GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF YIELD AND YIELD CONTRIBUTING TRAITS IN BRINJAL (*Solanum melongena* L.) GENOTYPES

SUMON CHANDRA SHELL

DEPARTMENT OF GENETICS AND PLANT BREEDING

SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

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SUMON CHANDRA SHELL
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APPROVED BY:

Shahanaz Parveen, Ph.D.	**Md. Harun-Ur-Rashid, Ph.D.**
Associate Professor	**Associate Professor**
Supervisor	**Co-supervisor**

Prof. Dr. Md. Abdur Rahim
Chairman
Examination Committee

Shahanaz Parveen, Ph.D.
Associate Professor
Department Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Mobile: +8801716519515
E-mail: muktasau@gmail.com

CERTIFICATE

*This is to certify that the thesis entitled, "*Genetic Variability and Character Association of Yield and Yield Contributing Traits in Brinjal (*Solanum melongena* L.) Genotypes" *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by Sumon Chandra Shell, Registration No. 19-10099 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2021
Place: Dhaka, Bangladesh

Shahanaz Parveen, Ph.D.
Supervisor

Dedicated to
my beloved parents
and
respected teachers
who always inspired me in
the quest for knowledge

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June, 2021 ***The Author***

SAU, Dhaka

LIST OF ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro Ecological Zone	AEZ
Bangladesh Agricultural Research Institute	BARI
Centimeter	cm
Square Centimeter	cm^2
Degree Centigrade	0^c
Gram(s)	g
Muriate of Potash	MP
Number	No.
Randomized Complete Block Design	RCBD
Triple Super Phosphate	TSP
Ton/hectare	t/ha
Percent	%
Days After Transplantation	DAT
Degree of freedom	df
Coefficient of Variance	CV
Standard Error	SE
Meter	M
Milligram	mg
Parts per Million	ppm
Concentrate of H^+	pH
Kilogram	Kg
Brinjal Shoot and Fruit Borer	BSFB
Phenotypic	P
Genotypic	G

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ABSTRACT

The experiment was carried out using 20 genotypes of brinjal at the farm of Sher-e-Bangla Agricultural University, Dhaka to determine the genetic variability, correlation and path coefficient for yield and its contributing traits during August 2019 to March 2020. Significant variations were observed among the brinjal genotypes for all the parameters under study. Mean comparison table shows variation exist among all the characters. Phenotypic variance and phenotypic coefficient of variation (PCV) was higher than the genotypic variance and genotypic coefficient of variation (GCV) for all the characters under studied. High estimate of heritability coupled with moderate to high GCV, PCV and genetic advance observed in plant height, fruit weight, fruit length, fruit diameter, pedicel length, number of fruits/plant, leaf are index, percent of BSFB infestation and yield/plant which indicated the effect of additive genes. The correlation coefficient revealed that yield per plant had the highly significant positive correlation with number of fruits per plant indicating this character can be considered for phenotypic selection for future brinjal improvement program. The path coefficient had direct positive effect with days to 1st fruit harvest, days to last fruit harvest, plant height, number of primary branches/plant, number of secondary branches/plant, fruit weight, number of fruits/plant and percent of BSFB infestation which indicated that promising selection would be rewarding for those traits. Among five clusters, cluster I had the maximum of nine and the cluster IV and V had the minimum of 1 genotype respectively. The highest intra-cluster distance was observed in cluster I followed by III. The highest inter-cluster distance was observed between cluster III and V and the lowest between the cluster I and IV. The characters such as fruit length, fruit diameter, leaf area index and yield/plant contributed maximum towards divergence among the genotypes. Analyzing genetic variation, cluster analysis, intra and inter cluster distance and agronomic performances, the genotype 6 from cluster III, genotype 15 from cluster V and genotype 17 from cluster IV might be selected as promising parents for future hybridization program.

CHAPTER I
INTRODUCTION

Vegetables are one of the crucial items of our daily demand. Brinjal is a vegetable of the Solanaceae family. Its scientific name is *Solanum melongena* L. having chromosome number 2n=2x=24. It is the native of India (Hazra *et al*., 2011). It is popularly known as Begoon in Bangladesh and aubergine in France and United Kingdom.

In 2019, the world production of eggplants was 55.2 million tons. China ranked first (35.5 million tons; 63% of world's total) after India (12.68 million tons; 24% of world's total), Egypt (1.18 million tons), Turkey (0.82 million tons), and Iran (0.7 million tons). Asia produce maximum (94.2%) brinjal in terms of production (FAOSTAT, 2020). In the year of 2019, Brinjal was the fifth most economically important vegetable crop after Tomato, Onion, Cucumber, and Cabbage according to its total production (Statista, 2020).

Brinjal or eggplant is indeed a warm loving crop mostly grown in tropical and subtropical regions of the world. Among different types of fruit vegetables, brinjal is one of the most important vegetables cultivated widely in Asian countries both in kitchen and commercial gardens mainly for its fleshy and fresh fruits. Eggplant is widely cultivated as a vegetable in both temperate and tropical areas, especially in Asia. *S. melongena* L. is a favored and regular vegetable grown in most parts of Bangladesh. To fulfill the market demand in Bangladesh, eggplant is widely grown during both the summer and winter seasons. It is cultivated in the summer that yields 170189 M. tons in the area of 47213 acres, and in the winter, it yields 360421 M. tons in the area of 82206 acres (BBS, 2020).

Eggplant is considered the healthiest vegetable for human health as it has a high content of vitamins, minerals, and bioactive compounds (Docimo *et al*., 2016). Fresh eggplant has 92% water, 6% carbohydrates, 1% protein, a negligible amount of fat, and low amounts of essential nutrients, with only manganese (Mn) having a moderate percentage (11%) of the Daily Value (San José *et al*., 2014). Minor changes in nutrient composition occur with the season, environment of cultivation, and genotype (San José *et al*., 2014).

Brinjal is graded among the top ten vegetables with reference to oxygen radical absorbance capacity (Cao *et al*., 1996). The bioactive properties of brinjal are mostly

linked with high content in phenolic compounds (Plazas *et al*., 2013), which are mainly phenolic acids, especially chlorogenic acid in the endocarp (Stommel *et al*., 2015) and anthocyanins in the fruit skin (Mennella *et al*., 2012). Both phenolic acids and anthocyanins are beneficial for human health (Braga *et al*., 2016).

In the face of an ever-growing population, there is a crying need for increased production and productivity levels of eggplant. Brinjal breeding programs focus not only to develop high-yielding varieties with high fruit quality, shelf-life, and resistance to major disease and insect pests but also on broad adaptation to environmental stress (Daunay and Hazra, 2012). Several factors are responsible for the low productivity of brinjal in Bangladesh. These include biotic factors as insect pests and pathogens. Brinjal shoot and fruit borer (*Leucinodes orbonalis* Guenee) is the key insect pest of this crop (Latif *et al*., 2010; Chakraborti and Sarkar, 2011; Saimandir and Gopal, 2012) and is predominant in brinjal producing countries all over the world (Dutta *et al.,* 2011). Due to its high reproductive potential, the rapid turnover of generations and intensive cultivation of brinjal in both wet and dry seasons, the pest poses a severe threat. Production losses due to this pest are very high in South Asia (Thapa, 2010) and range from 85%-90% (Mishra, 2008; Jagginavar *et al*., 2009). It feeds internally on fruit and its excretion inside the fruit unfit for human consumption (Baral *et al*., 2006). Since brinjal is attacked by many insect pests and pesticides are used extensively to reduce economic losses caused by these pests. The use of these chemicals results in many ecological hazards like environmental contamination, bioaccumulation, and biomagnification (Dadmal *et al*., 2004). The indiscriminate and continuous use of insecticides also leads to insecticide resistance in insect pests (Harish *et al.,* 2011).

The most crucial problem with chemical use is the retention and persistence of insecticide residues on the surface of vegetables. When human beings eat these vegetables, traces of the insecticides enter their bodies and may cause serious health problems. To avoid these hazards, it is urgently required to find an alternative and non-insecticide method for this pest. The use of resistant varieties is one of these alternate methods (Hossain *et al*., 2002). The screening of different brinjal varieties for resistance has been carried out by many workers. Some varieties have been field tested in different countries around the world. The use of resistant varieties is the more reliable control measure. Selected resistant brinjal varieties can be used in combination with other control methods to manage this insect pest economically and in an environmentally safer way (Lit, 2009). It is not necessary that the varieties be highly resistant. Even a

very low level of resistance can play a vital role in managing an insect pest when it is combined with other control methods that result in reduced use of insecticides (Srivastava, 1993). The knowledge of morphological variability, its nature, and magnitude are essential for selecting genotypes from the germplasm for successful utilization in the breeding program. So, it is vital to study local and available varieties to screen different brinjal varieties for identifying tolerance to BSFB under local conditions.

This study was tackled to approximate the nature and vastness of genetic diversity of brinjal and to study the achievability of employing all that information for the future improvement of the brinjal resistance to shoot and fruit borer. Therefore, this exploration was under taken with the following objectives:

1. To identify the high yielding brinjal germplasm;
2. To know the nature of association of traits, direct and indirect relation between yield and yield contributing characters;
3. To determine different bio-morphological characters of brinjal genotypes against brinjal shoot and fruit borer; and
4. To recommend the best genotype for the further breeding program.

CHAPTER II
REVIEW OF LITERATURE

For an efficient selection of parents for hybridization, it is important to a plant breeder to know the Information on genetic divergence, and it is established that genetically different parents are likely to provide preferable segregants. It was noted that the more different the parents, the greater are the chances of attaining high heterotic F1 and a wide range of variability in the segregating generation (Arunachalam, 1981).

A large number of analyses have been carried out in different crops on the basis of a survey of variance which qualified the study of genetic variance for different characters. But total genetic diversity among different natural populations could not attain which was vital to the plant breeding program. Advancement in yield and quality is generally attained by selecting genotypes with preferable character combinations present in nature or by hybridization. Selection of parents recognized on the basis of divergence analysis would be more promising for a plant hybridization program. Studies on quantitative and qualitative characters of eggplant are gaining much concentration in tropical and sub-tropical countries. Brinjal is one of the most famous vegetables occupying a wider area under its production in Bangladesh, but information on its growth pattern and productivity of different genotypes under different agro-ecological conditions are limited.

The information present in the literature concerning the diversity of the eggplant and some other vegetable crops of the Solanaceae family was evaluated in this segment.

2.1 Origin and domestication of brinjal

Vavilov (1951) reviewed *S. melongena* as being native to the "Indo-Chinese center of origin." According to Lester (1986), *S. aethiopicum* is classified into four cultivar groups (Gilo, Shum, Kumba, and Aculeatum) based on use and morphological characteristics. Characteristics are i) the Gilo group has edible fruits with different shapes, colors, and sizes, and hairy, inedible leaves; ii) the Shum group has glabrous and small leaves that are eaten as a green vegetable but the fruits are inedible; iii) the Kumba group has glabrous leaves and flattened large fruits, which are edible; iv) the Aculeatum group has more prickliness than other groups with flat-shaped fruit, and are used as ornamentals (Lester, 1986).

Both the scarlet and gboma species were domesticated in Africa, from their respective

wild ancestors, which are *S. anguivi* Lam. for *S. aethiopicum* (Lester and Niakan, 1986) and *S. dasyphyllum* Schumach and Thonn for S. *macrocarpon* (Bukenya and Carasco, 1994). It is proved that hybrids between cultivated brinjals and their respective wild ancestors are fully fertile (Lester and Thitai, 1989; Bukenya and Carasco, 1994).

S. melongena and *S. macrocarpon* are included in section Melongena Dunal (Lester and Daunay, 2003), whereas *S. aethiopicum* is included in section Oliganthes (Dunal) Bitter. Around the eighth century, eggplant spread eastward to Japan and then westward into Western Asia, Europe, and Africa by Arab traders during the fourteenth century (Prohens *et al*., 2005). The Old World (Africa and Eurasia) and Australia, are home to more than 300 *Solanum* species (Levin *et al*., 2006). *S. macrocarpon* is cultivated both for its fruits and leaves (Maundu *et al*., 2009). Although, the brinjal is considered to be of Asian origin, wildest relatives are from Africa (Weese and Bohs, 2010).

The *Solanum* genus can be divided into 13 clades, where brinjal is the member of the large *Leptostemonum* clade (subgenus *Leptostemonum* Bitter; Knapp *et al*., 2013), which is commonly known as the "Spiny *Solanum*" group due to the showing of sharp epidermal spines on stems and leaves (Vorontsova *et al*., 2013). The subgenus *Leptostemonum* contains around 450 species (Knapp *et al.*, 2013), many of which originated in the New World (Vorontsova and Knapp, 2012).

Four taxonomically informal groups, labeled E–H, were considered by Lester and Hasan (1991) to show the different types of wild and weedy brinjal and their distribution also. However, these four groups are considered as expressing two different species: the cultivated brinjal *S.* melongena and its wild ancestor *S. insanum* (Knapp *et al*., 2013). Groups E and F grow wild or weedy in India and Southeast Asia corresponding to extremely prickly that are now included within *S. insanum* (Ranil *et al*., 2017). The plants of group G bearing small fruits, while the plants of group H are less spiny than other groups and consist of modern cultivars (Daunay *et al*., 2001; Weese and Bohs, 2010). Both groups, G and H, constitute S. melongena (Knapp *et al*., 2013).

Archeological evidence proposes that the application of wild brinjals may have started earlier in India than China, with a subsequent auxiliary center of domestication in the Philippines (Meyer *et al*., 2012). Recent evidence suggests that brinjal had multiple independent domestications (Knapp *et al*., 2013). Based on data regarding crossing and biosystematics, nine wild species, along with S. melongena, form the "eggplant complex," which includes the cultivated brinjal and its nearest brinjal wild relatives

(Knapp *et al*., 2013).

S. melongena and the two other cultivated brinjal are allied to a large number of wild species (Vorontsova *et al*., 2013; Syfert *et al*., 2016) that may provide as sources of variation for successful breeding programs, not only for traits associated with adaptation to climate change but also traits associated with resistance to pest and disease (Rotino *et al*., 2014). Wild brinjals are very spiny and they produce small, bitter, and multi-seeded inedible fruits. Some of them hold high levels of chromogenic acid and other bioactive compounds, which have potential importance for human health (Meyer *et al*., 2015).

Wild relatives can be classified into primary, secondary, and tertiary genepools based on their crossability with cultivated species (genepool concept) (Harlan and de Wet, 1971). The primary genepool (GP1) of brinjal consists of cultivated brinjal and its wild ancestor *S. insanum* (Ranil *et al*., 2017) which can be crossed easily and generate fertile hybrids (Plazas *et al*., 2016). The secondary genepool (GP2) includes a large number (over 40) of wild relatives that are phylogenetically close to the brinjal, but the success of the crosses and the fertility of the hybrids with the brinjal may be lowered. For example, some interspecific hybrids derived from GP2 are partly sterile or weak due to reproductive barriers such as *S. dasyphyllum*, *S. linnaeanum* Hepper & P.M. L. Jaeger or *S. tomentosum* L. (Rotino *et al*., 2014; Kouassi *et al*., 2016). It is reported that the tertiary genepool (GP3) comprises more diversely related species, which are used in breeding programs for their resistance features, but specific breeding strategies are required for successful crossing (e.g., *S. torvum* Sw., *S. elaeagnifolium* Cav., and *S. sisymbriifolium* Lam.; Kouassi *et al*., 2016; Plazas *et al*., 2016; Syfert *et al*., 2016). *S. melongena* has been considered as the same taxonomic species than its wild ancestor *S. insanum* L. (Ranil *et al*., 2017).

2.2 Genetic diversity

Genetic diversity appears due to geographical detachment or due to genetic fence to cross ability. Variability differs from diversity in the sense that the former has noticeable phenotypic variations, whereas the latter may or may not have such an appearance. One of the vigorous strategies of evaluating genetic divergence is the D^2 static that was proposed by Mahalanobis in 1936. This strategy computes the forces of contrast of two levels, namely, intra-cluster and inter-cluster levels, and thus helps in the choice of genetically dissimilar parents for hybridization programs.

Genetic diversity takes part in a vital role in plant breeding programs because hybrids display greater heterosis. In addition to backing in the choice of dissimilar parents for hybridization, the D^2 statistic computes the degree of diversification and justifies the relative percentage of each component character to the total divergence. The genotypes clustered together are less dissimilar than the ones, which are placed in different groups. The groups, which are detached by the greatest statistical distance, appear the maximum divergence.

During the selection of parents on the basis of D^2 statistics, three important points should be taken into consideration. These points are i) the relative contribution of each character to the total divergence ii) the choice of clusters with the maximum statistical distance and iii) the selection of one or two genotypes from such clusters.

A study was worked by Quamruzzaman *et al*. (2020) at the experimental field of the Olericulture Division of Bangladesh Agricultural Research Institute to examine the extent of genetic diversity among 26 eggplant germplasm. The inter-cluster distance was higher than the intra-cluster distance. The maximum inter-cluster distance was observed in clusters IV and V followed by clusters II and IV, and the minimum was found in clusters II and V. The maximum intra-cluster distance was recorded in the germplasm under cluster I. Inbreeds belong to clusters III, IV and V will be given higher priority for successful breeding programs.

Nayak and Nagre. (2014) conducted an experiment comprised of 20 genotypes of brinjal and the experiment was laid out in randomized block design with three replications. Variability studies revealed that highly significant differences were recorded among the varieties for all characters under study. Correlation and path analysis revealed that fruit length, diameter, weight influenced the fruit yield in plants with high direct effect and positive correlation. Therefore, fruit length, diameter, weight

are important characters that may be included in selection criteria for improvement in fruit yield per plant.

The characters like single fruit weight, fruit diameter, seed yield/fruit, pulp seed ratio, fruits/plant, fruit yield/plant, and fruit length showed significant differences under the study conducted by Mili *et al.* (2014) with 36 different genotypes of eggplant. A study on Genetic divergence analysis among fourteen eggplant genotypes using Mahalanobis's D^2 statistic was conducted by Ramesh *et al.* (2013). Six clusters were formed. The highest number of genotypes (5) was found in cluster III. The maximum inter-cluster distance was observed between cluster II and cluster V. Genotypes belonging to these clusters may be utilized in hybridization programs for crop improvement.

Mishra *et al.* (2002) conducted a study in Uttar Pradesh, India, during the rabi season of 1999/2000 and 2000/01 to determine the genetic diversity among 38 potato genotypes. Based on the calculated mean performance for characters and genetic distance between genotype crosses, namely JP-100 × Kufri Pukhraj, JP-100 × JW-96, JP-100 × JX-23, JP-100 × Kufri Ashoka, JP-100 × JX-235, JP-100 × JX-216, and JP-100 × JX-371 were identified as encouraging and were likely to result in progenies with heterotic performance for tuber yield and its components.

Three hundred accessions of andigena group of potato (2n = 4x = 48) germplasms were evaluated by Sandhu *et al.* (2001) for genetic divergence based on 8 distinct traits, namely, plant height, number of stems, number of nodes, internode length, leaflet index, tuber yield, tuber number, and average tuber weight. Principal component analysis based on adjusted mean values yielded 8 each eigenvector. Eight genetically diverse and agronomically promising genetic stocks were identified which may be involved in the crossing program.

Diversity in the genetic composition is the basic characteristic that increases the chance of survival during natural selection. It leads to speciation in the long term due to the process of evolution (Raven *et al.,* 1999). Morphological similarity, eco-geographic diversity were the few simpler methods used to distinguish dissimilar populations which were restored by more scientific and advanced biometrical strategies viz. multivariate analysis based on Mahalanobis's D^2 statistics.

Genetic divergence among twenty cultivars of brinjal was estimated by Mishra *et al.* (1998) using D^2 statistics for eleven yield traits. The cultivars were grouped into 7 clusters. Maximum genetic distance was found between clusters IV and VI followed by

that between clusters I and IV, suggesting wide diversity among these groups. Considering cluster means and the genetic distances, the crosses of the cultivar of cluster VI (A-I) with the cultivars of clusters I and IV were likely to recombine the genes for high yield.

Amaral *et al.* (1997) observed that the efficiency in predicting the behavior of tomato hybrids based on the parents, genetic divergence was evaluated via D^2 analysis of data on 15 characteristics in 5 parents and their hybrids. Almost all correlations between D^2 and hybrid population means, heterosis, and combining abilities were positive, indicating that genetic divergence was a high-efficiency parameter for hybrid behavior prediction.

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

Randhawa *et al.* (1993) observed in a study that was conducted with 22 genotypes of brinjal on 24 quantitative characters, that fruits per plant and the number of branches per plant had the highest straight effect on yield.

Hybrids from a diallel set of crosses between 11 varieties of tomato were studied by Sidhu *et al.* (1993). The genetic divergence between the parents was not clearly connected to the execution of the hybrids.

Mandal and Dana (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that fruits/plant; secondary branches/plant and plant height were important traits for the selection of superior genotypes.

Vedivel and Bapu (1990) studied nineteen genotypes of eggplant including 7 from foreign sources, which were grown in a Randomized Block Design for observation on growth and yield-related traits. Plant height, fruit weight, and fruit/plant exhibited high genotypic variance. High heritability coupled with high genetic gain from fruit yield/plant, fruit/plant, and length indicated the predominance of additive gene effects.

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

was higher than the genotype coefficient of variation for all the characters since they showed high heritability values. They concluded that there was enough scope for improvement of quantitative characters in brinjal by selection.

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

Sidhu *et al.* (1981) evaluated 81 genotypes of potato for genetic divergence by using Mahalanobis's D^2 statistics. The 81 genotypes were grouped into six clusters of which cluster I was the largest accommodating 48 genotypes. Cluster VI had a large genetic distance from the remaining clusters.

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

2.3 Relationship between genetic and geographic diversity in brinjal

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

A study was conducted to evaluate yield attributed characters of 33 eggplant genotypes by Nikitha *et al*. (2020). The correlation coefficient analysis expressed fruit yield/plant showed a maximum positive association with the number of fruits/plant, yield/plant, number of branches/plant, fruit diameter, fruit weight, and days to first flowering respectively. Path coefficient analysis revealed the maximum positive direct effect on yield/plant through days to first fruit harvest, number of fruits/plant, fruit weight, days to first flowering, and number of branches/plant.

Ramesh *et al*. (2013) conducted a study that consisted of 54 genotypes where fruit yield was kept as a dependent character. Analysis of variance disclosed that considerable variability for all the characters. High estimation of phenotypic and genotypic coefficient of variation was studied for fruit length, the number of fruits per plant, calyx length, total phenol content, and fruit yield per plant. The study further expresses that simple phenotypic selection could be successful for the improvement of traits.

Muniappan *et al*. (2010) studied the genetic divergence that was carried out to examine the variability, direct and indirect effects of different morphological characters in 34 brinjal genotypes where high PCV and GCV were recorded in different characters. All the characters like as, fruit length, fruit breadth, number of fruits per plant, average fruit weight, and fruit yield per plant were gone along with high heritability and high genetic advance.

Genetic divergence was examined by Joshi *et al*. (2003) using nonhierarchical Euclidean cluster analysis in 73 tomatoes (*Lycopersicon esculentum* L.) genotypes of different origin for diverse quantitative and qualitative traits. The maximum value of the coefficient of variability (53.208) was found for the shelf life of fruits while it was minimum (69.208) for days to first picking. The grouping of the genotypes into 15 clusters showed the presence of a wide range of genetic diversity among the genotypes and expressed non- parallelism between geographic and genetic diversity.

Thirty-four genotypes of eggplant (Solanum melongena) of different origins were analyzed by Sarma *et al*. (2000). Data on yield and its components grouped the genotypes into ten clusters using Mahalanobis's D^2 statistic. Fruit circumference and average fruit weight were the main characters affecting the grouping of genotypes. The eco-geographic variation of the genotypes was not related to genetic diversity.

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

Genetic divergence of sweet potatoes (*Ipomoea batatas*) was studied by Naskar *et al.*

(1996) from Madhya Pradesh, was derived from data on 8 quantitative characters in 18 sweet potato genotypes using Mahalanobis's D^2 statistic. The genotypes were grouped into 7 diversified clusters. Cluster I had 8 genotypes, whereas clusters II and III had 2 genotypes each, and cluster IV had genetic divergence for yield contributing traits in sweet potato under this study.

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

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

2.4 Technique of multivariate analysis

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

Hundred brinjal accessions were studied and grouped into eight clusters by Rabbani *et al.* (2014) through genetic diversity based on multivariate analysis. The pattern of clustering expressed that the accessions of the same area did not fall in the same cluster which indicates that there was no relationship between genetic divergence and geographical distribution. The output of the PCA showed that the first four of the principal component axes considered for 78.07% of the variation among the genotypes considering ten characters. The maximum inter-cluster divergence (32.234) was recorded between cluster II and VI, and was minimum (2.841) between V and VII. Cluster II had the maximum intra-cluster divergence.

Caguiat and Hautea (2014) conducted a study for genetic diversity analysis of 64 Philippine brinjal germplasm. The morphological trait and SSR data were evaluated as separate and combined data sets using PCA and unweighted pair-group method with arithmetic averages (UPGMA) cluster analysis. This study showed significant

information for the need to increase the present eggplant collection and to widen the genetic diversity of cultivated brinjal varieties in the Philippines.

Genetic divergence in eighteen eggplant genotypes was examined by Uddin *et al.* (2014) using multivariate analysis. The genotypes were grouped into four diverse clusters. The clustering pattern of the genotypes was not correlated with their geographical distribution. The highest inter-cluster distance (764.67) was between cluster I and IV while it was the lowest (213.30) between cluster II and III. The highest and lowest intracluster distance was recorded in cluster II (94.14) and cluster I (28.79) respectively. The number of fruits per plant, plant canopy, fruit weight, fruit length, yield per plant, and the number of harvests had the maximum contribution towards total divergence.

An experiment was done by Saurabh *et al.* (2011) with 50 eggplant genotypes. The intra-cluster distance was minimum for cluster IV and maximum in cluster II. The maximum distance at the inter-cluster level was between clusters I and IV followed by II and IV which may serve as a potential genotype for a successful hybridization program. On the basis of mean performance of different clusters, genotypes having high yield along with fruit diameter, fruit index, and average fruit weight were observed in cluster V having genotypes like DBR-31 (Delhi), Green Long (Kalyani), KS-335 (Kalayanpur), DBR-8 (IARI, Delhi), SL-91-2 (Pantnagar), SL- 190-10-12 (Panipat), ABR-1 (Anand) Swarna Shree (Ranchi).

Genetic divergence among 19 brinjal genotypes was evaluated by Quamruzzaman *et al.* (2009) using Mahalanobis's D^2 statistic. Among five clusters, the highest intra-cluster distance (1.067) was observed for cluster V and the lowest (0.916) for cluster III. The highest inter-cluster distance (10.748) was observed between clusters IV and V. Cluster V recorded the highest mean for characters namely, plant height at last harvest, fruit pedicel length, leaf blade length, leaf blade diameter, leaf pedicel length, spines on calyx.

Prakash *et al.* (2008) reported high heritability (in broad sense) with the high genetic advance in the percentage of the mean for the number of fruits per plant, individual fruit weight and plant height by conducting an experiment with 50 brinjal genotypes. However, yield per plant showed moderate heritability and low genetic advance but highest genetic advance as a percentage of mean under selection.

It was reported by Dharmatti *et al.* (2001) using multivariate analysis that genetic diversity in a population of 402 tomato genotypes was analyzed, in a field experiment

carried out in Karnataka, India. The genotypes under study were grouped into four clusters based on the likeness of D^2 values. Significant diversity within and between the clusters was recorded, and it was shown that the characters like TLCV resistance, fruit yield/plant, and the number of whiteflies/plant provided the highest to the divergence. Therefore, the choice of dissimilar parents based on these characters may be effective for tomato breeding.

Thirty-six genotypes of potatoes were grown in 16 environments and were evaluated by Desai *et al.* (1997) for genetic divergence using Mahalanobis's D^2 statistic. Nine clusters were identified in the study; I being the largest, consisting of 7 genotypes. Cluster I, III, V, VI, and VII expressed larger genetic divergence. Genotypes in clusters III had the maximum tuber yields and other characters like the number of stems, maturity, number of leaves, shoot fresh weight, the number of tubers, average tuber weight, sugar content and harvest index. Cluster I had 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 varied significantly for all characters, suggesting a good scope of selection for a breeding program.

Estevez *et al.* (1994) reported that 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 programs.

The influence of four types of genetic divergence on the vigor and variability of the progenies was studied in two field experiments at Fredericton, Brunswick, Canada reported by Loiselle *et al.* (1991). The measures of genetic divergence were (1) the progenies inbreeding coefficients; (2) the Mahalanobis's distances between the parents obtained from their agronomic traits. These measures of divergence were not significantly related. Canonical correlation analysis between the divergence parameters and vigor-related traits produced significant relationships in one experiment only. The methods of estimating genetic divergence appeared to be a good predictor of either the mean on the variability of a progeny.

Birhman *et al.* (1991) constructed that genetic distance was evaluated by applying the D^2 statistic to data on nine yield contributing components in 26 potato genotypes consisting of 9 elite varieties and 17 advanced breeding genotypes. Genotypes were

grouped into 8 clusters. Cluster I comprising 12 genotypes and the others between clusters 1 and 4. Intercrossing of genotypes in clusters III, VI, and VIII was thought the most advantageous in terms of tuber yield gain.

However, literature related to efficient multivariate techniques for genetic diversity analysis is reviewed in the above paragraphs proving that genetic diversity analysis is mainly done on the basis of different multivariate techniques. During the last decade, different multivariate techniques have been developed which may be due to the improvement in statistical analysis.

CHAPTER III
MATERIALS AND METHODS

This chapter explicates the information respecting the methodology that was used in conveying this experiment. It carries a short explanation of the location of the experimental area, climate, characteristics of soil, planting materials, layout and design of the experiment, land preparation, fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording, and statistical analysis etc. which are introduced as follows.

3.1 Experimental site

The research work was carried out at the Farm of Sher-e-Bangla Agricultural University, Dhaka-1207 from August 2019 to March 2020.

3.2 Geographical location

The experimental area was situated at 23°77′N latitude and 90°33′E longitude at an altitude of 8.6 meters above sea level. The experimental field belongs to AEZ-28, the Agro-ecological zone called the Madhupur tract. This was a region of complex relief and soils developed over the Madhupur clay where floodplain sediments buried the dissected edges of the Madhupur tract leaving small hillocks of red soils as islands surrounded by floodplain. The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.3 Climate

The experimental area has a subtropical climate characterized by scanty rainfall associated with moderately low temperatures during the Rabi season (August-March). Meteorological data on rainfall, temperature, relative humidity from August 2019 to March 2020 were obtained from Bangladesh Meteorological Department (Climate and Weather Division), Dhaka-1207. Meteorological data that prevailed at the experimental site during the study period was presented in Appendix II.

3.4 Characteristics of soil

The soil of the experimental site had the general shallow red-brown terrace soils. The land of the experimental site was medium to high fertility level. Topsoil was clay loam texture. Soil pH ranged from 6.0-6.6 and had 0.82% organic matter. Soil samples taken from 0-15cm depths were collected from the experimental field under study. The analyses of soil under study were done by Soil Resource and Development Institute (SRDI), Dhaka. The experimental land was flat having available irrigation and

drainage system and above flood level. Appendix III shows the physicochemical properties of the soil under study.

3.5 Design and layout of the experiment

This study was assigned in Randomized Complete Block Design (RCBD) with 3 replications. The brinjal genotypes were distributed randomly in each block. Five plants were planted for each genotype in every single row. The spacing was maintained at 120 cm by 75 cm. The layout of the experimental plot is presented in Appendix IV.

3.6 Planting materials

Twenty genotypes of brinjal were used for this experiment. The purity and germination percentage were leveled as around 100 and 80 respectively. The genetically pure and physically healthy seeds of twenty genotypes were collected from the Department of Genetics and Plant Breeding and the local market. The experimental genotypes are presented in Table 1.

3.7 Seeds selection for sowing

Healthy and uniform seeds were selected for sowing to ensure better germination.

3.8 Land preparation

To bring about good tilth, the experimental plot was prepared by several ploughing followed by laddering and harrowing with tractor and power tiller in the middle of the third week of September, 2019. The experimental plot was leveled properly after removing weeds and other inert carefully.

3.9 Manure and fertilizer application

The experimental land was fertilized at the rate given in Table 2. The area of the experimental plot was 264 square meters. According to dose of fertilization and size of the plot 0.5 ton, 9 kg, 6.5 kg, and 2.5 kg of cow dung, urea, TSP, and MP were applied respectively to the experimental plot under study. A 50% amount of cow dung was applied during the last land preparation. The rest 50% of the cow dung, whole TSP and 33% Urea, and 50% of MP were applied before transplanting the seedling into the main plot. The rest of the Urea and MP was applied at equal three installments- the first was applied at 21 days after transplantation (DAT) and the second and the third were applied at 35 and 55 DAT respectively.

Table 1. List of genotypes along with their collection sources

Sl. No.	Genotypes	Identification mark	Collection source
01	Mukto Jhuri	G1	Local Market, Dhaka
02	Pobon-5	G2	Local Market, Dhaka
03	Green Line	G3	Local Market, Dhaka
04	BNB-478	G4	Local Market, Dhaka
05	Aveo Round	G5	Local Market, Dhaka
06	BT-4	G6	BARI, Gazipur
07	Altapon	G7	Local Market, Dhaka
08	Brinjal White	G8	Local Market, Barishal
09	Black Diamond	G9	Local Market, Barishal
10	Green Super	G10	Local Market, Dhaka
11	Chu-chu	G11	Local Market, Dhaka
12	Chumki	G12	Local Market, Dhaka
13	Choice Light	G13	Local Market, Jamalpur
14	Kushtia-2	G14	Local Market, Jamalpur
15	Shingnath	G15	BARI, Gazipur
16	Shabuj Sathi	G16	Local Market, Dhaka
17	Mukta Keshi	G17	Local Market, Dhaka
18	Katali Begun	G18	Local Market, Dinajpur
19	Pirgonj	G19	Local Market, Dinajpur
20	Borsharani	G20	Local Market, Mymensing

Table 2. Fertilizer/Manure dose (Agropedia, 2012)

Sl. No.	Fertilizer/Manure	Rate of Application
1	FYM	15-20 ton /hectare
2	Nitrogen	150 kg /hectare
3	P_2O_5	100 kg /hectare
4	K_2O	50 kg /hectare

Plate 1. Different field activities of the study (A- Seed bed, B-Field preparation, C- Transplanting seedlings in the main field, D- Stalking and tagging)

3.10 Raising of seedling

Individual seedbed was prepared for different varieties following standard method of bed preparation (Plate 1). Seeds were sown in lines in a well-prepared seedbed on the evening of 21 August 2019. The seeds were sown at about 1.25 cm depth and were covered uniformly with light soil for proper germination. Heptachlor was dusted over the seedbed to prevent the seedling from ant attack. To avoid varietal mixture adequate control measures were taken. The seedbed was watered as and when necessary for proper germination as well as for normal growth of the seedling. After germination shading was arranged to protect the young seedling from scorching sunshine and was kept exposed during the night, morning, and afternoon. Proper nursing was done for developing healthy seedlings. At the attainment of 45 days of sowing the seedlings were ready for transplanting.

3.11 Transplanting of seedlings

Healthy and vigorous seedlings of 30 days old were selected for transplanting in the main field (Plate 1). The seedlings were removed carefully from the seedbed by avoiding any injuries and sown one seedling per pit in the evening time. Slight watering was provided after transplantation.

3.12 Intercultural operations

For proper growth and development of the brinjal plants, intercultural operations like weeding, mulching, irrigation, etc. were done when necessary. But no insecticide was used to study the resistance capacity of the genotype against brinjal shoot and borer. Proper shadings were given in the morning at the first stage of transplanting to protect the young seedlings from scorching sunshine during day time. Shadings were removed in the afternoon. Extra soils were added around the base of plants for proper rooting. Sticks were given to protect the plant from falling due to strong wind (Plate 2). Gap filling was done twice, firstly 10 days after transplanting and 2nd time 20 days after transplanting (DAT). Weeding was done several times when necessary. In the early stage of transplanting watering was done twice a daily. In the mature stage, flood irrigation was done to the field.

Plate 2. Intercultural operations in the experimental plot

3.13 Harvesting

Fruits were harvested on the basis of horticultural maturity, size, color, and age. Fruits were picked with a sharp knife and care was taken to avoid injury to the plant. Frequent picking was done throughout the harvesting period.

3.14 Data recording

Three plants were selected randomly for each genotype from every blocks and tagged properly for collecting data. Data were recorded on the following parameters from the studied plants throughout their life cycle.

3.14.1 Growth habit

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

3.14.2 Hairiness

The presence of hairiness on leaf, stem was recorded properly.

3.14.3 Spiny character

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

3.14.4 Color of flower

Flower color of every plant of every genotypes were recorded.

3.14.5 Color of fruit

Fruit color of the brinjal genotypes was recorded.

3.14.6 Days to 1st flowering

Days from transplanting to 1st flowering of every plant of every genotypes were recorded.

3.14.7 Days to 50% flowering

Days from transplanting to 50% flowering of every plant of every genotypes were recorded.

3.14.8 Days to 1st fruit harvest

Days from transplanting to 1st fruit harvest of every plant of every genotypes were recorded.

3.14.9 Days to last fruit harvest

Days from transplanting to last fruit harvest of every plant of every genotypes were recorded.

3.14.10 Fruit shape

The fruit of different genotypes showed differences in shape. The shape of fruits was recorded.

3.14.11 Fruit length (cm)

Length from the top to the bottom of matured fruits per plant was recorded.

3.14.12 Fruit diameter (cm)

Measured average diameter along the whole part of the harvestable mature fruits.

3.14.13 Pedicel length (cm)

Length of pedicel of matured fruits per plant was recorded.

3.14.14 Number of primary branches/plant

Number of primary branches of each randomly selected plant was recorded.

3.14.15 Number of secondary branches/plant

Number of secondary branches of each randomly selected plant was recorded.

3.14.16 Number of fruits/plant

Total number of fruits harvested from individual plant was recorded.

3.14.17 Leaf area index (cm^2)

Leaf area index of randomly selected leaves was recorded using 1 cm^2 graph paper.

3.14.18 Plant height (cm)

Length of main stem from ground level to the tip of the stem was measured after harvest.

3.14.19 Fruit weight (g)

Weight of individual fruit per plant was recorded.

3.14.20 Yield/plant (kg)

Total fruits harvested from each selected plant in each replication were weighted together and yield per plant was recorded.

3.14.21 Percent of BSFB infestation

Brinjal genotypes were affected by shoot and fruit borers. Number of infected fruits were recorded. The rate of insect infestation against different genotypes was calculated in percentage and graded using the following grades (Subbaratnam and Butani, 1981) for shoot and fruit borer.

Infestation (%)	Grading for Resistance
1-15	Tolerant
16-25	Moderately Tolerant
26-40	Susceptible
>40	Highly Susceptible

3.15 Estimation of genetic variability, heritability and genetic advance

Collected data on the twenty genotypes were used to statistical analysis for each character, Analysis of variance (ANOVA), mean, range were calculated by using MSTATC software by Johnson *et al*. (1955).

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) for all characters was carried out individually.

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	

Where,
r = Number of replications
g = Number of genotypes
df = degree of freedom
MSS = Mean sum of square
EMSS = Expected values of MSS

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

a. **Genotypic variance**, $\boldsymbol{\delta^2 g}$ = [(MSG-MSE)/r]

   Where, MSG = Mean sum of square for genotypes

   MSE = Mean sum of square for error, and r = Number of replication

b. **Phenotypic variance,** $\boldsymbol{\delta^2 p} = \delta^2 g + \delta^2 e$

   Where, $\delta^2 g$ = Genotypic variance,

   $\delta^2 g$ = Environmental variance = Mean square of error

Genotypic and phenotypic coefficient of variation were calculated by the following formula given by Burton (1952).

GCV = ($\delta_g \times 100$)/ x

PCV = ($\delta_p \times 100$)/ x

Where, GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

x = Population

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

Heritability in broad sense, $h^2_b = \sigma^2_g / \sigma^2_p$

Where, h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

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

Genetic advance, $GA = K. h^2_b . \sigma_p$

Where, K= Selection Intensity

h^2_b = Heritability in broad sense

σ_p = Phenotypic standard deviation

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

Genetic Advance (% over mean) = (Genetic Advance/ Population Mean) × 100

3.16 Correlation analysis

Simple correlation coefficient (r) was estimated with the following formula (Singh and Chaudhary, 1985; Clark, 1973).

$$r = \frac{n(\Sigma xy) - (\Sigma x)(\Sigma y)}{\sqrt{[\, n\Sigma x^2 - (\Sigma x)^2 \,][\, n\Sigma y^2 - (\Sigma y)^2 \,]}}$$

Where, $\sum$ = Summation,

x and y are the two variables correlated and

n = Number of observation

3.17 Path coefficient analysis

Path coefficient analysis was done according to the procedure employed by Dewey and Lu (1959) that is also quoted by Singh and Chaudhary (1985) using simple correlation values.

In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$

$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$

$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$

Where, r's denotes simple correlation coefficient and P's denote path coefficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix form.

Total correlation, say between x1 and y is thus partitioned as follows:

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, residual effect (R) was calculated.

3.18 Estimation of genetic diversity

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Selection of parents in a hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analysis such as Mahalanobis's D^2 and canonical variate analysis (CVA), which quantify the differences among several quantitative traits are efficient methods of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. For univariate analysis of variance, analysis was done individually, and the least of significance was done by F- Test (Pense and Shukhatme, 1978). Mean, range, coefficient of variation (CV), and correlation were estimated using

the OPSTAT computer program. Multivariate analysis viz., principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis (CLU), and canonical variate analysis (CVA) were done by using the GEN STAT program. Peyne et al. (1989) reported that the hierarchical nature of the grouping into various classes could impose undue constraints and the statistical properties of the resulting groups were not at all clear. Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. They also reported that the squared distance between means was Mahalanobis's D^2 statistics when all the dimensions were used, which could be computed using Principal Coordinate Analysis (PCO). They also commended the Canonical Variate Analysis (CVA) for discriminatory purposes.

3.18.1 Principal component analysis (PCA)

Principal Component Analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters. It can be done from the sum of squares and products matrix for the characters. Principal components were computed from the correlation matrix and genotype scores were obtained for the first components and succeeding components with latent roots greater than unity (Jeger *et al.,* 1983). Contributions of different morphological characters towards divergence were discussed from the latent vectors of the first two principal components.

3.18.2 Principal coordinate analysis (PCO)

The principal coordinate analysis (PCO) is equivalent to principal component analysis but it is used to measure inter-unit distances. Through the use of all dimensions of P, it gives the maximum distances between each pair of the n point using a similarity matrix (Digby *et al.,* 1989).

3.18.3 Clustering

Clustering was done to separate the brinjal genotypes of the study into some number of groups using non-hierarchical classification. Starting from some initial classification of the genotypes into required groups, the algorithm of the statistics program repeatedly transfers genotypes from one group to another so long as such transfers improve the criterion, the algorithm converts to a second stage which measures the effect of swapping two genotypes of different classes and so on.

3.18.4 Average Intra-Cluster Distances

The average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the principal coordinate

analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotype included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

3.18.5 Canonical variate analysis (CVA)

Canonical variate analysis complementary to D^2 statistic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical variate analysis computed a linear combination of original variability that maximized the ratio between ground and within-group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformations sequentially maximized the ratio of the groups to within-group variations.

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

3.18.6 Cluster diagram

A cluster diagram was drawn using the measured values (D^2) of intra and inter-cluster distance from the study. The diagram expressed the brief idea of the diversity pattern among the brinjal genotypes and relationships between different genotypes included in different clusters.

CHAPTER IV
RESULTS AND DISCUSSION

As plant breeding is dependent on genetic variation, a new variation is fundamentally important for introducing new traits in breeding programs. Thus, accurate information on the nature and degree of diversity of the parents is the prerequisite of an effective breeding program. The knowledge of genotypic variation within genotypes in relation to morphology, phenology, and yield would help to screen better genotypes for the hybridization programs. The accessibility of transgressive segregants in the breeding programs relies upon the dissimilarities of the parents. So, appropriate data on the degree of diversity of the parent is necessary for an effective breeding program. Therefore, to generate information on the degree of diversity twenty genotypes of brinjal were raised in the growing season of 2019-2020 at the farm of Sher-e-Bangla Agricultural University, Dhaka. The data in respect of different morphological characters influencing the infestation of brinjal shoot and fruit borer were analyzed and presented in this chapter.

4.1 Morphological Characterization of Brinjal

Phenotypic expression of morphological characters in brinjal genotypes showed a wide range of variation under study. In the present study, the characters showing variation are explained. Thus, selection on the basis of these traits will be effective. Morphological characterization is considered to the first step for the description and classification of genetic resources. Different morphological characters of 20 brinjal genotypes is given in Table 3.

Table 3. Characterization of 20 brinjal genotypes

Genotypes		Growth habit	Hairiness	Spiny characters	Color of flower	Color of fruit	Fruit shape	Fruit curvature
Sl. No.	Names							
G1	Mukto Jhuri	Spreading	Leaf, Stem	Petal	Purple	Violet	Elongate	Slightly Curved
G2	Pobon-5	Spreading	Leaf, Stem	Calyx	Purple	Whitish Green	Oval	Slightly Curved
G3	Green Line	Spreading	Leaf, Stem	Calyx	Purple	Whitish Green	Elongate	Slightly Curved
G4	BNB-478	Spreading	Leaf, Stem	Calyx	Purple	Whitish Green	Oval	None
G5	Aveo Round	Spreading	Leaf, Stem	Leaf, Stem	Purple	White	Oval	None
G6	BT-4	Spreading	Leaf, Stem	Petal, Leaf	Purple	Green	Oval	None
G7	Altapon	Spreading	Leaf, Stem	Calyx	Purple	Purple	Elongate	Slightly Curved
G8	Brinjal White	Erect	Leaf, Stem	Stem	Purple	White	Oval	None
G9	Black Diamond	Spreading	Leaf, Stem	Calyx	Purple	Violet	Elongate	Slightly Curved
G10	Green Super	Erect	Leaf, Stem	Petal, Calyx	Purple	Green	Round	None
G11	Chu-chu	Erect	Leaf, Stem	Calyx	Purple	Violet	Oval	None
G12	Chumki	Spreading	Leaf, Stem	Stem	White	Violet	Elongate	Curved
G13	Choice Light	Spreading	Leaf, Stem	Petal, Calyx, Leaf	Purple	Purple	Round	None
G14	Kushtia-2	Semi erect	Leaf, Stem	Stem, Calyx	Purple	Green	Elongate	Slightly Curved
G15	Shingnath	Semi erect	Leaf, Stem	Calyx	Purple	Violet	Elongate	Curved
G16	Shabuj Sathi	Erect	Leaf, Stem	Leaf, Stem	White	Whitish Green	Round	None
G17	Mukta Keshi	Semi erect	Leaf, Stem	Stem	Purple	Violet	Elongate	None
G18	Katali Begun	Semi erect	Leaf, Stem	Leaf, Stem, Calyx	White	Whitish Green	Round	None
G19	Pirgonj	Semi erect	Leaf, Stem	No	Purple	Violet	Elongate	None
G20	Borsharani	Semi erect	Leaf, Stem	No	Purple	Violet	Oval	None

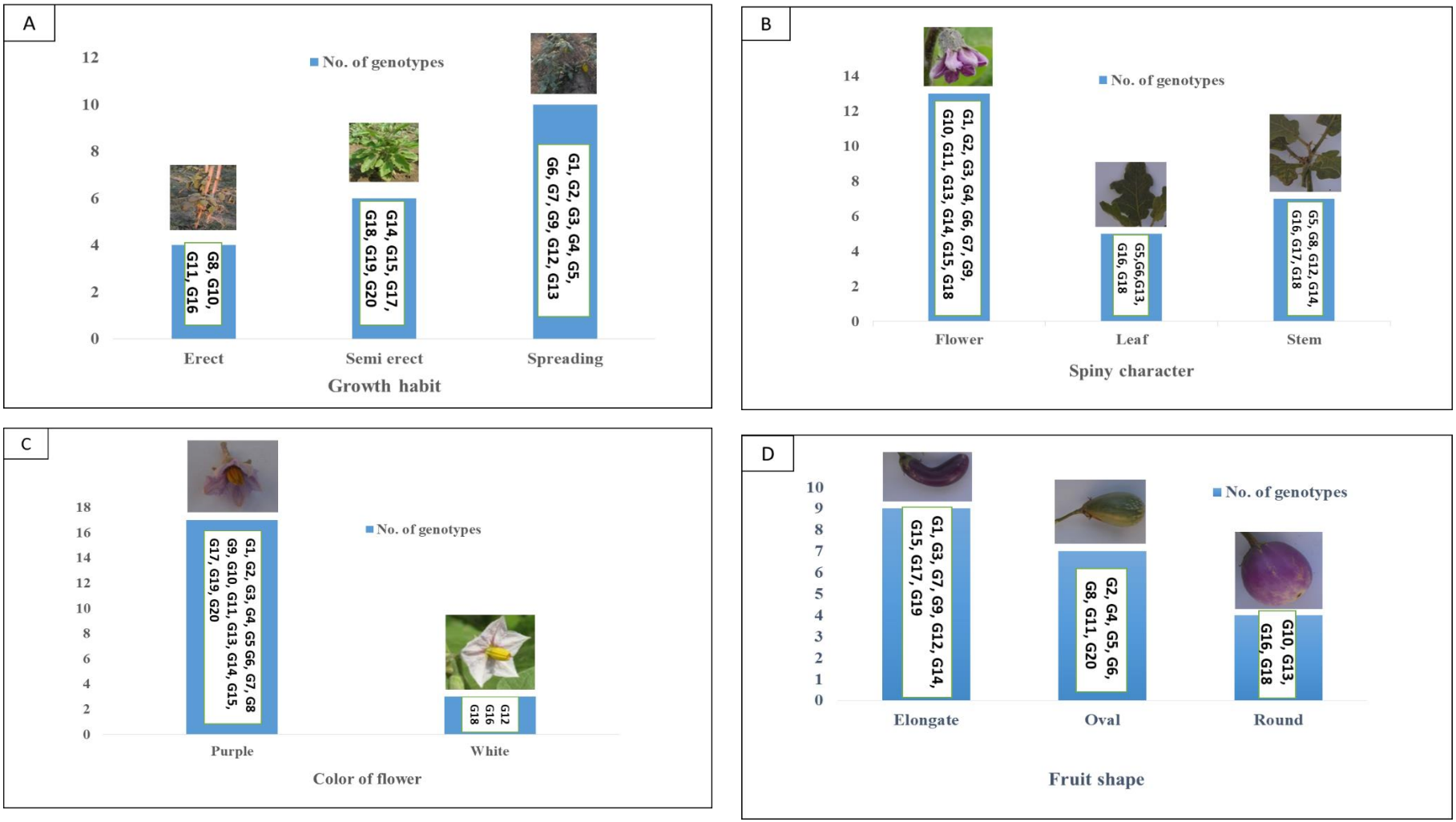
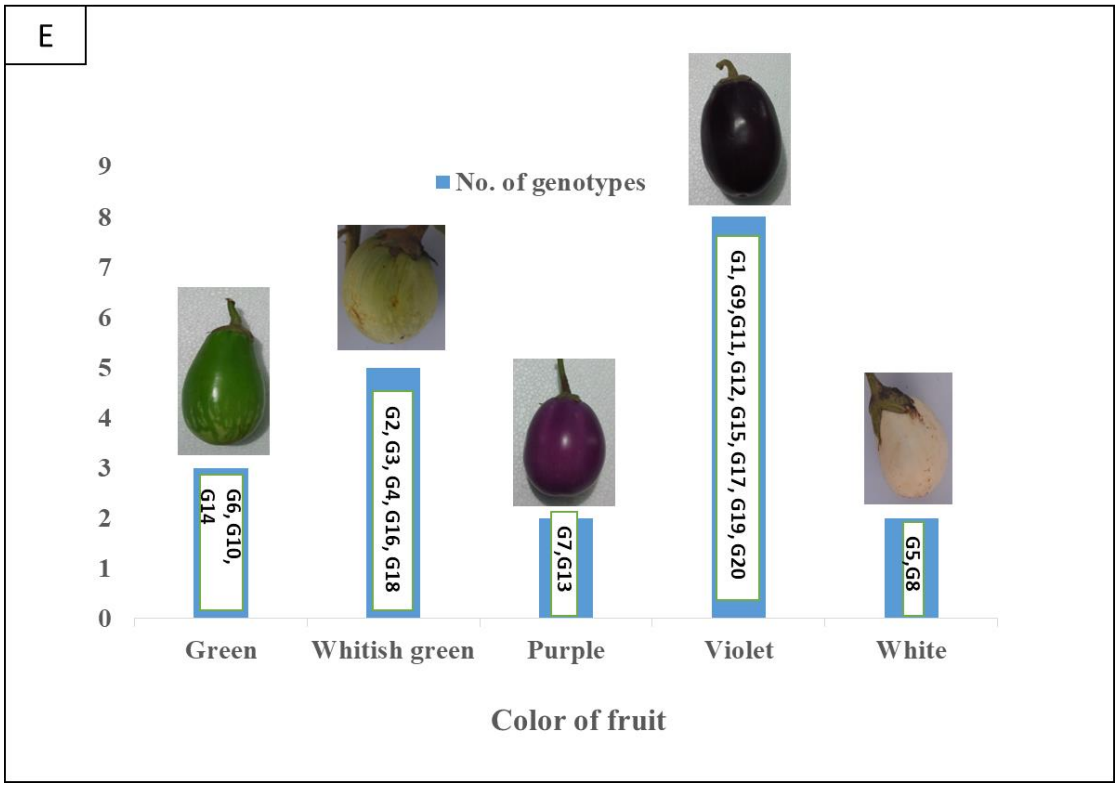


Plate 3a. Graphical representation of frequency distribution (A-Growth habit, B-Spiny character, C-Color of flower and D-Fruit shape)



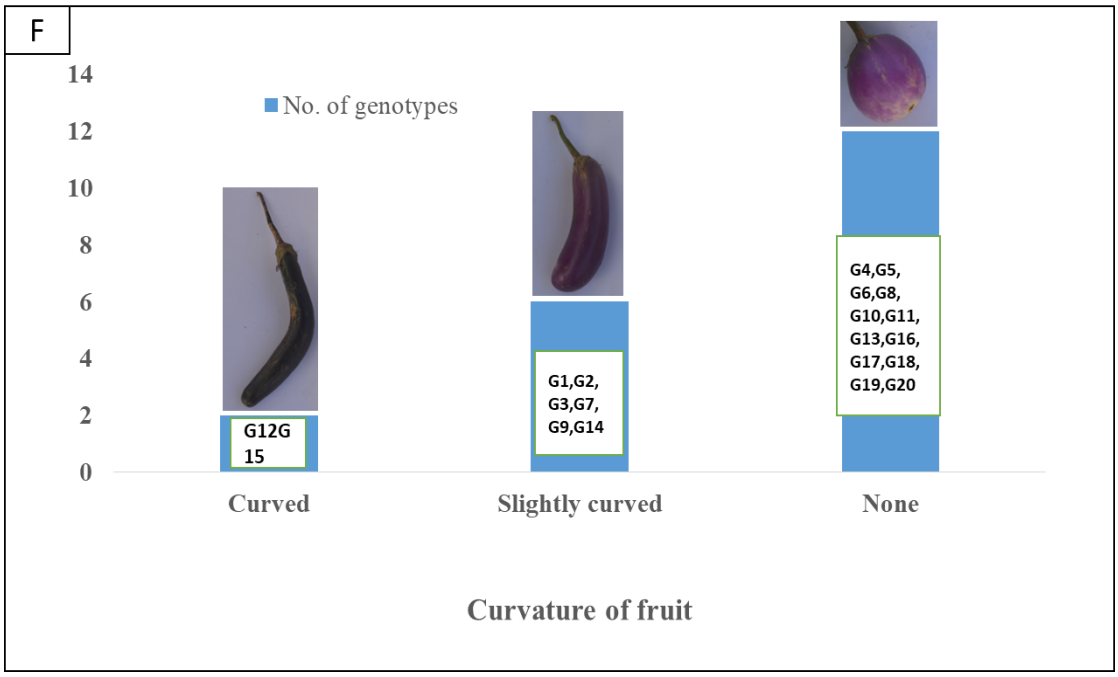


Plate 3b. Graphical representation of frequency distribution (E-Color of fruit and F-Curvature of fruit)

4.1.1 Growth habit

Plant architecture is an important character to the breeder for improvement of plant ideotype under given environment. The genotypes studied have been grouped into three distinct characteristics. The genotypes G1, G2, G3, G4, G5, G6, G7, G9, G12 and G13 were spreading; genotypes G8, G10, G11 and G16 were erect in plant growth habit and rest of the genotypes G14, G15, G17, G18, G19 and G20 were semi erect in growth habit in Table 3. Generally, farmers are looking for that types of materials that are suitable for intercultural operation in the field. In this study, it was found that spreading type genotypes were less infested by BSFB than erect type. Plate 3a (A) shows that among 20 genotypes of brinjal spreading type is maximum whereas the erect type of plant growth is minimum in number. Similar trend was also noted by Quamruzzaman *et al.* (2020).

4.1.2 Hairiness

Hairiness is an important character of the brinjal plant. This character is related to its resistance against pests. The hairs had significant role towards non-preference for fruit infestation by brinjal shoot and fruit borer, which is in conformity with the findings of Javed *et al.* (2017) and Kassi *et al.* (2018). The more densely hairy plant is more resistant to pest. All the genotypes under study were characterized by hairiness in Table 3. Hairiness was observed mostly at the leaf and stem.

4.1.3 Spiny character

Various types of brinjal genotypes are characterized by their spinyness. According to the findings of Javed *et al*. (2017) and Kassi *et al*. (2018) having spine is an important character that is related to insect resistance. Different genotypes were classified as having a spine in their flower, stem, or leaves. The genotype G5, G8, G12, G14, G16, G17 and G18 had spine in stem, the genotypes G1, G2, G3, G4, G6, G7, G9, G10, G11, G13, G14, G15 and G18 had spine in flower and the genotypes G5, G6, G13, G16 and G18 had spine in leaves. Genotype 5 had spines in stem and leaf. The genotypes G6, G13, and G18 had spines in flower and leaf. Genotype G14 had spines in stem and flower in Plate 3a (B).

4.1.4 Color of flower

According to Agrawal (1980), 48% cross-pollination was observed in the brinjal plants. Flower color is an important factor for the brinjal plants. Different genotypes were classified as having flower colors purple or white. The genotypes G12, G16 and G18 produced white color flowers whereas the genotypes G1, G2, G3, G4, G5, G6, G7, G8,

G9, G10, G11, G13, G14, G15, G17, G19 and G20 produced purple color flower in Plate 3a (C). Similar trend was also noted by Kumar *et al.* (2011). Genotypes producing white and purple color fruits were less infested by shoot and fruit borer.

4.1.5 Fruit shape

According to Das *et al.* (2017) *Solanum melongena* has three botanical varieties namely, var. *esculentum* (round to oval fruit shape), var. *serpentinum* (long and slender fruit shape), and var. *depressum* (dwarf and oblong fruit shape). The fruit of different genotypes showed differences in shape. It is an important consumer preference trait in brinjal marketing. Various types of brinjal were found according to their shape. The genotypes G1, G3, G7, G9, G12, G14, G15, G17 and G19 produced elongated fruits, genotypes G2, G4, G5, G6, G8, G11 and G20 produced ovate fruits and the rest of the genotypes produced more or less round fruits in Plate 3a (D).

4.1.6 Color of fruit

Fruit color is an important consumer preference trait in brinjal marketing. Generally, green and violet color fruits are common in the market. However, a lot of variations in fruit color were found in the present study which is similar to the findings of Das *et al.* (2017) and that was classified into distinct groups: violet, purple, white, green and whitish green. The violet genotypes were G1, G9, G11, G12, G15, G17, G19 and G20; purple genotypes were G7 and G13; white genotype were G5 and G8; green genotypes were G6, G10 and G14, and the rest of the genotypes were whitish green in Plate 3b (E). This variation offered a good scope for breeding consumer preference attributes.

4.1.7 Fruit curvature

Fruit curvature is an important trait of brinjal morphology. Consumer preference also depends on curvature of the fruit. Variations in fruit curvature were found in the present study and that could be classified into distinct groups: curved, slightly curved, and none. The genotypes G12 and G15 produced curved fruits, genotypes G1, G2, G3, G7, G9 and G14 produced slightly curved fruits and the rest of the genotypes produced fruits without curvature in Plate 3b (F). Similar trend was also noted by Parida *et al.* (2020).

4.2 Estimation of genetic variability, heritability and genetic advance

Analysis of variance showed that the brinjal genotypes varied significantly (5% level of probability) with each other in Table 4. Range, mean and coefficient of variation of 15 characters of brinjal genotypes namely days to first flowering, days to 50% flowering, first fruit harvest, last fruit harvest, plant height, no. of primary branches/plant, no. of secondary branches/plant, fruit weight, fruit length, fruit diameter, pedicel length, number of fruits/plant, leaf area index, yield/plant and percent of BSFB infestation have been presented in Table 5.

The genetic parameters revealed that PCV and GCV were high for fruit weight (33.94%, 32.80%) followed by number of fruits/plant (33.80%, 31.38%), yield/plant (31.60%, 28.53%), fruit length (25.65%, 24.58%) and pedicel length (23.66%, 23.10%) offering scope for further improvement by selection. These findings are in close agreement with the results obtained by Sherly and Shanthi (2009). The PCV was higher than corresponding GCV for all the traits which might be due to the interaction of genotypes with the environment to some degree or due to higher influence of environmental factors in the expression of these characters. Wide differences in PCV and GCV were observed for number of primary branches/plant, number of secondary branches/plant and percent of BSFB infestation depicting their susceptibility to environmental fluctuation. Narrow difference between PCV and GCV for rest of the characters implied their relative resistance to environmental variation, suggesting that genetic factors were predominantly responsible for expression of these attributes and selection could be made effectively on the basis of phenotypic performance. This result was in harmony with that of Mohanty and Prusti (2002).

The estimates of heritability in broad sense ranged from 96.88 % to 26.58% for all the traits. High values of broad sense heritability, found in all the traits except primary and secondary branches/plant, reflect that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable. Similar reports were given by Baswana *et al*. (2002) in brinjal. High estimates of genetic advance over mean were obtained for percent of BSFB infestation (109.21) and fruit diameter (87.56) while it was moderate for fruit weight, number of fruits/plant, yield/plant, number of secondary branches/plant, pedicel length, leaf area index, plant height and days to first flowering which illustrated that they could be improved to a large extent.

Table 4. Analysis of variance of 15 characters of 20 genotypes of brinjal

Source of Variation	df	Mean sum of square													
		DFF	**50%DF**	**DFFH**	**DLFH**	**PH**	**NPBPP**	**NSBPP**	**FW**	**FL**	**FD**	**PL**	**NFPP**	**LAI**	**%BI**	**YPP**
Replication	2	10.760	13.601	1.775	11.458	10.980	0.566	35.623	585.366	0.248	4.575	0.028	6.686	7.800	9.551	0.379
Genotypes	19	272.53**	131.30**	135.93**	202.24**	381.61**	6.04**	34.92**	16,971.86**	69.67**	196.02**	6.41**	17.14**	577.57**	100.28**	0.65**
Error	38	4.114	3.364	4.589	10.553	12.978	2.897	8.848	393.194	1.992	2.086	0.104	0.867	10.081	9.559	0.046

df = Degree of freedom, ** = 5% level of significance

DFF: Days to 1st flowering | 50%DF: Days to 50% flowering | DFFH: Days to 1st fruit harvest | DLFH: Days to last fruit harvest | PH: Plant height (cm)

NPBPP: No. of primary branches/plant | NSBPP: No. of secondary branches/plant | FW: Fruit weight (g) | FL: Fruit length (cm) | FD: Fruit diameter (cm)

PL: Pedicel length (cm) | NFPP: No. of fruits/plant | LAI: Leaf area index (cm^2) | %BI: Percent of BSFB infestation | YPP: Yield/plant (kg)

Table 5. Mean performance, range, standard error and coefficient of variation in respect of 15 characters of 20 brinjal genotypes

Genotypes	DFF	50%DF	DFFH	DLFH	PH	NPBPP	NSBPP	FW	FL	FD	PL	NFPP	LAI	%BI	YPP
G1	62.67fg	87.00 cd	91.56jkl	157.78abc	53.73i	12.33abcdef	27.11abc	205.33ef	24.23b	19.17f	6.20fgh	6.67efg	107.33a	15.10bc	1.37defghi
G2	60.55gh	80.89hi	91.44jkl	145.45fghi	65.33fg	10.33ef	24.11bcde	252.33cd	15.83hi	26.10cd	5.70hi	4.11ij	79.00ghij	8.18efg	1.07i
G3	74.00de	91.22b	97.45fgh	144.33ghij	75.17cd	11.67bcdef	20.45efg	234.00de	24.17b	21.53ef	5.83ghi	6.22fg	66.67l	16.36b	1.43defgh
G4	60.67gh	84.22defg	98.45efg	153.11cde	86.20b	13.33abcd	26.11abcd	295.33b	21.63cd	25.50cd	8.17b	5.56ghi	91.67c	4.23gh	1.67bcde
G5	64.11f	80.67i	94.44hij	135.11l	71.83de	11.00cdef	27.55abc	198.67fg	14.63ij	23.87de	6.80cde	9.78bc	55.00m	7.68fg	1.93b
G6	81.11ab	95.22a	107.11ab	155.00bcd	92.13ab	14.89a	26.00abcd	372.00a	17.53fgh	33.00a	6.57def	3.00j	98.33b	0.00h	1.10hi
G7	71.89e	94.67a	102.00cd	160.33ab	75.27cd	14.00ab	30.22a	192.33fgh	21.43de	16.37g	7.13c	7.78de	87.00cde	7.21fg	1.53cdefg
G8	60.00ghi	80.89hi	91.78jk	140.22ijkl	67.07efg	12.11abcdef	22.89cdef	195.67fg	19.20ef	19.47f	6.97cd	5.67gh	62.33l	13.62bcd	1.20ghi
G9	62.00fgh	83.78efgh	96.89ghi	139.89jkl	62.47gh	11.89bcdef	25.89abcd	193.33fgh	23.53bcd	12.70h	6.33efg	8.56cd	78.00gijk	12.94bcde	1.67bcde
G10	58.78hij	81.22ghi	90.67kl	138.66kl	63.70gh	13.44abc	28.33ab	342.00a	15.33hi	29.90b	5.60i	4.55hi	80.67fghi	17.27ab	1.57cdef
G11	81.89a	97.00a	108.22a	162.00a	87.63b	10.56def	17.22g	284.67bc	16.03ghi	26.33c	3.80m	6.44efg	88.33cd	22.31a	1.83bc
G12	56.11j	75.89j	84.77m	136.11l	79.27c	12.89abcde	28.11ab	203.33ef	21.27de	16.23g	6.63cdef	8.78cd	85.33def	10.61cdef	1.80bc
G13	56.67ij	84.33def	90.33kl	142.22hijk	58.43hi	12.22abcdef	21.67defg	161.33hi	12.67jk	22.50e	5.43ij	7.78de	73.33k	9.95def	1.30fghi
G14	79.22ab	94.47a	104.67bc	155.33bcd	95.03a	10.67cdef	25.45abcd	363.33a	23.87bc	26.47c	4.47l	4.56hi	109.67a	10.52cdef	1.70bcd
G15	59.00hij	79.78i	88.11lm	141.55ijk	67.87efg	13.22abcd	25.66abcd	126.00jk	31.10a	11.87hi	10.67a	10.44ab	74.33jk	4.25gh	1.33efghi
G16	75.33cd	95.00a	101.33cde	153.22cde	67.47efg	10.22ef	21.22defg	166.80ghi	14.67ij	7.80jk	7.07cd	9.33bc	82.67efgh	3.75gh	1.60bcdef
G17	63.33fg	86.44cde	93.44ijk	139.89jkl	66.43efg	10.00f	18.44fg	282.83bc	18.20fg	7.97jk	4.63kl	11.44a	76.67ijk	5.83fg	3.17a
G18	79.45ab	96.56a	106.67ab	148.22efg	64.80fg	10.22ef	22.00defg	199.47fg	11.13k	8.00jk	5.00jk	9.67bc	97.33b	3.45gh	1.93b
G19	81.67a	89.33bc	100.44def	150.78def	62.27gh	11.33bcdef	25.67abcd	111.80k	18.60f	7.50k	6.30efg	10.44ab	83.67defg	3.20gh	1.17hi
G20	78.22bc	82.33fghi	98.67defg	147.11fgh	70.33def	10.78cdef	25.11bcde	152.60ij	21.33de	10.10ij	6.27fg	7.67def	90.67c	4.37gh	1.13hi
Mean	**68.33**	**87.04**	**96.92**	**147.32**	**71.62**	**11.86**	**24.46**	**226.66**	**19.32**	**18.62**	**6.28**	**7.42**	**83.40**	**9.04**	**1.58**
Maximum	**81.89**	**97.00**	**108.22**	**162.00**	**95.03**	**14.89**	**30.22**	**372.00**	**31.10**	**33.00**	**10.67**	**11.44**	**109.67**	**22.31**	**3.17**
Minimum	**56.11**	**75.89**	**84.77**	**135.11**	**53.73**	**10.00**	**17.22**	**111.80**	**11.13**	**7.50**	**3.80**	**3.00**	**55.00**	**0.00**	**1.07**
SE	**1.66**	**1.50**	**1.75**	**2.65**	**2.94**	**1.39**	**2.43**	**16.19**	**1.15**	**1.18**	**0.26**	**0.76**	**2.59**	**2.52**	**0.18**
CV (%)	**13.95**	**7.70**	**7.06**	**5.77**	**16.02**	**16.53**	**17.42**	**33.42**	**25.21**	**43.18**	**23.25**	**33.83**	**16.64**	**68.92**	**31.65**

SE- Standard error, CV- Coefficient of variation

DFF: Days to 1st flowering	50%DF: Days to 50% flowering	DFFH: Days to 1st fruit harvest	DLFH: Days to last fruit harvest	PH: Plant height (cm)	NPBPP: No. of primary branches/plant	NSBPP: No. of secondary branches/plant	FW: Fruit weight (g)	FL: Fruit length (cm)	FD: Fruit diameter (cm)	PL: Pedicel length (cm)	NFPP: No. of fruits/plant	LAI: Leaf area index (cm^2)	%BI: Percent of BSFB infestation	YPP: Yield/plant (kg)

Table 6. Estimation of genotypic and phenotypic coefficient of variations, genetic advance, genetic advance percentage over mean and heritability percentage for 15 characters of brinjal

Characters	GCV	PCV	GA	GAPM	HP
Days to 1st flowering	13.84	14.16	19.05	27.88	95.60
Days to 50% flowering	07.50	07.79	12.95	14.88	92.69
Days to 1st fruit harvest	06.83	07.18	12.97	13.38	90.51
Days to last fruit harvest	05.43	05.86	15.26	10.36	85.83
Plant height (cm)	15.48	16.27	21.72	30.32	90.45
No. of primary branches/plant	08.64	16.75	01.09	09.17	26.58
No. of secondary branches/plant	12.05	17.12	04.28	17.48	49.55
Fruit weight (g)	32.80	33.94	147.96	65.28	93.36
Fruit length (cm)	24.58	25.65	09.38	48.54	91.89
Fruit diameter (cm)	43.19	43.88	16.30	87.56	96.88
Pedicel length (cm)	23.10	23.66	02.92	46.45	95.29
No. of fruits/plant	31.38	33.80	04.46	60.03	86.23
Leaf area index (cm^2)	16.49	16.93	27.61	33.10	94.94
Percent of BSFB infestation	60.82	69.77	09.88	109.21	75.98
Yield/plant (kg)	28.53	31.60	0.84	53.08	81.60

GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, GA- Genetic advance, GAPM- Genetic advance percentage over mean, HP- Heritability percentage

High estimate of heritability coupled with moderate to high GCV, PCV and genetic advance as observed in plant height, fruit weight, fruit length, fruit diameter, pedicel length, number of fruits/plant, percent of BSFB infestation and yield/plant might be attributed to additive gene action conditioning their expression and genetic improvement can be achieved in yield and its important components by simple method of selection.

4.2.1 Days to 1st flowering

Sambandam (1960) studied the number of days required for flowering in different brinjal genotypes and concluded that the variation was due to the varietal characteristics. A wide range of variability was observed in respect of flowering time among the genotypes. Genotype G12 took the shortest time (56.11 days) which is nearly identical to genotype G10, G13, G15 for flowering from seedling while genotype G11 took the longest time (81.89 days) to flower which is identical to genotypes G6 and G19 in Table 5.

4.2.2 Days to 50% flowering

A wide range of variability was observed in respect of 50% flowering time among the genotypes. Genotype G12 took the shortest time (75.89 days) for 50% flowering from seedling while genotype G11 took the longest time (97 days) to 50% flowering which is identical to genotype G18 in Table 5. Genotypes G19 and G20 took a very short time to 50% flowering from their first flowering whereas genotypes G1 and G13 took a long time to reach their 50% flowering from the first flowering. Sambandam (1960) studied the number of days required for flowering in different brinjal genotypes and concluded that the variation was due to the varietal characteristics.

4.2.3 Days to 1st fruit harvest

Genotype G12 took the shortest time (84.77 days) for the first fruit harvest while genotype G11 took the longest time (108.22 days) in Table 5. Genotypes G6 and G18 are nearly identical to genotype G11. These findings are in close agreement with the results obtained by Sherly and Shanthi (2009).

4.2.4 Days to last fruit harvest

Genotype G5 took the shortest time (135.11 days) for the last fruit harvest while genotype G11 took the longest time (162 days) in Table 5. Genotypes G6 and G18 are nearly identical to genotype G11. Genotypes G5 and G9 took a very short time to last fruit harvest from their first harvest whereas genotypes G1 and G7 took a long time to reach their last fruit harvest from the 1st fruit harvest. These findings are in close

agreement with the results obtained by Sherly and Shanthi (2009).

4.2.5 Fruit length (cm)

The fruits of genotype G15 (31.10 cm) were found to be the longest followed by genotype G1 (24.23 cm) and G3 (24.17 cm) while genotype G18 produced the smallest fruit (11.13 cm) in Table 5. Genotype G15 produced the longest fruit while the smallest fruit was produced by genotype G18. The coefficient of variation of this trait was 25.21 %. This result was in harmony with that of Mohanty and Prusti (2002).

4.2.6 Pedicel length (cm)

The pedicel length of the genotype G15 (10.67 cm) was found to be the longest followed by the genotypes G4 (8.17 cm) and G7 (7.13 cm). Genotype G11 produced the shortest pedicel length (3.80 cm) in Table 5. Genotype G15 produced the longest pedicel while the smallest was produced by genotype G11. The coefficient of variation of this trait was 23.25 %. This result was in harmony with that of Mohanty and Prusti (2002).

Genotype G15 produced the largest fruit length as well as pedicel. Genotype G14 produced long fruit compared with pedicel. The difference between fruit length and pedicel is maximum for genotype G14 followed by genotypes G3, G1, and G9.

4.2.7 Fruit diameter (cm)

The average diameter of the fruit showed marked differences among themselves. In respect of diameter, the experimental data showed that the fruit of genotype G6 was widest (33.00 cm) followed by the genotypes G10 (29.90 cm), G14 (26.47 cm), G11 (26.33 cm). The lowest diameter was observed in genotype G19 (7.50 cm) which was more or less identical with genotype G16 (7.80 cm) and genotype G17 (7.97) in Table 5. The coefficient of variation of this trait was 43.18%. It was found in this study that fruits with less diameter showed little chance of BSFB infestation.

Sarma *et al*. (2000) evaluated thirty-four genotypes of brinjal of diverse origin and reported that fruit diameter and average fruit weight were the main characters affecting grouping of genotypes.

4.2.8 Number of primary branches/plant

It was observed that the maximum numbers of primary branches were produced by genotype G6 (14.89) which is followed by genotypes G7 (14.00), G10 (13.44), G4 (13.33), and G15 (13.22). Genotype G10 (10.00) produced the least number of primary branches/plant which was more or less identical to genotype G16 (10.22), G18 (10.22), and genotype G2 (10.33) in Table 5. The coefficient of variation of this trait was 16.53%. Similar trend was also noted by Quamruzzaman et al. (2020).

4.2.9 Number of secondary branches/plant

The number of secondary branches is also an important morphological character. This is related to yield and the number of fruit per plant. The number of secondary branches of each plant was recorded and their average mean was calculated. It was observed that the maximum numbers of secondary branches were produced by genotype G7 (30.22) which is followed by genotypes G10 (28.33) and G12 (28.11). Genotype G11 (17.22) produced the least number of secondary branches which is followed by the genotypes G17 (18.44) and G3 (20.45) in Table 5. The coefficient of variation of this trait was 17.42%. Similar trend was also noted by Quamruzzaman et al. (2020).

Genotype G6 produced the largest number of primary branches whereas genotype G7 produced the largest number of secondary branches. Genotypes G4, G6, G7, G10, G12, G15, and G19 produced a larger number of primary and secondary branches compared with other genotypes.

4.2.10 Number of fruits/plant

The number of fruits was recorded maximum in genotype G17 (11.44). Genotypes G15 and G19 produced the second-highest number of fruits/plant (10.44). The least number of fruits (3.00) was produced in genotype G6.

Sambandam (1960) examined the number of fruits/plant of different genotypes of brinjal and recorded that the number of fruits/plant varied due to the difference in their yield potential.

In brinjal, it has been also reported that there is a strong association between the number of fruits/plant and yield/plant (Srivastava and Sachan, 1973 and Hiremath and Gururaja, 1974). Thus, the number of fruits/plant is considered an important character to select the best variety of brinjal for effective improvement of this crop.

4.2.11 Leaf area index (cm^2)

Leaf area index of randomly selected leaves was recorded using 1 cm^2 graph paper. Leaves are an important source of carbohydrates produced during photosynthesis.

Maximum biomass or dry matter of a plant is produced by leaves. Leaf area index is a reliable parameter for plant growth. Genotype G14 had the largest leaf area (109.67 cm^2) which is followed by genotype G1 (107.33 cm^2) whereas genotype G5 had the lowest leaf area (55.00 cm^2) which is followed by genotype G8 (62.33 cm^2) in Table 5. The coefficient of variation of this trait was 16.64%. Nikitha *et al.* (2020) showed in their experiment that plant spread is a reliable parameter for plant growth.

4.2.12 Plant height (cm)

The plant height of different genotypes exhibited wide variations. The plant height was maximum in genotype G14 (95.03 cm), which was followed by genotypes G6 (92.13 cm) and G11 (87.63 cm). Genotype G1 (53.73 cm) produced the shortest plant which was followed by the genotypes G19 (62.27 cm) and G9 (62.47 cm). The remaining genotypes were intermediate in this regard in Table 5. The coefficient of variation of this trait was 16.02%.

Mandal and Dana (1992) examined 20 genotypes of brinjal for the yield contributing characters and found that number of fruits/plant, number of secondary branches/plant and plant height are important traits for the choice of superior genotypes.

4.2.13 Fruit weight (g)

Twenty different brinjal genotypes under study showed variations in their fruit weight. Genotype G6 was found to have the highest fruit weight (372.00 g) which was statistically superior to the rest of the genotypes while genotype G14 produced the second-highest fruit weight (363.33 g) in Table 5 which was also statistically significant from the rest of the genotypes. The least individual fruit weight was produced by G19 (111.8 g) which is followed by the genotypes G15 (126.00 g) and G20 (152.60 g) while the other genotypes took intermediate positions. The coefficient of variation of this trait was 33.42%. Nikitha *et al.* (2020) showed in their experiment that fruit weight is an important trait and reliable parameter for the choice of superior genotypes.

4.2.14 Percent of BSFB infestation

Brinjal is mostly affected by shoot and fruit borer. It caused great harm to yield and reduced production of brinjal. So resistance is an efficient character of the brinjal plant. Their rates of attack against different genotypes were significantly different. The attack of insect of brinjal depends on its morphological i.e. spinyness, hairiness, the hardiness of fruit coat; physiological and genetic characteristics of the plant. The different genotypes are genetically different from each other. From the study, it was revealed that genotype G11 (22.31%) was highly affected and genotype G6 (0.0%) was the least

affected which mentioned that genotype G6 was the most tolerant and superior to the rest of the variety in Table 5. The coefficient of variation of this trait was 68.92%.

Table 7. The rate of BSFB infestation in percentage against different brinjal genotypes

Infestation (%)	Genotypes	Grading for resistance
1-15	G1, G2, G4, G5, G6, G7, G8, G9, G12, G13, G14, G15, G16, G17, G18, G19, G20	Tolerant
16-25	G3, G10, G11	Moderately Tolerant

The rate of insect infestation against different genotypes in Table 7 was calculated in percentage and graded using the grades mentioned by Subbaratnam and Butani in 1981 for shoot and fruit borer.

4.2.15 Yield/plant (kg)

Twenty different brinjal genotypes under study showed wide variation in their fruit yield/plant. Genotype G17 was found to give the highest yield per plant. This genotype produced fruits 3.17 kg/plant on average while the lowest yield was recorded in genotype G2 (1.07 kg/plant) in Table 5 which is nearly identical to genotypes G6 (1.10 kg/plant), G20 (1.13 kg/plant) and G19 (1.17 kg/plant). The coefficient of variation of this trait was 31.65%.

Ahmad (1968) and Siddique (1968) found identical results while carrying out experiments with different genotypes. Ahmad (1968) reported that the variety Nayankazal tended to out yield all other genotypes including Islampuri and D.R.C. while Siddique (1968) obtained superiority of Singnath over Islampuri.

Differences in yield might be due to environmental factors and for the use of different germplasms. Experimental data showed that the number of fruits per plant was influenced by the individual fruit weight. Genotype G17 produced the maximum number of fruits (11.44) per plant in Table 5 which is expected in successful breeding programs. The yield was influenced by both the number of fruits/plant and individual fruit weight. Sambandam (1960) and Siddique (1968) also obtained similar results.

4.3 Correlation coefficient analysis

Determination of correlation coefficient was provided the information how yield depends on different yield contributing characters. Yield is a complex product being influenced by several inter-dependable quantitative characters. Thus, selection for yield may not be effective unless the other yield components influence it directly or indirectly are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors. The correlation co efficient and the parameter correlated were shown in Table 8 and 9. Simple correlation was divided into phenotypic (directly observed) and genotypic (inherent association between character). At genotypic and phenotypic level, the results on characters association indicated positive and significant association of fruit yield/plant with number of fruits/plant whereas number of primary branches/plant and pedicel length showed negatively significant association shown in Table 8 and 9. It is also observed that characters association indicated positive and non-significant association of fruit yield/plant with days to 50% flowering, plant height, fruit weight and percent BSFB infestation whereas days to 1st flowering, last fruit harvest, fruit length and leaf area index showed negative non-significant association. On the basis of above results, it is found that the genotypic and phenotypic correlation of number of fruits/plant and fruit weight with the fruit yield/plant were high. Hence, these characters are to be considered as the prior criteria for selection in order to obtain the high yielding varieties of brinjal. The results on characters association indicated positive association of fruit yield/plant with days to 50% flowering (0.108P, 0.076G), plant height (0.048P, 0.063G), fruit weight (0.243P, 0.223G), number of fruits/plant (0.517P, 0.471G) and percent of BSFB infestation (0.006P, 0.067G) which indicates adequate interrelationship between fruit yield/plant and it's components creating ample scope in the improvement of yield by improving these characters as they are highly correlated. These results were in accordance with the findings of Ahmed *et al.* (2013), Shende *et al.* (2014), Ravali *et al.* (2017), and Tiwari *et al.* (2017).

Table 8. Genotypic correlation coefficient among different pairs of yield and yield contributing characters for 20 genotypes of brinjal

	DFF	50%DF	DFFH	DLFH	PH	NPBPP	NSBPP	FW	FL	FD	PL	NFPP	LAI	%BI
DFF														
50%DF	0.838**													
DFFH	0.921**	0.908**												
DLFH	0.661**	0.785**	0.738**											
PH	0.422**	0.376**	0.542**	0.400**										
NPBPP	-0.375**	-0.245^{NS}	-0.189^{NS}	0.032^{NS}	0.271*									
NSBPP	-0.308*	-0.430**	-0.295*	-0.109^{NS}	-0.030^{NS}	0.569**								
FW	0.122^{NS}	0.266*	0.313*	0.224^{NS}	0.644**	0.255*	-0.053^{NS}							
FL	-0.160^{NS}	-0.224^{NS}	-0.250^{NS}	0.053^{NS}	0.138^{NS}	0.422**	0.326*	-0.131^{NS}						
FD	-0.107^{NS}	-0.007^{NS}	0.054^{NS}	0.133^{NS}	0.509**	0.567**	0.191^{NS}	0.732**	-0.113^{NS}					
PL	-0.365**	-0.414**	-0.380**	-0.179^{NS}	-0.091^{NS}	0.695**	0.540**	-0.429**	0.550**	-0.182^{NS}				
NFPP	-0.054^{NS}	-0.128^{NS}	-0.204^{NS}	-0.333**	-0.455**	-0.496**	-0.171^{NS}	-0.716**	0.032^{NS}	-0.868**	0.207^{NS}			
LAI	0.443**	0.493**	0.472**	0.718**	0.324*	0.123^{NS}	0.186^{NS}	0.378**	0.124^{NS}	0.078^{NS}	-0.251^{NS}	-0.316*		
%BI	-0.211^{NS}	-0.079^{NS}	-0.179^{NS}	-0.023^{NS}	-0.046^{NS}	-0.194^{NS}	-0.286*	0.210^{NS}	0.044^{NS}	0.380**	-0.448**	-0.295*	-0.146^{NS}	
YPP	-0.093^{NS}	0.076^{NS}	-0.003^{NS}	-0.222^{NS}	0.063^{NS}	-0.516**	-0.434**	0.223^{NS}	-0.160^{NS}	-0.286*	-0.345**	0.471**	-0.066^{NS}	0.067^{NS}

*(5% level of significance) ** (1% level of significance) NS (Non- significant)

DFF: Days to 1st flowering | 50%DF: Days to 50% flowering | DFFH: Days to 1st fruit harvest | DLFH: Days to last fruit harvest | PH: Plant height (cm)

NPBPP: No. of primary branches/plant | NSBPP: No. of secondary branches/plant | FW: Fruit weight (g) | FL: Fruit length (cm) | FD: Fruit diameter (cm)

PL: Pedicel length (cm) | NFPP: No. of fruits/plant | LAI: Leaf area index (cm^2) | %BI: Percent of BSFB infestation | YPP: Yield/plant (kg)

Table 9. Phenotypic correlation coefficient among different pairs of yield and yield contributing characters for 20 genotypes of brinjal

	DFF	50%DF	DFFH	DLFH	PH	NPBPP	NSBPP	FW	FL	FD	PL	NFPP	LAI	%BI
DFF														
50%DF	0.779**													
DFFH	0.848**	0.863**												
DLFH	0.596**	0.746**	0.667**											
PH	0.412**	0.334**	0.465**	0.350**										
NPBPP	-0.188^{NS}	-0.081^{NS}	-0.165^{NS}	0.098^{NS}	0.150^{NS}									
NSBPP	-0.205^{NS}	-0.265*	-0.221^{NS}	-0.026^{NS}	0.034^{NS}	0.667**								
FW	0.120^{NS}	0.258*	0.297*	0.200^{NS}	0.600**	0.130^{NS}	-0.009^{NS}							
FL	-0.138^{NS}	-0.231^{NS}	-0.243^{NS}	0.035^{NS}	0.147^{NS}	0.270*	0.281*	-0.085^{NS}						
FD	-0.108^{NS}	0.002^{NS}	0.061^{NS}	0.141^{NS}	0.462**	0.311*	0.143^{NS}	0.721**	-0.092^{NS}					
PL	-0.359**	-0.397**	-0.359**	-0.169^{NS}	-0.097^{NS}	0.390**	0.371**	-0.411**	0.517**	-0.168^{NS}				
NFPP	-0.066^{NS}	-0.078^{NS}	-0.135^{NS}	-0.274*	-0.421**	-0.262*	-0.131^{NS}	-0.648**	-0.001^{NS}	-0.797**	0.183^{NS}			
LAI	0.415**	0.458**	0.439**	0.649**	0.309*	0.058^{NS}	0.132^{NS}	0.350**	0.117^{NS}	0.067^{NS}	-0.234^{NS}	-0.297*		
%BI	-0.166^{NS}	-0.036^{NS}	-0.140^{NS}	-0.002^{NS}	-0.050^{NS}	0.025^{NS}	-0.106^{NS}	0.200^{NS}	0.085^{NS}	0.350**	-0.384**	-0.284*	-0.111^{NS}	
YPP	-0.081^{NS}	0.108^{NS}	0.049^{NS}	-0.158^{NS}	0.048^{NS}	-0.267*	-0.252^{NS}	0.243^{NS}	-0.137^{NS}	-0.238^{NS}	-0.323*	0.517**	-0.080^{NS}	0.006^{NS}

*(5% level of significance) ** (1% level of significance) NS (Non- significant)

DFF: Days to 1st flowering | 50%DF: Days to 50% flowering | DFFH: Days to 1st fruit harvest | DLFH: Days to last fruit harvest | PH: Plant height (cm)

NPBPP: No. of primary branches/plant | NSBPP: No. of secondary branches/plant | FW: Fruit weight (g) | FL: Fruit length (cm) | FD: Fruit diameter (cm)

PL: Pedicel length (cm) | NFPP: No. of fruits/plant | LAI: Leaf area index (cm^2) | %BI: Percent of BSFB infestation | YPP: Yield/plant (kg)

4.3.1 Days to 1st flowering

Days to first flowering showed significant and positive correlation with days to 50% flowering (0.779P, 0.838G), days to first fruit harvest (0.848P, 0.921G), days to last fruit harvest (0.596P, 0.661G), plant height (0.412P, 0.422G) and leaf area index (0.415P, 0.443G). It showed negatively significant correlation with number of primary branches/plant (-0.375G), number of secondary branches/plant (-0.308G) and pedicel length (-0.365G, -0.359P). It showed positively non-significant correlation with fruit weight (0.122G, 0.120P). It showed negatively non-significant correlation with fruit length (-0.160G, -0.138P), fruit diameter (-0.107G, -0.108P), number of fruits/plant (-0.054G, -0.066P), percent of BSFB infestation (-0.093G, -0.166P) and yield/plant (-0.093G, -0.081P).

Alam *et al.* (2021) found that days to first flowering had negative correlation with plant height and non-significant correlation with plant height and number of branches per plant.

4.3.2 Days to 50% flowering

Days to 50% flowering showed significant and positive correlation with days to first fruit harvest (0.863P, 0.908G), days to last fruit harvest (0.746P, 0.785G), plant height (0.334P, 0.542G), fruit weight (0.258P, 0.266G) and leaf area index (0.458P, 0.493G). It showed negatively significant correlation with number of secondary branches/plant (-0.430G, -0.265P) and pedicel length (-0.414G, -0.397P). It showed positively non-significant correlation with yield/plant (0.076G, 0.108P). It showed negatively non-significant correlation with number of primary branches/plant (-0.245G, -0.081P), fruit length (-0.224G, -0.231P), fruit diameter (-0.007G), number of fruits/plant (-0.128G, -0.078P), and percent of BSFB infestation (-0.079G, -0.036P).

Gurve *et al.* (2020) showed that days to 50% flowering had negative and significant correlation with number of branches per plant where as negative and non-significant correlation with plant spread and plant height.

4.3.3 Days to 1st fruit harvest

Days to first fruit harvest showed significant and positive correlation with days to last fruit harvest (0.667P, 0.738G), plant height (0.465P, 0.542G), fruit weight (0.297P, 0.313G) and leaf area index (0.439P, 0.472G). It showed negatively significant correlation with number of secondary branches/plant (-0.295G) and pedicel length (-0.380G, -0.359P). It showed positively non-significant correlation with fruits diameter (0.054G, 0.061P). It showed negatively non-significant correlation with number of

primary branches/plant (-0.189G, -0.165P), fruit length (-0.259G, -0.243P), number of fruits/plant (-0.204G, -0.135P), percent of BSFB infestation (-0.179G, -0.140P) and yield/plant (-0.003G). Similar results were found in the study of Nikitha *et al.* (2020).

4.3.4 Days to last fruit harvest

Days to last fruit harvest showed significant and positive correlation with plant height (0.350P, 0.400G) and leaf area index (0.649P, 0.718G). It showed negatively significant correlation with number of fruits/plant (-0.333G, -0.274P). It showed positively non-significant correlation with number of primary branches/plant (0.032G, 0.098P), fruit weight (0.224G, 0.200P), fruit length (0.053G, 0.035P) and fruit diameter (0.133G, 0.141P). It showed negatively non-significant correlation with number of secondary branches/plant (-0.109G, -0.026P), pedicel length (-0.179G, -0.169P), percent of BSFB infestation (-0.023G, -0.002P) and yield/plant (-0.222G, -0.158P). Similar results were found in the study of Nikitha *et al.* (2020).

4.3.5 Fruit length (cm)

Fruit length showed significant and positive correlation with pedicel length (0.517P, 0.550G). It showed positively non-significant correlation with number of fruits/plant (0.032G), leaf area index (0.124G, 0117P) and percent of BSFB infestation (0.044G, 0.085P). It showed negatively non-significant correlation with fruit diameter (-0.113G, -0.092P) and yield/plant (-0.160G, -0.137P).

Kustagi *et al.* (2019) showed that fruit length had positive and non-significant correlation with number of fruits/plant.

4.3.6 Pedicel length (cm)

It showed negatively significant correlation with percent of BSFB infestation (-0.384P, -0.448G) and yield/plant (-0.323P, -0.345G). It showed positively non-significant correlation with number of fruits/plant (0.207G, 0.183P). It showed negatively non-significant correlation with leaf area index (-0.251G, -0.234P). Similar trends were found in the study of Nikitha *et al.* (2020).

4.3.7 Fruit diameter (cm)

Fruit diameter showed significant and positive correlation with percent of BSFB infestation (0.350P, 0.380G). It showed negatively significant correlation with number of fruits/plant (-0.868G, -0.797P) and yield/plant (-0.286G). It showed positively non-significant correlation with leaf area index (0.078G, 0.067P). It showed negatively non-significant correlation with pedicel length (-0.182G, -0.168P). Gurve *et al.* (2020) showed that fruit diameter had negative and significant correlation with number of

branches per plant and number of fruits/plant where as negative correlation with pedicel length.

4.3.8 Number of primary branches/plant

It showed significant and positive correlation with number of secondary branches/plant (0.667P, 0.569G), fruit weight (0.255G), fruit length (0.270P, 0.422G), fruit diameter (0.311P, 0.567G) and pedicel length (0.390P, 0.695G). It showed negatively significant correlation with number of fruits/plant (-0.496G, -0.262P) and yield/plant (-0.616G, -0.267P). It showed positively non-significant correlation with leaf area index (0.123G, 0.058P). It showed negatively non-significant correlation with percent of BSFB infestation (-0.194G).

Nikitha *et al.* (2020) showed in their experiment that number of branches had positive correlation with fruit length, number of fruits per plant and yield per plant whereas negative correlation with days to 50% flowering, fruit diameter and pedicel length.

4.3.9 Number of secondary branches/plant

It showed significant and positive correlation with fruit length (0.281P, 0.326G) and pedicel length (0.371P, 0.540G). It showed positively non-significant correlation with days to last plant height (0.34P), fruit diameter (0.191G, 0.143P) and leaf area index (0.186G, 0.132P). It showed negatively non-significant correlation with fruit weight (-0.053G, -0.009P), number of fruits and plants (-0.171G, -0.131P) percent of BSFB infestation (-0.106P) and yield/plant (-0.252P). It showed positively non-significant correlation with fruit diameter (0.191G, 0.143P) and leaf area index (0.186G, 0.132P). Nikitha *et al.* (2020) showed in their experiment that number of branches had positive correlation with fruit length whereas negative correlation with days to 50% flowering, fruit diameter and pedicel length.

4.3.10 Number of fruits/plant

Number of fruits/plant showed significant and positive correlation with yield/plant (0.517P, 0.471G). It showed negatively significant correlation with leaf area index (-0.316G, -0.297P) and percent of BSFB infestation (-0.295G, -0.284P). Gurve *et al.* (2020) showed that number of fruits per plant had positive and significant correlation with yield per plant. Konyak *et al.* (2020) showed similar results.

4.3.11 Leaf area index (cm^2)

It showed negatively non-significant correlation with percent of BSFB infestation (-0.111P, -0.146G) and yield/plant (-0.080P, -0.066G). Nikitha *et al.* (2020) showed in their experiment that plant spread had negative correlation with yield/plant.

4.3.12 Plant height (cm)

It showed significant and positive correlation with number of primary branches/plant (0.271G), fruit weight (0.600P, 0.644G), fruit diameter (0.462P, 0.509G) and leaf area index (0.309P, 0.324G). It showed negatively significant correlation with number of fruits/plant (-0.455G, -0.421P). It showed positively non-significant correlation with fruit length (0.138G, 0.147P) and yield/plant (0.063G, 0.048P). It showed negatively non-significant correlation with number of secondary branches/plant (-0.030G), pedicel length (-0.091G, -0.097P) and percent of BSFB infestation (-0.046G, -0.050P). Similar results were found in the study of Nikitha *et al.* (2020).

4.3.13 Fruit weight (g)

It showed significant and positive correlation with fruit diameter (0.721P, 0.732G) and leaf area index (0.350P, 0.378G). It showed negatively significant correlation with pedicel length (-0.429G, -0.411P) and number of fruits/plant (-0.716G, -0.648P). It showed positively non-significant correlation with percent of BSFB infestation (0.210G, 0.200P) and yield/plant (0.223G, 0.243P). It showed negatively non-significant correlation with fruit length (-0.131G, -0.085P). Nikitha *et al.* (2020) showed that fruit weight had positive correlation with yield/plant where as negatively significant correlation with fruit length.

4.3.14 Percent of BSFB infestation

It showed significant and positive correlation with fruit diameter (0.350P, 0.380G). It showed negatively significant correlation with number of secondary branches/plant (-0.286G), pedicel length (-0.448G, -0.384P) and number of fruits/plant (-0.295G, -0.284P). It showed positively non-significant correlation with fruit weight (0.210G, 0.200P) and fruit length (0.004G, 0.085P). It showed negatively non-significant correlation with days to 1st flowering (-0.211G, -0.166P), days to 50% flowering (-0.079G, -0.036P), days to 1st fruit harvest (-0.179G, -0.140P), days to last fruit harvest (-0.023G, -0.002P), plant height (-0.046G, -0.050P), number of primary branches/plant (-0.194G), number of secondary branches/plant (-0.106P) and leaf area index (-0.146G, -0.111P).

Sowmya and Pradeep (2020) showed that percent of BSFB infestation had negative correlation with fruit weight and yield/plant. Similar findings were reported by Hazra *et al*., 2004, there was a positive and significant effect of fruit weight (0.45) on the susceptibility to fruit infestation of the pest.

4.4 Path coefficient analysis

Path coefficient analysis indicates that the association of the independent character with dependent variable is due to their direct effect on it or is a consequence of their indirect effect through other characters. The path coefficient analysis was carried out considering fruit yield/plant as dependent variable and its attributes viz., plant height, number of primary branches/plant, number of secondary branches/plant, days to first flowering, days to 50% flowering, days to first fruit harvest, days to last fruit harvest, leaf area index, fruit weight, fruit length, pedicel length, fruit diameter and number of fruits/plant as independent variables.

Each component has two paths of action viz., direct influence on fruit yield and indirect effect through component characters which are not revealed from the correlation studies. The estimates of direct and indirect effects of yield related characters on fruit yield/plant are presented in Table 10. Path coefficient analysis showed that plant height (0.21546), number of primary branches/plant (0.08061), number of secondary branches/plant (0.08825), days to 1st fruit harvest (0.08216), days to last fruit harvest (0.39382), number of fruits/plant (1.0295), fruit weight (1.13944), and percent of BSFB infestation (0.05084) showed positive direct effect on fruit yield per plant. Similar results were reported in brinjal by Shende *et al*. (2014), Koundinya *et al*. (2017), Ravali *et al*. (2017), Dasmohapatra and Sharma (2018), Tripathy *et al*. (2017) and Nikitha *et al.* (2020). It clearly indicates that direct selection based on these characters would be effective for improvement in brinjal. The residual factor measures the average value across the standardized residuals. It ranges from zero (perfect fit) to one (very poor fit). It determines how best the causal factors account for the variability of the dependent factor, the fruit yield/plant in this case. The residual effects were 0.00662 which is of low magnitude at phenotypic and genotypic levels.

This analysis showed that fruit weight/plant exhibited maximum direct effects on yield which is followed by the number of fruits/plant. Similar results were reported in brinjal by Muniappan S. *et al.* (2010).

Table 10. Path coefficient analysis showing direct and indirect effects of different characters on yield/plant of brinjal

	DFF	50%DF	DFFH	DLFH	PH	NPBPP	NSBPP	FW	FL	FD	PL	NFPP	LAI	%BI	r
DFF	**-0.5890**	-0.0058	0.0756	0.2603	0.0910	-0.0302	-0.0272	0.1391	0.0011	0.0634	0.1634	-0.0555	-0.1694	-0.0107	-0.093
50%DF	-0.4931	**-0.0069**	0.0745	0.3092	0.0809	-0.0198	-0.0380	0.3029	0.0015	0.0040	0.1850	-0.1322	-0.1884	-0.0040	0.076
DFFH	-0.5423	-0.0063	**0.0821**	0.2906	0.1167	-0.0152	-0.0260	0.3563	0.0017	-0.0318	0.1701	-0.2097	-0.1805	-0.0091	-0.003
DLFH	-0.3891	-0.0054	0.0606	**0.3938**	0.0861	0.0026	-0.0097	0.2557	-0.0004	-0.0785	0.0800	-0.3424	-0.2743	-0.0012	-0.222
PH	-0.2486	-0.0026	0.0445	0.1574	**0.2154**	0.0218	-0.0027	0.7338	-0.0010	-0.3008	0.0405	-0.4684	-0.1237	-0.0024	0.063
NPBPP	0.2208	0.0016	-0.0155	0.0127	0.0583	**0.0806**	0.0502	0.2907	-0.0030	-0.3349	-0.3107	-0.5109	-0.0469	-0.0099	-0.516**
NSBPP	0.1815	0.0029	-0.0242	-0.0431	-0.0065	0.0458	**0.0882**	-0.0607	-0.0023	-0.1127	-0.2413	-0.1760	-0.0710	-0.0145	-0.434**
FW	-0.0719	-0.0018	0.0256	0.0884	0.1387	0.0205	-0.0047	**1.1394**	0.0009	-0.4327	0.1916	-0.7373	-0.1443	0.0106	0.223
FL	0.0940	0.0015	-0.0206	0.0207	0.0298	0.0340	0.0287	-0.1495	**-0.0071**	0.0666	-0.2458	0.0325	-0.0473	0.0022	-0.160
FD	0.0632	0.00005	0.0044	0.0523	0.1097	0.0456	0.0168	0.8344	0.0008	**-0.5909**	0.0813	-0.8939	-0.0298	0.0193	-0.286*
PL	0.2151	0.0028	-0.0313	-0.0705	-0.0195	0.0560	0.0476	-0.4883	-0.0039	0.1074	**-0.4472**	0.2135	0.0958	-0.0228	-0.345**
NFPP	0.0317	0.0008	-0.0167	-0.1310	-0.0980	-0.0400	-0.0151	-0.8161	-0.0002	0.5130	-0.0928	**1.0295**	0.1207	-0.0150	0.471**
LAI	-0.2610	-0.0034	0.0388	0.2827	0.0697	0.0098	0.0163	0.4304	-0.0009	-0.0460	0.1121	-0.3255	**-0.3820**	-0.0074	-0.066
%BI	0.1242	0.0005	-0.0147	-0.0091	-0.0100	-0.0157	-0.0252	0.2389	-0.0003	-0.2248	0.2003	-0.3037	0.0557	**0.0508**	0.067

Diagonal values indicate direct effects, Residual: 0.00662, r indicates genotypic correlation coefficient with 5% (*) and 1% (**) level of significance

DFF: Days to 1st flowering | 50%DF: Days to 50% flowering | DFFH: Days to 1st fruit harvest | DLFH: Days to last fruit harvest | PH: Plant height (cm)

NPBPP: No. of primary branches/plant | NSBPP: No. of secondary branches/plant | FW: Fruit weight (g) | FL: Fruit length (cm) | FD: Fruit diameter (cm)

PL: Pedicel length (cm) | NFPP: No. of fruits/plant | LAI: Leaf area index (cm^2) | %BI: Percent of BSFB infestation | YPP: Yield/plant (kg)

4.4.1 Days to 1st flowering

Days to 1st flowering showed negatively direct effect (-0.589) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st fruit harvest (0.07569), days to last fruit harvest (0.26033), plant height (0.09101), fruit weight (0.1391), fruit length (0.00113), fruit diameter (0.06346) and pedicel length (0.16342). This character showed negatively indirect effect on days to 50% flowering (-0.0058), number of primary branches/plant (-0.0302), number of secondary branches/plant (-0.0272), number of fruits/plant (-0.0555), leaf area index (-0.1694) and percent of BSFB infestation (-0.0107). Nikitha *et al.* (2020) and Shende *et al*. (2014) found similar result.

4.4.2 Days to 50% flowering

Days to 50% flowering showed negatively direct effect (-0.0069) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st fruit harvest (0.07459), days to last fruit harvest (0.30924), plant height (0.08097), fruit weight (0.30295), fruit length (0.00159), fruit diameter (0.00408) and pedicel length (0.18509). This character showed negatively indirect effect on days to first flowering (-0.4931), number of primary branches/plant (-0.0198), number of secondary branches/plant (-0.038), number of fruits/plant (-0.1322), leaf area index (-0.1884) and percent of BSFB infestation (-0.004). Konyak *et al.* (2020) showed similar trend in which days to 50% flowering showed negatively direct effect on yield/plant.

4.4.3 Days to 1st fruit harvest

Days to first fruit harvest showed positively direct effect (0.08216) on yield/plant in Table 10. This character showed positively indirect effect on days to last fruit harvest (0.29065), plant height (0.11679), fruit weight (0.35635), fruit length (0.00177) and pedicel length (0.17014). This character showed negatively indirect effect on days to 1st flowering (-0.5423), days to 50% flowering (-0.0063), number of primary branches/plant (-0.0152), number of secondary branches/plant (-0.026), fruit diameter (-0.0318), number of fruits/plant (-0.2097), leaf area index (-0.1805) and percent of BSFB infestation (-0.0091). Nikitha *et al.* (2020) showed that days to first fruit harvest showed positively direct effect on yield/plant.

4.4.4 Days to last fruit harvest

Days to last fruit harvest showed positively direct effect (0.39382) on yield/plant. This character showed positively indirect effect on days to 1st fruit harvest (0.06064), plant height (0.08613), number of primary branches/plant (0.0026), fruit weight (0.25576)

and pedicel length (0.08006). This character showed negatively indirect effect on days to 1st flowering (-0.3891), days to 50% flowering (-0.0054), number of secondary branches/plant (-0.0097), fruit length (-0.0004), fruit diameter (-0.0785), number of fruits/plant (-0.3424), leaf area index (-0.2743) and percent of BSFB infestation (-0.0012). Nikitha *et al.* (2020) showed that days to last fruit harvest showed positively direct effect on yield/plant.

4.4.5 Fruit length (cm)

Fruit length showed negatively direct effect (-0.0071) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st flowering (0.09405), days to 50% flowering (0.00154), days to last fruit harvest (0.02077), plant height (0.02982), number of primary branches/plant (0.03402), number of secondary branches/plant (0.02879), fruit diameter (0.0666), number of fruits/plant (0.03251) and percent of BSFB infestation (0.00224). This character showed negatively indirect effect on days to 1st fruit harvest (-0.0206), fruit weight (-0.1495), pedicel length (-0.2458) and leaf area index (-0.0473). Nikitha *et al.* (2020) showed that fruit length showed negatively direct effect (-0.0071) on yield/plant.

4.4.6 Pedicel length (cm)

Pedicel length showed negatively direct effect (-0.4472) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st flowering (0.21512), days to 50% flowering (0.00285), number of primary branches/plant (0.05601), number of secondary branches/plant (0.04762), fruit diameter (0.10749), number of fruits/plant (0.21355) and leaf area index (0.09584). This character showed negatively indirect effect on days to 1st fruit harvest (-0.0313), days to last fruit harvest (-0.0705), plant height (-0.0195), fruit weight (-0.4883), fruit length (-0.0039) and percent of BSFB infestation (-0.0228). Nikitha *et al.* (2020) showed that pedicel length showed negatively direct effect (-0.4472) on yield/plant. Similar results were reported in brinjal by Shende *et al*. (2014) and Tripathy *et al*. (2017).

4.4.7 Fruit diameter (cm)

Fruit diameter showed negatively direct effect (-0.5909) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st flowering (0.06322), days to 50% flowering (0.00005), days to 1st fruit harvest (0.00442), days to last fruit harvest (0.05234), plant height (0.1097), number of primary branches/plant (0.04569), number of secondary branches/plant (0.01683), fruit weight (0.83444), fruit length (0.0008), pedicel length (0.08135) and percent of BSFB infestation (0.01934). This character

showed negatively indirect effect on number of fruits/plant (-0.8939) and leaf area index (-0.0298). Nikitha *et al.* (2020) showed similar result. Konyak *et al.* (2020) showed similar trend where fruit diameter showed negatively direct effect on yield/plant.

4.4.8 Number of primary branches/plant

Number of primary branches/plant showed positively direct effect (0.08061) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st flowering (0.22085), days to 50% flowering (0.00169), days to last fruit harvest (0.01272), plant height (0.05834), number of secondary branches/plant (0.05024) and fruit weight (0.29074). This character showed negatively indirect effect on days to 1st fruit harvest (-0.0155), fruit length (-0.003), fruit diameter (-0.3349), pedicel length (-0.3107), number of fruits/plant (-0.5109), leaf area index (-0.0469) and percent of BSFB infestation (-0.0099). Konyak *et al.* (2020) showed similar results.

4.4.9 Number of secondary branches/plant

Number of secondary branches/plant showed positively direct effect (0.08825) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st flowering (0.18157), days to 50% flowering (0.00296) and number of primary branches/plant (0.04589). This character showed negatively indirect effect on days to 1st fruit harvest (-0.0242), days to last fruit harvest (-0.0431), fruit length (-0.0023), fruit diameter (-0.1127), pedicel length (-0.2413), number of fruits/plant (-0.176), leaf area index (-0.071) and percent of BSFB infestation (-0.0145). Konyak *et al.* (2020) showed similar trend.

4.4.10 Number of fruits/plant

Number of fruits/plant showed positively direct effect (1.0295) on yield/plant. This character showed positively indirect effect on days to 1st flowering (0.03173), days to 50% flowering (0.00088), fruit diameter (0.51304) and leaf area index (0.12079). This character showed negatively indirect effect on days to 1st fruit harvest (-0.0167), days to last fruit harvest (-0.131), plant height (-0.098), number of primary branches/plant (-0.04), number of secondary branches/plant (-0.0151), fruit weight (-0.8161), fruit length (-0.0002), pedicel length (-0.0928) and percent of BSFB infestation (-0.015).

In brinjal, it has been reported that there is a strong association between the number of fruits per plant and yield per plant (Srivastava and Sachan, 1973 and Hiremath and Gururaja, 1974). Similarly path analysis in brinjal was conducted by Srivastava and Sachan (1973) showed that the number of fruits per plant exhibited maximum direct

effects on yield. It is therefore to be considered useful to select the best variety of brinjal on the basis of number of fruits per plant for effective improvement of this crop.

4.4.11 Leaf area index (cm^2)

Leaf area index showed negatively direct effect (-0.382) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st fruit harvest (0.03881), days to last fruit harvest (0.2827), plant height (0.06978), number of primary branches/plant (0.00989), number of secondary branches/plant (0.01639), fruit weight (0.43044) and pedicel length (0.11218). This character showed negatively indirect effect on days to 1st flowering (-0.261), days to 50% flowering (-0.0034), fruit length (-0.0009), fruit diameter (-0.046), number of fruits/plant (-0.3255) and percent of BSFB infestation (-0.0074). Nikitha *et al.* (2020) showed that leaf area index showed negatively direct effect (-0.382) on yield/plant.

4.4.12 Plant height (cm)

Plant height showed positively direct effect (0.21546) on yield/plant in Table 10. This character showed positively indirect effect on days to 1st fruit harvest (0.04453), days to last fruit harvest (0.15743), number of primary branches/plant (0.02183), fruit weight (0.73388) and pedicel length (0.04055). This character showed negatively indirect effect on days to 1st flowering (-0.2486), days to 50% flowering (-0.0026), number of secondary branches/plant (-0.0027), fruit length (-0.001), fruit diameter (-0.3008), number of fruits/plant (-0.4684), leaf area index (-0.1237) and percent of BSFB infestation (-0.0024). Nikitha *et al.* (2020) showed similar result where plant height showed positively direct effect on yield/plant. Similar results were reported in brinjal Koundinya *et al*. (2017), Ravali *et al*. (2017) and Tripathy *et al*. (2017).

4.4.13 Fruit weight (g)

Fruit weight showed positively direct effect (1.13944) on yield/plant in Table 10. Similar observation was found by Muniappan S. *et al.* (2010). This character showed positively indirect effect on days to 1st fruit harvest (0.02569), days to last fruit harvest (0.0884), plant height (0.13877), number of primary branches/plant (0.02057), fruit length (0.00093), pedicel length (0.19164) and percent of BSFB infestation (0.01066). This character showed negatively indirect effect on days to 1st flowering (-0.0719), days to 50% flowering (-0.0018), number of secondary branches/plant (-0.0047), fruit diameter (-0.4327), number of fruits/plant (-0.7373) and leaf area index (-0.1443). Konyak *et al.* (2020) showed in their study that fruit weight showed positively direct effect on yield/plant. It is therefore to be considered useful to select the best genotype

of brinjal on the basis of fruit weight for effective improvement of this crop.

4.4.14 Percent of BSFB infestation

Percent of BSFB infestation showed positively direct effect (0.05084) on yield/plant in Table 10 which is opposite to Panja *et al*. (2013). This character showed positively indirect effect on days to 1st flowering (0.12422), days to 50% flowering (0.00054), fruit weight (0.23898), pedicel length (0.20034) and leaf area index (0.05574). It showed negatively indirect effect on days to 1st fruit harvest (-0.0147), days to last fruit harvest (-0.0091), plant height (-0.01), number of primary branches/plant (-0.0157), number of secondary branches/plant (-0.0252), fruit length (-0.0003), fruit diameter (-0.2248) and number of fruits/plant (-0.3037).

4.5 Multivariate analysis

Genetic diversity was analyzed using the GENSTAT software program. Genetic diversity analysis involves several steps, i.e., principal component analysis, clustering, and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2014; Juned *et al*., 1988 and Ario, 1987). In the analysis of genetic diversity in brinjal multivariate techniques were used.

4.5.1 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis (Appendix V), 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 1. The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the genotypes.

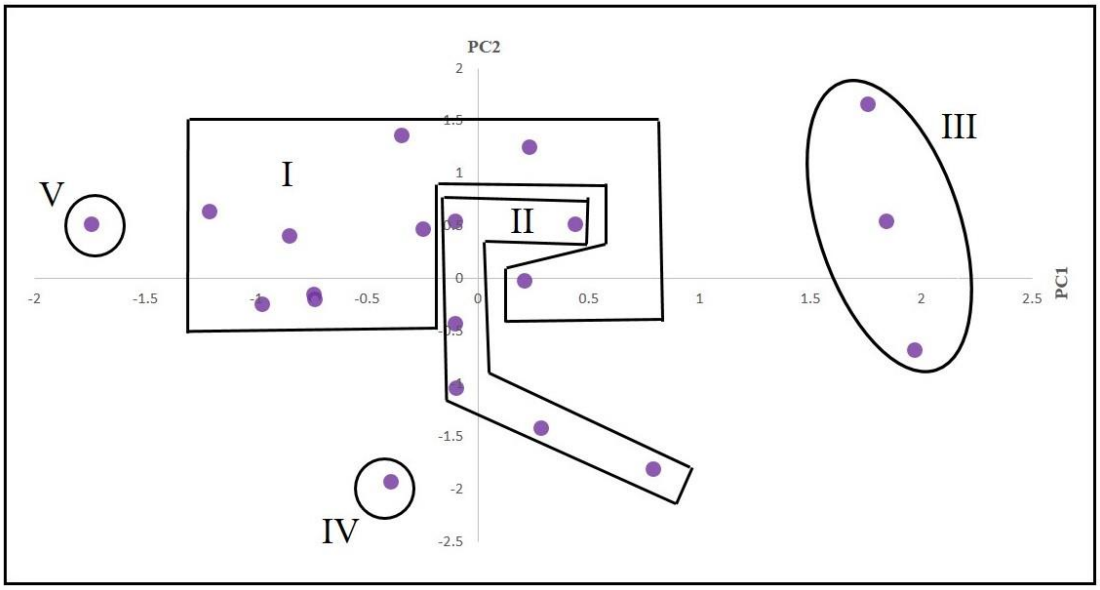


Figure 1. Scattered distribution of twenty brinjal genotypes on principal component score superimposed with clustering

Table 11. Eigen values and percentage of variation in respect of 15 characters in brinjal

Principal Component Axis	Eigen values	Percent Variation	Cumulative percent variation
Days to 1st flowering	4.49	30.0	30.0
Days to 50% flowering	2.98	19.8	49.8
Days to 1st fruit harvest	2.18	14.6	64.4
Days to last fruit harvest	1.26	8.4	72.8
Plant height (cm)	1.01	6.7	79.5
No. of primary branches/plant	0.93	6.2	85.7
No. of secondary branches/plant	0.73	4.8	90.5
Fruit weight (g)	0.47	3.1	93.6
Fruit length (cm)	0.29	1.9	95.5
Fruit diameter (cm)	0.24	1.6	97.1
Pedicel length (cm)	0.15	1.0	98.1
No. of fruit/plant	0.11	0.7	98.8
Leaf area index (cm^2)	0.09	0.6	99.4
Percent of BSFB infestation	0.08	0.5	99.9
Yield/plant (kg)	0.02	0.1	100.0

4.5.2 Principal component analysis

Principal components were computed using the correlation matrix and genotype scores obtained from the first components and succeeding components with latent roots greater than the unity contribution of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal components. The Principal Component Analysis yielded Eigen values of each Principal Component axes with the accounting for the variation among the genotypes. Six of these Eigen values above unity accounted for 85.7% in Table 11 of the total variation and the last nine principal axes accounted for 14.3% of the total variation.

Balasch *et al.* (1984) reported the use and the comparison of different multivariate techniques in classifying some important number of tomato varieties/genotypes. It was marked that three methods gave similar results.

Table 12. Distribution of 20 brinjal genotypes in five different clusters

Clusters	No. of genotypes	Name of genotypes
I	9	G2, G3, G4, G5, G8, G9, G10, G12, G13
II	6	G1, G7, G16, G18, G19, G20
III	3	G6, G11, G14
IV	1	G17
V	1	G15

The distribution pattern in Table 12 indicated that the maximum number of genotypes (9) was comprised in cluster I followed by cluster II (6), cluster III (3), cluster IV (1) and cluster V (1). Among five clusters, cluster I was composed of nine genotypes: G2, G3, G4, G5, G8, G9, G10, G12, and G13. From the clustering mean value shown in Table 13, it was observed that, in cluster I, the highest mean accounted for percent of BSFB infestation (11.20%), second-highest mean for plant height (69.94), the number of primary branches/plant (12.10), fruit diameter (21.98) and pedicel length (6.39) respectively. Cluster II produced the second-highest mean for days to 1st flowering (74.87), days to 50% flowering (90.81), days to 1st fruit harvest (100.11), days to last fruit harvest (152.91), number of the secondary branches/plant (25.22), and leaf area index (91.44) and the lowest mean values for plant height (65.64).

Table 13. Cluster mean for 15 characters of 20 genotypes of brinjal

Characters	Clusters				
	I	II	III	IV	V
Days to 1st flowering	61.43	74.87	80.74	63.33	59.00
Days to 50% flowering	82.57	90.81	95.56	86.44	79.78
Days to 1st fruit harvest	92.91	100.11	106.67	93.44	88.11
Days to last fruit harvest	141.68	152.91	157.44	139.89	141.55
Plant height (cm)	69.94	65.64	91.60	66.43	67.87
No. of primary branches/plant	12.10	11.48	12.04	10.00	13.22
No. of secondary branches/plant	25.01	25.22	22.89	18.44	25.66
Fruit weight (g)	230.67	171.39	340.00	282.83	126.00
Fruit length (cm)	18.70	18.57	19.14	18.20	31.10
Fruit diameter (cm)	21.98	11.49	28.60	7.97	11.87
Pedicel length (cm)	6.39	6.33	4.94	4.63	10.67
No. of fruits/plant	6.78	8.59	4.67	11.44	10.44
Leaf area index (cm^2)	74.67	91.44	98.78	76.67	74.33
Percent of BSFB infestation	11.20	6.18	10.94	5.83	4.25
Yield/plant (kg)	1.51	1.46	1.54	3.17	1.33

Cluster III showed the highest mean for days to 1st flowering (80.74), days to 50% flowering (95.56), days to 1st fruit harvest (106.67), days to last fruit harvest (157.44), plant height (91.60), fruit weight (340.00), fruit diameter (28.60) and leaf area index (98.78), and second-highest value for fruit length (19.14) and percent of BSFB infestation (10.94%) also the lowest value for the number of fruits/plant (4.67). Cluster IV had the highest mean for the number of fruits/plant (11.44) and yield/plant (3.17), second highest mean for fruit weight (282.83), and the lowest mean values for last fruit harvest (139.89), number of primary branches/plant (10.00), number of secondary branches/plant (18.44), fruit length (18.20), fruit diameter (7.97) and pedicel length (4.63). Cluster V produced the highest mean values for the number of the primary branches/plant (13.22), the number of the secondary branches/plant (25.66), fruit length (31.10 cm), and pedicel length (10.67).

Joshi *et al.* (2003) assessed the nature and magnitude of genetic divergence using non-hierarchical Euclidean cluster analysis in 73 tomato genotypes of diverse origin for different quantitative and qualitative traits. The maximum value of the coefficient of variability (53.208) was recorded for the shelf life of fruits while it was minimum

(69.208) for days to first picking. The grouping of the genotypes into 15 clusters indicated the presence of a wide range of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity.

Dharmatti *et al*. (2001) reported that genetic diversity in a population of 402 tomato genotypes was assessed using multivariate analysis. The 402 genotypes were grouped into 4 clusters based on the similarities of D^2 values. Considerable diversity within and between the clusters was noted, and it was observed that the characters TLCV resistance, fruit yield per plant, and the number of whiteflies per plant contributed the maximum to the divergence. Therefore, the selection of divergent parents based on these characters may be useful for heterosis breeding in summer tomatoes.

Table 14. Average intra (bold) and inter cluster distances (D^2) for 20 brinjal genotypes

Cluster	I	II	III	IV	V
I	**259.03**				
II	537.81	**215.85**			
III	726.56	650.58	**249.46**		
IV	468.41	617.15	1190.17	**0.0**	
V	799.86	613.41	1592.62	921.61	**0.0**

4.5.3 Principal coordinate analysis

By using inter-genotypic distances intra cluster genotypic distances were calculated as suggested by Singh *et al*. (1977). Results found in respect to inter and intra cluster divergences exhibited variations in the parameters in Table 14. The highest intra cluster distance was 259.03 in cluster I followed by cluster III (249.46) and cluster II (215.85) showed the lowest distance, while it was zero in case of cluster IV and V which indicated within-group diversity of the genotypes was maximum in cluster I and minimum in cluster II.

The genotypes grouped into the same cluster displayed the lowest degree of divergence from one another and in case crosses are made between genotypes belonging to the same cluster, no transgressive segregant is expected from such combinations.

Therefore, hybridization program should always be formulated in such a way that the parents belonging to different clusters with maximum genetic distance divergence could be utilized to get desirable transgressive segregants.

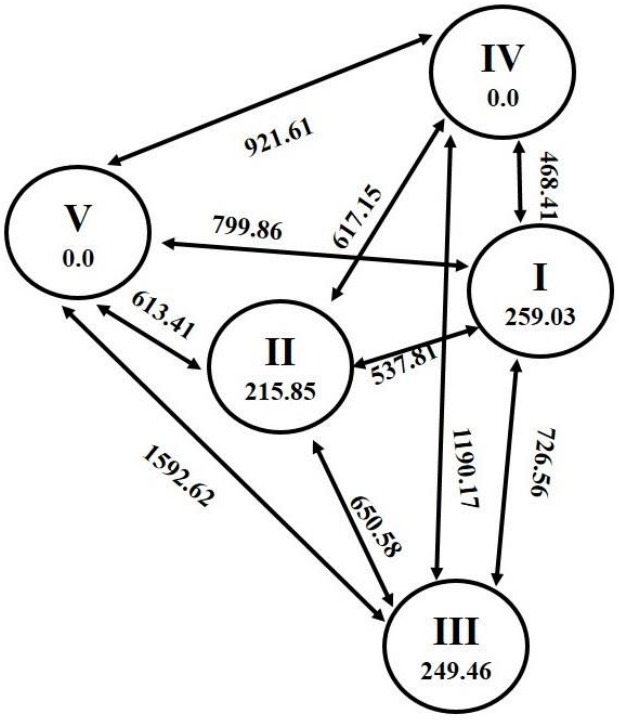


Figure 2. Diagram showing inter cluster (outside the circle) and intra cluster (inside the circle) distances of 20 genotypes of brinjal

4.5.4 Canonical variate analysis

Canonical variate analysis was performed to compute the inter cluster Mahalanobis's values. Statistical distances show the index of genetic diversity among the clusters. The average intra and inter cluster distance (D^2) values were presented in Table 14. In figure 2, results showed the maximum inter cluster distance was recorded between cluster III and V (1592.62), followed by between III and IV (1190.17), and IV and V (921.61). So, genotypes from these clusters if involved in hybridization might produce a wide range of segregating populations, as genetic variation was very distinct among these groups. The lowest inter cluster distance was found between the cluster I and IV (468.41) followed by I and II (537.81), II and V (613.41) representing a close relationship among these clusters. Inter cluster distances were greater than the intra cluster distances representing wider genetic diversity among the genotypes of different groups (Table 14 and Figure 2). Islam *et al*. (1995) found larger inter cluster distances

than the intra cluster distances in a multivariate analysis.

4.5.5 Non-hierarchical clustering

The computation from covariance matrix gave non-hierarchical clustering among 20 genotypes. By application of non- hierarchical clustering using covariance matrix, the 20 brinjal genotypes were grouped into five different clusters. These results confirmed the clustering pattern of the genotypes according to the Principal Component Analysis. So, the results obtained through PCA were confirmed by non-hierarchical clustering.

Joshi *et al.* (2003) assessed the nature and magnitude of genetic divergence using non-hierarchical Euclidean cluster analysis in 73 tomatoes (*Lycopersicon esculentum*) genotypes of diverse origin for different quantitative and qualitative traits. The grouping of the genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity.

Mandal and Dana (1992) studied 20 genotypes of brinjal for the yield contributing characters and indicated that fruits/plant, secondary branches/plant and plant height are important traits for the selection of superior genotypes.

From the clustering mean value shown in Table 13, it was observed that cluster I produced the highest mean for percent of BSFB infestation (11.20%), second-highest mean of plant height (69.94), the number of primary branches/plant (12.10), fruit diameter (21.98) and pedicel length (6.39). Fruit type of the different genotypes of this cluster has been presented in Plate 4.

Cluster II produced the second-highest mean for days to 1st flowering (74.87), days to 50% flowering (90.81), days to 1st fruit harvest (100.11), days to last fruit harvest (152.91), number of the secondary branches/plant (25.22), and leaf area index (91.44) and the lowest mean values for plant height (65.64). Fruit type of this cluster has been presented in Plate 4.

Cluster III produced the highest mean for days to 1st flowering (80.74), days to 50% flowering (95.56), days to 1st fruit harvest (106.67), days to last fruit harvest (157.44), fruit weight (340.00), fruit diameter (28.60) and leaf area index (98.78), and second-highest value for fruit length (19.14 cm) and percent of BSFB infestation (10.94%) also the lowest value for the number of fruits/plant (4.67). Fruit type of the genotypes of this cluster has been presented in Plate 4.

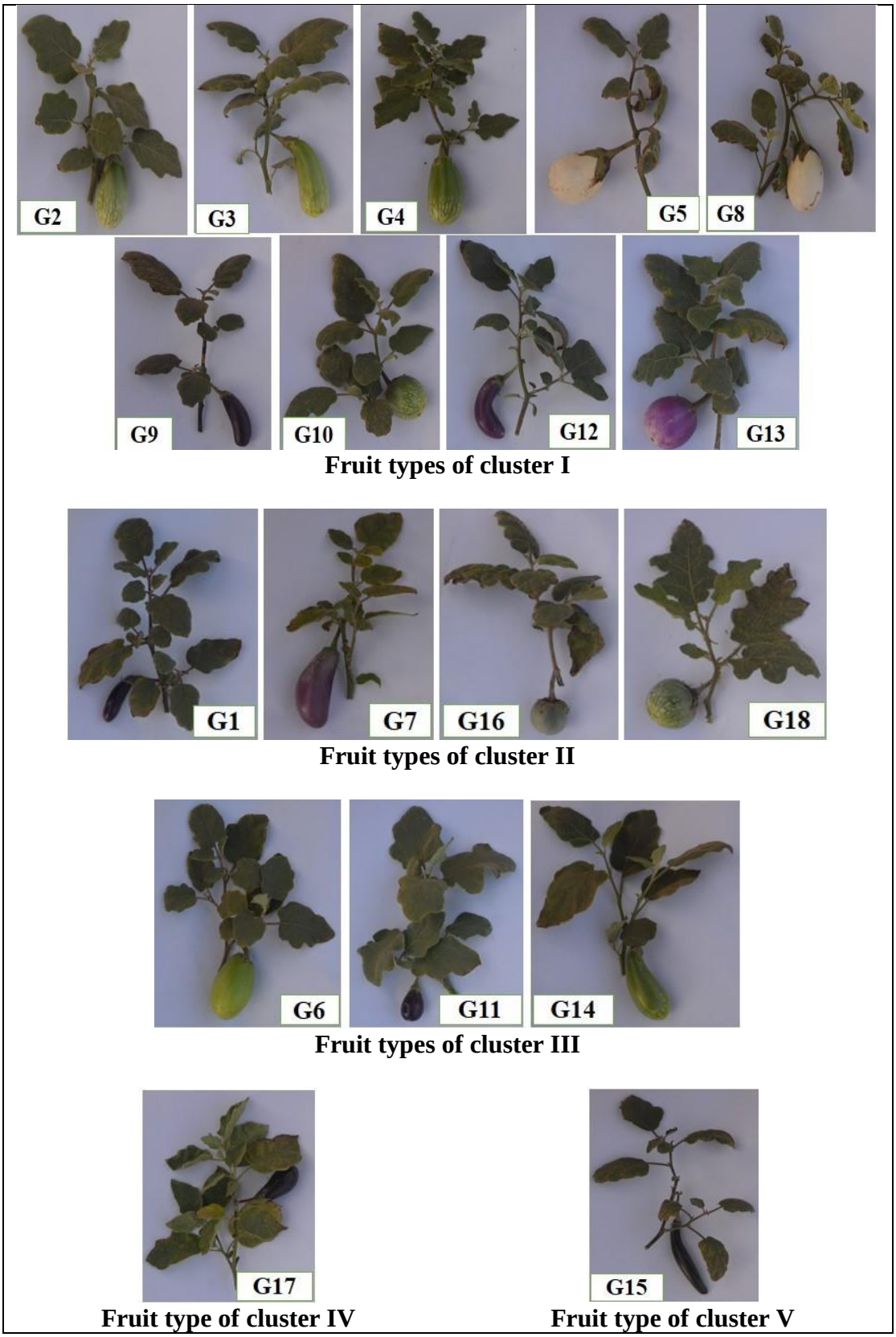


Plate 4: Different fruit types of the different genotypes of different clusters

Cluster IV produced the highest mean for the number of fruits/plant (11.44) and yield/plant (3.17), second highest mean for fruit weight (282.83), and the lowest mean values for days to last fruit harvest (139.89), number of the primary branches/plant (10.00), number of the secondary branches/plant (18.44), fruit length (18.20 cm), fruit diameter (7.97) and pedicel length (4.63). Its fruit type has been presented in Plate 4.

Cluster V produced the highest mean values for the number of the primary branches/plant (13.22), the number of the secondary branches/plant (25.66), fruit length (31.10 cm), and pedicel length (10.67 cm), the second-highest mean value for the number of fruits/plant (10.44), and lowest mean values for days to 1st flowering (59.00), days to 50% flowering (79.78), days to first fruit harvest (88.11), fruit weight (126.00), leaf area index (74.33), percent of BSFB infestation (4.25%), and yield/plant (1.33). Its fruit type has been presented in Plate 4.

Observing the class mean value, it was observed that all the cluster mean values for days to 50% flowering, days to last fruit harvest, number of primary branches/plant and number of secondary branches/plant were more or less similar. The range of variability was observed for yield (1.33 kg to 3.17 kg) among all the characters in five clusters. The range of variability was observed for percent of BSFB infestation (4.25% to 11.20%) among all the characters in five clusters. Cluster IV included mainly early flowering and early maturing genotypes with high yield and less percentage of BSFB infestation. To develop high yielding varieties/genotypes, genotype of this cluster could be used in hybridization program. Cluster II and V included mainly early flowering and early maturing genotypes with less percentage of BSFB infestation. To develop BSFB resistant varieties/genotypes, genotypes of cluster II, IV and V could be used in hybridization program.

4.6 Contribution of characters towards divergence of the genotypes

The character contributing maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization (Jagadev *et al*., 1991). The PCA revealed that in vector I the important characters responsible for genetic divergence in the major axis of differentiation were first fruit harvest (0.406), days to 50% flowering (0.393), days to first flowering (0.361), last fruit harvest (0.36), plant height (0.294) and fruit weight (0.28) in Table 15.

Table 15. Vector I and II from PCA for 15 characters of 20 brinjal genotypes

Characters	Vector I	Vector II
Days to 1st flowering	0.361	-0.184
Days to 50% flowering	0.393	-0.168
Days to 1st fruit harvest	0.406	-0.131
Days to last fruit harvest	0.36	0.026
Plant height (cm)	0.294	0.197
No. of primary branches/plant	-0.044	0.441
No. of secondary branches/plant	-0.121	0.348
Fruit weight (g)	0.28	0.242
Fruit length (cm)	-0.106	0.206
Fruit diameter (cm)	0.166	0.412
Pedicel length (cm)	-0.255	0.198
No. of fruits/plant	-0.223	-0.405
Leaf area index (cm^2)	0.292	0.082
Percent of BSFB infestation	0.025	0.079
Yield/plant (kg)	0.002	-0.281

In vector II, the second axis of differentiation, the number of primary branches/plant (0.441), fruit diameter (0.412), number of secondary branches/plant (0.348), fruit weight (0.242) and fruit length (0.206) were important.

The role of last fruit harvest, plant height, fruit weight, fruit diameter, leaf area index and percent of BSFB infestation for both the vectors were positive across two axes indicating the important components of genetic divergence in these materials.

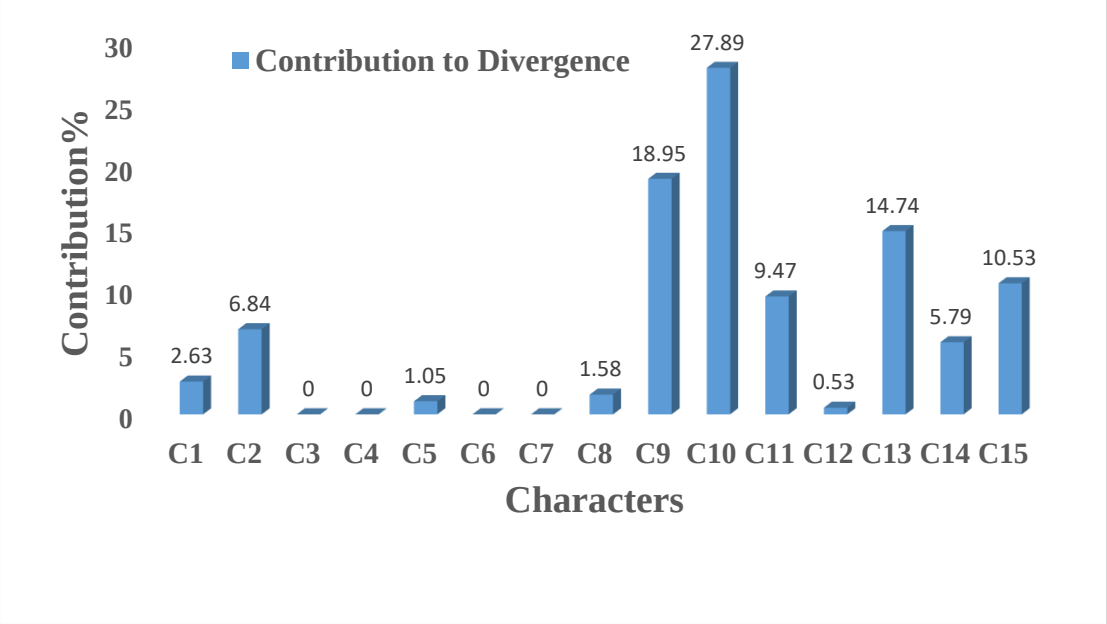


Figure 3. Graph showing relative contribution of 15 characters of 20 brinjal genotypes towards divergence

The relative contribution of 15 quantitative traits to genetic divergence among the 20

germplasms of brinjal is presented in Figure 3. Among the yield contributing characters, the maximum contribution towards divergence was made by fruit diameter (27.89%) followed by fruit length (18.95%), leaf area index (14.74%), yield/plant (10.53%), pedicel length (9.47%), days to 50% flowering (6.84%), percent of BSFB infestation (5.79%), days to first flowering (2.63%), fruit weight (1.58%), plant height (1.05%) and number of fruits/plant (0.53%).

Among the yield contributing characters, the maximum contribution towards divergence was made in accordance with study conducted by Naik (2005), Singh *et al*. (2006), Kumar *et al*. (2008), Das *et al*. (2010), and Sadarunnisa *et al*. (2015).

4.7 Selection of genotypes for future hybridization

Selection of genotypically distant parents are an important step for hybridization program. As a result, genotypes would be selected on the basis of specific objectives. Crosses between genetically distant parents able to produce higher heterosis (Falconer, 1960; Moll *et al*.; 1962; Ghaderi *et al.;* 1984; Main and Bhal, 1989).

Considering the agronomic performance, genotype 17 produced highest yield, maximum number of fruit, second-highest of minimum insect infestation from cluster IV than others. Genotype 15 from cluster V produced the highest values for the number of the primary branches/plant, number of the secondary branches/plant, fruit length, and pedicel length, the second-highest value for the number of fruits per plant. Genotype 6 produce 100% BSFB resistant fruit and maximum fruit weight.

Based on the results of this study, it may be concluded that a breeding program should be undertaken by picking parental genotypes from diverse distant clusters along with considering cluster mean values of different traits for finding the desirable characters which have an active relative contribution to the total divergence aimed at developing anticipated varieties by the selection of superior genotypes through the successive positive principal coordinate and canonical variants involvement generations. Therefore, considering group distance and other agronomic performances, the genotypes 17, 15 and 6 may be suggested to use for future hybridization program.

CHAPTER V
SUMMARY AND CONCLUSION

The experiment was carried out using 20 genotypes of brinjal at the farm of Sher-e-Bangla Agricultural University, Dhaka to determine the genetic variability, correlation and path coefficient for yield and its contributing traits during August 2019 to March 2020.

Bio-morphological study revealed that less BSFB infestation were reported in spreading type plant growth habit, more hairiness and spines, small fruit diameter and white and purple color fruit. Out of 20 genotypes, 17 brinjal genotypes showed less BSFB infestation i.e. tolerant type. Significant variations were observed among the brinjal genotypes for all the parameters under study. Mean comparison table shows variation exist among all the characters. Phenotypic variance and phenotypic coefficient of variation (PCV) was higher than the genotypic variance and genotypic coefficient of variation (GCV) for all the characters under studied. The genetic parameters expressed that PCV and GCV were higher for percent of BSFB infestation (69.77%, 60.82%), fruit diameter (43.88%, 43.19%) fruit weight (33.94%, 32.80%) followed by number of fruits/plant (33.80%, 31.38%), yield/plant (31.60%, 28.53%), fruit length (25.65%, 24.58%) and pedicel length (23.66%, 23.10%) offering possibility for further improvement. The estimates of heritability in broad sense are range from 96.88 % to 26.58% for all the traits. High values of broad sense heritability, found in all the traits except primary and secondary branches/plant, reveal that the phenotypes were the true representative of their genotypes and a reliable selection would be possible based on phenotypic performances. High estimates of genetic advance percentage over mean were calculated for percent of BSFB infestation (109.21) and fruit diameter (87.56), fruit weight (65.28), number of fruits/plant (60.03) while it was moderate for yield/plant (53.08), fruit length (48.54), pedicel length (46.45), leaf area index (33.10), plant height (30.32) and days to first flowering (27.88) which illustrated that they could be improved.

The correlation coefficient revealed that yield/plant had the highly significant positive correlation with number of fruits/plant (r_g=0.471, r_p=0.517) indicating this character can be considered for phenotypic selection for future brinjal improvement program. The path coefficient had direct positive effect with days to 1st fruit harvest (0.082), days to last fruit harvest (0.393), plant height (0.215), number of primary branches/plant

(0.080), number of secondary branches/plant (0.088), fruit weight (1.139), number of fruits/plant (1.029) and percent of BSFB infestation (0.050) which indicated that promising selection would be rewarding for those traits.

The first six principal component axis contributed a total of 85.7% variation. According to PCA, D^2 and Cluster analysis, the genotypes were grouped into five divergent clusters. Cluster I, II, III, IV and V composed of nine, six, three, one and one genotypes respectively. As the maximum inter-cluster distance was recorded between cluster III and V (1592.62), followed by between III and IV (1190.17), and IV and V (921.61) so genotypes from these clusters if involved in hybridization might produce a wide range of segregating populations which is desirable for successful breeding programs. The intra cluster divergence varied from 259.03 from cluster I which comprised of nine cultivars of diverse origin to 215.85 from cluster II which comprised six genotypes. Greater inter cluster distances reveals wider genetic diversity among the genotypes of different groups. The clustering pattern of this study revealed that genotypes collected from the same places did not form a single cluster.

Considering cluster distances, genetic parameters and other agronomic performances, genotype 17 produced highest yield, maximum number of fruit, second-highest of minimum insect infestation from cluster IV than others. Genotype 15 from cluster V produced the highest values for the number of the primary branches/plant, number of the secondary branches/plant, fruit length, and pedicel length, the second-highest value for the number of fruits/plant. Genotype 6 produce 100% BSFB tolerant fruit and maximum fruit weight. This study revealed that genotype 6 from cluster III, genotype 15 from cluster V and genotype 17 from cluster IV could be considered as better parents for future hybridization programs.

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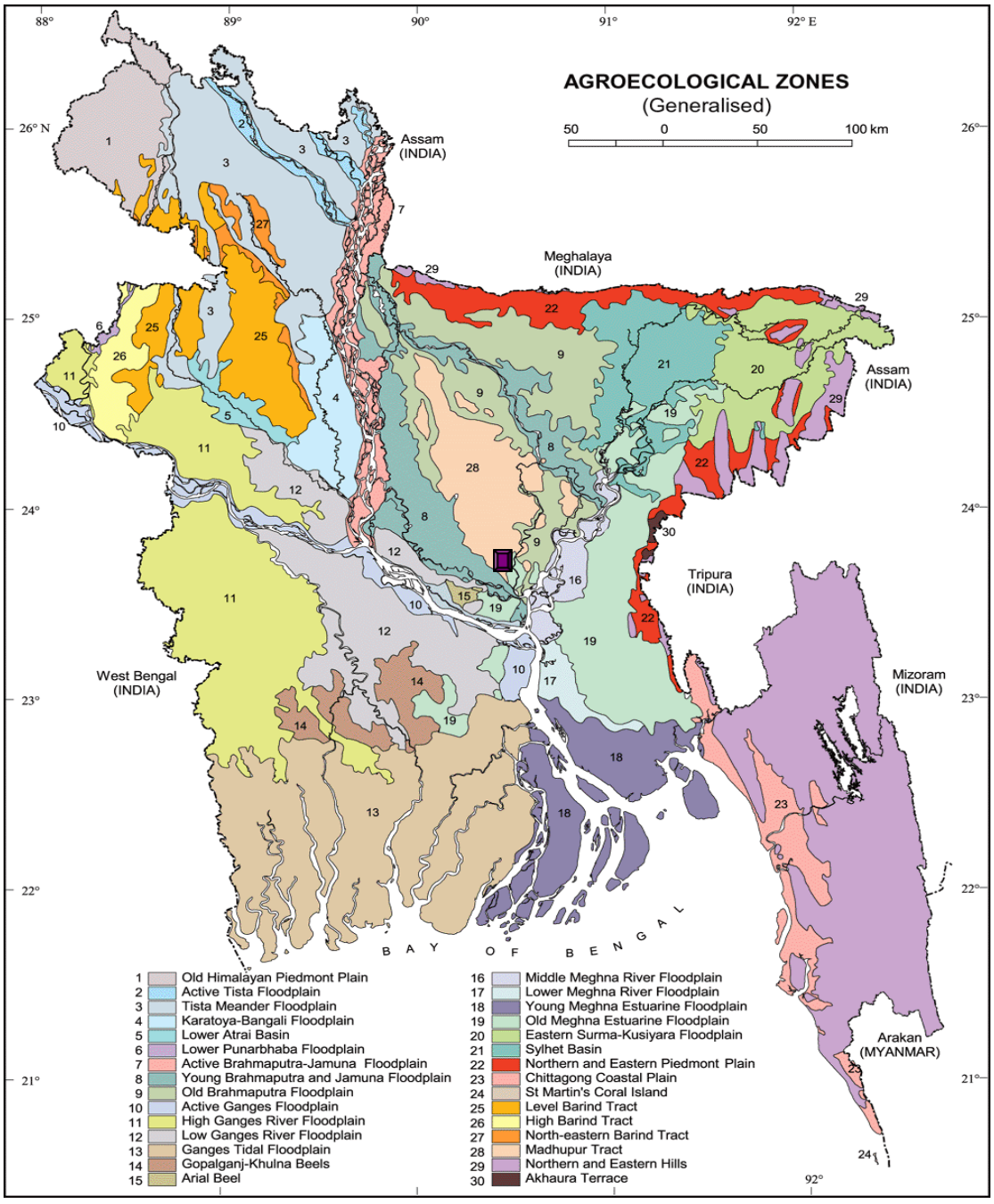
APPENDICES

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 (ºC)	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: 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

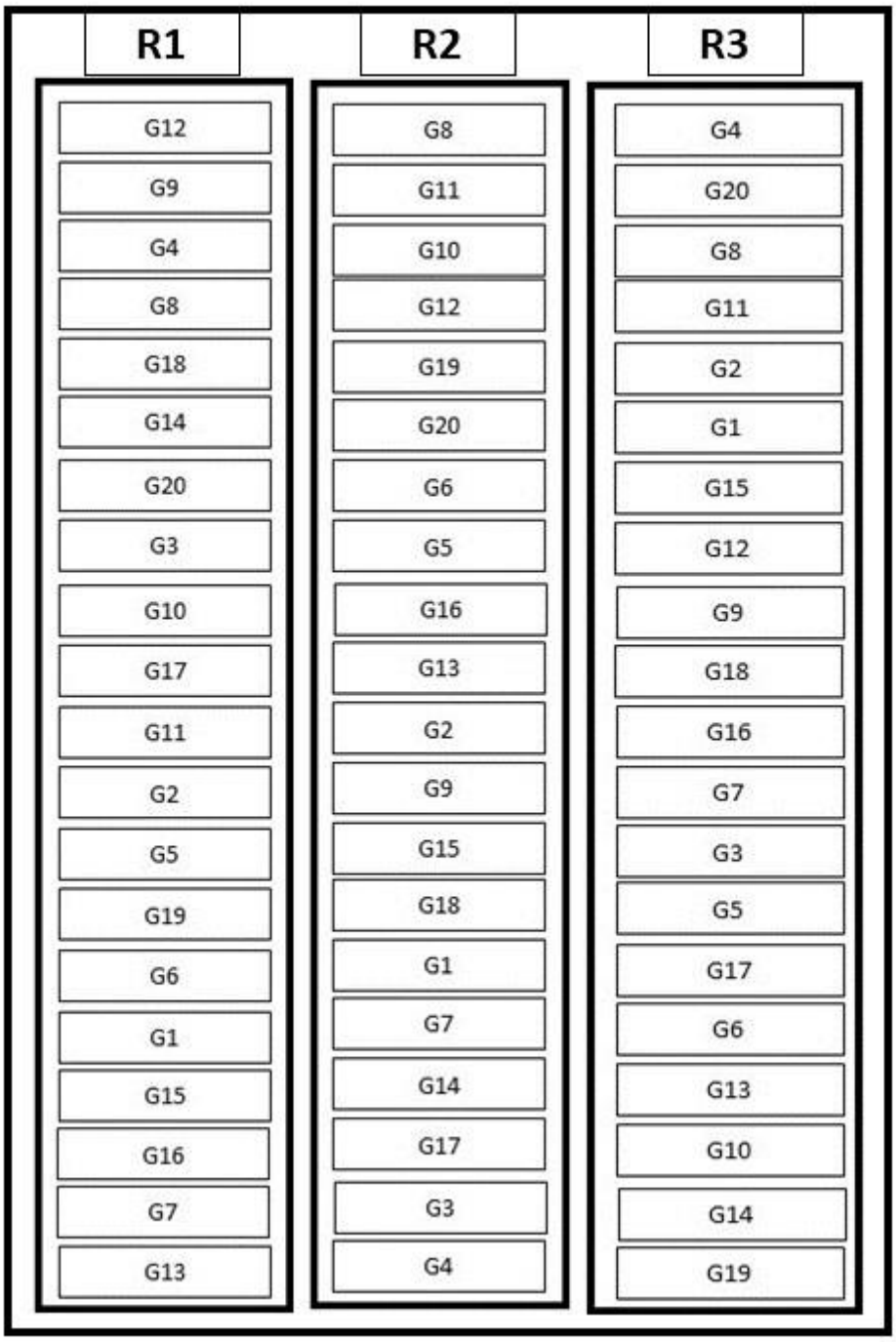
B. Chemical composition of the soil

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 IV: Layout of the field

Total Area: 24 × 11 = 264 sq. meter
Spacing: 120 cm × 75 cm



Appendix V: PC scores of 20 genotypes of brinjal

Genotypes	PC1	PC2
G1	-0.101	0.548
G2	-0.249	0.474
G3	0.209	-0.018
G4	0.234	1.253
G5	-0.972	-0.247
G6	1.76	1.66
G7	0.439	0.521
G8	-0.852	0.404
G9	-0.738	-0.15
G10	-0.343	1.358
G11	1.971	-0.679
G12	-1.213	0.637
G13	-0.734	-0.193
G14	1.841	0.55
G15	-1.743	0.522
G16	0.287	-1.423
G17	-0.391	-1.931
G18	0.792	-1.809
G19	-0.098	-1.045
G20	-0.1	-0.433

Appendix VI: 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%
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