"Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization".

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(MSH-2018-230)

Division of Vegetable Science

Faculty of Horticulture

Sher-e-Kashmir University of Agricultural Sciences and

Technology of Kashmir

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“Parents”

They hold us in arms as we enter this world, they nourish us to be human beings
Someone who encourages all our efforts and appreciate us wholeheartedly
Someone who listens patiently to our never ending doubts
Some who’s eyes shine with pride and happiness at our every little achievement
Someone who helps us to smile instead shedding a tear
Someone who is our life-long friend

DEDICATE MY THESIS

“To serve whom was my dream and
Dream of serving them remain
forever”

“MY BELOVED PARENTS”

Sher-e-Kashmir
University of Agricultural Sciences and Technology of Kashmir
Division of Vegetable Science, Shalimar Campus, Srinagar 190025

Certificate- I

This is to certify that the thesis entitled**, "Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization".** submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science in Horticulture (Vegetable Science)** to the **Faculty of Horticulture, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir** is a record of bonafide research work carried out by **Mr. Nawaz Ahmad Ganie (Regd. No. MSH-2018-230**) under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

It is further certified that any help or information received during the course of investigation has duly been acknowledged.

Dr. Ajaz Ahmed Malik
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Certificate – II

We, the members of the Advisory Committee of **Mr. Nawaz Ahmad Ganie (Regd. No. MSH-2018-230),** a candidate for the degree of **Master of Science in Horticulture (Vegetable Science)** have gone through the manuscript of the thesis entitled, **"Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization ".** and recommend that it may be submitted by the student in partial fulfillment of the requirements for award of the degree.

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Certificate – III

This is to certify that the thesis entitled, **"Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization".** submitted by **Mr. Nawaz Ahmad Ganie (Regd. No. MSH-2018-230)** to the **Faculty of Horticulture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir** in partial fulfillment of the requirements for award of the degree of **Master of Science in Horticulture (Vegetable Science)** was examined and approved by the Advisory Committee and External Examiner on ……...

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ABSTRACT

The present investigation entitled **"Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization".** was carried out at Experimental Field, Division of Vegetable Science, SKUAST-K, Shalimar during Kharif, 2019. The experiment was laid out in randomized complete block design (RCBD) with three replications. Forty one genotypes were evaluated for various quantitative and qualitative traits. Analysis of variance revealed significant differences among the genotypes for all the traits. The maximum fruit yield per plant was recorded in SK-BL-105 (1125.33) followed by 2017/BRL VAR-7 (1092.88), SK-BL-103 (1009.99) and minimum in SK-BL-116 (254.33). The estimates of phenotypic correlation coefficients, in general were higher in magnitude than genotypic correlation coefficients for all the characters indicating the little influence of environmental factors in the expression of traits. High Genotypic coefficient of variation and Phenotypic coefficient of variation were found in some characters viz., number of flowers per cluster, number of fruits per cluster, fruit length, fruit diameter, petiole length, number of fruits per plant, fruit yield plant per plant, fruit yield hectare per hectare, TSS, and ferulic acid. High heritability coupled with high genetic gain was recorded for number of flowers per cluster, number of fruits per cluster, fruit length, fruit diameter, petiole

length, number of fruits per plant, fruit yield plant per plant, fruit yield hectare per hectare, TSS, dry matter, FRAP, scavenging activity (DPPH), ferulic acid. Correlation was positively significant in case of number of flowers per cluster, number of fruits per cluster, plant height, number of branches per plant, number of fruits per plant, average fruit weight and fruit yield per plant with fruit yield per hectare at both genotypic and phenotypic levels. Genetic divergence analysis grouped forty one genotypes into four clusters, cluster I had maximum number of genotypes (16) followed by cluster II (11), cluster III (7) and cluster IV (7). The maximum intra-cluster distance was found in cluster II. The maximum inter-cluster distance was highest between cluster III and cluster IV followed by cluster II and III.

A total of 15 ISSR (Inter-simple sequence repeats) markers were used in this study to analyze the genetic diversity among the genotypes. Number of alleles per locus ranged from two (BGCO5 830, BGCO5 824, BGCO5 848) to twelve (BGCO5 860). The polymorphic information content (PIC) of the loci ranged from 0.261 (BGCO5 823, BGCO5 848) to 0.383 (BGCO5 860). The jaccards similarity quotient is minimum between G2 and G17 (0.05) that indicates these are more diverse than other genotypes. The present study indicates usefulness of assessing genetic diversity at DNA level using ISSR markers and its potential to determine the similarity between genotypes more precisely.

Key words: Solanum sps, Genetic divergence, PCV, GCV, ISSR

Signature of Student **Signature of Major Advisor**

Dated:_____ Dated:_____

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Nawaz Ahmad Ganie

Place: Shalimar, Srinagar
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CONTENTS

LIST OF TABLES

LIST OF FIGRUES

LIST OF PLATES

Chapter -1

INTRODUCTION

Brinjal or Eggplant or Aubergine (*Solanum melongena* L., 2n =2x= 24) belongs to family Solanaceae sub-family Solanoideae very large genus Solanum, sub genus, leptostemonus section Melongena and tribe Solaneae (Yang *et al.*, 2014). It is the third most important vegetable crop after tomato and potato in the genus Solanum. The genus Solanum has about 1500 species. Genus Solanum consists both tuberiferous and non-tuberiferous species. *Solanum melongena* is a non-tuberiferous species. It is a polymorphic taxon encompassing three horticultural varieties or groups viz., esculentum (round or egg-shaped cultivars), serpentinum (long slender varieties) and depressum (dwarf variety).

Most of the genus Solanum are representatives of new world. However, eggplants are phylogenetically distinct and are indigenous to old world with most related species reported to be orginated in India, Africa, and South America (Knapp *et al.,* 2013). Eggplant is widely cultivated vegetable in both temperate and tropical areas, especially in Asia. It has been revealed that the eggplant production has increased upto threefold in the last two decades. India is one of the largest brinjal producing country in the world grown in an area of 0.73 million hectare with a production of 12.80 million tonnes (Anonymous, 2018).

Importance of brinjal as food and medicine has been reported as early as 300 BC in several saniskrit documents (Nadkarni, 1927). Brinjal is highly nutritious vegetable being rich in vitamin C, vitamin A and minerals like calcium, magnesium and phosphorous (Bose and Som, 1986). It helps in minimizing blood cholesterol level. The de-cholestrolizing action is attributed to presence of poly unsaturated fatty acid (Linoleic acid and Linolenic acid) which are present in flesh and seeds of the fruit in higher amount (Thamburaj and Singh, 2015). In Ayurvedic, white types are recommended for diabetic patients and roots for treatment of asthama (Khan, 1979). Brinjal is a low calorie vegetable rich source

of potassium and high dietary fiber content which makes it ideal for diabetics, hypersensitive and obese patients. The unripe fruit is primarily used as cooked vegetable or mixed with other vegetables in fish curry, saubhar, mashed, fried, griffed and stuffed with spices and then fried (Barta) and also as a raw material in pickle making.

Crop improvement depends largely on availability of genetic variability in germplasm, there effective evaluation and utilization. This genetic variability is responsible for the different traits in species and has enabled crop species to adapt to variety of environments that exist in the world. Adequate genetic variability ensures better chances of producing new forms (Aremu, 2011). Knowledge of the magnitude and existence of variability in the available germplasm is important in order to bring about genetic improvement in this crop, which eventually helps to develop an appropriate breeding programe for high yield and other desirable characteristics and to understand the role of the environment in the expression of different plant traits. In the segregating population, successful selection of better genotypes primarily depends on the degree of genetic variability between the selected parent and the magnitude of genetic distance in the selected genotype.

Genetic diversity in plants has traditionally been established using morphological and biochemical markers. A morphological characterization is the first step in the description and classification of local genetic resources (Smith and Smith, 1989). Morphological identification using traditional descriptors has been helpful in describing and defining relationships between genetic resources of local eggplants (Boyaci *et al*., 2010). However, genetic diversity based on phenotypic evaluation of morphological traits demands collection of extensive data at different locations and most of these traits are polygenic in nature thus, influenced by environment. Also the level of polymorphism for morphological characteristic in elite germplasm is too limited and inadequate to allow for varietal discrimination. The cultivar evaluation and estimation of genetic diversity using phenotypic markers only have several limitations.

In contrast, all the drawbacks observed when using biochemical and morphological markers are resolved by molecular markers. They are a powerful tool for evaluating the relationship between accessions on the basis of genetic similarity estimation. They are more authentic, accurate, less dependent and influenced by environmental factors and are highly reproducible. There are primarily two kinds of molecular markers, molecular markers based on hybridization (RFLPs) and molecular markers based on PCR (RAPDs, AFLPs and SSRs). For genotype characterization, genome analysis and gene mapping in different crop species, the Simple Sequence Repeat (SSR) markers are widely preferred, as these are PCR-based, co-dominant, stable, accurate, reproducible, hypervariable, informative and easy to use. They may also have greater discrimination power than markers like RFLP or RAPD. SSRs or microsatellites are randomly repeated short nucleotide units of 1 to 6 nucleotides. These repeats are multi-allelic in nature, codominant, relatively abundant, provide extensive genome coverage with high resolution and are easily detectable by PCR using a small amount of genomic DNA as a template (Stàgel *et al.* 2008; Powell *et al*. 1996). In addition, the application of these markers is fairly inexpensive once SSR primers have been designed. (Nunome *et al.,* 2003) have developed genomic SSRs for eggplants, while (Stàgel *et al*., 2008) have developed genomic SSRs that have been tested primarily on eggplant cultivars. A large number of genotypes having ample variability for different traits are being cultivated in India and some of these variations are so localized which restricts their cultivation in that particular zone only and thus their cultivation is unknown beyond that particular zone. Due to their restricted distribution, some of these promising genotypes are yet to be known. So, it is important to estimate the performance of local and exotic genotypes of brinjal for finding out best genotypes under temperate conditions of Kashmir valley.

The present investigation shall be undertaken to estimate Morphological, Molecular and Biochemical diversity of brinjal and to study the feasibility of utilizing all these information for varietal improvement of the brinjal.

1. Assessment of Genetic divergence among brinjal genotypes based on qualitative and quantitative traits.
2. Molecular characterization and diversity analysis in brinjal using ISSR markers.

Chapter -2

REVIEW OF LITERATURE

The plant breeder is largely concerned with enhancement of both quantitative and qualitative traits. It is important to recognize the genetic makeup of various important traits and interrelationship among them. In the present investigation, an effort has been made to study morphological, molecular and biochemical characterization in brinjal (*Solanum melongena* L.). A brief review of available literature pertaining to the investigation is present in this chapter under the following headings.

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation analysis

2.3 Biochemical characterization

2.4 Genetic divergence

2.5 Molecular characterization

2.1 Genetic variability, heritability and genetic advance

The planning and implementation of any breeding program to improve quantitative characteristics depends on the extent of genetic variability and diversity present in the germplasm to a large extent. Hence, genetic variability is the pre-requisite for any crop improvement program. In terms of mendelian genetics, (Fisher, 1918) interprets quantitative traits, and subsequently the estimates of genotypic and phenotypic variations were used to predict the genetic response. To measure the degree of variability between two different traits, the variability coefficient is used. The phenotypic and genotypic variation coefficients were determined according to the Burton formula (1952).

Mohanty (2002) reported that high heritability accompanied by moderate to high genetic gain were observed for average fruit weight, number of fruits and branches per plant which could be improved by selection in early generation.

Naik (2006) at Karnataka conducted experiment to study genetic variability of sixty two genotypes of brinjal. The results showed that fruit length, number of fruits per cluster, number of fruits per plant, total yield per plant, and fruit length to diameter ratio were high for GCV and PCV. For fruit length, number of fruits per cluster, number of fruits per plant, total yield per plant, and fruit length to diameter ratio, high heritability coupled with high genetic advance over mean was observed, suggesting the predominance of additive gene action for these characteristics.

Kamani and Monpara (2006) conducted experiment with three brinjal varieties (H-7, PLR-1 and GBL-1), their F1 and F2 generations at Junagarh. Heritability and associations for ten traits were determined. All the traits were mostly genetically regulated in both crosses, with the exception of days to first picking in both crosses and plant height in one cross, for which environmental variation accounted for a substantial portion of the overall variability. Due to the major environmental variance, the heritability for days to first picking and plant height was unpredictable. For other traits, the high heritability estimates warrant good progress from selection.

Patel (2007) observed high estimates of PCV coupled with GCV in fruit weight, number of flowers per cluster, fruit length, fruit stalk length and fruit yield per plant. High heritability was observed for days to 50 percent flowering, fruit yield per plant, fruit weight, number of flowers per cluster, plant height, fruit length, fruit girth and fruit stalk length coupled with high genetic advancement as a percent of mean.

Ram *et al*. (2007) at Kalyanpur observed high genotypic and phenotypic c oefficient of variation for yield per plant, number of fruits per plant and plant

spread in parents. Characters including plant height, days to marketable maturity, plant spread, days to flowering, fruit yield per plant, fruit weight and number of branches per plant in F1s, F2s and parent populations showed high heritability coupled with high genetic advance suggesting additive gene action.

Senapati *et al*. (2009) recorded high heritability estimates for the number of fruits per plant, fruit weight and fruit yield per plant, coupled with high genetic advance.

Ansari (2010) at Raipur observed high GCV and PCV for number of number of fruit per picking, flower per inflorescence, and fruit girth, moderate for average fruit weight, number of fruits per cluster, total number of fruits per plant and fruit length whereas, low for days to first flowering, days to 50% flowering, days to first picking, days to first fruiting, number of primary branches/plant, plant height, total fruit yield/plant and total soluble solids. High heritability with high genetic advance was observed for average fruit weight and total number of fruits/plant, genetic advance coupled with moderate heritability for number of fruits/cluster.

Naik *et al*. (2010) reported high values of genetic advance over mean coupled with high estimates of heritability was observed for number of fruits per cluster, fruit length, yield per plot, number of fruits per plant, yield per hectare and fruit length diameter ratio in brinjal.

Ansari *et al*. (2011) estimated mean performance and genetic variability parameters in 7 parents and twenty one hybrids of brinjal from. The study revealed that highly significant differences were observed for most of the traits. Mean performance reported that IBWL had the highest fruit yield of 1004 g per plant, followed by PPC (974g), GL (931g), MK (918g) and PPR (872g), while F1 showed that PPC x PPR had a fruit yield of 1347 g per plant, followed by WBPF x PPR (1317 g), IBWL x PPR (1293g), IBWL x PPC, PPL x PPR (1287g), WBPF x PPC (1282g), IBWL x WBPF and PPL x PPC (1274g). Moderate estimates of

Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were observed for average fruit weight, number of fruits per cluster, fruit length, total number of fruits per plant. For the number of flowers per inflorescence, number of fruits per picking and fruit girth, maximum Genotypic Coefficient of Variation (GCV) & Phenotypic Coefficient of Variation (PCV) have been observed, suggesting that selection can be predicted to improve the brinjal genotypes for these characters. The highest heritability estimates, combined with the high estimated genetic advance for the average fruit weight and number of fruits per plant, showed the efficacy of simple selection to improve these characteristics.

Kumar *et al.* (2013) evaluated 54 genotypes of Brinjal which consisted of 14 parents (ten land races, four commercial varieties) and forty hybrids observed sufficient variability for all horticultural and quality traits. In parents, high estimates of the phenotypic and genotypic coefficient of variation for fruit length, calyx length, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant were observed. The characters viz., length of fruit, length of calyx, number of fruits per plant, little leaf incidence, total phenol content and fruit yield per plant also showed a high heritability magnitude coupled with genetic advancement.

Kumar S.R *et al*. (2013) conducted field experiment to find out variability in segregants of eggplant. The crosses L5 x T4 (Palamedu Local x EP 65) and L4 x T1 (Alagarkovil Local x Annamalai) had the maximum mean with high variability for individual fruit weight and fruit yield per plant. These crosses were best for using as a base population for further improvement in fruit weight and fruit yield as they had high heritability and genetic advance. Favorable low mean with high variability occurred for days to first flowering in the crosses L5 x T2 (Palamedu Local x KKM 1) and L4 x T2 (Alagarkovil Local x KKM 1). Direct selection may be executed, taking into account these genotypes for selection towards the improvement of early flowering and high yielding brinjal variety.

Ramesh Kumar (2014) studied mean performance and genetic variability parameters in 33 local types of brinjal to identify suitable parents for hybridization. The analysis showed that for most of the characteristics, highly significant variations were found. Mean performance showed that EP 27 (1.93 g) recorded the highest yield of fruit per plant, followed by EP 3, respectively (1.83 g). High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the number of primary branches per plant, inter nodal length and average number of fruits per plant, fruit weight, and fruit yield per plant have been observed, indicating that selection can be predicted to boost the genotypes of brinjal for these traits. High heritability estimates combined with high genetic advance as a percentage of the mean expected number of primary branches per plant, internodal length, length of fruit, mean fruit weight, ascorbic acid content, number of fruits per plant and yield of fruit per plant.

Dhaka and Soni (2014) observed highly significant differences among the 20 diverse brinjal genotypes for different traits. The average fruit weight displayed the highest coefficient of variation (phenotypic and genotypic), closely followed by yield per plant. The lowest values for days to first flowering were recorded, followed by days to first picking. The heritability figures for all the characters were high (above 85 percent). For the number of fruits per plant and average fruit weight, maximum heritability was observed. For average fruit weight, yield per plant, number of fruit per plant, and number of leaves per plant, the genetic advance as a percentage of mean was high. For yield per plant and number of fruit plants per plant high GCV and heritability coupled with high genetic advancement were observed, indicating that they are regulated by additive genes and could be effectively improved by selection.

Nayak and Nagre (2014) conducted field experiment consisting of 20 genotypes along with one brinjal as check and the experiment was laid out with three replications in randomized block design. Studies of variability showed that for all characters, significant differences were reported between the varieties.

which comprised of 20 genotypes along with one check 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 traits. Correlation and path analysis showed that diameter, fruit length, weight had a high direct impact on fruit yield in plants and a strong positive correlation.

Hassan (2015) characterized twenty two different Eggplant accessions for various agro-morphological traits. For most of the parameters analyzed, the study demonstrated an average to high variance like f ruit weight, angle of branching, flowering days and plant height. However, for leaf lobation, petiole thickness, inter node length and number of flower(s) per axil, low variance has been observed. In particular, the relationship between characteristics contributing to yield was important. The 22 Eggplant genotypes were grouped into three clusters by cluster analysis and each cluster was further sub-divided into two sub-clusters. The pattern of clustering showed no correspondence with the collection origin. As compared to other genotypes tested, the genotype 19326 remained outstanding in terms of better efficiency. The genotypes clustered in Cluster-I were typically tall with high mean values of different parameters, and followed by clusters-II and III. In the germplasm accessions, the fruit shape and color observed ranged from round form to elongated and dark purple to white. The predominant shape was round (40.9 percent) and purple (54 percent).While the germplasm examined consisted of only 22 accessions, it revealed diverse pattern based on different characteristics.

Reshmika P. K. (2015) reported that degree of genetic variability and divergence existing in the germplasm depends to the greater extent upon the planning and execution of a breeding program for the improvement of quantitative traits. For a genotype, selection is based upon the association of traits. Correlation coefficients become more evident when they are partitioned into their components in path analysis (Kalloo, 1994). By following suitable breeding strategies, the

existing variability can be used to further improve the yield level of the brinjal cultivars. For hybridization programme, diverse genotypes can be utilized also. Emphasis must be given to the traits having high direct and positive effect on yield like number of fruits plant per plant and fruit weight.

Solaimana *et al*. (2015) studied thirty five genotypes of brinjal and found significant variation for all the traits within genotypes. The phenotypic (PCV) was high than genotypic coefficient variation. The PCV estimates were high for number of fruit per plant, number branches, single fruit weight. For single fruit weight, heritability estimates were high with high genetic advance. The expected genetic advance as percentage of mean ranged from 19.92 to 121.51, inspite of high heritability values for most traits. The genotypes were summed into six clusters. The High inter-cluster distance was found between cluster II and III and lowest between V and VI. Maximum intra-cluster distance was showen by Cluster VI and II showed the lowest. Genotypes of cluster I were appropriate for number of branches per plant, cluster II for fruit length, cluster III for number of fruit per plant, cluster IV for single fruit weight and yield.During evaluation, genotypes SM-111, SM-84, EGN-27, SM-183, BARI begun-6 might be considered as suitable parents for efficient breeding program. Cluster III and cluster IV with traits of high yielding capacity could be useful for hybridization programme.

Das *et al*. (2017) evaluated and characterized twenty one brinjal genotypes during two consecutive autumn-winter season of 2014-2016. A sum of 47 traits viz. growth and yield characteristics were studied and significant difference observed amongst the genotypes collected across the country. Due to the effect of genotype, environment or their interaction the variability may be observed. For this experiment, a randomized block design of three replications was used. Mean data pooled over the years, except for the number of fruits per plant, fruit weight, number of seeds per fruit, yield per plant and yield per hectare, was given and statistically analyzed for all characteristics. Although the BCB-27 genotype, followed by BCB-8, is the highest yielder for two seasons per plant, BCB-8 is

superior in total fruiting period, fruit length and number of fruits per plant to all other genotypes.

Balas *et al*. (2019) carried out an investigation having three replications at Vegetable Research Station, Junagadh Agricultural University) in Randomized Block Design. There were 35 genotypes and 5 control varieties of the experimental material. The analysis of variance showed that for all 14 characters analyzed, the mean sum of square due to genotype was highly significant. High PCV, GCV, heritability combined with high genetic gain were observed for fruit borer infestation, number of fruits per plant, weight of fruit, length of fruit, number of branches per plant, height of plant and total yield of fruit per plant.

Sulaiman *et al.* (2020) conducted a study on twenty nine eggplant accessions by using agro-morphological traits studied under two cropping conditions namely glasshouse and open field. The experiments were laid out with three replications in a randomized block design (RCBD). Data on vegetative and yield traits were obtained and subjected to variance analysis (ANOVA) using SAS 9.4, while the variance components were manually calculated. The findings obtained from the ANOVA showed a highly significant difference ($p = 0.01$) in both cropping conditions for all the traits studied. Using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) Dendrogram, the evaluated accessions were grouped into six major clusters based on agro-morphological traits. Therefore, crosses could be used between group I with VI or V to achieve higher heterosis and vigor among the accessions. This evaluation may also be used as a selection criterion for major agronomic yield characteristics in eggplants.

Sakriya *et al*. (2020) carried out an investigation on 180 genotypes of brinjal to analyse the genetic variation, heritability and genetic advance of thirteen different traits. Highly considerable differences were seen among all the genotypes and traits except days to last picking under study signifying the presence of sufficient amount of variation in all the traits. PCV estimates were

high than their subsequent GCV for all traits studied. GCV was found low for all the traits whereas, PCV was moderate for fruit yield per plant (15.69%) followed by number of fruits per plant (15.43%). High heritability was noticed for fruit length (86.62%), plant height (76.73%), plant spread – EW (72.99%), number of branches per plant (72.12%) and TSS (63.38%). Expected genetic advance was observed to be low for all the traits

2.2 Correlation analysis

A correlation is the ratio of the appropriate covariance to the product of the two standard deviations. Essentially it is a measure of the intensity of association between any two traits.

Correlations were helpful to ascertain the real component of yield which is complex characteristic. The correlation coefficient indicates the degree of association between traits but it alone does not give the clear picture of association between yield and its components. The knowledge of direct and indirect influence of yield components is prime importance to select suitable genotype for improving the yield.

Genotypic correlation co-efficient provides measure of genotypic association among the traits and gives indication of more useful traits. They provide basic information that which species was useful to breeder with which they work.

Patel and Sarnaik (2004) at Raipur observed correlation coefficient on twenty four genotypes of brinjal and found that fruit yield per plant had positive correlation with number of branches, fruit size index and fruit width but significant positive association was observed with number of fruit length, fruits per plant and weight per fruit at genotypic level.

Katoch *et al.* (2005) conducted correlation studies on nineteen genotypes of brinjal at Palampur. The results expressed that yield per plant was positively and significantly corelated with number of fruits, gross yield and

total number of fruits per plant. Days taken to flowering were significantly associated with days taken to first picking.

Kushwah and Bandhyopadhya (2005) at Tehri Garhwal, conducted correla tion analysis study for thirteen traits of aubergine. Results showed that at the genetic level, the number of fruits per plant, fruit diameter and number of pickings showed a significant positive correlation with fruit yield per plant. At the phenotypic level, fruit yield was positively correlated with the number of pickings, fruit diameter and number of fruits per plant, but was negatively correlated with the number of days to first picking. Fruit weight and diameter were negatively correlated with the number of fruits per plant, number of fruits per cluster, fruit length and number of flowers per cluster.

Nair and Mehta (2007) conducted an experiment on twenty diverse aubergine genotypes to decide the correlation between yield and its components at phenotypic level besides estimating the direct and indirect effects through path coefficient analysis and reported that the correlation coefficient at the phenotypic level of yield per plant was significant and positive with number of fruits per plant, percentage fruit set, leaf area index and plant height. Negative and significant correlation was observed with days to flower initiation, number of branches per plant, days to first picking, number of fruits per cluster and days to last picking. Path coefficient analysis showed that weight of fruit, number of fruits per plant, days to flower initiation, seed weight per fruit, leaf area index, number of fruits per cluster, days to first picking, length of fruits and number of branches per plant exerted direct positive effect on yield per plant.

Patel (2007) estimated correlation coefficient in sixty three genotypes of brinjal and found that, at phenotypic level, number of branches per plant, fruit girth and fruit weight were positively associated with fruit yield per plant. Whereas, trait fruit girth expressed significant positive correlation with fruit yield per plant at genotypic level.

Lohakare *et al.* (2008) at Akola estimated the correlation in 23 genotypes of green fruited brinjal and reported yield per plant was closely associated with number of fruits per cluster, fruit index, number of fruits per plant and average fruit weight.

Bansal and Mehta (2008) studied the correlation in twenty six brinjal genotypes (Solanum melongena L.) expressed a positive association of yield per plant with plant height, branches per plant, plant spread, and fruits per plant, leaves per plant at genotypic level.

Ansari (2010) at Raipur studied the association analysis in total fruit yield per plant expressed positive and significant association with fruit yield per plant, number of fruits per picking, number of primary branches per plant and total number of fruit per plant in both the seasons; number of fruits per cluster in rainy season only, whereas, negative significant correlation with days to first picking, days to first flowering, days to 50 percent flowering, days to first fruiting in both seasons.

Nalini *et al*. (2009) studied correlation in 36 genotype and revealed that there was strong correlation for number of branches per plant, fruit weight and flower per inflorescence with fruit yield.

Lakshmi *et al.* (2014) studied correlation coefficient analysis of eighty four brinjal varieties revealed that the correlation between the number of flowers per cluster, the number of fruits per cluster, the average length of the fruit and the number of fruits per plant with the yield of fruit was positive and highly significant and these traits were regarded as components of yield. Thus, the genetic improvement of the fruit yield can be achieved by direct selection of these components of the yield. Path coefficient analysis revealed that the traits viz., fruit set percentage, fruit weight, number of fruits per plant, relative style length, number of flowers per cluster and number of fruits per cluster had high direct and

correlation values. Thus, the fruit yield per plant can be improved by making selection of these traits during yield improvement programme.

Thangamani *et al.* (2014) revealed that correlation studies for yield per plant showed positive correlation with number of branches per plant, percentage of long styled flowers, number of fruits per plant, fruit dry matter content and ascorbic acid content of 25 F1 hybrids in brinjal. For days to first flowering, significant negative association of yield was observed. A significant positive correlation for fruit borer incidence with calyx length and fruit girth was observed however, negative significant correlation with total phenols, ascorbic acid content and dry matter was observed. The path analysis study revealed that the number of fruits per plant is the most significant yield determinant trait that influence the yield through number of branches per plant and fruit weight. The yield is influenced by moderate effects exerted by fruit girth, fruit length and dry matter content by many other yield enhancing traits. Importance have to be given for traits having high direct effect like number of fruits per plant to enhance the yield.

Musa *et al*. (2015) conducted his research at the Student Research and Demonstration Farm of Kogi State University (Longitude 07 061 N; 43 ° E), Anyigba, Kogi State, to investigate the correlation of certain yield characteristics with yield in eggplant (*Solanum melongena* L.). Randomized complete block design (RCBD) with 4 replications was used in which two cultivars of eggplant NC-2 (green) and NC-1 (off-white) were laid out. Number of branches, fruit diameter, number of nodes and number of fruits shows significant and positive correlation with yield. Correlation coefficient for yield vs other growth and yield component: Plant height, number of branches, number of nodes, fruit diameter and number of fruits were found to be 0.983, 0.962, 0.959, 0.906 and 0.891 respectively.

In thirty eight locally collected genotypes, Kumar *et al.* (2020) examined genetic heterogeneity and association with the objective of improving yield through selection. The results showed that wide variability in brinjal was observed

for various characteristics. Higher values were invariably observed for the phenotypic coefficient of variation in comparison to the corresponding genotypic coefficient of variation, suggesting the effect of environmental factors on the expression of traits. High estimates of genotypic coefficient of variation, heritability (broad sense) and genetic advance as percentage of mean together at a glance were observed for the traits such as fruit yield per plant, number of fruits per plant, fruit weight, fruit girth and node at which first flowering appeared, suggesting additive gene action for expression of these traits indicated their possibility of enhancement with simple selection procedure in Brinjal. likewise, correlation studies among the traits indicated that there is a strong inherent association between yield per plant with traits like plant height and number of fruits per plant. Further, plant height, number of fruits per plant, fruit weight, fruit girth, days to 50% flowering, days to first fruiting and days to edible maturity showing significant positive association both at genotypic and phenotypic levels suggested that, these are important correlated traits contributing towards fruit yield of brinjal and simultaneous improvement in these traits will be helpful in brinjal improvement programme.

Chithra *et al.* (2020) studied the correlation and path analysis in 300 F2 segregating population of the bi-parental cross Surya × Harita for 12 different quantitative traits. The correlation study indicated that the total yield per plant had a positive and significant correlation with plant height, number of primary branches, number of flowers per cluster, number of fruits per cluster, fruit diameter, fruit length, average fruit weight and number of fruits per plant. The genetic improvement of fruit yield can be obtained by selection of these yield components. Path analysis revealed that the traits number of fruits per plant, average fruit weight, plant height, fruit length, fruit set percentage, fruit diameter, number of flowers per cluster, days to first picking had high positive direct effect on fruit yield per plant. Thus, the fruit yield per plant can be enhanced by making direct selection of these characters.

2.3 Biochemical characterization

Kandoliya *et al*. (2015) studied the nutritional quality along with various parameters contributing antioxidant activity from brinjal fruits of local varieties. The study revealed that varieties, shows 25.17-40.35% radical scavenging activity (DPPH) as comparable amount of flavanoids (7.42-13.25 mg per 100g) and anthocyanine content along with total phenol (32.89-39.12 mg.100g-1), ascorbic acid (9.43-16.75 mg.100g-1), protein (0.92-1.39 %) and titrable acidity (0.20-0.32 percent) in a pulp of brinjal fruits. The activity value for polyphenol oxidase (PPO), the enzyme responsible for the browning in brinjal ranges from 0.66 to 1.39 OD. min^{-1}. g^{-1} in a fresh pulp of brinjal.

Nayanathara *et al.* (2016) conducted a study on five eggplants genotypes and were evaluated for total phenolic activity, total flavonoid activity and anthocyanin activity. The results showed that the total phenolic and flavonoid content of eggplant extract ranged from 856.76 to 386.75 gallic acid equivalents mg/100 g extract and total flavonoid values from 102.01 to 22.62 catechin equivalents mg/100 g extract Violet suphol which contained high total phenolic and flavonoid content had good anthocyanin content as compared (129.29 mg/gm) to other varieties.

Kumari *et al*. (2018) conducted a study on 50 genotypes of brinjal bearing fruits of various colours were examined for anthocyanin content in peel, flesh part and whole fruit in fresh tissue in 2012 and 2013. The peel had highest anthocyanin in both years followed by whole fruit and flesh part. The fruits of green and white colour have low or negligible anthocyanin content in peel. The genotypes showed maximum anthocyanin content in peel, flesh and whole fruit were SR-312 (purple colour) SR-308 (green colour) and SR-303 (purple colour) respectively.

Koundinya *et al*. (2019) examined the different fruit quality parameters between the Spring-Summer (February-June) and Autumn-Winter (September-

March) seasons and the extent of variation contributed by the fruit quality parameters with 40 eggplant germplasm with the help of Principal Component Analysis (PCA). Two factorial ANOVA showed highly signifcant differences for total sugars, vitamin-A, anthocyanin in the peel, total phenols and DPPH free radical scavenging activity for the two factors viz., genotypes (G) and season (S) and their interaction (G X S). Paired t-test also confrmed the seasonal differences for all the fruit quality traits. First four Principal components (PCs), cumulatively contributing 74.4% of total variation, were selected. The first PC contributed 27.9% of total variation and was highly loaded with total phenols, vitamin-C and DPPH free radical scavenging capacity. TSS and total sugars; total phenols and DPPH free radical scavenging capacity; and moisture content and vitamin C were signifcantly positively correlated pairs. Vitamin-C had a significant negative association with total phenols and DPPH free radical scavenging capacity. Anthocyanin in the peel and phenol based DPPH free radical scavenging capacity were also negatively correlated. No outlier was found and the genotypes Kalo Makra, BCB-123 and KS-8103 had the maximum distance from the centroid indicating their diverse nature.

Bidaramali *et al*. (2020) conducted a study on nutrient compounds (on dry weight basis) and the bioactive compounds (on a fresh weight basis) in 20 diverse eggplant genotypes varying in colour and shape. The fruit moisture content ranged from 71.54 to 91.36 percent, while the carbohydrate content ranged from 2.80 to 6.82 percent, crude protein 16.98 to 31.85 percent, nitrogen 2.49 to 4.35 percent, phosphorus 0.29 to 0.51 percent, potassium 1.65 to 4.54 percent, calcium 0.83 to 0.35 percent, iron 106.21 to 235.34 mg/kg, manganese 89.01 to 245.54 mg/kg, copper 18.73 to 98.56 mg/kg, and zinc 60.73 to 245.54 mg/kg. Biochemically related parameters like total soluble solids ranged from1.27 to 3.94 ^{o}Brix, total sugar content 2.26 to 4.65%, ascorbic acid 0.66 to 3.53 mg/100g, total anthocyanin content 0.35 to 18.85 mg/100g FW, total chlorophyll 0.11 to 2.70 mg/100g FW, total phenol 1.03 to 15.65 mg catechol equivalent/100g FW,

total antioxidant 1.16 to 2.26 µmol Trolox equivalent/g FW and radical scavenging activity 50.52 to 96.48 percent. Proximate nutrients were maximum in Pusa Uttam, Pant Rituraj and BRBL -01, quality parameters in BRBL 07 and 71-19, while bioactive compounds were maximum in Pant Rituraj, Pusa Purple cluster, Pusa Purple Long, and BRBL-01.

2.4 Genetic divergence

Sharma and Maurya (2004) studied 40 genotypes of aubergine for genetic divergence. They divided the genotypes into seven clusters. Characteristics such as the number of fruits per plant, the weight of 1000 seeds and the average fruit width have the maximum contribution to genetic divergence. The inter-cluster distance between clusters V and VII was the highest. There was no association between genetic divergence distribution and geographic distribution.

Singh *et al.* (2005) conducted a study on 35 genotypes of brinjal for genetic diversity and grouped them into 11 clusters. The grouping of genotypes was irrespective of geographic distribution. Three genotypes, namely Punjab Sadabahar, Punjab Jamunigola and HP-14, showed maximum diversity from other genotypes and can therefore be used effectively as one of the parents in the hybrid breeding program to utilize heterotic expressions of fruit yield and other economic characteristics.

Naik (2006) analysed genetic divergence in 61 genotypes of brinjal based on D^2 and assembling them into eight clusters. The maximum intra-cluster distance was observed for cluster III and the maximum inter-cluster distance between clusters III and VIII. Fruit length contributed sufficiently towerds diversity among the 16 traits, followed by the number of primary branches, plant height and number of fruits per cluster.

Kumar *et al.* (2008) evaluated morphological diversity in a set of 622 accessions of brinjal, comprising 543 indigenous accessions and 79 accessions of exotic origin. A wide range of variations were recorded for 31 descriptors (13

quantitative and 18 qualitative). For plant, flower and fruit descriptors, the wide regional variations revealed sufficient scope for improving yield traits by selection.

Quamruzzaman *et al*. (2009) assessed genetic divergence among 19 eggplant genotypes and grouped them into five clusters based on D^2 values. Cluster I had the highest number of genotypes (7), and Clusters IV and V had the lowest number of genotypes (7). (2). the distribution pattern of genotypes from different geographical locations into five clusters was random, showing that the only factor causing genetic diversity may not be geographical isolation. For cluster V, the highest intra-cluster distance was observed (1.067) and the lowest for cluster III (0.916). The highest inter-cluster distance between clusters IV and V was observed (10.748). Further emphasis should therefore be placed on cluster V for the selection of genotypes as parents for crossing with cluster II genotypes, which may produce new recombinants with desired characteristics.

Roosevelt and Shanti (2009) studied the divergence in 24 genotypes of brinjal. Cluster-I contains 3 genotypes, cluster-II contains 14 genotypes, cluster-III had two genotypes and cluster-IV had five genotypes on the basis of the relative magnitude of D^2 values. The maximum inter-cluster distance between cluster II and cluster IV was observed (43.45), while the minimum distance between cluster I and cluster III was reported (43.45). (24.39). The genotypes of cluster-IV with the genotypes of cluster III is likely to recombine the genes for high yield, taking into account cluster means and genetic distances. The fruit yield per plant is the highest contributiing factor towerds genetic divergence.

Muniappan *et al*. (2010) conducted a study on genetic divergence to determine the heterogeneity, interaction, direct and indirect effects of eight morphological traits in thirty four genotypes of eggplants. The characteristics viz., number of branches per plant, fruit length, fruit breadth, number of fruits per plant, average fruit weight, and fruit yield per plant have been recorded for high PCV and GCV. Except for days to 50 percent flowering, all the characteristics

were accompanied by high heritability and high genetic advancement. The characteristics were mostly controlled by the additive gene action so, it could be concluded that simple selection for these characteristics would be effective. Characteristics such as the number of branches per plant, the width of the fruit, the number of fruits per plant and the average fruit weight showed a positive and significant association with the yield of the fruit per plant.

Rahman *et al*. (2014) conducted a study on multivariate analysis of genetic divergence in 100 brinjal genotypes and obtained 8 clusters. Cluster I had the largest number of accessions (22), followed by Cluster V(19), Cluster III(17), Cluster IV(17), Cluster VII(10), Cluster VIII(7), Cluster II(6) and Cluster VIII(6) (2). The pattern of clustering showed that the accessions obtained from the same area did not fall within the same cluster, suggesting that there was no association between the accessions' genetic divergence and geographical distribution. The results of the PCA showed that 78.07 percent of the difference between the genotypes considering ten traits accounted for the first four of the principal component axes. The highest inter-cluster divergence between clusters II and VI was found (32.234) and the minimum was between V and VIII (32.234). (2.841).

Madhavi *et al*. (2015) evaluated 21 genotypes of egg plant. Mahalanobis D^2 statistics grouped the 21 genotypes into six clusters Cluster IV, with 7 genotypes, was the largest. Cluster III contains 4 genotypes whereas clusters I, II and V contains three genotypes in each. The VI cluster only had one genotype. Cluster IV (628.54) and cluster I have the highest and lowest intra-cluster distances (93.87). The maximum genetic distance between the inter-clusters was between clusters V and VI (3041.06), while the minimum was between clusters II and III (778.03). Cluster V (Punjab Nagini, Pusa Shyamal and Azad B-3) showed the highest cluster mean for plant height at 50% flowering (51.67 cm), length of fruit (20.33 cm), number of fruits per plant (31.82), number of pickings (6.00) and yield of fruit per plant (1.57 kg). The highest contribution towards total divergence was shown by fruit weight (31.90 percent), number of pickings and

fruit yield per plant (14.29 percent), leaf area and fruit volume (12.86 percent), number of fruits per plant (4.76 percent), plant height at final picking (4.29 percent) and dry matter content (1.90 percent).

Sindhuja *et al.* (2019) conducted a study on genetic divergence based on twelve agronomic traits among fifty six brinjal (*Solanum melongena* L.) genotypes. Significant variations among the genotypes of brinjal were observed for all the traits studied. Fifty six genotypes were resolved by D^2 analysis into as many as eight clusters. Maximum genotypes were obtained in Cluster V (27 genotypes), followed by Cluster IV (11 genotypes), Cluster VII (07 genotypes), Cluster I and Cluster I, contains 4 respectively There were two genotypes in Cluster II, III and IV each. Cluster VIII contains only one genotype. The intra-cluster distance was highest for cluster one.

Silambarasan *et al*. (2020) evaluated fifty assessions of brinjal (*Solanum melongena* L.) for twelve traits to identify genetically diverse genotypes, for the use in cross breeding programme. Analysis of variance revealed significant differences among the genotypes for all the traits of interest. The genotypes viz., VR-2, JBH-3 and Utkalkeshari were called out as elite genotypes, based on per se performance. Clustering of 50 genotypes by utilizing the Mahalanobi's D^2 statistic, gatherd the genotypes into as many as seven clusters. Cluster VII encompassed of with as many as 21 genotypes. Maximum inter-cluster distance was observed between cluster VI and VII. Cluster VI showed earliness coupled with high number of fruits per cluster and comprised of four genotypes. The genotypes gathered in these groups may be used in cross breeding programme to evolve high yielding but early lines or hybrids.

2.5 Molecular characterization

Khorsheduzzaman et *al.* (2008) used Simple Sequence Repeats markers (SSR) for characterization of five brinjal genotypes. In relation to morphological, anatomical and biochemical aspects, all the genotypes showed significant

variation. Based on Jaccard's coefficient value, the genetic similarities of SSR profiles were estimated. Two clusters were formed by the dendrogram and were clearly distinct and distinguished from each other. Cluster-I consisted of genotypes TURBO and BL009; genotypes EG058, EG075 and ISD006 were included in cluster-II. The TURBO and BL009 genotypes were classified as diverse genotypes and showed a maximum dissimilarity of 17 percent to EG058, EG075 and ISD006. The similarity value ranged from 0.83 to 1.00, suggesting the existence at the narrow range of genetic diversity at molecular level, but also having the probability of crossing between the two cluster genotypes. It was possible to use the banding pattern of various genotypes as a reference for further comparisons.

Tiwari *et al.* (2009) studied the description of ninteen superior cultivars and landraces of brinjal using RAPD and ISSR markers. A total of 240 amplified fragments were generated by twenty-nine RAPD primers, while 299 fragments were produced by 23 anchored and non-anchored ISSR primers. Of these, 66 RAPD (27.5 percent) and 56 ISSR fragments (18.73 percent) were polymorphic. It was possible to classify all cultivars based on RAPD and/or ISSR profiles. To differentiate all the 19 cultivars, a set of two RAPD primers, OPW 11 and OPX 07, were sufficient. A minimum of ten ISSR primers were required to achieve the same result. The unique presence or absence of one to four markers could recognize eleven cultivars. It was calculated that the average Jaccard similarity coefficient between cultivars based on combined RAPD and ISSR data was 0.9. Cultivars were grouped into three major clusters by the UPGMA study. While New Delhi formed a sub-cluster of cultivars bred at the Indian Agricultural Research Institute, others did not show a prominent region-based grouping.

Demir *et al.* (2010) conducted a study on molecular diversity of eggplant genotypes gatherd from diverse geographical regions of Turkey using SSR and RAPD markers. The number of alleles per locus of the microsatellite ranged from 2 to 10, with 24 alleles in total.The largest number of alleles was located at

emf21H22 (10 alleles), followed by the five and four alleles of emh11O01 and emf21C11, respectively. The average per-locus number of alleles was 4.8. 100 bands were amplified using 11 decamer RAPD primers, of which 29 were polymorphic. The number of bands per primer was from 7 (OPH10, OPH19, OPH20, OPH03) to 14 (OPH10, OPH19, OPH20, OPH03) (OPB07). Primer OPB07 was the most polymorphic, producing 64 percent polymorphic bands; less than 50 percent polymorphism was provided by the rest of the primers. To analyze the genetic relatedness of the genotypes, UPGMA dendrograms were used.

Ali *et al*. (2011) analyzed the diversity of 143 using ISSR and RAPD markers eggplant using ISSR and RAPD markers. For the identification of genetic diversity, ISSR markers were more efficient than RAPD markers, ranging from 0.10-0.51, slightly lower than what is known from other crops. ISSR/RAPD data provide molecular evidence which, with the exception of two groups, agrees with the morphological classification into three varieties and further subdivision into eight groups.

Hurtado *et al.* (2012) conducted a study on molecular data derived from SSR markers with the morphological descriptors by several workers. Twenty eight morphological descriptors and 12 SSR markers were used to assess the genetic diversity and relationships of 52 accessions of melongena from three geographically distant secondary centres of diversity viz. China, Spain, and Sri Lanka. Accessions from each of the three countries presented a typical combination of morphological characteristics. Many unique alleles confined to each origin were identified by the SSR characterization, but for any of the origins, no universal alleles were found. Most of the accessions were clustered by origin, but there was also evidence of displacement between these three centres.

Verma *et al*. (2012) assessed genetic diversity in 29 popular Indian brinjal varieties using 11 RAPD and 6 SSR primers. The 11 RAPD primers generated 64 polymorphic markers with an average of 5.81 polymorphic bands per primer. Genetic distance based on RAPD markers among all the varieties ranged from

0.07 to 0.78 with an average of 0.33. All the six SSR primer pairs were polymorphic with a total of 25 detected alleles. The number of alleles per primer ranged from 2 to 10, with a mean of 4.67. UPGMA clustering for RAPD and SSR markers grouped all the brinjal varieties into two clusters, but grouping patterns were different for each of the marker system. The maximum genetic gap of One between Pusa Bhairav and Green Long, Green Long and KS-224, Green Long and SL-195, Green Long and KS 331, and between Pusa Kranti and SL-195 was identified on the basis of SSR markers, followed by 0.85 between Pusa Kranti and KS-224, and between NDB-25 and Pusa Kranti. However, majority of the cultivated varieties did not cluster concordant to the collection site information or phenotypic data such as fruit shape or any other known traits.

Channe *et al*. (2013) measured genetic diversity amoung five brinjal varieties by using eleven ISSR markers. 69 scorable bands were generated.

Cluster analysis performed with the markers grouped the genotype into 2 major clusters where cluster A include only one genotype (Pusa Purple long) and cluster B is biggest cluster which include three genotypes. For the first time, the selected primers were used in Brinjal, representing useful tools for future assessments, with focus on the characterization of diversity and genetic mapping.

Naegele *et al*. (2014) used twenty two SSR markers in order to assess the genetic diversity, population structure and resistance to Phytophthora fruit rot, among 99 genotypes of eggplant germplasm representing landraces and heirloom cultivars of S. Ok, Melongena, S. Incanum, S. Incanum S. and Linnaeanum. Gilo, from 32 countries and five continents, obtained. The polymorphism (PIC) for the population was found to be moderate (0.49).

Divya, Konan *et al*. (2020) assessed the genetic variation of nine exotic and local eggplants commonly cultivated in Côte d'Ivoire, using five inter-simple sequence repeat (ISSR) primers. The results revealed for the exotic cultivars 42 ISSR loci of which 31 were polymorphic (73.81 %), and for local cultivars 51 loci of which 49 (96.08%) were polymorphic. The Nei's genetic diversity and

Shannon's information index of local cultivars (He = 0.3333 and I = 0.4863) were higher than those of exotic cultivars (He = 0.2000 and I = 0.2971). The Gst value and the AMOVA analysis found more than 70% of the total genetic diversity within the groups. The Jaccard's dissimilarity coefficients between the cultivars, ranged from 0.324 to 0.966 with an average of 0.741. The clustering of genotypes with the neighbor-joining unrooted tree and PCoA analysis differentiated three main clusters with exotic cultivars grouped in cluster I and local cultivars in cluster II and III. In view of these results, the local eggplants had higher genetic diversity and constitute an interesting germplasm which needs to be conserved for potential breeding programs.

Chapter – 3

MATERIALS AND METHODS

The present investigation entitled **"Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization''** was undertaken at Experimental Farm of Division of Vegetable Science, SKUAST-Kashmir, Shalimar during Kharif 2019. The experimental field is located at 34^{o} N latitude and 74.89^{o} E longitude, 1685 meters above sea level. The climate is temperate characterized by mild summers. June and July are the hottest months while January and February are the coldest. The maximum rain fall is received from March to April.

3.1 Experiment I: Genetic diversity for different morphological traits

3.1.1 Experimental material

Forty one genotypes of brinjal, were evaluated for various yield and yield attributing traits at the Experimental field during Kharif 2019. The list of genotypes along with their source are given in the Table-1.

3.1.2 Experimental Procedure

The experiment was laid out in Randomised Complete Block Design with three replications. The plots of size 2.43 m^2 consisted of 3 rows of each genotype in each replication at spacing of 45 cm x 45 cm. The experimental fields were well prepared and standard agronomic practices were followed to ensure a healthy crop.

Table 1: List of brinjal (*Solanum melongena* L.) genotypes used in the present study

S.NO.	Genotype	Source
1.	SK-BL-100	IIVR
2.	SK-BL-101	IIVR
3.	SK-BL-102	IIVR
4.	SK-BL-103	IIVR
5.	SK-BL-104	IIVR
6.	SK-BL-105	IIVR
7.	SK-BL-106	IIVR
8.	2017/BRL VAR-7	AICRP on vegetable crops
9.	2018/BRL VAR-5	AICRP on vegetable crops
10.	SK-BL-107	IIVR
11.	SK-BL-108	IIVR
12.	SK-BL-109	IIVR
13.	SK-BL-110	IIVR
14.	SK-BL-111	IIVR
15.	SK-BL-112	IIVR
16.	SK-BL-113	IIVR
17.	SK-BL-114	IIVR
18.	SK-BL-115	IIVR
19.	SK-BL-116	IIVR
20.	SK-BR-117	IIVR
21.	SK-BR-118	IIVR

22.	SK-BR-119	IIVR
23.	SK-BR-120	IIVR
24.	SK-BR-121	IIVR
25.	SK-BR-122	IIVR
26.	SK-BR-123	IIVR
27.	SK-BSR-124	IIVR
28.	SK-BSR-125	IIVR
29.	SK-BSR-126	IIVR
30.	SK-BSR-127	IIVR
31.	SK-BSR-128	IIVR
32.	SK-BR-129	IIVR
33.	SK-BR-130	IIVR
34.	SK-BR-131	IIVR
35.	SK-BR-132	IIVR
36.	SK-BR-133	IIVR
37.	SK-BR-134	IIVR
38.	SK-BR-135	IIVR
39.	SK-BR-136	IIVR
40.	SK-BR-137	IIVR
41.	Local Long	Local variety

3.1.3 Morphological traits studied and observational procedures

The descriptors were recorded as per the Minimal Descriptor List of Agri-Horticultural crops, NBPGR (Srivastava *et al.,* 2001).

3.1.3 Descriptor traits

3.1.3.1 Fruit colour

To be recorded on marketable fruits

i. Milky white
ii. Green
iii. Deep yellow
iv. Fire red
v. Scarlet red
vi. Lilac red
vii. Purple
viii. Purple black
ix. Black
x. Light purple
xi. Others

3.1.3.2 Fruit shape

To be recorded on marketable fruits

i. Long
ii. Round
iii. Oblong
iv. Oval
v. Others

3.1.3.3 Plant growth habit

To be recorded at peak fruiting stage

i. Upright
ii. Intermediate
iii. Prostrate
iv. Others

3.1.3.4 Petiole colour

To be recorded on 5th leaf from top at full foliage stage

i. Green
ii. Greenish violet
iii. Violet
iv. Dark violet
v. Dark brown
vi. Others

3.1.3.5 Leaf blade lobing

To be recorded on 5th leaf from top at full foliage stage

i. Very weak
ii. Weak
iii. Intermediate
iv. Strong
v. Very strong
vi. Others

3.1.3.6 Leaf blade tip angle

To be recorded on 5th leaf from top at full foliage stage

i. Very acute «=15 degree)
ii. 3 Acute (>15-45 degree)

iii. Intermediate (>45-75 degree)
iv. Obtuse (>75-110 degree)
v. Very obtuse (>110 degree)
vi. Others

3.1.3.7 Fruit length-breadth ratio

To be recorded as average of same 5-10 fruits at marketable stage

i. Broader than long
ii. As long as broad
iii. Slightly longer than broad
iv. 7 Twice as long as broad
v. Three times as long as broad
vi. Several times as long as broad

3.1.3.8 Fruit curvature

To be recorded on marketable fruits

i. None
ii. Slightly curved
iii. Curved
iv. Snake shaped
v. Sickle shaped
vi. U shaped
vii. Others

3.1.3.9 Presence or absence of spines on fruit calyx

Presence or absence of spines on fruit calyx for each genotype was recorded.

3.1.3.10 Clustering or non clustering habit of flowers

Record for clustering or non clustering habit of flowers for each genotype was carried out.

3.1.3.11 Days to 50% flowering

The plots were observed on daily basis and exact date was noted, when 50% plants of the plot bloomed and half the number of flowers bloomed per plant, the number of days were counted from the date of transplanting.

3.1.3.12 Number of flowers per cluster

Number of flowers on five randomly selected clusters (one cluster from each selected plant) was counted at three stages i.e. after first, second and third picking. Average number of flowers per cluster was calculated at each stage and finally mean value was worked out by dividing summation of averages by three.

3.1.3.13 Number of fruits per cluster

Number of fruits at a single fruiting position was recorded on five randomly selected clusters (one cluster from each selected plant) was counted at three stages i.e. after first, second and third picking. Average number of fruits per cluster was calculated at each stage and finally mean value was worked out by dividing summation of averages with three.

3.1.3.14 Days to first fruit set

The days were recorded from the date of transplanting to the date of first fruit set of the selected plants.

3.1.3.15 Days to first fruit picking

The days were recorded from the date of transplanting to the date of first fruit picking of the selected plants.

3.1.3.16 Plant height (cm)

The plant height was recorded from the ground level to the tip of the plant at the time of final picking.

3.1.3.17 Plant spread (cm)

Plant spread was measured from north to south and east to west directions in 5 randomly selected plants. Average value was calculated per plant.

3.1.3.18 Number of branches per plant

Branches arising on the main stem were counted from the five selected plants.

3.1.3.19 Fruit length (cm)

Five fruits were randomly selected from each tagged plant and fruit length was measured from the base of the fruit to the tip of the fruit (leaving the stalk).The average value was calculated as fruit length.

3.1.3.20 Fruit diameter (cm)

Fruit diameter was measured from the middle portion of the five randomly selected fruits with the help of digital vernier caliper and average value was calculated as fruit diameter.

3.1.3.21 Petiole length (cm)

Petiole length was measured on ten randomly selected leaves of each selected plant with the help of scale and average value was calculated as petiole length.

3.1.3.22 Number of fruits per plant

The number of fruits from each picking were pooled and the total number of fruits per plant was noted.

3.1.3.23 Average fruit weight (g)

Average fruit weight was calculated by dividing the total fruit yield per plant in grams by total number of fruits.

3.1.3.24 Fruit yield per plant (g)

The total weight of fruits obtained from each picking of the tagged plants was pooled and the average fruit yield per plant was worked out.

3.1.3.25 Yield (q/ha)

The fruit yield per plant was converted to fruit yield per hectare using the multiplication factor.

3.2 Biochemical traits

The genotypes under study were used for biochemical characterization.

3.2.1 Total phenols (mg/100g)

Total phenols were estimated by using Folin-Ciocalteu method developed by (Thimmaiah, S. R.1999). In this procedure 5 ml of methanolic extract was evaporated to dryness and the residue was dissolved in 6.5 ml of distilled water. To this 0.5 ml of Folin-Ciocalteu reagent was added and shaken thoroughly followed by addition of 1 ml of standard solution of Na_2CO_3 after interval of 3 minutes and the volume was made up 25ml with distilled water. The blue colour was developed in the reaction mixture whose absorbance was read after 1 hour at 760 nm against the blank. A standard curve was prepared by using catechol and the results were expressed as mg catechol per 100g dry weight.

3.2.2 Anthocyanin (mg/100g)

The 100 g fruit sample was blended in a blender at full speed with 100 ml of ethanolic HCL and then transferred to a 500 ml glass stopper bottle using approximately 50 ml of ethanolic HCL to wash the blender jar. It was then stored at 4^0C in the refrigerator overnight. The sample was then filtered using a Buchner funnel on the whatman no.1 filter paper. The residue was then washed repeatedly with ethanolic HCL on filter paper. Until an extract of approximately 450 ml was collected. The extract was then transferred to a volumetric flask of 500 ml and made to volume. The extract was then filtered by polymidfilterdchromafil AO

45/25 and the sample absorbance was measured at a wavelength of 535nm using ethanolic HCl as blank HCl (Rangana, 1986).

3.2.3 Antioxidant potential (FRAP mmol/gm)

Ferric reducing antioxidant power (FRAP) assay was performed according to the method explained by Kriengask *et al*. (2006) with modifications. The FRAP reagent included 10 mM TPTZ, 20 mM $FeCl_3$, and 0.3 M acetate buffer at 1:1:10 (v/v) ratio. FRAP reagent (3 mL) at 37 °C was mixed with 150 µl of the extract. After a lapse of 4 min, the absorbance was read at 593 nm against a reagent blank and the results were expressed as mmol of Fe^{2+}/g fresh weight using a Fe^{2+} (0.05-0.50 mmol) standard curve.

3.2.4 Determination of Antioxidant Activity by DPPH (%)

A volume of 900 ml Tris HCl buffer (50 mM, pH 7.4) and 2 ml of DPPH were added to the methanol extract (100 ml) of the sample (0.1 mM in methanol). For 30 minutes, the solution was incubated at room temperature and the absorbance was read at 517 nm. The percentage of scavenging activity (DPPH) was determined as follows, DPPH Radical Scavenging Activity (percent) = [(A0-A1)/A0] x100 where control absorbance is A0 and sample absorbance is A1 (Gyamfi *et al*. 1999).

3.2.5 Vitamin C (mg/100g)

A known weight of sample was titrated with 2, 6-dichloro phenol indophenol dye using metaphosphoric acid as stablising agent as per A.O.A.C (1984) method of titration.

Five grams of samples were ground in a stabilizing medium with the help of pestle and mortar (1:5). It was centrifuged. Supernatant was taken and up to 50 ml with stabilizing medium volume was made up and filtered. 10ml of the aliquot was titrated against the 2, 6-dichloro phenol indophenols dye. It calculated the dye factor as:

Five ml of 3% HPO_3 was added to standard ascorbic acid and titrated with the dye solution to a pink colour. The dye factor i.e. mg of ascorbic acid per ml of dye was determined by using the following formula:

Dye factor = 0.5/titre

The vitamin C content of the sample was calculated by the formula given below:

$$\text{Vitamin C (mg/100 mg)} = \frac{\text{Titre value} \times \text{dye factor} \times \text{volume made up x100}}{\text{Total weight of the sample} \times \text{aliquot of sample}}$$

3.2.6 Dry matter (%)

Weighed samples of fruit were chopped and dried in an oven. The dried samples were weighed again and loss in weight was calculated. The dry matter %age was calculated as :

$$\text{Moisture content} = \frac{\text{Fresh weight} - \text{Dry weight}}{\text{Fresh weight}} \times 100$$

$$\text{Dry matter (\%)} = 100\% - \text{Moisture content}$$

3.2.7 TSS (^{o}Brix)

Total soluble solids content was determined by using ERMS hand refractometer. 2-3 drops of juice obtained by crushing a sample of fruit were placed on the prism of refractometer and directly recording the total soluble solid content on scale. Five observations from each treatment were recorded and average calculated. The total soluble solids content was expressed in brix.

3.2.8 Estimation of quercetin and ferullic acid (mg/g) by HPLC Method

3.2.9 Sample preparation for HPLC

Mature fruits were separated from the plants and kept at -20^{o}C. At the time of extraction the fruits were taken out and put in liquid nitrogen, ground in a blender until a fine powder was obtained. 5 g of fine powder was taken in falcon's

tubes and 10ml of methanol: acetone HPLC grade (Hi-media) in the ratio of 70:30 was added and kept in water bath for 10 minutes and then centrifuged for 10 minutes at 10,000 rpm. The supernatants formed was taken out and transferred into rotatory evaporator. The dry extract was dissolved in methanol: acetonitrile (75:25) HPLC grade. Different aliquots were filtered using MCE-hydrophillic syringe driven filters (0.22 µm, Himedia, India) prior to injection into the chromatographic systems.

3.2.10 HPLC analysis

The HPLC analysis of samples was carried out in a Shimadzu HPLC (Kyoto, Japan) equipped with quaternary pumps, degasser coupled to a photo-diode-array detector and injection valve with a 20 µL loop. An injection volume of 20µl, a flow rate of 1ml min^{-1} with 1h run time was used for separation process. Quercetin was detected at 262 nm and the retention time was 1.915 mins. Quercetin, and ferullic acid standard were obtained from Sigma Aldrich. Chromatographic separations were performed on C18 (250 mm 4.6 mm), 5 mm column using a solvent system in gra- dient mode followed by isocratic run as run. The filtration of mobile phase was done through a 0.45 lm membrane filter (Millipore, Bedford, MA, USA) and was subjected to 40 mins ultrasonication. Instrument control, data acquisition and data processing were done by using Class WP software (version 6.1) from Shimadzu. Quantitative determinations were made by taking into account the respective peak areas of standards at particular retention time versus concentration and expressed in mg/g of apple leaves (Shafi *et al*., 2019).

3.3 Experiment II: Molecular characterization of Brinjal (*Solanum melongena* L.) genotypes using ISSR markers

3.3.1 Collection of leaf material

Young, fresh, disease and insect free leaves from all forty genotypes were used for DNA extraction. Leaf samples were collected in butter paper bags and

placed in ice containers while transferring from field to laboratory. They were stored in deep freezer at -80^{o}C for DNA isolation at molecular biology laboratory, ICAR- Central Institute of Temperate Horticulture Srinagar.

3.3.2 Extraction of DNA

DNA was extracted by a cetyl-tri-methyl ammonium bromide (CTAB) protocol given by Sharma *et al*. (2000) with some modifications.

3.3.3 Protocol for DNA isolation

i. Two gram fresh leaf sample from a single seedling was ground in liquid nitrogen to obtain the fine powder.

ii. The powder was immediately transferred to 50 ml polypropylene centrifuge tubes containing 7 ml pre warmed (60 ^{o}C) extraction buffer and was mixed by inversion.

iii. The mixture was incubated for 60 min at 65 ^{o}C in hot water bath followed with intermediate shaking after every 10 min.

iv. 7 ml of Chloroform: lsoamyl alcohol (24:1) was added and mixed gently.

v. Centrifugation was carried out at 15000 rpm for 10 min at room temperature.

vi. The upper aqueous phase was transferred in new pre sterilized centrifuge tubes without disturbing the interface.

vii. 500µl of ice cold isopropanol was added to precipitate the DNA. Centrifugation for 8000 rpm for seven minutes was done and the supernatant was discard.

viii. 1ml of 70% ethanol was added and kept for 10 minutes. Then tubes were centrifuged at 10000 rpm for 5 minutes, supernatant was discarded and DNA pellet at bottom of tube was dried at room temperature.

ix. The DNA pellet was air- dried for 30 minutes and then dissolved in 100µl of TE buffer.

x. The DNA pellets were allowed to dissolve completely overnight at 4 ^{o}C without agitation.

Table 2: List of selected ISSR primers along with their primer sequence

Primer	Primer Sequence	Annealing Temperature (^{o}C)	Expected amplicon size (bp)
BGCO5 860	TGTGTGTGTGTGTGTGCA	49	300-1000
BGCO5 825	ACACACACACACACACT	46.4	150-1000
BGCO5 824	TCTCTCTCTCTCTCTCG	43.5	350-800
BGCO5 847	CACACACACACACACAGC	46	300-900
BGCO5 857	ACACACACACACACACGGTC	53	200-1500
BGCO5 856	ACACACACACACACACG	46	300-700
BGCO5 827	ACACACACACACACACGG	46	250-750
BGCO5 830	TGTGTGTGTGTGTGTGG	47	200-1000
BGCO5 842	GAGAGAGAGAGACCCGGG	51	300-700
BGCO5 814	CTCTCTCTCTCTCTCTA	40	250-700
BGCO5 822	TCTCTCTCTCTCTCAC	40	300-750
BGCO5 848	CACACACACACACACAGC	49	300-900
BGCO5 851	GTGTGTGTGTGTGTGTCG	49	250-750
BGCO5 818	CACACACACACACACAG	46	250-700
BGCO5 823	TCTCTCTCTCTCTCTCC	43	200-1000

3.3.4 Quality assessment of DNA

The concentration and purity of DNA was checked by Agarose gel electrophoresis. Different steps followed were as:

Step 1:1g of agarose was dissolved in 100ml of 1X TBE electrophoresis buffer (Tris base-45 Mm, Boric acid- 45mM and EDTA- 1mM).

Step 2: The mixture was heated in microwave oven for 2 minutes till the agorose dissolved completely i.e., when solution became transparent and clear. It was allowed to cool for a couple of minutes and then stained with ethidium bromide (0.5 µg/ml) of buffer and stirred for some time.

Step 3: It was then poured in the casting tray with combs in it and allowed to solidify for 20-25 minutes at room temperature.

Step 4: Sample DNA along with concentration standards were loaded to estimate the concentration of DNA in each sample.

Step 5: The electrophoresis was carried out at 75V for 2 hours.

Step 6: It was then viewed under gel documentation system.

Step 7: The concentration of DNA was determined by comparing the intensity of bands with that of standards.

3.3.5 DNA Quantification

DNA Quantification was done by using Thermo Scientific Nano Drop™ 1000 Spectrophotometer (Version 3.7.1), which measures 1µl samples with high accuracy and reproducibility. Blank was run using 1 µl of TE buffer (pH 8) and quantification of DNA samples was done by using the same volume (1 µl) of the DNA samples. The results were recorded in nano gram per micro litre (ng/µl) of the sample.

3.3.6 Dilution of DNA samples

An aliquot of DNA from each sample was diluted with appropriate amount of nuclease free water to yield a working concentration of 25 ng/µl and these samples were stored at 4^0C. Remaining DNA sample was stored at -20^oC. The following formula was used for dilution:

$C_1V_1=C_2V_2$

Where,

C1 = Concentration of the DNA in the sample as determined by DNA quantification

V1 = The amount of DNA sample to be taken to make the final concentration of 25 ng/µl

C2 = Required working concentration of the DNA (25 ng/µl)

V2 = Final volume of the DNA sample of 25 ng/µl concentration to be prepared (100 µl).

The volume of sterile distilled water required to make 100 µl of final DNA sample of 25 ng/µl concentration = 100- Volume of DNA sample taken.

3.3.7 ISSR primer optimization

A total of 15 primers were used in this study. Details of primers are provided in Table-2. The primers were synthesized by GCC Biotech India Pvt. Ltd. The primers were then diluted to make a working concentration of 10 mM/µl. Annealing temperatures of different primers ranged from 40-53^{o}C.

3.3.8 PCR amplification by ISSR

PCR tubes containing master mix and DNA template were thoroughly mixed and subjected to the thermal profile. The amplification reaction was carried out in gradient thermo cycler (Takara PCR). As shown in the Table-4 an initial denaturation step of 5 minutes was programmed in the thermo-cycler, followed by

a loop of 35 cycles each consisting of denaturation (at 94°C for 40 seconds), annealing (at 40-53°C for 40 seconds), elongation (at 72°C for 1 minute) and the final extension was performed (at 72 °C for 7 minutes). The composition of PCR reaction mixture is given in the Table-3.

Table 3: The composition of PCR reaction mixture for ISSR analysis

Ingredients	Name of the brand	Stock concentration	Required concentration	Vol. for one reaction	Vol. for 40 reaction
Millipore water	-	-	-	4.2 µl	168 µl
Taq buffer	GeNei™	10X	1X	1 µl	40 µl
dNTPs	Thermo scientific	10mM	1mM	1 µl	40 µl
$MgCl_2$	GeNei™	25mM	1.5mM	0.6 µl	24 µl
Primer	GCC BIOTECH	100µM	10µM	1 µl	40 µl
Taq Polymerase	GeNei™	5 Units/µl	1Unit/µl	0.2 µl	8 µl
DNA Template	-	25ng/µl	50ng/reaction	2 µl	-
Total Volume				10 µl	400 µl

Table 4: Optimum PCR conditions for ISSR analysis

Step	Temperature (°C)	Time	Number of cycles
Initial denaturation	94	5 minutes	1
Denaturation	94	40 seconds	35
Annealing	40-53	40 seconds	35
Elongation	72	1 minute	35
Final Extension	72	7 minutes	1

3.3.9 Electrophoresis of amplified DNA

Amplified DNA fragments were resolved in horizontal electrophoresis using 2% agarose gel and visualized by staining with ethidium bromide. Gel casting plate was washed with distilled water and ethanol and subsequently dried. 2% agarose gel solution was prepared by heating it in oven. The solution was cooled to about 50ºC by keeping it at room temperature for 5-10 minutes. Ethidium bromide was added in the gel at a concentration of 5 µl/100 ml of and mixed. Agarose gel was then poured into the gel casting plate inserted with an appropriate comb with required well number and size to get a 0.5 cm thick gel. Gel was allowed to solidify for 20 minutes. Gel plate was then placed in the electrophoresis chamber and submerged using 1 X TAE (Tris-Acetate- EDTA) buffer. The comb was removed gently. DNA samples were prepared by adding loading dye solution (2µl/PCR reaction) containing bromophenol blue and xylenecyanol. The samples were loaded in the wells using micropipette. Electrophoresis was carried out at constant voltage (3 V/cm of gel) until the dye had moved to 3/4 length in the gel. PCR amplification products were viewed under Gel documentation system by using UV light.

3.3.10 Scoring of ISSR allele profile

Each ISSR band was considered an independent locus, and only distinct, reproducible, and well-resolved fragments were scored visually, as absent (0) or present (1), for each of the 40 genotypes. A locus was considered polymorphic if a consistent band was present in one or more, but not all genotypes of the experiment. Qualitative differences in band intensity were not considered.

3.3.11 Statistical analysis of molecular characterization

The potential of the marker for estimating genetic variability of brinjal was examined by assessing the marker informativeness through the bands scoring. Primer banding characteristics such as number of total bands (TB), number of polymorphic bands (PB), and percentage of polymorphic bands (PPB) were

obtained. In order to analyze the suitability of marker for genetic profile evaluation, the performance of 15 ISSR markers used was measured using three parameters: polymorphic information content (PIC), marker index (MI), and resolving power (RP). The PIC value for each primer was calculated as described by (Roldan-Ruiz *et al*., 2000); PIC*i* = 2f*i* (1-f*i*), where PIC*i* is the polymorphic information content of the locus *i*, fi is the frequency of the amplified allele, and 1-fi is the frequency of non amplified allele. The frequency was calculated as the proportion between the number of amplified alleles at each locus and the total number of accessions. The PIC of each primer was calculated using the average PIC value from all loci of each primer. Marker index for each primer was calculated as product of polymorphic information content and effective multiplex ratio according to (Varshney *et al*., 2007); MI = PIC x EMR, where EMR is the effective multiplex ratio. Effective multiplex ratio was estimated as EMR = n x β, where n is the average number of alleles amplified by accession to a specific system marker (multiplex ratio) and β is estimated after considering the number of polymorphic loci (PB) and non polymorphic loci (MB); β = PB/ (PB+MB). Resolving power is the ability of a primer to distinguish genotypes, which was calculated as RP = ΣIb, where Ib represents the informative bands (Prevost and Wilkinson, 1999). The Ib can be represented into a 0/1 scale by using the following formula: Ib = 1 – (2 x |0.5 - p*i* |), where p*i* is the ratio of accessions comprising the *i*th band. iMEC software was used to measure heterozygosity index (H), polymorphism information content (PIC), discriminating power (D), effective multiplex ratio (EMR), marker index (MI), arithmetic mean heterozygosity (Havp), and resolving power (RP) all these parameters are used for calculating the marker efficiency (Amiryousefi *et al*., 2018).

3.3.12 Statistical analysis using NTSYS-PC version 2.02e

Numerical Taxonomic and Multivariate Analysis System (NTSYS-pc) version 2.02e (Rohlf, 1997) software programme was used to analyze molecular data. Data from 15 primers were used to estimate the similarity based on the

number of shared amplified bands. Similarity was estimated using SIMQUAL function of NTSYS, which computes a variety of similarity coefficient for qualitative data (nominal data). Dendrogram, was constructed using UPGMA (Unweighted Pair Group Method using Arithmetic Averages) by using Jaccard's similarity co-efficients available in NTSYS.

3.4 Statistical and biometrical analysis of morphological and biochemical traits

The data recorded during the present investigation was subjected to the following statistical and biometrical analysis.

- Analysis of variance and estimation of the components of variability,
- Estimation of heritability and expected genetic gain,
- Estimation of phenotypic and genotypic correlation coefficient,
- Divergence analysis

3.4.1 Analysis of variance and estimation of the components of variance

3.4.1.1 Analysis of variance

Analysis of variance for all the traits in randomized block design was carried out for testing variation among the genotypes.

The Analysis of variance table was set up as under:

Source of variation	d.f	SS	MSS	Fcal
Replications	r-1	SSQr	MSR= SSQr/r-1	
Treatments	t-1	SSQt	MST= SSQt/t-1	MST/MSE
Error	(r-1) (t-1)	SSQe	MSE= SSQe/(r-1)(t-1)	
Total	rt-1			

Where,

R	=	Number of replications
T	=	number of treatments
SS	=	sum of squares
MSS	=	mean sum of squares
SSQr	=	Sum of square due to replications
MSR	=	Mean sum of square due to replications
SSQe	=	Sum of square due to error
MSE	=	Mean sum of square due to error
SSQt	=	Sum of square due to treatments
MST	=	Mean sum of square due to treatments

The significance of varietal differences was tested by F-test comparing calculated F-value at 5 and 1 per cent level of significance at treatment (t-1) and error (t-1) (r-1) degrees of freedom

3.4.1.2 Genotypic variance

Genotypic variance was calculated using the method suggested by (Johnson *et al*., 1955).

$$\hat{\sigma}^2_g = \frac{MSG - MSE}{r}$$

Where,

$\hat{\sigma}^2 g$ = Genotypic variance,

MSG = mean sum of squares due to genotypes,

MSE = mean sum of squares due to error, and

R = number of replications

3.4.1.3 Phenotypic variance

Phenotypic variance was calculated as per the procedure given by (Johnson *et al*., 1955).

$$\hat{\sigma}^2 p = \hat{\sigma}^2 g + \hat{\sigma}^2 e$$

Where,

$\hat{\sigma}^2 p$ = Phenotypic variance

$\hat{\sigma}^2 g$ = genotypic variance, and

$\hat{\sigma}^2 e$ = error variance

3.4.1.4 Phenotypic and genotypic co-efficient of variation

The magnitude of phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) existing in a trait was worked out by the formula given by (Burton, 1952):

$$PCV = \frac{\sqrt{\hat{\sigma}^2 p}}{\overline{x}} \times 100$$

Where,

$\hat{\sigma}^2 p$ = Phenotypic variance, and

$\overline{X}$ = grand mean of the trait studied

$$GCV = \frac{\sqrt{\hat{\sigma}^2 g}}{\bar{x}} \times 100$$

Where,

$\hat{\sigma}^2 g$ = Genotypic variance, and

$\bar{x}$ = grand mean of the trait studied

3.4.2 Estimation of heritability genetic advance and expected genetic gain

3.4.2.1 Heritability (broad sense)

It was estimated as per the procedure presented by (Burton, 1952); (Johnson *et al.,* 1955)

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

h^2 = Estimate of heritability in broad sense,

$\sigma^2 g$ = Genotypic variance, and

$\sigma^2 p$ = Phenotypic variance

3.4.2.2 Genetic advance

Genetic advance at 5 per cent selection intensity was worked out by using the formula given by (Lush, 1949) and Johnson *et al*., 1955).

$$GA = \frac{\sigma^2 g}{\sigma^2 p} \times (\sigma^2 p)^{0.5} \times K$$

Where,

GA = Genetic advance of the trait,

$\sigma^2 g$ = genotypic variance of the trait,

$\sigma^2 p$ = phenotypic variance of the trait, and

K = selection differential; (K= 2.06 at 5 per cent selection intensity)

3.4.2.3 Expected genetic gain (genetic advance as per cent of mean)

It was estimated as per the method suggested by (Johnson *et al*., 1955).

$$\text{Genetic gain} = \frac{GA}{\overline{x}} \times 100$$

Where,

GA = Genetic advance of the trait, and

$\overline{x}$ = mean of the trait

3.4.3 Estimation of genotypic and phenotypic covariances and correlation coefficients

Covariance analysis followed the same pattern as the variance analysis. The genotypic and phenotypic covariances between two traits were obtained in the same fashion as corresponding variances. Estimate of genotypic and phenotypic variances and covariances were substituted in the following formula suggested by (Panse and Sukatme, 1985) to calculate correlation co-efficient between all possible pairs of traits.

Genotypic correlation co-efficient

$$r_{xy}\,(g) = \frac{\hat{\sigma}^2{}_{xy}\,(g)}{\sqrt{\hat{\sigma}^2{}_x\,(g)\;\hat{\sigma}^2{}_y\,(g)}}$$

Phenotypic correlation coefficient

$$r_{xy}\ (p) = \frac{\hat{\sigma}^2{}_{xy}\ (p)}{\sqrt{\hat{\sigma}^2{}_{x}\ (p)\ \hat{\sigma}^2{}_{y}\ (p)}}$$

Where,

$\hat{\sigma}^2 xy(g), \hat{\sigma}^2 xy(p)$ = Genotypic and phenotypic covariances, respectively, for a pair of traits x and y

$\hat{\sigma}^2 x(g), \hat{\sigma}^2 y(g)$ = Genotypic variance for traits x and y, respectively, and

$\hat{\sigma}^2 x(p), \hat{\sigma}^2 y(p)$ = Phenotypic variance for character x and y, respectively.

Test of significance

The significance of a correlation co-efficient was tested by the following formula:

$$t = \frac{r\ (n-2)^{0.5}}{(1-r^2)^{0.5}}$$

Where,

r = Correlation coefficient and

n = number of observations

Any value (±) exceeding the table value of t at n-2 d.f is significant.

3.4.4 Estimates of genetic divergence

The genetic divergence was computed using the procedure as described by (Rao, 1952). The details of analysis are described under the following heads:

1. Test of Wilk's criterion,

2. Transformation of correlated variables,
3. Computation of D^2 values,
4. Relative contribution of individual traits towards total divergence, and
5. Group constellation

3.4.4.1 Test of Wilk's criterion

Variances and covariances were obtained from analysis of variance and covariance tables and the following analysis of dispersion table was constructed:

Analysis of dispersion

		Matrix due to			
Dispersion due to	**d.f.**	**Sum of squares**		**sum of products**	
		X^2_1	X^2_2…..	$X_1 X_2$	X_1X_3……
Replications	r-1	A	B	C	d……..
Between genotypes (Q)	Q	a′	b′	c′	d′…..
Genotypes (W)	By subtraction	A-(a)	B-(b)	C-(c)	D-(d)…
Total	**N**	**A**	**B**	**C**	**D……**

The determination of error and error + variety variance-covariance matrix were calculated by pivotal condensation method of using 'V' statistics which, in turn, utilizes Wilk's criteria. A simultaneous test of differences between mean values of traits from all the genotypes in the present study was performed, as per the details given below:

The Wilk's test is:

$$V = -m\log e\,\lambda$$

Where,

$$\lambda = \frac{W}{W + Q}$$

$$= \frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}}$$

$$m = n - \frac{q + k + 1}{2}$$

Where,

N = Total number of observations minus one,

Q = number of variable minus one, and

K = number of traits under study

'V' Statistics so obtained was compared with the tabulated value of χ^2 for 2qk degrees of freedom.

3.4.4.2 Transformation of correlated variables

Plot means of the varieties corresponding to the traits studied were transformed to uncorrelated variables by Pivotal Condensation Method, which rendered the computation of D^2 values between any combinations of two varieties to simple summation of squares of differences in transformed values for various traits. The skeleton procedure of obtaining transformed variables by Pivotal Condensation Method is described below:

Let dispersion matrix of original variables $x_1, x_2 \ldots\ldots\ldots x_p$ be

λ_{11}	λ_{12}	……	λ_{1p}
λ_{21}	λ_{22}	……	λ_{2p}
•	•	……	•
•	•	……	•
•	•	……	•
•	•	……	•
•	•	……	•

λ_{p1} λ_{p2} ..... λ_{pp}

and consider the extended matrix

λ_{11} λ_{12} ..... $\lambda_{1p\ x\ 1}$

λ_{21} λ_{22} ..... $\lambda_{2p\ x\ 2}$

• • ..... •

• • ..... •

• • ..... •

• • ..... •

• • ..... •

λ_{p1} λ_{p2} ..... $\lambda_{pp\ x\ p}$

taking λ_{11} as the first pivotal element, the first row is replaced by

$$1 \quad \frac{\lambda_{12}}{\lambda_{11}} \quad \ldots\ldots\ldots\ldots\ldots\ldots \quad \frac{\lambda_{1p}}{\lambda_{11}} \quad \frac{X\ 1}{\lambda_{11}}$$

Sweeping out first column and using the first pivotal row, following reduced matrix is obtained

$$\begin{pmatrix} \lambda_{22'} & \ldots\ldots\ldots & \lambda_{2p'} \\ \bullet & & \bullet \\ \bullet & & \bullet \\ \bullet & & \bullet \\ \bullet & & \bullet \\ \lambda_{p2'} & \ldots\ldots\ldots & \lambda_{pp'} \end{pmatrix} \begin{pmatrix} X_{2'} \\ \bullet \\ \bullet \\ \bullet \\ \bullet \\ x_{p'} \end{pmatrix}$$

Where,

$$\lambda_{ij} = - \frac{\lambda_{ij}}{\lambda_{11}} \lambda_{ij} x_i$$

$$x_i = - \frac{\lambda_{il}}{\lambda_{ll}} X_1$$

$$\text{Now, } = V_{(xi)} = V_{(xi)} - \frac{2\lambda_{il}}{\lambda_{ll}} \text{Cov.} (x_i x_1) + \frac{2\lambda_{il}}{\lambda_{ll}} V(X_1)$$

$$= \lambda_{ii} - \frac{\lambda_{il}^2}{\lambda_{ll}} X_{1i}$$

$$\text{Now, } V_{(xi')} = + \frac{\lambda_{il}}{\lambda_{ii}} V(xl)$$

Similarly, Cov. $(x'_{i1}\ x'j) = \lambda_{ij}'$

Similarly, Cov. $(x'_i{}'\ x'j') = \lambda_{ij}'$

$$\text{also, cov. } (x\ 1\ x'i) = \text{cov. } (xlxi) - \frac{\Lambda il}{\Lambda ll} v(xi)$$

$$= \lambda il - \lambda il = 0$$

So the new variables are uncorrelated.

Considering the second pivotal row

$$\frac{\lambda 23}{\lambda 22'} \qquad \frac{\lambda 2p'}{\lambda 22'} \qquad \frac{x2'}{22'}$$

the further reduced matrix is

λ33″ ……. λ3p″			λx3″
•			•
•			•
•			•
λp3″	λpp″		xp″

resulting into variables

x1′ x 2′ x 3″ …… with variance

x11′ x λ22′ λ33″ ……..

They are all mutually uncorrelated as shown above and further x'_2, depends on x_1 and x_2', and x_3 on x_1', x_2 and x_3 only.

3.4.4.3 Computation of D^2 values

For each pair-wise combination of the varieties the differences in transformed values for various traits were computed and D^2-values were calculated according to the following formula:

$$D^2 = \sum_{i-1}^{p} (\overline{Y}_{ij} - Y_{ik})^2$$

Where,

P = number of traits studied, and

Y_{ij} and Y_{ik} = are two transformed variables of the i^{th} character for two genotypes

3.4.4.4 Relative contribution of individual traits towards total divergences

The ranking of differences in uncorrelated means between all the traits for all pair-wise combinations of varieties was carried out, with first rank being assigned to the highest differences. Finally relative contribution of a trait towards total divergence was estimated by calculating the percentage of first rank in that trait.

3.4.4.5 Group constellation

Wards D^2 method was used for assigning various varieties to different clusters. The two varieties having smallest distance from each other were considered first to which a third variety having smallest average D^2 value from the first two varieties was added. Next come the nearest fourth variety and the process continued till the average D^2 value increased. The remaining varieties were then considered for the next cluster and the process was continued till all varieties were included in various clusters.

The spatial distances between clusters were arrived at by taking square root of average intra and inter cluster D^2 values.

For each combination (pair of genotypes) the mean deviation (d^2i) i.e. Y_1-Y_1 with I = 1, 2, 3 …….. p was computed and D^2 values were calculated as sum of these deviations i.e. (y_i^1-y_i^2), where, y_i is the transformed variable from the original variable xi. Accordingly D^2 values for all combinations were calculated. The D^2 values so obtained for each pair of population were treated as x^2 and were tested against the tabulated values of λ^2 for p degrees of freedom, where p is the number of traits considered.

In all combinations each trait was ranked on the basis of $d_i = y_{ij} - y_{ik}$ values. Rank I was given to the highest mean difference and rank p to the lowest mean difference, where p is the total number of traits. In this manner contribution of each trait to the total divergence was computed.

Wards hierarchical clustering method for grouping of varieties into various clusters was adopted. All the above computations were carried out using the R software.

Chapter- 4

EXPERIMENTAL FINDINGS

The experimental results obtained through statistical analysis have been presented under the following headings.

4.1 Characterization on the basis of morphological traits

4.2 Mean performance and analysis of variance

4.3 Variability and genetic components of variation

4.4 Characterization on the basis of biochemical traits

4.5 Correlation between various characteristics and genetic divergence studies

4.6 Characterization on the basis of ISSR markers

4.1 Characterization on the basis of morphological traits

Analysis of variance revealed highly significant difference among all forty one genotypes of brinjal Table-7.1 and Table-7.2 for all the traits observed viz., plant height, plant spread, number of primary branches, days to 50% flowering, days taken to first fruit set, fruit diameter, fruit length, petiole length, average fruit weight, number of fruits per plant, fruit yield per plant, number of seeds per fruit, average dry fruit weight and fruit yield per hectare. The result indicated presence of adequate amount of variability in the germplasm under study. Morphological characterization of brinjal genotypes (Table-5) and their mean performance for each trait is presented in Table-6.1 and Table-6.2.

Components of variation**:** Phenotypic variation could represent only rough estimates of the variation or magnitude of divergence present among different genotypes. The estimates of phenotypic and genotypic coefficients of variation are more reliable estimates of genetic variability. As the estimates of phenotypic variability cannot differentiate between genetic and environmental effects, it is necessary to divide the phenotypic or observed variation into heritable (variation

due to genotype) and environmental components. For this purpose, mean, range, phenotypic and genotypic coefficients were computed and their estimates are presented in Table-8. A relative amount of variation for different traits can be judged by comparing the coefficients of genotypic and phenotypic variation.

Heritability is a estimate of genetic relationship between parent and progeny and has been widely used in determining the degree to which a trait may be transmitted from parent to off springs. Knowledge of heritability for the trait helps to measure the genetic advance from selection. The result pertaining to heritability and percentage genetic advance are present in Table-8. Selection of a particular trait is made on the basis of phenotype, which is outcome of interaction between genotype and environment.

4.1.1 Fruit colour

Out of forty-one genotypes twelve genotypes SK-BL-101, SK-BL-105, SK-BL-109, SK-BL-110, SK-BL-111, SK-BL-112, SK-BL-114, SK-BR-119, SK-BSR-125, SK-BSR-126, SK-BR-137 and Local Long (29.26%) had purple colour However, fourteen genotypes (34.14%) 2018/BRL VAR-5, SK-BL-115, SK-BL-116, SK-BR-117, SK-BR-118, SK-BR-121, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BSR-128, SK-BR-130, SK-BR-134, SK-BR-135 and SK-BR-136 showed light purple colour. Nine genotypes (21.95%) SK-BL-103, SK-BL-104, SK-BL-106, SK-BL-107, SK-BL-108, SK-BSR-127, SK-BR-129, SK-BR-132 and SK-BR-133 showed dark purple colour. Three genotypes (7.31%) SK-BL-102, SK-BL-113 and SK-BR-131 showed light green colour. Two genotypes (4.87%) showed green variegated colour viz., SK-BL-100 and SK-BR-120 and one genotype (2.43%) 2017/BRL VAR-7 showed white colour.

4.1.2 Fruit shape

Out of forty-one genotypes, nine genotypes (21.95%) SK-BL-102, SK-BL-103, SK-BL-104, SK-BL-105, SK-BL-110, SK-BL-114, SK-BL-115, SK-BL-116 and Local Long showed long fruit shape. Eight genotypes (19.51%) SK-BL-

101, SK-BL-106, SK-BL-107, SK-BL-108, SK-BL-109, SK-BL-111, SK-BL-112 and SK-BL-113 showed medium long shape. Four genotypes (9.75%) 2017/BRL VAR-7, SK-BL-100, SK-BR-120, SK-BR-134 showed oblong fruit shape. Eight genotypes (19.51%) SK-BR-117, SK-BR-119, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BSR-126, SK-BSR-127 and SK-BSR-128 showed oval fruit shape. Eleven genotypes (26.82%) SK-BR-118, SK-BR-121, SK-BSR-125, SK-BR-129, SK-BR-130, SK-BR-131, SK-BR-132, SK-BR-133, SK-BR-135, SK-BR-136 and SK-BR-137 showed round fruit shape and one genotype (2.43%) 2018/BRL VAR-5 showed very long fruit shape.

4.1.3 Plant growth habit

Twenty six genotypes (63.41%) SK-BL-100,SK-BL-101,SK-BL-102,SK-BL-103,SK-BL-104,SK-BL-105, 2017/BRL VAR-7, SK-BL-109, SK-BL-110, SK-BL-111, SK-BL-113, SK-BL-114, SK-BL-115, SK-BL-116, SK-BR-120, SK-BR-122, SK-BSR-124, SK-BSR-125, SK-BSR-126, SK-BSR-128, SK-BR-129, SK-BR-130, SK-BR-131, SK-BR-132, SK-BR-133 and Local Long showed intermediate plant growth habit. Six genotypes (14.63%) showed SK-BL-106, 2018/BRL VAR-5, SK-BL-112, SK-BR-118, SK-BR-119 and SK-BR-121 upright plant growth habit. Nine genotypes (21.95%) SK-BL-107, SK-BL-108, SK-BR-117, SK-BR-123, SK-BSR-127, SK-BR-134, SK-BR-135, SK-BR-136 and SK-BR-137 showed prostrate plant growth habit.

4.1.4 Petiole colour

Twenty nine genotypes (70.73%) SK-BL-100, SK-BL-101, SK-BL-102, SK-BL-106, 2017/BRL VAR-7, 2018/BRL VAR-5, SK-BL-109, SK-BL-111, SK-BL-112, SK-BL-115, SK-BR-117, SK-BR-118, SK-BR-119, SK-BR-121, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BSR-125, SK-BSR-127, SK-BSR-128, SK-BR-129, SK-BR-130, SK-BR-131, SK-BR-132, SK-BR-133, SK-BR-134, SK-BR-135, SK-BR-136 and SK-BR-137 showed greenish violet petiole colour. Nine genotypes (21.95%) SK-BL-105, SK-BL-3, SK-BL-107, SK-BL-

110, SK-BL-113, SK-BL-114, SK-BL-116, SK-BR-120 and SK-BSR-126 showed green petiole colour. Three genotypes (7.31%) SK-BL-104, SK-BL-108 and Local Long showed light green petiole colour.

4.1.5 Leaf blade lobing

Out of forty one genotypes thirty two genotypes (78.04%) SK-BL-100, SK-BL-101, SK-BL-102, SK-BL-105, SK-BL-108, SK-BL-110, SK-BL-111, SK-BL-113, SK-BL-114, SK-BL-115, SK-BL-116, SK-BR-117, SK-BR-118, SK-BR-119, SK-BR-120, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BSR-125, SK-BSR-126, SK-BSR-127, SK-BSR-128, SK-BR-129, SK-BR-130, SK-BR-131, SK-BR-132, SK-BR-133, SK-BR-134, SK-BR-135, SK-BR-136, SK-BR-137 and Local Long showed intermediate leaf blade lobing. Five genotypes (12.19%) SK-BL-103, SK-BL-106, 2018/BRL VAR-5, SK-BL-112 and SK-BL-109 showed strong leaf blade. Four genotypes (9.75%) SK-BL-104, 2017/BRL VAR-7, SK-BL-107 and SK-BR-121 showed weak leaf blade lobing.

4.1.6 Leaf blade tip angle

Thirty five genotypes (85.36%) SK-BL-100, SK-BL-101, SK-BL-103, SK-BL-104, 2017/BRL VAR-7, SK-BL-107, SK-BL-108, SK-BL-110, SK-BL-111, SK-BL-113, SK-BL-114, SK-BL-115, SK-BL-116,SK-BR-117, SK-BR-118, SK-BR-119, SK-BR-120, SK-BR-121, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BSR-125, SK-BSR-126, SK-BSR-127, SK-BSR-128, SK-BR-129, SK-BR-130, SK-BR-131,SK-BR-132, SK-BR-133, SK-BR-134, SK-BR-135, SK-BR-136, SK-BR-137 and Local Long showed acute leaf blade tip angle. Six genotypes (14.63%) SK-BL-103, SK-BL-104, SK-BL-106, 2018/BRL VAR-5, SK-BL-109 and SK-BL-112 showed intermediate leaf blade tip angle.

4.1.7 Fruit length breadth ratio

Out of forty-one genotypes, ten genotypes (24.39%) SK-BL-100, 2017/BRL VAR-7, SK-BL-8, SK-BR-119, SK-BR-123, SK-BR-129, SK-BR-130, SK-BR-131, SK-BR-135, SK-BR-136 and SK-BR-137 showed slightly longer

than broad fruit length breadth ratio. Ten genotypes (24.39%) SK-BL-101, SK-BL-103, SK-BL-106, SK-BL-108, SK-BL-111, SK-BL-112, SK-BL-115, SK-BL-116, SK-BR-120 and Local Long showed twice as long as broad fruit length breadth ratio. Eight genotypes (19.51%) SK-BL-102, SK-BL-113, SK-BL-104, SK-BL-105, SK-BL-107, SK-BL-109, SK-BL-110 and SK-BL-114 showed three times as long as broad fruit length breadth ratio. Twelve genotypes (29.26%) SK-BR-117, SK-BR-118, SK-BR-122, SK-BSR-124, SK-BSR-125, SK-BSR-126, SK-BSR-127, SK-BSR-128, SK-BR-132, SK-BR-133 and SK-BR-134 showed as long as broad fruit length breadth ratio and one genotype (2.43%) namely 2018/BRL VAR-5 showed several times as long as broad fruit length breadth ratio.

4.1.8 Fruit curvature

Out of forty-one genotypes, twenty nine genotypes (70.73%) SK-BL-100, SK-BL-101, SK-BL-106, 2017/BRL VAR-7, SK-BL-107, SK-BL-111, SK-BL-112, SK-BL-115, SK-BR-117, SK-BR-118, SK-BR-119, SK-BR-120, SK-BR-121, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BSR-125, SK-BSR-126, SK-BSR-127, SK-BSR-128, SK-BR-129, SK-BR-130, SK-BR-131, SK-BR-132, SK-BR-133, SK-BR-134, SK-BR-135, SK-BR-136 and SK-BR-137 showed no fruit curvature. Eleven genotypes (26.82%) SK-BL-102, SK-BL-103, SK-BL-104, SK-BL-105, SK-BL-108, SK-BL-109, SK-BL-110, SK-BL-113, SK-BL-114, SK-BL-116 and Local Long showed slightly curved fruit structure and one genotype (2.43%) namely 2018/BRL VAR -5 showed snake shaped fruit curvature.

4.1.9 Clustering and non clustering habit of flowers

Thirty five genotypes (85.36%) SK-BL-100, SK-BL-102, SK-BL-103, SK-BL-104, SK-BL-105, SK-BL-106, SK-BL-101, 2017/BRL VAR-7, SK-BL-107 , SK-BL-108, SK-BL-109, SK-BL-110, SK-BL-111, SK-BL-112, SK-BL-113, SK-BL-114, SK-BL-115, SK-BL-116, SK-BR-117, SK-BR-118, SK-BR-119, SK-BR-120, SK-BR-123, SK-BSR-124, SK-BSR-125, SK-BSR-126, SK-

BSR-127, SK-BSR-128, SK-BR-129, SK-BR-130, SK-BR-133, SK-BR-134, SK-BR-135, SK-BR-136, SK-BR-9 and Local Long showed clustering habit of flowers. However, six genotypes (14.63%) 2018/BRL VAR-5, SK-BR-121, SK-BR-122, SK-BR-131 and SK-BR-132, SK-BR-137 showed non clustering habit of flowers.

4.1.10 Presence or absence of spines on fruit calyx

Out of forty-one genotypes twenty nine genotypes (70.73%) SK-BL-100, SK-BL-101, SK-BL-102, SK-BL-103,SK-BL-104, SK-BL-105,SK-BL-106, 2017 BRL VAR-7, SK-BL-107, SK-BL-108, SK-BL-110, SK-BL-111, SK-BL-112, SK-BL-113, SK-BL-114, SK-BL-115, SK-BR-117, SK-BR-118, SK-BR-119, SK-BSR-125, SK-BSR-126, SK-BSR-127, SK-BSR-128, SK-BR-130, SK-BR-131, SK-BR-132, SK-BR-136, SK-BR-137 and Local Long showed absence of spines on fruit calyx. Twelve genotypes (29.26%) 2018/BRL VAR-5, SK-BL-109, SK-BL-116, SK-BR-120, SK-BR-121, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BR-129, SK-BR-133, SK-BR-134 and SK-BR-135 showed presence of spines on fruit calyx.

4.2 Mean performance and analysis of variance

The mean value of various morphological and biochemical traits is present in Table- 6.1 and 6.2. The Analysis of variance for all the traits under study is present in Table- 7.1 and 7.2. Perusal of tables revealed significant mean sum of squares due to yield and attributing traits suggesting existence of considerable variability in the material studied.

4.3 Variability and genetic components of variances

The genetic variability estimates including genotypic mean, range, genotypic variances (GV), phenotypic variance (PV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (bs) and genetic advance as percent of mean were estimated for each qualitative and.

Plate 1: View of experimental field

Table 5: Morphological description of brinjal genotypes (Solanum *melongena* L.)

S. No	Genotype	Fruit colour	Fruit shape	Plant growth habit	Petiole colour	Leaf blade lobbing	Leaf blade tip angle	Fruit length breadth ratio	Fruit curvature	Presence or absence of spines on fruit calyx	Clustering or non clustering habit of flowers
1	SK-BL-100	Green variegated	Oblong	Intermediate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Absent	Clustering habit
2	SK-BL-101	Purple	Medium long	Intermediate	Greenish violet	Intermediate	Acute	Twice as long as broad	None	Absent	Clustering habit
3	SK-BL-102	Light Green	Long	Intermediate	Greenish violet	Intermediate	Acute	Three times as long as broad	Slightly curved	Absent	Clustering habit
4	SK-BL-103	Dark purple	Long	Intermediate	Greenish	Strong	Intermediate	Twice as long as broad	Slightly curved	Absent	Clustering habit
5	SK-BL-104	Dark purple	Long	Intermediate	Light green	Weak	Acute	Three times as long as broad	Slightly curved	Absent	Clustering habit
6	SK-BL-105	Purple	Long	Intermediate	Greenish	Intermediate	Intermediate	Three times as long as broad	Slightly curved	Absent	Clustering habit
7	SK-BL-106	Dark purple	Medium long	Upright	Greenish violet	Strong	Intermediate	Twice as long as broad	None	Absent	Clustering habit
8	2017/BRLVAR-7	White	Oblong	Intermediate	Greenish violet	Weak	Acute	Slightly longer than broad	None	Absent	Clustering habit

Contd:-

S. No	Genotype	Fruit colour	Fruit shape	Plant growth habit	Petiole colour	Leaf blade lobbing	Leaf blade tip angle	Fruit length breadth ratio	Fruit curvature	Presence or absence of spines on fruit calyx	Clustering or non clustering habit of flowers
9	2018/BRL VAR-5	Light purple	Very long	Upright	Greenish violet	Strong	Intermediate	Several times as long as broad	Snake shaped	Present	Clustering habit
10	SK-BL-107	Dark purple	Medium long	Prostrate	Greenish	Weak	Acute	Three times as long as broad	None	Absent	Clustering habit
11	SK-BL-108	Dark purple	Medium long	Prostrate	Light green	Intermediate	Acute	Twice as long as broad	Slightly curved	Absent	Clustering habit
12	SK-BL-109	Purple	Medium long	Intermediate	Greenish violet	Strong	Intermediate	Three times as long as broad	Slightly curved	Present	Clustering habit
13	SK-BL-110	Purple	Long	Intermediate	Greenish	Intermediate	Acute	Three times as long as broad	Slightly curved	Absent	Clustering habit
14	SK-BL-111	Purple	Medium long	Intermediate	Greenish violet	Intermediate	Acute	Twice as long as broad	None	Absent	Clustering habit
15	SK-BL-112	Purple	Medium long	Upright	Greenish violet	Strong	Intermediate	Twice as long as broad	None	Absent	Clustering habit
16	SK-BL-113	Light Green	Medium long	Intermediate	Greenish	Intermediate	Acute	Three times as long as broad	Slightly curved	Absent	Clustering habit

Contd:-

S. No	Genotype	Fruit colour	Fruit shape	Plant growth habit	Petiole colour	Leaf blade lobbing	Leaf blade tip angle	Fruit length breadth ratio	Fruit curvature	Presence or absence of spines on fruit calyx	Clustering or non clustering habit of flowers
17	SK-BL-114	Purple	Long	Intermediate	Greenish	Intermediate	Acute	Three times as long as broad	Slightly curved	Absent	Clustering habit
18	SK-BL-115	Light purple	Long	Intermediate	Greenish violet	Intermediate	Acute	Twice as long as broad	Slightly curved	Absent	Clustering habit
19	SK-BL-116	Light purple	Long	Intermediate	Greenish	Intermediate	Acute	Twice as long as broad	Slightly curved	Present	Clustering habit
20	SK-BR-117	Light purple	Oval	Prostrate	Greenish violet	Intermediate	Acute	As long as broad	None	Absent	Clustering habit
21	SK-BR-118	Light purple	Round	Upright	Greenish violet	Intermediate	Acute	As long as broad	None	Absent	Clustering habit
22	SK-BR-119	Purple	Oval	Upright	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Absent	Clustering habit
23	SK-BR-120	Green variegated	Oblong	Intermediate	Greenish	Intermediate	Acute	Twice as long as broad	None	Present	Clustering habit
24	SK-BR-121	Light purple	Round	Upright	Greenish violet	Weak	Acute	As long as broad	None	Present	Non clustering habit

Contd:-

S. No	Genotype	Fruit colour	Fruit shape	Plant growth habit	Petiole colour	Leaf blade lobbing	Leaf blade tip angle	Fruit length breadth ratio	Fruit curvature	Presence or absence of spines on fruit calyx	Clustering or non clustering habit of flowers
25	SK-BR-122	Light purple	Oval	Intermediate	Greenish violet	Intermediate	Acute	As long as broad	None	Present	Non clustering habit
26	SK-BR-123	Light purple	Oval	Prostrate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Present	Clustering habit
27	SK-BSR-124	Light purple	Oval	Intermediate	Greenish violet	Intermediate	Acute	As long as broad	None	Present	Clustering habit
28	SK-BSR-125	Purple	Round	Intermediate	Greenish violet	Intermediate	Acute	As long as broad	None	Absent	Clustering habit
29	SK-BSR-126	Purple	Oval	Intermediate	Greenish	Intermediate	Acute	As long as broad	None	Absent	Clustering habit
30	SK-BSR-127	Dark purple	Oval	Prostrate	Greenish violet	Intermediate	Acute	As long as broad	None	Absent	Clustering habit
31	SK-BSR-128	Light purple	Oval	Intermediate	Greenish violet	Intermediate	Acute	As long as broad	None	Absent	Clustering habit
32	SK-BR-129	Dark purple	Round	Intermediate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Present	Clustering habit

S. No	Genotype	Fruit colour	Fruit shape	Plant growth habit	Petiole colour	Leaf blade lobbing	Leaf blade tip angle	Fruit length breadth ratio	Fruit curvature	Presence or absence of spines on fruit calyx	Contd:- habit of flowers
33	SK-BR-130	Light purple	Round	Intermediate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Absent	Clustering habit
34	SK-BR-131	Light Green	Round	Intermediate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Absent	Non clustering habit
35	SK-BR-132	Dark purple	Round	Intermediate	Greenish violet	Intermediate	Acute	As long as broad	None	Absent	Non clustering habit
36	SK-BR-133	Dark purple	Round	Intermediate	Greenish violet	Intermediate	Acute	As long as broad	None	Present	Clustering habit
37	SK-BR-134	Light purple	Oblong	Prostrate	Greenish violet	Intermediate	Acute	As long as broad	None	Present	Clustering habit
38	SK-BR-135	Light purple	Round	Prostrate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Present	Clustering habit
39	SK-BR-136	Light purple	Round	Prostrate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Absent	Clustering habit
40	SK-BR-137	Purple	Round	Prostrate	Greenish violet	Intermediate	Acute	Slightly longer than broad	None	Absent	Non clustering habit
41	Local Long	Purple	Long	Intermediate	Light green	Intermediate	Acute	Twice as long as broad	Slightly curved	Absent	Clustering habit

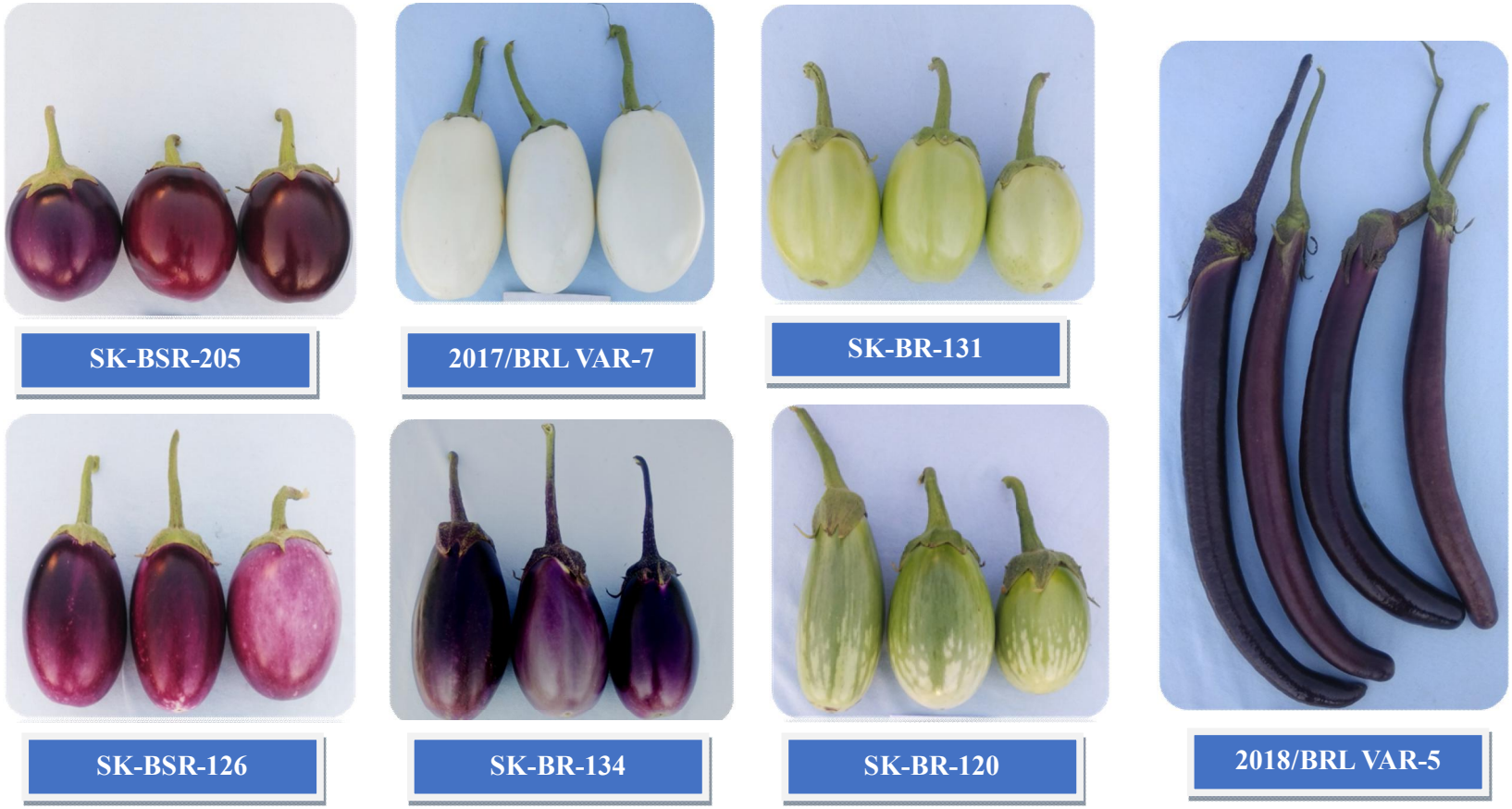

Plate 2: Variability observed among different genotypes

quantitative trait and are represented in Table-8. A comparative performance of all genotypes under the study has been described as follows

4.3.1 Days to 50% flowering

There were significant differences among genotypes under study for days to 50% flowering. Days to 50% flowering ranged from 44.55 to 56.99 days with a mean of 49.55 days. The maximum number of days to 50% flowering were taken by Local Long (56.99) was statistically at par with SK-BR-123 (56.33) and SK-BR-136 (55.10) and the minimum number of days to 50% flowering were observed in SK-BL-105 (44.55) was statistically at par with SK-BL-116 (46.29), SK-BL-113 (46.21), SK-BL-109 (45.26), SK-BL-104 (45.66), SK-BL-10 3 (45.22), SK-BL-102 (45.77) and SK-BL-101 (45.77). The phenotypic and genotypic variance for this trait were 10.56 and 9.08 respectively. The phenotypic and genotypic coefficient of variation were low i,e, 6.59 and 6.12 respectively. High heritability (86%) along with moderate genetic advance as a per cent of mean (11.69) was observed for the trait.

4.3.2 Days taken to first fruit set

Days to first fruit set showed considerable variation from 52.88 to 64.77 with an overall mean of 56.65. The maximum number of days to first fruit set was observed in Local Long (64.77) followed by SK-BR-123 (63.11) and SK-BR-136 (61.44). The minimum days to first fruit set was found in SK-BL-102 (52.88) was statistically at par with SK-BL-100 (54.33), SK-BL-101 (53.10), SK-BL-103 (53.33), SK-BL-108 (54.33), SK-BL-109 (53.99), SK-BL-115 (54.22) and SK-BL-116 (54.33).The phenotypic and genotypic variance for the trait were 9.25 and 8.22 respectively. The phenotypic coefficient of variation (5.36) and genotypic coefficient of variation (5.06) were low for this trait. High heritability (88%) along with low genetic advance as a percent of mean (9.82) was observed for this trait.

4.3.3 Days to first fruit picking

Days to first fruit picking showed considerable variation. Number of days to first fruit picking ranged from 71.33 to 84.99 with an overall mean of 77.38. The minimum number of days to first fruit picking were observed in SK-BL-113 (71.33) was statistically at par with SK-BL-109 (71.44), SK-BL-102 (72.66) and SK-BL-104 (72.44). The maximum number of days to first fruit picking were observed in SK-BR-136 (84.99) was statistically at par with SK-BR-123 (84.11). The phenotypic and genotypic variances for this trait were 12.11 and 11.08, respectively. Low phenotypic coefficient of variation (4.49) and low genotypic coefficient of variation (4.30) were observed for this trait. High heritability (91%) coupled with low genetic advance as a per cent of mean (8.47) were found for this trait.

4.3.4 Number of flowers per cluster

Number of flowers per cluster ranged from 1.00 to 7.21 with an overall mean of 3.56. Maximum number of flowers per cluster was recorded in SK-BSR-124 (7.21) was statistically at par with SK-BL-102 (6.99). The minimum number of flowers per cluster were observed in 2018/BRL VAR-5, SK-BR-121, SK-BR-122, SK-BR-131, SK-BR-132, SK-BR-137 (1) followed by SK-BR-134 (2.44) and Local Long (2.44).The phenotypic and genotypic variance for this trait were 2.46 and 2.29 respectively. The phenotypic and genotypic coefficient of variation were high i.e., (43.95) and (42.41) respectively. High heritability (93%) along with high genetic advance as a per cent of mean (84.31) was observed for the trait.

4.3.5 Number of fruits per cluster

The number of fruits per cluster ranged from 1.00 to 5.44 with an overall average of 3.91. Maximum number of fruits per cluster was recorded in SK-BSR-124 (5.44) was statistically at par with SK-BL-102 (5.33), SK-BSR-127 (4.77) and SK-BSR-126 (4.55). The minimum number of fruits per cluster were observed in SK-BR-122, SK-BR-131 (1.00), SK-BR-122 (1.00) and SK-BR-137

(1.00) was statistically at par with SK-BR-134 (1.44) and Local Long (1.66). The phenotypic and genotypic variance for this trait were 1.61 and 1.37 respectively. The phenotypic (49.42) and genotypic (45.70) coefficient of variation were high. High heritability (85%) along with high genetic advance as a per cent of mean (87.08) was observed for the trait.

4.3.6 Plant height (cm)

The genotypes under study showed considerable variation. Plant height of genotypes ranged from 65.06 cm to 89.77 cm with an average of 73.55 cm. The maximum plant height was recorded in 2018/BRL VAR-5 (89.77cm) followed by SK-BL-104 (85.17cm) and SK-BL-106 (83.22 cm). The minimum plant height was recorded in SK-BR-121 (65.06 cm) was statistically at par with SK-BL-101 (66.40 cm) and SK-BR-122 (66.38 cm). The phenotypic and genotypic variance for the trait was found to be 33.76 and 32.83, respectively. Low phenotypic coefficient of variation (7.89) and genotypic coefficient of variation (7.79) were found for the trait. High heritability (97%) along with moderate genetic advance as a per cent of mean (15.82) were observed for the trait.

4.3.7 Plant spread (cm)

The genotypes under study possessed a large amount of variability for this trait. Plant spread of all genotypes ranged from 31.22 to 58.90 cm with a mean of 45.60 cm. The minimum plant spread was observed in SK-BR-120 (31.22 cm) was statistically at par with SK-BR-121 (31.49 cm). The maximum plant spread was observed in 2018/BRL VAR-5 (58.90) followed by SK-BL-111 (57.05 cm). T he phenotypic and genotypic variance for the trait was found to be 51.80 and 51.23, respectively. Moderate phenotypic coefficient of variation (15.78) and genotypic coefficient of variation (15.69) were observed for this trait. High heritability (98%) coupled with high genetic advance as per cent of mean (32.15) were observed for the trait.

4.3.8 Number of branches per plant

Number of branches per plant showed variation from 5.00 to 6.90 with a mean of 5.33. The maximum number of branches per plant were recorded in SK-BL-102 (6.99) followed by SK-BL-105 (6.44). The minimum number of branches per plant were observed in SK-BL-107, SK-BL-109, SK-BL-110, SK-BL-114, SK-BL-115, SK-BL-116, SK-BR-117, SK-BR-118, SK-BR-119, SK-BR-120, SK-BR-121, SK-BR-122, SK-BR-123, SK-BSR-124, SK-BSR-128, SK-BR-129, SK-BR-130, SK-BR-131, SK-BR-132, SK-BR-135, SK-BR-136 and SK-BR-137 (5.00) was statistically at par with SK-BL-111 (5.33), SK-BL-112 (5.33), SK-BL-113 (5.33), SK-BSR-125, SK-BR-133, SK-BR-134 and Local Long (5.11). Phenotypic and genotypic variance was found to be 0.32 and 0.26 respectively. Moderate phenotypic coefficient of variation (10.59) and low genotypic coefficient of variation (9.45) along with high heritability (82%) and moderate genetic advance as a per cent of mean (17.37) was observed for the trait.

4.3.9 Fruit length (cm)

The genotypes under study possessed a large amount of variability for this trait. Fruit length of genotypes ranged from 4.36 to 23.96 cm with an average of 10.32 cm. The maximum value was recorded in 2018/BRL VAR-5 (23.96 cm) followed by SK-BL-105 (15.67 cm). The minimum fruit length was recorded in SK-BSR-124 (4.36 cm) was statistically at par with SK-BSR-128 (4.64 cm). The phenotypic and genotypic variance was found to be 16.73 and 16.60 respectively. High phenotypic coefficient of variation (39.60) and genotypic coefficient of variation (39.45) was observed for this trait. High heritability (99%) coupled with high genetic advance as a per cent of mean (80.94) was observed for this trait.

4.3.10 Fruit diameter (cm)

There were significant difference among all the genotypes for this trait. Fruit diameter ranged from 2.85 to 8.46 cm with a mean of 5.42 cm. SK-BR-132 recorded the maximum fruits diameter (8.46 cm) was statistically at par with SK-

BR-133 (8.39 cm). 2018/BRL VAR-5 recorded the minimum fruit diameter (2.85 cm) followed by Local Long (3.51 cm), and SK-BL-111 (3.52 cm). The phenotypic and genotypic variance was found to be 2.04 and 2.02 respectively. High phenotypic coefficient of variation (26.36) and genotypic coefficient of variation (26.23) were observed for this trait. High heritability (99%) coupled with high genetic advance as a per cent of mean (53.78) was recorded for this trait.

4.3.11 Petiole length (cm)

Leaf petiole length showed considerable variation from 0.91 cm to 4.08 cm with an average of 2.31 cm. SK-BL-109 recorded maximum value of (4.08 cm) was statistically at par with SK-BR-119 (3.90cm). The lowest value was observed in SK-BR-120 (0.91 cm) followed by SK-BL-102 (1.47) SK-BL-106 (1.48cm). The phenotypic and genotypic variance was found to be (0.49) and (0.47) respectively. The phenotypic coefficient of variation (30.42) and genotypic coefficient of variation (29.84) were high for this trait. High heritability (96%) coupled with high genetic advance as a per cent of mean (60.29) was observed for this trait.

4.3.12 Number of fruits per plant

It is an important yield contributing trait. Average number of fruits per plant ranged from 3.21 to 18.99 with a mean of 8.16. Maximum number of fruits were recorded in SK-BL-102 (18.99) was statistically at par with SK-BSR-124 (18.77) and SK-BSR-126 (17.66). Minimum number of fruits were recorded in SK-BR-134 (3.21) followed by SK-BL-116 (3.66) SK-BR-123 (3.44) and SK-BR-137 (3.55). The phenotypic and genotypic variance was observed to be 15.74 and 14.73 respectively. High phenotypic (48.60) and genotypic (47.01) coefficient of variation was observed for the trait. High heritability (93%) along with high genetic advance as a per cent of mean (93.65) was observed for this trait.

4.3.13 Average fruit weight (g)

In present investigation average fruit weight expressed the considerable variation from 43.66 g to 162.66 g with a mean of 92.85 g. Maximum weight was recorded in SK-BSR-125 (162.66 g) followed by SK-BR-123 (135 g) and SK-BR-134 (133.02). SK-BSR-124 recorded minimum fruit weight (43.66 g) which was followed by SK-BL-101 (48.33 g). The phenotypic and genotypic variance was found to be 894.35 and 886.16 respectively. The phenotypic coefficient of variation (31.85) and genotypic coefficient of variation (31.70) were observed to be high for this trait. High heritability (99%) along with high genetic advance as a per cent of mean (65.01) was observed for this trait.

4.3.14 Fruit yield per plant (g)

Fruit yield per plant ranged from 254.33 g to 1125.33 g with an average mean of 680.96 g. The maximum yield per plant was observed in SK-BL-105 (1125.33) followed by 2017/BRL VAR-7 (1092.88 g) and SK-BL-103 (1003.99 g). The lowest yield was found in SK-BL-116 (254.33) followed by SK-BL-114 (416.53) and SK-BR-134 (427.00 g). The phenotypic and genotypic variance was found to be 38774.00, 38756.99 respectively. The phenotypic (28.91) and genotypic (28.91) coefficient of variation was observed to be high for this trait. The high heritability 99% along with high genetic advance (59.54) was observed for this trait.

4.3.15 Fruit yield per hectare (q/ha)

Fruit yield per hectare ranged from 122.33 to 540.33 q/ha with an average mean of 325.89 q/ha. The maximum yield per hectare was observed in SK-BL-105 (540.33 q/ha) was statistically at par with 2017/BRL VAR-7 (525.29 q/ha). The lowest yield was found in SK-BL-116 (122.33 q/ha) followed by SK-BL-114 (200.33 q/ha) and Local Long (205.10 q/ha). The phenotypic and genotypic variance was found to be (27802.88) and (27628.26) respectively. The phenotypic and genotypic coefficient of variation (29.92) and (28.98) was observed to be high for this trait. The high heritability 99% along with high genetic advance (57.84) was observed for this trait.

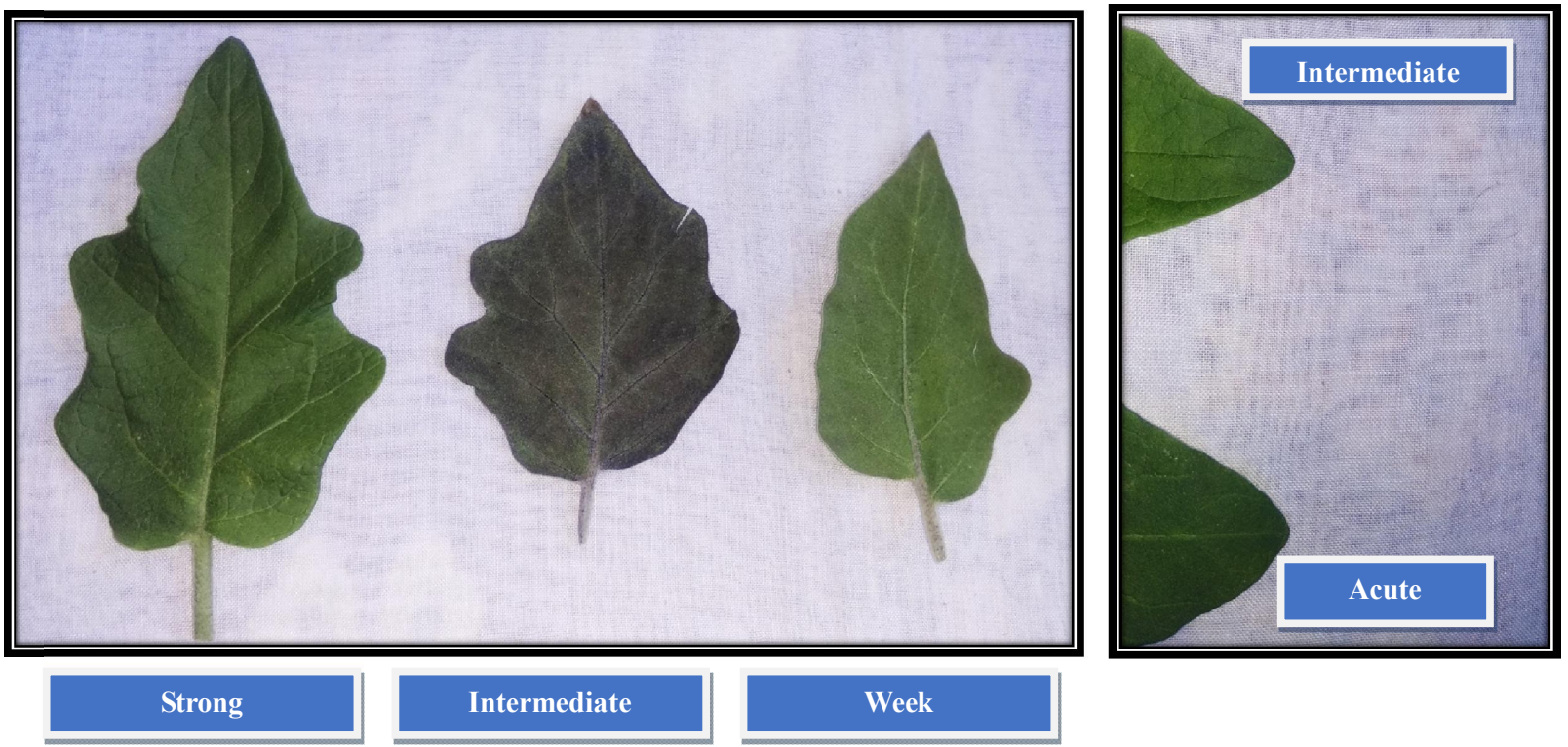

Plate 3: Leaf blade lobing

Table 6.1 : Mean performance of brinjal (*Solanum melongena* L.) genotypes with respect to different quantitative traits

S.NO	Genotypes	Days taken to 50% flowering	Days taken to first fruit set	Days taken to first fruit picking	No. of flowers per cluster	No. of fruits per cluster	Fruit length (cm)	Fruit diameter (cm)	Plant height (cm)	Plant spread (cm)	No. of branches per plant	Petiole length (cm)	Number of fruits per plant	Average fruit weight (g)	Fruit yield per plant (g)	Fruit yield per hectare (q)
1	SK-BL-100	46.99	54.33	71.66	2.99	2.10	9.62	5.82	72.31	43.82	5.55	2.18	4.55	95.33	437.00	210.22
2	SK-BL-101	45.77	53.10	75.55	2.99	1.88	10.96	5.95	66.40	48.65	5.99	2.22	9.10	48.33	431.99	207.23
3	SK-BL-102	45.77	52.88	72.66	6.99	5.33	12.63	4.02	78.65	56.89	6.99	1.47	18.99	52.33	985.99	473.96
4	SK-BL-103	45.22	53.33	73.33	3.77	2.99	12.21	4.10	79.59	48.76	5.99	2.29	9.77	101.66	1003.99	482.65
5	SK-BL-104	45.66	53.55	72.44	3.77	2.77	14.36	3.63	85.17	51.92	6.33	2.51	9.55	88.33	833.55	400.10
6	SK-BL-105	44.55	52.88	75.10	4.12	3.10	15.67	4.61	83.01	56.11	6.44	2.64	10.77	105.77	1125.33	540.33
7	SK-BL-106	48.77	56.77	73.44	5.55	3.99	16.03	4.79	83.22	52.92	5.99	1.48	10.55	75.33	803.00	385.32
8	2017/BRLVAR-7	47.50	54.84	75.99	5.77	4.22	11.09	5.62	82.57	51.67	6.11	2.18	11.21	99.33	1092.88	525.29
9	2018/BRL VAR-5	48.66	55.22	76.33	1.00	1.00	23.96	2.85	89.77	58.90	6.33	2.29	7.99	96.03	802.88	386.29
10	SK-BL-107	47.84	55.83	75.88	3.99	2.77	14.61	4.55	76.23	53.01	5.00	2.36	7.99	87.76	679.10	326.24
11	SK-BL-108	46.55	54.33	78.44	3.55	2.66	13.83	4.51	78.49	53.92	5.11	2.00	3.77	117.40	462.22	222.35
12	SK-BL-109	45.26	53.99	71.44	3.55	2.33	14.39	4.10	70.52	49.96	5.00	4.08	7.33	85.36	625.00	238.82
13	SK-BL-110	47.33	55.22	77.00	2.88	1.55	13.64	3.87	68.10	47.50	5.00	2.12	5.22	99.91	541.21	260.25
14	SK-BL-111	50.55	58.00	73.33	3.99	2.99	13.29	3.52	74.41	57.05	5.33	1.92	7.33	84.23	608.66	292.24
15	SK-BL-112	47.33	54.55	76.10	3.66	2.66	11.17	5.73	68.22	52.98	5.33	3.53	8.66	83.86	729.66	350.33
16	SK-BL-113	46.21	52.99	71.33	3.44	2.66	14.62	3.93	70.58	50.55	5.33	3.53	10.44	79.06	822.88	395.33
17	SK-BL-114	47.99	54.99	77.22	3.10	1.99	13.73	4.15	72.44	53.83	5.00	2.43	5.33	79.61	416.53	200.33
18	SK-BL-115	47.44	54.22	76.22	3.66	2.77	13.23	4.30	71.58	48.74	5.00	3.35	8.66	73.36	635.44	305.33
19	SK-BL-116	46.29	54.33	75.33	3.44	2.22	13.18	4.47	73.6	53.14	5.00	2.24	3.66	77.36	254.33	122.33
20	SK-BR-117	53.16	59.77	76.55	3.44	2.44	7.68	6.33	69.82	48.46	5.00	2.27	6.33	95.41	614.44	295.16
21	SK-BR-118	51.33	58.77	76.33	3.99	2.99	7.01	6.42	71.96	41.38	5.00	3.39	8.77	83.68	735.33	353.21

S.NO	Genotypes	Days taken to 50% flowering	Days taken to first fruit set	Days taken to first fruit picking	No. of flowers per cluster	No. of fruits per cluster	Fruit length (cm)	Fruit diameter (cm)	Plant height (cm)	Plant spread (cm)	No. of branches per plant	Petiole length (cm)	Number of fruits per plant	Average fruit weight (g)	Fruit yield per plant (g)	Fruit yield per hectare (q)
22	SK-BR-119	48.44	56.55	76.33	3.77	2.77	7.89	6.17	73.32	38.54	5.00	3.90	8.10	85.23	645.99	310.32
23	SK-BR-120	51.66	58.99	79.33	3.66	2.21	8.32	6.41	68.35	31.22	5.00	0.91	7.44	77.66	583.21	280.33
24	SK-BR-121	53.33	60.55	78.33	1.00	1.00	7.56	7.82	65.06	31.49	5.00	2.02	5.77	96.46	562.66	270.33
25	SK-BR-122	50.33	57.55	79.22	1.00	1.00	7.01	6.20	66.38	37.00	5.00	2.39	5.33	128.00	670.99	332.33
26	SK-BR-123	56.33	63.11	84.11	2.77	1.99	7.41	6.11	69.39	36.65	5.00	1.82	3.44	135.00	458.55	219.92
27	SK-BSR-124	52.10	60.32	82.77	7.21	5.44	4.36	4.43	68.25	36.49	5.00	1.50	18.77	43.66	797.55	383.18
28	SK-BSR-125	50.77	58.44	82.33	3.77	2.55	5.32	5.10	69.90	39.75	5.11	2.80	5.10	162.66	822.33	395.44
29	SK-BSR-126	48.21	56.10	80.55	5.88	4.55	5.26	5.09	79.37	42.97	5.66	3.16	17.66	49.66	854.33	409.73
30	SK-BSR-127	49.10	56.66	81.33	5.55	4.77	5.17	5.27	78.48	39.98	5.88	1.90	12.88	65.33	833.10	400.40
31	SK-BSR-128	48.77	56.66	78.66	5.55	3.88	4.64	4.40	75.51	40.82	5.00	1.51	8.99	65.66	583.44	280.46
32	SK-BR-129	49.88	55.77	78.22	3.99	2.88	8.09	6.82	71.29	40.19	5.00	2.35	8.33	104.00	833.10	400.00
33	SK-BR-130	49.22	56.33	78.88	3.33	2.11	7.95	7.47	79.31	42.23	5.00	1.90	4.66	132.33	606.44	291.00
34	SK-BR-131	52.33	59.88	80.33	1.00	1.00	8.02	7.33	70.60	40.70	5.00	1.77	5.55	151.33	812.10	390.44
35	SK-BR-132	49.77	56.33	78.44	1.00	1.00	8.02	8.46	69.37	41.81	5.00	2.41	7.10	80.00	572.99	275.18
36	SK-BR-133	47.55	54.77	78.00	3.55	2.33	8.05	8.39	72.25	41.80	5.11	2.36	9.88	89.00	875.33	420.17
37	SK-BR-134	50.88	57.66	81.66	2.44	1.44	5.68	5.53	71.43	40.40	5.11	1.41	3.21	133.02	427.00	205.25
38	SK-BR-135	48.33	55.55	80.11	4.55	3.55	8.23	6.80	74.54	41.34	5.00	1.55	12.55	59.00	750.10	360.14
39	SK-BR-136	55.10	61.44	84.99	2.99	1.99	7.51	6.27	69.04	40.89	5.00	2.31	5.44	127.66	708.21	340.34
40	SK-BR-137	54.33	61.22	77.99	1.00	1.00	8.09	7.48	66.65	40.96	5.00	2.28	3.55	123.66	454.10	218.41
41	Local Long	56.99	64.77	79.22	2.44	1.66	13.84	3.51	70.88	44.40	5.11	2.12	4.88	88.33	427.10	205.10
Mean		**49.25**	**56.65**	**77.38**	**3.56**	**3.91**	**10.32**	**5.42**	**73.55**	**45.60**	**5.33**	**2.31**	**8.16**	**92.85**	**680.96**	**325.89**
CV		**2.46**	**1.79**	**1.31**	**11.53**	**18.79**	**3.52**	**2.60**	**1.30**	**1.65**	**4.51**	**5.93**	**12.36**	**3.04**	**0.66**	**5.25**
CD (P≤ 0.05)		**1.97**	**1.64**	**1.65**	**0.66**	**0.78**	**0.59**	**0.22**	**1.56**	**1.22**	**0.41**	**0.22**	**1.64**	**4.65**	**6.70**	**39.32**

4.4 Characterization on the basis of biochemical traits

Observation recorded for biochemical traits viz., total phenol, anthocyanin, TSS, vitamin C, dry matter, FRAP, DPPH, quercetin, ferulic acid, content in case of forty one genotypess are presented in Table-6.2.

4.4.1 Total Phenol content (mg/100g)

Total Phenol content of the genotypes ranged from 63.75 to 103.66 mg/100g with an overall mean of 86.55 mg/100g. Highest total phenol content was recorded in SK-BR-129 (103.66 mg/100g) was statistically at par with SK-BSR-128 (101.33 mg/100g), SK-BR-132 (102.98 mg/100g), and SK-BR-133 (102.46 mg/100g). Lowest total phenol content was recorded in 2017/BRL VAR-7 (63.75 mg/g) followed by 2018/BRL VAR-5 (73.09 mg/g). The phenotypic and genotypic variance was found to be (92.53) and (87.72) respectively. The phenotypic coefficient of variation (11.11) and genotypic coefficient of variation (10.82) was found to be moderate. High heritability (94%) along with high genetic advance as a per cent of mean (21.70) was observed for the trait.

4.4.2 Anthocyanin content (mg/100g)

Anthocyanin content of the genotypes ranged from 0.42 to 1.15 mg/100g with an overall mean of 0.84 mg/100g. Highest anthocyanin content was recorded in SK-BR-129 (1.15mg/100g) was statistically at par with SK-BR-132 (1.11mg/100g). Lowest anthocyanin content was recorded in 2017/BRL VAR-7 (0.42 mg/g) followed by SK-BL-101 (0.53 mg/g). The phenotypic and genotypic variance was found to be 0.02 and 0.01, respectively. The phenotypic coefficient of variation (17.08) and genotypic coefficient of variation (16.38) were found to be moderate. High heritability (92%) along with high genetic advance as a per cent of mean (32.37) was observed for the trait.

4.4.3 TSS (^{o}Brix)

TSS of the genotypes ranged from 3.13 to 7.20 ^{o}Brix with an overall mean of 4.58 ^{o}Brix. Highest TSS was recorded in SK-BL-107 (7.20 ^{o}Brix) was statistically at par with SK-BL-108 (7.13) and SK-BL-104 (6.70 ^{o}Brix). Lowest TSS was recorded in SK-BSR-125 (3.13 ^{o}Brix) was statistically at par with SK-BL-103 (3.53^{o}Brix), SK-BL-106 (3.46 ^{o}Brix), SK-BR-118 (3.43 ^{o}Brix) and SK-BSR-127 (3.43°Brix). The phenotypic and genotypic variance was found to be 1.06 and 0.92 respectively. High phenotypic coefficient of variation (22.54) and genotypic coefficient of variation (20.94) was observed for the trait. High heritability (86%) along with high genetic advance as a per cent of mean (40.01) was observed for the trait.

4.4.4 Vitamin-C content (mg/100g)

Vitamin-C content ranged from 10.91-17.39 (mg/100g) with an overall mean of 14.14mg/100g. The highest vitamin-C content was recorded in SK-BL-107 (17.39 mg/100g) was statistically at par with SK-BSR-128 (17.10), SK-BR-118 (15.94 mg/100g), SK-BR-119 (15.94 mg/100g), SK-BR-122 (15.82 mg/100g) and SK-BR-117(16.93 mg/100g). The lowest vitamin-C content was recorded in SK-BR-136 (10.91 mg/100g) was statistically at par with SK-BL-116 (11.57 mg/100g), SK-BSR-126 (11.10 mg/100g), SK-BSR-127 (12.16 mg/100g), SK-BR-134 (11.86 mg/100g), SK-BR-136 (10.91 mg/100g). The phenotypic and genotypic variance were found to be 5.98 and 1.14, respectively. Moderate phenotypic coefficient of variation (17.29) and low genotypic coefficient of variation (7.57) was observed for the trait. Low heritability (19%) coupled with low genetic advance as a per cent of mean (6.82) was observed for the trait.

4.4.5 Dry matter content (%)

Dry matter content of the genotypes ranged from 5.49 to 8.38 per cent with an overall mean of 7.16 %. Minimum dry matter content was recorded in SK-BL-103 (5.49 %) was statistically at par with SK-BL-104 (5.57 %) and SK-BL-108

(5.65 %). The maximum dry matter content was recorded in SK-BR-118 (8.38 %), SK-BR-119 (8.38 %) each was statistically at par with SK-BL-110 (8.36 %), SK-BL-111 (8.18 %), SK-BSR-124 (8.33 %) and SK-BR-110 (8.31 %). The phenotypic and genotypic variance was observed to be 0.59 and 0.55 respectively. Moderate phenotypic coefficient of variation (10.71) and genotypic coefficient of variation (10.35) were observed for the trait. High heritability (93%) along with high genetic advance as a per cent of mean (20.62) was observed for this trait.

4.4.6 Ferric reducing antioxidant potential (FRAP) (mmol/g)

FRAP potential of the genotypes ranged from 4.52 to 8.12 mmol/g with an overall mean of 6.04 mmol/g. Minimum antioxidant potential content was recorded in SK-BL-110 (5.41 mmol/g), followed by 2017/BRL VAR-7 (4.52 mmol/g.) The maximum antioxidant potential was recorded in SK-BR-129 (8.12mmol/g) was statistically at par with SK-BR-133 (8.00mmol/g). The phenotypic and genotypic variance was observed to be 0.59 and 0.58, respectively. Moderate phenotypic coefficient of variation (12.80) and genotypic coefficient of variation (12.60) were observed for the trait. High heritability (96%) along with high genetic advance as a per cent of mean (25.55) was observed for this trait.

4.4.7 2,2-diphenyl-1-picryl-hydrazyl-hydrate free radical scavenging activity DPPH (%)

DPPH (radical scavenging activity) of the genotypes ranged from 25.31 to 40.78 % with an overall mean of 30.27 %. Minimum DPPH scavenging activity was recorded in SK-BL-111 (25.31 %) was statistically at par with SK-BL-101 (25.71 %), SK-BL-105 (26.07 %), SK-BL-110 (25.63 %), 2017/BRL VAR-7 (25.48 %), 2018/BRL VAR-5 (25.50 %), SK-BL-114 (26.27 %), SK-BL-115 (25.56 %), SK-BL-116 (25.43 %), SK-BL-117 (25.71 %) and SK-BR-118 (25.46 %). The highest DPPH scavenging activity was recorded in SK-BR-129 (40.78 %) followed by SK-BR-133 (38.83 %) and SK-BR-132 (37.72 %). The

phenotypic and genotypic variance was observed to be 18.88 and 17.87, respectively. Moderate phenotypic coefficient of variation (14.35) and genotypic coefficient of variation (13.96) were observed for the trait. High heritability (94%) along with high genetic advance as a per cent of mean (27.98) was observed for this trait.

4.4.8 Quercetin (mg/g)

Quercetin content ranged from 7.10 to 8.00 (mg/g) with a mean of 7.63 mg/g. The highest quercetin content was recorded in SK-BR-129 (8.00 mg/g) was statistically at par with SK-BL-104 (7.94 mg/g), SK-BR-123 (7.93 mg/g), SK-BSR-125 (7.92 mg/g), SK-BSR-127 (7.96 mg/g), SK-BSR-128 (7.97 mg/g), SK-BR-130 (7.95 mg/g) SK-BR-132 (7.99 mg/g), and SK-BR-133 (7.98 mg/g). The lowest quercetin content was recorded in 2017/BRL VAR-7 (7.10 mg/g) was statistically at par with SK-BL-110 (7.12 mg/g) and 2018/BRL VAR-5 (7.16 mg/g). The phenotypic genotypic variance was found to be 0.11 and 0.07, respectively. The phenotypic coefficient of variation (4.02) and genotypic coefficient of variation (3.83) was low. High heritability (90%) coupled with low genetic advance as a per cent of mean (7.51) was observed. Peak value of quercitin using HPLC is shown in Fig. 1.

4.4.9 Ferulic acid (mg/g)

Ferulic acid content ranged from 0.07 to 0.25 (mg/g) with an overall mean of 0.12 mg/g. The highest ferulic acid content was recorded in SK-BR-129 (0.25mg/g) was statistically at par with SK-BR-132 (0.24 mg/g), SK-BR-133 (0.23 mg/g), SK-BSR-127 (0.21 mg/g), SK-BSR-128 (0.22 mg/g) and SK-BR-130 (0.20 mg/g). The lowest ferulic acid content was recorded in 2017/BRL VAR-7, 2018/BRL VAR-5, SK-BL-110, SK-BL-111 (0.07 mg/g) was statistically at par with SK-BL-100 (0.09), SK-BL-101 (0.08), SK-BL-102 (0.10), SK-BL-103 (0.09), SK-BL-105 (0.08), SK-BL-107 (0.09), SK-BL-108 (0.09), SK-BL-109 (0.09), SK-BL-112 (0.12), SK-BL-113 (0.08), SK-BL-114 (0.09), SK-BL-115

(0.08), SK-BL-116 (0.08), SK-BR-117 (0.08), SK-BR-118 (0.08), SK-BR-119 (0.09), SK-BR-120 (0.09), SK-BR-121 (0.08), SK-BSR-124 (0.11), SK-BR-135 (0.09), SK-BR-136 (0.09), SK-BR-137 (0.09) and Local Long (0.08). The phenotypic and genotypic variance was found to be 0.004 and 0.003, respectively. The phenotypic coefficient of variation (42.94) and genotypic coefficient of variation (42.72) was high. High heritability (98%) coupled with high genetic advance as a per cent of mean (87.57) was observed for the trait.

4.5 Correlation and genetic divergence studies

4.5.1 Correlation coefficient

In plant breeding, the degree of association among plant traits has always been useful for selection. The existence of association between different traits is usually determined by studying correlation existing between them. For this purpose, it is important to know the genetic correlation among different traits which may provide information regarding the correlated response to selection. In this study, correlation coefficients were determined using variances and co variances to obtain relationship among various traits and their relationship with economically desirable trait i.e., fruit yield per plant, both at genotypic and phenotypic levels. Phenotypic and genotypic correlations between different traits are present in Table-9.

Table 6.2: Mean performance of brinjal (*Solanum melongena* L.) genotypes with respect to different quality traits

S.NO	Genotypes	Total phenol (mg/100g)	Anthocyanin (mg/100g)	Vitamin-C (mg/100g)	TSS (^{o}Brix)	Dry Matter (%)	FRAP mmol/g	Scavenging activity (DPPH %)	Quercetin (mg/g)	Ferulic acid (mg/g)
1	SK-BL-100	85.99	0.71	13.39	3.80	7.21	5.80	29.55	7.74	0.09
2	SK-BL-101	82.70	0.53	15.14	4.30	6.43	5.69	25.71	7.40	0.08
3	SK-BL-102	90.06	0.81	12.96	4.86	6.56	5.81	29.38	7.84	0.10
4	SK-BL-103	85.66	0.85	12.79	3.53	5.49	5.79	29.85	7.70	0.09
5	SK-BL-104	95.16	0.95	13.14	6.70	5.57	6.34	34.49	7.94	0.19
6	SK-BL-105	75.65	0.75	13.49	4.53	6.57	5.65	26.07	7.28	0.08
7	SK-BL-106	90.68	0.90	14.34	3.46	6.54	5.83	30.28	7.85	0.10
8	2017/BRLVAR-7	63.75	0.42	14.74	5.06	8.30	4.52	25.48	7.10	0.07
9	2018/BRL VAR-5	73.09	0.71	15.47	3.86	7.02	5.60	25.50	7.16	0.07
10	SK-BL-107	83.36	0.83	17.39	7.20	7.05	5.74	27.93	7.44	0.09
11	SK-BL-108	84.35	0.82	15.46	7.13	5.65	5.74	28.80	7.60	0.09
12	SK-BL-109	87.89	0.86	13.29	4.76	6.62	5.79	28.79	7.78	0.09
13	SK-BL-110	69.99	0.65	13.94	4.93	8.36	5.41	25.63	7.12	0.07
14	SK-BL-111	73.30	0.65	14.79	4.76	8.18	5.56	25.31	7.20	0.07
15	SK-BL-112	91.13	0.88	14.33	5.10	7.30	5.87	32.76	7.87	0.12
16	SK-BL-113	83.11	0.82	11.17	4.43	7.48	5.78	29.26	7.42	0.08
17	SK-BL-114	83.96	0.84	12.96	3.76	6.46	5.70	26.27	7.50	0.09
18	SK-BL-115	75.94	0.75	12.66	4.26	7.43	5.67	25.56	7.30	0.08
19	SK-BL-116	78.32	0.76	11.57	4.20	6.98	5.65	25.43	7.32	0.08
20	SK-BR-117	74.73	0.65	16.93	4.36	6.63	5.62	25.71	7.26	0.08
21	SK-BR-118	79.13	0.77	15.94	3.43	8.38	5.65	25.46	7.36	0.08
22	SK-BR-119	84.02	0.86	15.94	6.03	8.38	5.72	27.43	7.55	0.09

S.NO	Genotypes	Total phenol (mg/100g)	Anthocyanin (mg/100g)	Vitamin-C (mg/100g)	TSS (^{o}Brix)	Dry Matter (%)	FRAP mmol/g	Scavenging activity (DPPH %)	Quercetin (mg/g)	Ferulic acid (mg/g)
23	SK-BR-120	83.42	0.81	13.49	3.86	7.47	5.70	27.70	7.47	0.09
24	SK-BR-121	81.65	0.82	13.07	3.83	7.30	5.65	27.51	7.38	0.08
25	SK-BR-122	91.63	0.89	15.82	3.90	6.63	5.81	30.02	7.88	0.13
26	SK-BR-123	95.09	0.94	16.14	4.30	7.28	6.21	33.57	7.93	0.18
27	SK-BSR-124	91.09	0.90	15.52	3.93	8.33	5.80	31.13	7.86	0.11
28	SK-BSR-125	94.38	0.93	13.52	3.13	8.03	5.95	33.82	7.92	0.17
29	SK-BSR-126	93.00	0.94	11.10	4.93	7.60	5.96	34.71	7.90	0.15
30	SK-BSR-127	96.01	0.92	12.16	3.43	7.29	7.42	35.73	7.96	0.21
31	SK-BSR-128	101.33	1.01	17.10	4.30	6.63	7.74	35.81	7.97	0.22
32	SK-BR-129	103.66	1.15	15.19	5.13	7.03	8.12	40.78	8.00	0.25
33	SK-BR-130	95.86	0.94	14.83	4.20	7.40	7.21	35.69	7.95	0.20
34	SK-BR-131	92.90	0.93	15.09	5.53	8.31	6.26	34.58	7.89	0.14
35	SK-BR-132	102.98	1.11	15.49	6.13	7.92	7.85	37.72	7.99	0.24
36	SK-BR-133	102.46	1.06	15.44	5.26	7.15	8.00	38.83	7.98	0.23
37	SK-BR-134	93.70	0.92	11.86	4.60	6.86	6.09	34.55	7.91	0.16
38	SK-BR-135	89.73	0.90	13.32	3.76	7.22	5.80	30.53	7.82	0.09
39	SK-BR-136	89.53	0.91	10.91	3.73	6.96	5.86	32.52	7.80	0.09
40	SK-BR-137	84.70	0.81	13.65	4.00	6.86	5.76	29.48	7.65	0.09
41	Local Long	73.66	0.77	14.11	5.33	6.93	5.50	25.98	7.24	0.08
	Mean	**86.55**	**0.84**	**14.14**	**4.58**	**7.16**	**6.04**	**30.27**	**7.63**	**0.12**
	CV	**2.53**	**4.84**	**15.55**	**8.38**	**2.74**	**2.26**	**3.31**	**1.71**	**2.33**
	CD (P≤ 0.05)	**3.56**	**0.06**	**1.57**	**0.62**	**0.31**	**0.22**	**1.63**	**0.08**	**0.05**

Table 7.1: Analysis of variance for various quantitative traits in brinjal (*Solanum melongena* L.)

Source of variation	d.f	Mean sum of squares													
		Days taken to 50% flowering	Days taken to first fruit set	Days taken to first fruit picking	No. of flowers per cluster	No. of fruits per cluster	Fruit length (cm)	Fruit diameter (cm)	Plant height (cm)	Plant spread (cm)	No. of branches per plant	Petiole length (cm)	Number of fruits per plant	Average fruit weight (g)	Fruit yield per plant (g)	Fruit yield per hectare (q)
Replication	2	0.0065	0.27	2.01	1.61	1.33	3.15	0.01	7.57	2.23	0.03	0.04	1.16	2.18	47.24	144
Genotypes	40	28.73**	25.68**	34.28**	7.04**	4.36**	49.93**	6.10**	99.43**	154.28**	0.82**	1.45**	45.20**	2666.68**	116287**	27355**
Error	80	1.47	1	1.03	0.16	0.23	0.13	0.01	0.92	0.56	0.06	0.01	1.01	8.19	17.01	586

*, **- Significant at 5% and 1% level of significance respectively.

Table 7.2: Analysis of variance for various quality traits in brinjal (*Solanum melongena* L.)

Source of variation	d.f	Mean sum of squares								
		Total phenol (mg/100g)	Anthocyanin (mg/100g)	Vit.C (mg/ 100g)	TSS°Brix	Dry Matter (%)	FRAP mmol/g	Scavenging activity DPPH (%)	Quercetin (mg/g)	Ferulic acid (mg/g)
Replication	2	27.45	0.000791	13.92	0.066	0.12	0.032	5.31	0.12	0.00 4
Genotypes	40	267.99**	0.058985**	8.27**	2.90**	1.69**	1.75**	54.64**	0.25**	0.036**
Error	80	4.80	0.001668	4.83	0.14	0.03	0.01	1.01	0.009	0.001

*, **- Significant at 5% and 1% level of significance respectively

Table 8: Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability and genetic advance for various quantitative and biochemical traits in brinjal (*Solanum melongena* L.)

S. No.	Parameters	Mean	Range	Phenotypic variance (PV)	Genotypic variance (GV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability (h^2) (broad sense)	Genetic advance as % of mean
1.	Days taken to 50 flowering	49.25	44.55-56.99	10.56	9.08	6.598	6.12	0.86	11.69
2.	Days taken to first fruit set	56.65	52.88-64.77	9.25	8.22	5.369	5.06	0.88	9.82
3.	Days taken to first fruit picking	77.38	71.33-84.99	12.11	11.08	4.498	4.30	0.91	8.47
4.	Number of flowers per cluster	3.56	1.00-7.20	2.46	2.29	43.95	42.41	0.93	84.31
5.	Number of fruits per cluster	2.56	1.00-5.44	1.61	1.37	49.42	45.70	0.85	87.08
6.	Fruit length (cm)	10.32	4.36-23.96	16.73	16.60	39.60	39.45	0.99	80.94
7.	Fruit diameter (cm)	5.42	2.85-8.46	2.04	2.02	26.36	26.23	0.99	53.78
8.	Plant height (cm)	73.55	65.06-89.77	33.76	32.83	7.89	7.79	0.97	15.82
9.	Plant spread (cm)	45.60	31.22-58.90	51.80	51.23	15.78	15.69	0.98	32.15
10.	Number of branches per plant	5.33	5.00-6.90	0.32	0.26	10.59	9.45	0.82	17.37
11.	Petiole length (cm)	2.31	0.91-4.08	0.49	0.47	30.42	29.84	0.96	60.29
12.	Number of fruits per plant	8.16	3.21-18.99	15.74	14.73	48.60	47.01	0.93	93.65
13.	Average fruit weight (g)	93.89	43.66-175.33	894.35	886.16	31.85	31.70	0.99	65.01
14.	Fruit yield per plant (g)	680.96	254.33-1125.33	38774.00	38756.99	28.91	28.91	0.99	59.54
15.	Fruit yield per hectare (q)	325.89	78.29-709.99	27802.88	27628.26	29.92	28.98	0.99	57.84
16.	Total phenols (mg/100g)	86.55	63.75-103.66	92.53	87.72	11.11	10.82	0.94	21.70
17.	Anthocyanin (mg/100g)	0.84	0.42-1.15	0.02	0.01	17.08	16.38	0.92	32.37
18.	Vitamin-C (mg/100g)	14.14	10.91-17.39	5.98	1.14	17.29	7.57	0.19	6.82
19.	TSS^{o} Brix	4.58	3.13-7.20	1.06	0.92	22.54	20.92	0.86	40.01
20.	Dry Matter (%)	7.16	5.49-8.38	0.59	0.55	10.71	10.35	0.93	20.62
21.	FRAP(mmol/g)	6.04	4.52-8.12	0.59	0.58	12.80	12.60	0.96	25.55
22.	Scavenging activity DPPH (%)	30.27	25.31-40.78	18.88	17.87	14.35	13.96	0.94	27.98
23.	Quercetin (mg/g)	7.63	7.10-8.00	0.11	0.07	4.02	3.83	0.90	7.51
24.	Ferulic acid (mg/g)	0.12	0.07-0.25	0.004	0.003	42.94	42.72	0.98	87.57

4.5.1.1 Days to 50% flowering

Days to 50% flowering showed positive and significant correlation with days to first fruit set (r_g = 0.990, r_p = 0.966), days taken to first fruit picking (r_g = 0.693, r_p= 0.623), fruit diameter (r_g = 0.362, r_p= 0.332), average fruit weight (r_g = 0.368, r_p = 0.335) both at genotypic and phenotypic levels. However, it depicted negative significant association with number of flowers per cluster (r_g = -0.332, r_p = -0.310), number of fruits per cluster (r_g = -0.321, r_p = -0.294), fruit length (r_g = -0.441, r_p = -0.411), plant height (r_g = -0.472, r_p = -0.426), plant spread (r_g = -0.606, r_p = -0.555), number of branches per plant (r_g = -0.520, r_p = -0.435), petiole length(r_g = -0.302, r_p = -0.285), number of fruits per plant (r_g = -0.351, r_p = -0.309), fruit yield per plant (r_g = -0.322, r_p = -0.299),fruit yield per hectare (r_g = -0.300, r_p = -0.270).

4.5.1.2 Days to first fruit set

Days taken to first fruit set had positive significant association with days to first fruit set (r_g = 0.990, r_p = 0.996), days to first fruit picking (r_g = 0.675, r_p = 0.611), fruit diameter (r_g = 0.298, r_p = 0.277), average fruit weight (r_g = 0.338, r_p = 0.314) at both genotypic and phenotypic level and it expressed negative and significant correlation with number of flowers per cluster (r_g = -0.278, r_p = -0.262), number of fruits per cluster (r_g = -0.273, r_p = -0.254), fruit length (r_g = -0.442, r_p = -0.413), plant height (r_g = -0.449, r_p = -0.416), plant spread (r_g = -0.605, r_p = -0.567), number of branches per plant (r_g = -0.525, r_p = -0.428), petiole length (r_g = -0.290, r_p = -0.277), number of fruits per plant (r_g = -0.324, r_p = -0.286), fruit yield per plant (r_g = -0.315, r_p = -0.296).and fruit yield per hectare (r_g = -0.294, r_p = -0.296).

4.5.1.3 Days to first fruit picking

Days taken to first fruit picking showed significant positive association with days to 50% flowering (r_g = 0.693, r_p = 0.623), days to first fruit set (r_g = 0.675, r_p = 0.611), fruit diameter (r_g = 0.392, r_p = 0.370) and average fruit weight

(r_g = 0.363, r_p = 0.342) at both genotypic and phenotypic level and it expressed non significant negative correlation with number of flowers per cluster (r_g = -0.094, r_p = -0.094), number of fruits per cluster (r_g = -0.100, r_p = -0.086), number of fruits per plant (r_g = -0.132, r_p = -0.111), fruit yield per plant (r_g = -0.142, r_p = -0.135) and fruit yield per hectare (r_g = -0.112, r_p = -0.135). It expressed negative significant correlation with fruit length (r_g = -0639, r_p = -0.602), plant height (r_g = -0.325, r_p = -0.303) plant spread (r_g = -0.664, r_p = -0.626), number of branches per plant (r_g = -0.467, r_p = -0.415) and petiole length (r_g = -0.345, r_p = -0.319).

4.5.1.4 Number of flowers per cluster

Number of flowers per cluster showed significant positive association with number of fruits per cluster (r_g = 0.995, r_p = 0.954), plant height (r_g = 0.369, r_p = 0.346), plant spread (r_g = 0.186, r_p = 0.177), number of branches per plant (r_g = 0.378, r_p = 0.326), number of fruits per plant (r_g = 0.783, r_p = 0.733), fruit yield per plant (r_g = 0.461, r_p = 0.444) and fruit yield per hectare (r_g = 0.459, r_p = 0.444) at both genotypic and phenotypic level. However, it expressed non significant negative correlation with days to first fruit picking (r_g = -0.094, r_p = -0.094), fruit length (r_g = -0.132, r_p = -0.128), petiole length (r_g = -0.106, r_p = -0.092), It expressed negative significant correlation with days to 50% flowering (r_g = -0.332, r_p = -0.310), days to first fruit set (r_g = -0.278, r_p = -0.262), fruit diameter (r_g = -0.347, r_p = -0.334) and average fruit weight (r_g = -0.551, r_p = -0.530).

4.5.1.5 Number of fruits per cluster

Number of fruits per cluster showed positive and significant association with number of flowers per cluster (r_g = 0.995, r_p = 0.954), plant height (r_g = 0.427, r_p = 0.378), plant spread (r_g = 0.193, r_p = 0.176), number of branches per plant (r_g = 0.493, r_p = 0.366), number of fruits per plant (r_g = 0.885, r_p = 0.755), fruit yield per plant (r_g = 0.524, r_p = 0.484) and fruit yield per hectare (r_g = 0.524,

r_p = 0.463) at both genotypic and phenotypic level respectively. However, it showed negative and non significant correlation with days to first fruit picking (r_g = -0.100, r_p = -0.086), fruit length (r_g = -0.124, r_p = -0.113), petiole length (r_g = -0.086, r_p = -0.060), It expressed negative significant correlation with days to 50% flowering (r_g = -0.321, r_p = -0.294), days to first fruit set (r_g = -0.273, r_p = -0.254), fruit diameter (r_g = -0.342, r_p = -0.313) and average fruit weight (r_g = -0.595, r_p = -0.549).

4.5.1.6 Fruit length

Fruit length exhibited significant positive association with plant height (r_g = 0.515, r_p = 0.504), plant spread (r_g = 0.814, r_p = 0.807), number of branches per plant (r_g = 0.472, r_p = 0.414), at both genotypic and phenotypic level but showed negative but non significant correlation with number of flowers per cluster (r_g = -0.132, r_p = -0.128), number of fruits per cluster (r_g = -0.124, r_p = -0.113) and number of fruits per plant (r_g = -0.058, r_p = -0.057). It also depicted positive but non significant correlation with fruit yield per plant (r_g = 0.075, r_p = 0.075), petiole length (r_g = 0.166, r_p = 0.162), fruit yield per hectare (r_g = 0.057, r_p = 0.054). It showed significant negative correlation with days to 50% flowering (r_g = -0.441, r_p = -0.411), days to first fruit set (r_g = -0.442, r_p = -0.413), days to first fruit picking (r_g = -0.639, r_p = -0.602), fruit diameter and (r_g = -0.619, r_p = -0.611).

4.5.1.7 Fruit diameter

Fruit diameter showed significant positive association with days to 50% flowering (r_g = 0.362, r_p = 0.332), days to first fruit set (r_g = 0.298, r_p = 0.277), days to first fruit picking (r_g = 0.392, r_p = 0.370), average fruit weight (r_g = 0.250, r_p = 0.249) at both genotypic and phenotypic level respectively. However, it expressed non significant negative correlation with fruit yield per plant (r_g = -0.076, r_p = -0.075). Petiole length (r_g = -0.096, r_p = -0.094) and fruit yield per hectare (r_g = -0.060, r_p = -0.058). It expressed negative significant correlation with number of flowers per cluster (r_g = -0.347, r_p = -0.334), number of fruits per

cluster (r_g = -0.342, r_p = -0.313), fruit diameter (r_g = -0.619, r_p = -0.611), plant height (r_g = -0.447, r_p = -0.441), plant spread (r_g = -0.642, r_p = -0.636), number of branches per plant (r_g = -0.421, r_p = -0.379) and number of fruits per plant (r_g = -0.205, r_p = -0.203).

4.5.1.8 Plant height

Plant height exhibited significant positive association with number of flowers per cluster (r_g = 0.369, r_p = 0.346), number of fruits per cluster (r_g = 0.427, r_p = 0.378), fruit length (r_g = 0.515, r_p = 0.504), plant spread (r_g = 0.577, r_p = 0.567), number of branches per plant (r_g = 0.726, r_p = 0.637), number of fruits per plant (r_g = 0.346, r_p = 0.326), fruit yield per plant (r_g = 0.507, r_p = 0.501) and fruit yield per hectare (r_g = 0.513, r_p = 0.491) at both genotypic and phenotypic level respectively and It showed negative and non significant correlation with petiole length (r_g = -0.077, r_p = -0.078) and average fruit weight (r_g = -0.129, r_p = -0.128). It expressed negative significant correlation with days to 50% flowering (r_g = -0.472, r_p = -0.426), days to first fruit set (r_g = -0.449, r_p = -0.416), days to first fruit picking (r_g = -0.325, r_p = -0.303), fruit diameter (r_g = -0.447, r_p = -0.441).

4.5.1.9 Plant spread

Plant spread exhibited significant positive association with number of flowers per cluster (r_g = 0.186, r_p = 0.177), number of fruits per cluster (r_g = 0.193, r_p = 0.176), fruit length (r_g = 0.814, r_p = 0.807), plant height (r_g = 0.577, r_p = 0.567), number of branches per plant (r_g = 0.575, r_p = 0.513), petiole length (r_g = 0.198, r_p = 0.197) and fruit yield per plant (r_g = 0.179, r_p = 0.179) at both genotypic and phenotypic level respectively and It showed negative significant correlation with days to 50% flowering (r_g = -0.606, r_p = -0.555), days to first fruit set (r_g = -0.605, r_p = -0.567), days to first fruit picking (r_g = -0.664, r_p = -0.626), fruit diameter (r_g = -0.642, r_p = -0.636) and average fruit weight (r_g = -0.218, r_p = -

0.216). It expressed positive non significant correlation with number of fruits per plant (r_g = 0.133, r_p = 0.125), plant spread (r_g = 0.166, r_p = 0.162).

4.5.1.10 Number of branches per plant

Number of branches per plant showed significant positive association with number of flowers per cluster (r_g = 0.378, r_p = 0.326), number of fruits per cluster (r_g = 0.439, r_p = 0.366), fruit length (r_g = 0.472, r_p = 0.414), plant height (r_g = 0.726, r_p = 0.637), plant spread (r_g = 0.575, r_p = 0.513), number of fruits per plant (r_g = 0.548, r_p = 0.488), fruit yield per plant (r_g = 0.598, r_p = 0.534) and fruit yield per hectare (r_g = 0.611, r_p = 0.521), at both genotypic and phenotypic level respectively and It showed significant negative correlation with days to 50% flowering (r_g = -0.520, r_p = -0.435), days to first fruit set (r_g = -0.525, r_p = -0.428), days to first fruit picking (r_g = -0.467, r_p = -0.415), fruit diameter (r_g = -0.421, r_p = -0.379) and average fruit weight (r_g = -0.278, r_p = -0.250). It expressed non significant negative correlation with petiole length (r_g = -0.094, r_p = -0.097).

4.5.1.11 Petiole length

Petiole length showed significant positive association with plant spread (r_g = 0.198, r_p = 0.197 at both genotypic and phenotypic level respectively and It showed significant negative correlation with days to 50% flowering (r_g = -0.302, r_p = -0.285), days to first fruit set (r_g = -0.290, r_p = -0.277), days to first fruit picking (r_g = -0.345, r_p = -0.319). It expressed non significant positive correlation with fruit length (r_g = 0.166, r_p = 0.162), fruit yield per plant (r_g = 0116, r_p = 0.114) and fruit yield per hectare (r_g = 0.073, r_p = 0.075). It expressed non significant negative correlation with number of flowers per cluster (r_g = -0.106, r_p = -0.092), number of fruits per cluster (r_g = -0.086, r_p = -0.060), fruit diameter (r_g = -0.096, r_p = -0.094), plant height (r_g = -0.077, r_p = -0.078), number of branches per plant (r_g = -0.094, r_p = -0.097) and number of fruits per plant (r_g = -0.010, r_p = -0.003), average fruit weight (r_g = -0.075, r_p = -0.069),

4.5.1.12 Number of fruits per plant

Number of fruits per plant showed significant positive association with number of flowers per cluster (r_g = 0.783, r_p = 0.733), number of fruits per cluster (r_g = 0.855, r_p = 0.755), plant height (r_g = 0.346, r_p = 0.326), number of branches per plant (r_g = 0.548, r_p = 0.488), fruit yield per plant (r_g = 0.671, r_p = 0.649) and fruit yield per hectare (r_g = 0.668, r_p = 0.639) at both genotypic and phenotypic level. It expressed non significant negative correlation with days to first fruit picking (r_g = -0.132, r_p = -0.111), fruit length (r_g = -0.058, r_p = -0.057), petiole length (r_g = -0.010, r_p = -0.003). It expressed significant negative correlation with days to 50% flowering (r_g = -0.351, r_p = -0.309), days to first fruit set (r_g = -0.324, r_p = -0.286), fruit diameter (r_g = -0.205, r_p = -0.203), average fruit weight (r_g = -0.697, r_p = -0.673). It showed non significant positive correlation with plant spread (r_g = 0.133, r_p = 0.125).

4.5.1.13 Average fruit weight

Average fruit weight showed significant positive association with days to 50% flowering (r_g = 0.368, r_p = 0.335), days to first fruit set (r_g = 0.338, r_p = 0.314), days to first fruit picking (r_g = 0.363, r_p = 0.342), fruit diameter (r_g = 0.250, r_p = 0.249), fruit yield per plant (r_g = 0.098, r_p = 0.106) and fruit yield per hectare (r_g = 0.106, r_p = 0.094) at both genotypic and phenotypic level. It showed non significant negative correlation with fruit length (r_g = -0.148, r_p = -0.147), plant height (r_g = -0.129, r_p = -0.128) and petiole length (r_g = -0.075, r_p = -0.069). It expressed negative significant correlation with number of flowers per cluster (r_g = -0.551, r_p = -0.530), number of fruits per cluster (r_g = -0.595, r_p = -0.549), plant spread (r_g = -0.218, r_p = -0.216), (r_g = -0.278, r_p = -0.250) and number of fruits per plant (r_g = -0.697, r_p = -0.673).

4.5.1.14 Fruit yield per plant

Fruit yield per plant showed significant positive association with number of flowers per cluster (r_g = 0.461, r_p = 0.444), number of fruits per cluster (r_g =

0.524, r_p = 0.484), plant height (r_g = 0.507, r_p = 0.501), plant spread (r_g = 0.179, r_p = 0.179), number of branches per plant (r_g = 0.589, r_p = 0.534), number of fruits per plant (r_g = 0.671, r_p = 0.649), average fruit weight (r_g = 0.098, r_p = 0.106) and fruit yield per hectare (r_g = 0.986, r_p = 0.974), at both genotypic and phenotypic level. It showed non significant negative correlation with days to first fruit picking (r_g = -0.142, r_p = -0.135), fruit diameter (r_g = -0.076, r_p = -0.075). It expressed negative significant correlation with days to 50% flowering (r_g = -0.322, r_p = -0.299) and days to first fruit set (r_g = -0.315, r_p = -0.296). It shows non significant positive association with fruit length (r_g = 0.075, r_p = 0.075), petiole length (r_g = 0.116, r_p = 0.114).

4.5.1.15 Fruit yield per hectare

Fruit yield per hectare showed significant positive association with number of flowers per cluster (r_g = 0.459, r_p = 0.422), number of fruits per cluster (r_g = 0.524, r_p = 0.463), plant height (r_g = 0.513, r_p = 0.491), number of branches per plant (r_g = 0.611, r_p = 0.521), number of fruits per plant (r_g = 0.668, r_p = 0.639), average fruit weight (r_g = 0.106, r_p = 0.094) and fruit yield per plant (r_g = 0.986, r_p = 0.974) at both genotypic and phenotypic level. It showed non significant negative correlation with days to first fruit picking (r_g = -0.112, r_p = -0.102), fruit diameter (r_g = -0.060, r_p = -0.058), It expressed negative significant correlation with days to 50% flowering (r_g = -0.300, r_p = -0.270), days to first fruit set (r_g = -0.294, r_p = -0.282). It expressed non significant positive association with fruit length (r_g = 0.057, r_p = 0.054), plant spread (r_g = 0.166, r_p = 0.162) and petiole length (r_g = 0.073, r_p = 0.075).

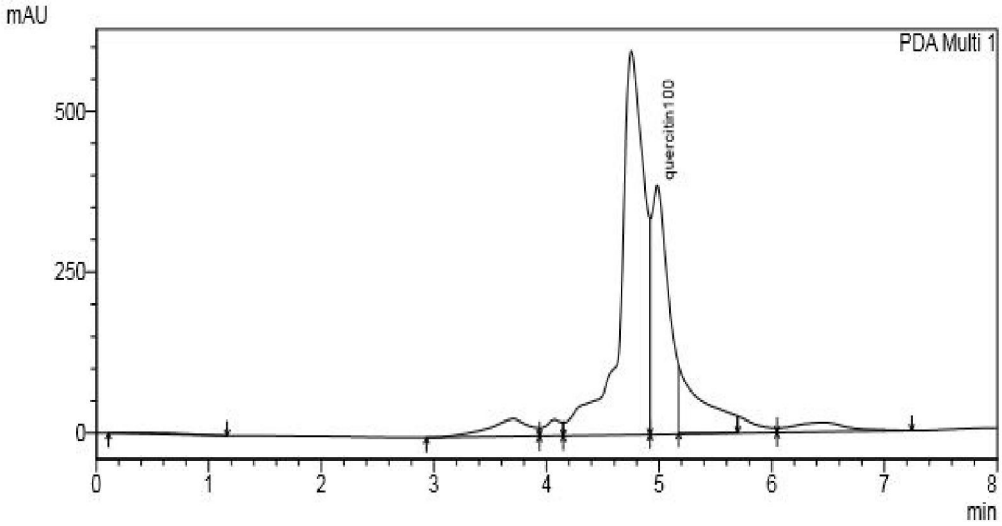

Fig.1: Shows peak value of quercitin using HPLC

Table 9: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among different traits in brinjal (*Solanum melongena* L.)

	D50%	DFFS	DFFP	NfPC	NFPC	FL	FD	PH	PS	NBPP	PL	NFPP	AFV	FYPP	FYPH
D50%	**1.00**	0.990**	0.693**	-0.332**	-0.321**	-0.441**	0.362**	-0.472**	-0.606**	-0.520**	-0.302**	-0.351**	0.368**	-0.322**	-0.300**
DFFS	0.966**	**1.00**	0.675**	-0.278**	-0.273**	-0.442**	0.298**	-0.449**	-0.605**	-0.525**	-0.290**	-0.324**	0.338**	-0.315**	-0.294**
DFFP	0.623**	0.611**	**1.00**	-0.094	-0.1	-0.639**	0.392**	-0.325**	-0.664**	-0.467**	-0.345**	-0.132	0.363**	-0.142	-0.112
NfPC	-0.310**	-0.262**	-0.094	**1.00**	0.995**	-0.132	-0.347**	0.369**	0.186*	0.378**	-0.106	0.783**	-0.551**	0.461**	0.459**
NFPC	-0.294**	-0.254**	-0.086	0.954**	**1.00**	-0.124	-0.342**	0.427**	0.193*	0.439**	-0.086	0.855**	-0.595**	0.524**	0.524**
FL	-0.411**	-0.413**	-0.602**	-0.128	-0.113	**1.00**	-0.619**	0.515**	0.814**	0.472**	0.166	-0.058	-0.148	0.075	0.057
FD	0.332**	0.277**	0.370**	-0.334**	-0.313**	-0.611**	**1.00**	-0.447**	-0.642**	-0.421**	-0.096	-0.205*	0.250**	-0.076	-0.06
PH	-0.426**	-0.416**	-0.303**	0.346**	0.378**	0.504**	-0.441**	**1.00**	0.577**	0.726**	-0.077	0.346**	-0.129	0.507**	0.513**
PS	-0.555**	-0.567**	-0.626**	0.177*	0.176*	0.807**	-0.636**	0.567**	**1.00**	0.575**	0.198*	0.133	-0.218*	0.179*	0.166
NBPP	-0.435**	-0.428**	-0.415**	0.326**	0.366**	0.414**	-0.379**	0.637**	0.513**	**1.00**	-0.094	0.548**	-0.278**	0.598**	0.611**
PL	-0.285**	-0.277**	-0.319**	-0.092	-0.060	0.162	-0.094	-0.078	0.197*	-0.097	**1.00**	-0.01	-0.075	0.116	0.073
NFPP	-0.309**	-0.286**	-0.111	0.733**	0.755**	-0.057	-0.203*	0.326**	0.125	0.488**	-0.003	**1.00**	-0.697**	0.671**	0.668**
AFV	0.335**	0.314**	0.342**	-0.530**	-0.549**	-0.147	0.249**	-0.128	-0.216*	-0.250**	-0.069	-0.673**	**1.00**	0.098**	0.106**
FYPP	-0.299**	-0.296**	-0.135	0.444**	0.484**	0.074	-0.075	0.501**	0.179*	0.534**	0.114	0.649**	0.106**	**1.00**	0.986**
FYPH	-0.270**	-0.282**	-0.102	0.422**	0.463**	0.054	-0.058	0.491**	0.162	0.521**	0.075	0.639**	0.094**	0.974**	**1.00**

*, **- Significant at 5% and 1% level of significance respectively. D50% =Days to 50% flowering, DFFS= Days to first fruit set, DFFP= Days to first fruit picking, NfPC= Number of flowers per cluster, NFPC= Number of fruits per cluster, FL= Fruit length, FD= Fruit diameter.PH= Plant height, PS=Plant spread, NBPP= Number of branches per plant ,PL= Petiole length, NFPP=Number of fruits per plant, AFW= Average fruit weight ,FYPP= Fruit yield per plant, PYPH= Fruit yield per ha.

4.5.2 Clustering pattern based on D^2 analysis

Knowledge of genetic diversity of a crop and its quantitative assessment usually helps a plant breeder in choosing desirable parents for breeding programme. Geographic diversity in crop plants, very often fails to convey information about the genetic divergence. Therefore, it is worthwhile to use suitable tool like D^2 statistics (Mahalanobis, 1936) as a quantitative measure of genetic divergence.

4.5.3 Distribution of genotypes into different clusters

In the present study, D^2 analysis grouped the test genotypes into four clusters (Table-10) and pictorially represented in Fig-2 with cluster I containing maximum number of genotypes sixteen, cluster II with eleven genotypes, cluster III with seven genotypes and cluster IV with seven genotypes. Cluster I consisted of SK-BR-117, SK-BL-111, SK-BL-110, SK-BL-108, SK-BL-107, SK-BL-101, SK-BL-100, SK-BL-116, SK-BL-114, SK-BL-112, SK-BL-109, SK-BL-115, SK-BL-113, SK-BR-119, SK-BR-118 and Local Long. SK-BSR-125, SK-BR-136, SK-BR-122, SK-BR-131, SK-BR-123, SK-BR-130, SK-BR-134, SK-BR-121, SK-BR-137, SK-BR-120 and SK-BR-135 were included in cluster II. SK-BSR-128, SK-BR-132, SK-BR-129, SK-BR-133, SK-BSR-124, SK-BSR-126 and SK-BSR-127 were included in cluster III. Cluster IV, included genotypes SK-BL-104, SK-BL-103, SK-BL-105, SK-BL-102, SK-BL-106, 2017/BRL VAR-7, 2018/BRL VAR-5. The formation of different clusters with variable number of entries in each cluster indicated diversity among genotypes. The genotypes distributed randomly to different clusters irrespective of geographical origin. The clustering pattern of these genotypes under the study suggested that geographic diversity may not be necessarily related with genetic diversity.

The cluster mean values for fifteen traits are presented in Table-12. The perusal of data indicated considerable differences for all the traits among clusters. It is inferred from the cluster means that each cluster has its uniqueness that

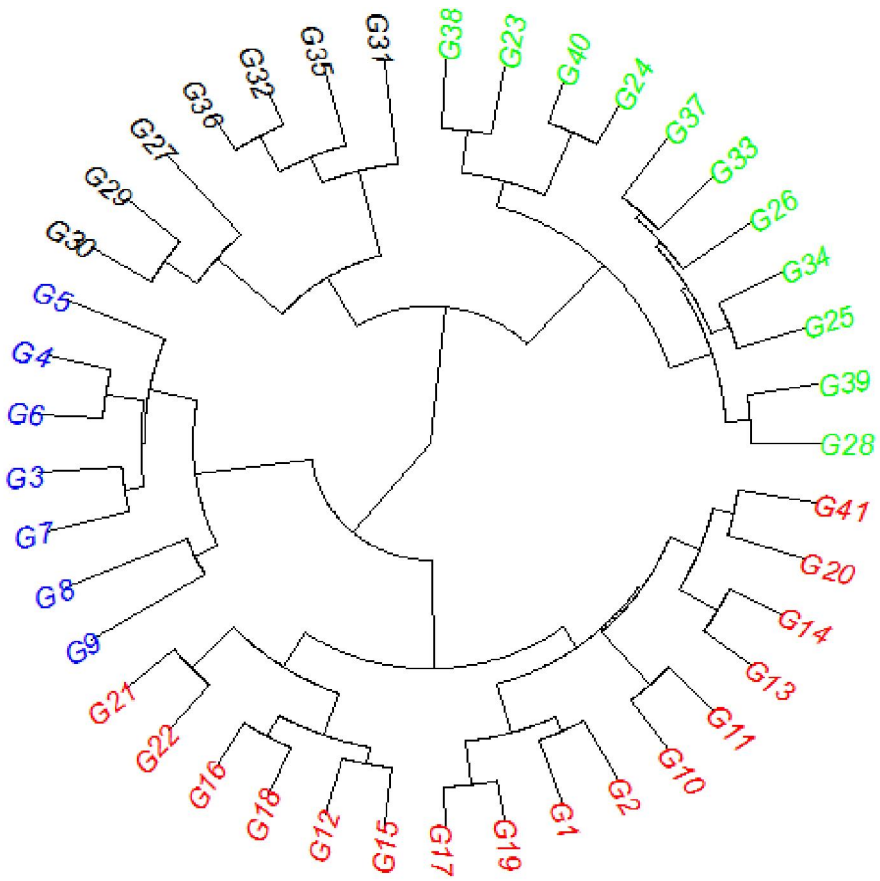

Fig. 2: Dendrogram showing morphological clustering of brinjal genotypes

separated it from other clusters. Lowest cluster mean for days to 50% flowering (46.59) was found in Cluster IV while the highest cluster mean for days to 50% flowering (52.05) was found in cluster II. The lowest cluster mean for days taken to first fruit set (54.21) was found in cluster IV and highest cluster mean for days taken to first fruit set (59.15) was found in cluster II. The lowest cluster mean for days taken to first fruit picking (74.18) was found in cluster IV while the highest cluster mean for days taken to first fruit picking (80.66) in cluster II. The highest cluster mean for number of flowers per cluster (4.67) and number of fruits per cluster (3.55) was found in cluster III and the lowest cluster mean for number of flowers per cluster (2.50) and number of fruits per cluster (1.68) were found in cluster II. The highest cluster mean for fruit length (15.13 cm) in cluster IV while lowest (6.22 cm) in cluster III. Highest cluster mean for fruit diameter (6.59 cm) existed in cluster II while lowest (4.23 cm) in cluster IV. Highest cluster mean for plant height (83.14 cm), plant spread (53.88) and number of branches per plant (6.31) were found in cluster IV while lowest cluster mean for plant height (70.05 cm), plant spread (38.42 cm), number of branches per plant (5.02 cm) was found in cluster II. Highest cluster mean for petiole length (2.72 cm) was found in cluster I and lowest cluster mean (1.92 cm) was found in cluster II. Highest cluster mean for number of fruits per plant (11.94) was found in cluster III and lowest (5.64) in cluster II. Highest cluster mean for average fruit weight (124.46 g) was found in cluster II while lowest cluster mean (71.04 g) in cluster III. Highest cluster mean for fruit yield per hectare (456.27g) was found in cluster IV while lowest cluster mean (268.42 g) in cluster I.

4.5.4 Identification of diverse and desirable genotypes

Non- hierarchical cluster analysis was also performed in addition to grouping of genotypes into different clusters so as to identify the diverse and desirable genotypes in terms of inter cluster distance and mean performance of clusters for various traits, respectively. For this purpose, intra and inter cluster distances (Table-11) and the mean performance of each cluster for different traits

was studied. The intra cluster distance ranged from 79.1 (cluster IV) to 104.3 (cluster II) indicating that the genotypes in clusters have dissimilarity for morphological traits and performance. The members of cluster II exhibited maximum divergence (intra cluster distance 104.3) followed by members of cluster III (92.4). The inter cluster distance were larger than the intra cluster distances indicating a wider genetic diversity between genotypes of cluster with respect to traits considered. Maximum inter-cluster distance indicates that genotypes falling in these clusters had wide diversity and can be used for hybridization programme to get better recombinants in the segregating generation. The inter cluster distance D^2 values was highest between cluster III and IV (885.53) followed by I and IV (550.24) and II and IV (273.58).

Table 10: Distribution of brinjal (*Solanum melongena* L.) genotypes into clusters based on D^2 statistics

Cluster number	Number of genotypes	Genotypes
I	16	SK-BR-117, SK-BL-111, SK-BL-110, SK-BL-108, SK-BL-107, SK-BL-101, SK-BL-100, SK-BL-116, SK-BL-114, SK-BL-112, SK-BL-109, SK-BL-115, SK-BL-113, SK-BR-119, SK-BR-118, Local Long.
II	11	SK-BSR-125, SK-BR-136, SK-BR-122, SK-BR-131, SK-BR-123, SK-BR-130, SK-BR-134, SK-BR-121, SK-BR-137, SK-BR-120, SK-BR-135.
III	7	SK-BSR-128, SK-BR-132, SK-BR-129, SK-BR-133, SK-BSR-124, SK-BSR-126, SK-BSR-127.
Iv	7	SK-BL-104, SK-BL-103, SK-BL-105, SK-BL-102, SK-BL-106, 2017/BRL VAR-7, 2018/BRL VAR-5.

Table 11: Average intra cluster (Diagonal) and inter cluster (Above Diagonal) distance values in brinjal (*Solanum melongena* L.)

S. No.	Cluster	I	II	III	Iv
1	I	**79.2**	285.54	340.05	550.24
2	II		**104.2**	617.82	273.58
3	III			**92.4**	885.53
4	Iv				79.1

Table 12: Mean performance studies of different clusters for evaluated morphological traits of brinjal (*Solanum melongena* L.) genotypes

Clusters	Days taken to 50% flowering	Days taken to first fruit set	Days taken to first fruit picking	Number of flowers per cluster	Number of fruits per cluster	Fruit length (cm)	Fruit diameter (cm)	Plant height (cm)	Plant spread (cm)	Number of branches per plant	Petiole length (cm)	Number of fruits per plant	Average fruit weight (g)	Fruit yield per plant (g)	Fruit yield per hectare (q)
I	48.46	55.98	75.49	3.43	2.40	12.04	4.83	71.80	49.12	5.17	2.72	6.88	85.26	566.68	268.42
II	52.05	59.15	80.66	2.50	1.68	7.37	6.59	70.05	38.42	5.02	1.92	5.64	124.46	623.24	300.35
III	49.34	56.65	79.71	4.67	3.55	6.22	6.12	73.50	40.58	5.23	2.17	11.94	71.04	764.26	367.01
Iv	46.59	54.21	74.18	4.42	3.34	15.13	4.23	83.14	53.88	6.31	2.12	11.26	88.39	949.66	456.27

4.5.5 Principal component analysis (PCA)

The first five principal components contributing 30.02%, 22.47%, 11.42%, 6.70% and 6.23%, respectively, with a cumulative variation of 76.86% (Table-13) are pictorially represented in Fig-3. The relative discriminating power of the principal axes as indicated by the Eigen value was high for axis 1 (7.20%) and low for axis 5 (1.50%).

4.5.5.1 Principal component analysis (PCA) for morphological traits

From PC1, plant spread and fruit length showed 80% and 75% variation, respectively. PC2 revealed number of fruits per cluster (69%) and fruit yield per hectare (67%) as the key traits which significantly contributed to total genetic variance. Number of fruits per cluster (49%) and number of flowers per cluster (48%) were considered as the most important parameters that contributed to the total genetic variance as revealed by PC3. PC4 showed that average fruit weight (62%) and fruit yield per hectare (45%) were the traits which made substantial contribution to total variation among the genotypes. Petiole length (56%) and fruit yield per hectare (37%) were the most promising traits explaining the diversity as shown by PC5.

4.5.5.2 Principal component analysis (PCA) for biochemical traits

From PC1, (total phenol, scavenging activity) showed 72% and 71% variation, respectively. PC2 revealed scavenging activity (61%) and quercetin (60%) as the key traits which significantly contributed to total genetic variance. Dry matter (56%) and TSS (44%) were considered as the most important parameters that contributed to the total genetic variance as revealed by PC3. PC4 showed that TSS (13%) dry matter and FRAP (12%) were the traits which made substantial contribution to total variation among the genotypes. Dry matter and vitamin C showed 53% and 39% variation respectively towards PC5.

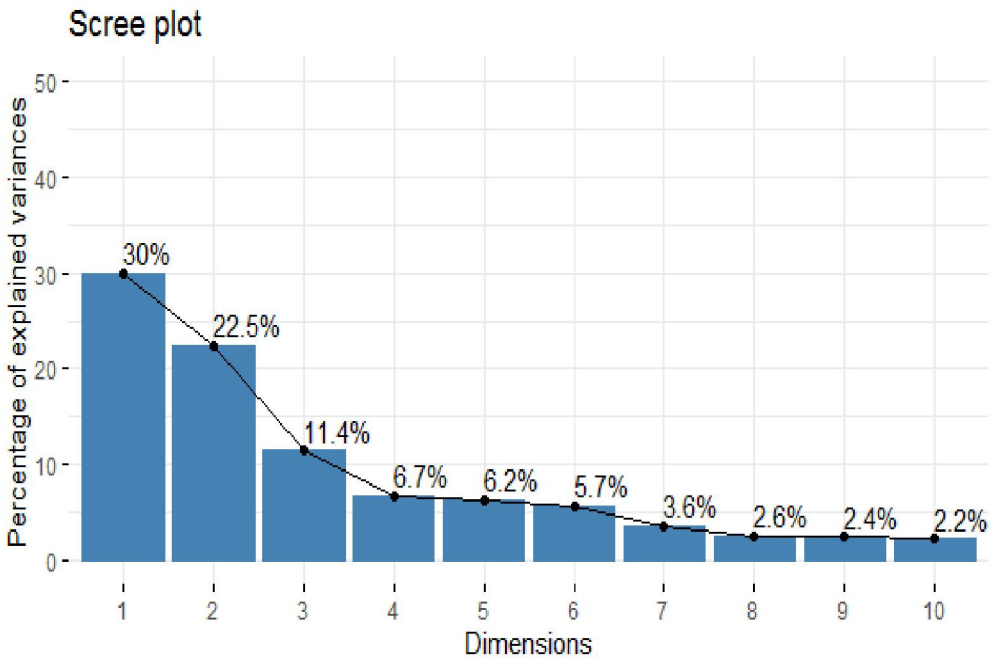

Fig. 3: Contribution of variables towards principal components

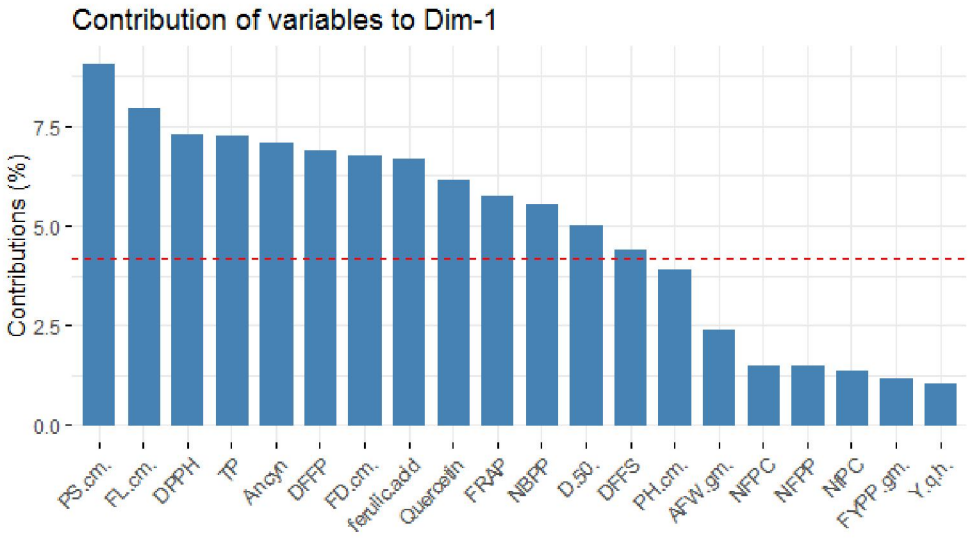

Fig. 3a: Contribution of variables towards dimension one

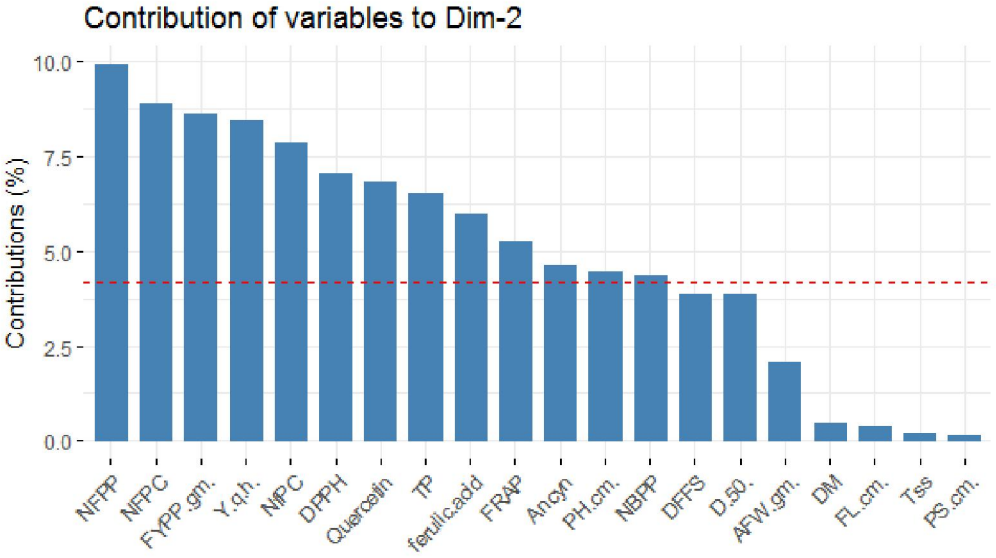

Fig. 3b: Contribution of variables towards dimension two

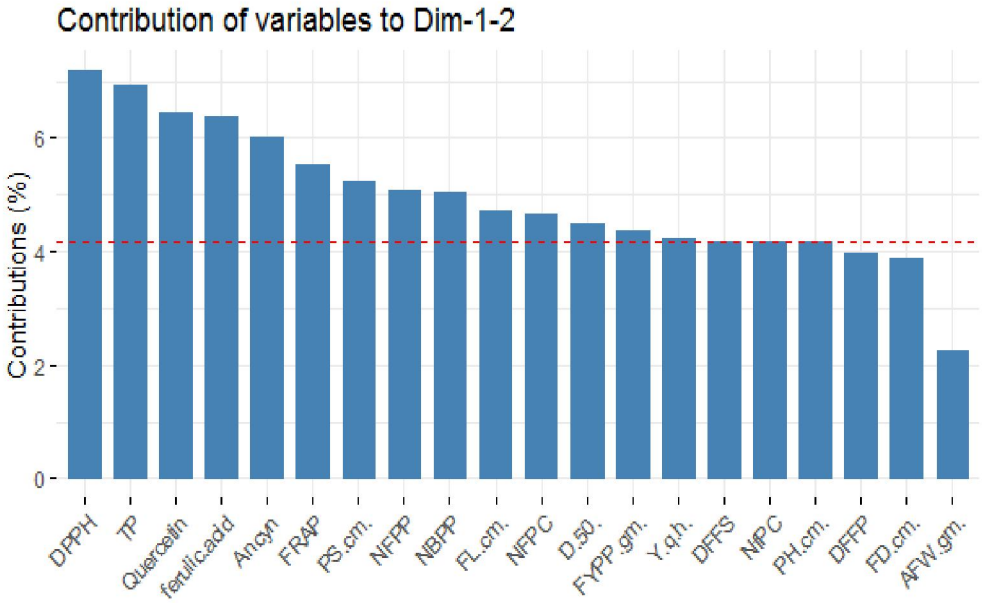

Fig. 3c: Contribution of variables towards dimension one and two

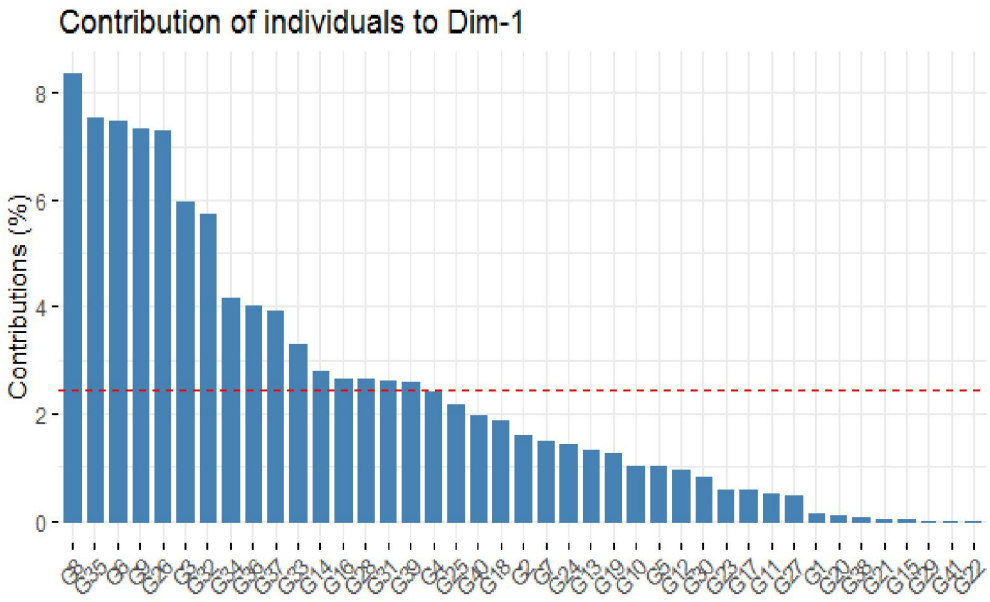

Fig. 3d: Contribution of variables towards dimension one

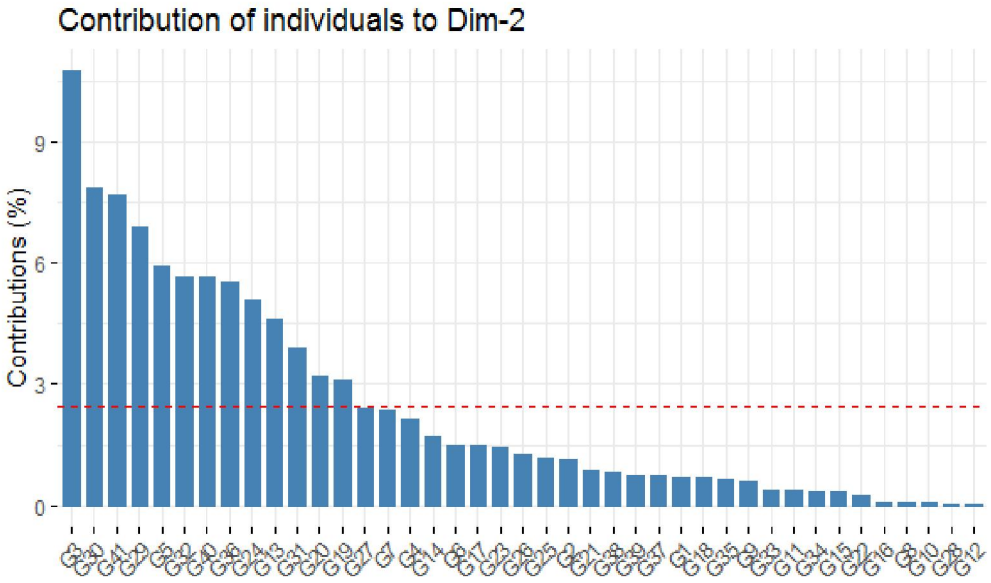

Fig. 3e: Contribution of variables towards dimension two

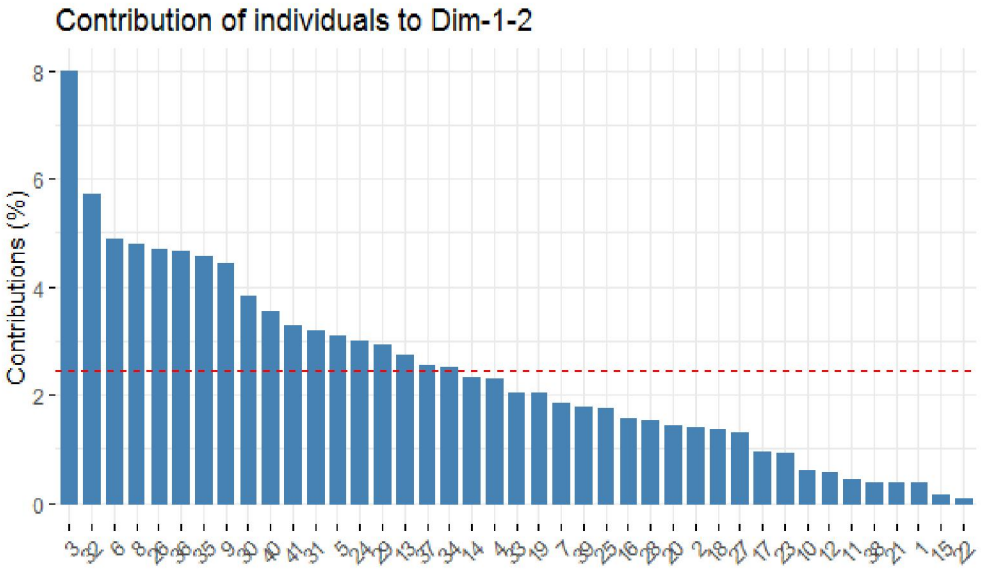

Fig. 3f: Contribution of variables towards dimension one and two

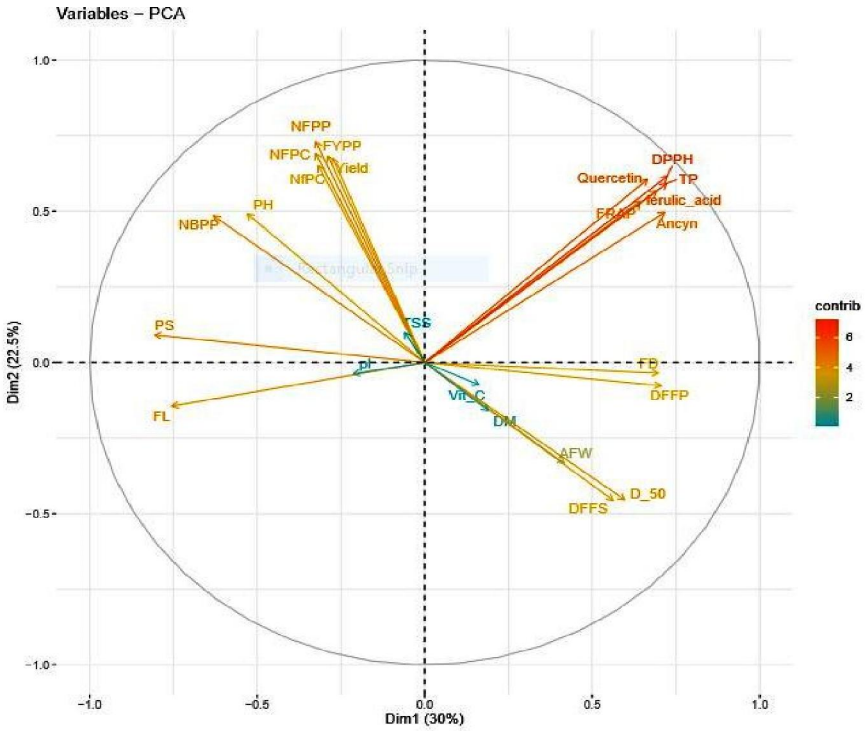

Fig. 4: Correlation circle showing contribution of studied variables towards principal components

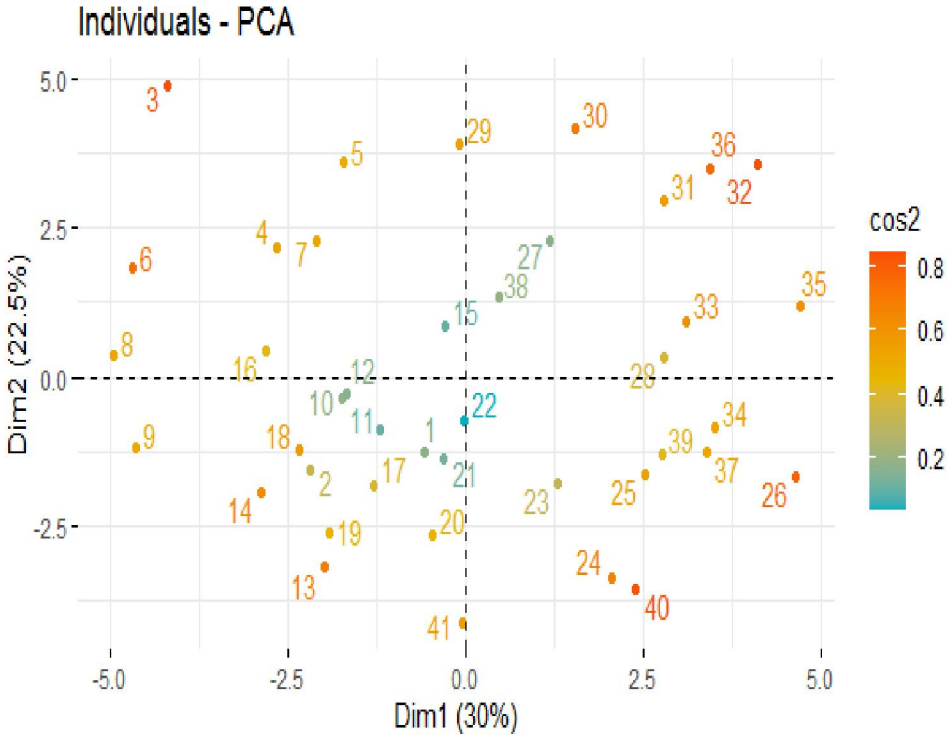

Fig. 5: Contribution of brinjal individuals towards PCA analysis based on cos2 value

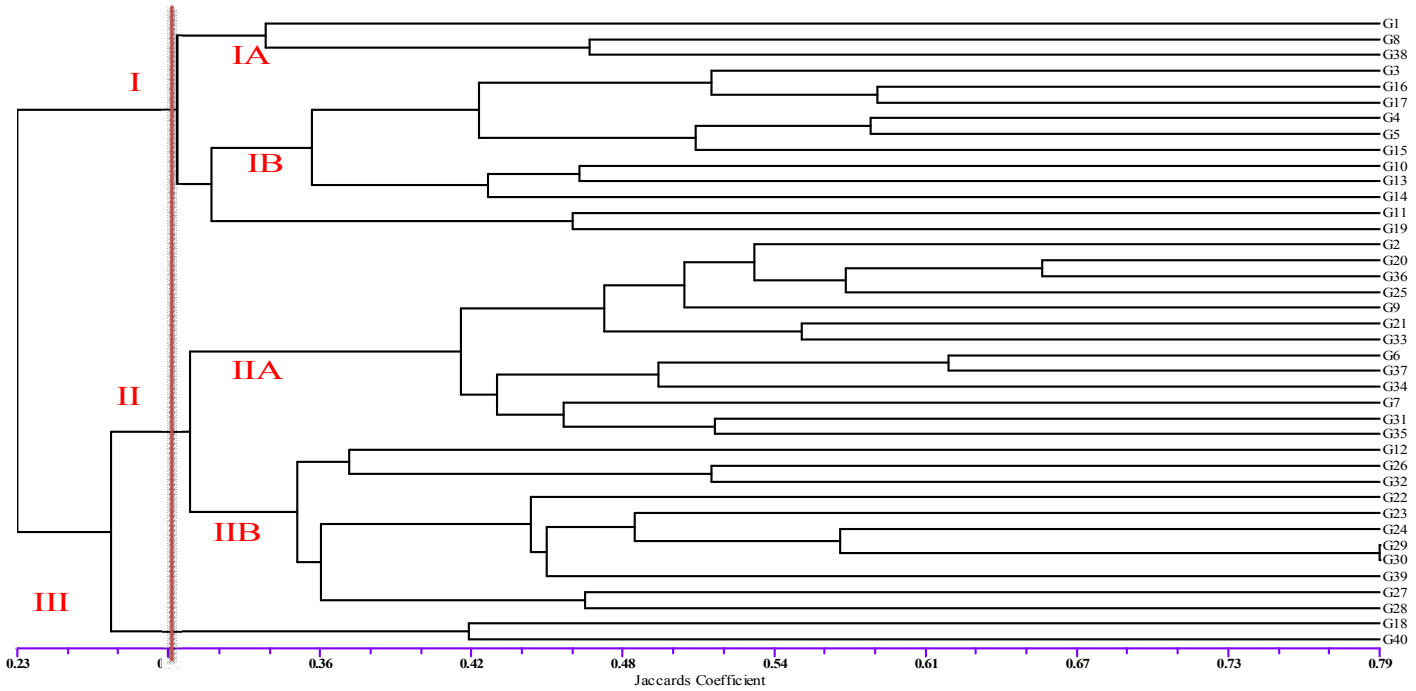

Fig. 6: Dendrogram showing clustering of brinjal genotypes based on ISSR markers

4.5.5.3 Contribution of variables and individuals towards dimension one and dimension two

Scavenging activity (DPPH) showed maximum contribution towards dimension one and dimension two and average fruit weight showed minimum contribution towards dimension one and dimension two (Fig-3c) while as individual 3 shows maximum contribution towards dimension one and dimension two and individual 22 showed minimum contribution towards dimension one and dimension two (Fig-3f). Fig-4 represents the correlation circle and it shows the contribution of variables towards principal components. Fig-5 represents the scatter plot and it shows the contribution of brinjal individuals towards PCA analysis based on cos2 value.

4.6 Characterization on the basis of ISSR markers.

4.6.1 ISSR marker analysis

The summarized data of 15 ISSR primers used for identification and evaluation of genetic diversity of forty brinjal genotypes is present in Table-2. All 15 ISSR primers, produced sharp and consistent amplification bands in all selected genotypes. A total of 83 alleles were amplified by 15 polymorphic ISSR loci and the numbers of alleles ranged from 2 amplified by primer BGCO5 848 and BGCO5 830 to 12 amplified by primer BGCO5 860 with an average of 5.53 alleles per locus with band size varying from 150-1200. The total numbers of bands amplified were 83 out of which 53 were polymorphic. The number of polymorphic bands ranged from 1 in primer BGCO5 830, BGCO5 824, BGCO5 848 to 11 in primer BGCO5 848 with an average value of 3.53. No single band was specific to any individual genotype. The variation in number of alleles produced by ISSR markers demonstrates heterozygosity of alleles at a given locus and shows great genetic variability. Band size ranged between 150 to 1200 bp. The percentage of polymorphism ranged from 40% to 91.67% with an average value of 60.59%.The maximum percentage of polymorphism was found in primer

Table 13: Latent vectors for twenty four traits in brinjal (*Solanum melongena* L.)

Trait	Eigen vector				
	PC1	**PC2**	**PC 3**	**PC 4**	**PC 5**
Days taken to 50 flowering	0.59	-0.45	0.41	0.27	-0.08
Days taken to first fruit set	0.56	-0.45	0.45	0.24	-0.09
Days taken to first fruit picking	0.70	-0.07	0.39	0.23	-0.12
Number of flowers per cluster	-0.31	0.65	0.48	-0.25	-0.17
Number of fruits per cluster	-0.32	0.69	0.49	-0.21	-0.14
Fruit length	-0.75	-0.14	-0.44	0.173	-0.02
Fruit diameter	0.69	-0.03	0.04	0.05	0.33
Plant height	-0.53	0.49	-0.18	0.41	-0.08
Plant spread	-0.80	0.09	-0.37	0.05	-0.03
Number of branches per plant	-0.63	0.48	-0.03	0.36	-0.15
Petiole length	-0.21	-0.03	-0.21	-0.31	0.56
Number of fruits per plant	-0.32	0.73	0.47	-0.15	0.03
Average fruit weight	0.41	-0.33	-0.27	0.62	0.10
Fruit yield per plant	-0.28	0.68	0.24	0.43	0.38
Fruit yield per hectare	-0.27	0.67	0.26	0.45	0.37
Total phenol	0.72	0.59	-0.24	-0.09	-0.12
Anthocyanin	0.71	0.49	-0.25	-0.02	-0.04
Vitamin-C	0.16	-0.07	-0.04	-0.03	0.39
TSS ^{o}brix	-0.06	0.09	-0.44	-0.13	0.37
Dry matter	0.19	-0.15	0.54	-0.12	0.55
FRAP	0.64	0.53	-0.32	-0.12	0.02
Scavenging activity (DPPH)	0.72	0.61	-0.20	0.07	0.01
Quercetin	0.66	0.60	-0.16	-0.01	-0.16
Ferulic acid	0.69	0.56	-0.26	0.01	0.04
Eigen values	7.20	5.39	2.74	1.61	1.50
Percentage variance	30.02	22.47	11.42	6.70	6.23
Cumulative percentage variance	30.02	52.49	63.92	70.62	76.86

BGCO5 860 and the minimum percentage of polymorphism (40%) was realized in BGCO5 823.The average percentage of polymorphism was 60.59%. Among 15 primers only seven primers had percentage of polymorphism greater than average. The maximum number of amplified bands (144) were observed in BGCO5 842 and the minimum number of bands amplified (14) was found in primer BGCO5 860.The average number of bands amplified by each primer were 57.46.

The information on the genetic profile of each accession obtained using the fifteen ISSR primers was used to estimate the marker performance through evaluation of seven parameters: polymorphic information content (PIC), effective multiplex ratio EMR, marker index (MI), resolving power (RP), discriminating power (DP), heterozygocity (H), average heterozygocity (H.av) (Table-14). High PIC value was detected for primer BGCO5-860 and BGCO5-814 at 0.383 and 0.380, respectively and low PIC value of 0.261 for primers, namely, BGCO5 848 and BGCO5 823.The average of PIC value per primer, was 0.37.The expected heterozygosity varied from 0.057 to 0.498. The maximum value of H 0.498 was found in primer BGCO5 823 and the minimum value of H 0.057 BGCO5 860, with mean value of 0.002. The maximum value of expected heterozygosity (H) and PIC for binary data is 0.5, because two alleles per locus are assumed, and both are influenced by the number and frequency of the alleles for codominant markers, these values varies between 0 and 1. The ISSR effective multiplex ratio (EMR) may be influenced by the fraction of polymorphic loci. The highest EMR (3.60) was detected with the primer BGC05 842 and the lowest was shown by the primer BGCO5 860 (0.35), with a mean EMR of 1.44 per primer. General usefulness of the ISSR markers was determined by the calculation of marker index (MI) for each ISSR primer. The highest MI was shown by the primer BGCO5 824 and BGCO5 848 (0.007) and the lowest in the primer BGCO5 814 (0.00), BGCO5 860 (0.00) with a mean MI of 0.003 per primer. The resolving power (RP) is the ability of a primer to differentiate between genotypes. The

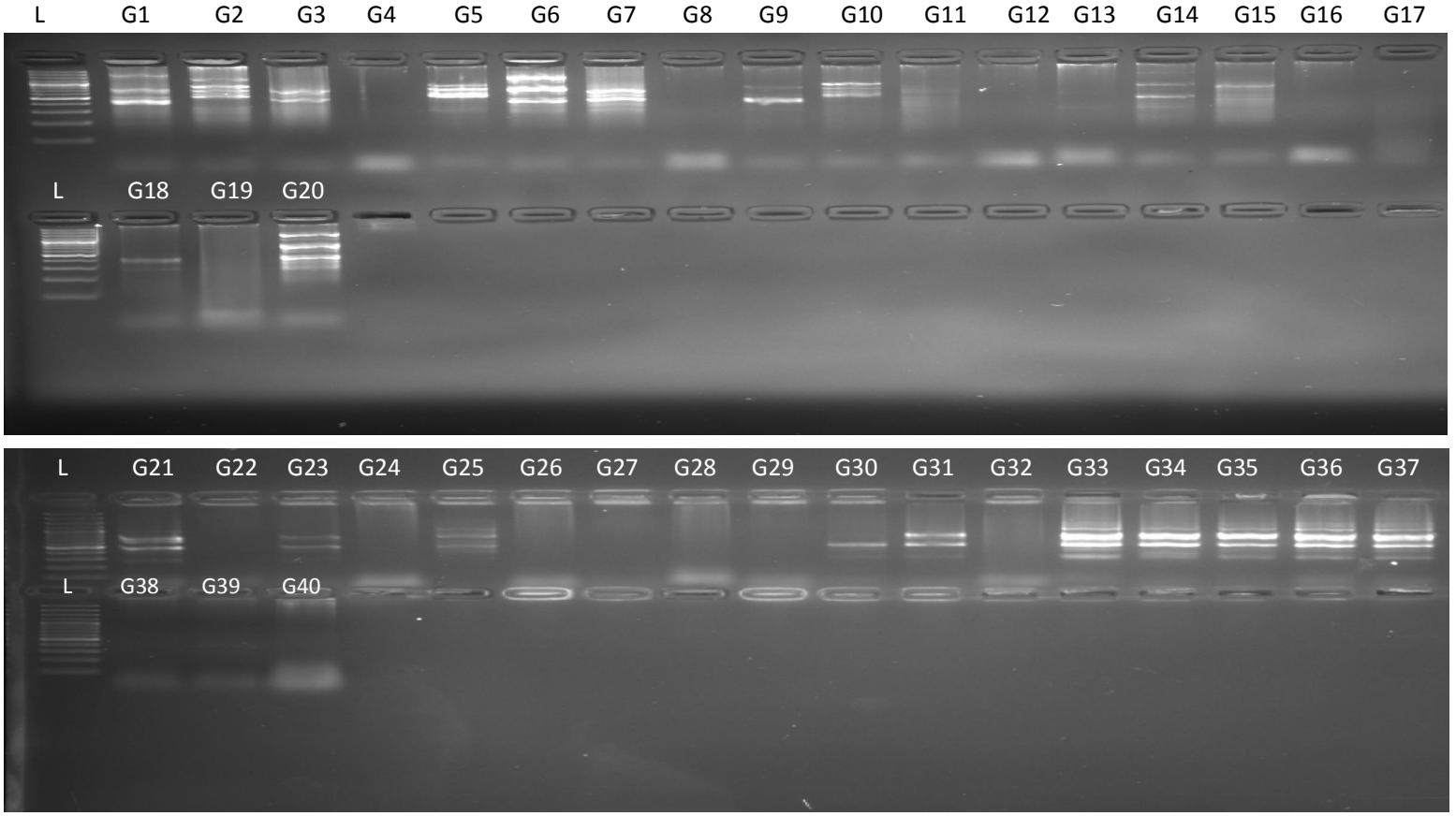

Plate 4: Primer: BGCO5 842

average RP was 2.28 per ISSR primer. The highest RP value was detected with the primer BGCO5 842 (6.70) and the lowest with the primer BGCO5 860 (0.70). Primer BGCO5860 showed the highest discrimination power (0.999) and the lowest discrimination power were observed in BGCO5824 with the value of 0.658 with an average value of 0.876. The mean heterozygosity (H.av) ranged from 0.00 in BGC05 814 to 0.006 in BGC 848 with an average value of 0.002.

4.6.2 Cluster Analysis based on ISSR.

The genetic relationship of forty brinjal genotypes was obtained from the scoring data using Jaccard's similarity coefficient. Cluster analysis was conducted to group genotypes into a dendrogram. The dendrogram was constructed using Jaccards similarity coefficient. The forty genotypes were grouped into three major clusters at a coefficient value of 0.30 (Fig-6) and the similarity coefficient value ranged from 0.23 to 0.79. Cluster I comprised 14 genotypes, which was divided into two sub clusters (IA and IB) which contain 3 genotypes, SK-BL-100, 2017/BRL VAR-7 and SK-BR-135 and 11 genotypes, SK-BL-102, SK-BL-113, SK-BL-114, SK-BL-103, SK-BL-104, SK-BL-112, SK-BL-107, SK-BL-110, SK-BL-111, SK-BL-108, SK-BL-116 respectively. Cluster II consisted of 24 genotypes which was further divided into two sub-clusters (IIA, IIB) which contained 13 genotypes, SK-BL-101, SK-BR-117, SK-BR-133, SK-BR-122, 2018/BRL VAR-5, SK-BR-118, SK-BR-130, SK-BL-105, SK-BR-134, SK-BR-131, SK-BL-106, SK-BSR-128, SK-BR-132 and 11 genotypes SK-BL-109, SK-BR-123, SK-BR-129, SK-BR-119, SK-BR-120, SK-BR-121, SK-BSR-126, SK-BSR-127, SK-BR-136, SK-BSR-124, SK-BSR-125, respectively ; cluster III contained 2 genotypes SK-BL-115 and SK-BR-137.

Table 14: Performance and marker efficiency of fifteen ISSR primers in brinjal

S. No	Marker	No. of bands	Polymorphic bands	% of polymorphism	Total no. of bands amplified	PIC value	RP	DP	EMR	MI	H	H.av
1	BGCO5 818	3	2	66.67	48	0.271	1.150	0.849	1.175	0.005	0.477	0.004
2	BGCO5 830	2	1	50.00	18	0.324	0.900	0.952	0.450	0.002	0.349	0.004
3	BGCO5 822	5	3	60.00	112	0.264	2.300	0.688	2.800	0.007	0.493	0.002
4	BGCO5 814	7	5	71.43	15	0.380	0.750	0.997	0.375	0.000	0.101	0.000
5	BGCO5 856	7	4	57.14	45	0.349	2.250	0.975	1.125	0.001	0.270	0.001
6	BGCO5 823	5	2	40.00	94	0.261	2.700	0.780	2.350	0.006	0.498	0.002
7	BGCO5 824	2	1	50.00	47	0.268	1.650	0.658	1.175	0.007	0.485	0.006
8	BGCO5 825	8	5	62.50	62	0.333	3.250	0.959	1.625	0.002	0.324	0.001
9	BGCO5 827	6	3	50.00	53	0.326	2.650	0.952	1.325	0.002	0.344	0.001
10	BGCO5 847	4	3	75.00	48	0.297	2.400	0.911	1.200	0.003	0.420	0.003
11	BGCO5 857	4	3	75.00	29	0.341	1.450	0.968	0.725	0.001	0.297	0.002
12	BGCO5 842	9	6	66.67	144	0.270	6.700	0.841	3.600	0.005	0.480	0.001
13	BGCO5 851	7	3	42.86	90	0.290	3.800	0.897	2.250	0.004	0.436	0.002
14	BGCO5 860	12	11	91.67	14	0.383	0.700	0.999	0.350	0.000	0.057	0.000
15	BGCO5 848	2	1	50.00	43	0.261	1.550	0.714	1.075	0.007	0.497	0.006
	Average	**5.533**	**3.533**	**60.59**	**57.46**	**0.307**	**2.280**	**0.876**	**1.440**	**0.003**	**0.368**	**0.002**

PIC=Polymorphism information content, RP= Resolving power, DP= Discriminating power, EMR= Effective multiplex ratio, MI= Marker index, H= Heterozygocity, H.av=Average heterozygoci

Table 15: Jaccards similarity quotient

	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27	G28	G29	G30	G31	G32	G33	G34	G35	G36	G37	G38	G39	G40
G1	1.00																																							
G2	0.27	1.00																																						
G3	0.29	0.18	1.00																																					
G4	0.28	0.27	0.35	1.00																																				
G5	0.31	0.38	0.38	0.58	1.00																																			
G6	0.16	0.40	0.19	0.15	0.37	1.00																																		
G7	0.20	0.31	0.18	0.17	0.26	0.44	1.00																																	
G8	0.37	0.23	0.26	0.46	0.41	0.15	0.27	1.00																																
G9	0.24	0.46	0.22	0.26	0.31	0.39	0.46	0.32	1.00																															
G10	0.23	0.35	0.36	0.32	0.44	0.38	0.33	0.28	0.34	1.00																														
G11	0.25	0.30	0.29	0.39	0.39	0.32	0.32	0.31	0.48	0.41	1.00																													
G12	0.10	0.19	0.15	0.21	0.20	0.25	0.30	0.24	0.45	0.30	0.35	1.00																												
G13	0.23	0.30	0.38	0.44	0.39	0.21	0.32	0.38	0.48	0.46	0.45	0.29	1.00																											
G14	0.17	0.33	0.31	0.30	0.35	0.41	0.42	0.26	0.32	0.46	0.39	0.33	0.39	1.00																										
G15	0.30	0.24	0.50	0.46	0.56	0.23	0.32	0.34	0.33	0.36	0.28	0.22	0.43	0.34	1.00																									
G16	0.19	0.09	0.55	0.39	0.39	0.13	0.21	0.38	0.22	0.36	0.31	0.35	0.39	0.34	0.54	1.00																								
G17	0.20	0.05	0.49	0.39	0.39	0.14	0.12	0.27	0.11	0.28	0.20	0.15	0.31	0.26	0.47	0.59	1.00																							
G18	0.23	0.30	0.16	0.35	0.39	0.37	0.19	0.27	0.43	0.17	0.40	0.29	0.27	0.26	0.28	0.15	0.24	1.00																						
G19	0.20	0.18	0.23	0.40	0.29	0.12	0.22	0.34	0.38	0.23	0.46	0.23	0.46	0.17	0.24	0.27	0.23	0.31	1.00																					
G20	0.22	0.55	0.20	0.26	0.38	0.48	0.34	0.23	0.50	0.34	0.42	0.22	0.29	0.37	0.27	0.14	0.13	0.47	0.25	1.00																				
G21	0.25	0.48	0.21	0.15	0.23	0.37	0.42	0.27	0.43	0.28	0.31	0.15	0.31	0.34	0.19	0.10	0.05	0.20	0.19	0.38	1.00																			
G22	0.16	0.29	0.19	0.22	0.21	0.26	0.20	0.29	0.38	0.21	0.30	0.33	0.30	0.23	0.13	0.18	0.13	0.30	0.24	0.37	0.46	1.00																		
G23	0.26	0.39	0.15	0.23	0.30	0.29	0.25	0.32	0.39	0.16	0.32	0.26	0.22	0.20	0.20	0.20	0.15	0.41	0.21	0.42	0.41	0.46	1.00																	
G24	0.14	0.17	0.09	0.19	0.18	0.10	0.21	0.30	0.33	0.10	0.21	0.28	0.26	0.07	0.17	0.15	0.06	0.26	0.30	0.33	0.21	0.42	0.48	1.00																
G25	0.17	0.50	0.17	0.20	0.32	0.48	0.38	0.19	0.57	0.32	0.41	0.17	0.31	0.35	0.24	0.11	0.09	0.31	0.31	0.54	0.46	0.24	0.37	0.25	1.00															
G26	0.28	0.31	0.17	0.28	0.33	0.32	0.24	0.34	0.38	0.22	0.24	0.30	0.21	0.19	0.32	0.16	0.18	0.44	0.24	0.30	0.28	0.30	0.48	0.36	0.27	1.00														
G27	0.06	0.23	0.18	0.13	0.14	0.25	0.18	0.13	0.38	0.30	0.24	0.33	0.29	0.22	0.11	0.13	0.11	0.24	0.29	0.38	0.24	0.41	0.21	0.35	0.35	0.25	1.00													
G28	0.08	0.13	0.11	0.12	0.10	0.19	0.22	0.19	0.24	0.14	0.10	0.29	0.14	0.11	0.14	0.12	0.10	0.18	0.12	0.25	0.22	0.44	0.33	0.47	0.16	0.37	0.47	1.00												
G29	0.26	0.28	0.14	0.26	0.24	0.18	0.30	0.45	0.52	0.22	0.33	0.45	0.33	0.19	0.26	0.22	0.11	0.33	0.38	0.35	0.38	0.43	0.43	0.60	0.33	0.52	0.38	0.41	1.00											
G30	0.24	0.44	0.17	0.26	0.27	0.26	0.33	0.39	0.54	0.26	0.36	0.36	0.41	0.27	0.23	0.20	0.10	0.36	0.37	0.42	0.55	0.46	0.55	0.54	0.46	0.44	0.42	0.38	0.79	1.00										
G31	0.20	0.31	0.18	0.24	0.30	0.33	0.45	0.31	0.40	0.29	0.42	0.24	0.28	0.36	0.25	0.17	0.12	0.28	0.32	0.39	0.48	0.36	0.38	0.32	0.57	0.32	0.30	0.27	0.40	0.48	1.00									
G32	0.13	0.15	0.15	0.21	0.17	0.29	0.23	0.20	0.40	0.20	0.23	0.44	0.23	0.17	0.18	0.21	0.19	0.32	0.27	0.26	0.16	0.30	0.33	0.32	0.27	0.52	0.44	0.40	0.46	0.38	0.23	1.00								
G33	0.16	0.43	0.21	0.18	0.29	0.41	0.48	0.24	0.54	0.28	0.35	0.35	0.35	0.34	0.25	0.21	0.11	0.27	0.27	0.52	0.56	0.40	0.50	0.36	0.52	0.28	0.29	0.27	0.38	0.50	0.42	0.32	1.00							
G34	0.29	0.29	0.25	0.27	0.36	0.41	0.45	0.38	0.38	0.30	0.29	0.27	0.33	0.32	0.33	0.30	0.23	0.23	0.26	0.31	0.43	0.28	0.40	0.25	0.36	0.36	0.20	0.29	0.42	0.47	0.41	0.37	0.51	1.00						
G35	0.20	0.33	0.16	0.18	0.29	0.40	0.46	0.26	0.41	0.20	0.23	0.19	0.19	0.25	0.28	0.12	0.10	0.26	0.18	0.36	0.43	0.20	0.44	0.30	0.50	0.42	0.14	0.26	0.32	0.39	0.52	0.27	0.54	0.50	1.00					
G36	0.19	0.56	0.14	0.18	0.33	0.43	0.33	0.21	0.50	0.21	0.28	0.15	0.28	0.27	0.23	0.07	0.05	0.41	0.23	0.65	0.41	0.26	0.42	0.32	0.61	0.29	0.30	0.19	0.30	0.42	0.38	0.20	0.58	0.37	0.45	1.00				
G37	0.18	0.33	0.20	0.21	0.32	0.62	0.36	0.20	0.41	0.24	0.30	0.23	0.23	0.29	0.19	0.15	0.16	0.34	0.22	0.41	0.39	0.33	0.44	0.25	0.56	0.34	0.28	0.31	0.28	0.39	0.46	0.41	0.54	0.59	0.52	0.50	1.00			
G38	0.30	0.13	0.29	0.28	0.26	0.17	0.32	0.47	0.33	0.37	0.27	0.35	0.40	0.22	0.32	0.44	0.35	0.20	0.36	0.19	0.27	0.35	0.25	0.31	0.19	0.28	0.29	0.32	0.54	0.45	0.28	0.37	0.24	0.47	0.19	0.14	0.23	1.00		
G39	0.19	0.31	0.22	0.25	0.19	0.18	0.17	0.28	0.33	0.18	0.28	0.25	0.31	0.23	0.17	0.16	0.12	0.28	0.20	0.33	0.39	0.44	0.40	0.36	0.27	0.25	0.25	0.23	0.47	0.58	0.28	0.21	0.31	0.30	0.21	0.29	0.27	0.31	1.00	
G40	0.18	0.32	0.15	0.30	0.25	0.19	0.11	0.20	0.31	0.13	0.19	0.22	0.19	0.14	0.24	0.12	0.16	0.42	0.14	0.31	0.13	0.23	0.27	0.20	0.18	0.37	0.18	0.25	0.27	0.27	0.15	0.26	0.16	0.17	0.15	0.26	0.22	0.16	0.41	1.00

Chapter-5

DISCUSSION

Brinjal (*Solanum melongena* L.) is one of the most important vegetable crops grown extensively in tropical and subtropical areas of the world. The chief immediate and long term objective of plant breeding is to increase the productivity and to meet the requirements of increasing population. Crop improvement largely depends on the existence of variability and its exploitation by the plant breeder. For this, plant breeder needs to identify sources of favorable genes, incorporate them into breeding populations/lines and select for a combination of desirable traits that might result in the isolation of productive genotypes. Plant breeder needs to know the extent of variability present in a population to achieve these goals. Effective evaluation and identification of potentially useful germplasm forms the first and foremost step in a crop improvement programme.

This study was carried out to characterize brinjal genotypes with respect to morphological and biochemical traits. Also diversity analysis was done with ISSR markers. The aim of this study was to examine genetic diversity in forty one widely adapted brinjal genotypes of India. Their diversity analysis will be beneficial not only in designing hybridization programme but also in conserving and maintaining them as genetic resources. This is aimed at widening the genetic base of the cultivars and preventing genetic erosion (Yuzbapyoglu *et al.,* 2006).

5.1 Morphological characterization of brinjal genotypes

Morphological characterization of brinjal genotypes was done as per the minimal descriptor list published by NBPGR, New Delhi. The genotypes were characterized for ten scorable traits (Table-5). Fruit colour revealed different classes like green variegated, purple, white, light green with majority of the genotypes showed light purple colour followed by purple colour. Different genotypes showing different fruit shapes like oblong, medium long, long, very

long, oval and round. Majority of genotypes expressed long fruit shape and only one genotype had very long fruit shape. Plant growth habit was found to be intermediate, upright or prostrate with majorty of genotypes showing intermediate followed by prostrate plant growth habit. Petiole colour was classified into greenish violet, greenish or green, light green with majorty of genotypes showing greenish violet colour followed by green colour. Based on extent of lobing, leaves of different genotypes were grouped into those with intermediate, strong or weak lobing with majorty of genotypes expressing intermediate leaf blade lobbing followed by strong leaf blade lobbing. Different genotypes had either acute or intermediate leaf blade tip angle. Genotypes were classified on the basis of fruit length breadth ratio like slightly longer than broad, twice as long as broad, three times as long as broad, several time as long as broad with majorty of genotypes showing as long as broad fruit length breadth ratio and only one genotype expressed several times as long as broad fruit length breadth ratio. Based on fruit curvature different genotypes were grouped into slightly curved, none or snake shaped with majorty of genotypes expressing slightly curved fruit. On the basis of presence or absence of spines on fruit calyx, genotypes were classified into present and absent. Majorty of genotypes showed absence of spines on fruit calyx. On the basis of clustering habit, genotypes were classified as having clustering habit or non clustering habit. Majorty of genotypes showed clustering habit. These results are in corroboration with studies by Solaimana *et al.* (2015); Dash *et al.* (2019); Khan and Singh (2014) and Shinde *et al*. (2012). These variations among the genotypes for the traits studied could be used in future brinjal improvement programmes.

5.2 Mean performance of genotypes

In this study, brinjal genotypes showed wide range of variability for most of the morphological, growth, yield attributing and quality traits. The estimates of mean values from Table-6.1 and Table-6.2 revealed that no genotype was superior for all the traits under study. However SK-BL-105 (44.55) statistically at par with

SK-BL-116 (46.29), SK-BL-113 (46.21), SK-BL-109 (45.26), SK-BL-104 (45.66), SK-BL-103 (45.22), SK-BL-102 (45.77) and SK-BL-101 (45.77) were superior for days to 50% flowering as these take minimum number of days from transplanting to 50% flowering; SK-BSR-124 (7.21) statistically at par with SK-BL-102 (6.99) for number of flowers per cluster. SK-BSR-124 (5.44) statistically at par with SK-BL-102 (5.33), SK-BSR-127 (4.77) and SK-BSR-126 (4.55) for number of fruits per cluster; SK-BL-102 (52.88) statistically at par with SK-BL-100 (54.33), SK-BL-101 (53.10), SK-BL-103 (53.33), SK-BL-108 (54.33), SK-BL-109 (53.99), SK-BL-115 (54.22) and SK-BL-116 (54.33) for days taken to first fruit set, because these take minimum number of days from transplanting to first fruit set; SK-BL-113 (71.33) statistically at par with SK-BL-109 (71.44), SK-BL-102 (72.66) and SK-BL-104 (72.44) for days first fruit picking; 2018/BRL VAR-5 attained the maximum plant height (89.77cm) followed by SK-BL-104 (85.17) and SK-BL-106 (83.22). For plant spread 2018/BRL VAR-5 (58.90) followed by SK-BL-111 (57.05 cm). SK-BL-102 (6.99) followed by SK-BL-105 (6.44) for number of branches per plant; 2018/BRL VAR-5 recorded the maximum fruit length (23.96 cm) followed by SK-BL-105 (15.67 cm). SK-BR-132 recorded the maximum fruits diameter (8.46 cm) statistically at par with SK-BR-133 (8.39 cm). SK-BL-109 recorded maximum value of petiole length (4.08 cm) statistically at par with SK-BR-119 (3.90 cm). Maximum number of fruits per plant were recorded in SK-BL-102 (18.99) statistically at par with SK-BSR-124 (18.77) and SK-BSR-126 (17.66). SK-BSR-125 (162.66 g) recorded maximum average fruit weight followed by SK-BR-123 (135 g) and SK-BR-134 (133.02 g). The maximum yield per plant was observed in SK-BL-105 (1125.33) followed by 2017/BRL VAR-7 (1092.88) and SK-BL-103 (1003.99). For fruit yield per hectare SK-BL-105 (540.33 q) was statistically at par with 2017/BRL VAR-7 (525.29 q/ha) were found to be superior.

A general review of Table-6.1 and Table-6.2 on the performance of genotypes revealed that certain genotypes exhibited superior performance for

some economically important traits. SK-BL-102 was superior for number of branches per plant, number of fruits per plant. 2018/BRL VAR-5 for plant height, plant spread, fruit length. SK-BSR-124 was found to be superior for number of flowers per cluster, number of fruits per cluster. SK-BL-107 for vitamin C, TSS. SK-BR-129 for total phenol, anthocyanin, FRAP, DPPH (scavenging activity), quercetin and ferulic acid.

Since no genotype could be identified to have superior performance for all the traits, the genotype with diverse characteristics could be used in a well-planned hybridization programme to select superior performing lines in the successive segregating lines.

5.3 Biochemical characterization

Brinjal is a rich source of ascorbic acid, phenolics and anthocyanin compounds which supply a good amount of antioxidants to the human body (Chanasut and Rattanaponone, 2008). Percentage of dry matter in fruit is an important criteria for processing.

The highest total phenol content was recorded in SK-BR-129 (103.66 mg/100g) statistically at par with SK-BSR-128 (101.33 mg/100g), SK-BR-132 (102.98 mg/100g), and SK-BR-133 (102.46 mg/100g). Similar results were found by Nisha *et al*. (2009) The findings revealed that total phenol content varies from 80.31± 1.8 - 106.98 ± 2.2 mg.100g^{-1}, Hussain *et al.* (2018) The findings revealed that total phenol content varies from 73.89- 105.92 mg/100g), Somawathi *et al.* (2014). The highest anthocyanin content was recorded in SK-BR-129 (1.15mg/100g) was statistically at par with SK-BR-132 (1.11mg/100g). The results were in conformity with Nisha *et al.* (2009), Kumari *et al.* (2018), Jung *et al.* (2011). Highest TSS was recorded in SK-BL-107 (7.20° Brix) statistically at par with SK-BL-108 (7.13) and SK-BL-104 (6.70°Brix). Similar results were also found by Koundinya *et al.* (2019), Oluoch and Chadha (2007). The highest vitamin-C content was recorded in SK-BL-107 (17.39 mg/100g) statistically at

par with SK-BSR-128 (17.10), SK-BR-118 (15.94 mg/100g), SK-BR-119 (15.94 mg/100g), SK-BR-122 (15.82 mg/100g) and SK-BR-117 (16.93 mg/100g). The results were in conformity with Kandoliya *et al* (2015). The findings revealed that ascorbic acid content varies from 9.43-16.75 mg.100g^{-1}, Ghadsingh *et al*. (2012) The findings revealed that ascorbic acid content varies from 8.9-13 mg.100g^{-1}, Kumar and Arumugam (2013) and revealed that mean value was found to be 11.38 mg.100g^{-1} , Jayalakshmi and Praneetha (2018) which revealed that ascorbic acid content varies between 7.27-12.46 mg.100g^{-1}. The maximum dry matter content was recorded in SK-BR-118, SK-BR-119 (8.38 %) each, statistically at par with SK-BL-110 (8.36 %), SK-BL-111 (8.18 %), SK-BSR-124 (8.33 %) and SK-BR-110 (8.31 %). The results were in conformity with Jayalakshmi and Praneetha (2018), Reshmika *et al.* (2016), Maik KCK (2005), Adamczewska-Sowieska and Krygier (2013). The maximum antioxidant potential (FRAP) was recorded in SK-BR-129 (8.12 mmol/g) statistically at par with SK-BR-133 (8.00 mmol/g). The results were in conformity with Somawathi *et al.* (2014) and found that antioxidant potential (FRAP) varied from 4.19±0.11 to 7.46±0.26 mmol of FeS04/g fresh weight. The maximum scavenging percentage (DPPH) was recorded in SK-BR-129 (40.78 %) followed by SK-BR-133 (38.83 %) and SK-BR-132 (37.72 %). Similar results were also found by Kandoliya *et al.* (2015). The findings revealed from all the variety studied, showed 25.17-40.35% radical scavenging activity (DPPH).

High performance liquid chromatography method was used to determine the Quercitin and ferulic acid concentration of 41 brinjal genotypes. The highest Quercitin concentration was recorded in SK-BR-129 (8.00 mg/g) statistically at par with SK-BL-104 (7.94 mg/g), SK-BR-123 (7.93 mg/g), SK-BSR-125 (7.92 mg/g), SK-BSR-127 (7.96 mg/g), SK-BSR-128 (7.97 mg/g), SK-BR-130 (7.95 mg/g) SK-BR-132 (7.99 mg/g), and SK-BR-133 (7.98 mg/g). The results were in conformity with Elekofehinti *et al.* (2013) The findings revealed that quercetin concentration was found to be 7.39 ± 0.05) mg/g. The highest ferulic acid

concentration was recorded in SK-BR-129 (0.25 mg/g) was statistically at par with SK-BR-132 (0.24 mg/g), SK-BR-133 (0.23 mg/g), SK-BSR-127 (0.21 mg/g), SK-BSR-128 (0.22 mg/g) and SK-BR-130 (0.20 mg/g). Similar results were also found by Zhao and Moghadasian (2008) and Sakakibara *et al*. (2003). The findings revealed that ferulic acid concentration was found to be 0.07- 0.35 mg/100gm.

5.4 Genetic variability, heritability and genetic advance (as per cent of mean)

The success of any crop improvement programme depends upon the nature and magnitude of the genetic variability existing in the breeding material (Prabhu *et al.,* 2009). Success of selection directly depends upon the amount of heritability and genetic advance as percent of mean for that trait (Prabakaran, 2010).

The range of values reflects the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype × environmental interaction components and does not reveal as to which trait is showing higher degree of genetic variability Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable), epistasis (no allelic interaction) and GxE interaction. Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation and genotypic coefficient of variation, which ultimately indicates the extent of genetic variability existing for various traits.

The analysis of variance revealed that all the traits exhibited highly significant differences among the genotypes (Table-7.1 and Table-7.2). The estimates of phenotypic and genotypic coefficients of variation of all the traits studied are presented in Table-8. In general, the phenotypic and genotypic coefficients of variation were almost similar with slight higher phenotypic coefficients of variation, which indicates the role of environment in the expression

of traits under observation. This was in agreement with the study of Kumar *et al.* (2013).

It is evident from the data that number of flowers per cluster (43.95, 42.41), number of fruits per cluster (49.42, 45.70), Fruit length (cm) (39.60, 39.45), Fruit diameter (cm) (26.36, 26.23), petiole length (cm) (30.42, 29.84), number of fruits per plant (48.60, 47.01), average fruit weight (g) (31.85, 31.70), fruit yield per plant (28.91, 28.91), fruit yield per hectare (29.92, 28.98) recorded high phenotypic and genotypic coefficients of variation indicating that genotypes had broad genetic base for these traits. Similar results were obtained by Dasmohapatra and Sharma (2019), Balas *et al* (2019), Kumar *et al* (2020), Solaimana *et al*. (2015), Muniappan *et al*. (2010), Prabakaran (2010), Pujer *et al.* (2017). Rest of the traits such as days taken to 50 flowering (6.59, 6.12), days to first fruit set (5.36, 5.06), days to first fruit picking (4.49, 4.30), plant height (cm) (7.89, 7.79) and number of branches per plant (10.59, 9.45), showed low phenotypic and genotypic coefficients of variation. Thus these traits were less amenable for improvement through selection.

Among quality parameters, TSS (22.54, 20.92) and ferulic acid (42.94, 42.72), recorded high phenotypic and genotypic coefficients of variation but the total phenol (11.11, 10.82), anthocyanin (17.08, 16.38), vitamin-C (17.29, 7.57) contents showed moderate phenotypic and genotypic coefficients indicating that genotypes under study have broad genetic base for these traits as well. Similar results were obtained by Srivastava *et al.* (2019). Traits which possessed moderate to high coefficients of variation suggested that there is better potential for improvement through selection. A wide range of variability, high estimates of phenotypic and genotypic coefficients of variation further, along with high GCV and PCV ratio indicate that these attributes would respond to selection.

Even phenotypic and genotypic coefficients of variation do not give a true picture of the extent of inheritance of the trait. Therefore, the heritability of a trait can be relied upon, as it enables the breeder to decide the extent of selection

pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. The estimation of heritability has a greater role to play in determining the effectiveness of selection of a trait provided it is considered in conjunction with the predicated genetic advance as suggested by Johnson *et al.* (1955) as the heritability is influenced by bio-metrical method, generation of hybrid, sample size of experimental material and environment. Furthermore, the progress in selection is also directly proportional to the amount of genetic gain. Therefore, the effect of selection is realized more quickly in those traits which have high heritability as well as high genetic gain. The relative amount of heritable portion of variation was, therefore, estimated with the help of heritability estimates and genetic advance.

Heritability (Broad sense) was high for all the traits except vitamin-C and ranged from 19 to 99 percent indicating that the traits are less influenced by environmental effects and the traits are effectively transmitted to the progeny, suggesting major role of genetic constitution in the expression of a trait and thus selection based on phenotypic expression could be relied upon. Sometimes, a trait has low heritability, under such situation another trait having high heritability and high correlation with the former trait is chosen to make selection more effective. Thus genetic improvement is achieved using indirect selection through component traits with high heritability. High heritability was observed for days taken to first fruit set (88%), days taken to first fruit picking (91%), number of flowers per cluster (93%), number of fruits per cluster (85%), plant height (97%), plant spread (98%), number of branches per plant (82%), petiole length (96%), number of fruits per plant (93%), fruit length (99%), fruit diameter (99%), average fruit weight (99%), fruit yield per plant (99%) and fruit yield per hectare (99%). This is in accordance with the findings of Arun kumar (2014), Kumar *et al.* (2013). Priyanka Verma *et al.* (2018). High heritability values for these traits indicates that variation observed mainly under genetic control and was less influenced by environment.

Among quality traits high heritability estimates were recorded for total phenol (94%), anthocyanin (92%), TSS (86%), dry matter (93%), FRAP (96%), DPPH (scavenging activity) (94%), quercetin (90%) and ferulic acid (98%). Finding of the present investigation were in conformity with Sangam *et al.* (2020), C. Karak *et al.* (2012), Pallavi Chaudhary and Sanjay Kumar (2014) which also found the high heritability for these traits.

High estimate of heritability along with genetic gain (per cent of mean) is more reliable than heritability alone for predicting the effect of selection (Johnson *et al.*, 1955). The traits *viz.,* number of flowers per cluster (93%, 84.31), number of fruits per cluster (85%, 87.08), plant spread (98%, 32.15), petiole length (96%, 60.29), number of fruits per plant (93%, 93.65), fruit length (99%, 80.94), fruit diameter (99%, 53.78), average fruit weight (99%, 65.01), fruit yield per plant (99%, 59.54), fruit yield per hectare (99%, 57.84), total phenol (94%, 21.70), anthocyanin (92%, 32.37), TSS (86%, 40.01), dry matter (93%, 20.62), FRAP (96%, 25.55), DPPH (scavenging activity) (94%, 27.98) and ferulic acid (98%, 87.57) showed the high estimates of heritability coupled with high genetic advance as per cent of mean (GAM) respectively, indicating the preponderance of additive gene action in control of these traits. This suggests that real progress in improvement through selection could be made for yield. These results are in conformity with the work of several workers *viz*., Dasmohapatra and Sharma (2019), Balas *et al* (2019), Islam and Uddin (2009), Singh *et al.* (2013). Rani *et al* (2019), Bende *et al.* (2019), Arti *et al.* (2018) and Srivastava *et al.* (2019).

Fruit yield is an important trait, which decides the commercial viability of the hybrid/variety. Thus the trait deserves the highest priority in any breeding programme. High heritability (>60%) along with high genetic advance (>20%) as per cent of mean for this trait suggested the possibility of selecting high yielding cultivars from the present collection. This was supported by Kumar *et al*. (2013), Verma *et al.* (2018).

5.5 Correlation coefficient

Yield is an ultimate criterion which a plant breeder has always to keep in view for evolving improved cultivars of any crop. However, yield is a polygenic trait and highly influenced by environment. Knowledge of the association of quantitative traits specifically for yield and its attributes is of immense practical value during selection. Variability studies provide information on the extent of improvement possible in different traits, but they do not throw light on the extent and nature of relationship existing between various contributing traits and economically important traits. Hence, a knowledge regarding association of various traits among themselves and with economic trait is necessary for making indirect selection for improvement of economical traits. Correlation studies pave way to know the association prevailing between highly heritable traits with most economic traits and gives better understanding of the contribution of each trait in building up the genetic makeup of the crop. The phenotypic correlations indicate the extent of the observed relationship between two traits. This does not give true genetic picture of the relationship because it indicates both heritability as well as environmental influences. Genotypic correlations provide an estimate of inherent association between genes controlling any two traits. Hence, it is of greater significance and could be effectively utilized in formulating an effective selection scheme. Perusal of Table-9 indicated that in the present investigation, the estimates of genotypic correlation were in general slightly higher than phenotypic correlation showing that masking effects of the environment was little indicating the presence of inherent association between various traits. In all instances, however, more reliance may be placed on the genotypic correlations. The nature of genotypic correlation was more or less similar to phenotypic correlation under study. Similar results were reported by Lakshmi *et al*. (2014), (Nalini *et al.,* 2009; Muniappan *et al.,* 2010).

The economically important trait i.e., fruit yield per hectare exibited significant positive association with number of flowers per cluster (r_g = 0.459,

r_p = 0.422), number of fruits per cluster (r_g = 0.524, r_p = 0.463), plant height (r_g = 0.513, r_p = 0.491), number of branches per plant (r_g = 0.611, r_p = 0.521), number of fruits per plant (r_g = 0.668, r_p = 0.639), average fruit weight (r_g = 0.106, r_p = 0.094) and fruit yield per plant (r_g = 0.986, r_p = 0.974). It depicted positive but non significant association with fruit length (r_g = 0.057, r_p = 0.054), plant spread (r_g = 0.166, r_p = 0.162) and petiole length (r_g = 0.073, r_p = 0.075). It also showed negative non significant association with days to first fruit picking (r_g = -0.112, r_p = -0.102), fruit diameter (r_g = -0.060, r_p = -0.058), at both phenotypic and genotypic levels, which suggested that rational improvement in yield is possible through simultaneous selection for these component traits which clearly indicated the independent nature of these traits and selection for fruit yield based on these is not reliable. These results are in conformity with findings of Chaitanya (2017), Chauhan *et al.* (2017), Kumar *et al*. (2020), Mishra *et al*. (2007) and Lohakare *et al.* (2008).

5.6 Genetic diversity

As an initial step to develop high yielding and superior quality brinjal varieties for cultivation in any geographical region, it is imperative to evaluate a large number of existing genotypes. These genotypes must have been selected on the basis of their *per se* performance from diverse sources. Superior genotypes are selected and may be used as parents in hybridization programmes. However, the selection of superior parents from a large number of genotypes is a difficult task to perform. Genetic divergence analysis among genotypes is helpful to screen the genetically diverse parents that are likely to produce high heterotic effects among crosses and also generate large spectrum of variability during segregation and recombination of genes at heterozygous polygenic blocks. Multivariate technique using D^2 statistic is a powerful tool in quantifying the degree of divergence among the genotypes. This would help to identify putative parents for executing an effective breeding strategy to obtain high heterotic response and transgressive segregants. Estimation of genetic divergence helps in reducing the large data of

genotypes to manageable proportions. It is assumed that the parents showing wide genetic divergence are best suited for being used in the hybridization programme. In the process of formulating the brinjal improvement programme through hybridization and creating variability for the improvement of yield and other desirable traits, it is essential to understand the nature and degree of genetic divergence present in the available germplasm.

The utility of multivariate analysis in quantifying the degree of divergence between populations so as to understand the trend of their evolutionary pattern and assess the relative contribution of different components to the total divergence together with the nature of forces operating at intra and inter cluster levels had greatly been emphasized (Murty and Qadri, 1966; Anand and Murty, 1968; Mishra *et al*., 1994).

In the present study, forty one genotypes of brinjal were evaluated to estimate the genetic divergence for identification of potential parents using Mahalanobis D^2 statistics. Analysis of variance for divergence revealed that the value of D^2-statistic were significant indicating substantial genetic diversity in the material.

The genotypes were grouped into four clusters. Cluster I had the highest number of genotypes (16) followed by cluster II (11) while remaining III and IV clusters contained seven genotypes each (Table-10).

In brinjal, utility of multivariate analysis in selecting genetically divergent parents for successful hybridization has been discussed by Kumar *et al.* (2013), Rahman *et al*. (2014) and Dutta *et al.* (2009). Intracluster distance (D^2) in this study was maximum in cluster II (104.3), followed by the cluster III (92.4). The intercluster distance (D^2) was maximum between cluster III and IV (885.53) followed by I and IV (550.24), cluster II and IV (273.58) (Table-11). The maximum intra cluster distance (D^2) (cluster II) indicated high heterogenity in genetic constitution of genotypes in that cluster while minimum intra cluster

distance (D^2) (cluster IV) indicated homogenity in genetic constitution of genotypes in that cluster. The highest value of intercluster distance (cluster III and IV) indicated also more heterogeneous genetic constitution of genotypes included in both clusters. In contrast, minimum intercluster distance (cluster II and IV) indicated closer relationship among the genotypes included (Mehta, 2004; Shinde, 2014).

The traits that contribute maximum towards the divergence should be given great emphasis for deciding the clusters to be chosen for hybridisation and the subsequent selection of the parents from the clusters be based on their per se performance. In brinjal, maximum contribution from traits towards divergence has been reported to be different for different sets of materials used in experimentation depending upon the genotypes under study (Banerjee *et al* (2018), Ravali *et al*. (2017), Madhavi *et al.* (2015), Vindhya *et al.* (2019). They concluded that promising genotypes selected from divergent clusters on the basis of observed traits could be utilized in future breeding programmes.

Persual of the results representing cluster means (Table-12) for different growth traits revealed that lowest cluster mean for days to 50% flowering (46.59) was found in Cluster IV while the highest cluster mean for days to 50% flowering (52.05) was found in cluster II. The lowest cluster mean for days taken to first fruit set (54.21) was found in cluster IV and highest cluster mean for days taken to first fruit set (59.15) was found in cluster II. The lowest cluster mean for days taken to first fruit picking (74.18) was found in cluster IV while the highest cluster mean for days taken to first fruit picking (80.66) in cluster II. The highest cluster mean for number of flowers per cluster (4.67) and number of fruits per cluster (3.55) was found in cluster III and the lowest cluster mean for number of flowers per cluster (2.50) and number of fruits per cluster (1.68) were found in cluster II. The highest cluster mean for fruit length (15.13 cm) was in cluster IV while lowest (6.22 cm) in cluster III. Highest cluster mean for fruit diameter (6.59cm) in cluster II while lowest (4.23 cm) in cluster IV. Highest cluster mean for plant

height (83.14 cm), plant spread (53.88), number of branches per plant (6.31) was found in cluster IV while lowest cluster mean for plant height (70.05 cm), plant spread (38.42 cm), number of branches per plant (5.02 cm) was found in in cluster II. Highest cluster mean for petiole length (2.72 cm) was found in cluster I and lowest cluster mean (1.92 cm) was found in cluster II. Highest cluster mean for number of fruits per plant (11.94) was found in cluster III and lowest (5.64) in cluster II. Highest cluster mean for average fruit weight (124.46 g) was found in cluster II while lowest cluster mean (71.04 g) in cluster III. Highest cluster mean for fruit yield per plant (949.66 g) was found in cluster IV while lowest cluster mean (566.68 g) in cluster I. Highest cluster mean for fruit yield per hectare (456.27g) was found in cluster IV while lowest cluster mean (268.42 g) in cluster I. Thus the traits showing high contribution towards genetic divergence can be improved upon by selecting the genotypes from those clusters having maximum cluster means for the respective traits, which in turn depends upon the objective of the breeding programme.

It is clear from the above discussion that tremendous potential exists for converging the elite allelic resources present in the present set of brinjal genotypes through a systematic breeding and selection approach so as to recover high yielding recombinants, with good quality charactertistics. Selection of the parents for hybridization should be done from different clusters having wide inter-cluster distance and those selected parents should have high *per se* performance for the traits contributing maximum towards divergence (Singh *et al.,* 1996).

5.7 Principal Component Analysis (PCA)

In genetic diversity studies using morphological traits, the most important variables describing phenotypic variation are defined by principal component analysis (PCA). According to Chahal and Gosal (2002) traits with largest absolute value closer to unity within the first principal component influence the clustering more than those with lower absolute value closer to zero. Therefore, in the present study, differentiation of the genotypes into different clusters was because of

relatively high contribution of few traits rather than small contribution from each trait. The principal component analysis in this study showed that 76.86 % of the total genetic variance encountered among the brinjal genotypes was accounted for by first five principal components taking into account all the traits studied (Table-13). The relative discriminating power of the principal axes as indicated by the Eigen value was high for axis 1 (7.20%) and low for axis 5 (1.50%). PC1 contributed 30.02% to total variance in which plant spread and fruit length showed 85% and 75% variation respectively. Plant spread and fruit length were the most important trait explaining the diversity within the brinjal genotypes. PC2 contributed 22.50% to total variance among number of fruits per cluster (69%) and fruit yield per hectare (67%) as the key traits which significantly contributed to total genetic variance. Number of fruits per cluster (49%) and number of flowers per cluster (48%) were considered as the most important parameters that contributed to the total genetic variance as revealed by PC3 which contributed 11.40% to total variance, PC4 which contributed 6.70% to total variance showed that average fruit weight (62%) and fruit yield per hectare (45%) were the traits which made substantial contribution to total variation among the genotypes. Petiole length (56%) and fruit yield per hectare (37%) were the most promising traits explaining the diversity as shown by PC5 which contributed 6.20% to total variance. The results of the present investigation are supported by the findings of Kumar *et al*. (2016), Ullah *et al*. (2014), Solaiman *et al*. (2014)

Among the quality traits total phenol and scavenging activity (DPPH) showed 72% and 71% variation respectively towerds PC1. PC2 contributed 61% scavenging activity (DPPH) and 60% (quercetin) to the variation. Dry matter (56%) and TSS (44%) were considered as the most important parameters that contributed to the total genetic variance as revealed by PC3. PC4 showed that TSS (13%) and dry matter, FRAP (12%) were the traits which made substantial contribution to total variation among the genotypes. Dry matter and vitamin C showed 53% and 39% variation respectively towerds PC5. The results of the

present investigation are supported by the findings of Koundinya *et al*. (2019), Kumar *et al.* (2016) and Kaur *et al*. (2014).

5.8 Molecular Chatacterization

ISSR markers are widely used in plant research such as phylogenic studies, genetic mapping, and population genetics studies as well as in cultivar identification and germplasm management Isshiki *et al.* (2008). In this study, an attempt was made to evaluate genetic diversity among 40 brinjal genotypes using 15 ISSR primers, amplified alleles across 40 genotypes with varying degree of polymorphism.

15 ISSR primers were used for molecular characterization of forty brinjal genotypes. A total of 83 alleles were amplified by 15 polymorphic ISSR loci and the numbers of alleles ranged from 2 to 12 with an average of 5.53 alleles per locus. The total number of bands amplified were 83 out of which 53 were polymorphic.The number of polymorphic bands ranged from 1 to 11 with an average value of 3.53. Similar results have been observed by Thakkar *et al*. (2014) by using six ISSR primers for diversity analysis in brinjal found that out of total 47 numbers of bands amplified 38 were polymorphic with an average of 7.83 and 6.33, respectively. Edris *et al.* (2014) reported an average number of polymorphic bands of 3.5. The percentage of polymorphism ranged from 40% to 91.67% with an average value of 60.59%. Mao *et al*. (2006) reported each primers resulted in 9.67 DNA fragments of eggplant, 84 fragments were polymorphic (percentage of polymorphic bands was 71%). Mahmoud and El-Mansy (2012) studied ten cultivars of eggplant with four ISSR primers found high levels of polymorphism ranging from 70.00% to 100%. Likewise, Isshiki *et al.* (2008) used ISSR markers on eight Japanese eggplants and 12 related Solanum species reported a high percentage of polymorphism (99.1%). Mansour *et al.* (2010) reported high polymorphism in ISSR analysis (100%). The high polymorphism effectiveness of this dominant microsatellite-based molecular marker is due to its ability to access variation in the numerous microsatellite regions dispersed across the genomes

Mahmoud and El-Mansy, (2012) and is based on inter-tandem repeats of short DNA sequences Shrivastava *et al*. (2018). These regions lie within the microsatellite repeats and offer great potential to determine intra-genomic and inter genomic differences (Shrivastava *et al*., 2018; Husnudin *et al*., 2019).The high levels of polymorphism found among the eggplants studied are consistent with the important morphological differences presented by their fruits in terms of shape, size, and color. Morphological variations of fruits are among the most notable distinguishing features of eggplants and they are the result of genes involved in adaptive evolution (Tumbilen *et al*., 2011; Cakir *et al*., 2017; Gramazio *et al*., 2019). The ISSR primers produced 862 total numbers of amplified products with 57.46 products per primer. Thakkar *et al*. (2014) also found six ISSR primers produced 313 total numbers of amplified products with 52.17 products per primer. Weihai *et al.* (2006) reported that 12 primers produced total 116 DNA fragments from 57 samples. The ISSR effective multiplex ratio (EMR) may be influenced by the fraction of polymorphic loci. The highest EMR ratio ranged from 0.35 to 3.60 with a mean value of 1.44 per primer. The results of our (EMR) effective multiplex ratio are less than reported by Pandey *et al*. (2019) in bitter gourd (5.75 to 28). The MI values ranged from 0.00 to 0.007 with a mean value of 0.003 per primer. The resolving power (RP) is the ability of a primer to differentiate between genotypes. The highest RP value was 6.70 and the lowest was 0.70 with an average value 2.28 per ISSR primer. These results are in agreement with the results reported by Tiwari *et al*. (2009) in brinjal and found the highest (3.894) and the lowest resolving power (0.00). The discrimination power of primers ranged from 0.65 to 0.999 with an average value of 0.876. Prevost and Wilkinson (1999) described resolving power as an interesting tool to assess the capacity of a given primer to distinguish genotypes.

5.9 Jaccards similarity and cluster Analysis

Jaccards similarity coefficient ranged from 0.05 between the distant genotypes G17 and G2 genotypes to 0.79 between the closest genotypes, G30 and

G29 (Table-15). Mahmoud and El-Mansy (2012) also found the Jaccards similarity between two closest genotypes of eggplants as 0.775 and the most distant had similarity of 0.042. Tiwari *et al.* (2009) reported Jaccards similarity values ranged from 0.894 to 0.985 with an average similarity of 0.935 in brinjal genotypes through ISSR fingerprinting. The genotypes that showed most molecular dissimilarity are expected to contain the greatest number of different genes Souframanien and Gopalakrishna, (2004).The high similarity values observed between the present genotypes are in accordance with the earlier studies on brinjal using ISSR Isshiki *et al*. (2008). Karihaloo *et al.* (1995) attributed the high genetic similarity to a narrow gene pool from which the cultivated forms arose, while Nunome *et al.* (2003) suggested intense selection efforts and/or a narrow genetic background to be the reason. Cluster analysis divided 40 genotypes into three major clusters at a coefficient value of 0.30 with various degrees of sub-clustering. The Cluster I comprised 14 genotypes, Cluster II consisted of 24 and cluster III contained 2 genotypes. Similar study done by Isshiki *et al* (2008) found cluster analysis of ISSR markers divided the examined solanum species into seven groups at a 0.04 distance. Mahmoud and El-Mansy (2012) also classified the ten genotypes into two main clusters with various degrees of sub-clustering. The clustering among the studied accessions was random. Weihai *et al.* (2006) also found that cultivars tested through ISSR and cluster analysis divided cultivars into six groups, and they added that the pedigree relations had no connection with regions of cultivars origin. Thus, all main clusters includes accessions originated from different countries. Hence, there was a tendency of together clustering for accessions from the same or adjacent geographic origin, the accessions collected or originated from different geographic regions were also found placed into the same cluster, or from same geographic area placed into different clusters. This indicates that, the geographical origin of accessions has no influence on the clusters obtained. Such results were also obtained in a number of studies and explained that the accessions from different regions might have similar genetic background and those from the same

origin might also have different genetic background (Keneni *et al*., 2005; Gashaw *et al*., 2007; Celka *et al*., 2010; Sharifova *et al*., 2013). All those results suggested that selection of parent genotypes based on geographical origin only was not an accurate indicator of genetic diversity.

Chapter - 6

SUMMARY AND CONCLUSION

Genetic diversity studies through morphological and molecular markers are vital tools in generating useful information on the genetic diversity within a species. Genetic variability revealed through morphological, molecular and biochemical characterization helps in germplasm conservation and maintenance. The estimation of genetic variability also forms the basis of successful breeding programmes.

The present investigation entitled **"Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization''** was conducted at Division of Vegetable Science, Faculty of Horticulture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Srinagar and Molecular Biology lab, ICAR- Central Institute of Temperate Horticulture, Srinagar. All the forty one genotypes were evaluated in Randomized Complete Block Design (RCBD) with three replications. The genetic diversity was assessed using morpho-biochemical characteristics and ISSR (Inter Simple Sequence Repeats) markers.

For morphological characterization, the genotypes were evaluated for various traits viz., presence or absence of spines on fruit calyx, clustering or non clustering habit of flowers, fruit colour, fruit shape, plant growth habit, petiole colour, leaf blade lobbing, leaf blade tip angle, fruit length-breadth ratio, fruit curvature, days to 50% flowering, number of flowers per cluster, number of fruits per cluster, days to first fruit set, days to first fruit picking, plant height, plant spread, number of branches per plant, fruit length, fruit diameter, petiole length, number of fruits per plant, average fruit weight, fruit yield per plant, fruit yield per hectare and biochemical traits viz., total phenols**,** anthocyanin, FRAP, scavenging activity (DPPH), vitamin-C, drymatter, TSS, quercitin and ferulic acid.

Taking into consideration the morphological characterization, it was observed that the studied brinjal accessions present great variation. Among forty one genotypes twelve genotypes (29.26%) showed purple fruit colour, Forteen genotypes (34.14%) showed light purple fruit colour, Nine genotypes (21.95%) showed dark purple fruit colour, Three genotypes (7.31%) showed light green fruit colour, Two genotypes (4.87%) showed green variegated fruit colour and one genotype (2.43%) namely 2017/BRL VAR-7 showed white fruit colour. Nine genotypes (21.95%) expressed long fruit shape, eight genotypes (19.51%) expressed medium long shape, four genotypes (9.75%) showed oblong fruit shape, eight genotypes (19.51%) showed oval fruit shape, eleven genotypes (26.82%) expressed round fruit shape and one genotype (2.43%) showed very long fruit shape. Twenty-six genotypes (63.41%) showed intermediate plant growth habit, six genotypes (14.63%) showed upright plant growth habit, nine (21.95%) genotypes showed prostrate plant growth habit. Twenty nine genotypes (70.73%) showed greenish violet petiole colour, nine genotypes (21.95%) showed green petiole colour, three genotypes (7.31%) showed light green petiole colour. Thirty two genotypes (78.04%) showed intermediate leaf blade lobing. five genotypes (12.19%) showed strong leaf blade lobing, four genotypes (9.75%) showed weak leaf blade lobing. Thirty five genotypes (85.36%) showed acute leaf blade tip angle, six genotypes (14.63%) showed intermediate leaf blade tip angle. Ten genotypes (24.39%) showed slightly longer than broad fruit length breadth ratio, ten genotypes (24.39%) showed twice as long as broad fruit length breadth ratio, eight genotypes (19.51%) showed three times as long as broad fruit length breadth ratio, twelve genotypes (29.26%) showed as long as broad fruit length breadth ratio, one genotype (2.43%) showed several times as long as broad fruit length breadth ratio. Twenty-nine genotypes (70.73%) showed no fruit curvature, eleven genotypes (26.82%) showed slightly curved fruit structure and one genotype (2.43%) showed snake shaped fruit curvature. Thirty-five genotypes (85.36%) showed clustering habit of flowers, six genotypes (14.63%) showed non

clustering habit of flowers. Twenty- nine genotypes (70.73%) showed absence of spines on fruit calyx whereas, twelve genotypes (29.26%) showed their presence.

Analysis of variance showed that mean square values were highly significant for all the traits. The maximum range was recorded for fruit yield per plant, followed by fruit yield per hectare, average fruit weight, total phenol, plant spread, plant height while the lowest range was observed for ferulic acid, anthocyanin, quercetin, number of branches per plant, petiole length, dry matter. On the basis of mean performance of the genotypes the maximum fruit yield per hectare was recorded in SK-BL-105 (540.33 q) was statistically at par with 2017/BRL VAR-7 (525.29 q/ha). The lowest fruit yield was recorded in SK-BL-116 (122.33 q) followed by SK-BL-114 (200.33 q) and Local Long (205.10 q).

The phenotypic and genotypic coefficients of variation ranged from 4.02-49.42 and 3.83- 47.01 respectively. However, there were narrow differences between magnitude of phenotypic and genotypic coefficients of variation for all the traits studied, indicating low environmental effect on expression of these traits, which implies that phenotypic variability is a reliable measure of genotypic variability. High phenotypic and genotypic coefficients of variation were observed for number of flowers per cluster (43.95 ,42.41), number of fruits per cluster (49.42 ,45.70), fruit length (cm) (39.60, 39.45), fruit diameter (cm) (26.36, 26.23), petiole length (cm) (30.42, 29.84), number of fruits per plant (48.60, 47.01), average fruit weight (g) (31.85, 31.70), fruit yield per plant (28.91, 28.91), fruit yield per hectare (29.92, 28.98), TSS (22.54, 20.92), ferulic acid (42.94, 42.72) while moderate phenotypic and genotypic coefficient of variation were showed by total phenol (11.11, 10.82), anthocyanin (17.08, 16.38), vitamin-C (17.29, 7.57). Rest of the traits such as days taken to 50 flowering (6.59, 6.12), days to first fruit set (5.36, 5.06), days to first fruit picking (4.49, 4.30), plant height (7.89, 7.79) and number of branches per plant (10.59, 9.45), showed low phenotypic and genotypic coefficients of variation.

High heritability coupled with high genetic gain was recorded for number of flowers per cluster, number of fruits per cluster, plant spread, petiole length, number of fruits per plant, fruit length, fruit diameter, average fruit weight, fruit yield per plant, fruit yield per hectare, total phenols, anthocyanin, TSS, dry matter, FRAP, DPPH and ferulic acid indicating that most likely the heritability is due to additive gene effects and thus the chances of fixing by selection are more to improve such traits through pure line selection, mass selection, progeny selection, hybridization and through pedigree breeding.

The biochemical traits included total phenol, anthocyanin, vitamin C, TSS, dry matter, FRAP, scavenging activity (DPPH), quercetin and ferulic acid. The highest total phenols were recorded in SK-BR-129 (103.66 mg/100g) statistically at par with SK-BSR-128 (101.33 mg/100g), SK-BR-132 (102.98 mg/100g), and SK-BR-133 (102.46 mg/100g). The highest anthocyanin content was recorded in SK-BR-129 (1.15 mg/100g) statistically at par with SK-BR-132 (1.11mg/100g). Highest TSS was recorded in SK-BL-107 (7.20 °Brix) was statistically at par with SK-BL-108 (7.13) and SK-BL-104 (6.70°Brix). The highest vitamin-C content was recorded in SK-BL-107 (17.39 mg/100g) statistically at par with SK-BSR-128 (17.10), SK-BR-118 (15.94 mg/100g), SK-BR-119 (15.94 mg/100g), SK-BR-122 (15.82 mg/100g) and SK-BR-117(16.93 mg/100g). The highest dry matter content was recorded in SK-BR-118 and SK-BR-119 (8.38 %) in both statistically at par with SK-BL-110 (8.36 %), SK-BL-111 (8.18 %), SK-BSR-124 (8.33 %) and SK-BR-110 (8.31 %). The maximum antioxidant potential was recorded in SK-BR-129 (8.12mmol/g) statistically at par with SK-BR-133 (8.00mmol/g). The maximum scavenging percentage was recorded in SK-BR-129 (40.78 %) followed by SK-BR-133 (38.83 %) and SK-BR-132 (37.72 %). High performance liquid chromatography method was used to determine the quercetin and ferulic acid content of brinjal genotypes. The highest quercetin content was recorded in SK-BR-129 (8 mg/g) was statistically at par with SK-BL-104 (7.94 mg/g), SK-BR-123 (7.93 mg/g), SK-BSR-125 (7.92 mg/g), SK-BSR-127 (7.96 mg/g), SK-BSR-

128 (7.97 mg/g), SK-BR-130 (7.95 mg/g) SK-BR-132 (7.99 mg/g), and SK-BR-133 (7.98 mg/g). The highest ferulic content was recorded in SK-BR-129 (0.25 mg/g) was statistically at par with SK-BR-132 (0.24 mg/g), SK-BR-133 (0.23 mg/g), SK-BSR-127 (0.21 mg/g), SK-BSR-128 (0.22 mg/g) and SK-BR-130 (0.20 mg/g).

In the present investigation, the estimates of genotypic correlation coefficients were in general slightly higher than phenotypic correlation coefficients showing that masking effects of the environment was little indicating the presence of inherent association between various traits. Correlation coefficients revealed that the economically important trait i.e., fruit yield per hectare exhibited positive and significant association with with number of flowers per cluster, number of fruits per cluster, plant height, number of branches per plant, number of fruits per plant, fruit yield per plant. It depicted positive but non significant association with fruit length, plant spread and petiole length. It also showed negative non significant association with days to first fruit picking, fruit diameter, average fruit weight at both phenotypic and genotypic levels.

In the present study, 41 genotypes of brinjal were evaluated to estimate the genetic divergence for identification of potential parents using Mahalanobis D^2 statistics. The genotypes were grouped into four clusters. Cluster I had the highest number of genotypes (16) followed by cluster II (11) while remaining III and IV clusters contained seven genotype each. The inter cluster distance (D^2) was maximum between cluster III and IV (885.53) followed by I and IV (550.24), cluster II and IV (273.58). In contrast, minimum inter cluster distance (cluster II and IV) indicated closer relationship among the genotypes included. The maximum intra cluster distance (D^2) was observed in cluster II. The minimum intra cluster distance (D^2) was observed in cluster IV. The inter cluster distance were larger than the intra cluster distance indicating a wider genetic diversity between genotypes of clusters with respect to trait studied. Therefore, superior

recombinants can be obtained through hybridization between genotypes across the clusters.

The formation of different clusters with variable number of entries in each cluster indicated diversity among genotypes. The genotypes from different agro-ecological zones were found to be scattered in different clusters, which suggested that a pattern of clustering of accessions was independent of their geographical origin. Considering the genetic divergence and mean performance of genotypes in respect of various traits, genetically diverse genotypes were identified. The highest cluster mean for number of flowers per cluster (4.67) and number of fruits per cluster (3.55) was found in cluster III. The highest cluster mean for fruit length (15.13 cm) in cluster IV. Highest cluster mean for fruit diameter (6.59cm) in cluster II. Highest cluster mean for plant height (83.14 cm), plant spread (53.88), number of branches per plant (6.31) was found in cluster IV. Highest cluster mean for petiole length (2.72 cm) was found in cluster I. Highest cluster mean for number of fruits per plant (11.94) was found in cluster III. Highest cluster mean for average fruit weight (124.46 g) was found in cluster II. Highest cluster mean for fruit yield per hectare (456.27g) was found in cluster IV. Thus the traits showing high contribution towards genetic divergence can be improved upon by selecting the genotypes from those clusters having maximum cluster means for the respective traits, which inturn depends upon the objective of the breeding programme.

15 ISSR primers were used for molecular characterization of forty brinjal genotypes. The amplified bands were recorded as 1 (band present) and 0 (band absent) in a binary matrix. Polymorphic Information Content (PIC) values for each ISSR marker were determined. Cluster analysis of genotypes using binary data generated by micro satellite markers was conducted. A total of 83 alleles were amplified by 15 polymorphic ISSR loci and the numbers of alleles ranged from 2 to 12 with an average of 5.53 alleles per locus. The total number of bands

amplified were 83 out of which 53 were polymorphic. The number of polymorphic bands ranged from 1 to 11 with an average value of 3.53.

High PIC value was detected for primer BGCO5-860 and BGCO5-814 at 0.383 and 0.380, respectively and low PIC value of 0.261 for primers, namely, BGCO5 848 and BGCO5 823.The average of PIC value per primer, was 0.37.The expected heterozygosity varied from 0.057 to 0.498. The maximum value of H 0.498 was found in primer BGCO5 823 and the minimum value of H 0.057 was found in BGCO5 860, with mean value of 0.002. The maximum value of expected heterozygosity (H) and PIC for binary data is 0.5, because two alleles per locus are assumed, and both are influenced by the number and frequency of the alleles for codominant markers, these values varies between 0 and 1. The ISSR effective multiplex ratio (EMR) may be influenced by the fraction of polymorphic loci. The highest EMR (3.60) was detected with the primer BGC05 842 and the lowest was shown by the primer BGCO5 860 (0.35), with a mean EMR of 1.44 per primer. General usefulness of the ISSR markers was determined by the calculation of marker index (MI) for each ISSR primer. The highest MI was shown by the primer BGCO5 824 and BGCO5 848 (0.007) and the lowest in the primer BGCO5 814 (0.00), BGCO5 860 (0.00) with a mean MI of 0.003 per primer. The resolving power (RP) is the ability of a primer to differentiate between genotypes. The average RP was 2.28 per ISSR primer. The highest RP value was detected with the primer BGCO5842 (6.70) and the lowest with the primer BGCO5860 (0.70). Primer BGCO5860 showed the highest discrimination power (0.999) and the lowest discrimination power were observed in BGCO5824 with the value of 0.658 with an average value of 0.876.The mean heterozygosity (H.av) ranged from 0.00 in BGC05 814 to 0.006 in BGC 848 with an average value of 0.002.

The genetic relationship of forty brinjal genotypes was obtained from the scoring data using Jaccard's similarity coefficient. Cluster analysis was conducted to group genotypes into different clases. The dendrogram was constructed using Jaccards similarity coefficient. Jaccards similarity coefficient ranged from 0.05

between the distant genotypes G17 and G2 genotypes to 0.79 between the closest genotypes, G30 and G29. Cluster analysis divided 40 genotypes into three major clusters at a coefficient value of 0.30 with various degrees of sub-clustering. Cluster I comprised 14 genotypes, which was divided into two sub clusters (IA and IB) which contain 3 genotypes, SK-BL-100, 2017/BRL VAR-7 and SK-BR-135 and 11 genotypes, SK-BL-102, SK-BL-113, SK-BL-114, SK-BL-103, SK-BL-104, SK-BL-112, SK-BL-107, SK-BL-110, SK-BL-111, SK-BL-108, SK-BL-116 respectively. Cluster II consisted of 24 genotypes which was further divided into two sub-clusters (IIA, IIB) which contained 13 genotypes, SK-BL-101, SK-BR-117, SK-BR-133, SK-BR-122, 2018/BRL VAR-5, SK-BR-118, SK-BR-130, SK-BL-105, SK-BR-134, SK-BR-131, SK-BL-106, SK-BSR-128, SK-BR-132 and 11 genotypes SK-BL-109, SK-BR-123, SK-BR-129, SK-BR-119, SK-BR-120, SK-BR-121, SK-BSR-126, SK-BSR-127, SK-BR-136, SK-BSR-124, SK-BSR-125, respectively ; cluster III contained 2 genotypes SK-BL-115 and SK-BR-137.

Based on the findings of the present investigation, the following conclusions could be drawn:

- Analysis of variance indicated existence of significant variation among various genotypes under study.
- High heritability coupled with high genetic gain was recorded for number of flowers per cluster, number of fruits per cluster, plant spread, petiole length, number of fruits per plant, fruit length, fruit diameter, average fruit weight, fruit yield per plant, fruit yield per hectare, total phenol, anthocyanin, TSS, dry matter, FRAP, scavenging activity (DPPH), ferulic acid indicating the preponderance of additive gene action.
- Correlation studies indicated that traits viz., number of flowers per cluster, number of fruits per cluster, number of branches per plant, number of fruits per plant should be considered for improving quantitative traits in brinjal.

- The inter cluster distance (D^2) was maximum between the cluster III and IV followed by cluster II and III which suggested that members of these clusters are very diverse. Selection of parents from these clusters have high cluster means and showing high performance can be used in hybridization programme for developing of high yielding varieties.
- ISSR markers showed genetic variability in the studied brinjal genotypes and they are powerful tools for estimating genetic similarities and diversity. The genetic relationships presented among the genotypes are helpful for future breeding programmes through selection of genetically diverse parents.
- 15 ISSR primers were used for molecular characterization of forty brinjal genotypes. A total of 83 alleles were amplified by 15 polymorphic ISSR loci and the numbers of alleles ranged from 2 to 12 with an average of 5.53 alleles per locus.
- Molecular UPGMA clustering classified 40 genotypes into 3 clusters and showed considerable diversity among the genotypes.
- The Jaccards similarity quotient is minimum between G2 and G17 (0.05) that indicates these are more diverse than other genotypes.
- The results have proven that both morphological and ISSR markers are effective tools in studying genetic diversity in brinjal species.

LITERATURE CITED

Adamczewska-SowiEska K. and Krygier. M. 2013 Yield quantity and quality of field cultivated eggplant in relation to its cultivar and the degree of fruit maturity. *Acta ScientiarumPolonorumHortorumCultus***12** (2):13-23.

Ali, Z., Xu, Z. L., Zhang, D. Y., He, X. L., Bahadur, S. and Yi, J. X. 2011. Molecular diversity analysis of eggplant (*Solanummelongena*) genetic resources. *Genetics and Molecular Research***10** (2): 1141-1155.

Amiryousefi, A., Hyvönen, J. and Poczai, P. 2018. iMEC: Online Marker Efficiency Calculator. *Applications in Plant Sciences* **6**(6): e1159.

Anand, I. J. and Murty, M. B. R. 1968. Genetic divergence and hybrid performance in linseed. *The Indian Journal of Genetics and Plant Breeding* **28**: 178-185.

Anderson, J. A., ChurchilL, G. A., Autrique, J. E., Tanksley, S. D. and Sorrells, M.E. 1993. Optimizing parental selection for genetic linkage maps Genome **36**: 18 1-186.

Anonymous, 2018. Horticulture Statistics Division Department of Agriculture, Cooperation & Farmers' Welfare Ministry of Agriculture & Farmers' Welfare Government of India. *Horticultural Statistics at a Glance,* pp. 188.

Ansari, S. F. 2010. Genetic analysis for earliness and heat tolerance along with yield attributing traits in Brinjal (*Solanummelongena* L.). Ph. D. thesis submitted to Indira Gandhi Agricultural University, Raipur.

Ansari, S. F., Mehta, N., Ansari, S. and Gavel, J. P.2011. Variability studies in brinjal (*Solanummelongena* L.) in Chattisgarh Plains. *Food and Agricultural Organisation of the United Nations* **2**(2): 275-281.

AOAC, 1984. Official Methods of Analysis. Association of official Analytical Chemists 13th edition, Washington D.C., p. 497.

Aremu. 2011. Genetic diversity a review for need and measurements for Intraspecific crop improvement. *Journal of Microbiogical and Biotechnological Research* **2**: 80-85.

Arti, D. and Sharma, A. K. 2018. Genetic variability studies for yield and quality parameters in Brinjal (*Solanummelongena* L.) *Journal of Pharmacognosy and Phytochemistry* **7**(5): 2494-2496.

Arti, D., Sharma, A. K. and Kumar, R. 2018. Assessment of Genetic Divergence in Brinjal (*Solanummelongena* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences* **7**(9): 2567-2572.

Arunkumar. 2014. Genetic variability and divergence studies in brinjal (*Solanummelongena* L.) *Bioinfolet.* **10**(2B): 739- 744.

Balas, A., Jivani, L. L., Valu, M. G., Sakriya, S. G., Gamit, U. C. and Rathod, R. K. 2019. Study of genetic variability and heritability in brinjal (*Solanummelongena* L.). The *Pharma Innovation Journal* **8**(9): 44-46.

Banerjee, S., Bisht, Y. S. and Verma, A. 2018. Genetic Diversity of Brinjal (*Solanummelongena* L.) in the Foot Hills of Himalaya.*International Journal of Current Microbiology and Applied Sciences* **7**(4): 3240-3248.

Bansal, S. and Mehta, A. K. 2008. Genotypic correlation and path analysis in brinjal (*Solanummelongena* L.). *National Journal of Plant Improvement* **1 0**(1): 34-36.

Bende, T. S., Bagade, A. B., Deshmukh, J. D. and Shinde, A. V. 2019.Variability studies for yield and yield components in brinjal (*Solanummelongena* L.). *International Journal of Chemical Studie*s **7**(2):56-58.

Bidaramali, V., Akhtar, S. and Das, A. 2020.Proximate Composition and Bioactive Compounds in Diverse Eggplant Genotypes.*Current Journal of Applied Science and Technology* **39**(4): 113-121.

Bose, T. K. and Som, M. G. 1986. Vegetable Crops in India. MitraNayaProkash, 206, BidhanSarani, Calcutta, India. pp. 4-293.

Boyaci, F., Unlu, A. and Abak, K. 2010. Screening for resistance to fusarium wilt of some cultivated eggplants and wild Solanum accessions. *Acta Horticulturae* **935**: 23-27.

Burton, G. M.1952. Quantitative inheritance in grasses. *Grassland Cong.* **1**: 277-285.

Cakir, Z., Balkaya, A., Saribas, S. and Kandemir, D. 2017. The morphological diversity and fruit characterization of Turkish Eggplant (*Solanummelongena* L.) populations. *Ekin Journal of Crop Breed and Genetics* **3**(2): 34-44.

Celka, Z., Buczkowska, K., Baczkiewicz, A. and Drapikowska, M. 2010.Geneticd ifferentiation among geographically close populations of *Malvaalcea*. *Acta Biological Cracoviensia Series Botanical* **52**(2): 32-41.

Chahal, G. S. and Gosal, S. S. 2002. Principles and Procedures of Plant Breeding: Biotechnology and Conventional Approaches. *Narosa Publishing House, New Delhi*. **21**:64-89.

Chaitanya. 2017. Variability and Trait Association Studies in Brinjal (*Solanummelongena* L.), *Indian Horticulture Journal* **7**(1):58-63.

Chanasut, U. and Rattanaponone, N. 2008. Screening methods to measure antioxidant activities of phenolic compounds extracts from some varieties of Thai eggplants. *Acta Horticulture* **765**: 291-96.

Channe, J. B., More, N. B. and Kadam, R. S. 2013. Assortment of Genetic Diversity in Brinjal (*Solanummelongena*) Genotypes Using ISSR markers. *Indian Journal of Applied Research* **3**(6):44-46.

Chauhan, A., Chandel, K. S. and Singh, S. P. 2017.Studies on Correlation and Path Analysis for Yield and Yield Contributing Traits in Eggplant

(*Solanummelongena* L) Involving Bacterial Wilt Resistant Genotypes. *Vegetos* **30**(4):118-121.

Chithra, K., Devaraju., Srinivasa, V., Varalakshm, B., Kolakar, S. S. and Asha, A. B.2020. Correlation and path analysis in segregating population of brinjal (*Solanummelongena* L.) *Journal of Pharmacognosy and Phytochemistry* **9**(5): 2457-2459.

Das, A., Pandit, M. K., Saheb, P., Muthaiah, K. and Santanu, L. 2017.Characteriz ation of Brinjal Genotypes for Growth, Yield and Morphological Traits. *Research Journal of Agricultural Sciences* **8**(4): 789-796.

Dash, S. P., Singh, J. and Sharma. D. 2019. Morphological characterization of brinjal (*Solanummelongena* L.) germplasm. *Journal of Pharmacognosy and Phytochemistry* **8**(2): 1574-1578.

Dasmohapatra, A. and Sharma, D. 2019. Mean Performance & Variability Analysis in Long Fruited Brinjal (*Solanummelongena* L.) for Chhattisgarh.*Bulletin ofEnvironment, Pharmacology and LifeSciences* **8**(2) : 28-31.

Demir, K., Bakır, M., Sarıkamış, G. and Acunalp, S. 2010. Genetic diversity of eggplant (*Solanummelongena L.*) germplasm from Turkey assessed by SSR and RAPD markers. *Genetics and Molecular Research* **9** (3): 1568-1576.

Dewey, D. R. and Lu, K. H. 1959. A correlation and path coefficient analysis of components of crested wheat-grass seed production. *Agronomy Journal* **51**: 515-518.

Dhaka, S. K. and Soni, A. K. 2014.Genetic variability in brinjal (*Solanummelonge na* L.). *The Asian Journal of Horticulture* **7**(2): 537-540.

Dutta, R., Mandal, A. K., Maity, T. K. and Hazra. P. 2009. Multivariate genetic divergence in brinjal (*Solanummelongena* L.). *Journal of Crop and Weed* **5**(1):67-70.

Elekofehinti, O. O., Kamdem, J. P., Bolingon, A. A., Athayde, M. L., Lopes, S.R., Waczuk, E. P., Kade, I. J., Adanlawo, I. G. and Rocha, J. B. T. 2013. African eggplant (*Solanumanguivi* L.) fruit with bioactive polyphenolic compounds exerts in vitro antioxidant properties and inhibits Ca_2 induced mitochondrial swelling. *Asian Pacific Journal of Tropical Biomedicine* **3**(10): 757-766.

Fisher, R. A. 1918. The correlation between relatives on the supposition of Mendelian inheritance. Trans. Roy. *Society Edinburgh* **52**: 399-433.

Gashaw, A., Mohammed, H. and Singh, H. 2007. Genetic divergence in selected durum wheat genotypes of Ethiopian plasm. *African Crop Science Journal* **15**(2): 67-72.

Ghadsingh, P. G. and Mandge, S. V. 2012. Nutritional spoilage of tomato and brinjal fruits due to postharvest fungi. *Current Botany* **3** (4):10-12.

Golani, I. J., Mehta, D. R., Naliyadhara, M. V., Pandya, H. M. and Purohit, V. L. 2007. A study on genetic diversity and genetic variability in brinjal (*Solanummelongena* L.). *Agricultural Science Digest* **27**(1): 22-25.

Gramazio, P., Chatziefstratiou, E., Petropoulos, C., Chioti, V., Mylona, P., Kapotis, G., Vilanova, S., Prohens, and J. Papasotiropoulos, V. 2019. Multilevel characterization of eggplant accessions from Greek Islands and the mainland contributes to the enhancement and conservation of this germplasm and reveals a large diversity and signatures of differentiation between both origins. *Agronomy* **9**: 887.

Gyamfi, M. A., Yonamine, M. and Aniya, Y. 1999. Free radical scavenging activity of medicinal herb of Ghana: Thonningiasanguinea

on experimentally induced liver injuries. *General Pharmacology* **32**(6): 661-667

Halliwell, B., Aeschbach, R., Lo Liger, J. and Arouma, O.I. 1995. The characterization of antioxidants. *Food and Chemical Toxicology* **33**: 601–617.

Han, S. W., Tae, J., Kim, J. A., Kim, D. K., Seo, G. S., Yun, K., Choi, S. C., Kim, T.Y., Nah, Y.H. andLee, Y.M. 2003. The aqueous extract of *Solanum melongena* inhibits PAR2 agonist-induced inflammation. *Clinica Chimica Acta* **328**: 39-44.

Hassan, I., Ahmad, S. Arif, M., Siddiqui, S. U. and Ahson, M. 2015. Genetic variability in eggplant for Agro-morphological traits. *Science, Technology and Development* **34**(1): 45-49.

Hurtado, M., Vilanova, S., Plazas, M., Gramazio, P., Fonseka, H. H., Fonseka, R. and Prohens, J. 2012. Diversity and relationships of eggplants from three geographically distant secondary centers of diversity. *PLoS ONE* **7**(7): 41748

Husnudin, U. B., Daryono, B. S., Purnomo. 2019. Genetic variability of Indonesian Eggplant (*Solanummelongena L.*) based on ISSR markers. *Biodiversitas* **20**(10): 3049-3055.

Hussain, K., Khan, S. H., Parveen, K., Narayan, S., Afroza, B., Mukhdoomi, M.I., Quratul-Ain., Zehra, B., Farwah, S., Hussain, S. M., Rizvi, S., Dar, Z. A. and Pala, M. M. 2018. Comparative performance of Brinjal (*Solanummelongena* L.) genotypes. *Bulletin of Environment Pharmacology and Life Sciences* **7** (9): 91-93.

Islam, M.S. and Uddin, M.S.2009. Genetic variation and trait relationship in the exotic and local eggplant germplasm. *Bangladesh Journal of Agricultural Research* **34**(1): 91-96.

Isshika, S., Iwata, N. and Khan, M. M. R. 2008. ISSR variations in eggplant (*Solanummelongena* L.) and related *Solanum* species. *Scientia Horticultur ae* **117**(3): 186-190.

Jayalakshmi. K. and Praneetha, S. 2018. Evaluation of brinjal (*Solanummelongena* L.) local types for yield and its quality traits. *International Journal of Chemical Studies* **6**(3): 292-297.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal* **47**: 477-483.

Jung, E. J., Bae, M. S., Jo, E. K., Jo, Y. H. and Lee, S. C. 2011. Antioxidant activity of different parts of eggplant. *Journal of Medicinal Plants Research* **5**(18): 4610-4615.

Kamani, J. M. and Monpara, B. A. 2006. Extent of genetic variation and associations among yield traits in f_2 generation of two brinjal crosses. *National Journal of Plant Improvement* **8**(2):109-114.

Kandoliya, U. K., Bajaniya, V. K., Bhadja, N. K., Bodar, N. P. and.Golakiya, B. A. 2015. Antioxidant and nutritional components of Egg plant (*Solanummelongena* L) fruit grown in Saurastra Region. *International Journal of Current Microbiology and Applied Science* **4**(2): 806-813.

Kaneyuki, T., Noda, Y., Traber, M. G., Mori, A. and Packer, L. 1999. Superoxide anion and hydroxyl radical scavenging activities of vegetable extracts measured using electron spin resonance. *Biochemistry and Molecular Biology International* **47***:* 979-989.

Karak. C., Ray. U., Akthar. S. and Naik. A. Hazara. P. 2012. Genetic variation and trait association in fruit yield components and quality traits in brinjal (*Solanummelongena* L.). *Journal of Crop and Weed* **8**(1):86-89.

Karihaloo, J. L., Baruner, S. and Gottlieb, L. D. 1995. *Theoretical and* Applied *Genetics* **90**:767.

Katoch, V., Katoch, R. and Pathania, N. K. 2005. Correlation and path analysis for some biometric traits in brinjal (*Solanummelongena* L.). *Annals of Biology* **21** (2): 193-197.

Kaur, C., Nagal, S., Nishad, J., Kumar, R. and Sarika 2014.Evaluating eggplant (*Solanummelongena* L) genotypes for bioactive properties: A chemometric approach.*Food Research International***60**: 205–211.

Keneni, G., Jarso, M., Wolabu, T. and Dino, G. 2005. Extent and pattern of genetic diversity for morpho-agronomic traits in Ethiopian highland pulse landraces II. Faba bean (*Viciafaba* L.). *Genetic Resources and Crop Evolution* **52**(5): 551-561.

Khan, R. 1979. *Solanummelongena*and its ancestral forms. *J. G. Hawkes*, pp.629-636.

Khan, R. and Singh, Y. V. 2014. Germplasm characterization in eggplant (*Solanummelongena* L.). *The Asian Journal of Horticulture* **9**(2):356-359.

Khorsheduzzaman, A. K. M., Alam, M. Z., Rahman, M. A. K., Mian, M. I. and H ossain, M. M. 2008. Molecular characterization of five selected brinjal (*Solanummelongena* L) genotypes using SSR markers. *Bangladesh Journal of Genetics and Plant Breeding* **21**(1): 01-06.

Knapp, S., Vorontsova, M. S. and Prohens, J. 2013. Wild relatives of the eggplant (*Solanummelongena* L.: Solanaceae): new understanding of species names in a complex group. *PloS ONE* **8**(2): 57039.

Konan, N. O., Akaffou, M. A., Kouadio, L., Akaffou, D. S. and Mergeai, G. 2020. Genetic diversity of exotic and local eggplants (Solanum spp.) cultivated in Côte d'Ivoire based on ISSR markers. *Biodiversitas* **21**: 3651-3658.

Koundinya, A. V. V., Pandit, M. K., Dolui, S., Bhattacharya, A. and Hegde, V. 2019.Multivariate analysis of fruit quality traits in brinjal. *Indian Journal of Horticulture* **76** (1):94-103.

Kriengsak, T., Unaroj, B., Kevin, C., Luis, C. and David, H. B. 2006. Comparison of ABTS, DPPH, FRAP, and ORAC assays for estimating antioxidant activity from guava fruitextracts. *Journal of Food Composition and Analysis***19**:669 - 675.

Kumar, A., Sharma, S., Pratap, A., Joshi, A., Singh, M. and Das, P.2018. Screening and identification of molecular marker of brinjal hybrid (*Solanummelongena* L.) revealed by issr and rapd marker. *World Journal of Pharmacy and Pharmaceutical Sciences* **7**(7): 1350-1357.

Kumar, M. K., Mishra, H. N., Manas, P. and Nayak, D. P. 2020. Genetic variability and correlation studies in brinjal (*Solanummelongena* L.). *The Pharma Innovation Journal* **9**(2): 416-419.

Kumar, R. S. and Arumugam, T. 2013. Phenotypic evaluation of indigenous brinjal types suitable for rainfed conditions of South India (Tamilnadu). *African Journal of Biotechnology* **12**(27): 4338-4342.

Kumar, S. R., Arumugam, T., Anandakumar, C. R. and Premalakshmi, V.2013. Genetic variability for quantitative and qualitative traits in Brinjal (*Solanummelongena* L.). *African Journal of Agricultural Research* **8** (39): 4956-4959.

Kumar, S. R., Arumugam, T. and Ulaganathan, V. 2016. Genetic diversity in eggplant germplasm by principal component analysis. *SABRAO Journal of Breeding and Genetics* **48** (2) 162-171.

Kumar, S. R., Arumugam, T. and Premalakshmi, V. 2014. Evaluation and variability studies in local types of brinjal for yield and quality (*Solanummelongena* L.). *Electronic Journal of Plant Breeding* **3**(4) 129-135.

Kumar, G., Meena, B. L., Kar, R. Tiwari, S. K., Gangopadhyay, K.K. and Bisht, I.S. and Mahajan, R. K. 2008. Morphological diversity in brinjal

(*Solanum melongena* L.) germplasm accessions. *Plant Genetic Resources characterization and Utilization* **6**(3): 232-236.

Kumari, A., Chawla, N. and Dhatt, A. S. 2018. Genotypic differences for Anthocyanins in different parts of Eggplant (*Solanum melongena* L.). *International Journal of Advanced Research in Biological Sciences* **5**(1): 12-18.

Kushwah, S. and Bandhyopadhya, B. B. 2005. Variability and correlation studies in brinjal. *Indian Journal of Horticulture* **62** (2): 210-212.

Lakshmi, R. R., Padma, S. S. V., Naidu. L.N. and Umajyothi.K.2014. Correlation and path analysis studies ofyield and yield components in brinjal. *Plant Archives* **14** (1): 583-591.

Lohakare, A. S., Dod, V. M. and. Peshattiwar, P. D. 2008. Correlation and path analysis studies in green fruited brinjal. *Asian Journal of Horticulture* **3**(1): 173-175.

Lush, J. L. 1949. Heritability of quantitative characters in farm animals. Proceedings of the Eight International Congress on Genetics. *Heredits* **35**(1).356-395.

Madhavi, N., Mishra, A.C., Pushpavathi, Y. and Kumari, V. L. P. 2015. Genetic diversity in brinjal (*Solanummelongena* L.) under temperate hills of Uttrakhand, India. Department of Vegetable Science, Uttarakhand University of Horticulture and Forestry, Ranichauri Campus, TehriGarhwal - 249 199 (Uttarakhand), India**15** (2): 1107-1110.

Mahalanobis P. C. 1936. On the generalized distance in statistics, Proc. Nat. *Indian Institute of Science* **2**: 49-55.

Mahmoud, M.I and El-Mansy, A. B. 2012.Molecular Identification of Eggplant cultivars (*Solanum melongena* L.) using ISSR Markers. *Journal of Applied Sciences Research* **8**(1):69-77.

Maik, K. C. K 2005 Genetic variability and divergence studies in brinjal (*Solanummelongena* L.). MSc thesis. University of Agricultural Science, Dharwad, India.

Mansoor, S., Sharmaa, V. Mudasir A. M., Javid I. M., Sajad, N., Nazeer A., Jawaher, A., Mona, S. and A. Khalid, Z. M. 2020. Quantification of polyphenolic compounds and relative gene expression studies of phenylpropanoid pathway in apple (*MalusdomesticaBorkh*) in response to Venturia inaequalis infection. *Saudi Journal of Biological Sciences*.

Mao, W**.,** Du, L., Bao, C., Hu, T., Zhu, Q and Hu, H. 2006. Genetic Diversity and Genetic Relatives Analysis of Southern Long-eggplant Germplasm Based on Inter-simple Sequence Repeat (ISSR) **33**(5):1113-1116.

Matsubara, K., Kaneyuki, T., Miyake, T. and Mori, M. 2005. Antiangiogenic activity of nasunin, an antioxidant anthocyanin, in eggplant peels. *Journal of Agricultural Food Chemistry* **53**: 6272–6275.

Mazza, G., Cacace, J. E. and Kay, C. D. 2004. Methods of analysis for anthocyanins in plants and biological fluids. *Journal of AOAC International* **87**: 129-145.

Mehta, D. R. Golani, I. J., Pandya, H. M., Patel, R. K. and Naliyadhara, M.V. 2004. Genetic diversity in Brinjal (*Solanummelongena* L.) *Vegetable Science* **31**(2): 142-145.

Mishra, S. B., Singh, U. K. and Sahu, P. K. 1994. Studies on genetic divergence in five landraces of rice in Northern Bihar. *Annals of Agricultural Research* **15** (2): 217-221.

Mishra, S. V., Warade S.D. and M. B. Nayakwadi, 2007. Correlation and path coefficient analysis in brinjal. *Journal of Maharashtra Agricultural University* **32**(1): 74-76.

Mohanty, B. K. 2002. Variability, heritability and genetic advance studies in brinjal (*Solanum melongena* L.). *Indian Journal of Agricultural Research* **36**(4): 290-292.

Muniappan, S., Saravana, K. and Ramya, B. 2010. Studies on Genetic Divergence and Variability for Certain Economic Traits in Eggplant (*Solanummelongena* L.). *Electronic Journal of Plant Breeding* **1**(4): 462-465.

Murty, B. R. and Qadri, M. I. 1966. Analysis of divergence in some self compatible forms of *Brassica compestris* var.Brown sarson. *The Indian Journal of Genetics and Plant Breeding***26**: 45-55.

Musa, U. and Yusuf, J. 2015. Corelation studies on the yield and yield traits of Eggplant (*Solanummelongena* L.). *IISTE***5** (19).

Nadkarni, K. M. 1927. Indian Materia Medica Bombay.

Naegele, R. P., Boyle, S., Quesada-Ocampo, L. M. and Hausbeck, M. K. 2014. Genetic diversity, population structure, and resistance to *Phytophthora capsici*of a worldwide collection of eggplant germplasm. *Plos One* **9**(5):e95930.

Naik, C. K. K. 2006. Genetic variability and divergence studies in brinjal (*Solanum melongena* L.). *Karnataka Journal of Agricultural Sciences* **19** (2): 488-492.

Naik, K., Sreenivasulu, G. B., Prashnath, S. J., Jayprakashnarayan, R. S., Madalgiri, M. B. and Mulge, R. 2010. Studies on genetic variability and its importance in brinjal (*Solanum melongena* L*). Asian journal of Horticulture* **4**(2): 380-382.

Nair, R. and Mehta, A. K. 2007. Phenotypic correlation and Path coefficient analysis for some metric in brinjal (*Solanum melongena* L.). *Asian Journal of Horticulture* **2**(2): 164-168.

Nalini, A. D., Salimath, P. M. and Patil, S. A. 2009. Association and path coefficient analysis in elite germplasm lines of brinjal (*Solanum melongena* L.). *Karnataka Journal of Agricultural Science* **22**(5): 965-966.

Naliyadhara, M. V., Golani, I. J., Mehta, D. R. and Purohit, V. L. 2007. Genetic variability, correlation coefficient and path analysis in Brinjal. *The Orissa Journal of Horticulture* **35**(2):92-96.

Nayak, B. R. and Nagre, P. K. 2014. Genetic Variability and Correlation studies in brinjal (*Solanum melongena* L.) *International Journal of Applied Biology and Pharmaceutical Technology* **4**(4):211-215.

Nayanathara, A. R., Mathews, A., Aalolam, K. P. and Reshma, J. K. 2016. Valuationof total Phenol, Flavonoid and Anthocyanin Content in Differen t Varieties of Eggplant. *Emergent Life Sciences Research* **2**(2):63-65.

Nisha. P., Nazar, A. P. and Jayamurthy. P. 2009. A comparative study on antioxidant activities of different varieties of *Solanum melongena.Food and Chemical Toxicology* **47:**2640-2644

Noda, Y., Kaneyuki, T., Igarashi, K., Mori, A. and Packer, L. 2000. Antioxidant activity of nasunin, an anthocyanin in eggplant peels. *Toxicology* **148:** 119-123.

Nunome, T., Suwabe, K., Iketani, H. and Hirai, M.2003.Identification and charact erization of microsatellites in eggplant. *Plant Breeding***122**: 256-262.

Pallavi Chaudhary and Sanjay Kumar. 2014. Variability, Heritability and Genetic advance studies in egg-plant (*Solanunm melongena* L.). *Plant Archives* Vol. **14**(1):483-486.

Pandey, P., Ansari, W. A., Kashyap S. P., Bhardwaj, D. R., Tiwari, S. K. and Singh, B.2019. Genetic diversity of Indian bitter gourd (*Momordica chara ntia*) by ISSR and morphological markers. *Indian Journal of Agricultural Sciences* **89** (12): 2037–42.

Panse, V. G. and Sukhatme, P. V. 1985. Statistical methods for agricultural workers. *Indian Council of Agricultural Research, New Delhi* pp. 157-165.

Patel, D. 2007. Studies on genetic diversity for fruit characteristics in brinjal (*Solanum melongena* L.). M. Sc. (Ag.) Thesis submitted to IGAU, Raipur (CG) 86.

Patel, K., Patel, N. B., patel, A. I., Rathod, H. and Patel, D.2015. Study of variability, correlation and path analysis in brinjal (*Solanum melongena*l.).*The bioscan.* **10**(4): 2037-2042,

Patel, K. K., Sarnik, D. A., Asati, B.S. and Tirkey, T. 2004. Studies on variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). *Agricultural Science Digest* **24**(4): 256-259.

Powell, W., Machray, G. C. and Provan, J. 1996. Polymorphism revealed by Simple Sequence Repeats. *Trends in Plant Science***1**: 215-222.

Prabakaran, S. 2010. Evaluation of local types of brinjal (*Solanum melongena* L.). M.Sc., (Hort.) Thesis, Agricultural College and Research Institute, TNAU, Madurai.

Prabhu M, Natarajan and S, Pugalendhi L (2009). Variability and heritability studies in F5 and F6 progenies of brinjal. *American-Eurasian Journal of Sustainable Agriculture* **3**(3):306-309.

Prevost, A. and Wilkinson, M. J. 1999. A new system of comparing PCR primers applied to ISSR fingerprinting of potato cultivars. *Theoretical and Applied Genetics* **98**:107-112.

Pujer, P., Jagadeesha, R. C. and Cholin, S. 2017. Genetic variability, Heritability and Genetic Advance for yield, yield related components of brinjal (*Solanum melongena* (L.)) genotypes, *International Journal of Pure and Applied Bioscience* **5**(5): 872-878.

Quammruzaman, A. K. M., Rashid, M. A., Ahmad, S. and Moniruzzaman, A. 2009. Genetic divergence analysis in egg plant (*Solanum melongena* L.). *Bangladesh Journal of Agricultural Research* **34**(4):705-712.

Rahman, M. O., Rabbani, M. G., Yesmin, R. and Garvey, E. J. 2014. Genetic diversity of brinjal (*Solanum melongena* Linn.) through multivariate analysis.*International Journal of Natural and Social Sciences***1**: 85-93.

Ram, K., Singh, P. and Singh, R. 2007. Studies on genetic variability and selection parameters for economic traits in egg plant. *International Journal of Natural and Social Sciences* **2** (1): 99-102.

Ramesh Kumar. 2014. Evaluation and variability studies in local types of brinjal for yield and quality (*Solanum melongena* L.). *ElectronicJournal of Plant Breeding* **3**(4): 977-982.

Ranganna, S. 1986. Hand Book of Analysis and Quality Control of Fruit and Vegetable Products. *Tata McGraw Hill Publication*, NewDelhi.

Rani, K. R., Sharma, A. and Pandey, N. 2019. Genetic variability and correlation between yield and its component traits in brinjal (*Solanum melongena L.*). *International Journal of Chemical Studies* SP **6**: 668-671.

Rao, C. R. 1952. Advanced statistical Methods in Biometrical Research. *Wiley and Sons, New York.*

Ravali, B., Reddy, K. R., Saidaiah, P. and Shivraj, N. 2017. Genetic diversity in brinjal (*Solanum melongena* L.). *International Journal of Current Microbiology and Applied Sci*ence **6**(6): 48-54.

Reshmika, P.K. 2015. Genetic variability divergence and corelation studies in brinjal. *International Journal of Agricultural Science and Research* **5**(6): 103-110.

Reshmika, P. K., Gasti, V. D., Evoor, S., Jayappa, J., Mulge, R. and Basavaraj, L.B. 2016. Evaluation of Brinjal (*Solanum melongena* L.) Genotypes for Yield and Quality Traits. *Environment and Ecology* **34**(2): 531-535.

Rohlf, F. J. 1997. NTSYS-PC 2.1: Numerical Taxonomy and Multivariate Analysis System. Setauket, Newyork: Exeter software.

Rold-an-Ruiz, Dendauw, J., Bockstaele, V.EDepicker, A. and Loose, M. D. 2000. "AFLP markers reveal high polymorphic rates in ryegrasses (*Lolium*spp.)," *Molecular Breeding* **6**(2):125–134.

Roosevelt, J. S. and Shanti, S. 2009. Diversity studies in brinjal (*Solanum melongena* L.). *The Asian Journal of Horticulture* **4**(1): 13-15.

Sakakibara, H., Honda, Y., Nakagawa, S., Ashida, H. and Kanazawa, K. 2003. Simultaneous determination of all polyphenols in vegetables.fruits, and teas. *Journal of Agricultural and Food Chemistry* **51:** 571–581.

Sakriya, S. G., Vaddoria, M. A., Dudhat, M. A., Gamit, U. C. and Jivani, L. L.2020. Genetic variability, heritability and genetic advance in brinjal (*Solanum melongena* L.).*International Journal of Chemical Studies* **8**(4): 1768-1770.

Sangam, S., Kant, K., Akhtar, S., Kumari, N., Chattopadhyay, T. and Kumar, R.2020. Genetic Variability in Summer Brinjal (*Solanum melongena* L.*). International Journal of Plant & Soil Science* **32**(14): 44-50

Sao, A. 2006. Line X Tester analysis for fruit yield and its component in brinjal (*Solanum melongena* L.). Ph.D. Thesis, IGKV, Raipur. pp 158.

Senapati, N., Mishra, H. N., Bhoi, M. K., Dash, S. K. and Prasad, G. 2009. Genetic variability and divergence studies inbrinjal (*Solanum melongena* L.). *Vegetable Science* **36**(2): 150-154.

Shafi, W., Mansoor, S., Jan, S., Singh, D. B., Kazi, M., Raish, M., Alwadei, M., Mir, J. L. and Ahmad,P.2019.Varibility in catechin and rutin contents and

their antioxidant potential in diverse apple genotypes. *Molecules* **24**(5):943.

Shailesh, K., Tiwari1, J. L., Karihaloo1., Hameed, N. and Ambika, B Gaikwad 2009. Molecular characterization of Brinjal (*Solanum melongena* L) Cultivars using RAPD and ISSR Markers *Journal of Plant Biochemistry and Biotechnology* **18**(2): 189-195.

Sharifova, S., S. Mehdiyeva, K. and Roubos, T. K. 2013. Assessment of Genetic Diversity in Cultivated Tomato (*Solanum lycopersicum* L.) Genotypes Using RAPD Primers. *Journalof Horticultural Research* **21**(1):83-89.

Sharma, A. D., Gill, P. K. and P. Singh 2000. DNA isolation from dry and fresh samples of polysccaharide rich plants. *Plant Molecular Biology Reporter* **20**: 415-415.

Sharma, A. and Maurya, I. B. 2004. Genetic divergence in brinjal (*Solanum melongena* L.). *Orissa Journal of Horticulture* **32** (2): 22-25.

Shinde, K. G., Birajdar, U. M., Bhalekar, M. N. and Patil, B.T. 2014. Genetic divergence in Brinjal (*Solanum melongena* L.). *Vegetable Science* **39**(1): 103-104.

Shindhe, K. G., Bhalekar, M. N. andPatil, B. T. 2012. Characterization in brinjal (*Solanum melongena* L.) germplasm. *Vegetable Science* **9**(2):186:188.

Shrivastava, S., Sharma, S. and Das, P. 2018. Screening and identification of molecular marker for fingerprinting of brinjal hybrids and its parental lines. *International Journal of Current Biotechnology* **6** (1):1-5.

Silambarasan, V., Eswaran, R., Senthil, N.k., Thangavel, P and Thirugnanakumar, S.2020. Studies on genetic diversity in brinjal (*Solanum melongena* L.). *Plant Archives* **20** (1): 9-15.

Sindhuja, K., Vinithra, S., Senthilkumar, N., Senthilkumar, P., Ponsiva, S. T., BarathKumar, T. R. and Thirugnanakumar, S. 2019. Studies on genetic

diversity in brinjal (*Solanum melongena* L.). *Electronic Journal of Plant Breeding,* **10** (4): 1554-1559.

Singh, A. K., Singh, S. B. and Singh, S. M. 1996. Genetic divergence in scented and five genotypes of rice (*Oryza sativa* L.). *Annals of Agricultural Research* **17** (2): 163-166.

Singh, J., Kaur, A. and Thakur, J. C. 2005. Genetic divergence in rainy season brinjal (*Solanum melongena* L.). *Crop Improvement* **32** (2): 200-204.

Singh, O., Singh, B., Singh, K. V., Chand, P. and Vaishali. 2013. Studies on genetic variability in brinjal (*Solanum melongena* L.). *Annuals of Horticulture* **6** (2): 279 – 283.

Smith, J. S. C. and Smith, O. S. 1989. The description and assessment of distances between inbred lines of maize: the utility of morphological, biochemical and genetic descriptors and a scheme for the testing of distinctiveness between inbred lines. *Maydica* **34**: 151-161.

Solaimana, A. H. M., Nishizawa, T., Khatun, M. and Ahmed, S. 2015. Physio morphological characterization genetic variability and correlation studies in brinjal genotypes of Bangladesh. *Computational and Mathematical Biology* **4**(1):1-36.

Solaimana, A. H. M., Nishizawab, T., Khatuna, M. and Ahmad, S. 2014. Morphological characterization and genetic diversity studies of promising brinjal genotypes for hybridization program in Bangladesh. *Journal of Advance in Agricultural Research* **3**:225-234.

Somawathi, K. M., Rizliya, V., Wijesingh, D. G. N. G. andMadhujith, W. M. T. 2014. Antioxidant Activity and Total Phenolic Content of Different Skin ColouredBrinjal (*Solanum melongena L.*). *Tropical Agricultural Research* **26** (1): 152 –161.

Souframanien, J. andGopalakrishna, T. 2004. A comparative analysis of genetic diversity in blackgram genotypes using RAPD and ISSR markers. *Theory of Applied Genetics***109**: 1687–1693.

Srivastava, S., Saidaiah, P., Shivraj, N. and Reddy, K.R.2019. Study of genetic variability, heritability and genetic advance for yield and yield related components of brinjal (*Solanum melongena* L.) genotypes. *Journal of Pharmacognosy and Phytochemistry* **8**(4): 917-919.

Srivastava, U., Mahajan, R. K. and Gangpadhyay, K. K. 2001. *Minimal Descriptors of Agri-Horticultural Crops (part II). NBPGR New Delhi/India*.

Stàgel, A., Portis, E. and Toppino, L. 2008. Gene-based microsatellite development for mapping and phylogeny studies in eggplant. *BMC Genomics,* **9**: 357- 361.

Sulaiman, N. N. M., Rafii, M.Y., Duangjit, J., Ramlee, S. I., Phumichai, C., Oladosu, Y., Datta, D. R. and Musa. I. 2020.Genetic variability of eggplant germplasm evaluated under open field and glasshouse cropping conditions. *Agronomy***10**: 436-439.

Swain, T. and Hill, W. E. 1959. The phenolic constituents of prunisdomestica.The quantitative analysis of phenolic constituents. *Journal of Science and Food Agriculture* **10**:63-84.

Tasing, K., Deo, C., Ramjan, M. D. and Semba, S. 2019. Assessment of genetic variability, heritability and genetic advance in Brinjal (*Solanum melongena* L.) Genotypes. *International Journal of Chemical Studies* **7**(5): 2452-2457.

Thakkar, J. R., Mandavia, M. K., Golakiya. B. A.and Sabara, P. H. 2014. Analysis of Genetic Diversity among Brinjal (*Solanum melongena* L.)Genotypes through dominant markers. *Indian Journal of Agricultural Biochemistry* **2 7** (2): 165-169.

Thamburaj, S., Singh, N. 2015. Text book of vegetables, Tuber crops and Spices. ICAR, New Dehli, pp.30.

Thangamani, C. and Jansirani, P.2014. Corelation and path coefficient analysis studies on yield and attributing traits in brinjal (*Solanum melongena*L.). *Electronic Journal of Plant Breeding* **3**(3): 939-944.

Thimmaiah, S. R. 1999. Standard Methods of Biochemical Analysis Kalyani Publishers New Dehli, pp. 534.

Tiwari, S. K., Karihaloo, J. L., Hameed, N. and Gaikwad, A. B. 2009. Molecular characterization of brinjal (*Solanum melongena*L) cultivars using RAPD and ISSR markers.*Journal of Plant Biochemistry and Biotechnology* **18**(2): 189-195.

Tümbilen,Y., Frary, A., Mutlu, S. andDoganlar, S. 2011.Genetic diversity in Turkish eggplant (*Solanum melongena*) varieties as determined by morphological and molecular analyses. *International Research Journal of Biotechnology* **2** (1): 16- 25.

Ullah, S., Ijaz, U., Shah T. I., Najeebullah, M. andNiaz, S. 2014.Association and Genetic Assessment in Brinjal.*European Journal of Biotechnology and Bioscience* **2**(5): 38-40.

Varshney, R. K., Chabane, K., Hendre, P. S., Aggarwal, R. K and. Graner, A.2007 Comparative assessment of EST-SSR, ESTSNP and AFLP markers for evaluation of genetic diversity and conservation of genetic resources using wild, cultivated and elite barleys, *Journal of Plant Sciences* **173**(6): 638-649.

Verma, M., Rathi, S., Munshi, A. D., Kumar, A., Arya, L., Bhat, K.V. and Kumar, L. 2012. Genetic diversity of Indian brinjal revealed by RAPD and SSR markers. *Indian Journal of Horticulture* **69**(4): 517-522.

Verma, P., Kushwaha, M. L. and Panchbhaiya. A. 2018. Studies on Variability, Heritability and Genetic Advance for Yield Attributing Traits in Brinjal (*Solanum melongena* L.) for Two Different Seasons. *International Journal of Current Microbiology and Applied Sciences* **7**(9): 1543-1552

Vindhya Rani, P., G. Subbi Reddy, M. Rajasekhar and Usharani, M. 2019. Genetic Divergence in Brinjal (*Solanum melongena* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences* **8**(7): 571-574.

Vinson, J. A., Hao, Y., Su, X. and Zubik, L.,1998. Phenol antioxidant quantity and quality in foods:vegetables. *Journal of Agricultural and Food Chemistry* **46**: 3630–3634.

Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research***20**: 557-585.

Yang, R.Y. 2006. Application of Antioxidant Activity Analytical Methods for Studies on Antioxidant Activities of Vegetables. Ph.D. Dissertation. Institute of Tropical Agriculture and International Cooperation of National Ping-tung University of Science and Technology, Taiwan.

Yang, X., Cheng, Y. F., Deng, C. Ma. Y., Wang, Z.W. and Chen, X.H. 2014. Comparative transcriptome analysis of eggplant (*Solanum melongena*L.) and turkey berry (*Solanum torvum*Sw.): phylogenomics and disease resistance analysis. *BMC Genomics* **15**(1):412.

Yuzbapyoglu, E., Ozcan, S. and Acik, L. 2006. Analysis of genetic relationships among Turkish Cultivars and breeding lines of Lens CulinatisMestile using RAPD markers *Genetic resources and Crop Evolution* **53**: 507-514.

Zhao, Z. and Moghadasian, M.H.2008. Chemistry, natural sources, dietary intake and pharmacokinetic properties of ferulic acid: A review. *Food Chemistry* **109**:691-702.

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C E R T I F I C A T E

Certified that all the corrections/amendments as suggested by External Examiner **Dr. Harish Vardhan Chowdhary** (Principal Scientist) Division of Vegetable Science, IARI, PUSA, New Delhi during Viva-Voce examination held on **09-06-2021** have been incorporated in the manuscript entitled **"Diversity studies in Brinjal (*Solanum melongena* L.) through Morphological, Molecular and Biochemical characterization"** submitted by **Mr. Nawaz Ahmad Ganie (Regd. No. MSH-2018-230).**

(Dr. Ajaz Ahmad Malik)
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