular and important vegetables occupying a wider acreage under its cultivation in Bangladesh. Knowledge on brinjal's growth habit and productivity of different varieties/lines under varied agro-ecological conditions are not well informed in Bangladesh and elsewhere in the world, research effort on characterization, diversity analysis of brinjal and comparative studies of brinjal seems to be negligible. Thinking about magnitude of diversity for yield and its component characters, considerable interest to the plant breeders for planning and execution of genetic improvement program; a large number of such investigations have been carried out. All these studies were carried out on the basis of simple analysis of variance which enabled to compute genetic variance for different characters. In order to obtain desired genotypes in breeding progenies, superior parents with high breeding values are needed. To evolutionary and breeding point of view, total genetic diversity among different natural populations is very important. Variability and genetic diversity are the fundamental law of plant breeding which are the major tools which are used in parent selection for efficient hybridization progarmme (Bhatt, 1973). Under these circumstances, statistical analysis such as variability, interrelationship, path coefficient analysis, heritability, genetic advance, Mahalanobis's D^2, multivariate analysis was of great importance. Therefore, related information available in the literature pertaining to the characterization, variability and diversity of the brinjal and some other crops of the same family were reviewed in this section. Moreover, literatures related to the efficient multivariate techniques for diversity analysis were also reviewed in the following section.

2.1 Characterization and variability of brinjal genotypes

Nazir *et al.* (2019) observed variance for quality and yield traits revealed highly significant differences using 13 parents and 30 F_1 hybrids of brinjal. For all the traits phenotypic variances were slightly higher than corresponding genotypic variances. Broad sense heritability was high for all the characters with medium to high genetic

advance as percentage of mean. Correlation studies revealed that fruit yield/ha had a positive direct correlation with number of fruits/plant and fruit weight.

Bende *et al.* (2019) analyzed 41 brinjal genotypes and observe that the phenotypic coefficient of variations was higher than the genotypic coefficients of variation for all the characters. The genotypic coefficient of variation was highest for fruit borer infestation and lowest for plant height also recorded. As well as the high heritability with high genetic advance as per cent of mean for fruit borer infestation, shoot borer infestation, fruit yield per plant, fruit weight per plant, fruit per cluster and fruit length per plant was observed which indicating that these characters were least influenced by the environmental effects.

Tirkey *et al.* (2018) analyzed genetic variability, heritability, genetic advance, correlation coefficient and path coefficient analysis for growth and yield contributing characters in 18 brinjal genotype among 14 different the genotype. High heritability in broad sense along with high genetic advance in percent of mean for fruit length, single fruit weight and plant height 60 days was observed. Also, high genotypic coefficient of variation (GCV) was recorded for number of fruits per plant, fruit yield per plot and phenotypic coefficient of variation (PCV) for number of fruits per plant followed by fruit yield per plant.

Dutta *et al.* (2018) examined significant variability among the qualitative traits of 25 brinjal genotypes. Close estimates between GCV and PCV values indicated lower influence of environmental factors on the expression of traits. The proportion of genetic contribution was very high to the phenotypic expression of most of the studied traits, suggesting their use as important discriminatory variables for brinjal classification. High GCV coupled with high broad sense heritability and genetic advance was observed in all the characters except days to 1st flowering and days to 50% flowering, which indicating predominant control of additive genes, and these traits could be improved upon by selection without progeny testing. Positive phenotypic correlation was observed in number of fruits/plant and plant height exhibited significantly with fruit yield/plant. However, number of fruits/plant and fruit weight was recorded highly positive direct effects on fruit yield/plant.

Parvati *et al.* (2018) investigated genetic variability, heritability, genetic advance and genetic diversity of 55 genotypes of brinjal. PCV were slightly higher than the GCV

and the difference was very low for majority of the characters, indicating that prevalence of more of genetic effects than environment in their expression. It was observed high GCV, PCV, heritability coupled with high genetic advance indicating more of genetic inheritance and selection is effective.

Patel *et al.* (2017) investigated the phenotypic and genotypic variances, heritability, genetic advances, correlation and path coefficient for yield and yield contributing traits in 72 eggplant genotypes. The highest GCV was observed in fruit shape, followed by average fruit weight. High heritability in the broad sense with moderate to high genetic gain and GCV was observed for number of fruits per plant followed by yield per ha. The high genetic advance was noticed for yield per plant, indicating the prevalence of additive gene action for inheritance of these characters. Correlation and path coefficient (genotypic and phenotypic) showed that number of fruits per plant and average fruit weight had maximum direct effect resulted significantly positive correlation with yield/plant. These traits must be considered in selection program for the improvement of the yield potential of eggplant.

Pujer *et al.* (2017) investigated 55 brinjal genotypes to assess the mean performance, genetic variability, heritability and genetic advance. GCV were slightly lower than the corresponding PCV and the difference was very low for majority of the characters, suggesting that presence of more of genetic effects than environment in their expression. High GCV, PCV, heritability coupled with High genetic advance expressing more of genetic inheritance and selection is effective. Therefore, direct selection helps in selecting good genotypes with high growth, quality and yield for brinjal hybrids.

Sujin *et al.* (2017) investigated the extent of genetic variability, heritability, correlation and path coefficient analysis of 60 genotypes of brinjal for yield and shoot and fruit borer tolerance. The highest phenotypic and genotypic variation was observed in fruit yield per plant followed by fruit weight, fruit girth, number of fruits per plant and brinjal shoot and fruit borer incidence. High heritability along with high estimates of GCV, genetic advance and genetic gain were noted for fruit yield per plant, fruit weight, number of secondary branches per plant and shoot and fruit borer incidence. Number of long styled flowers per plant, number of short styled flowers per plant, number of fruits per plant, fruit weight, days to 1st harvesting and shoot and fruit borer incidence

showed positive direct effect. Positive and significant correlation was found in fruit weight, fruit girth and number of fruits per plant.

Nilakh *et al.* (2017) conducted a field trial to assess the magnitude of genetic variability and correlation in segregating generation of brinjal. The traits, number of branches per plant, days to initiation of flowering, days to 50 per cent flowering and fruit length showed comparatively higher estimates of genotypic and phenotypic coefficients of variation which indicating high level of variability and scope for effective improvement. High heritability coupled with high genetic advance as percentage of mean was found in days to initiation of flowering and fruit yield per plant, indicating additive gene action for the above characters.

Koundinya *et al.* (2017) did an experiment at AB District Seed Farm, BCKV, Kalyani Simanta, West-Bengal, India during autumn-winter 2013-14 and 2014-15. The traits that showed higher Phenotypic and Genotypic Coefficient of variation values were number of fruits per plant, fruit weight, harvest index, fruit yield per plant, anthocyanin in peel, total phenols and DPPH (2,2-diphenyl-l-picryl hydrazyl) free radical scavenging (FRS) capacity indicating that a greater amount of genetic variability was present for these characters which provide greater scope for selection. High heritability coupled with high genetic advance as percent of mean was recorded for the characters like plant height, days to 1st flowering, days to 50% flowering, number of fruits per plant, fruit weight, harvest index, fruit yield per plant, total sugar, anthocyanin in peel, total phenols and DPPH FRS capacity. Highly positive significant correlation was found in number of primary branches per plant, number of fruits per plant, harvest index, vitamin-A and total phenols and significant negative correlation with days to 1st flowering, TSS, total sugars and total protein with fruit yield per plant.

Yadav *et al.* (2016) evaluated 40 brinjal genotypes for thirteen quantitative characters and found significant differences among all studied traits. Highly significant differences were recorded among all the genotypes and characters under study indicating the presence of sufficient amount of variability in all the characters. PCV were higher than their corresponding GCV for all characters. High heritability coupled with high genetic advance was observed for plant height, fruits per plant, flowers per cluster, fruit length, fruit diameter, fruit weight, yield per plant, leaf width and fruit length to width ratio.

Kumar *et al.* (2013) analyzed the variability for all the characters using 14 parents and 40 hybrids of brinjal in RCBD. High phenotypic and genotypic coefficient of variation was observed in the parents for fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant. High magnitude of heritability coupled with genetic advance was also found for fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant.

Naik *et al.* (2010) conducted an experiment during kharif season of 2004- 05 to evaluate 61 genotypes using randomized block design on 24 characters. High heritability values and high percentages of genetic advance were observed in fruits length, number of fruits per cluster, number of fruits per plant, total yield per plant, yield per plot, yield per hectare indicating that there were a greater number of additive factors for these characters and improvement in yield could be brought about by selection, based on phenotypic observations.

Singh *et al.* (2010) carried out a study with 99 genotypes (76 F_1 s, 19 lines and 4 testers) of brinjal to assess the character association and contribution of quantitative trait towards yield. Number of flowers per plant, number of fruits per plant, fruit length, fruit weight, fruit volume, number of fruit picking, plant height, plant girth, leaf area and plant spread were positively correlated with yield per hectare (in both direction), while days to first fruit harvest and per cent of plant wilted showed significant negative association with fruit yield. The path analysis suggested that fruit weight and fruit per plant had high direct effect on fruit yield. However, the indirect contribution of fruit diameter, leaf area and plant spread (in both direction) were observed to affect fruit yield in brinjal.

Jadhao *et al.* (2009) investigated 50 F4 progenies and six parents of for correlation and path analysis among eleven yield contributing characters. The PCV was greater than the respective GCV for all the characters studied. Path coefficient analysis showed positive direct effect of the plant height, number of branches per plant, days to Initiation of flowering, days to first picking, days to last picking, fruit length and fruit weight with fruit yield per plant, indicating these characters had direct relation with yield, so while for improvement in yield attributes, these characters may get priority.

Aramendiz *et al.* (2009) carried out an experiment with 24 cultivars of eggplant to analysis the phenotypic, genotypic and environmental correlations. The genetic correlations were of higher or equal magnitude to the phenotypic correlations, while the environmental ones had low effects on the results. The number of fruits and the yield showed a positive and highly significant genetic correlation. It was suggested that the number of fruits per plant could be used as a selection criterion to obtain high yield eggplant cultivars.

2.2 Genetic diversity

Banerjee *et al.* (2018) evaluated 38 genotypes for the analysis of genetic divergence. All genotypes were grouped into 7 clusters. Cluster III was having highest fourteen genotypes followed by cluster I, cluster II, cluster IV, cluster V, cluster VI and cluster VII had minimum genotypes. Between geographical distribution and genetic distance there is no direct relationship. Cluster III showed maximum intra-cluster distance followed by cluster II. Based on inter-cluster distances, the maximum divergence was recorded between cluster IV and cluster VII indicating that the genotypes of these clusters could be used as parents in hybridization program to develop high heterotic hybrids. Number fruit per plants showed maximum contribution towards the diversity.

Sultana *et al.* (2018) investigated Bangladesh Agricultural Research Institute (BARI) released 11 varieties of brinjal to assess genetic diversity using PCR-based randomly amplified polymorphic DNA (RAPD) markers. A total of 44 distinct DNA amplified bands were observed for five primers (OPB-04, OPB-08, OPD-02, OPP-13 and OPW-08). The overall gene diversity was detected 0.216 and level of polymorphism was found 63.64%. The 11 genotypes of brinjal were segregated into two main clusters. The first major cluster contained only one genotype (BARI begun 6) and the second major cluster had rest of ten genotypes. BARI begun 6 vs BARI begun 1 presented the highest Nei's genetic distance as they are released from different parental origin. On the other hand, BARI begun 9 vs BARI begun 7 varietal pair was recorded the lowest genetic distance as they are released from same parental origin. The experiment reveals genetic diversity among 11 brinjal genotypes which may be informative for the future varietal identification and genetic improvement of brinjal.

Patel *et al.* (2018) investigated 35 germplasm accessions of brinjal to analyze genetic diversity among sixteen different traits. PCA indicated that characters like plant height, leaf area per plant at 50 % flowering, transpiration rate at 50 % flowering, chlorophyll content at 50 % flowering, number of fruits per plant, fruit girth, total phenol content and total soluble sugar, could be used to distinguish the germplasms of brinjal in the heavy rainfall zone. The result of present study will help in planning and execution of future breeding strategies in brinjal.

Ravali *et al.* (2017) evaluated genetic divergence among 35 genotypes of brinjal for 19 characters aimed at improving yield potential by using Mahalanobis D^2 statistics. The genotypes were segregated into ten clusters suggesting considerable amount of genetic diversity in the material. The cluster V had maximum 10 genotypes followed by II and IV cluster having 6 and 4 genotypes, respectively. These clusters having maximum number of genotypes, indicating narrow genetic diversity. The maximum intra cluster distance was recorded by cluster II followed by cluster V and cluster X. The maximum inter-cluster D^2 value was noted between VIII and IX. Maximum contribution towards the total divergence was exhibited by fruit yield per plant followed by average fruit weight and ascorbic acid content. The cluster VIII and X exhibited high cluster means for fruit yield per plant, average fruit weight, number of fruits per plant and these clusters can be successfully utilized in hybridization programs of brinjal.

Dissanayake *et al.* (2017) evaluated 38 brinjal genotypes in Sri Lanka, to characterize brinjal germplasm using morphological traits and to assess the genetic diversity within germplasm. Genetic distance of each accession was calculated using Manhattan distance and linkage was computed. All genotypes were accessions into three main clusters. Cluster II recorded the highest average fruit weight; however, highest yield was recorded in accessions in cluster I. Cluster III was observed lowest yield with intermediate branching habit. There was a high similarity coefficient among accessions, though all the accessions differ from each other. It was found that, morphology-based analysis was effective in differentiating brinjal accessions.

Shailesh (2016) analyzed the extent of diversity among 96 accessions of brinjal with morphologically diverse characters. The results could clearly distinguish prickly and non-prickly types of accessions. High correlation was found among the prickliness of plant parts i.e., stem, leaves and calyx. The cluster analysis presented low intra-cluster

distances compared to the inter-cluster distances, indicating homogenous and heterogenous nature of accessions within and between the clusters respectively.

Rahman *et al.* (2014) investigated 100 brinjal accessions to access genetic diversity based on multivariate analysis and they were grouped into 8 clusters. The cluster I having 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 results of the PCA showed 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 noted between the cluster II and VI, while minimum between V and VII. The maximum intra-cluster divergence was observed between accessions falling in the cluster II. On the basis of the mean performance of different clusters, acceptable yield was placed in brinjl accessions of cluster IV, VI and VIII.

Saurabh *et al.* (2011) carried out an experiment to evaluate the breeding potentiality using D^2 analysis. All the genotypes were grouped into 5 clusters, which exhibited no association between geographical and genetic divergence. The intra-cluster distance was recorded maximum in cluster II and minimum for cluster IV. The inter-cluster maximum distance was observed between clusters I and clusters IV followed by II and IV which may serve as a potential genotype for hybridization program.

Dharwad *et al.* (2011) conducted a study on 28 F_1 hybrids and 8 parents of brinjal derived from germplasm lines to access the heterosis and diversity. It was recorded that high heterosis for fruit yield was attributed to increased fruit weight and number of fruits per plant. Thirty-six entries comprising 28 F_1 hybrids and 8 parents were segregated into six clusters. The combination of the analysis of heterosis and diversity, indicating the high frequency of hybrids classified under DC_2 and DC_3 suggesting moderate genetic diversity is most desirable to produce highly heterotic hybrids of brinjal.

Dharwad *et al.* (2011) conducted a study to analysis the heterosis and diversity on 28 F_1 hybrids of brinjal derived from germplasm lines and a local cultivar. Fruit weight (g), number of fruits per plant and fruit yield (g) showed considerably high magnitude of heterosis. High heterosis for fruit yield was attributed to increased fruit weight and number of fruits per plant. Thirty-six entries comprising 28 F_1 hybrids and 8 parents

were segregated into six clusters. Based on parental divergence, all 28 hybrids were grouped in 4 divergence classes. The combination of heterosis and diversity analysis indicated the genetic diversity is most desirable to produce highly heterotic hybrids.

Das *et al.* (2010) investigated on 40 genotypes of brinjal collected from different places in the country and abroad were evaluated for different morphophysiological characters and genetic diversity was measured among the genotypes through D^2 statistics. The range of D^2 values range from 8.13 to 8015.95 which revealed high variability among the genotypes. Based on the degree of divergence the genotypes were segregated into ten clusters among which cluster ten was the largest having 22 genotypes. The top two characters which contributed most towards the genetic divergence were fruit yield and fruit weight. Dendrogram among the genotypes also showed high diversity along with strong intra and inter cluster relationships.

Demir *et al.* (2010) carried out an experiment to access molecular characterization of eggplant genotypes collected from different geographical regions of Turkey by using SSR and RAPD markers. With amplification of five SSR loci, the number of alleles per microsatellite locus ranged from 2 to 10, with a total of 24 alleles. The greatest number of alleles was noted at the emf21H22 locus (10 alleles); followed by emh11O01 and emf21C11 as five and four alleles, respectively. The average number of alleles per locus was 4.8. Using 11 decamer RAPD primers, 100 bands were amplified, among which 29 were polymorphic. The number of bands per primer ranged from 7 (OPH10, OPH19, OPH20, OPH03) to 14 (OPB07). Primer OPB07 was the most polymorphic, generating 64% polymorphic bands; the rest of the primers gave less than 50% polymorphism. UPGMA dendrograms were utilized to examine the genetic relatedness of the genotypes.

Golani *et al.* (2007) conducted an experiment on 23 genotypes of brinjal in Junagadh, Gujarat, India to determine the nature and magnitude of genetic divergence and genetic variability for fruit yield and its contributing characters: plant height, plant spread, fruit length, fruit girth and 10-fruit weight. The population was segregated into 6 clusters. Cluster I having largest 6 number genotypes, followed by clusters II and III, each with 5 genotypes, while cluster VI was a solitary cluster. The cluster pattern indicating that there was no association between the geographical distribution of the genotypes and genetic divergence. The maximum inter-cluster D^2 Genetic diversity was observed in 5

traits, i.e. plant height, branches per plant, fruits per plant, average fruit weight and fruit yield, was evaluated in 15 genotypes of *S. melongena* grown during value was reported between clusters II and III. The genotypic coefficient of variation, heritability and genetic advance as percentage of mean were high for fruit length, fruit girth and 10-fruit weight, indicating additive gene action, which contributed to maximum divergence and played a major role in the improvement of brinjal yield.

2.3 Relationship between genetic and geographic diversity

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

Valadares *et al.* (2019) carried out an experiment to estimate the genetic divergence among eggplant genotypes for agronomic traits in order to gather information for the selection of genotypes in eggplant breeding programs for tolerance to high temperatures among ten traits in 24 genotypes, using the generalized Mahalanobis distance (D^2) as dissimilarity measure. The genotypes exhibited considerable genetic variability for all agronomic traits analyzed and can be used in eggplant genetic breeding programs for high temperatures.

Genetic diversity is an important prerequisite for improving the genetic makeup of any crop. Genetic divergence is the one of the main criteria of selection of parents to produce potential hybrids and for isolation of transgressive segregants from hybrids in further filial generations. Vidhya & Kumar (2014) conducted a study to investigate the genetic diversity among 30 genotypes of brinjal (*Solanum melongena* L.) against ten characters. Present study expressed that the cluster pattern based on D^2 statistics grouped 30 genotypes into five distinct clusters. Cluster I had 26 genotypes and cluster II, cluster III, cluster IV, cluster V had one genotype each. Maximum intra-cluster distance was observed by cluster I. The highest inter cluster distance of was recorded between cluster IV and V followed by cluster II and V and cluster I and IV, indicating there is presence of wide of wide range of genetic diversity among the brinjal

genotypes. Such genotypes with high degree of genetic diversity based on their mean values can be utilized through inter varietal hybridization program.

Hurtado *et al.* (2012) conducted an experiment to assessed the diversity and relationships of 52 accessions of eggplant from three geographically distant secondary centers of diversity (China, Spain, and Sri Lanka) using 28 morphological descriptors and 12 highly polymorphic genomic SSRs. A wide variation was observed for most morphological traits, and significant differences among the three centers of diversity were detected. The PCA analysis showed that eggplants from the three origins were morphologically differentiated, and accessions from each of the three secondary centers of diversity showed a typical combination of morphological characteristics. The SSR characterization identified 110 alleles and allowed to obtain a unique genetic fingerprint for each accession. Many alleles were found to be private to each origin, but no universal alleles were observed for any of the origins. The PCA analysis showed that the genetic differentiation among origins was less clear than for morphological traits, although the analysis of the population structure exhibited that accessions mostly group according to the origin, but also provides evidence of migration among the three secondary centers of diversity. These results were relevant for the management of genetic resources, breeding programs, and further evolutionary studies of eggplant.

Rathi *et al.* (2011) carried out an investigation where all the brinjal genotypes were grouped into five clusters based on D^2 values, which showed no association between geographical and genetic divergence. The intra-cluster distance was observed minimum for cluster IV and maximum in cluster II and the maximum distance at inter-cluster level was between clusters I and clusters IV, which may serve as a potential genotype for hybridization program.

Das *et al.* (2010) studied 40 genotypes of brinjal collected from different places and abroad were evaluated for different morphophysiological characters and genetic diversity was measured among the genotypes through D^2 statistics. The range of D^2 values varied from 8.13 to 8015.95 which presented high variability among the genotypes. Based on the degree of divergence the genotypes were gsegregated into ten clusters among which cluster ten was the largest having 22 genotypes. The divergence within the cluster showed medium and consistent level of divergence in all the clusters except cluster ten which had highest intra-cluster distance. The top two characters

which contributed most towards the genetic divergence were fruit yield and fruit weight. Dendrogram among the genotypes also revealed high diversity along with strong intra and inter cluster relationships.

The nature and magnitude of genetic divergence was evaluated by Joshi *et al.* (2003) using non-hierarchical Euclidean cluster analysis in 73 tomato (*Lycopersicon esculentum*) genotypes of diverse origin for different quantitative and qualitative traits. Maximum value of coefficient of variability (53.208) was observed for shelf life of fruits while it was minimum (69.208) for days to first picking. The genotypes were grouped into 15 clusters indicated that 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.

Rio and Bamberg (2002) carried out an investigation and collecting germplasm to broaden breeding resources is an essential activity of genebanks to understand how genetic diversity is partitioned in nature might help to identify collections rich in diversity. Previous studies among wild populations of *Solanum fendleri* (a disomic polyploid selfer) and *S. jamesii* (a diploid outcrosser) presented no significant associations between genetic and ecogeographic variation. Even physical separation could not predict genetic differences. In that study, 28 populations of *S. sucrense* Hawkes (2n=4x=48), a Bolivian species with another breeding system (polysomic polyploid oucrosser), were evaluated. The objective was to identyfy whether genetic differences between populations are predicted by differences in geographic parameters at the natural site of origin. They eventually found that geographic origin data is not very useful in gauging inter population genetic diversity in the genebank.

Sarma *et al.* (2000) evaluated 34 genotypes of brinjal (*Solanum melongena*) grouped them into 10 clusters using Mahalanobis's D^2 statistic. Fruit circumference and average fruit weight were the main characters affecting the grouping of genotypes. Eco-geographic diversity of the genotypes was not related to genetic diversity.

Joseph *et al.* (1999) conducted a study on 17 potato genotypes for estimation of genetic divergence using Mahalanobis's D^2. Clustering pattern was different under the sub-tropical and the temperate conditions where the 17 genotypes were segregated into 8 and 6 clusters, respectively. There was very little common with regard to distribution

of different genotypes into different clusters under the two conditions. Cluster I was observed the largest in both the growing conditions. The maximum genetic distance was noted between cluster II and V and the minimum genetic distance was recorded between cluster .VI and VII under subtropical conditions, whereas, the maximum genetic distance was observed between cluster II and VI and the minimum genetic distance was between cluster II and IV under temperate conditions. Intra-cluster distances were lower than the inter-cluster distances and the major contributor to genetic divergence was presented by tuber yield under both the conditions. The genetic diversity was not related to geographic diversity.

Gopal (1999) investigated 22 potatoes were evaluated by for ten morphological characters under four in vivo seasons (2 springs and 2 autumns) in the field. Mahalanobis's generalized intra-cluster and inter-cluster genetic distance and the distribution of genotypes into different clusters, led to the same conclusions under both in vitro and in vivo conditions. It was found 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.

Naskar *et al.* (1996) gave information on genetic divergence of sweet potatoes (*Ipomoea batatas*) 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.

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

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

2.4 Technique used for multivariate analysis

Multivariate statistics or multivariate statistical analysis in statistics describes a

collection of procedures which involve observation and analysis of more than one statistical variable at a time. Sometimes a distinction is made between univariate (e.g., ANOVA, t-tests) and multivariate statistics (Jupp and Mardia 1979). Genetic diversity analysis is based on different multivariate techniques. During last decade different multivariate techniques have been developed which may be due to the improvement of computer and internet. However, literature related to efficient multivariate techniques for genetic diversity analysis are reviewed in the following paragraphs:

Karim *et al.* (2016) conducted a multivariate analysis of twenty-six genotypes of eggplant to estimate the genetic diversity and to select the potential parents for a successful hybridization program. For PCA, D^2 and cluster analysis, the genotypes were grouped into five clusters. The highest inter-cluster distance was between Cluster II and Cluster III and the lowest between Cluster I and Cluster III were observed. Cluster III showed the maximum intra-cluster distance, whereas Cluster II showed the lowest intra-cluster distance. Depending on the analysis high yielding genotypes and genotypes which can be used for further hybridization program were selected.

Amaral (2005) conducted an experiment to evaluate the genetic divergence among 56 accessions of chilli and sweet pepper (*Capsicum spp.*) by using multivariate techniques. Eleven quantitative descriptors proposed by International Plant Genetic Resources Institute were use in a field experiment carried out in Campos dos Goytacazes, Rio de Janeiro State, Brazil. Generalized Mahalanobis distance (D^2) was used as the dissimilarity measure. Canonical variate analyses, cluster analysis using Tocher's optimization method and distances in the plan were applied. The variables: fruit length, fruit diameter, number of seeds per fruit, fruit average weight, plant height, plant canopy width, 1000- seed weight, days to flowering, days to fruiting, fruit number per plant and fruit weight per plant were evaluated. There were significant differences among accessions for all descriptors evaluated. General agreement among all multivariate techniques used was recorded and it was possible to separate the accessions in eight distinct groups, indicating that there is genetic variability for the evaluated traits.

Subrahmanyam *et al.* (2003) carried out an investigation to determine the extent of genetic divergence with respect to eleven characters in 85 sunflower genotypes consisting of 80 inbreds and five check cultivars. Univariate and multivariate analysis

of variance revealed the presence of significant differences among the genotypes. Mahalanobis' D^2 analysis indicated the presence of substantial genetic diversity. The genotypes were segregated into fifteen clusters. Based on inter-cluster distance and cluster mean for various characters, potential lines were identified from clusters III, IV, VI, VIII, XI, XII and XIV for crossing program. Among the investigated characteristics, the number of filled seeds per head, test weight, kernel to hull ratio and seed yield per plant exhibited high contribution towards the genetic divergence.

It was reported by Dharmatti *et al.* (2001) that genetic diversity in a population of 402 tomato lines was assessed by using multivariate analysis, in a field experiment carried out. Observations were noted for plant height, number of branches/plant, number of fruits per plant, yield per plant, incidence of tomato leaf curl virus (TLCV), and number of whiteflies per plant. The 402 lines were segrgated 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 25 contributed maximum to the divergence. Therefore, selection of divergent parents based on these characters might be useful for heterosis breeding in summer tomato.

Desai *et al.* (1997) conducted an experiment on thirty-six genotypes of potato to evaluat by for genetic divergence by Mahalanobis's D^2 statistic. Nine clusters were identified; I being the largest, containg 7 genotypes. Cluster I, III, V, VI and VII showed larger genetic divergence. Genotypes in clusters III had the highest tuber yields and other characters like number of stems, number of leaves, maturity, shoot fresh weight, number of tubers, average tuber weight, sugar content and harvest index. Cluster I contained genotypes with high dry matter and starch contents, cluster IV those with dwarf plant height and early maturity and cluster VI those with high protein content. The genotypes differed significantly for all characters, suggesting a good scope of selection of potato.

Estevez *et al.* (1994) conducted an analysis of data on yield and its components from tests of 15 varieties enabled the varieties to be classified into 7 groups on the basis of genetic divergence (measured by values for the Mahalanobis's D^2 statistics). A group comprising Lipsi and Allrad and another comprising Simcoe showed the greatest

divergence between themselves and from other types which suggested that they would be suitable for use as parents in breeding.

Birhman and kaul (1991) evaluated by applying the D^2 statistic to data on 9 yield components in 26 potato genotypes comprising 9 elite varieties and 17 advanced breeding lines. Genotypes were segregated into 8 clusters, cluster I having 12 genotypes and the others between 1 and 4. Inter-crossing of genotypes in clusters III, VI and VIII was thought the most advantageous in terms of tuber yield gain.

The influence of four types of genetic divergence on the vigour and variability of the progenies was studied in two field experiments by Loiselle *et al.* (1991). The measures of genetic divergence were; (1) the progenies inbreeding coefficients; (2) the Mahalanobis's distances between the parents obtained from their agronomic traits. These measures of divergence were not significantly related. Canonical correlation analysis between the divergence parameters and vigour related traits produced significant relationships in one experiment only.

CHAPTER III

MATERIALS AND METHODS

The present research work was intitled as "Morphological characterization, genetic variability and phenotypic diversity analysis in brinjal (*Solanum melongena* L.) genotypes" and was carried out in the experimental field of Sher-e-Bangla Agricultural University, Dhaka during the period from August, 2019 to March, 2020. The explicit information regarding the materials and methods of this experiment is discussed below:

3.1 Site of experiment

The experimental site was at 90° 22" E longitude and 23° 41" N latitude at an altitude of 8.6 meters from the sea level (www.distancesfrom.com).

3.2. Characteristics of soil

The experimental site's soil is a medium-high land in the Modhupur Tract of the Agro Ecological Zone (AEZ) 28 (www.banglapedia.com). The Madhupur Clay has created a region with complex relief and soils. There are eleven different types of soil in the area, with deep red brown terrace, shallow red brown terrace, and acid basin clays being the most common. Dark grey thick clays make up the soil. They have a high acidity level, with limited moisture retention capacity, and a low fertility level. The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.3. Climate

The experiment was largely carried out during the Rabi season (August to March). In Kharif-2, seeds are sowed (August). In August, there was a lot of rain, while in January and February; there was little or no rain. During the experiment, the humidity percentage and temperature was moderate. Details of the meteorological data in respect of temperature, rainfall and relative humidity during the period of the experiment were collected from Bangladesh Meteorological Department, Agargon, Dhaka- 1207 (Appendix II).

3.4 Planting materials

The materials used in the experiment were collected from local market of Bangladesh and India. The name of the genotypes along with the source are showed in Table 1.

Table 1. Name of selected 20 genotypes used in the experiment with their source

Sl. No.	Name	Identification marker	Source
1	India 1	G1	India
2	Luna	G2	Local market
3	Magic ball	G3	Local market
4	Green super	G4	Local market
5	Chumki	G5	Local market
6	Choice light	G6	Local market
7	Shinghnath	G7	Local market
8	Ventura	G8	Local market
9	Borsharani	G9	Local market
10	DNJ katali	G10	Local market (Dinajpur)
11	Sobuj sathi	G11	Local market
12	Pirgonj	G12	Local market
13	BNB 422	G13	Local market
14	KB 2031	G14	Local market
15	Bt	G15	Local market
16	Aveo Round	G16	Local market
17	Kushtia-2	G17	Local market
18	Altapon	G18	Local market
19	Green Line	G19	Local market
20	Brinjal White	G20	Local market

3.5 Design and layout of the experiment

The experiment was laid out Randomized Complete Block Design (RCBD) with three replications. Five plants for each genotype per replication were used. Plant to plant distance was 0.75 m and row to row distance was 1.20 m. The genotypes were randomly distributed to each block. The layout of the experiment has been shown Appendix III.

3.6 Raising of seedlings

Seeds of selected genotypes were sown in the well-prepared seedbed on 21th August, 2019. All care and precautions were taken to raise healthy seedlings. When seedlings become 30 days old, those were transplanted to poly bags. The seedbeds were watered before uprooting the seedlings. At the time of uprooting, care was taken so that root damage was minimized and some soil remained with the roots. After 30 days, seedlings are transplanted to the main field.

3.7 Land preparation

The experiment plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller. Weeds and other stables were removed carefully from the experimental plot. Manures and fertilizers were applied as per the recommended dose before the final land preparation and plots were prepared as per layout.

Plate 1. Preparation of land

3.8 Manure and fertilizers application

Total FYM and TSP were applied in the field during final land preparation. Urea and MOP were applied at two equal installments. The first top dressing was done 25 days after transplanting and the 2nd at the time of flowering. Doses of manure and fertilizers used in the study are shown in Table 2. Organic manure was applied for two times, 1st dose was 2 weeks after transplanting and another one was 5 weeks after transplanting.

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

Sl. No.	Fertilizer/Manure	Dose
1.	FYM	15 – 20 ton/hector
2.	Nitrogen	150 kg/hector
3.	P_2O_5	75 kg/ha
4.	K_2O	75 kg/ha
6.	Organic manure	100g/m^2

Source: Kumar, 2012

3.9 Transplanting of seedling

Healthy, uniform sized and 60 days old seedlings were transplanted in the experimental field. Then stalking and tagging was done for each genotype.

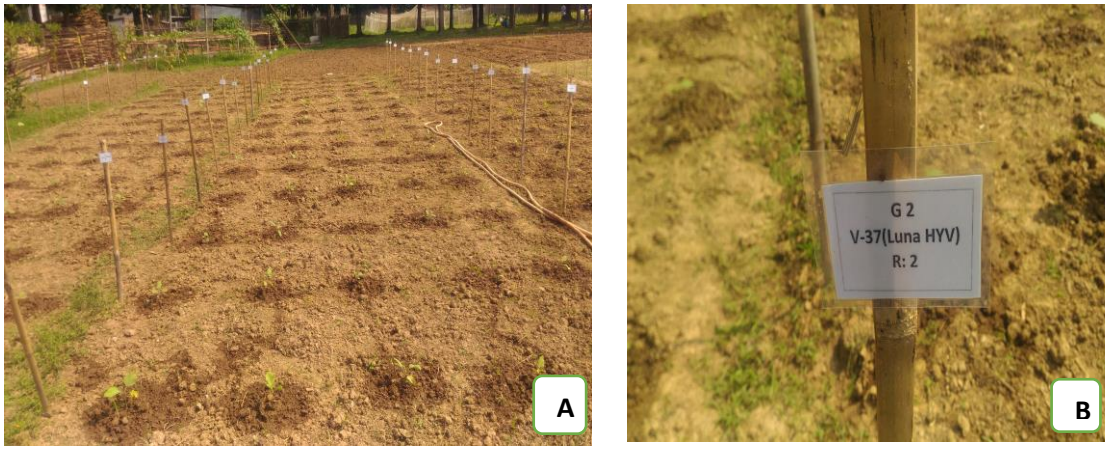


Plate 2. A- Field after transplantation; B- Stalking and tagging

3.10 Intercultural operations

Intercultural operations such as weeding, mulching, irrigation etc. were done when it was necessary for proper growth and development of the plants. Hence, no insecticide was used to study the tolerance capacity of the genotypes against fruit and shoot borer. Proper shading was given in the morning at the first stage of transplanting to protect the young seedlings from scorching sunshine during the day time.

3.10.1 Gap filling

Some of seedlings were damaged after transplanting and the damaged seedlings were replaced by new and healthy seedlings from the same stock. Seedlings were transplanted with a high mass of soil with roots to minimize transplanting shock. Gap filling was done twice. The first gap filling was done just after 10 days of transplanting and the 2nd one was one week after first gap filling.

3.10.2 Weeding

The first weeding was done after 20 days of transplanting to keep the crop free from weeds. After that it was done at every 15 days interval until the peak flowering stage. Spading was done from time to time specially to break down the soil crust and keep the land weed free after irrigation was done.

3.10.3 Irrigation

Irrigation was done more or less three times in a week or when it was needed. Irrigation was given throughout the growing period. Each fertilizer application was followed by irrigation.

Plate 3. Different intercultural operations (A- Irrigation to the plant, B- Earthing up)

3.10.4 Earthing up

Earthing up was done as and when required by piling soil up around the base of a plant and the soil from the space between the rows to regulate soil moisture and temperature and suppress the weeds.

3.11 Data collection

For studying various genetic parameters and inter-relationships, thirteen characters were taken into account such as plant types, growth habit, hairiness, spines on leaf, calyx and stem, flower color, shape and color of fruits, days to 1st flowering, days 1st fruiting, days to 1st harvesting, plant height, no. of primary branches per plant, no. of secondary branches per plant, no. of flowers per plant, no. of fruits per plant, fruit length, fruit diameter, fruit weight, % infested fruit by BSFB and yield per plant.

3.12 Data collection methods

The data were recorded on three selected plants of each genotype from each replication on the following traits-

3.12.1 Growth habit

Plant growth characters were recorded according to their spreading, branches, dwarfness and erect habit

3.12.2 Hairiness

The presence of hairiness on leaf, stem, and calyx was recorded.

3.12.3 Spiny character

The spiny characters of leaf, stem, calyx, and fruit of the brinjal plants was recorded.

3.12.4 Flower color

Flower color of selected plant of each genotype was observed.

3.12.5 Fruit shape and color

Different shapes and color of fruit of each genotype was observed.

3.12.6 Days to 1st flowering

When the genotype of each row showed the 1st flowering, then the data was recorded. Counting should be started from the sowing date to the date of appearance of 1st flower bloom.

3.12.7 Days to 1st fruiting

Days to 1st fruiting were counted from the sowing date to the date of appearance of 1st fruit.

3.12.8 Days to 1st harvest

At the mature stage, 1st harvesting was done. Recording data was started from the sowing date to the date of harvest of 1st mature fruit.

3.12.9 Plant height (cm)

Measurement of plant height was done in centimeter (cm) which was starting from the base of the plant to the tip of the plant. After harvesting, data of plant height was noted.

3.12.10 No. of primary branches per plant

The total no. of branches derived from the main stem of a plant was considered primary branches and the record was kept after counting.

3.12.11 No. of secondary branches per plant

The total no. of branches originated from the primary branches of a plant was counted and deliberated as the no. of secondary branches per plant.

3.12.12 No. of flowers per plant

The total no. of flowers of each plant was counted and considered as the no. of flowers per plant.

3.12.13 No. of fruits per plant

The total no. of fruits of each plant was counted and considered as the no. of fruits per plant.

3.12.14 Fruit length (cm)

The length of each fruit from each plant was measured with scale in cm and consider as individual fruit length.

3.12.15 Fruit diameter (cm)

The diameter of each fruit in cm from each plant was measured with slide calipers and consider as individual fruit diameter.

3.12.16 Fruit weight (gm)

The weight in gram of each fruit from each plant was measured with electric balance and consider as individual fruit weight.

3.12.17 % of Fruit infestation

By cutting each fruit into pieces with the help of sharp knife, observing the presence of tunnel or larvae inside the fruit of BSFB and counted the number of infested fruits per plant.

To find out the % of infested fruits per plant, given formula is followed.

$$\textbf{Percent of infested fruits per plant} = \frac{\textbf{The number of infested fruits per plant}}{\textbf{Total number of fruits per plant}} \times 100$$

3.12.18 Yield per plant (kg)

Fruits produced by a representative plant were weighted in kilogram and considered as the yield per plant.

3.13 Statistical analysis

Collected data were statistically analyzed using STATICTIX-10 computer software program to find out the significance among the brinjal genotypes. To test the differences between the means of the genotypes, Duncan's Multiple Range Test (DMRT) at 5% level of significance was performed for all the characters (Gomez and Gomez, 1984). Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Mean, range and coefficient of variation (% CV) were also estimated using OPSTAT computer software program. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz.,

Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.13.1 Analysis of Variance

The variance analysis for different characters was carried out utilizing mean data to assess the genetic variability among populations as given by Cochran and Cox (1957). The level of significance was tested at 5% and 1% using the F test. The model of ANOVA used is presented below:

Source of variation	df	MSS	EMSS	F-Ratio
Replication (r)	r-1	M1		M1/M3
Genotypes (g)	g-1	M2	$\delta e^2+\delta g^2$	M2/M3
Error (e)	(r-1) (g-1)	M3	δe^2	

Here,

r = Number of replications;
g = Number of genotypes;
df = degree of freedom;
MSS = Mean sum of square; and
EMSS = Expected values of MSS.

To test the significance of the difference between any two-adjusted genotypic mean, the standard error of the mean was computed using the formula**:**

$$S.E = \sqrt{\frac{2Me}{r}}\ (1 + \frac{rqu}{q+1})$$

Here,

S. E = Standard error of mean;
Me = Mean sum of square for error (Intra block);
r = Number of replications;
q = Number of populations in each sub-block; and
u = Weightage factor computed.

3.13.2 Estimation of Least Significant Differences (LSD)

Least Significant Differences were estimated according to the formula of Gomez and Gomez (1984).

$$LSD_\alpha = t_\alpha\sqrt{\frac{s^2}{r}}$$

Here,

α = Level of significance;
t= tabulated t-value with concerned df at same level of significance;
s^2= Error Mean Sum of Square; and
r = Number of replications.

3. 13.3 Study of Variability parameters

Estimation of the variability among the populations for traits related to yield per plant in brinjal were narrated below:

3.13.3.1 Estimation of Genotypic and Phenotypic Variances

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

a. Genotypic variance, $\sigma_g^2 = \frac{\text{MSG}-\text{MSE}}{\text{r}}$

Here,

MSG = Mean sum of square for genotypes;
MSE = Mean sum of square for error; and
r = Number of replications.

b. Phenotypic variance, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Here,
σ_p^2= Phenotypic variance;
σ_g^2= Genotypic variance; and
σ_e^2 = Environmental variance = Mean square of error (MSE).

3.13.3.2 Estimation of genotypic and phenotypic coefficient of variation

The following formula was given by Burton (1952) to calculate the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the characters.

$$\mathbf{GCV} = \frac{\sigma_g \times 100}{\bar{x}}$$

Here,
GCV = Genotypic coefficient of variation;
σ_g= Genotypic standard deviation; and
$\bar{x}$ = Population mean.

$$\mathbf{PCV} = \frac{\sigma_p \times 100}{\bar{x}}$$

Here,
PCV = Phenotypic coefficient of variation;
σ_p= Phenotypic standard deviation; and
$\bar{x}$ = Population mean.

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were categorized by Sivasubramanian and Madhavamenon (1973).

- High (>20%);
- Moderate (10-20%); and
- Low (0-10%).

3.13.3.3 Estimation of heritability in broad sense

To compute broad sense heritability, a formula was given by Singh and Chaudhary (1985), which is presented below:

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Here,

h_b^2=Heritability in broad sense;

σ_g^2= Genotypic variance; and

σ_p^2= Phenotypic variance.

Categories for heritability estimation in cultivated plants were suggested by Robinson *et al.* (1966). They are:

- Low: 0-30%;
- Moderate: 30-60%; and
- High: >60%.

3.13.3.4 Estimation of genetic advance

To calculate the expected genetic advance for different characters under selection a formula was suggested by Allard (1960). These are given below:

$$GA = \frac{\sigma_g^2}{\sigma_p^2} . K . \sigma_p$$

Here,

GA = Genetic advance;

σ_g^2 = Genotypic variance;

σ_p^2 = Phenotypic variance;

σ_p = Phenotypic standard deviation; and

K= Standard selection differential which is 2.06 at 5% selection intensity.

Johnson *et al.* (1955) suggested categories for genetic advance. They are:

- Low (<10%);
- Moderate (10-20%); and
- High (>20%).

3.13.3.5 Estimation of genetic advance in percentage of mean

To calculate genetic advance in the percentage of mean following formula was given by Comstock and Robinson (1952).

$$\text{GA in percent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Johnson *et al.* (1955) suggested categories for genetic advance in percent of mean. They are:

- Low (<10%);
- Moderate (10-20%); and
- High (>20%).

3.13.3.6 Correlation coefficient analysis

The correlation coefficients were calculated to estimate the level of relationship of characters with yield and among the yield parts. Both genotypic and phenotypic correlation coefficients between two characters were computed by utilizing the variance and covariance products, using the formula which is suggested by Al-Jibouri *et al.* (1958).

- $r_{gxy} = \frac{Cov_{gxy}}{\sqrt{\sigma^2_{gx}}.\sqrt{\sigma^2_{gy}}}$

Here,
$r_g(xy)$= The genotypic correlation coefficients of x;
Cov_{gxy}= The genotypic covariance of x;
σ^2_{gx}= Genotypic variance of the trait x; and
σ^2_{gy} = Genotypic variance of the trait y.

- $r_{pxy} = \frac{Cov_{pxy}}{\sqrt{\sigma^2_{px}}.\sqrt{\sigma^2_{py}}}$

Here,
$r_p(xy)$= The phenotypic correlation coefficients y;
Cov_{pxy} = The phenotypic covariance of y;
σ^2_{px}= Phenotypic variance of the trait x; and
σ^2_{py}= Phenotypic variance of the trait y.

The estimated value of 'r' was compared with table 'r' value with n-2 degrees of freedom at 5% and 1% level of significance, where, n is stand for the number of pairs of observation. Thus, the data obtained from various experimental objectives were

subjected to pertinent statistical analysis to draw relevant inference towards the genetic divergence of brinjal populations.

3.13.3.7 Path coefficient analysis

According to the procedure given by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), Path coefficient analysis was done utilizing simple correlation values. In path analysis, the correlation coefficient is segregate into direct and indirect independent variables on the dependent variable.

$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$ +……..+ $P_{yx11}.r_{x1x11}$

$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$ +……..+ $P_{yx11}.r_{x2x11}$

$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$ +……..+ $P_{yx11}.r_{x3x11}$

To calculate direct and indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is needed to be formulated as presented below:

Here,

r= simple correlation coefficient; and

P= path coefficient (unknown).

P's in the above equations may be conveniently decoded by arranging them in matrix form. Total correlation, say between x1 and y is thus partitioned as given bellow:

P_{yx1} = the direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = the indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = the indirect effect of x1 via x3 on y.

After calculating the direct and indirect effect of the characters, the residual effect (R) was computed by using the formula given below (Singh and Chaudhary, 1985):

- $P_{RY}^2 = 1 - \sum P_{iy} \cdot r_{iy}$

Here,

$P_{RY}^2 = (R^2)$;

Hence, residual effect, $R = (P_{RY}^2)^{1/2}$;

P_{iy}= Direct effect of the character on yield; and

r_{iy}=Correlation of the character with yield;

Categories:

- Negligible (0.00 to 0.09);
- Low (0.10 to 0.19);
- Moderate (0.20 to 0.29);
- High (0.30 to 1.0); and
- Very High (>1.00)

3.13.4 Analysis of diversity

Among the genotypes genetic diversity was assessed by Mahalanobis's (1936) distance (D^2) general statistic and its auxiliary analyses. Clustering was done using non-hierarchical classification. In GENSTST, to search for optimal values of chosen criterion proceeds the algorithm is used as follows. Starting from some initial grouping of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. The quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program (Rao, 1952). Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Canonical Vector analysis (CVA), Non-Hierarchical Clustering, and Cluster Diagram which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity (Bashar, 2002 and Uddin, 2001). These are as follows:

3.13.4.1 Principal Component Analysis (PCA)

Principal Component analysis is one of the multivariate techniques which is used to examine the inter-relationships among several traits and it can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations that maximize the variation contained within them, thereby presenting most of the original variability in a smaller number of dimensions. Therefore, Principles components were calculated from the correlation matrix and genotypes scores obtained for the first products (which has the item of accounting for maximum variance) and flourishing components with latent roots greater than unity (Jeger *et al.*, 1983). Different morphological character's contribution towards divergence is discussed from the latent vectors of the first two principal components.

3.13.4.2 Principal Coordinate Analysis (PCO)

Principal Coordinates Analysis is a method to explore and to visualize similarities or dissimilarities of data. It starts with a similarity matrix or dissimilarity matrix (=

distance matrix) and assigns for each item a location in a low-dimensional space. By using PCO we can visualize individual and/or group differences. Individual differences can be used to show outliers. Principal Coordinate analysis is equivalent to PCA but it is used to compute inter unit distances and used for dissimilarities.

3.13.4.3 Canonical Vector Analysis (CVA)

Canonical vector analysis (CVA) observes linear combination of original variabilities that maximize the ratio of between groups to within group variation. It's also giving functions of the original variables that help to discriminate between the groups. Consequently, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among the groups to the within group variations. The canonical vector is based upon the roots and vectors of WB, where W is pooled within the groups covariance matrix and B is the among groups covariance matrix.

3.13.4.4 Cluster Analysis (CA)

The genotypes of a data set are divided into some number of mutually exclusive groups by cluster analysis. Clustering was done by using non-hierarchical classification. In GENSTST, the algorithm is used to search for optimal values of chosen criterion proceeds such as: Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.13.4.5 Calculation of D^2 values

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

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

Here,

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

X = Number of characters

3.13.4.6 Calculation of average intra-cluster distances

Average intra-cluster distances were estimated by the following formula as suggested by Singh and Chaudhury (1985). Statistic is defined by the formula

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

Here,

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

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

3.13.4.7 Calculation of average inter-cluster distances

Average inter-cluster distances were computed by the following formula which was suggested by Singh and Chaudhury (1985).

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

Here,

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

n_i = Number of populations in cluster I; and

n_j = Number of populations in cluster j.

3.13.4.8 Cluster diagram

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

3.13.4.9Selection of genotypes for future hybridization program

Divergence analysis is usually performed to identify the diverse genotypes for hybridization program. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) disclose the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization program according to Singh and Chaudhury (1985). According to them

the following points should be considered while selecting genotypes for hybridization program- (i) Choice of cluster from which genotypes are selected for use as parent(s),

(ii) Selection of particular genotype(s) from the selected cluster(s),

(iii) Relative contribution of the characters to the total divergence, and

(iv) Other important characters of the genotypes performance.

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted in the central farm of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka during the period from July, 2019 to March, 2020 to evaluate the performance of yield contributing characters of twenty brinjal genotypes. As plant breeding depend on genetic variation, a new variation is fundamentally vital for introducing new cultivars in breeding programs. Thus, accurate information on the nature and degree of diversity of the parents is the prerequisite for an effective breeding program. The knowledge of genotypic variation within genotypes in relation to morphology, phenology, and yield would help to screen out better genotypes for the hybridization or further breeding programs. The accessibility of transgressive segregants in the breeding methods relies upon the dissimilarities of the parents. So, appropriate data on the degree of diversity of the parent is important for an effective breeding program. The results on different parameters have been interpreted, discussed and presented in following sub-headings:

4.1 Morphological Characterization of Brinjal

Phenotypic expression of morphological traits of different brinjal genotypes exhibited remarkable variations under study. In this research, the characters presenting variations are explained. Consequently, selection on the basis of these characters will be effective. Characterization on the basis of morphological traits is considered to the 1st step for classification of genetic resources. Various morphological traits of 20 genotypes of brinjal are given in Table 3.

4.1.1 Growth habit

To the breeder, plant architecture is a crucial parameter for the improvement of plant ideotype under the given environment. The observed genotypes have been assembled into three distinct groups. The genotypes G1, G3, G5, G8, G9, G10, G15, G16, G18, and G19 were spreading; genotypes G2, G6, G7, G12 and G17 were observed semi erect in plant growth habit and rest of the genotypes G4, G11, G13, G14, and G20 exhibited erect growth habit. Generally, genotypes which are easy to maintain for interculture operation, are preferable to the farmers. In this research, it was noted that,

spreading type genotypes were less infested by BSFB than erect types. Similar result was also disclosed by Quamruzzaman *et al.* (2020).

Table 3. Morphological characterization of twenty brinjal Genotypes

Genotypes	Growth habit	Hairiness	Presence of spines	Flower color	Fruit shape	Color of fruits
G1	Spreading	Stem, Leaf	Stem, Leaf, Calyx	Purple	Oblong	Deep green
G2	Semi erect	Stem, Leaf	Stem	Purple	Oval	Green
G3	Spreading	Stem, Leaf	Calyx	Purple	Oval	Green
G4	Erect	Stem, Leaf	Absent	Purple	Round	Green
G5	Spreading	Stem, Leaf	Absent	White	Oval	Green
G6	Semi erect	Stem, Leaf	Absent	Purple	Round	Violet
G7	Semi erect	Stem, Leaf	Absent	Purple	Long	Violet
G8	Spreading	Stem, Leaf	Stem, Calyx	Purple	Oval	Green
G9	Spreading	Stem, Leaf	Absent	Purple	Oblong	Violet
G10	Spreading	Stem, Leaf	Stem, Leaf, Calyx	Purple	Round	Green
G11	Erect	Stem, Leaf	Stem	White	Round	Deep green
G12	Semi erect	Stem, Leaf	Absent	Purple	Long	Violet
G13	Erect	Stem, Leaf	Calyx	Purple	Oval	Green
G14	Erect	Stem, Leaf	Absent	Purple	oblong	Green
G15	Spreading	Stem, Leaf	Stem, Leaf, Calyx	Purple	Round	Green
G16	Spreading	Stem, Leaf	Stem,	Purple	Oval	White
G17	Semi erect	Stem, Leaf	Stem, Calyx	Purple	Oblong	Green
G18	Spreading	Stem, Leaf	Calyx	Purple	Oval	Purple
G19	Spreading	Stem, Leaf	Calyx	Purple	Oval	Whitish green
G20	Erect	Stem, Leaf	Stem	Purple	Round	White

4.1.2 Hairiness

Hairiness is a major character of the brinjal plants as it is related to the resistance against pests. The hairs have a noteworthy role towards non-preference for fruit infestation by BSFB insect (Javed *et al.*, 2017 and Kassi *et al.*, 2018). In this study, it was observed that, the more densely hair present on plant's body is more resistant to pest. All the 20

genotypes were characterized by hairiness, which was mostly observed at the leaf and stem.

4.1.3 Spiny character

Presence of spines on brinjal plant is considered one of the major characteristics. According to the observation of Javed *et al.* in 2017 and Kassi *et al.* in 2018, spine gives resistance from the insect pest. In this present study, different genotypes having a spine in their different body part such as, stem, leaves, and calyx. The genotypes G1, G10, and G15 had spine in stem, leaf, and calyx. The genotypes G2, G11, G16, and G20 had spine in only stem. The genotypes G3, G13, G18, and G19 had spine in calyx only. Genotype 8 had spines in stem and calyx, while, some genotypes G4, G5, G6, G7, G9, G12, and G14 didn't show any spine (Table 3).

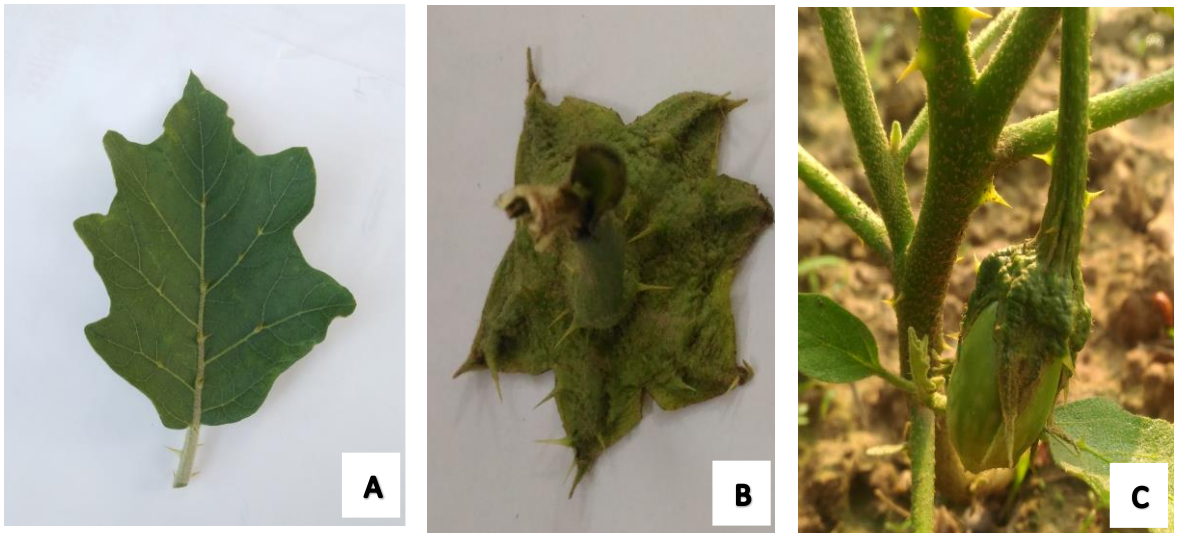


Plate 4. Spiny character **(**A- Spines on a leaf, B- A calyx with spines and C- A whole plant with spines)

4.1.4 Color of flower

About 48% cross-pollination was recorded in the brinjal plants (Agrawal, 1980), and flower color plays a major role in brinjal fruit setting. Two color white or purple were observed in different genotypes. Purple is more common than other colors in case of brinjal flower. The genotypes G5 and G11 produced white color flowers whereas, all the rest genotypes produced purple color flower. Different colors for brinjal flower were reported by Kumar *et al.* (2011) in his study.

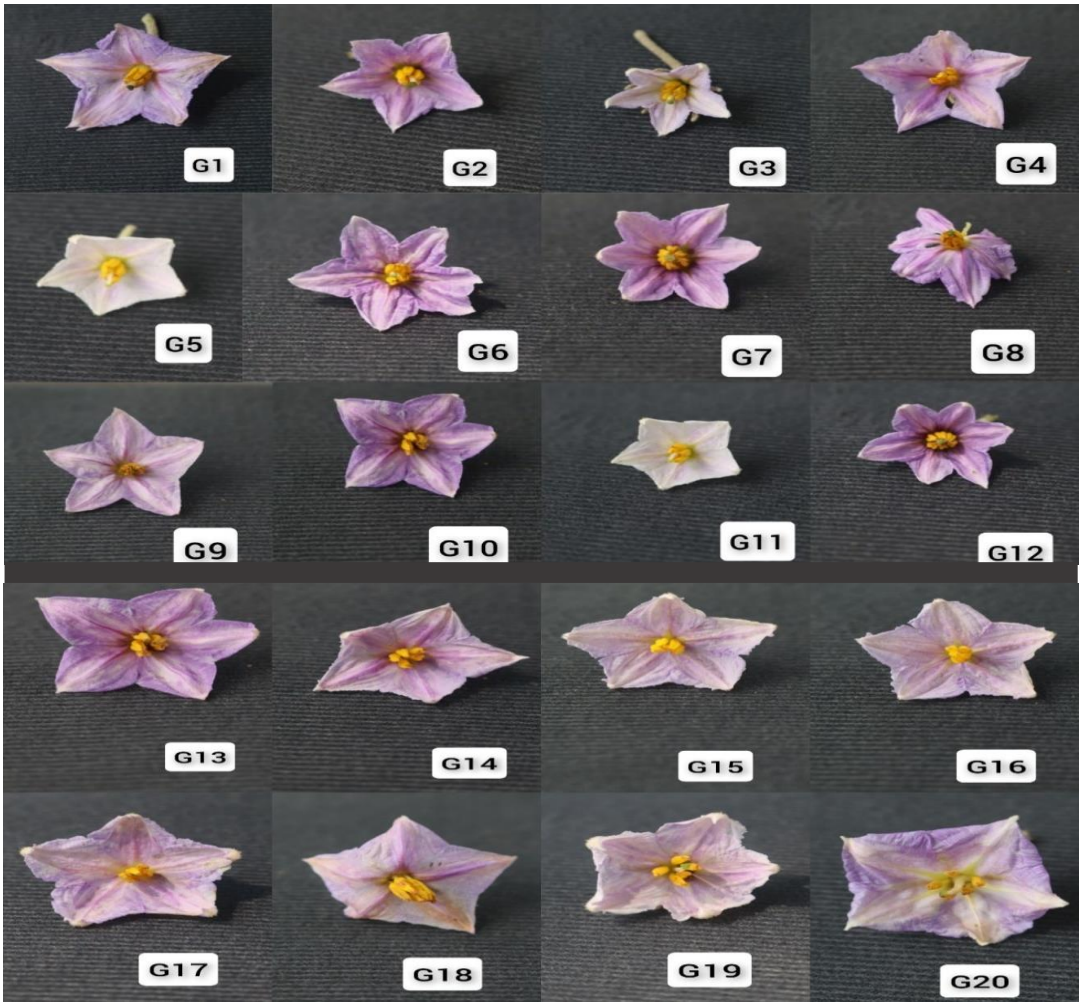


Plate 5. Different color flower from 20 genotypes of brinjal

4.1.5 Fruit shape

According to (Das *et al.*, 2017), three botanical types are present in brinjal, which are- var. *esculentum* (round to oval type fruit shape), var. *serpentinum* (long and slender type fruit shape), and var. *depressum* (dwarf and oblong type fruit shape). Different genotypes exhibited different shapes of fruit and it plays an important role in consumer preference as well market value. The genotypes G4, G6, G10, G11, G15, and G20 produced round fruits, genotypes G1, G9, G14, and G17 produced oblong fruits. The genotype G2, G3, G5, G8, G13, G16, G18, and G19 produced oval shaped fruit and the rest two G7 and G12 produced long shaped fruits.

4.1.6 Color of fruit

Fruit color is a serious consumer preference character in brinjal marketing. Usually, green and violet color fruits are common in the market but a lot of variations in fruit color were observed in the present experiment, which is similar to the observation of Das *et al.* (2017) and color of brinjals was classified into distinct groups: violet, purple,

white, green, and whitish green. The green color brinjal is noted in maximum genotypes, they were G2, G3, G4, G5, G8, G10, G13, G14, G15, and G17; white color genotypes were G16 and G20; violet genotypes were G6, G7, G9, and G12; purple color observed for only G18 only and the rest one G19 was whitish green.

4.2 Estimation of genetic variability, heritability and genetic advance

Analysis of variance exhibited that, the brinjal genotypes varied remarkably (5% level of probability) with each other in Table 4. Range, mean, LSD and standard error of thirteen parameters of brinjal genotypes namely, days to 1st flowering, days to 1st fruiting, days to 1st harvesting, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of flowers per plant, no. of fruits per plant, fruit length (cm), fruit diameter (cm), fruit weight (g), % of infested fruit and yield per plant (kg) have been showed in Table 5. Phenotypic variance (PV), Genotypic variance (GV), Environmental variance (EV), Phenotypic coefficient variance (PCV), Genotypic coefficient variance (ECV), Environmental coefficient variance (ECV), heritability, genetic advance (GA) and genetic advance as % mean of the observed thirteen characters of brinjal genotype have been illustrated in Table 6.

4.2.1 Days to 1st flowering

Significant variations were noticed for the character of days to 1st flowering, and presented highly significant mean sum of square (61.39**) due to genotypic differences (Table 4).

The shortest duration for 1st flowering was recorded in G16 (71.78), followed by G1 (72.00), G20 (72.67) and G18 (73.34). On the other hand, the longest duration for 1st flowering was noted in G4 (86.00), followed by G11 (85.00), G3 (84.89) and G6 (84.78) (Table 5). Hassan *et al.* (2015) reported that, the no. of days to flowering exhibited a wide range of variation, ranging from 44 days to 88 days. Dutta *et al.* (2018) also observed the minimum days to 1st flowering was 35.33 days and maximum days were 51 days in their study.

In this experiment, the phenotypic variance (21.41) was recorded higher than genotypic variance (19.99) and the difference between them was low, which indicated that, environment has little influence for the expression of this parameter. Both the GCV (5.59) and PCV (5.79) were observed low. The estimated heritability was noticed high

Table 4. Analysis of variance for thirteen characters of brinjal

Sources of variation	df	Mean Sum of Square												
		DFF	**DFFR**	**DFH**	**PH**	**NPB**	**NSB**	**NFP**	**NFRP**	**FRL**	**FRD**	**FRW**	**PIF**	**YP**
Replications	2	2.21	0.23	0.17	6.75	1.38	1.45	0.04	0.30	0.38	0.41	407.90	9.17	0.001
Genotypes	19	61.39**	78.63**	182.48**	429.79**	6.58**	8.27**	136.64**	22.66**	87.82**	16.16**	18916.00**	1085.93**	0.46**
Error	38	1.42	1.16	1.42	21.20	0.65	0.74	0.44	0.21	0.75	0.21	181.50	8.21	0.01
CV (%)		1.49	1.15	1.01	5.99	7.40	6.17	3.35	6.51	5.57	6.43	5.67	8.85	8.14

*= Significant at 5 % level of probability, **= Significant at 1 % level of probability, and df = Degree of freedom,

Here,

DFF= Days to 1st flowering;
DFFR= Days to 1st fruiting;
DFH= Days to 1st harvesting;
PH= Plant height (cm);
NPB= No. of primary branches per plant;
NSB= No. of secondary branches per plant;
NFP= No. of flowers per plant;
NFRP= No. of fruits per plant;
FRL= Fruit length (cm);
FRD= Fruit diameter (cm);
FRW= Fruit weight (g);
PIF= % of infested fruit; and
YP= Yield per plant (kg).

Table 5. Mean performance of thirteen characters of twenty genotypes of brinjal

Geno types	DFF	DFFR	DFH	PH	NPB	NSB	NFP	NFRP	FRL	FRD	FRW	PIF	YP
G1	72.00i	85.56hi	105.33j	52.76h	10.00d-f	12.00gh	26.78d	10.11c	10.77ij	4.01h	94.14j	7.70j	0.95i
G2	82.22de	97.44cd	118.33g	79.25bc	11.33b-d	13.33d-g	12.78l	4.89hi	11.98hi	7.48f	287.39c	56.57a	1.40fg
G3	84.89ab	99.45ab	121.44f	63.57fg	9.11fg	11.11h	11.44mn	4.11j	14.98de	8.30c-e	310.67b	56.66a	1.28gh
G4	86.00a	99.67a	123.67de	75.95b-d	10.89b-e	12.89e-g	18.33i	6.78f	10.32jk	9.03bc	262.93d	55.56a	1.78b-d
G5	84.22a-c	97.67bc	127.89ab	56.24gh	8.56g	11.22h	12.67l	3.89j	22.03b	4.76gh	238.33ef	42.76c	0.93i
G6	84.78ab	100.67a	125.67c	74.97c-e	9.67e-g	12.67fg	22.00e-g	7.67de	10.49j	7.32f	207.61gh	30.41de	1.59d-f
G7	79.11f-h	93.45f	117.56g	92.58a	13.00a	16.00ab	30.78b	12.00a	22.15b	2.96i	103.38j	14.82i	1.24gh
G8	78.67gh	94.67ef	122.22ef	83.13b	12.00a-c	15.00bc	22.78e	7.22d-f	13.63e-g	8.82b-d	328.43b	26.22ef	2.36a
G9	79.33f-h	94.78ef	126.78a-c	81.49bc	10.78c-e	14.11c-e	22.78e	7.33d-f	22.85b	4.18h	162.37i	54.49a	1.19h
G10	82.33c-e	97.67bc	126.45bc	68.45d-f	8.78fg	12.78e-g	16.78 j	5.67 g	9.05k	9.13b	315.23b	58.84a	1.79bc
G11	85.00ab	100.33a	128.67a	75.73b-d	8.67fg	12.67fg	13.00kl	3.78j	9.07k	7.67ef	230.51ef	20.49gh	0.88i
G12	79.89fg	93.11f	114.22h	96.19a	12.89a	16.89a	33.78a	12.67a	30.02a	2.60i	112.07j	3.55jk	1.42fg
G13	83.89b-d	97.78bc	125.00cd	74.04c-e	11.22b-d	15.22bc	13.89k	5.11gh	14.75d-f	7.63ef	310.23b	24.06fg	1.58d-f
G14	80.78ef	93.56f	121.00f	74.63c-e	11.00b-e	14.67b-d	21.33f-h	7.56de	17.95c	5.28g	220.45fg	19.08hi	1.67c-e
G15	80.11fg	95.78de	117.44g	93.67a	12.00a-c	15.00bc	11.00n	3.56j	14.81de	8.95b-d	326.18b	0.00k	1.16h
G16	71.78i	84.33i	105.78 j	76.89bc	12.78a	15.78ab	28.11c	11.11b	13.32f-h	8.26de	195.04h	38.95c	2.17a

Table 5. Mean performance of thirteen characters of twenty genotypes of brinjal (cont.)

Geno types	DFF	DFFR	DFH	PH	NPB	NSB	NFP	NFRP	FRL	FRD	FRW	PIF	YP
G17	80.11fg	94.56ef	115.22h	96.52a	10.89b-e	13.89c-f	12.11lm	4.22ij	17.35c	10.62a	375.12a	15.90hi	1.58d-f
G18	73.34i	86.55h	105.22j	76.22bc	12.22ab	15.22bc	20.89h	7.78d	15.32d	8.77b-d	197.55h	31.40d	1.54ef
G19	77.89h	90.67g	110.44i	78.74bc	9.78e-g	12.78e-g	22.11ef	7.67de	17.88c	9.25b	248.67de	42.05c	1.90b
G20	72.67i	86.11hi	109.78i	67.38ef	12.78a	15.78ab	21.00gh	7.00ef	12.34gh	7.80ef	222.17fg	47.64b	1.55ef
Min	71.78	84.33	105.22	52.76	8.56	11.11	11.00	3.56	9.05	2.60	94.14	0.00	0.88
Max	86.00	100.67	128.67	96.52	13.00	16.89	33.78	12.67	30.02	10.62	375.12	58.84	2.36
Mean	79.95	94.19	118.41	76.92	10.92	13.95	19.72	7.01	15.55	7.14	237.42	32.36	1.50
$LSD_{0.05}$	1.97	1.78	1.97	7.61	1.33	1.42	1.09	0.75	1.43	0.76	22.27	4.73	0.20
SE	0.97	0.88	0.97	3.76	0.66	0.70	0.54	0.37	0.71	0.37	11.00	2.34	0.10

Here,

DFF= Days to 1st flowering;
DFFR= Days to 1st fruiting;
DFH= Days to 1st harvesting;
PH= Plant height (cm);
NPB= No. of primary branches per plant;
NSB= No. of secondary branches per plant;
NFP= No. of flowers per plant;
NFRP= No. of fruits per plant;
FRL= Fruit length (cm);
FRD= Fruit diameter (cm);
FRW= Fruit weight (g);
PIF= % of infested fruit; and
YP= Yield per plant (kg).

Table 6. Estimation of genetic parameters of thirteen characters of twenty brinjal genotypes

Parameters	σ^2p	σ^2g	σ^2e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to 1st flowering	21.41	19.99	1.42	5.79	5.59	0.19	93.38	8.90	11.13
Days to 1st fruiting	26.99	25.82	1.16	5.52	5.40	0.12	95.69	10.24	10.87
Days to 1st harvesting	61.77	60.36	1.42	6.64	6.56	0.08	97.70	15.82	13.36
Plant height (cm)	157.39	136.20	21.20	16.31	15.17	1.14	86.53	22.36	29.07
No. of primary branches per plant	2.63	1.98	0.65	14.85	12.88	1.97	75.20	2.51	23.01
No. of secondary branches per plant	3.25	2.51	0.74	12.92	11.36	1.57	77.19	2.87	20.55
No. of flower per plant	45.84	45.40	0.44	34.34	34.17	0.16	99.05	13.81	70.06
No. of fruits per plant	7.69	7.48	0.21	39.59	39.05	0.54	97.30	5.56	79.35
Fruit length (cm)	29.77	29.02	0.75	35.08	34.64	0.45	97.48	10.96	70.45
Fruit diameter (cm)	5.53	5.32	0.21	32.92	32.28	0.63	96.19	4.66	65.23
Fruit weight (g)	6426.33	6244.83	181.50	33.76	33.28	0.48	97.18	160.47	67.59
% of infested fruit	367.45	359.24	8.21	59.24	58.58	0.67	97.77	38.61	119.31
Yield per plant (kg)	0.16	0.15	0.01	27.04	25.78	1.25	90.93	0.76	50.65

Here,

σ^2p= Phenotypic variance; PCV= Phenotypic co-efficient variance;
σ^2g= Genotypic variance; GCV= Genotypic co-efficient variance; and
σ^2e= Environmental variance; ECV= Environmental co-efficient variance.

(93.38%) associated with moderate genetic advance as percentage of mean (11.13 %) of mean were noted in Table 6. Moderate PCV and GCV were reported in days to 1st flowering by Dutta *et al.* (2018).

4.2.2 Days to 1st fruiting

Considerable variations were noted in Table 4 for the character of days to 1st fruiting expressed highly significant mean sum of square (78.63**) due to genotypic differences.

The shortest duration for 1st fruiting was recorded in G16 (84.33), followed by G1 (85.56), G20 (86.11) and G18 (86.55), while, the longest duration for 1st fruiting was observed in G6 (100.67), followed by G11 (100.33), G4 (99.67), and G3 (99.45) in Table 5.

The phenotypic variance (26.99) was higher than genotypic variance (25.82) and the difference between them was low, which indicated influence of environment was so little for the appearance of this character. Both the GCV (5.40) and PCV (5.52), were low. The estimated heritability was also high (95.69 %) with moderate genetic advance (10.24 %) and moderate genetic advance (10.87 %) in % of mean were noted in Table 6, which suggesting presence of additive gene action.

4.2.3 Days to 1st harvesting

Significant variations were observed for the character of days to 1st harvesting showed highly significant mean sum of square (182.48**) due to genotypic differences (Table 4).

The minimum duration for 1st harvesting was recorded in G18 (105.22), followed by G1 (105.33), G16 (105.78), and G20 (109.78). On the other hand, the maximum duration for 1st harvesting was noted in G11 (128.67), followed by G5 (127.89), G9 (126.78), and G10 (126.45) (Table 5). Patel *et al.* (2017) reported that, days to 1st harvesting ranges from 60.74–82.30 days.

In this present experiment, the phenotypic variance (61.77) was slightly higher than genotypic variance (60.36) and the difference between them was (1.41) minimum, indicating that, environment had a little influence for the appearance of this character. Both the GCV (6.56) and PCV (6.64) were low. Low PCV and GCV along with moderate heritability was recorded in days to 1st harvest by Patel *et al.* (2017) in their

study. Vaishya *et al.* (2017) also reported low PCV and GCV along with high heritability for days to 1st fruit harvest. The estimated heritability was also high (97.70 %) with moderate genetic advance (15.82 %) and moderate genetic advance (13.36 %) in % of mean were also noted (Table 6).

4.2.4 Plant height (cm)

Considerable variations were observed for the character of plant height. Due to genotypic differences, it showed highly significant mean sum of square (429.79**) (Table 4).

The minimum plant height was observed in G1 (52.76 cm), followed by G5 (56.24 cm) and G3 (63.57 cm). On the other contrary, the maximum plant height was observed in G17 (96.52 cm), followed by G12 (96.19 cm), G15 (93.67 cm) and G7 (92.58 cm) (Table 5). Hassan *et al.* (2015) observed the variability in plant height ranged from 55 cm to 94 cm. Dutta *et al.* (2018) also recorded maximum plant height 129 cm and minimum plant height 71.67 cm.

It was observed that, the phenotypic variance (157.39) was considerably higher than genotypic variance (136.20) and the difference between them was high, which indicated that, environment had a great influence for the expression of this parameter. Both the GCV (15.17) and PCV (16.31) were moderate. Similar results were reported for plant height by Dutta *et al.* (2018). The estimated heritability was high (86.53 %) coupled with high genetic advance (29.07 %) in % of mean, which indicated the presence of additive gene action and simple selection can be effective for this trait (Table 6). Hazra *et al.* (2003) found medium to low variation among the brinjal for plant height.

4.2.5 No. of primary branches per plant

Due to genotypic differences, considerable variations were observed for the no. of primary branches per plant and it exhibited highly significant mean sum of square (6.58**) in Table 4.

The maximum no. of primary branches per plant was observed in G7 (13), followed by G12 (12.89), G16 (12.78), and G20 (12.78). On the other hand, the minimum no. of primary branches per plant was observed in G5 (8.56), followed by G11 (8.67), G10 (8.78), and G3 (9.11) (Table 5). Dutta *et al.* (2018) presented the range of the no. of primary branches per plant was from 2.33 to 5.33 in their study selected to brinjal.

In this study, the phenotypic variance (2.63) was slightly higher than genotypic variance (1.98) and the difference between them was low, which indicated that, environment had little influence for the expression of this character. Both the GCV (12.88) and PCV (14.85) were moderate. High heritability (75.20 %) associated with high genetic advance (23.01 %) as % of mean were recorded, which indicated the existence of additive gene action and simple selection can be possible for this trait (Table 6). Primary branches per plant was showing the relatively lower differences, reported by Saha *et al.* (2019). Similar result was reported by Muniappan *et al.* (2010).

4.2.6 No. of secondary branches per plant

Considerable variations were noted for the character of no. of secondary branches per plant and that, exhibited highly significant mean sum of square (8.27**) due to genotypic differences (Table 4).

In Table 5, the minimum no. of secondary branches per plant was recorded in G3 (11.11), followed by G5 (11.22), G1 (12), and G6 (12.67), while, the maximum no. of secondary branches per plant was noticed in G12 (16.89), followed by G7 (16), G16 (15.78), and G20 (15.78).

The phenotypic variance (3.25) was a bit higher than genotypic variance (2.51) and the differences between them was low, which indicated that, environment had a little influence for the expression of this character. Both the GCV (11.36) and PCV (12.92) were moderate. The estimated heritability was also high (77.19 %) coupled with high genetic advance (20.55 %) in % of mean were noted in Table 6, which was indicating additive gene action for the character. Similar result was reported by Patel *et al.* (2015) and Saha *et al.* (2019).

4.2.7 No. of flowers per plant

Due to genotypic differences, significant variation was noted for no. of flowers per plant and showed highly significant mean sum of square (136.64**) in Table 4.

The maximum no. of flowers per plant was observed in G12 (33.78), followed by G7 (30.78), G16 (28.11), and G1 (26.78), while, the minimum no. of flowers per plant was observed in G15 (11.00), followed by G3 (11.44), G17 (12.11), and G5 (12.67) in Table 5.

It was recorded that, the phenotypic variance (45.84) was slightly higher than genotypic variance (45.40) and the difference between them was low, which indicated that, environment has a bit influence for the expression of this character. Both the GCV (34.17) and PCV (34.34) were observed high. The estimated heritability was high (99.05 %) combined with high genetic advance (70.06 %) in % of mean, indicating the appearance of additive gene action and simple selection for further breeding for this character is possible (Table 6). No. of flowers per plant showed higher estimates of GCV and PCV observed by Bende *et al.* (2019).

4.2.8 No. of fruits per plant

Considerable variations were noticed for no. of fruits per plant which showed highly significant mean sum of square (22.66**) due to genotypic differences in Table 4.

The maximum no. of fruits per plant was observed in G12 (12.67), followed by G7 (12), G16 (11.11), and G1 (10.11). On the other hand, the minimum no. of fruits per plant was observed in G15 (3.56), followed by G11 (3.78), G5 (3.89), and G3 (4.11) (Table 5). Dutta *et al.* (2018) found the maximum no. of fruits per plant was 16.02 and the minimum number was 3.39 in their study.

The phenotypic variance (7.69) was a little higher than genotypic variance (7.48) and the difference between them was a bit low, which indicated that, environment had a little influence for the expression of this character. Both the GCV (39.05) and PCV (39.59) were observed high. It was noticed that, high heritability (97.30 %) associated with high genetic advance (79.35 %) in % of mean were recorded, which indicated the presence of additive gene action and simple selection for this parameter is considerable (Table 6). Bende *et al.*, (2019) reported higher estimates of GCV and PCV in fruits per plant in their study.

4.2.9 Fruit length (cm)

For fruit length, considerable variations were recorded and exhibited highly significant mean sum of square (87.82**) due to genotypic differences (Table 4).

The maximum length of fruit was noticed in G12 (30.02 cm), followed by G9 (22.85 cm), G7 (22.15 cm), and G5 (22.03 cm). On the other hand, the smallest length of fruit was recorded in G10 (9.05 cm), followed by G11 (9.07 cm), G4 (10.32 cm) and G6

(10.49 cm) (Table 5). Hasan *et al.* (2015) found fruit length ranges from 1.8 to 22.9 cm in their study.

The phenotypic variance (29.77) was a little higher than genotypic variance (29.02) and the difference between them was slightly low, which indicated that, environment had a little influence for the appearance of this character. Both the GCV (34.64) and PCV (35.08) were high. The estimated heritability was observed high (97.48 %) and associated with high genetic advance (70.45 %) as % of mean, which indicated the presence additive gene action (Table 6). Relatively lower difference was found in fruit length by Saha *et al.* (2019). Similar results were reported by Banerjee *et al.* (2018) and Kumar *et al.* (2013). High heritability with high genetic advance was observed for fruit length (Bende *et al.*, 2019).

4.2.10 Fruit diameter (cm)

Considerable variations were noted in Table 4 for fruit diameter and showed highly significant mean sum of square (16.16**) due to genotypic differences.

The minimum measurement of fruit diameter was observed in G12 (2.60 cm), followed by G7 (2.96 cm), G1 (4.01 cm), and G9 (4.18 cm). On the other hand, the maximum measurement of fruit diameter was recorded in G17 (10.62 cm), followed by G19 (9.25 cm), G10 (9.13 cm), and G4 (9.03 cm) (Table 5). Solaimana *et al.* (2015) found 2.6 to 9.0 cm fruit breadth his study. Fruit breadth ranged from 2.40 cm to 10.60 cm noted by Islam *et al.* (2018).

The phenotypic variance (5.53) was slightly higher than the genotypic variance (5.32) and the difference between them was a bit low, which indicated that, environment has a little influence for the expression of this parameter. Both the GCV (32.28) and PCV (32.92) were observed high. High heritability was also high (96.19 %) combined with high genetic advance (65.23 %) in % of mean indicating the existing of additive gene action (Table 6). High PCV and GCV were reported in fruit diameter by Dutta *et al.* (2018) in their study. Hassan *et al.* (2015) found medium to low variation among the germplasm in fruit width.

4.2.11 Fruit weight (gm)

For fruit weight, considerable variations were noticed and it exhibited highly significant mean sum of square (18916.00**) due to genotypic differences (Table 4).

The maximum weight of individual fruit was observed in G17 (375.12 g), followed by G8 (328.43 g), G15 (326.18 g), and G10 (315.23 g), while, the minimum weight of individual fruit was observed in G1 (94.14 g), followed by G7 (103.38 g), G12 (112.07 g), and G9 (162.37 g) (Table 5). Fruit weight ranging from 13 g to 95.20 g was reported by Islam *et al.* (2018). Hasan *et al.* (2015) found 12.1 g to 214.0 g fruit weight and Solaimana *et al.* (2015) found 35.5 g to 313.30 g fruit weight in their study.

The phenotypic variance (6426.33) was considerably higher than genotypic variance (6244.83) and the difference between them was high, which indicate that, environment had a great influence for the expression of this character. Both the GCV (33.28) and PCV (33.76) were high. High heritability was also high (97.18 %) coupled with high genetic advance (67.59 %) in % of mean were noted, which indicated the presence of additive gene action and simple selection can be possible for this particular trait (Table 6). High heritability with high genetic advance was observed for fruit weight per plant by Bende *et al.* (2019) in their study.

4.2.12 % of infested fruit

For % of fruit infestation, remarkable variations were recorded and expressed highly significant mean sum of square (1085.93**) due to genotypic differences in Table 4.

The minimum % of fruit infestation was noticed in Table 5 for G15 (0.00), followed by G12 (3.55), and G1 (7.70). On the other hand, the maximum % of fruit infestation was observed in G10 (58.84), followed by G3 (56.66), G2 (56.57), and G4 (55.56).

The phenotypic variance (367.45) was higher than genotypic variance (359.24) and the difference between them was low, which indicate that, environment has little influence for the expression of this character. Both the GCV (58.58) and PCV (59.24) were high. The estimated heritability was also high (97.77 %) and associated with high genetic advance (119.31 %) in % of mean, suggesting the existence of additive gene action (Table 6). Fruit borer infestation showed higher estimates of GCV and PCV. High heritability with high genetic advance was observed for fruit and shoot borer infestation (Bende *et al.*, 2019).

The rate of BSFB infestation in percentage against different brinjal genotypes

Infestation (%)	Genotypes	Grading for resistance
0%	G15	Resistance
1-15%	G1, G7, G12	Tolerant
15-30%	G8, G11, G13, G14, G17,	Moderately Tolerant
>30%	G2, G3, G4, G5, G6, G9, G10, G16, G18, G19, G20	Susceptible

4.2.13 Yield per plant (kg)

Yield per plant exhibited remarkable variations due to genotypic differences and presented highly significant mean sum of square (0.46**) in Table 4.

The maximum yield per plant was observed in G8 (2.36 kg), followed by G16 (2.17 kg), G19 (1.90 kg), and G10 (1.79 kg). On the contrary, the lowest yield per plant was observed in G11 (0.88 kg), followed by G5 (0.93 kg), G1 (0.95 kg), and G15 (1.16 kg) (Table 5). In 2018, Dutta *et al.* reported the highest fruit yield per plant was 3.02 kg and the lowest fruit yield per plant was 1.05 kg in their study.

The phenotypic variance (0.16) was slightly higher than genotypic variance (0.15) and the difference between them was low, which indicated that, environment had a little effect for the expression of this character. Both the GCV (25.78) and PCV (27.04) were high. Similar results were noted by Dutta *et al.* (2018). High heritability was also high (90.93 %) associated with high genetic advance (50.65 %) in % of mean, indicating the presence of additive gene action and simple selection for further breeding program for this character can be possible (Table 6).

4.3 Correlation coefficient analysis

Analysis of correlation coefficient provides the details how yield depends on different yield attributes. Yield is a complex product and being affected by several inter-dependable quantitative and qualitative parameters. Thus, selection for yield may not be efficient, unless the other yield related products directly or indirectly is taken into consideration. When selection is exercised for improving characters highly associated with yield, a number of other correlated characters are affected simultaneously. Hence, knowledge regarding to the association of traits with yield and other yield contributing character, provided information to the plant breeder for making advancement through

selection provide a clear knowledge about the contribution in respect of building the association by genetic and non-genetic factors. The correlation coefficient (genotypic and phenotypic) and the parameter correlated were shown in Table 7. It was conspicuous that, genotypic correlation coefficients were higher than their phenotypic ones which suggested that these traits were highly correlated in genetically and the environment has less influence on the phenotypic appearance of these characters. In some cases, the phenotypic correlation coefficient was higher than their corresponding genotypic correlation coefficient, which suggested that, at the phenotypic level, both environmental and genotypic correlation worked in the same direction and in the end maximized their expression.

4.3.1 Days to 1st flowering

Days to 1st flowering showed a highly significant and positive correlation with days to 1st fruiting (r_g=0.991, r_p=0.960), days to 1st harvesting (r_g=0.886, r_p=0.848), and fruit weight (r_g=0.429, r_p=0.390). It also observed that, highly significant and negative correlation with no. of primary branches per plant (r_g=-0.579, r_p=-0.508), no. of secondary branches per plant (r_g=-0.478, r_p=-0.424), no. of flowers per plant (r_g=-0.546, r_p=-0.522), no. of fruits per plant (r_g=-0.548, r_p=-0.528), while, non-significant and positive correlation with plant height (r_g=0.042, r_p=0.032), fruit diameter (r_g=0.091, r_p=0.068), % of infested fruit per plant (r_g=0.207, r_p=0.191) and non-significant but negative correlation with fruit length (r_g=-0.042, r_p=-0.048) and yield per plant (kg) (r_g=-0.198, r_p=-0.215). Koundinya *et al.* (2017) reported that, days to 1st flowering are significant and negatively correlated with fruit yield per plant.

4.3.2 Days to 1st fruiting

Days to 1st fruiting showed a highly significant and positive correlation with days to 1st harvesting (r_g=0.909, r_p=0.882), and fruit weight (r_g=0.456, r_p=0.435). It also observed that, highly significant and negative correlation with no. of primary branches per plant (r_g=-0.583, r_p=-0.468), no. of secondary branches per plant (r_g=-0.484, r_p=-0.388), no. of flowers per plant (r_g=-0.560, r_p=-0.548), and no. of fruits per plant (r_g=-0.577, r_p=-0.563). Days to 1st fruiting exhibited non-significant and positive correlation with plant height (r_g=0.085, r_p=0.073), fruit diameter (r_g=0.120, r_p=0.101), % of infested fruit per plant (r_g=0.190, r_p=0.187) and non-significant but negative correlation with fruit length (r_g=-0.106, r_p=-0.103), and yield per plant (r_g=-0.205, r_p=-0.212).

Table 7. Genotypic (r_g) and phenotypic (r_p) correlation coefficients among different pairs of yield and yield contributing characters in brinjal genotypes

Characters		DFF	DFFR	DFH	PH	NPB	NSB	NFP	NFRP	FRL	FRD	FRW
DFFR	r_g	0.991**										
	r_p	0.960**										
DFH	r_g	0.886**	0.909**									
	r_p	0.848**	0.882**									
PH	r_g	0.042	0.085	-0.048								
	r_p	0.032	0.073	-0.038								
NPB	r_g	-0.579**	-0.583**	-0.585**	0.616**							
	r_p	-0.508**	-0.468**	-0.470**	0.495**							
NSB	r_g	-0.478**	-0.484**	-0.407**	0.688**	0.909**						
	r_p	-0.424**	-0.388**	-0.319*	0.562**	0.922**						
NFP	r_g	-0.546**	-0.560**	-0.455**	0.190	0.559**	0.559**					
	r_p	-0.522**	-0.548**	-0.444**	0.178	0.479**	0.483**					
NFRP	r_g	-0.548**	-0.577**	-0.521**	0.193	0.592**	0.561**	0.986**				
	r_p	-0.528**	-0.563**	-0.501**	0.190	0.520**	0.494**	0.979**				
FRL	r_g	-0.042	-0.106	-0.047	0.433**	0.334**	0.396**	0.414**	0.398**			
	r_p	-0.048	-0.103	-0.043	0.397**	0.299*	0.365**	0.404**	0.385**			
FRD	r_g	0.091	0.120	-0.041	0.059	-0.156	-0.185	-0.589**	-0.576**	-0.630**		
	r_p	0.068	0.101	-0.038	0.066	-0.138	-0.163	-0.574**	-0.554**	-0.598**		
FRW	r_g	0.429**	0.456**	0.337**	0.105	-0.271*	-0.251	-0.801**	-0.800**	-0.391**	0.819**	
	r_p	0.390**	0.435**	0.332**	0.104	-0.233	-0.216	-0.791**	-0.781**	-0.370**	0.809**	
PIF	r_g	0.207	0.190	0.252	-0.440**	-0.353**	-0.443**	-0.276*	-0.286*	-0.286*	0.298*	0.252
	r_p	0.191	0.187	0.246	-0.386**	-0.294*	-0.379**	-0.272*	-0.275*	-0.277*	0.290*	0.246
YP	r_g	-0.198	-0.205	-0.198	0.215	0.355**	0.356**	0.243	0.224	-0.187	0.494**	0.326*
	r_p	-0.215	-0.212	-0.174	0.220	0.314*	0.315*	0.242	0.248	-0.164	0.489**	0.333**

* and ** indicate significant at 5% and 1% level of probability respectability and NS indicates non-significant;

r_g= genotypic correlation coefficients, r_p= phenotypic correlation coefficients;

Here,

DFF= Days to 1st flowering;
DFFR= Days to 1st fruiting;
DFH= Days to 1st harvesting;
PH= Plant height (cm);
NPB= No. of primary branches per plant;
NSB= No. of secondary branches per plan
NFP= No. of flowers per plant;
NFRP= No. of fruits per plant;
FRL= Fruit length (cm);
FRD= Fruit diameter (cm);
FRW= Fruit weight (g);
PIF= % of infested fruit; and
YP= Yield per plant (kg).

4.3.3 Days to 1st harvesting

Days to 1st harvesting showed a highly significant and positive correlation with fruit weight (r_g=0.337, r_p=0.332). It also observed that, highly significant and negative correlation with no. of primary branches per plant (r_g=-0.585, r_p=-0.470), no. of secondary branches per plant (r_g=-0.407, r_p=-0.319), no. of flowers per plant (r_g=-0.455, r_p=-0.444), and no. of fruits per plant (r_g=-0.521, r_p=-0.501). On the other hand, it expressed non-significant and positive correlation with % of infested fruit per plant (r_g=0.252, r_p=0.246) and non-significant but negative correlation with plant height (r_g=-0.048, r_p=-0.038), fruit length (r_g=-0.047, r_p=-0.043), fruit diameter (r_g= -0.041, r_p=-0.038), and yield per plant (r_g=-0.198, r_p=-0.174).

4.3.4 Plant height (cm)

Plant height exhibited a highly significant and positive correlation with no. of primary branches per plant (r_g=0.616, r_p=0.495), no. of secondary branches per plant (r_g=0.688, r_p=0.562), and fruit length (r_g=0.433, r_p=0.397). It also observed that, highly significant and negative correlation with % of infested fruit per plant (r_g=-0.440, r_p=-0.386) and non-significant and positive correlation with no. of flowers per plant (r_g=0.190, r_p=0.178), no. of fruits per plant (r_g=0.193, r_p=0.190), fruit diameter (r_g=0.059, r_p=0.066), fruit weight (r_g=0.105, r_p=0.104), and yield per plant (r_g=0.215, r_p=0.220). Patel *et al.* (2017) reported that, the character yield per plant was found to be significantly and positively correlated with plant height.

4.3.5 No. of primary branches per plant

No. of primary branches per plant showed a highly significant and positive correlation with no. of secondary branches per plant (r_g=0.909, r_p=0.922), no. of flowers per plant (r_g=0.559, r_p=0.479), no. of fruits per plant (r_g=0.592, r_p=0.520), fruit length (r_g=0.334, r_p=0.299), and yield per plant (r_g=0.355, r_p=0.314). It also observed that, highly significant and negative correlation with fruit weight (r_g=-0.271), % of infested fruit per plant (r_g=-0.353, r_p=-0.294) and non-significant but negative correlation with fruit diameter (r_g=-0.156, r_p=-0.138), and fruit weight (r_p=-0.233). Highly significant and positive correlation was also noticed between plant height and primary branches per plant, which indicated if plant height increased primary branches per plant also increased (Saha *et al.*, 2019)

4.3.6 No. of secondary branches per plant

No. of secondary branches per plant expressed significant and positive correlation with no. of flowers per plant (r_g=0.559, r_p=0.483), no. of fruits per plant (r_g=0.561, r_p=0.494), fruit length (r_g=0.396, r_p=0.365), and yield per plant (r_g=0.356, r_p=0.315). It also observed that, highly significant and negative correlation with % of infested fruit per plant (r_g=-0.443, r_p=-0.379) and non-significant but negative correlation with fruit diameter (r_g=-0.185, r_p=-0.163), and fruit weight (r_g=-0.251, r_p=-0.216). Patel *et al.* (2017) reported that, the branches per plant had significant and strongly positive association with plant height, fruit length, fruit shape, average fruit weight and yield per plant in both genotypic and phenotypic levels. It indicated that, these traits are useful for taking them as the basis of selection for higher yield.

4.3.7 No. of flowers per plant

No. of flowers per plant showed a highly significant and positive correlation with no. of fruits per plant (r_g=0.986, r_p=0.979), and fruit length (r_g=0.414, r_p=0.404). It also observed that, highly significant and negative correlation with fruit diameter (r_g=-0.589, r_p=-0.574), fruit weight (r_g=-0.801, r_p=-0.791), and % of infested fruit per plant (r_g=-0.276, r_p=-0.272). Non-significant and positive correlation was found with yield per plant (r_g=0.243, r_p=0.242). No. of flowers per axil presented a considerable negative trend with fruit diameter and fruit weight, which means a greater no. of flowers per axil results in less fruit diameter and low fruit weight and a smaller no. of flowers per axil produce fruit with high diameter and more fruit weight (Hasan *et al.*, 2015).

4.3.8 No. of fruits per plant

No. of fruit per plant exhibited a highly significant and positive correlation with fruit length (r_g=0.398, r_p=0.385). It also observed that, highly significant and negative correlation with fruit diameter (r_g=-0.576, r_p=-0.554), fruit weight (r_g=-0.800, r_p=-0.781), and % of infested fruit per plant (r_g=-0.286, r_p=-0.275). It also showed non-significant and positive correlation with yield per plant (kg) (r_g=0.224, r_p=0.248). Fruit yield per plant (ha) showed significant positive correlation with no. of fruits per plant at both genotypic and phenotypic levels (Nazir *et al.* 2019).

4.3.9 Fruit length (cm)

Fruit length showed a highly significant and negative correlation with fruit diameter (r_g=-0.630, r_p=-0.598), fruit weight (r_g=-0.391, r_p=-0.370), and % of infested fruit per plant (r_g=-0.286, r_p=-0.277). It also observed that, non-significant and negative

correlation with yield per plant (r_g=-0.187, r_p=-0.164). Saha *et al.* (2019) reported that, fruit length showed non-significant and positive correlation with yield per plant.

4.3.10 Fruit diameter (cm)

Fruit diameter showed a highly significant and positive correlation with fruit weight (r_g=0.819, r_p=0.809), % of infested fruit per plant (r_g=0.298, r_p=0.290), and yield per plant (r_g=0.494, r_p=0.489). Saha *et al.* (2019) reported that, fruit diameter showed non-significant and positive correlation with yield per plant.

4.3.11 Fruit weight (gm)

Fruit weight reported a highly significant and positive correlation with yield per plant (r_g=0.326, r_p=0.333). It also observed that, non-significant and positive correlation with % of infested fruit per plant (r_g=0.252, r_p=0.246). Fruit yield per plant per hector showed significant positive correlation with fruit weight at both genotypic and phenotypic levels (Nazir *et al.* 2019).

4.4 Path coefficient analysis

Path coefficient analysis means that, the association of the independent traits with dependent variable is due to their direct influence on it or it is a consequence of their indirect effects through the other characters. The path coefficient analysis was carried out considering fruit yield per plant as dependent variable and its attributes as independent variables namely, days to 1st flowering, days to 1st fruiting, days to 1st harvesting, plant height, no. of primary branches per plant, no. of secondary branches per plant, no. of flowers per plant, no. of fruits per plant, fruit length, fruit diameter, fruit weight, and % of infested fruit. Each component has two paths of actions, one is direct influence on fruit yield and another is indirect impact through component traits which are not revealed from the correlation observation. The estimates of direct and indirect effects of yield related characters on fruit yield/plant are presented in Table 8.

4.4.1 Days to 1st flowering

Path coefficient analysis revealed that, days to 1st flowering had a positive direct effect (0.589) on yield per plant. Days to 1st flowering had a positive indirect effect on yield

per plant through days to 1st fruiting (0.167), no. of fruits per plant (0.713), fruit diameter (0.058), fruit weight (0.388) and % of infested fruit (0.021), while, negative indirect effect was found via days to 1st harvesting (-0.321), plant height (-0.028), no. of primary branches per plant (-0.190), no. of secondary branches per plant (-0.164), no. of flowers per plant (-1.428), and fruit length (-0.004). It had non-significant and negative genotypic correlation (-0.198) with yield per plant. Koundinya *et al.* (2017) observed that, days to first flowering had a negative direct effect on fruit yield per plant.

4.4.2 Days to 1st fruiting

Path coefficient analysis revealed that, days to 1st fruiting had a positive direct effect (0.169) on yield per plant. Days to 1st fruiting had a positive indirect effect on yield per plant through days to 1st flowering (0.584), no. of fruits per plant (0.752), fruit diameter (0.076), fruit weight (0.413), and % of infested fruit (0.019), while, negative indirect effect was found via days to 1st harvesting (-0.329), plant height (-0.055), no. of primary branches per plant (-0.191), no. of secondary branches per plant (-0.167), no. of flower per plant (-1.465), and fruit length (-0.010). It had non-significant and negative genotypic correlation (-0.205) with yield per plant.

4.4.3 Days to 1st harvesting

Path coefficient analysis exhibited that, days to 1st harvesting had a negative direct effect (-0.362) on yield per plant. Days to 1st harvesting had a positive indirect effect on yield per plant through days to 1st flowering (0.522), days to 1st fruiting (0.153), plant height (0.031), no. of fruits per plant (0.679), fruit weight (0.305), and % of infested fruit (0.026), while, negative indirect effect was found via no. of primary branches per plant (-0.192), no. of secondary branches per plant (-0.140), no. of flowers per plant (-1.189), fruit length (-0.004), and fruit diameter (-0.026). It had non-significant and negative genotypic correlation (-0.198) with yield per plant. Patel *et al.* (2017) observed positive and direct effect by days to 1st harvest in their study.

4.4.4 Plant height (cm)

Path coefficient analysis revealed that, plant height had a negative direct effect (-0.654) on yield per plant. Plant height had a positive indirect effect on yield per plant through days to 1st flowering (0.025), days to 1st fruiting (0.014), days to 1st harvesting (0.017),

Table 8. Path analysis showing direct and indirect effects of different characters on yield per plant of twenty brinjal genotypes

Trait	DFF	DFFR	DFH	PH	NPB	NSB	NFP	NFRP	FRL	FRD	FRW	PIF	Genotypic correlation with YP
DFF	**0.589**	0.167	-0.321	-0.028	-0.190	-0.164	-1.428	0.713	-0.004	0.058	0.388	0.021	-0.198
DFFR	0.584	**0.169**	-0.329	-0.055	-0.191	-0.167	-1.465	0.752	-0.010	0.076	0.413	0.019	-0.205
DFH	0.522	0.153	**-0.362**	0.031	-0.192	-0.140	-1.189	0.679	-0.004	-0.026	0.305	0.026	-0.198
PH	0.025	0.014	0.017	**-0.654**	0.202	0.237	0.498	-0.251	0.040	0.037	0.095	-0.045	0.215
NPB	-0.341	-0.098	0.212	-0.403	**0.328**	0.313	1.463	-0.770	0.031	-0.099	-0.245	-0.036	0.355**
NSB	-0.281	-0.082	0.147	-0.450	0.298	**0.344**	1.463	-0.731	0.037	-0.118	-0.227	-0.045	0.356**
NFP	-0.322	-0.095	0.165	-0.124	0.184	0.192	**2.616**	-1.283	0.038	-0.375	-0.725	-0.028	0.243
NFRP	-0.323	-0.097	0.189	-0.126	0.194	0.193	2.579	**-1.302**	0.037	-0.366	-0.724	-0.029	0.224
FRL	-0.025	-0.018	0.017	-0.283	0.110	0.136	1.084	-0.517	**0.093**	-0.400	-0.353	-0.029	-0.187
FRD	0.054	0.020	0.015	-0.038	-0.051	-0.064	-1.541	0.750	-0.058	**0.636**	0.741	0.031	0.494**
FRW	0.253	0.077	-0.122	-0.068	-0.089	-0.086	-2.095	1.042	-0.036	0.521	**0.905**	0.026	0.326*
PIF	0.122	0.032	-0.091	0.288	-0.116	-0.152	-0.723	0.373	-0.027	0.189	0.228	**0.102**	0.226

Here, Residual effect: 0.02

Bold figures indicate direct effects

***** and ****** indicate significant at 5% and 1% level of probability, respectively.

DFF= Days to 1st flowering;
DFFR= Days to 1st fruiting;
DFH= Days to 1st harvesting;
PH= Plant height (cm);
NPB= No. of primary branches per plant;
NSB= No. of secondary branches per plant;
NFP= No. of flowers per plant;
NFRP= No. of fruits per plant;
FRL= Fruit length (cm);
FRD= Fruit diameter (cm);
FRW= Fruit weight (g);
PIF= % of infested fruit; and
YP= Yield per plant (kg).

no. of primary branches per plant (0.202), no. of secondary branches per plant (0.237), no. of flowers per plant (0.498), fruit length (0.040), fruit diameter (0.037), and fruit weight (0.095), while, negative indirect effect was found via no. of fruit per plant (-0.251), and % of infested fruit (-0.045). It had non-significant and positive genotypic correlation (0.215) with yield per plant. Patel *et al.* (2017) noted positive and direct effect by plant height in their study.

4.4.5 No. of primary branches per plant

Path coefficient analysis revealed that, no. of primary branches per plant had a positive direct effect (0.328) on yield per plant. No. of primary branches per plant had a positive indirect effect on yield per plant through days to 1st harvesting (0.212), no. of secondary branches per plant (0.313), no. of flower per plant (1.463), and fruit length (0.031), while, negative indirect effect was found via days to 1st flowering (-0.341), days to 1st fruiting (-0.098), plant height (-0.403), no. of fruit per plant (-0.770), fruit diameter (-0.099), fruit weight (-0.245), and % of infested fruit (-0.036). It had highly significant and positive genotypic correlation (0.355) with yield per plant. Primary branches per plant indicated direct positive influence with yield both genotypic and phenotypically (saha *et al.*, 2019). A similar trend has been reported by Sharma and Swaroop (2000).

4.4.6 No. of secondary branches per plant

Path coefficient analysis expressed that, no. of secondary branches per plant had a positive direct effect (0.344) on yield per plant. No. of secondary branches per plant had a positive indirect effect on yield per plant through days to 1st harvesting (0.147), no. of primary branches per plant (0.298), no. of flower per plant (1.463), and fruit length (0.037), while, negative indirect effect was found via days to 1st flowering (-0.281), days to 1st fruiting (-0.082), plant height (-0.450), no. of fruit per plant (-0.731), fruit diameter (-0.118), fruit weight (-0.227), and % of infested fruit (-0.045). It had highly significant and positive genotypic correlation (0.356) with yield per plant. Direct positive influence with yield both genotypic and phenotypically was found with secondary branches per plant (Saha *et al.*, 2019, Pravu, *et al.* (2008).

4.4.7 No. of flowers per plant

Path coefficient analysis exhibited that, no. of flowers per plant had a positive direct effect (2.616) on yield per plant. No. of flowers per plant had a positive indirect effect on yield per plant through days to 1st harvesting (0.165), no. of primary branches per plant (0.184), no. of secondary branches per plant (0.192), and fruit length (0.038),

while, negative indirect effect was found via days to 1st flowering (-0.322), days to 1st fruiting (-0.095), plant height (-0.124), No. of fruits per plant (-1.283), fruit diameter (-0.375), fruit weight (-0.725), and % of infested fruit (-0.028). It had non-significant and positive genotypic correlation (0.243) with yield per plant.

4.4.8 No. of fruits per plant

Path coefficient analysis revealed that, no. of fruits per plant had a negative direct effect (-1.302) on yield per plant. No. of fruits per plant had a positive indirect effect on yield per plant through days to 1st harvesting (0.189), no. of primary branches per plant (0.194), no. of secondary branches per plant (0.193), no. of flowers per plant (2.579), and fruit length (0.037), while, negative indirect effect was found via days to 1st flowering (-0.323), days to 1st fruiting (-0.097), plant height (-0.126), fruit diameter (-0.366) fruit weight (-0.724), and % of infested fruit (-0.029). It had non-significant and positive genotypic correlation (0.224) with yield per plant. No. of fruits per plant was found highly positive direct effects on fruit yield per plant by Dutta *et al.* (2018). Similar result was also found by Sujin and Saravanan *et al.* (2017). Patel *et al.* (2017) found the highly significant and positive correlation of amount of fruits per plant in yield per plant due to their maximum direct and indirect effect via fruit shape respectively.

4.4.9 Fruit length (cm)

Path coefficient analysis revealed that, fruit length had a positive direct effect (0.093) on yield per plant. Fruit length had a positive indirect effect on yield per plant through days to 1st harvesting (0.017), no. of primary branches per plant (0.110), no. of secondary branches per plant (0.136), and no. of flowers per plant (1.084), while, negative indirect effect was found via days to 1st flowering (-0.025), days to 1st fruiting (-0.018), plant height (-0.283), no. of fruits per plant (-0.517), fruit diameter (-0.400), fruit weight (-0.353), and % of infested fruit (-0.029). It had non-significant and negative genotypic correlation (-0.187) with yield per plant. Negative direct effect of the fruit length was observed by Patel *et al.* (2017) in their study.

4.4.10 Fruit diameter (cm)

Path coefficient analysis expressed that fruit diameter had a positive direct effect (0.636) on yield per plant. Fruit diameter had a positive indirect effect on yield per plant through days to 1st flowering (0.054), days to 1st fruiting (0.020), days to 1st harvesting (0.015), no. of fruits per plant (0.750), fruit weight (0.741), and % of infested fruit

(0.031), while, negative indirect effect was found via plant height (-0.038), no. of primary branches per plant (-0.051), no. of secondary branches per plant (-0.064), and no. of flowers per plant (-1.541) and fruit length (-0.058). It had highly significant and positive genotypic correlation (0.494) with yield per plant. Negative direct effect of the fruit diameter was noticed by Saha *et al.* (2019) in their study.

4.4.11 Fruit weight (gm)

Path coefficient analysis revealed that, fruit weight had a positive direct effect (0.905) on yield per plant. Fruit weight had a positive indirect effect on yield per plant through days to 1st flowering (0.253), days to 1st fruiting (0.077), no. of fruits per plant (1.042), fruit diameter (0.521), and % of infested fruit (0.026), while, negative indirect effect was found via days to 1st harvesting (-0.122), plant height (-0.068), no. of primary branches per plant (-0.089), no. of secondary branches per plant (-0.086), and no. of flowers per plant (-2.095) and fruit length (-0.036). It had significant and positive genotypic correlation (0.326) with yield per plant. Average fruit weight indicated direct positive influence with yield both genotypic and phenotypically (Saha *et al.,* 2019). A similar trend has been reported by Sharma and Swaroop (2000) and Shinde *et al.* (2012). Fruit weight was found highly significant and positive direct effects on fruit yield per plant (Dutta *et al.,* 2018 and Mangi *et al.,* 2016).

4.4.12 % of infested fruit

% of infested fruit weight had a positive direct effect (0.102) on yield per plant. % of infested fruit had a positive and indirect effect on yield per plant through days to 1st flowering (0.122), days to 1st fruiting (0.032), plant height (0.288), no. of fruits per plant (0.373), fruit diameter (0.189), and fruit weight (0.228), while, negative indirect effect was found via days to 1st harvesting (-0.091), no. of primary branches per plant (-0.116), no. of secondary branches per plant (-0.152) and no. of flowers per plant (-0.723), and fruit length (-0.027). It had non-significant and positive genotypic correlation (0.226) with yield per plant.

4.5 Genetic diversity of twenty brinjal genotypes

Multiple multivariate techniques (PCA, PCO, CVA, non-hierarchical clustering, and cluster diagram) are required to more clearly describe the results of a genetic diversity investigation (Bashar, 2002 and Uddin, 2001). The genetic diversity of twenty brinjal genotypes was examined using the GENSTAT software program and the results are shown.

4.5.1 Principal component analysis (PCA)

Principal component analysis can easily access important polygenic characters which are of importance in plant breeding program. Principal components were computed from the correlation matrix and genotype scores obtained from first components and succeeding components with latent roots greater than the unity. Eigen values corresponding thirteen principal component axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in Table 9. Eigen values represents that the cumulative eigen values of five principal components accounted for 92.5% of the total variation among traits of brinjal genotypes. Out of five principal component PC1, PC2, PC3, PC4 and PC5 accounted for 43.74%, 19.3%, 16.01%, 8.69%, and 4.76% of the total variation, respectively.

Table 9. Eigen values, and Principal components showing the proportion of variance explained and cumulative variance (%) for thirteen characters in twenty brinjal genotypes

Principal Component	Eigen Value	proportion of variance	Cumulative variance (%)
1	5.687	43.74	43.74
2	2.509	19.30	63.04
3	2.081	16.01	79.05
4	1.129	8.69	87.74
5	0.618	4.76	92.50
6	0.432	3.33	95.83
7	0.288	2.21	98.04
8	0.138	1.06	99.10
9	0.064	0.49	99.59
10	0.026	0.20	99.79
11	0.017	0.13	99.92
12	0.008	0.06	99.98
13	0.003	0.02	100

4.5.2 Construction of scatter diagram

Based on the values of principal component scores l and 2 obtained from the principal component analysis, a two-dimensional scatter diagram, using component score 1 as X-axis and component score 2 as Y-axis was constructed, which has been presented in Figure 6. The position of the genotypes in the scatter diagram was apparently distributed into four groups, which indicated that there existed considerable diversity among the genotypes.

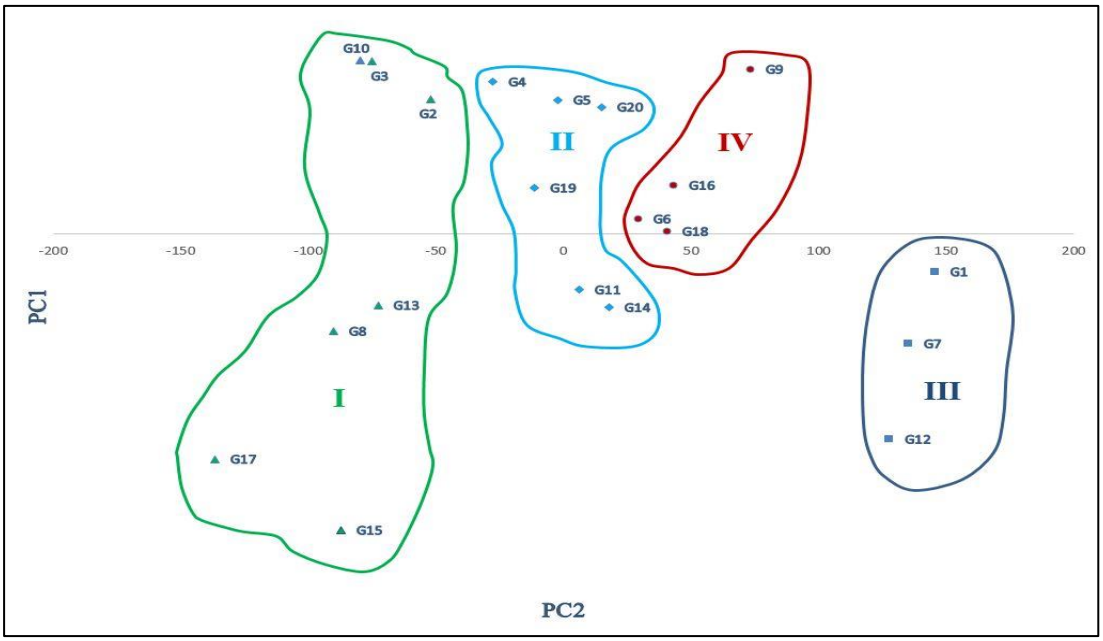


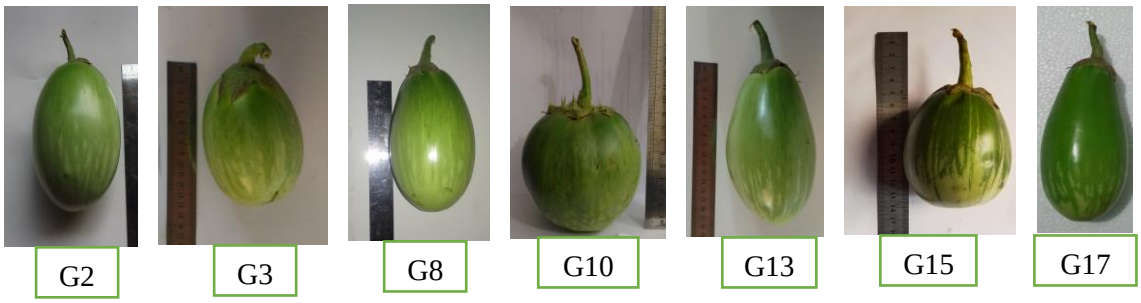
Figure 1. Scatter distribution of twenty brinjal genotypes based on their principal component scores

4.5.3 Non- hierarchical clustering

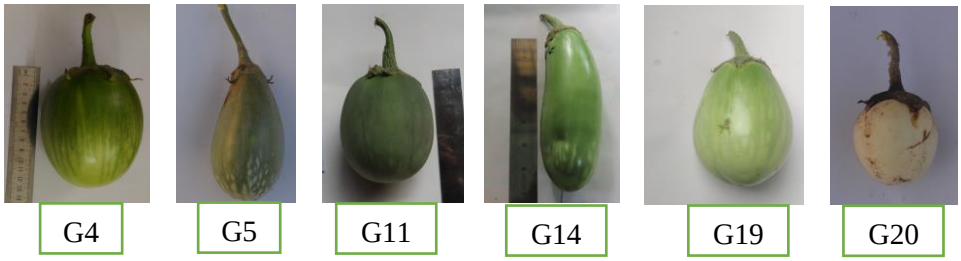
By using covariance matrix with the application of non-hierarchical clustering, the twenty brinjal genotypes were grouped into four different clusters. Cluster III consists of three genotypes, which is smallest cluster. Cluster I composed of seven genotypes that was largest cluster. Finally, cluster II composed of six genotypes and cluster IV composed of four genotypes (Table 10). These results confined the clustering pattern of the genotype according to the principal component analysis. Kumar *et al.* (1998) reported six distinct clusters in brinjal. Compositions of different clusters with their corresponding genotypes in each cluster were presented in Table 10. According to the principal component analysis, these findings corroborated the genotype clustering patterns. The nonhierarchical clustering corroborated the PCA findings, thereby confirming the PCA results. Genotypes were grouped into clusters, indicating a broad variety of genetic variation. Brinjal genotypes clustering revealed a non-parallel relationship between spatial and genetic diversity.

Table 10. Distribution of D^2 cluster of twenty brinjal genotypes

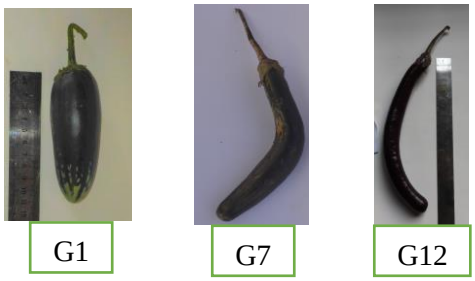
Cluster	Number of genotypes	Genotypes
I	7	G2, G3, G8, G10, G13, G15, G17
II	6	G4, G5, G11, G14, G19, G20
III	3	G1, G7, G12
IV	4	G6, G9, G16, G18



Fruit type of cluster I



Fruit type of cluster II



Fruit type of cluster III

Fruit type of cluster IV

Plate 7. Genetic divergence of fruits of the twenty brinjal genotypes grouping into different clusters

Cluster I

Cluster I had seven genotypes as G2, G3, G8, G10, G13, G15, and G17 (Table 10). From the clustering mean values (Table 11), it was observed that cluster I produced the highest mean values for days to 1st flowering (81.74 days), days to 1st fruiting (96.76 days), days to 1st harvesting (120.87 days), fruit diameter (8.71 cm), and fruit weight (321.89 g) and the lowest mean value for number of flowers per plant (14.4), and fruit length (13.79 cm) in comparison with other clusters (Table 10). These group possessed genotypes with the second highest cluster mean for plant height (79.8 cm), and yield per plant (1.59 kg). Mandal and Dada (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that fruits per plant, secondary branches per plant, and plant height were important traits for the selection of superior genotypes.

Cluster II

Cluster II was associated with six genotypes namely G4, G5, G11, G14, G19, and G20 (Table 10). It was observed that cluster II produced the lowest mean values for plant height (71.45 cm), no. of primary branches per plant (10.28), and no. of secondary branches per plant (13.33) and the second highest mean value for days to 1st flowering (81.09 days), days to 1st fruiting (94.67 days), days to 1st harvesting (120.24 days), fruit diameter (7.3 cm), fruit weight (237.18 g), and % of infested fruit (37.93) (Table 11).

Cluster III

Cluster III composed of three genotypes. The genotypes were G1, G7, and G12 (Table 10) It was observed that cluster III produced the highest mean values for plant height (80.51 cm), no. of primary branches per plant (11.96), no. of secondary branches per plant (14.96), no. of flower per plant (30.44), no. of fruit per plant (11.59), and fruit length (20.98 cm) and the lowest mean value for days to 1st flowering (77 days), days to 1st fruiting (90.7 days), days to 1st harvesting (112.37 days), fruit diameter (3.19 cm), fruit weight (103.2 g), % infested fruit (8.69), and yield per plant (1.2 kg) (Table 11).

Cluster IV

Cluster IV consisted of four genotypes, namely G6, G9, G16, and G18 (Table 10). From the clustering mean values (Table 11), it was observed that cluster IV produced the highest mean values for % infested fruit (38.81), and yield per plant (1.62 kg). These group possessed genotypes with the second highest cluster mean for no. of primary

branches per plant (11.36), no. of secondary branches per plant (14.44), no. of flowers per plant (23.45), no. of fruits per plant (8.47), and fruit length (15.5 cm).

Table 11. Cluster mean for thirteen characters of twenty brinjal genotypes

Characters	Cluster			
	I	**II**	**III**	**IV**
Days to 1st flowering	81.74	81.09	77	77.31
Days to 1st fruiting	96.76	94.67	90.7	91.58
Days to 1st harvesting	120.87	120.24	112.37	115.86
Plant height (cm)	79.8	71.45	80.51	77.39
No. of primary branches per plant	10.76	10.28	11.96	11.36
No. of secondary branches per plant	13.76	13.33	14.96	14.44
No. of flowers per plant	14.4	18.07	30.44	23.45
No. of fruits per plant	4.97	6.11	11.59	8.47
Fruit length (cm)	13.79	14.93	20.98	15.5
Fruit diameter (cm)	8.71	7.3	3.19	7.13
Fruit weight (g)	321.89	237.18	103.2	190.64
% of infested fruit	34.03	37.93	8.69	38.81
Yield per plant (kg)	1.59	1.45	1.2	1.62

4.5.4 Principal coordinate analysis

Principal coordinate analysis (PCO) was performed on auxiliary principal component analysis. This analysis helps in estimating distances (D^2) for all combinations between pairs of varieties. The highest inter genotype distance (4.252) was observed between the genotype G9 and G15 followed by the genotype G10 and G15 (4.186), G4 and G15 (4.135), and G3 and G15 (4.093). The fifteen highest pair distance was (3.358) observed between genotype G3 and G12. The lowest distance (0.364) was observed between the genotypes G4 and G10 followed by the varieties genotype G2 and G3 (0.456). The fifteen lowest distance (0.657) was observed between the genotype G8 and G13. The difference between the highest and the lowest inter-genotypes distance indicated the prevalence of variability among the twenty genotypes of brinjal (Table 12).

Table 12. Inter-genotypic distance (D^2) of some genotypes of brinjal of different clusters

Sl. No.	Between genotype (G)	Distance (Highest)	Sl. No.	Between genotype	Distance (Lowest)
1	9-15	4.252	1	4-10	0.364
2	10-15	4.186	2	2-3	0.456
3	4-15	4.135	3	4-20	0.504
4	3-15	4.093	4	18-19	0.505
5	2-15	4.08	5	18-20	0.508
6	15-20	4.016	6	2-4	0.527
7	15-16	3.981	7	2-10	0.54
8	5-15	3.909	8	16-18	0.55
9	15-19	3.909	9	6-18	0.552
10	15-18	3.638	10	19-20	0.572
11	6-15	3.635	11	16-20	0.616
12	7-15	3.461	12	6-20	0.643
13	8-15	3.457	13	4-19	0.654
14	10-12	3.368	14	13-17	0.656
15	3-12	3.358	15	8-13	0.657

4.5.5 Canonical variate analysis

By using inter-genotypic distances and intra-cluster genotypic distances were calculated (Table 13) as suggested by Singh *et al.* (1977). Cluster I which (1.74) composed of seven genotypes showed the maximum intra cluster distances and cluster IV showed the lowest intra-cluster distance (0.83) which composed of 4 genotypes. The coordinates obtained from the Principal Component analysis (PCA) were used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al.* (1989). PCA was used for the graphical representation of the points while PCO was used to calculate the minimum distance straight line between each pair of points.

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. Table 13, indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances indicating wider genetic diversity among the genotypes of different groups. Results indicated that the highest inter cluster distance was observed between

cluster I and cluster III (32.04) followed by between cluster II and cluster III (23.86) and cluster III and IV (17.2). The lowest inter-cluster distance was observed between the cluster II and Cluster IV (7.15) (Table 13). The inter-cluster distances were larger than the intra-cluster distances indicating wider genetic diversity among the genotypes of different groups. Thus, crosses can be made between genotypes of these clusters to obtain heterotic hybrids and desirable segreants. Yatung *et al* (2014) studied genetic diversity in 30 chilies and reported the highest (459.81) inter cluster distance between cluster II and IV and the lowest (36.04) between cluster I and IV. Cluster III (D^2 = 67.66) have exhibited highest intra cluster distance and the lowest was observed in cluster II (D^2 =11.19). However, Matin *et al.* (2016) screened out suitable parents for hybridization programme. They found the maximum inter-cluster distance between cluster II and V (532.214) and the minimum inter-cluster distance was obtained between the cluster I and IV (91.948). Islam (1995) was carried out an experiment on groundnut (*Arachis hypogaea* L.) and obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis. Genotypes from the cluster I and Cluster III (32.04) if involved in hybridization might produce a wide spectrum of segregating population, as genetic variation was very distinct among these groups.

Table 13. Intra (Bold) and inter cluster distance of twenty brinjal genotypes

Cluster	I	II	III	IV
I	**1.74**			
II	13.3	**1.06**		
III	32.04	23.86	**1.32**	
IV	15.98	7.15	17.2	**0.83**

4.5.6 Relative contribution of individual character to genetic divergence in brinjal

Relative contribution of individual characters towards divergence was measured through vectors (vector I and II) for different quantitative traits. Vectors (Vector I and II) for different quantitative traits in this experiment are presented in Table 14. In vector I, the important characters responsible for genetic divergence in the major axis of differentiation were days to 1st flowering, days to 1st harvesting, no. of primary branches per plant, no. of flowers per plant, no. of fruits per plant, fruit length and fruit diameter

and in vector II, the second axis of differentiation days to 1st flowering, days to 1st harvesting, plant height, no. of primary branches per plant, no. of flowers per plant, fruit diameter, % of infested fruit, and yield per plant. Days to 1st flowering (1.19 and 4.363), days to 1st harvesting (0.366 and 0.281), no. of primary branches per plant (1.886 and 1.635), no. of flowers per plant (0.938 and 1.84) and fruit diameter (1.987 and 0.405) was positive for both indicating this trait contributes maximum towards divergence. Srinivas *et al.* (2013) and Hasan *et al.* (2015) found similar result that was maximum contribution of yield per plant towards divergence. However, Matin *et al.* (2016) found fruit diameter contributed maximum to the total divergence.

Table 14. Latent vectors for thirteen characters of twenty brinjal genotypes

Character	**Vector-1**	**Vector-2**
Days to 1st flowering	1.19	4.363
Days to 1st fruiting	-1.244	-4.335
Days to 1st harvesting	0.366	0.281
Plant height (cm)	-0.031	0.211
No. of primary branches per plant	1.886	1.635
No. of secondary branches per plant	-2.109	-1.636
No. of flowers per plant	0.938	1.84
No. of fruits per plant	1.747	-6.737
Fruit length (cm)	0.114	-0.361
Fruit Diameter (cm)	1.987	0.405
Fruit weight (g)	-0.042	-0.084
% of infested fruit	-0.08	0.011
Yield per plant (kg)	-15.11	5.109

4.6 Comparison of different multivariate techniques

Along with non-hierarchic clustering a cluster pattern of D^2 analysis has taken care that all characters studied differ simultaneously. However, in various clusters of the D^2 analysis the distribution of genotypes has followed more or less like trends in main component analysis, which have proven to be an alternative method to give information on the genotype classification pattern. The main component analysis however contains information about the contribution of characters to brinjal divergence.

4.7 Selection of genotypes for future hybridization program

Genetically diverse selection of parents is a major step in hybridization. Multivariate analysis is a useful tool for measuring the divergence of the genotype of biological populations and for assessing the relative contribution of the various components to the overall difference at intra and intersectional cluster levels. The study of brinjal genetic diversity has allowed genotypes of different levels to be used for the development of desired high yield species in distant clusters. D^2 statistics clusters are useful in this field. Three important points are considered while selecting the genotypes-1) Choice of the particular cluster from which genotypes are to be used as parents 2) Selection of particular genotype from the selected cluster, and 3) Relative contribution of characters to total divergence (Singh and Chaudhary, 1985). Contribution of individual characters towards divergence was also observed in this study. In respect of cluster mean performance of different clusters revealed that cluster I produced was important for the maximum mean values for days to 1^{st} flowering, days to 1^{st} fruiting, days to 1^{st} harvesting, fruit diameter, and fruit weight. Cluster III is important for highest mean values for plant height, no. of primary branches per plant, no. of secondary branches per plant, no. of flowers per plant, no. of fruits per plant, and fruit length and cluster IV produced the highest mean values for % infested fruit, and yield per plant. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G12 for maximum value for number of secondary branches per plant, number of flowers per plant, number of fruits per plant, and fruit length from cluster III, G16 for minimum days to 1^{st} flowering and days to 1^{st} fruiting, G18 for minimum days to 1^{st} harvesting from cluster IV and G17 for highest individual fruit diameter and fruit weight, G15 for minimum % infested fruit and G8 for high yield per plant from cluster I would be considered as better parents for further use in future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

An experiment was conducted with 20 brinjal genotypes to evaluate the performance of yield and yield contributing character. It was executed by following Randomized complete block design (RCBD) with three replications in the experimental field of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, during the period from August 2019 to March 2020. Data on different morphological and yield contributing characters were recorder. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

From the experiment, it was observed the highest number of fruits per plant was observed in G12 (12.67) and the lowest number of fruits per plant was observed in G15 (3.56). The longest fruit was produced by G12 (30.02 cm), while the smallest fruit was observed in G10 (9.05 cm). The maximum diameter of an individual fruit was obtained in G17 (10.62) while the minimum was in G12 (2.60). The maximum weight of an individual fruit was found in G17 (375.12), while the minimum weight was in G1 (94.14). The minimum percent of fruit infestation was observed in G15 (0.00) and the maximum percent of fruit infestation was observed in G10 (58.84). Phenotypic variance was considerably higher than the genotypic variance for all the studied characters. Differences between the genotypic and phenotypic variances was minimum in days to 1st flowering, days to 1st fruiting, days to 1st harvesting, no. of primary branches per plant, no. of secondary branches per plant, no. of flower per plant, no. of fruit per plant, fruit length, fruit diameter, % of infested fruit, and yield per plant indicating the less environmental effect to control these characters. Plant height and fruit weight showed high difference between phenotypic variance and genotypic variance which indicates high influence of environment on these characters. The high genotypic coefficient of variation was observed for the characters of percent % of infested fruit indicating that this character can be improved by selection. High heritability with low genetic advance was observed in days to 1st flowering, no. of primary branches per plant, no. of secondary branches per plant, no. of fruit per plant, fruit diameter, and yield per plant

indicating non-additive gene action for expression of the characters. High heritability with high genetic advance was observed in plant height and fruit weight, indicating the additive gene action for expression of the characters and effective selection of the populations for these traits. Significant genotypic and phenotypic positive association was with no. of primary brunches, no. of secondary brunches, fruit diameter, and fruit weight through the correlation analysis. According to the path coefficient analysis, direct positive effect on seed yield per plant was observed by days to 1st flowering, days to 1st fruiting, no. of primary branches per plant, no. of secondary branches per plant, no. of flowers per plant, fruit length, fruit diameter, fruit weight, % of infested fruit, and yield per plant (kg).

Eigen values represents that the cumulative eigen values of five principal components accounted for 92.5% of the total variation among traits of brinjal genotypes. The twenty brinjal genotypes were grouped into four different clusters. Cluster I contain the maximum number of genotypes, which are G2, G3, G8, G10, G13, G15, and G17, followed by cluster II (G4, G5, G11, G14, G19, and G20) and cluster IV (G6, G9, G16, and G18). Cluster III consists G1, G7, and G12, which is smallest cluster. cluster I produced the highest mean values for days to 1st flowering (81.74 days), days to 1st fruiting (96.76 days), days to 1st harvesting (120.87 days), fruit diameter (8.71 cm), and fruit weight (321.89 g). It was observed that cluster II produced the second highest mean value for days to 1st flowering (81.09 days), days to 1st fruiting (94.67 days), days to 1st harvesting (120.24 days), fruit diameter (7.3 cm), fruit weight (237.18 g), and % of infested fruit (37.93). cluster III produced the highest mean values for plant height (80.51 cm), no. of primary branches per plant (11.96), no. of secondary branches per plant (14.96), no. of flowers per plant (30.44), no. of fruits per plant (11.59), and fruit length (20.98 cm). cluster IV produced the highest mean values for % infested fruit (38.81), and yield per plant (1.62 kg). The highest intra cluster distance value was found in cluster I and the highest inter cluster distance was observed between cluster I and cluster III (32.04) followed by between cluster II and cluster III (23.86) and cluster III and IV (17.2). The inter-cluster distances were larger than the intra-cluster distances indicating wider genetic diversity among the genotypes of different groups. Therefore, considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotype G12

for maximum value for number of secondary branches per plant, number of flowers per plant, number of fruits per plant, and fruit length from cluster III, G16 for minimum days to 1st flowering and days to 1st fruiting, G18 for minimum days to 1st harvesting from cluster IV and G17 for highest individual fruit diameter and fruit weight, G15 for minimum % infested fruit and G8 for high yield per plant from cluster I would be considered as better parents for further use in future hybridization program.

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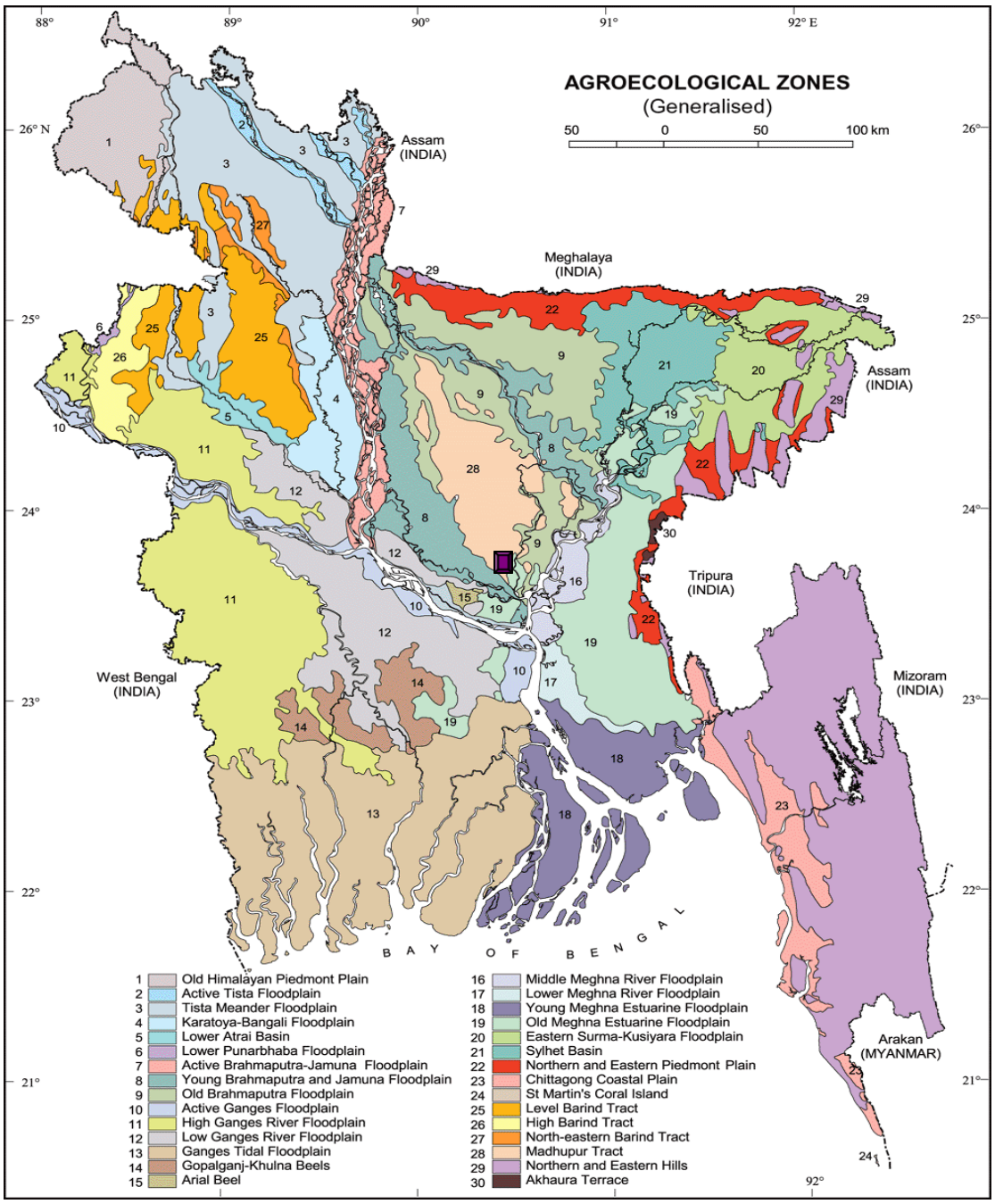
APPENDICES

Appendix I. Map showing the experimental site under the study



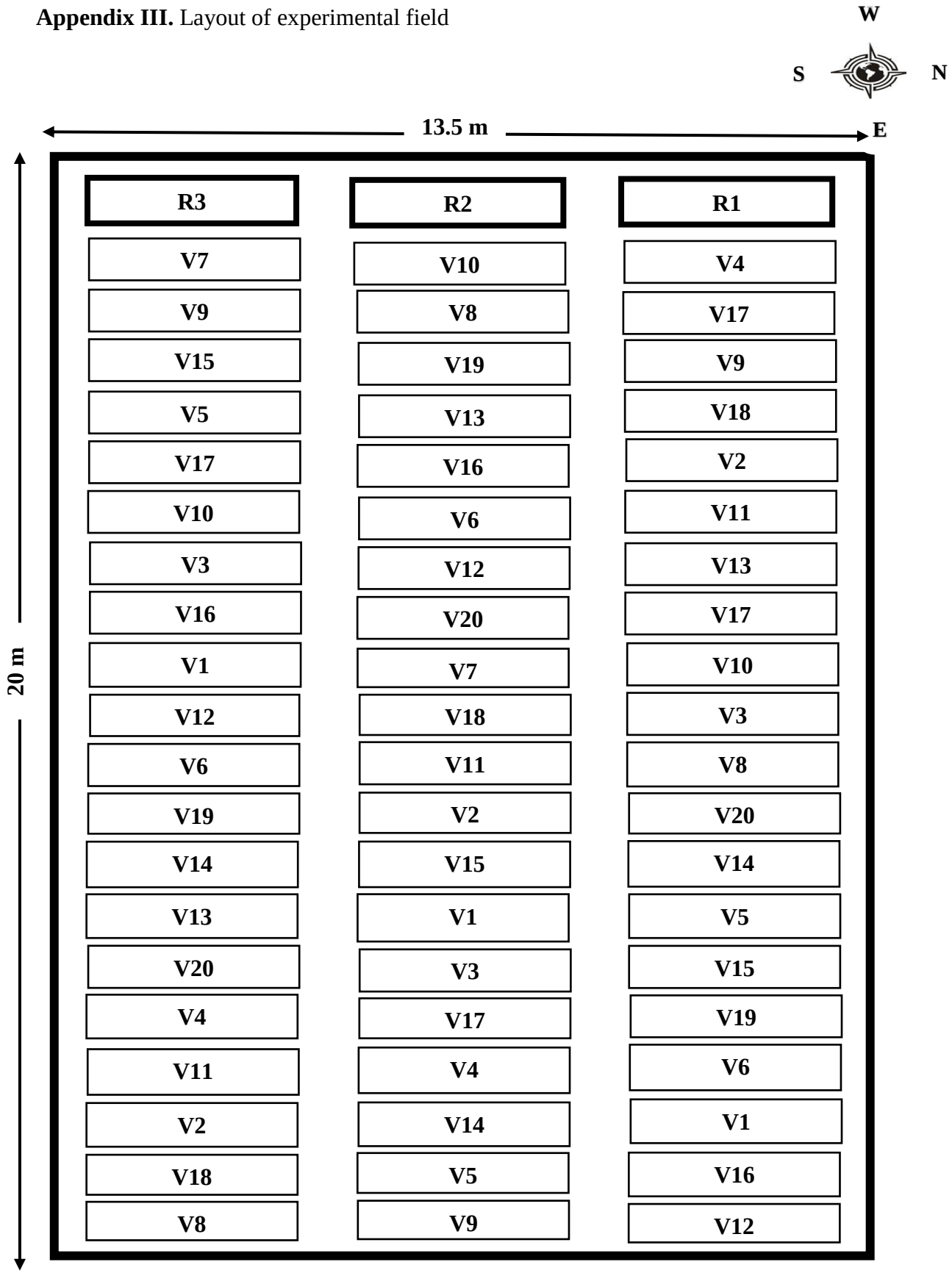
The experimental site under study

Appendix II. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from September, 2019 to March, 2020

Month	Avg. Temperature (°C)	Relative Humidity (%)	Total Rainfall (mm)
September, 2019	29.1	80	161
October, 2019	27.6	78	188
November, 2020	24.9	74	37
December, 2020	19.3	74	5
January, 2020	18.5	76	21
February, 2020	21.6	59	1
March, 2020	26.4	57	30

Source: Bangladesh Meteorological Department (Climate Division, Dhaka Station), Agargaon, Dhaka – 1207

Appendix III. Layout of experimental field



Appendix IV. Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	**%**
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

Sl. No.	**Soil characteristics**	**Analytical data**
1	Organic carbon (%)	0.82
2	Total N (kg/ha)	1790.00
3	Total S (ppm)	225.00
4	Total P (ppm)	840.00
5	Available N (kg/ha)	54.00
6	Available P (kg/ha)	69.00
7	Exchangeable K (kg/ha)	89.50
8	Available S (ppm)	16.00
9	pH (1:2.5 soil to water)	5.55
10	CEC	11.23

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix V: Nutrition profile of brinjal (per 100 g raw)

Principle	Nutrient Value	% of RDA
Energy	24 Kcal	1%
Carbohydrates	5.7 g	4%
Protein	1 g	2%
Total Fat	0.19 g	1%
Cholesterol	0 mg	0%
Dietary Fiber	3.40 g	9%
Vitamins		
Folates	22 µg	5.50%
Niacin	0.649 mg	4%
Pantothenic acid	0.281 mg	6%
Pyridoxine	0.084 mg	6.50%
Riboflavin	0.037 mg	3%
Thiamin	0.039 mg	3%
Vitamin A	27 IU	1%
Vitamin C	2.2 mg	3.50%
Vitamin E	0.30 mg	2%
Vitamin K	3.5 µg	3%
Vitamin B-6	0.1 mg	
Electrolytes		
Sodium	2 mg	0%
Potassium	230 mg	5%
Minerals		
Calcium	9 mg	1%
Copper	0.082 mg	9%
Iron	0.24 mg	3%
Magnesium	14 mg	3.50%
Manganese	0.250 mg	11%
Zinc	0.16 mg	1%

RDA- Recommended Dietary Allowance

Source: USDA National Nutrient data base