STUDIES ON INDUCTION OF FLOWER THROUGH GROWTH REGULATORS AND GENETIC DIVERSITY ANALYSIS BY MOLECULAR MARKERS IN BRINJAL (*Solanum melongena* L.)

THESIS

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KAUSHELENDRA PRATAP SINGH
Id. No. 3674

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Kaushelendra Pratap Singh

August, 2022 ***Author***

Dr. Bijendra Singh
Professor & Dean

Department of Horticulture
Sardar Vallabhbhai Patel
University of Agriculture and
Technology, Meerut – 250110
(U.P.), India

CERTIFICATE

This is to certify that the thesis entitled "**Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in Brinjal (*Solanum melongena* L.)**" submitted in partial fulfillment of the requirements for the degree of **Doctor of Philosophy** with major in **Horticulture** and minor in **Agricultural Biotechnology** of the College of Post-Graduate Studies, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut is a record of *bona fide* research carried out by **Mr. Kaushelendra Pratap Singh, Id. No. 3674**, undermy supervision and no part of the thesis has been submitted for the awardof any other degree or diploma.

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(Bijendra Singh)
Chairman
Advisory Committee

SARDAR VALLABHBHAI PATEL UNIVERSITY OF AGRICULTURE AND TECHNOLOGY, MEERUT – 250110 (U.P.), INDIA

CERTIFICATE

We, the undersigned, members of the Advisory Committee of **Mr. Kaushelendra Pratap Singh, Id. No. 3674**, a candidate for the degree of **Doctor of Philosophy** with major in **Horticulture** and minor in **Agricultural Biotechnology** agree that the thesis entitled **"Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in Brinjal (*Solanum melongena* L.)"** may be submitted by **Mr. Kaushelendra Pratap Singh** in partial fulfillment of the requirements for the degree.

(Bijendra Singh)
Chairman Advisory
Committee

(Satya Prakash)	**(L. K. Gangwar)**	**(R. S. Sengar)**	**(Vipin Kumar)**
Member	**Member**	**Member**	**Member**

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Cm	Centimeter	/	Per
Mm	Millimeter	etc.	And the rest
%	Percentage	No.	Number
e*t al.*	And others/ co – worker	@	At the rate of
Syn.	Synonymous	Viz.	Namely
^{0}C	Degree centigrade	Max.	Maximum
i.e.	That is	Min.	Minimum
SS	Sum of square	%	Percentage
SI. No.	Serial Number	Bp	Base pairs
MS	Mean sum of square	C:I	Chloroform : Isomyl Alcohal
SSEr	Error sum of square	CTAB	Cetyl trymethyl Ammonium Bromide
MSEr	Error Mean sum of square	EDTA	Ethylene-diamine-tetra acetic acid
SE(m)±	Standard error of mean	EtBr	Ethedium Bromide
DF	Degrees of Freedom	HCL	Hydrochloride acid
CD	Critical difference	Kb	Kilobase
ANOVA	Analysis of Variance	M	Molar (= gram molecular weight)

Fig.	Figure	mM	Milli molar (= mg molecular weight)
Mol	Gram molecular weight	ng	Nanogrm
OD	Optical Density	UV	Ultraviolet (light)
V/V	Volume by Volume	W/V	Weight by Volume
W/W	Weight by Weight	SSR	Simple sequence repeat
rpm	Revolution per minute	min	Minute

CHAPTER-1 INTRODUCTION

Vegetables comprise of a large number of plants, mostly annual, of which different parts like leaf, stem, flower bud, flower, fruit, root etc. are eaten. They are rich in nutrients and are essential items of a balanced diet. Vegetables are called protective food as their consumption can prevent several diseases. Many vegetables are important items of commerce and thus can play a major role in the economic development**. (S. Thamburaj and Narendra Singh 2001)**

Eggplant (*Solanum melongena* L. 2n=24) is a member of the Solanaceae, a large plant family comprising over 3000 species including important crops such as tomato (*Solanum lycopersicum* L.), potato (*Solanum tuberosum* L.), pepper (*Capsicum annuum* L.), and tobacco (*Nicotiana tabacum* L.). Eggplant is represented by three cultivated species: *S. macrocarpon* L. and *S. aethiopicum* L., which is indigenous to a vast area of Africa and is locally cultivated, and the world wide-cultivated *S. melongena* L. Unlike most of the other Solanaceae crops, which are native of the New World **(Fukuoka *et al.* 2010; Albert and Chang, 2014; Hirakawa *et al.* 2014)**, eggplant has a phylogenetic uniqueness, due to its exclusive Old-World origin **(Lester and Hasan, 1991)** located in Asia as a result of two/three separate domestication events **(Daunay and Hazra, 2012; Meyer *et al.* 2012; Cericola *et al.* 2013; Knapp *et al.* 2013).** Eggplant was introduced to the Mediterranean Basin **(Daunay, 2008)** and, at present, it is one of the most consumed vegetables in the world. During 2020-21 (2nd Advance Estimates), the area under Brinjal crop is estimated at 0.758 million hectares with a production of 13.154 million tons in India **(National Horticulture Board 2020-21).** Its global production is estimated to be around 52,309,119 Metric tons and is mainly concentrated in Asia (93% of both the world

production and harvested area), with China, India, Indonesia, Iran, representing the major producers. Egypt, Turkey, and Italy are the main producers of the Mediterranean countries **(FAO, 2017; http://faostat3.fao.org/ browse/Q/QC/E).**

Brinjal is considered as one of the top ten vegetables in terms of scavenging capacity. The major phenolic content present in fruit is responsible for the high oxygen radical scavenging capacity **(Cao *et al.* 1996)**

There is an increasing demand for its varieties for different culinary purpose. It is considered as brain food and poor man's caviar. The immature fruits is primarily used as cooked vegetable and utilized in the preparation of various dishes like sliced bhaji, stuffed curry, bertha, and chutney in different parts of the world. Brinjal has good nutritive value and contrary to the common belief, it is quite rich in nutrition and can be compared with tomato **(Choudhry, 1976).** It is an important source of carbohydrate (4.0 g), protein (1.4 g), fiber (1.3 g), vitamin A (124 IU), phosphorus (47 mg), potassium (2.0 mg) and iron (0.3 mg), per 100 g of edible portion and recommended for patients suffering from diabetes, asthma, cholera, bronchitis and it protects the brain cell membranes from damage. In Ayurveda, an Indian system of medicine, white fruited types are recommended for diabetic patients, and roots for the treatment of asthma **(Khan, 1979).**

The oblong fruited eggplant cultivars are rich in total soluble sugars, whereas the long fruited cultivars contain a higher content of free reducing sugars, anthocynin, phenols, glycoalkaloides, dry matter and amide proteins **(Bajaj *et al.* 1979).** High anthocynin content and low glycoalkaloides content are considered essential, regardless of how the fruit is to be used. Bitterness in eggplants of Solanaceae family. The glycoalkaloides contents in the Indian commercial cultivars vary from 0.37 mg/100g fresh weight to 4.83

mg **(Bajaj *et al.* 1981).** Generally, the high content of glycoalkaloides (20mg/100 g fresh weight), produce a bitter taste and off flavour. The discoloration in eggplant fruit is attributed to high polyphenol oxidase activity.

Eggplant is a photo-periodically inert plant with bisexual and partially self-pollinating flowers, although cross-pollination increases the effectiveness of fruit setting **(Pandit *et al.* 2010).**

The downward-facing flowers are born solitary or in clusters. The eggplant produces three types of flowers: With a long-style pistil, where the stigma is localized above the anthers; with a medium-style pistil, where the stigma is at the same level as the anthers; and with a short-style pistil, where the stigma is below the anthers. This flower character promotes outcrossing between morphs via delivery and uptake of pollen by pollinators **(Jagatheeswari, 2014 and Keller *et al*. 2014).** The stamen pores of the long- and medium-styled pistils are localized above or close to the stigma, favouring self-pollination. On the contrary, the stigmas of short-styled pistils are inside the downward-facing anther cone, making self-pollination difficult **(Glover *et al.* 2004, Karapanos *et al.* 2008 and Sekara *et al.* 2008)**

Brinjal is usually self pollinated, but extent of cross pollination has been reported to be as high as 48% and hence it is classified as often cross pollinated crop. **(Gobu *et al*. 2017)**. Flowering is the primary factor of any species which have direct relation with fruit yield. Keeping genetic, biotic and abiotic factors of flowering constant the yield will be directly proportion to the flowering. Maximum fruit set occurs in long and medium styled flower which are found approximately 50% in brinjal. Hence, PGR like GA_3 when applied

in brinjal more fruit setting was observed in pseudo short and medium styled flower in brinjal **(Krishnamurthi and Subramanian, 1954)**

Commercially eggplant is grown as an annual crop but it is a perennial herb. It can grow in soil ranging from light sand to heavy clay. The optimum pH for growth and development is 6.0-6.8 for optimum growth of brinjal, long and warm season are favorable. The most favorable temperature for optimum growth and yield is 13 to 21^{o}C. It is susceptible to insects such as stem and fruit borer, pests, root-knot nematodes, beetle, diseases such as wilt and temperature **(Singh, 2007).**

Beneficial effects of growth substances on fruit-set in brinjal have been reported by several workers. Application of 2, 4-D (2ppm) at flowering induces parthenocarpy, increases fruit-set, advances fruit maturation and significantly increases the total yield. A significant increase in yield (50%) was obtained by whole plant spray of 2, 4-D at 2 ppm at intervals of one week over a period of 60-70 days from commencement of flowering. Spraying of 2, 4-D (2.5 ppm), 4 CPA (20ppm) and n-metatolylphthalamic acid (0.5%) promotes fruit-set in brinjal. NAA (60ppm) alone or in combination with BA (30ppm) applied on open flowers improved fruit set and their development and spraying of n-metatolylphthalamic acid at 250-500ppm considerably increases the early yield. **(Textbook of Vegetables, Tuber crops and Spices)**

Experiments made by **Nothmann *et al.* (1983)** revealed that treating the eggplant flowers with 2,4-D at concentration of 2.5 mg·l-1 four times every 3 weeks considerably improved the fruit setting. Variety, flower structure, and localization within an inflorescence were important for fruit setting and seed formation processes. Percentage of

high-pistil flowers in total fruit setting was 90%. Although harmonization increased the fruit setting from low-pistil flowers four times as compared to the control, maximum fruit setting (8%) was still very poor. Fruits formed from so-called additional flowers were of worse quality than those from main flowers. (**Handique and Sarma, 1995)** applied NAA at 10 ppm concentration and observed the increase of high-pistil flowers number only at some varieties, whereas higher rates (25 ppm) significantly decreasing the number of low-pistil flowers at all tested varieties. Treating the eggplants with kinetins considerably decreased the number of low-pistil flowers; however, higher concentration (40 ppm) was more efficient for all varieties than 20 ppm rate. There is a hypothesis that hormones such as kinetins are more focused on female preferences, while Gibberellic acid favors male expression.

Molecular markers are the markers based on DNA sequences **(Bostein *et al.* 1980).** These markers provide a genetic diagnostic tool that permits direct identification of genotype in an environment independent manner in any tissue and at any developmental stage.

Molecular diversity reveals the germplasm evaluation for identification of diverse genotypes which can be utilized by breeders for creation of variation. Low number of availability of morphological markers and poor genetic control and influence of environmental stress on phenotypic expression creates limitation to use of these markers in selection programmes. Evaluation of genotypes on the basis of the molecular markers has recently attained great attention due to their stability and reliability and no fluctuation through environmental constraints. Now a day, SSR markers are used at majority levels due to its high level of polymorphism and reproducibility **(Varshney *et al.* 2005, 2009).**

The study of genetic diversity and relationships of collections of local genotypes provides information of relevance for the breeding programmed. DNA marker technology and molecular characterization are immensely helpful in selective breeding from diverse parents to widen the breeding gene pool **(Fu, 2006).** Several molecular studies **(Cericola *et al*. 2013; Prohens *et al*. 2005; Tumbilen *et al*. 2011)** have shown that eggplant cultivar groups are genetically diverse. SSR markers indicated a strong genetic affinity of eggplant (*Solanum viarum*, *Solanum melongena* and *Solanum aethiopicum*; *Aculeatum* group) and also assayed informative for the potential to serve as perfect markers for studying variation **(Adeniji *et al*. 2012).** Genetic diversity and relatedness may be informative for the varietal identification and genetic improvement of brinjal **(Sultana *et al*. 2018).** However, despite its widespread cultivation and nutritional and economic importance, the eggplant genome has not yet been extensively evaluated as for the other solanaceous vegetables such as tomato, potato and pepper, all of which have high density linkage maps **(Barchi *et al*. 2007; Jacobs *et al*. 2004).** Morphological, molecular and combined trait analyses consistently recognized the main groups of eggplants (cultivars and land races). It also exhibited higher variation compared to the landraces and cultivars. For eggplants landraces, morphological variability was moderately high but low diversity was observed on SSR and combined data analyses **(Caguiat and Hautea, 2014).** High degree of diversity of brinjal cultivars may be attributable to genetic improvement programme based on the molecular clustering patterns. It also provides support for selection of crossing combinations from parental genotypes and for broadening the genetic basis of breeding programs. The use of molecular markers in eggplant breeding has been limited compared to other relevant crops of the same family **(Barone *et al*. 2009; Jo *et al*. 2010; Danan *et***

***al*. 2006).** A number of SSR markers have been identified in Solanaceae **(Yi *et al*. 2006; Bindler *et al*. 2007),** but the numbers are less in eggplant. **Portis *et al*. (2018)** developed an "Eggplant Microsatellite DataBase" (EgMiDB) which permits identification of SSR markers in terms of their location on the genome, type of repeat (perfect vs. imperfect), motif type, sequence, repeat number and genomic/gene context. It also suggests forward and reverse primers and also employed an in-silico PCR analysis to validate these SSR markers, using as templates two CDS sets and three assembled transcriptomes obtained from diverse eggplant accessions.

SSRs or microsatellites are tandemly repeated short nucleotide units of 1 to 6 nucleotides. These repeats are multi-allelic in nature, co-dominant, relatively abundant, provide extensive genomi coverage with high resolution and easily detected by PCR using a small amount of genomic DNA as a template **(Stagel *et al*. 2008; Powell *et al*. 1996)** and can be located in genes (genic SSRs) or non-coding regions (genomic SSR) of the nuclear genome and also in cytoplasmic genomes **(Jones *et al*. 1997; Varshney *et al*. 2005).** In the nuclear genome, genomic SSRs are reported to be collected around particular regions of the chromosomes, such as centromeric areas **(Areshchenkova *et al*. 1999).** Both types of SSR markers are easy to apply and have a high level of polymorphism, which makes them ideal for mapping and diversity studies, fingerprinting, population genetics and map-based gene cloning **(Powell *et al*. 1996' Mohan *et al*. 1997; Jones *et al*. 1997).** More ever, once SSR primers have been designed, application of these markers is fairly inexpensive. Genomic SSRs for eggplant have been developed by **Nunone *et al*. (2003)** while **Stagel *et al*. (2008)** have developed genic SSRs, which they tested primarily on eggplant cultivars.

Keeping this point in view, the present investigations have been entitled "**Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in brinjal (*Solanum melangena* L.)"** with the following objectives.

1. To study the effect of plant growth regulators on flower induction in brinjal
2. To evaluate the brinjal genotype through morpho-physiological and antioxidant properties
3. To study the molecular profile of different brinjal genotype using molecular marker

CHAPTER-2 REVIEW OF LITERATURE

The updated relevant literature pertaining to different aspects of the present study to accumulate knowledge about the present investigation in brinjal has been reviewed in this chapter under following heads:

To study the effect of plant growth regulators on flower induction in brinjal

To evaluate the brinjal genotype through morpho-physiological and antioxidant properties

To study the molecular profile of different brinjal genotype using molecular marker

To study the effect of plant growth regulators on flower induction in brinjal

The role of plant growth regulators in various physiological and biological processes in plants is well known, which enables a rapid phenotypic change in the plant. Plant growth regulators are known to affect seed germination, vegetative growth, flowering, fruit development, fruit maturity and fruit yield. Further the physic-chemical properties of the crop are also influenced by plant growth regulators.

An attempt has been made to present the impact of plant growth regulators on plant morphological, physiological and yield parameters of brinjal. The literature on the use of growth regulators in brinjal is merge and hence the work on other closely related brinjal, chilli and tomato, there effect on morphological, physiological and yield attributes are considered to support the present investigation.

Jayaram and Neelakandan (2000) investigated the role of PGR such as, IAA, GA_3 and Ascorbic Acid (AA) at different concentration (10 ppm, 25 ppm and 50 ppm) on development of flowers in brinjal (*Solanum melongena* Linn.). He was observed that 25 ppm and 50ppm AA treated plants produced significant number of female flowers and same concentrations of IAA and GA_3 produced significant number of male flowers.

These finding help to alter the sex of brinjal flowers to femaleness and maleness by external application of AA, IAA and GA_3.

Lahshmi *et al.* (2006) studied the effect of nitrobenzene and other growth regulators on Brinjal under glass house for increasing the yield and flower sets. Foliar applications of nitrobenzene were carried out and 95 percent earliness along with 26 flower plant^{-1} out of which 12 fruit i.e. 46 % of the total flower were obtained.

M. D. Sharma (2006) reported that the effect of different PGR such as, NAA (40 ppm), GA_3(10 ppm), 2,4-D (2 ppm), ethephon (300 ppm), BAP (30 ppm) and triacontanol (5 ppm) by foliar spray on growth and yield of two varieties of brinjal (*Solanum melongena* Linn.). The finding concluded that the higher fruit yield is observed at NAA (40 ppm) in PPL variety and BAP (30 ppm) in PPC variety.

Moniruzzaman *et al.* (2014) noticed that the GA_3 (Gibberellic acid) and NAA had no significant effect on plant height and stem diameter at the end of the crop period and days to 100% flowering. NAA 40 ppm produced highest percentage of long and medium styled-flower, leaf photosynthesis, number of fruits/plant and fruit yield.

Netam and Sharma (2014) reported the role of different PGR on growth characters and yield attributes in brinjal (*Solanum melongena* L.). It was concluded that the combined application of GA3, NAA and 2,4-D @ 10 ppm, 20 ppm and 1 ppm of 2,4-D respectively had significantly affected the plant growth, flowering, quality and yield potential.

Ahmad *et al.* (2017) evaluate the influence of different plant growth promoters on growth and yield of JP-27 summer cherry tomato line. Four different growth promoters including control viz. F0= Control (Water), F1= Flora (Nitrobenzene 20% w/w) @ 2.5ml/L, F2= 4-CPA @ 2.5 ml/L and F3= GA_3 @ 200ppm was used. Maximum plant height, no. of leaves, no. of branches, days to first flower, no. of

flowers, no. of fruits, fruit length, single fruit weight, yield/plant and yield/ha were found in F3 treatment and maximum fruit diameter were found in F2.

Kohombange *et al.* (2017) reported that the effect of different concentration of nitrobenzene (15%, 20%, and 25%) as a foliar spray on bell pepper yield. The finding concluded that 25% nitrobenzene applied plants showed highest flowering, fruit setting, yield quality as well as postharvest performances as compared to other treatments under greenhouse condition.

Arivazhagan *et al.* (2018) experiment was carried out to study the effect of different plant growth regulators on growth and yield of brinjal cv. ANNAMALAI. Different concentrations viz., NAA (25, 50 and 100 ppm), GA_3 (50, 100 and 200 ppm) and ethrel (50, 100 and 200 ppm) has been taken. Highest total soluble solids and ascorbic acid content recorded in GA_3 @200 ppm treated fruits and GA_3 @ 50 ppm was found to produce best results in improving the growth and yield of brinjal cv. ANNAMALAI.

Jakhar *et al.* (2018) studied the impact of plant growth regulators on growth and yield of tomato. The researcher has taken three concentrations (25, 50 and 75 ppm) of each PGR viz., GA_3, NAA along with the control. Based on results, it was concluded that GA_3@50 ppm were found significantly superior to improve growth and yield of tomato.

Mukati *et al.* (2019) examine the role of different concentration of GA_3 on two varities of growth and yield of tomato. Different concentration of GA_3 viz., 12.5ppm, 25 ppm, 37.5 ppm, 50 ppm and 62.5 ppm were taken for experiment. It was observed that the application of GA_3 at 62.5 ppm shown superior result to other treatments.

Kropi and Amit Phonglosa (2020) assess the response of different Plant Growth Regulators on fruit yield of Brinjal. Different concentration (25, 50 and 100 ppm) of

each A_3, IAA and NAA were taken. The finding has concluded that GA_3 proved to be the best in improving the physiological and yield attributing parameters in brinjal.

To evaluate the brinjal genotype through morpho-physiological and antioxidant properties

Variability

The back bone of selection in any crop improvement programme used by numerous researchers is genetic variability. Genetic variability is the actual criteria of selection for variability in a population, whereas the phenotypic variability is a result of the interaction of genotype, environment and interaction between them. The "genetic coefficient of variation" single handily provides real picture of variability. The occurrence of "genetic variability" existing in a crop is of utmost relevance, as genetic diversity increases, the scope of selection also increased. **Frankel (1974)** stated the value of variability in the population of plant for achieving the most effective breeding programme.

Kumar *et al.* (2011) studied thirty-three genotypes of brinjal and establish high estimates of "genotypic coefficient of variance" and "phenotypic coefficient of variance" for per plant branches number, average wt. of fruit, and per plant fruits no. and per plant fruit yield.

Kumar and Arumugam (2013) examine variability in thirty-four brinjal genotypes which had higher values of "phenotypic coefficient of variance" and "genotypic coefficient of variance" for per unit no. of branches, fruit breadth, length of fruit, per unit no. of fruits, and per unit fruit yield.

Vidhya and Kumar (2015) studied thirty genotypes of brinjal for the eleven characters high significant differences in almost all traits were observed in study. "Genotypic coefficients of variations" and "phenotypic coefficients of variations" were

observed to be greatest for fruit girth. The large genetic advance and large heritability observed for fruit girth, weight of single fruit and per unit marketable yield.

Koundinya *et al.* (2017) studied forty genotypes of brinjal and various yield and yield governing traits and found highest "Phenotypic and Genotypic Co-efficient of variation" for per unit fruits number, weight of fruit, harvest index, per unit fruit yield, total phenols content and anthocyanin content in peel. Large "heritability coupled with high genetic advance as percent of mean" was found for traits such as "days to 1st flowering, days to 50% flowering, plant height, number of fruits per plant, 9 fruit weight, harvest index, fruit yield per plant, total sugar, anthocyanin in peel and total phenols" indicating that characters were under the influence of "additive gene action" and there for selection based on the basis of phenotypic performance of characters would be of great significance.

Sujin *et al.* (2017) investigated sixty brinjal genotypes for yield and tolerance to shoot and fruit borer. Great estimates of "genotypic coefficient of variance" were recorded for fruit yield, weight of fruit, secondary branches number and incidence of shoot and fruit borer. Great "phenotypic and genotypic coefficient of variation" was found for fruit yield, wt. of fruit and per plant secondary branches number suggesting greater genetic variability and selection of these traits will be effective.

Banerjee *et al.* (2018) observed great "genotypic coefficient of variation" for length of fruit, diameter of fruit, per plant fruits number, weight of fruit and per plant marketable yield. Length of fruit, fruit diameter, weight of fruit and per plant fruit number showed great "heritability, as well as great genetic advance as percent over mean

Jirankali *et al.* (2019) were considered high estimates of "phenotypic coefficient of variation and genotypic coefficient of variation", "high heritability coupled with high

genetic advance" were calculated for weight of fruit, number of fruits per cluster and shoot borer infestation.

Heritability and Genetic Advance Studies

For planning successful breeding program evidence on heritability estimates and genetic advance are quite necessary and this is an effective tool for predicting the genetic gain and can be found by selection of morphological characters. "Heritability 10 is the heritable part of phenotypic variance". It is of utmost importance for investigating the inheritance of traits from parents to their successors.

For evaluating genetic gain under selection another tool is extensively used which is called genetic advance. It is defined as "the enhancement in the mean genotypic value of the selected plants over the base population". Genetic variability, heritability and selection intensity are the factors which determine the success of the genetic advance. When heritability estimation is used in accord with genetic advance, the efficacy of heritability is increased.

Thangavel *et al.* (2011) showed that White Brinjal × Annamalai showed greatest values of "heritability and high genetic advance" for characters like height of plant, days to first flowering and fruit length. "High heritability and moderate genetic advance was shown by the trait like per plant branches number whereas, per plant fruit yield showed moderate "heritability with low genetic advance".

Solieman *et al.* (2012) recorded high standards of "heritability in broad sense" for the majority of the characters with a range of 73.51 to 97.91 per cent in black oval 12 genotypes of brinjal, 35.20 to 94.96 per cent in black long and 53.24 to 94.74 per cent in white long cultivars.

Kumar *et al.* (2013) evaluated high "heritability and genetic advance" for per plant branches number, length of fruit, fruit breadth, per plant fruits number, average wt. fruit and per plant fruit yield in brinjal.

Lokesh *et al.* (2013) studied 60 brinjal genotypes for 14 quantitative characters. "Genetic advance as per cent of mean" found to be high for height of plant, plant spread, average wt. of fruit and incidence of shoot and fruit borer. "High heritability coupled with high genetic advance" was calculated for plant height, plant spread, average fruit weight and incidence of shoot and fruit borer on shoot signifying that only selection will be operative to fix and improve such kinds of traits.

Chaudhary and Kumar (2014) observed high "heritability coupled with high genetic advance" for characters like fruit weight, fruit yield per plant, leaves per plant, fruit length, yield per plot, yield per hectare and total reducing sugar, suggesting that the characters were determined by "additive gene action".

Mili *et al.* (2014) observed high heritability for characters like per plant fruit yield, ratio of pulp to seed, height of plant, weight of single fruit and per plant fruits number and fruit diameter. High heritability associated with high genetic advance was calculated for per fruit seed yield, weight of single fruit, per plant fruits.

Sabolu *et al.* (2014) studied brinjal genotypes and recorded higher estimates of broad and narrow- sense heritability's in all the crosses for all the quality traits under the investigation but had least magnitude of dominance and environmental variances in genotypes of brinjal.

Akpan *et al.* (2016) studied ten accessions of brinjal and calculated high significant differences among various accessions for all traits under examination. "Broad sense heritability (h2bs)" was recorded high for per plant fruits number, fruit circumference and per hectare fruit yield during late planting and same trend was

obtained for early planting. Correlation analysis during early season exhibited that fruit yield had positive correlation with fruit 13 circumference and fruit diameter. Per plant fruits number showed significant and positive correlation with per plant branches number, per plant leaves number and height of plant.

Ravali *et al.* (2017) studied thirteen genotypes of brinjal and studied nineteen traits. The heritability studies exhibited that heritability were greater for the characters which were examined. Great "heritability coupled with high genetic advance" were found for the days for fifty percent flowering, number of flower cluster per plant, number of flower per cluster, number of fruit per cluster, number of fruits per plants, average fruit weight, fruit yield per plant and total phenol content as these governed by "additive genes" and thus selection can be utilized in improvement of traits.

Sujin *et al.* (2017) calculated sixty genotypes of brinjal and studied sixteen morphological traits of brinjal. The studies revealed that there were great heritability for all characters under study except days to first harvesting, number of short styled flowers and no. of primary branches per plant.

Koundinya *et al.* (2017) calculated 40 genotypes of brinjal and studied various yield and yield related traits. Heritability studies revealed that there exist great heritability coupled with great genetic advance as per cent of mean for the traits viz., plant height, days to first flowering, days to fifty per cent flowering, number of fruits per plant, fruit weight, harvest index, fruit yield per plant and total phenol content telling that these characters were under the influence of additive gene action and simple selection based on the phenotypic performance of these characters will be of great significance.

Correlation Studies

To develop the efficiency of selection the relative extent of relationship between pairs of characters is examined. The investigation of correlation gives us an idea about that the selection of one character will have the positive correlation with all the other positive correlated characters. Correlation coefficients must be significant between the yield and all other characters which will aid in improving the yield of the crop as they exhibit complex inheritance. Genotypic correlation 15 coefficient provides real association between two traits and used broadly in the process of selection **(Johnson *et al*. 1955).**

Thangamani and Jansirani (2012) find fruit yield to be "positive correlated" with traits such as "per plant branches number, percentage of long styled flowers, per plant fruits number, ascorbic acid content and fruit dry matter content". Negative significant correlation had been observed for yield with days to first flowering in brinjal genotypes under study.

Angadi *et al.* (2017) calculated "values" of "genotypic correlation coefficient" were superior than "phenotypic correlation coefficient" and significant and +ve correlation was shown for the fruit yield per plant with height of plant, per plant fruits number, length of fruit, per cent fruit set, seed weight of hundred seeds, per cluster fruits number and weight of fruit.

Chauhan *et al.* (2017) investigated correlation coefficient for 84 brinjal cultivars and exposed that the association of "per cluster flowers number, per cluster fruits number, average length of fruit and per plant fruits number with fruit yield and among them was positive and highly significant and these traits were recognized as yield components. The genetic improvement of fruit yield thus can be obtained by direct selection of these yield components. Path coefficient analysis identified that the characters viz., percentage of fruit set, weight of fruit, per plant fruits number, relative

length of style, per cluster flowers number and per cluster fruits number had high direct and correlation values."

Neha *et al.* (2017) revealed that there was positive genotypic correlation for per plant branches number, per cluster fruits number, per cluster flowers number and height of plant with fruit yield.

Koundinya *et al.* (2017) evaluated forty brinjal genotypes and studied various yield and yield related traits. "Genotypic and phenotypic correlation" was studied for seventeen morphological characters of brinjal for yield and fruit quality characters. genotypic correlation were found to be higher than the phenotypic correlation values for all characters. Fruit yield per plant exhibited highly positive significant correlation with per plant primary branches number, per plant fruits number, harvest index. Fruit yield showed negative correlation with days to first flowering, total sugars and total protein.

Tripathy *et al.* (2018) studied "character correlation and path analysis" in diverse brinjal genotypes for fourteen traits. The Genotypic correlation of fruit yield was found to be significantly positive with plant spread and these traits were described as yield components. On path analysis, found that fruit length was most essential determinative of yield. So, these characters must be given much importance in selection program of brinjal.

Yadav *et al.* (2018) studied correlation in brinjal with material thirty-two genotypes of two different groups (long purple and round purple) it was found that 20 genotypic correlation coefficient was similar in nature and larger in extent compared to repective "phenotypic correlation coefficient" values for most of the traits studied. Total fruit yield per plant showed "significant and positive correlation" with characters such as fruits per plant.

Path Coefficient Analysis Studies

"Path analysis" popularly used for studying the magnitude of "correlation" with yield and its governing parameters. **Wright (1921)** first of all developed the concept of path analysis, but it was **Deway and Lu in 1959** that used path analysis for better selection. It deals with characters which affect the final product may be directly or indirectly, told that each component exhibits "direct effect" towards yield and "indirect effect" through yield governing characters.

Path coefficient analysis are extensively utilized for enhancement of yield and therefore work done by numerous researcher for studying direct effects of yield governing traits were studied as under:

Arunkumar *et al.* (2013) path analyzed 31 genotypes and examined 8 characters of brinjal. Characters namely no. of fruit plant-1 and avg. weight of fruit possessed greater direct effect and serve as the essential criteria for enhancing the yield of brinjal.

Shende *et al.* (2014) proposed that "length of fruit", "number of fruit per cluster", "height of plant", "days to last picking", "average weight of fruit" and "number of fruits per plant" would serve as selection criteria for yield improvement of brinjal genotypes.

Siavkumar *et al.* (2016) also suggested that traits like fruit weight, per plant fruits number alongwith leaf width and plant height have significant positive association with yield of the brinjal.

Sujin *et al.* (2017) studied sixty brinjal genotypes and suggested that characters such as per plant of long styled flowers number, per plant of short styled flowers number, per plant fruits number, weight of fruit, days to first harvesting incidence of shoot and fruit borer had positive direct effect on yield per plant which were evident from the path coefficient analysis studies of the brinjal genotype.

Mangi *et al.* (2017) examined sixty genotypes for studying path analysis and character association they studied seventeen morphological characters of brinjal and suggested that path analysis had significant +ve interrelationship at genotypic level 23 for traits such as height of plant, leaf area, days to1st maturity of fruit, per cluster fruits no. and per plant yield had shown true coalition with yield. The apparent selection of such traits will be of great importance for enhancing total yield of the brinjal genotypes.

Neha *et al.* (2017) examined "forty genotypes" of brinjal and found "high +ve" direct influence of aubergine yield and was succeeded by per cluster of flower no. and per plant fruit yield on the other hand, length of peduncle contributed significant and -ve association with perplant branches no. Path analysis studies showed that no. of branches and fruits in one plant had high direct effect and per cluster flowers number had indirect effect via per plant branches number with per plant fruit yield.

Tripathy *et al.* (2018) studied eighteen diverse genotypes of brinjal for fourteen characters and the path analysis examination gives an idea that fruits length was most essential yield determining factor as it showed high direct effect and indirect effect on yield through per plant clusters number, height of plant and plant spread. Therefore, above mentioned traits must be given due consideration in designing effective breeding programme.

Kustagi *et al.* (2019) studied the path analysis in Brinjal (Solanum melongena L.). In C-I it was found that length of fruit (0.8351) and height of plant (0.1554) had highest direct positive effects on fruit yield. The direct effect of height of plant on fruit yield was mainly due to the indirect effects through length of fruit (0.3572) and fruit width (0.0246). In C-II fruit length (0.9324), per cluster fruit number (0.3028) and per plant fruits number (0.2544) exhibited highest direct positive effects on per plant fruit

yield. Direct effect shown by per cluster fruit no. on per plant fruit yield was mainly due to the indirect effects through fruit set per cent (0.0321).

Genetic Divergence Studies

Mahalanobis D2 statistics technique is based on multivariate analysis of quantitative traits, and is used for measuring genetic divergence. The degree of genetic diversity is find out between two populations for all characters under study. The Genetically divergent population categorized into different groups on clustering which enables parent's selection. The genetic diversity is compared with the geographic distribution of genotypes very often this exhibit parallelism.

This distance method has been extensively used in various crop plants for getting information on the available genetic diversity. The outcome of various studies using Mahalanobis D2 analysis is briefly reviewed as follow:

Patel *et al.* (2014) Thirty-five genotypes of brinjal were studied for genetic diversity. The genotypes were grouped into six clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. Cluster I was very large comprising of 30 genotypes.

Rahamn *et al.* (2014) studied hundred eggplant accessions and categorized them into eight diverse clusters. The "maximum inter- cluster distance" was found between II and VI cluster and minimum distance was between V and VII. The accessions falling in cluster no. II showed maximum intra-cluster divergence. Based on the mean performance accessions exhibiting sufficiently high yield were grouped in cluster IV, VI and VIII.

Khan and Singh (2015) evaluated one ninety-two genotypes of eggplant and grouped these genotypes into five different clusters. The highest "intra-cluster distance"

was found in cluster I and lowest in cluster V and highest inter-cluster value (18.031) was obtained between cluster II and V, and lowest between cluster I and III (2.869).

Chaitanya (2015) evaluated fifty-one brinjal lines for studying genetic divergence and classified them into 8 clusters. Geographical distribution and genetic diversity exhibits no association between them which was indicated by pattern of distribution of genotypes. The traits such as ascorbic acid content, average fruit weight and total number of fruits per plant were the characters that had maximum contribution towards total divergence.

Rekha and Celine (2015) evaluated twenty-seven round fruited brinjal accessions for various biometric character based on D2 statistical values, these accessions were grouped into five clusters. It was concluded that the maximum numbers of accessions were observed in cluster I and maximum intra cluster distance were obtained for cluster IV. The highest inter cluster distance was calculated for cluster II and V which means that these two clusters exhibit maximum genetic divergence and can be utilized in hybridization programmes to obtained the heterotic advantage.

Kumar *et al.* (2016) to studied the thirty-three brinjal genotypes from different geographical locations into 10 clusters. Cluster I contained the most genotypes (15) followed by cluster IX (5), cluster II (1), V (1), VII (1) and X (1). Inter-mating between genotypes of clusters I and IX would produce more desirable transgressive segregants for breeding.

Das and Das (2017) investigated the twenty-six brinjal genotypes into 11 clusters based on D 2 values. Cluster I and V contained maximum 4 genotypes each. On the basis of the cluster means, the important cluster was cluster IV for fruit circumstances, average fruit weight, marketable and total yield per plot. The result of cluster mean

clearly indicated that genotypes like UBB-8, Suphal-2, Green (Malda) and Black Beauty could be selected as parents for future hybridization programme. The genotypes from the cluster I, IV and IV could be selected for hybridization programme to produce highly heterotic genotypes as these were found to be most divergent with a number of desirable traits.

Nand *et al.* (2018) to studied "genetic divergence among 30 genotypes" which formed 6 distinct "clusters". Cluster III consisted of "maximum number of genotypes" (8)" followed by cluster I and VI" (5), while "cluster II", IV and V contained 4 "genotypes" each. "The highest intra cluster distance was recorded for cluster I followed by cluster II and the lowest intra-cluster distance was recorded for cluster V. However, the highest inter-cluster distance was observed between cluster IV and V.

Antioxidant properties

Brinjal is rich source of phenols and flavonoids, due to which ranks amongst top ten vegetables as far as antioxidant capacity is concerned **(Singh. 2009, Huang *et al*., 2004).** A human of health benefits of brinjal are reported, including scavenging of reactive oxygen species (antioxidant), ant-diabetic properties and its anticancer nature. These properties are directly attributed to its phenolic and anthocyanin content **(Akanitapichat *et al*., 2010).** Brinjal is great storehouse of vitamin and minerals **(Dias 2012).** Literature related to present study has been reviewed under below:

Bilal *et al.* (2009) were examine the total water soluble antioxidant activity and phenolic content on cultivars of eggplant (*Solanum melongena* L. Total water soluble antioxidant activity of the cultivars varied from 2664 to 8247 mmol Trolox/kg, a 3.1-fold difference and total phenolic contents ranging from 615 to 1376 mg/kg, a 2.2-fold difference were observed among different cultivars. The two traits were significantly

correlated and results of this study suggested that breeders can use the information to develop eggplant cultivars with high antioxidant activity.

P. Nisha *et al.* (2009) investigated the antioxidant potential of four different varieties of eggplant (long green, purple coloured big size, purple coloured moderate size and purple coloured small size). It was observed that extracts from purple colour small size eggplant fruit demonstrated better antioxidant activities than the other samples which may be attributed to the higher phenolic and anthocyanin content since a linear relation was observed between the TPC and the antioxidant parameters.

Jung *et al.* (2011) Evaluated the antioxidant activity of different parts i.e. calyx, leaf, peel, pulp, and stem of eggplant. The finding suggested that the calyx part of fruit had strong antioxidant activity

Li *et al.* (2012) investigated the total anthocyanin content in twelve highly pigmented vegetable including eggplant (Black Beauty variety) and they reported that the anthocyanin content was found to be 29.55 mg Cya-3-gluE/100g on dry weight basis.

Makhlouf *et al.* (2013) assayed antioxidants from the byproduct (peel) of eggplant (*Solanum melongena*) byusing three extraction solvents: 70% methanol, 70% ethanol and 70% acetone. For each solvent, content of total phenolics, flavonoids, tannins, and total anthocyanins were quantified. It was concluded that 70% methanol is the best solvent for the extraction of anthocyanins, whereas 70% acetone is the best solvent for the extraction of total phenolics, flavonoids and tannins and the phenolic extracts have shown the highest metal chelating activity.

Mishra *et al.* (2013) investigated the activity of Polyphenol oxidase (PPO) catalyses oxidation of phenolics on affecting post-cut browning in eight variety of eggplants. In fresh eggplant, browning was found to be dependent on both the phenolic

content and PPO specific activity, whereas, total phenolic content played a major role in browning of stored fruits. Interestingly, although browning index increased in stored eggplant fruits, PPO activity reduced in four out of eight cultivars studied. Phenolic level was found to increase in all these cultivars during storage. Although a significant level of homology was observed in PPO nucleotide and conceptually translated protein sequence, two cultivars, which displayed highest PPO specific activity, differed in the 38 amino acid stretch in the peptide region 301–338.

San Jose *et al.* (2013) investigated the diversity of composition in seven eggplant cultivars of occidental type (BBS118, CS16, Dourga, H11, IVIA371, LF3-24, Listada Clemente) and they reported Vitamin C content ranged between 2.91 and 6.54 mg/100g.

Kaur *et al.* (2014) conducted a study on 34 Indian eggplant genotypes belonging to four different group (8 wild, 4 green, 2 white and 20 purple) to evaluate the total phenolic content and they found values in the range of 22.00-234.00, 44.00-90.00, 50.00-56.00, 22.00-73.00 mg GAE/100g FW for wild, green, white and purple genotypes respectively.

Medina *et al.* (2014) investigated the nutritional and nutraceutical component of Chinese, Philippine, American, Hindu and Thai type of eggplant grown in Sinloa region of Mexico and thy reported the ascorbic acid content among the varieties ranged between 7.40 to 22.00 mg/100g with Hindu variety showing the highest vitamin C content.

Salerno *et al.* (2014) the aim of this study was to extract polyphenols from eggplant entire fruit, pulp, or skin, both fresh and dry, and compare results between conventional extraction and microwave-assisted extraction (MAE). The effects of time exposure (15, 30, 60, and 90 min) and solvent (water 100% or ethanol/water 50%) were

also evaluated. The highest amount of polyphenols was found in the extract obtained from dry peeled skin treated with 50% aqueous ethanol, irradiated with microwave; this extract contained also high quantity of flavonoids and showed good antioxidant activity expressed by its capacity to scavenge superoxide anion and to inhibit lipid peroxidation.

Tripathi *et al.* (2014) conducted a study on antioxidant and biochemical changes in round as well as long varieties of eggplant in Indo-Gangetic plains of Eastern Uttar Pradesh and they found that the total phenolic content in the round varieties ranged between 79.33-103.42 mg/100g and 84.32-95.18 mg/100g in long varieties with highest content Pusa Purple Round (103.42 mg/100g) and Pusa Purple Long (95.18 mg/100g).

Kandoliya *et al.* (2015) studied the antioxidant and nutritional components of fruit of six varieties of eggplant viz., JBGR-1, GOB-1, GBL-1, GBL-2, GBL-3 and GBH-2 grown in saurastra region and they recorded the Vitamin C content in the fruit ranging from 9.43-16, 75 mg/100g. The GBL-1 variety is having the highest content and GBH-2 is having the lowest content of Vitamin C.

Zambrano-Moreno *et al.* (2015) conducted a study in organically and conventionally grown eggplant to determine the levels of anthocyanins, polyphenols, and flavonoids and antioxidant capacity along with effect of three thermal preparation methods i.e., boiling, baking or steaming. The results showed anthocyanin content was greater in conventionally grown eggplant i.e., 97.95 mol TE/g FW. They concluded that the steamed eggplant contained higher anthocyanin levels as well as greater antioxidant capacity in comparison to fresh, boiled and baked fruit.

Ahmed *et al.* (2016) conducted a study on comparative phytochemical composition, antibacterial activity, cytotoxicity and antioxidant potentiality of seven commercial eggplant cultivars of Bangladesh and thy reported the phenolic content in the range 6.08 to 9.29 mg GAE/g among the eggplant cultivars.

Lo Scalzo *et al.* (2016) investigated the anthocyanin content of three eggplant genotype viz. 'Tunisina' (round violet pale purple) 'Buia' (oval, deep purple black) and 'L305' (long, deep purple) and the authors reported the contents in three genotypes as 41.00, 155.00 and 96.00 mg Del-3-glu/100g in 'Tunisina', 'Buia' and 'L305', respectively.

Nayanathara *et al.* (2016) in this study, five eggplants genotypes (violet nadan, long green, small round green, violet suphol and violet with white stripes) were evaluated for total phenolic activity, total flavonoid activity and anthocyanin activity. Finding concluded that Violet suphol has contained high total phenolic and flavonoid content had better anthocyanin value as compared to other varieties.

Uthumporn *et al.* (2016) investigated the antioxidant and physic-chemical properties of eggplant flour of four varieties (Chinese eggplant. Indian eggplant, White eggplant and Thailand eggplant) grown in Malaysia and they reported that the highest total phenolic content was shown by Indian type dried at 40 ^{o}C is 3545.80 mg GAE/100g while the lowest was shown by Thailand eggplant type dried at 50 ^{o}C (1184.30 mg GAE/100g).

Kumari *et al.* (2018) conducted a study on genotypic differences for anthocyanins in different parts of fifty genotypes of eggplant and they reported anthocyanin content in the peel is found to be in the range of 0.04-113.93 mg/100g in 2012 and 0.05-109.02 mg/100g in 2013. In the flesh the range is of 0.01-9.89 mg/100g in 2012 and range of 0.03-6.84 mg/100g in 2013. In 2012, the whole fruit contained anthocyanin in the range of 0.55-88.24 mg/100g while in 2013, the content was found in the range of 1.87-88.91 mg/100g.

Sharma *et al.* (2022) investigated the bioactive properties and enzymatic activities in twenty-three different long and round type eggplant genotypes to ascertain

their amenability for processable traits. This finding is concluded that the biochemical screening showed maximum phenolics content in Kashi Taru. Additionally, total flavonoids content varied from 1.86 (IVBHL-UT-6 and IVBHR-18) to 5.83 mg rutin equivalent/100 g fresh weight (IVBHL-UT-1). The total antioxidant capacity among different eggplant cultivars varied by about 1.3-fold

To study the molecular profile of different brinjal genotype using molecular marker

Molecular markers are the markers based on DNA sequences (Bostein *et al.* 1980). These markers provide a genetic diagnostic tool that permits direct identification of genotype in an environment independent manner in any tissue and at any developmental stage.

Molecular diversity reveals the germplasm evaluation for identification of diverse genotypes which can be utilized by breeders for creation of variation. Low number of availability of morphological markers and poor genetic control and influence of environmental stress on phenotypic expression creates limitation to use of these markers in selection programmes. Evaluation of genotypes on the basis of the molecular markers has recently attained great attention due to their stability and reliability and no fluctuation through environmental constraints. Now a day, SSR markers are used at majority levels due to its high level of polymorphism and reproducibility (Varshney *et al.* 2005, 2009).

Nunome *et al.* (2009) reported that they constructed simple sequence repeat (SSR) enriched genomic libraries in order to develop SSR markers, and sequenced more than 14000 colnes. On the basis of the segregating markers to 14 linkage map, and mapped the 236 segregating markers to 14 linkage groups. According to him the

markers should be a useful resource for qualitative and quantitative trait mapping and for marker assisted selection in eggplant breeding.

Bora (2010) conducted an experiment for the molecular diversity studies in seventeen genotypes of Solanum melongena and one line of *Solanum aethiopicuk* based on microsatellite (SSR) markers and revealed that the similarity coefficients among all the 18 genotypes ranged from 0.14 to 1.00. The Solanum aethiopicum showed least similarity with the Solanum melongena genotypes.

Demir *et al.* (2010) was carried out molecular characterization of eggplant genotypes collected from different geographical regions of Turkey using SSR markers. They found that number of alleles per microsatellite locus ranged from 2 to 10, with a total of 24 alleles with the amplification of five SSr loci. The greatest number of alleles was found at the *emf21H22* locus (10 alleles); followed by *emh11001* and *emf21C11* as five and four alleles, respectively. The average number of alleles per locus was 4,8.

Pritesh *et al.* (2010) employed twenty-three SSR primers to scan 25 tomato cultivars with determinate, indeterminate habit and different geographical location to determine genetic similarity, unraveling of genetic diversity and genetic relationship.

Awady *et al.* (2012) amplified 38 alleles of Tomato cultivars using SSR primers with scorable fragment sizes ranging from approximately 75 to 275 bp. 23 alleles were polymorphic thus revealing 60.5% of polymorphism. The genetic similarity estimated according to SSR data was scaled between 17.6 and 93.2%, suggesting the potential of SSR markers in discriminating among plants of close or distant genetic backgrounds. The genetic distance information obtained in this study might be useful to breeder for planning crosses among these cultivars.

Parmar *et al.* (2013) introduced a new SSR marker (TOM-144) which was deduced after evaluation of eight microsatellite loci amongst the twenty-one different

tomato cultivars. The marker selected was inherited and segregated in mendelian fashion as demonstrated in successive generation of a cross between H-24 x GT-2.

Saravanan *et al.* (2014) investigated 18 genotypes for studying its genetic diversity using five SSR markers. Observed high genetic diversity between the genotypes i.e., LE-150 and LE-22 and researcher suggested that SSR markers detected medium locus polymorphism among the 18 tomato genotypes, which could further be utilized in strengthening tomato breeding programme.

Singh *et al.* (2014) studied the twenty-four determinate and indeterminate cultivars of tomato with twenty SSR primers and four lycopene gene specific primers in order to determine genetic identities, genetic diversity and genetic relationship. Researcher suggested that the genetic distance information obtained in this study might be useful to breeder for planning the breeding programs.

Ansari *et al.* (2015) assessed the genetic diversity among 14 genotypes of *Solanum melongena* and *Solanum aethiopicum* by using 12, 16 and 12 polymorphic markers of SSR, ISSR and RAPD respectively. Researcher observed that forty markers of RAPD, ISSR and SSR detected a total of 57 unique/novel alleles with *aethiopicum* whereas 19 unique/novel alleles were generated in different genotypes of *melongena*. Each marker system individually as well as altogether exhibited least similarity coefficients of 0.24 to 0.29 between *aethiopicum* and *melongena* species of *Solanum* whereas higher order of similarity was observed within *melongena* group.

Mutegi *et al.* (2015) used 10 natural and 3 cultivated populations of wild brinjal (*Solanum insanum*= *Solanum melongena*) for analysis of genetic diversity, population structure and out crossing by using 14 SSR markers in South India. The rate of over cross varied from 5-33% in wild populations.

Zhou *et al.* (2015) used molecular markers to assess the genetic diversity of 29 cultivated tomatoes, 14 wild tomatoes and seven introgression lines. 15 polymorphic genomic SSR and 13 polymorphic EST-SSR markers used to identify the genetic diversity. It was observed that the polymorphism information content was slightly higher in genomic-SSR than in EST-SSR. The mean similarity coefficient among the wild tomatoes was lower than the mean similarity coefficient among the cultivated tomatoes.

Kumar *et al.* (2017) studied the diversity by using SSR markers to determine the distinctiveness of 30 Bhut Jolokia within the germplasm collected from different region of North East, India. Finding revealed 100 per cent polymorphism and polymorphic information content (PIC) ranging from 0.11to 0.37 has been observed.

Rongali *et al.* (2017) accessed thirty alleles were detected using twenty-two SSR primer pairs and Polymorphic Information Content (PIC) values ranged from 0.1491 to 0.5293 were observed. Researcher suggested that SSRs were able to differentiate exotic collections and commercially grown check varieties into different groups to some extent, indicating that SSRs is a more accurate and reliable method than RAPD to study the genetic diversity in brinjal.

Boureima *et al.* (2018) investigated the molecular characterization of forty-nine accessions collected from three climatic zones. Diversity accessed by using EST-SSRs molecular markers revealed moderate genetic variability within the collection, structured into three molecular groups. Indeed, 19 of the 29 markers tested were polymorphic. Expected heterozygosity (He) for the all collection ranged from 0.075 for smSSR41 marker to 0.507 for smSSR27 and smSSR35 markers. The Shannon diversity index (I), it ranged from 0.163 for smSSR41 marker to 1.307 for smSSR09 marker. It

was concluded the organization of this genetic diversity is weakly influenced by the climatic zone.

Pattanaik *et al.* (2018) accessed identify the SSR markers that could be used to test the hybrid purity of two commercial brinjal hybrids (viz., Arka Anand and Brinjal Asha) and to optimize the minimum sample size that can be used for purity assessment of the brinjal hybrids. Among 120 SSR markers studied, two markers were found to be suitable for testing the purity of these hybrids. The analysis of plant-to-plant variation within the parental lines of all the hybrids, using the identified hybrid specific markers, showed highly homogenous SSR profile, which further indicated the scope of application of these markers in maintenance and purity testing of hybrids and parental lines.

Sharmin *et al.* (2018) studied the molecular genetic diversity of 20 local chilli genotypes by using SSR markers. Result shown that total 10 alleles were detected for the five polymorphic SSR loci, with a mean of 2.00 alleles per primer. Gene diversity ranged from 0.333 to 1.00 with an average of 0.567. Polymorphic Information Content (PIC) values of the SSR primers ranged from 0.255 to 0.500 with an average value of 0.371. The similarity index matrix ranged from 0.00 to 1.000. Dendrogram indicated the segregation of 20 chilli genotypes into two main clusters. As per researcher SSR markers showed genetic variability in the studied pepper genotypes and they are powerful tools for estimating molecular diversity of chilli.

Ahmed *et al.* (2019) analysed genetic variability of 48 brinjal genotypes by Simple Sequence Repeat (SSR) markers. This is observed that the highest level of gene diversity value 0.8672 was observed in loci smSSR11 and the lowest level of gene diversity value 0.6580 was observed in the loci smSSR14 with a mean diversity of 0.7847. As a measure of the in formativeness of microsatellites, the PIC value ranges

from a low of 0.6413 (smSSR14) to a high of 0.8536 (smSSR11) and averaged 0.7660. The genetic distance (GD) between genotypes was computed from combined data for the four primers, ranging from 0.250 to 1.000.

Kaur *et al.* (2020) accessed twenty-six eggplant genotypes were characterized using seventy simple sequence repeat (SSR) markers. This research concluded that Out of 70 SSR markers used, 40 were polymorphic and 30 monomorphic. The average PIC value and number of alleles observed 0.50 and 2.55 per markers, respectively. Emi03K06 was most informative polymorphic marker on the basis of PIC values and number of alleles.

Khan *et al.* (2020) accessed the genetic diversity of Tomato (*Lycopersicon esculentum* Mill.) genotypes by using 30 Simple Sequence Repeats (SSR) markers based on fingerprinted. This finding found that all the genotypes of tomato showed genetic distances between range 1.0 - 2.20 and the most distant accessions were G7-1059 and G45-19212. Researcher suggested that the SSR marker-based fingerprints will assist for their future potential in crop improvement.

TG *et al.* (2020) examine the molecular diversity of Indian chilli genotypes were by using SSR markers. Researcher used 43 SSR marker and only nine has the polymorphism ranged from 2 to 16, and an average of 6.9 alleles in the locus, the Hpms1-1c marker recorded the highest alleles and the PIC rang varied between 0.28 to 0.89 by an average of 0.73. Cluster analysis of molecular diversity Shown that SSR markers grouped into 3 major clusters with 2 and 3 sub-clusters, and observed genetic variability for SSR markers revealed in the chilli genotypes.

Datta *et al.* (2022) accessed the genetic diversity among eggplant accessions collected from three countries by using SSR markers to determine suitable parents for heterotic hybridization. The estimation of genetic diversity among genotypes range

varied from 0.57 to 0.74 and average PIC value of 0.83 has been observed. This finding revealed that 77% total variation within the population from three different countries and 23% total variation among the populations. Researcher suggested high genetic differentiation among the eggplant germplasm while the accessions that are farther from each other show a high level of diversity.

CHAPTER-3 MATERIALS METHOD

All the experiments related to the study entitled **"Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in Brinjal (*Solanum melongena* L.)"** had been conducted carefully in a systematic manner under *in vivo* and laboratory conditions. The details regarding experimental site, climatic conditions during the study period, strategy applied, materials and methods adopted and statistical procedures followed in the experiment for experiments and data analysis are presented in this chapter.

EXPERIMENTAL SITE

The experiment was conducted at, Horticulture Research Centre (HRC), during *Rabi* season of 2020-21 and 2021-22, molecular work regarding the experiment was performed at Molecular Biology Laboratory (MBL), College of Agriculture, Department of Genetics & Plant Breeding, Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut U.P. India. Meerut comes under the semi-arid region and agro-climatic plain zone of Uttar Pradesh state and lies at North West Plain Zone, India, 28.99° N Latitude and 77.7° E Longitude with an altitude of 220 m above the mean sea level.

The outline of the methods and technical programme of different experiments has been described under the following heads:

METEOROLOGICAL DATA

Location Meerut comes under the semi-arid region and agro-climatic plain zone of Uttar Pradesh state. Geographically, it is situated between 29° 01 latitude in the North and 77° 43 longitudes in the Eastern elevation of about 219.75 m above MSL and represented North Western zones in India.

Season

The experiment was conducted during *Rabi,* 2020-21 and 2021-22.

Weather

Table 3.1: Mean weekly weather parameters for the period of experiment October 2020 to First week of April 2021

S.W.	Date	Temperature (^{0}C)		Relative humidity %		Rainfall (mm)
		Max.	Min.	Mor.	Eve.	
43	19 Oct. - 25 Oct.	33.00	16.10	85.40	45.10	0.00
44	26 Oct. - 01 Nov	31.00	13.40	81.60	43.70	0.00
45	02 Nov. - 08 Nov	28.40	11.30	83.40	45.30	0.00
46	9 Nov. - 15 Nov	27.60	9.90	84.30	44.40	1.30
47	16 Nov. - 22 Nov.	25.00	9.50	82.40	54.70	1.40
48	23 Nov. - 29 Nov.	25.80	8.40	83.90	45.70	0.00
49	30 Nov. - 06 Dec	26.30	7.90	85.00	45.00	0.00
50	07 Dec. - 13 Dec	22.90	6.40	85.60	49.90	5.90
51	14 Dec. - 20 Dec	20.30	6.00	87.40	51.30	0.00
52	21 Dec. - 27 Dec	18.70	4.90	92.10	54.40	0.20
1	28 Dec. - 03 Jan.	19.00	6.20	94.10	66.10	24.00
2	04 Jan. - 10 Jan.	18.80	5.70	94.90	63.60	0.00
3	11 Jan. - 17 Jan.	18.10	7.20	93.30	62.30	0.00
4	18 Jan. - 24 Jan.	18.80	6.50	90.00	57.30	0.00
5	25 Jan. - 31 Jan.	21.60	7.10	85.70	56.00	1.10
6	01 Feb. - 07 Feb.	23.90	7.70	86.00	55.30	5.60
7	08 Feb. - 14 Feb.	26.60	9.80	84.30	43.00	0.00
8	15 Feb. - 21 Feb.	29.40	12.00	83.30	40.40	0.00
9	22 Feb. - 28 Feb.	30.50	14.10	76.60	41.30	0.20
10	01 Mar. - 07 Mar.	32.30	14.50	72.60	35.40	0.00
11	08 Mar. - 14 Mar.	31.70	15.70	71.00	32.90	0.10
12	15 Mar. - 21 Mar.	33.00	16.60	75.60	38.00	0.00
13	22 Mar. - 28 Mar.	34.00	16.90	71.90	35.10	0.00
14	29 Mar. - 04 Apr.	35.10	17.80	48.60	26.60	0.00

Table 3.2: Mean weekly weather parameters for the period of experiment October 2021 to First week of April 2022

S.W.	Date	Temperature (^{0}C)		Relative humidity %		Rainfall (mm)
		Max.	Min.	Mor.	Eve.	
43	25 Oct. - 31 Oct.	30.94	18.00	69.86	49.57	12.60
44	01 Nov. 07 Nov.	30.06	14.86	72.00	50.14	0.00
45	08 Nov. - 14 Nov	28.73	12.86	76.86	48.00	0.00
46	15 Nov. - 21 Nov.	29.01	13.86	76.43	49.71	0.00
47	22 Nov. - 28 Nov.	28.11	11.00	80.57	46.86	0.00
48	29 Nov. - 05 Dec	26.76	9.71	81.57	46.29	0.00
49	06 Dec. - 12 Dec	23.07	11.64	84.29	48.14	0.90
50	13 Dec. - 19 Dec	22.40	9.36	83.43	39.43	0.00
51	20 Dec. - 26 Dec	20.74	7.17	82.43	38.43	0.00
52	27 Dec. - 02 Jan.	20.00	6.49	88.63	49.50	2.50
1	03 Jan. - 09 Jan.	20.60	7.50	84.60	61.10	9.90
2	10 Jan. - 16 Jan.	17.70	5.30	91.90	80.60	67.50
3	17 Jan. - 23 Jan.	16.20	4.70	92.60	71.10	3.70
4	24 Jan. - 30 Jan.	16.60	5.30	91.60	67.90	33.90
5	31 Jan. - 06 Feb.	20.10	6.00	88.60	67.00	18.40
6	07 Feb. - 13 Feb.	20.50	7.30	85.90	64.10	4.50
7	14 Feb. - 20 Feb.	24.30	8.30	82.60	57.40	0.00
8	21 Feb. - 27 Feb.	25.90	9.90	82.70	50.30	0.70
9	28 Feb. - 06 Mar.	26.00	10.50	88.60	53.10	31.50
10	07 Mar. - 13 Mar.	30.30	13.40	76.00	43.00	0.00
11	14 Mar. - 20 Mar.	34.20	17.10	71.10	39.60	0.00
12	21 Mar. - 27 Mar.	37.50	20.10	67.40	34.30	0.00
13	28 Mar. - 03 Apr.	38.70	20.30	58.90	28.40	0.00
14	04 Apr. - 10 Apr.	40.10	22.80	52.60	23.20	0.00

Technical programme: -

Design and layout of the experiment

The experiment was laid out in randomized block design (RBD) with three replications. The detail of experiment is given below broad outline of work and methodology.

Name of the experiment:

Studies on induction of flower through growth regulators and genetic diversity analysis by molecular marker in brinjal (*Solanum melangena* L.)

Planting material **:** 20 varieties

Spacing **:** 60 x 60 cm

Season **:** *Rabi* 2020-21 & *Rabi* 2021-22

Agronomic practice **:** Need based

Plant protection **:** Need based

Plant growth regulators: GA_3 **(50ppm)**, Nitrobenzene **(150ppm)**

PLANT MATERIAL

The details of all twenty brinjal genotypes included in the present study along with their sources are given in Table 3.2

METHODOLOGY

All the twenty accessions were evaluated during *Rabi* 2020-21 and 2021-22 at Horticultural Research Centre (HRC) in SVPUAT in Randomized Block Design (RBD) with three replications. Seedling were raised in pro-trays having 99 cavities with coco peat and vermicompost (2:1) under intensive care and with high survival percentage under college of horticulture shade net house during the month of September and transplanted in

the first week of October. Seedlings of each genotype were transplanted on 15cm raised ridges measuring 60×60 cm spacing between rows and 60×60 cm between plants. The recommended intercultural practices and recommended doses of fertilizers (RDF) were applied to ensure a healthy crop growth and development.

OBSERVATIONS FOR MORPHOLOGICAL CHARACTERS

Thirteen morphological traits of brinjal were recorded on four randomly selected plants in each of the accession per replication at appropriate growth stages. The mean values were utilized for statistical analysis.

Days to 50 per cent flowering:

This particular observation was recorded as day taken by plants after transplanting to the 50 percent plants from each treatment attained the flowering.

Plant height (cm):

Plant height was measured in cm. from ground level to the tip of the growing point of main shoot with the help of meter scale at the final harvest stage and the average plant height was calculated.

Stem diameter at harvesting:

Stem diameter was taken just above the soil surface with the help of digital verniar calipers in cm.

Number of primary branches per plant:

Four plant were randomly selected from each treatment and branches were counted, average was calculated by addition of branches from all four selected plant and dividing them with their numbers i.e. (Four).

Plant spread (cm):

The spread of the plant in East -West and North -South directions were measured and recorded in centimeters and the spread is expressed in square centimeters.

Flowers per plants:

The number of flower were counted day from the first flower emergence to the last harvesting of fruit.

Number of Flowers attained the fruits:

Fruit attainments from flower were counted from shedding of petals to the fruit emergence from the peduncle.

Length of fruit (cm):

The length of fruit was measured by using a digital vernier caliper of four randomly selected fruits and the averages fruit length (cm) was calculated**.**

Diameter of fruit (cm):

The width of fruit was recorded in cm with help of digital vernier calipers.

Average fruit weight (gm):

The weight of four randomly selected fruits was measured on digital electric balance and average fruit weight was calculated in gram.

Number of fruit per plant:

Number of fruit per plant harvested at each picking were recorded and added together after final harvesting of fruits which was recorded as number of fruits per plant among the selected plants.

Fruit index:

Fruit index was simply calculated by multiplying the length of fruit with diameter of the fruit.

Yield per plant (gm):

Yield per plant was calculated by multiplying the average number of fruit from each plant with the average fruit weight of the corresponding variety in grams.

Growth regulator treatment:-

GA_3 and Nitrobenzene growth promoters were sprayed with 50ppm and 150ppm concentrations respectively, both the PGRs ware applied together in two attempts before the flowering. First spry was carried out on 25th day after transplanting followed by the second on 15 days later from the first spry.

Table 3.2: List of 20 brinjal genotypes used for the present study:-

S.No.	Genotype	Source	S.No.	Genotype	Source
1	SVT-9	CSA, Kanpur	**11**	EG-01-03-02	IIVR, Varanasi
2	Azad Kranti	IIVR, Varanasi	**12**	PR-5	IIVR, Varanasi
3	SVT-4	CSA, Kanpur	**13**	Pant Samrat	IIVR, Varanasi
4	SVT-11	CSA, Kanpur	**14**	Pusa Ankur	IIVR, Varanasi
5	SVT-3	CSA, Kanpur	**15**	Swamani	IIVR, Varanasi
6	SVT-1	CSA, Kanpur	**16**	Pusa Shyamla	IIVR,

					Varanasi
7	B-3-L	IIVR, Varanasi	**17**	SVT-2	CSA, Kanpur
8	KS-224	IIVR, Varanasi	**18**	SVT-12	CSA, Kanpur
9	SVT-6	CSA, Kanpur	**19**	Kashi Taru	IIVR, Varanasi
10	AB-1	IIVR, Varanasi	**20**	Pant Rituraj	IIVR, Varanasi

STATISTICAL ANALYSIS

The observations recorded were subjected to statistical scrutiny. The results of the following parameters were analyzed. The following statistical procedure were followed in the present investigation

Analysis of variance

Variability, Heritability and Genetic Advance

Correlation coefficient analysis

Path coefficient analysis

Genetic divergence

3.7.1 ANALYSIS OF VARIANCE (ANOVA)

ANOVA was worked out for all the characters by making use of means of replication, as suggested by **Goulden (1959)** and the ANOVA table is presented below.

Source of variation	**Degrees of freedom**	**Mean squares**	**F ratio**

Replication	(r-1)	MSr	MSr/MSe
Genotype	(t-1)	MSt	MSt/MSe
Error	(r-1)(t-1)	MSe	

r = Number of replications, t = Number of treatments

MSr = Replication mean square, MSt = Treatment mean square

MSe = Error mean square

The test of significance was worked out by referring to the standard 'F' table suggested by **Snedecor (1967).**

VARIABILITY, HERITABILITY, GENETIC ADVANCE AND GENETIC ADVANCE AS PERCENT MEAN

Phenotypic and genotypic variances

Phenotypic and genotypic variances were estimated according to the formula given by **Lush (1940).**

a) Genotypic variance ($\sigma^2 g$) = $\frac{MS1 - MS2}{r}$

Where, MS_1 = Mean sum of squares for genotypes.

MS_2 = Mean sum of squares for error or error variance,

r = Number of replications.

b) Phenotypic variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Where, $\sigma^2 g$ = Genotypic variance.

$\sigma^2 e$ = Error variance.

Phenotypic coefficient of variation and genotypic coefficient of variation

The Phenotypic and Genotypic Coefficient of Variations were worked out as per the methods suggested by **Burton (1952).**

$$\text{Phenotypic coefficient of variation} = \frac{\sqrt{\sigma^2 p}}{\text{General mean}} \times 100$$

$$\text{Genotypic coefficient of variation} = \frac{\sqrt{\sigma^2 g}}{\text{General mean}} \times 100$$

$$\text{Environmental coefficient of variation} = \frac{\sqrt{\sigma^2 e}}{\text{General mean}} \times 100$$

PCV and GCV were classified as noted below and suggested by **Sivasubramaniam and Menon (1973).**

GCV and PCV	Category
Less than 10 %	Low
10-20 %	Moderate
More than 20 %	High

Heritability (h^2)

Heritability in the broad sense (h^2) was estimated based on the formula proposed by **Lush (1940)** and expressed in per cent.

$$\text{Heritability},(h^2) = \frac{(\sigma 2g)}{(\sigma 2p)} \times 100$$

Where, ($\sigma^2 g$) - Genotypic Variance

($\sigma^2 p$) - Phenotypic Variance

As suggested by **Johnson *et al.* (1955)**, heritability values are categorized as follows:

Heritability	Category
Less than 30 %	Low
30 – 60 %	Moderate
More than 60 %	High

Genetic advance and Genetic advance as percent mean

Genetic advance was estimated by the following formula as per the method suggested by **Johnson *et al*. (1955).**

$$\text{Genetic advance} = \frac{\sigma^2 g}{\sqrt{\sigma^2 p}} \text{ x k}$$

Where,

$\sigma^2 g$ - Genotypic variance,

$\sigma^2 p$ - Phenotypic standard deviation

K - Selection differential, the value of which is 2.06 at 5% selection intensity

$$\text{Genetic advance as per cent of mean} = \frac{\text{GA}}{\text{General mean}} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by **Johnson *et al*. (1955)**

Genetic advance	Category
0-10	Low
10-20	Moderate
> 20	High

ASSOCIATION ANALYSIS

Correlation coefficient

Genotypic and Phenotypic correlation co efficient for yield and other traits were computed using the method given by **Johnson *et al*. (1955).**

Genotypic correlation coefficient

$$rg\,(xy) = \frac{GCOV(xy)}{\sqrt{\sigma^2 g\,x\,x\,\sigma^2 g\,y}}$$

Where,

$r_g\,(xy)$ = Genotypic correlation coefficient between the traits x and y

GCOV(xy) = Genotypic covariance between the traits 'x'and 'y

$\sigma^2 g_x$ = Genotypic variance of the trait – 'x'

$\sigma^2 g_y$ = Genotypic variance of the trait – 'y'

Phenotypic correlation coefficient

$$r_p\,(x, y) = \frac{PCOV(xy)}{\sqrt{\sigma^2 p_x \times \sigma^2 p_y}}$$

Where,

$r_p\,(xy)$ = Phenotypic correlation coefficient between the traits 'x' and 'y'

PCOV(xy) = Phenotypic covariance between the traits 'x' and 'y'

$\sigma^2 p_x$ = Phenotypic variance of the trait 'x'

$\sigma^2 p_y$ = Phenotypic variance of the trait 'y'

The significance of the phenotypic and genotypic correlation co efficient was tested by referring the standard table given by **Panse and Sukhatme, 1967**.

PATH COEFFICIENT

Path coefficient analysis was suggested by **Wright (1921),** and illustrated and carried out separately by **Dewey and Lu (1959)** to know the direct and indirect effects of the important component traits on total yield per plant. Standard path coefficients, which

are the standardised partial regression coefficients were obtained by solving the following set of 'P' simultaneous equations through 'Doolittle technique' as given by **Goulden (1959).**

$P_{01} + P_{02}\, r_{12} + \ldots\ \ldots\ \ldots + P_{op}\, r_{1p} = r_{01}$

$P_{01}\, r_{12} + P_{02} + \ldots\ \ldots\ \ldots + P_{op}\, r_{2p} = r_{02}$

$P_{op}\, r_{1p} + P_{02}\, r_{2p} + \ldots\ \ldots\ \ldots + P_{op} = r_{op}$

where, P_{01}, P_{02} … P_{op} are the direct path effects of 1, 2, …, P variable on zero variables and r_{12}, r_{13}, …, r_{1p} $r_p(P\text{-}1)$ are the possible coefficients between dependent variable and independent variables and r_{01}, r_{02}, …, r_{op} are the correlation coefficients between dependent variables and independent variables. The indirect effect of i^{th} variable on dependent character through j^{th} variable was worked out (P_{oj} x r_{ij}).

The contribution of the remaining unknown was measured as the residual factor and calculated as given below:

$$P^2_{ox} = 1 - (P^2_{01} + 2P_{01}\, P_{02}\, r_{12} + 2P_{01}\, P_{03}\, r13 + \ldots + P^2_{02} + 2P_{02}\, P_{03}\, r_{23} + \ldots + P^2_{OP})$$

Residual factor (R) = $\sqrt{P^2 ox}$

The path coefficients were ranked on the scales given below **(Lenka** and **Misra, 1973).**

Negligible	:	0.00 to 0.09
Low	:	0.10 to 0.19
Moderate	:	0.20 to 0.29
High	:	0.30 to 0.99
Very high	:	> 1.00

(f) Contribution of individual characters towards divergence

In all the combinations, each character was ranked on the basis of (y_i^1 - y_i^2). Rank one was given to the highest mean difference and the rank 'p' to the lowest mean difference where 'p' is the total number of characters. The number of times appearing first in ranking for each character was counted and the per cent contribution was calculated taking the total number of combinations as hundred.

Antioxidant properties of different Brinjal Genotypes: -

The present study was conducted on the brinjal genotypes for their phenolic compounds, and antioxidant activities. A significant difference was found among the 20 different genotypes in terms of Total phenol, anthocyanin content, polyphenol oxidase and Total ascorbic acid content the result so obtained are presented under this section as follow: -

Estimation of total phenols

Determination of total phenolic content For determination of total phenolic content 0.5 g of moisture free sample were extracted with 10 ml of 80% ethanol and centrifuged at 10,000 rpm for 20 minutes. The extraction was done twice and the supernatant was collected together and evaporated to dryness. The residue was dissolved in a known amount of distil water (20 ml) and used for further analysis. Folin-Ciocalteau assay with slight modification by Slinkard and Singleton (1997) was used to determine the total phenolic content of eggplant extract. For the analysis, 20 µl of each of extract and gallic acid standard were taken in different test tubes and volume was made up to 2 ml with distilled water. 100 µl of Folin-Ciocalteau reagent (1N) was added to each tube and kept for 8 minutes, and then 300 µl of sodium carbonate was added and mixed well by using

vortex mixture. A blank was also prepared in the same way. The contents were allowed to incubate in dark for 30 minutes at 40°C. The absorbance was recorded at 765 nm. The phenolic content in the sample was expressed in mg GAE/100g of sample on dry weight basis

Extraction & estimation of anthocynin

Anthocyanin content was determined by using the method described by Abdel-Aal and Hucl (1999). For determining the anthocyanin content in eggplant 3 g of fresh sample was extracted by centrifuge using 50 ml of extraction solvent (Ethanol and HCl 1.0 N, 85:15 v/v). Then the solution was adjusted to pH 1 with 4 N HCl, shaken and readjusted to pH 1 if necessary, and shaken for additional 15 minutes. The mixture was centrifuged at 12000 rpm for 15 minutes and the supernatant was poured in 50 mL 31 volumetric flask and made up to volume with acidified ethanol. Absorbance was measured at 535 nm against a reagent blank. Cyanidin-3-glucoside was used as standard pigment. A series of cyanidin 3-glucoside standard solutions was prepared at 0–0.02 mmol (0–27 µg/3 mL). Absorbance was read at 535 nm against a reagent blank. The concentrations showed a linear relationship against absorbance. The total anthocyanin content was calculated in terms of cyanidin-3-O-glucoside (Cya-3-Glu). The concentration was calculated by using the following formula-

C (mg/kg) = (A/ε) × (vol/1,000) ×MW× (1/sample weight) ×106

Where, A= absorbance reading

ε= molar absorptivity (25,965 cm-1 M -1 for cyanidin-3-O-glucoside)

Vol. = total volume of anthocyanin extract

MW= molecular weight of cyanidin-3-glucoside

Extraction and assay of polyphenol oxidase (Zauberman *et* al 1991) Reaction

A) Extraction

Fruit part (200 mg) was extracted with 1.5 ml of 100mM sodium phosphate buffer (pH 6.8) using pre-chilled pestle and mortar. Homogenate was centrifuged at 4°C for 20 min and the clear supernatant was used for enzyme assay.

Reagents

i) 0.1 M sodium phosphate buffer (pH 6.8)

ii) 100 mM 4-methylcatechol

Assay

To the spectrophotometric cuvette, 1.3 ml of 100 mM phophate buffer (pH 6.8), 0.5 ml of 100 mM 4-methylcatechol and 0.2 ml of enzyme extract was added. Absorbance was recorded at 420 nm in a spectrophotometer at an interval of 1 minute upto 3 min. One unit of enzyme activity has been defined as increase of 0.01 in absorbance. Polyphenol oxidase activity was expressed as units min-1 g -1 of FW.

Estimation of ascorbic acid

Vitamin C content was determined by using method given in AOAC (1970). For determination of ascorbic acid 5 g of fresh sample was taken and extracted with 100 ml of 4% oxalic acid and centrifuged. To standardize dye, standard ascorbic acid was titrated against with 2,6-dichlorophenol indophenol dye and the value was recorded as titter value, which gives the dye factor. Then 5 ml of sample aliquot of the supernatant was taken and 10 ml of 4% oxalic acid was added and it was titrated against the 2,6-dichlorophenol indophenol dye until it gives a pink colour which persists for at least 15 seconds.

$$\text{Mg of Ascorbic acid per 100g} = \frac{\text{X (mg)} \times \text{V2} \times \text{volume made up (ml)} \times 100}{\text{Aliquot taken} \times \text{dye factor (V1)} \times \text{wt.of sample (g)}}$$

Where,

X = mg of standard ascorbic acid

V2 = titter value of sample against dye

The estimation of ascorbic acid was done in triplicate for each sample and the mean of them was recorded as mg per 100g of fresh sample.

MOLECULAR CHARACTERIZATION

The general chemicals used during this study were purchased from Bangalore Genie, Qualigens (India), Merck (Germany), Himedia and Imperial (IDT). The specific chemicals used for PCR i.e. Taq. Polymerase, Taq Buffer, dNTPs and $MgCl_2$ were obtained from Hi Media, Mumbai. The primers used for molecular profiling were synthesized by Macflow Engineering Pvt. Ltd.

Isolation of Genomic DNA

Isolation of DNA was done based on modified protocol of CTAB (Cetyl-Trimethyl-Ammonium Bromide) by **Doyle** and **Doyle (1987)**

3.8.1.1 Reagents and Chemicals Used

Reagent / Chemical	Specifications	Manufacturer
Liquid Nitrogen		
Agarose	Molecular Biology Grade	Himedia
CTAB powder	High Purity	Himedia
NaCl	High Purity	Himedia
Tris Base	Molecular Biology	Himedia
EDTA	Ultra-Pure Grade	Himedia
2- β Mercaptoethanol	Molecular Biology Grade	Himedia
Chloroform	Molecular Biology Grade	Himedia
Isoamyl alcohol	Analytical Grade	SRL

Isopropanol	Molecular Biology Grade	SRL
RNase - (10 mg/ml)	-	
Proteinase - (10 mg/ml)	-	
Ethanol	Analytical Grade	

Preparation of stock solutions

TrisHCl [1 M] (pH 8.0) 100 ml

15.76 g of TrisHCl was dissolve in 80 ml of distilled water. Its pH was adjusted to 8.0 with 0.1N HCl and volume was made up to 100 ml. Autoclaved and stored at room temperature.

EDTA [0.5 M] (pH 8.0) 100 ml

18.6 g of Ethylene diamine tetra acetic acid, disodium salt (EDTA Na_2) was dissolved in 80 ml of distilled water, pH was adjusted to 8.0 by adding 0.1N NaOH and it was mixed vigorously on magnetic stirrer to ensure that all the solutes were dissolved (Note that EDTA Na_2 will not dissolve completely in distilled water in the absence of NaOH). The final volume was made up to 100 ml, autoclaved and stored at room temperature.

NaCl [5 M] 100 ml

29.22 g of NaCl was dissolved in 80 ml of distilled water. NaCl was dissolved in distilled water properly and volume was made up to 100 ml. Autoclaved and stored at room temperature.

CTAB extraction buffer 10 X (pH 8.0) 500 ml

CTAB extraction buffer was prepared with a final concentration of CTAB 2.0 %, NaCl 1.4 M, Trisbuffer 100m M, EDTA 20mM, β-Mercaptoethanol 0.2 %. To prepare 500 ml extraction buffer add 10.0 g of CTAB, 43.837 g of NaCl, 50 ml TrisHCl from stock of 100mM, 125 ml of EDTA from stock of 20 mM, .03 ml β-Mercaptoethanol in 15 ml of

buffer (just before use) and 0.15 g of PVP in 15 ml of buffer (just before use) and adjust the pH to 8 and made the volume up to 500 ml. Autoclaved and stored at room temperature.

TE buffer (pH 8.0) 100 ml

1.0 ml of 1M TrisHCl and 0.2 ml of 0.5M EDTA were added in 98.8 ml of double distilled water from stock solution and made the final concentration of 0.05 M and 0.01 M, respectively.

Chloroform: Iso-amyl alcohol

Chloroform and Isoamylalcohol were mixed in the ratio of 24:1 and stored in a brown bottle. Vapour of Isoamyl alcohol is poisonous, so care should be taken.

RNase A (10 mg/ml)

10 mg RNase A was taken & dissolved in 1 ml of double distilled water. Dispensed into aliquots and stored at- 20°C.

Ethanol 70 %

70 ml of ethanol was mixed with 30 ml of distilled water and stored in a tight capped bottle.

Collection of leaf samples for DNA extraction

Premature leaves were collected from all plants during 2022, *Rabi* season. Then, leaf samples were packed into sterilized plastic poly-bags and stored at -40^{o}C in deep freezer for the purpose of isolation of genomic DNA.

DNA extraction and purification procedure

Principle

CTAB is a cationic detergent, which solubilizes membranes and forms a complex with DNA. After cell disruption and incubation with hot CTAB isolation buffer, proteins are extracted by chloroform: isoamyl alcohol. CTAB-DNA complex is precipitated with isopropanol. The DNA pellet resulting after centrifugation was washed, dried and re-dissolved. *RNase* treatment removes RNA and some polysaccharides.

Protocol

1. 200 mg frozen leaves of each brinjal genotype were taken and crushed in liquid nitrogen using mortar and pestle. Powdered leaves were transferred into centrifuge tube, and 1 ml of pre-warmed (65°C) extraction buffer was added to it. The samples were homogenized well by inverting the tubes several times.
2. The centrifuge tubes containing the samples were incubated for 1 hour in a shaking water bath at 65°C.
3. After which the tubes were cooled at room temperature and 1 ml of chloroform: iso-amyl alcohol (24:1) was added and mixed gently and properly by inverting centrifuge tubes for about 15-20 minutes.
4. Samples were centrifuged at 10,000 rpm for 10 minute at 5°C temperature.
5. After centrifugation, add 170µl NaCl and 500µl Isopropanol and put overnight the samples at 4° C temperature.
6. Next day samples were centrifuged at 12000 rpm for 15 minutes at 5° C temperature.
7. After centrifugation, discard the supernatant without disturbing the pellet and subsequently wash with 100 µl ice cold 70% ethanol and centrifuge at 6000 rpm for 5 minutes at 4° C temperature.
8. Decant the ethanol. Remove residual ethanol by drying in a Speed Vac.

9. Dry the pellet long enough to remove alcohol, but without completely drying the DNA. Dissolve DNA in 50 µl TE buffer (10 mM Tris, pH 8, 1 mM EDTA). The pellet may need warming in order to dissolve.
10. Finally, pellet was re-suspended in 50 µl of TE buffer and stored at 4°C for immediate use. However, for long term storage double volume of absolute ethanol was added and stored in -80^{0}C.

Quantification of Genomic DNA

Quantification by Spectrophotometer

The genomic DNA dissolved in TE buffer was used for quantification by Ultra Violet (UV) absorbance at 260 nm. To measure the concentration, BIO RAD Smart tech spectrophotometer was used. Reference was set against TE and then after thorough rinsing of quartz cuvette, the absorbance of the sample was measured at 260 nm and 280 nm. The ratio of Optical Density (OD) 260/280 provides estimate of nucleic acid purity. According to standard, properly purified DNA sample has the ratio between1.8 - 2.0 and the concentration in µg/ml was calculated as 1 OD at 260 nm is equivalent to 50 µg/ml of double stranded DNA **(Sambrook *et al.,* 1989)**.

If, DNA sample is free of contamination from protein, phenol, or RNA, its concentration can be measured accurately by determination of the amount of UV radiation that is absorbed by the bases present in an aliquot of the sample.

Procedure for DNA quantification by Spectrophotometer

1. Make sure that the spectrophotometer's UV light source has been turned on and allow it to warm up for at least 10 minutes before using.
2. Pipette 3000 µl of TE into cuvette (path length: 10mm) to be used.

3. Set spectrophotometer for DNA measurement, then wavelength to be measured for 260 nm and 280 nm. Follow instructions in the instrument manual. Insert cuvette.
4. Zero spectrophotometer using cuvette containing TE as a blank, then set reference.
5. Remove TE from blank cuvette with a Pasteur pipette.
6. Pipette 3ul of each sample into different 200µl PCR tube.
7. Pipette 3 ml of TE into 4 ml cuvette and 3µl of sample was added. Mix solution by pipetting up and down.
8. Cuvette containing the sample was into the spectrophotometer, OD260 and OD280 of each sample was recorded.
9. Cuvette was rinsing using double distilled water several times or rinsing with cuvette washing device. Replace cuvette in holder. The same process was repeated to record all samples' OD.

DNA concentration calculations

For calculation of DNA concentration of samples free of RNA, the following conversion factor was used:

OD260 = 50 mg of DNA/ml.

A. DNA concentration in mg/ml was calculated as follows

$$\text{mg DNA/ml} = \frac{\text{OD260 x 50 mg DNA/ml x Dilution Factor}}{\text{1000 ml/ml}}$$

With a dilution factor of 25 (i.e., 2 ml in 48 ml), this formula reduces to:

$$\text{mg DNA/ml} = \text{OD260X1.25}$$

B. Calculation and implication of ratio

$$\frac{OD\ 260}{OD\ 280} = 1.7 - 1.8$$

A value out of this range was not acceptable. It indicated that the DNA sample was not in solution or that there were contaminants (i.e., protein/RNA) in the sample that might inhibit subsequent reactions. (Results of the spectrophotometer readings for genomic DNA can be found in Table 3.3 (Appendix). The DNA was purified or re-extracted using phenol/chloroform/isoamyl (25:24:1) again. Sample were placed inside DNA container box and stored in -80°C deep freezer

Semi – quantitation and quality analysis by Gel-electrophoresis

Agarose gel electrophoresis of the isolated genomic DNA was performed in electrophoresis assembly (Hi Media, Mumbai) to know about the quality of DNA. Larger molecule migrate slower because of greater frictional drag and because they can pass through the pores of gel less efficiently than smaller molecules. As the size of genomic DNA is quite big, a 0.8% gel was used to visualize the genomic DNA, as it can resolves DNA molecules in the range of 0.7 to 8.5 kb.

3.8.2.2.1Reagents and Chemicals Used

Reagent / Chemical	Specifications	Manufacturer
Agarose	Type 1 grade	Himedia
Ethidium bromide		Himedia
100bp ladder		Himedia

Preparation of stock solutions

Electrophoresis buffer [TAE].

Weighed 242 gm of Tris base, 57.1 ml of glacial acetic acid and 100 ml of EDTA. All the constituents were dissolved in 750 ml double distilled water. pH was adjusted to 8.0 using NaOH. Filtered and adjust final volume to 1 liter. Autoclaved and kept at room temperature.

DNA loading dye (6X)

0.25 gm (25 % w/v) of Bromophenol blue and 40 gm of sucrose were dissolved in 100 ml double distilled water. The pH was adjusted to 8.0 with 1 N NaOH. The dye was aliquoted into eppendorff tubes and stored at 4^0C. Working solution was diluted to 3X

Ethidium Bromide.

Weighed 10 mg Ethidium Bromide and dissolved in 1 ml of double distilled water and stored at room temperature (Proper care and appropriate caution was taken with *Et Br* highly).

Protocol of agarose gel electrophoresis

1. Weighed 4g of agarose powder and suspended it in 500ml of 1X TAE buffer.
2. Boiled it in the Microwave oven and allow it to cool to about 45-50 °c.
3. Added 25ul of ethidium bromide and mix well by swirling.
4. The gel was casted in a gel casting tray fixed in a gel caster which kept on horizontal surface.
5. Combed were placed in a way that 2 mm gap was maintained between the bottom of the gel and the comb tip.
6. The gel was allowed to solidify and then combs were removed.
7. Gel was placed in the electrophoresis tank and 1X TAE buffer was added to fill the chamber and submerge the surface of the gel.
8. The isolated genomic DNA samples (5µl) were mixed with loading dye (2ul each) and the mixture was loaded into the well following a serial pattern.
9. The samples were electrophoresed on 0.8% agarose gel in 1X TAE buffer at 75volts for 1 hour.

Primers

SSR primers were used in the molecular characterization of twenty genotypes of Brinjal are presented in Table 3.3. The primers were adopted and synthesized from earlier studies **(Singh *et al.*, 2008 and 2011).** Primer sequences were synthesized from GCC Biotech, New Delhi. Further, these primers were diluted in 0.1X Tris-EDTA buffer solution for making primer stocks and later further diluted to appropriate working concentrations using ion free double distilled water.

Table 3.3 List of SSR primer Sequence and annealing temperature

SSR Primers			
S.No	**Marker name**	**Forward Primer (5'-3')**	**Reverse Primer (3'-5')**
1	CSM4	GCGTACCAATTCTAACCACAAG	GTAATCCGCTTCCCATTTCTC
2	CSM9	TGCGTACCAATTCGACATTCT	GCATTTGCTAGGAATTTACCG
3	CSM15	TCGGTCCTTTTGTTAAGCATC	GATATGAGTGTCGAGAGACCCC
4	CSM16	ACGTGCCATTTCAAACTTGG	TCCTTTTCTTGAGCTGAATTTG
5	CSM25	TCCACCAGCGTTAACCTCAG	TATCTTTGTGCGGGCTTTTC
6	CSM26	CCCAGAAAAGGCTCATTGTTAG	GTCGAGGCAATCCAAATTACTC
7	CSM27	TGTTTGGAGGTGAGGGAAAG	TCCAACTCACCGGAAAAATC
8	CSM36	CCTCAATGGCAGTAGGTCAGA	GTTCTTTGAGCCTCCAGTGC
9	CSM41	AACCTTGAGGGGCATTCAG	GTCACGGCTTGGAACAGAAG
10	CSM42	ACGCCCATGAGGTTCTAGTG	CATGCATTAGTGACTTGAAAGTTG
11	CSM43	ATTTTAACCCCGGGAAAATG	ACCGCTTCTAGGTTTTGCAC

12	CSM44	CGTCGTTGTAACCCATCATC	TTGCCAAATTCCTTGTGTTC
13	CSM48	GAGACTGGCTGTTTATGGTGTG	TTTTCTAATTGGACCAGAGACTTC
14	CSM49	GGTGTGGTGTTAGGGAAACG	GCATCCTTCTTTGCCATCAG
15	CSM54	ATGTGCCTCCATTCTGCAAG	TGGGTGGGATGCTGAGTAAG
16	CSM65	CAACCCCCAAATCCCTAAAT	GAGGAAGAGAAGCGGTGGTC

PCR Reaction for SSR

Based on amount of DNA, PCR reaction was setup. DNA amplification for SSR was performed in a total volume of 20µl. Following components were mixed gently in 0.2ml thin walled PCR-tubes.

Components	**Volume (µl)**
Taq Buffer 10x with $MgCl_2$	2.0
1mM each dNTPs Mix	4.0
Primer (5 µm)	2.0
Taq Polymerase (1U/µl)	1.0
DNA (25 ng/µl)	8.0
Water (Milli Pore)	3.0
Total	**20µl**

Tubes were transferred to the DNA thermal cycler. Amplification reactions were performed in BIO-RAD My Cycler^{TM} Thermal cycler with the following thermal profile mentioned.

Step	**Temperature (^oC)**	**Time**

Initial denaturation	94	5 min
Denaturation	94	1min
Annealing		
Extension	72	
Cycles		
Final extension	72	
Final hold		

Template DNA

Template DNA was extracted from leaves samples as described above. It was then diluted in sterile distilled water and makes the concentration of working solution at 25ng/µl.

Red Taq DNA polymerase

The enzyme used for polymerization obtained from Hi Media, Mumbai (1unit/µl) was stored at -80°C.

The Assay buffer

A readymade buffer supplied by Hi Media, Mumbai with the following component TAPS 100 mM, KCl 500 mM, $MgCl_2$ 15 mM and Gelatin 0.1 % was used.

dNTPs set

dNTPs set were used from Hi Media, Mumbai. Concentrations for each (dATP, dTTP, dCTP, dGTP) were 25mM and stored at - 80^0C.

Preparation of 1.5% (w/v) Agarose Gel for amplified products

Weighed 7.5gm of agarose powder and suspended it in 500 ml 1X TAE buffer. The solution was heated to boiling point using Microwave oven. After cooling to 45-50°c, then

25µl ethidium bromide was added and careful swirl, gel was cast in a trough, kept on horizontal surface. A comb was placed in such a way that 2 mm gap was maintained between the bottom of the gel and the comb tip was placed inside the gel to make wells. The gel was allowed to solidify and then comb was removed. Gel was placed in the electrophoresis chamber and 1X TAE buffer was added to fill the chamber and submerge the surface of the gel.

Electrophoresis

The amplified DNA samples were mixed with 3X loading dye, in 5:1 proportion and were loaded into the well with a micropipette, after which the gel was electrophoresed in 1x TAE buffer at 3-5 volt/ cm for 2-3 hours.

Calculation of PIC Value

After scoring the bands for every SSR locus, Polymorphism Information Content (PIC) was calculated as described by Botstein and co-workers using the formula below;

$$PIC = 1 - \left[\sum_{i=1}^{n} p_i^2\right] - \left[\sum_{i=1}^{n-1}\sum_{j=i+1}^{n} 2p_i^2 p_j^2\right]$$

Where p_i equals the frequency of the i^{th} allele and p_j the frequency of the $(I + 1)^{th}$ allele. Only data from polymorphic SSR loci were used for this analysis. The above mentioned methods used for finding of the result of the above said objectives **(Botstein *et al.*, 1980).**

Resolving Power

The power of each primer to distinguish among the studied genotypes was evaluated by the Resolving Power (RP) **(Prevost and Wilkinson, 1999).**

Resolving power is the capacity of any primer to distinguish among different varieties.

It is defined per primer as: Rp= Σ Ib

Where Ib is the band in formativeness, that takes the values of: 1-(2 x [0.5-p]), being p the proportion of the rice varieties containing the band.

Data analysis

The gel was photographed using CCD camera attached to a gel documentation system with the Quantity One software (Alpha Innotech). Scoring was done manually for each of the gel sections and alleles were determined based on the positions of the bands. Band pattern for each of the microsatellite marker were recorded for each genotype by assigning a letter to each band.

Using various commercially synthesized DNA ladders (Bangalore Genei, Bangalore), respective allele sizes were estimated and alleles were numbered as 'a1', 'a2' etc. In the data matrix, presence of a band was represented by '1' and '0' for absence. These binary data matrix was then utilized to generate similarity data among genotypes.

Only unambiguous bands were scored for the estimation of genetic similarity between the varieties using Jaccard's similarity coefficient based on these data, UPGMA (Unweighted Pair Group Method with Arithmetic Mean) clustering was carried out by applying the software NTSYS-pc **(Rohlf, 1997).**

The results obtained in respect of the study entitled "**Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in brinjal (*Solanum melangena* L.)"** Conducted under the present investigation have been described in this chapter under the following heads:

Effect of Gibberellic acid and Nitrobenzene on flowering characters of brinjal genotypes

Analysis of variance (ANOVA)

Mean performance of genotypes

Genetic variability

Heritability and genetic advance

Correlation coefficients

Path coefficients analysis

Genetic divergence

Antioxidant properties of different Brinjal Genotypes

Molecular characterization

Effect of Gibberellic acid and Nitrobenzene on flowering characters of brinjal genotypes: -

Response of 20 different brinjal genotypes to GA_3 and NBZ in terms of different flowering parameters like, days to 50% flowering, Number of flowers per plant and number of flowers that attained the fruits was evaluated with 50 ppm of GA_3 in combination 150 ppm NBZ during the study and the results from the recorded observations are as follow: -

Days to 50% flowering: -

The data presented in Table 4.1 and Figure 4.1 indicates that the days to 50% flowering significantly influenced with the treatment applied among all the 20 genotypes in the investigation. The result reveled that an application of GA_3 (50ppm) with NBZ (150ppm) induced earliness in flowering on an average of 5.48 days during (2020-2021) and 5.06 days during (2021-2022) in comparison of the control. However maximum difference (7 days) earlier flowering was observed under Pant Samrat during 2020-21- and 7.67-days early flowering was observed in Pant Rituraj during 2021-22. Whereas, under germplasm SVT-12 least difference between control and treated was observed for both the year of study i.e., 4 days and 3.80 days during 2020-21 and 2021-22 respectively.

Number of flowers per plant: -

Effect of GA_3 and NBZ on number of flowers per plant was evaluated in 20 different germplasm of brinjal are presented in Table 4.2 and Figure 4.2 it is evident that number of flowers per plant was higher on an average by 5.66 in 2020-2021 and 4.31 during 2021-2022 in comparison of control for both the years. When all the germplasm was compared with control the maximum difference (between control and treatment) was observed under SVT-12 where 7.66 more flower was recorded during 2020-2021. During 2021-2022, 7.41 more flowers was observed in Pusa Ankur. However, minimum difference between the control and the treated germplasm was observed in B-3-L (4.33 flowers) during 2020-2021 and 2.33 flowers in EG-01-03-02 during 2021-2022.

Number of flowers attained the fruiting: -

It is evidenced from the Table 4.3 and Figure 4.3 GA_3 and Nitrobenzene significantly improve the fruit setting in brinjal. During 2020-2021 on an average 3.61 and during 2021-2022, 3.43 more flowers was observed which attained the fruit when compared with the control (plants without any treatment of PGRs.) for both the year of investigation. When the effect of PGR was studied in all the germplasm while comparing with control the highest fruit was attained by the flowers of KS-224 (4.5) during 2020-21 and Kashi Taru (4.67) during 2021-22. In this way the lowest fruit attainment by the flower was recorded under SVT-9 (3.01) during 2020-21 and Azad Kranti 2.42 during 2021-22.

Analysis of Variance (ANOVA)

The data collected on different parameters under study was subjected to the standard statistical analysis describe in the previous chapter the analysis of variance was done for all the characters to test the significance among the genotypes under study (Table-4.4).

The sum squares due to genotypes were further partitioned in to Replication, Genotypes and Error the highly significance variance was observed for all thirteen characters under study. This analysis revealed that significant differences exist among the material used in the present investigation for all the thirteen characters studied viz., Plant height (cm), Number of primary branches per plant, Days to 50% flowering, Number of flowers per plant, Number of flower attained the fruit, Plant spread (cm), Length of fruit (cm), Diameter of fruit (cm), Stem diameter at harvesting(cm), Average fruit weight (gm), Number of fruit per plant, Fruit index, Average yield (g/plant).

Mean Performance of Genotypes

Plant height (cm)

The data presented in Table 4.5 exhibits the morphological observations of 20 genotypes of Brinjal. The observation recorded in terms of plant height reveled 84.49 as average. The tallest genotype (102.70 cm) recorded under SVT-4 and followed by Kashi Taru (99.81 cm). However, the shortest genotype ABH-1 attained only 71.32 cm height.

Number of primary branches per plant: -

Study for number of primary branches per plant among the 20 different genotypes of Brinjal varied significantly. SVT -1 proven to be best in terms of primary branches and produces 9.29 branches, which was 3.42 higher than the Average (5.87) primary branches, whereas the minimum 4.63 primary branches recorded in SVT-4.

Days to 50 per cent flowering: -

It is evident from Table 4.5 that the Days taken to 50 % flowering are statistically significant among the 20 genotypes of Brinjal. The average genotypes among the treatments attained 50% flowering in 60.62 days. The minimum 50.34 days was observed under ABH-1 and considered best for early flowering, however maximum number of days to 50 % flowering was observed in SVT- 6 which took 76.50 days and found late among all the genotypes which indicates that the studied genotypes were morphologically varied from each other in terms of flowering.

Flowers per plants: -

Number of flowers per plant of brinjal varied significantly for different lines. The maximum number of flowers per plant (62.88) was recorded in SVT-3, whereas the average number of flowers per genotype was 45.99 flower/ plant and less than 50% lines produced more than the average number of primary branches per plant. However, least number of flowers (30.71) per plant was recorded in PR-5.

Number of Flowers attained the fruits: -

Statistically significant variation was recorded for different genotypes in number of flowers attained the fruits (Table 4.5). The highest number of successful fruit attainment was recorded in SVT-3 in which 30.30 fruit was counted out of the total flowers on the plant in the entire season. Whereas the average flower attains the fruit was 21.28. The minimum number of flower (13.88) attained the fruit found in SVT-12.

Plant spread (cm): -

The 20 different genotypes of Brinjal were studied in terms of horizontal spreading of plant presented in Table 4.5. The maximum (95.33cm) plant spread among all the genotype was recorded in Pant Samrat and the minimum spreading (59.07 cm) was seen in Pusa Shyamla. The average plant spread was 76.67cm which was recorded in less than 50 % of the studied genotype.

Length of fruit (cm): -

The morphological observation in terms of Fruit length is presented in Table 4.5. Fruit length was found significantly different in all 20 genotypes of Brinjal. The maximum fruit length (19.86 cm) was recorded in Kashi Taru and the average fruit length was 12.04cm. However, the minimum length (7.28 cm) was observed in Swamani.

Fruit Diameter (cm): -

The study of fruit diameter in brinjal was carried out and presented in Table 4.5. The maximum diameter of fruit recorded in SVT-12 which was 9.70 cm and the minimum diameter was found in Pant Samrat (3.60cm). The average fruit diameter was 6.12 cm.

Stem diameter (cm): -

The maximum stem diameter was recorded in SVT-2 which was 1.94 cm and the minimum (1.52 cm) was found in SVT-9. Whereas the average stem diameter of the 20 genotypes was calculated as 1.73 cm.

Average fruit weight (gm): -

Data presented in Table 4.5 showed that among the 20 genotypes SVT-1 resulted in maximum (170.40 g) fruit weight. However, the minimum fruit weight 65.56 g was observed in Azad Kranti and the average fruit weight of all the genotypes was 97.32 g.

Fruit per plant: -

The maximum fruit per plant was recorded in Azad Kranti which was 26.46 and the minimum fruits per plant was recorded in PR-5 i.e., 10.46 fruit per plant. The average fruit per plant of all the genotypes was 18.27.

Fruit index: -

Data revealed that the average fruit index was 70.08 and about 50% brinjal lines produced the higher fruit index than that average fruit index. The maximum fruit index (116.62) was found in SVT-12, whereas, the minimum (47.17) was observed in Pusa Ankur.

Yield per plant (g): -

The morphological observation in terms of yield per plant is presented in table 4.5. Yield per plant observation was found statistically significant in brinjal genotypes. The maximum yield per plant was recorded in SVT-3 genotype which was 2477.50 g and the

minimum (1050.50 g) yield per plant was found in SVT-2. The average yield per plant in the study was 1703.68 g.

Genetic Variability

The estimates of genotypic and phenotypic coefficient of variation for thirteen characters of brinjal germplasm are presented in Table 4.6. The data showed that magnitude of phenotypic coefficients of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all thirteen characters studied. The estimates revealed that Fruit length showed maximum phenotypic variation (32.13) as well as genotypic variation (31.57) followed by fruit diameter (30.34) and (29.79), fruit index (29.60) and (28.53), number of fruit per plant (27.55) and (26.81), average fruit weight (26.13) and (26.08), number of flower attained the fruit (24.49) and (23.28), yield per plant (22.59) and (21.81), flower per plant (22.44) and (21.35), primary branches (19.84) and (18.24), plant spread (14.13) and (13.89), and the days of 50% flowering (12.91) and (12.52), plant height (10.56) and (9.38) and stem diameter showed minimum phenotypic variation (7.53) as well as genotypic variation (7.03).

Heritability and Genetic Advance

Estimates of heritability and genetic advance for thirteen characters are given in Table 4.6. It was revealed that the maximum heritability above 60% (in broad sense) found in average fruit weight (99.58) followed by plant spread (96.59), fruit length (96.55), fruit diameter (96.44), fruit per plant (94.72), days to 50% flowering (94.11), yield per plant (93.26), fruit index (92.92), flower per plant (90.56), number of flowers attained the fruit (90.31), stem diameter (87.23), primary branches per plant (84.53) and the minimum heritability was found plant height (78.88). Expected genetic advance (GA) as percentage

of mean was observed minimum in stem diameter (13.53) and maximum in fruit length (63.91) fruit diameter (60.27), fruit index (56.66), number of fruits per plant (53.76), average fruit weight (53.60), number of flowers attained the fruit (45.56), average yield (43.40), number of flowers per plant (41.86), number of primary branches per plant (34.54), plant spread (28.12), days to 50% flowering (25.03) and plant height (17.16).

The contribution of various characters under study toward the expression of genetic divergence as presented in Table 4.6. Shows that plant height (10.98) followed by number of primary branches (10.53), flower per plant (9.22), number of flowers attained the fruit (8.62), stem diameter (8.40), days to 50% flowering (7.99), fruit per plant (7.52), fruit index (7.51), plant spread (6.79), fruit length (6.51), yield per plant (6.41), fruit diameter (6.18) and the minimum contribution by fruit weight (3.35).

Correlation coefficients

Phenotypic correlation coefficients.

The inter character phenotypic correlation coefficients are presented in Table 4.7. Data revealed that highly significant positive correlation for yield per plant was found with number of fruits per plant (0.581**), number of flower attained the fruit (0.554**), flower per plant (0.503**) and primary branches per plant (0.332**) and significant positive correlation found with average fruit weight (0.276*) and positive non-significant correlation with plant height (0.196), fruit index (0.180), fruit length (0.145), days to 50 % flowering (0.039) and fruit diameter (0.008). While highly negative non-significant correlation found correlation with stem diameter (-0.485**), negative non-significant correlation found correlation with plant spread (-0.113).

Fruit index showed highly significant positive correlation with average fruit weight (0.515**), fruit diameter (0.511**) fruit length (0.451**) and positive non-significant correlation with primary branches per plant (0.184), plant spread (0.096) Days to 50% flowering (0.095) and plant height (0.082). While negative significant correlation, correlation with number of flowers attained the fruit (-0.226), fruit per plant (-0.201), flower per plant (-0.186) and stem diameter (-0.096).

Fruits per plant showed highly positive significant correlation with number of flowers attained the fruit (0.959**) followed by flower per plant (0.920**) and fruit length (0.350) and positive non-significant correlation with plant height (0.080). And highly negative significant correlation with average fruit weight (-0.581**), fruit diameter (-0.547**) and negative significant correlation with stem diameter (-0.306) negative non-significant correlation with plant spread (-0.206), primary branches per plant (-0.065) and days to 50% flowering (-0.037).

Average fruit weight showed highly positive significant correlation with fruit diameter (0.685**) followed by primary branches per plant (0.528**) and positive non-significant correlation, correlation with plant spread (0.129) highly negative significant correlation, correlation with flower per plant (-0.576**) followed by number of flower attained the fruit (-0.558**) and negative non – significant correlation, correlation with fruit length (-0.219), stem diameter (-0.119), Days to 50% flowering (-0.057) and plant height (-0.035).

Stem diameter showed positive non-significant correlation with fruit length (0.059) highly negative significant correlation, correlation with flower per plant (-0.361**) and number of flowers attained the fruit (-0.331**) negative significant correlation, correlation

with primary branches per plant (-0.278*) negative non-significant correlation, correlation with fruit diameter (-0.129), plant height (-0.108), Plant spread (-0.049) and Days to 50% flowering (-0.036).

Fruit diameter shows positive non-significant correlation with primary branches per plant (0.227), Days to 50% flowering (0.089) and plant spread (0.073) and highly negative significant correlation with fruit length (-0.524**), number of flowers attained the fruit (-0.499**) and flower per plant (-0.498**) and negative non-significant correlation with plant height (-0.194).

Fruit length showed the positive significant correlation with flower per plant (0.309*), plant height (0.297*) and number of flowers attained the fruit (0.272*) and positive non-significant correlation with Days to 50% flowering (0.037) and plant spread (0.001) and negative non-significant correlation with primary branches per plant (-0.103).

Plant spread showed the highly positive significant correlation with plant height (0.465**) and positive non- significant correlation with Days to 50% flowering (0.218), primary branches per plant (0.026) and negative non- significant correlation with flower per plant (-0.193) and number of flowers attained the fruit (-0.167).

Number of flowers attained the fruit showed the highly positive significant correlation with flower per plant (0.927**) and positive non- significant correlation with plant height (0.090) and negative non-significant with Days to 50% flowering (-0.060) primary branches per plant (-0.014).

Number of flowers per plant shows positive non- significant correlation with plant height (0.120) and negative non-significant correlation with Days to 50% flowering (-0.105) and primary branches per plant (-0.071).

Days to 50% flowering shows positive significant correlation with plant height (0.329*) and negative non-significant correlation with primary branches per plant (-0.228). Primary branches per plant shows negative non-significant correlation with plant height (-0.221)

Genotypic correlation coefficients

The inter character genotypic correlation coefficients are also presented in Table 4.8. In this yield per plant showed highly positive significant correlation with number of flowers attained the fruit (0.576**) followed by fruits per plant (0.561**), flower per plant (0.551**) and primary branches per plant (0.383**) and positive significant correlation with average fruit weight (0.286*) and positive non-significant correlation with plant height (0.212), fruit index (0.20), fruit length (0.152), days of 50% flowering (0.064) and fruit diameter (0.012). However negative non-significant with plant spread (-0.118).

Fruit index showed highly positive significant correlation with average fruit weight (0.532**) followed by fruit diameter (0.502**) and fruit length (0.439**) and positive non-significant correlation with primary branches per plant (0.180), days of 50% flowering (0.095), plant spread (0.092) and plant height (0.069). However negative non-significant with number of flowers attained the fruit (-0.229), fruit per plant (-0.214), flower per plant (-0.211) and stem diameter (-0.121).

Number of fruits per plant shows highly positive significant correlation with number of flowers attained the fruit (1.004**) followed by flower per plant (0.995**) and fruit length (0.365**) and positive non-significant correlation with plant height (0.074). Whereas negative highly significant shows with number of average fruit weight (-0.598**), fruit diameter (-0.572) and negative significant with stem diameter (-0.327*) and negative

non-significant with plant spread (-0.218), primary branches per plant (-0.066) and days of 50% flowering (-0.019).

Average fruit weight shows highly positive significant correlation with fruit diameter (0.698**) and primary branches per plant (0.575**) and positive non-significant correlation with plant spread (0.132). However, negative highly significant shows with flower per plant (-0.607**) and number of flowers attained the fruit (-0.586**) and negative non-significant with fruit length (-0.224), stem diameter (-0.130), days of 50% flowering (-0.061) and plant height (-0.043).

Stem diameter shows positive non-significant correlation with fruit length (0.041). However, negative highly significant shows with number of flowers attained the fruit (-0.373**) followed by flower per plant (-0.363**) and primary branches per plant (-0.334**) and negative non-significant shows with fruit diameter (-0.138), plant height (-0.092), plant spread (-0.072) and days of 50% flowering (-0.038).

Fruit diameter shows positive non-significant correlation with primary branches per plant (0.244), days of 50% flowering (0.094) and plant spread (0.073). Whereas negative highly significant shows with fruit length (-0.552**), flower per plant (-0.533**) and number of flowers attained the fruit (-0.526**) and negative non-significant shows with plant height (-0.249).

Fruit length shows highly positive significant correlation with plant height (0.349**) and positively significant correlation with flower per plant (0.324*) and number of flowers attained the fruit (0.299*) and positive non-significant correlation with days of 50% flowering (0.037). However, negative non-significant shows with primary branches per plant (-0.117) and plant spread (-0.004).

Plant spread highly positive significant correlation with plant height (0.521**) and positive non-significant with days of 50% flowering (0.229) and primary branches per plant (0.029). However, negative non-significant shows with flower per plant (-0.196) and number of flowers attained the fruit (-0.191).

Number of flowers attained the fruit shows highly positive significant correlation with flower/plant (1.007**) and positive non-significant correlation with plant height (0.104). However, negative non-significant shows with days of 50% flowering (-0.027) and primary branches per plant (-0.014)

Number of flowers per plant shows positive non-significant correlation with plant height (0.086). Whereas, negative non-significant shows with days of 50% flowering (-0.111) and primary branches per plant (-0.092)

. Days to 50% flowering shows highly positive significant correlation with plant height (0.397**). Whereas, negative non-significant shows with primary branches per plant (-0.244).

Number of primary branches per plant shows negative significant shows with plant height (-0.326*).

Path coefficients analysis

Genotypic path coefficient analysis.

Direct effect

The direct and indirect effect of different characters on fruit yield at genotypic level is presented in Table 4.9. The highest positive direct effect on fruit yield per plant was observed by Number of fruits per plant (1.4975) followed by average fruit weight (1.0308), number of flowers attained the fruit (0.3609), plant height (0.2357) and Days to 50%

flowering (0.0102). Negative direct effect was exerted by flower per plant (-0.7466) followed by fruit length (-0.5051), fruit diameter (-0.4177), primary branches per plant (-0.1238), plant spread (-0.1236) and stem diameter (-0.0709).

Indirect effect

Plant height had direct and positive effect of (0.2357) on fruit yield per plant via fruits per plant (0.1109), fruit diameter (0.0139), primary branches per plant (0.0433), Number of flowers attained the fruit (0.0374), Fruit index (0.0236), stem diameter (0.0065), Days to 50% flowering (0.0040). Negative indirect effect was observed by fruit length (-0.1761), plant spread (-0.0691), flower per plant (-0.0643) and average fruit weight (-0.0440).

Primary branches per plant had direct and negative effect of (-0.1328) on fruit yield via average fruit weight (0.5927), flower per plant (0.0684), fruit index (0.0615), fruit length (0.0592), stem diameter (0.0237). Negative indirect effect was observed by fruits diameter (-0.1021), fruits per plant (-0.0990), plant height (-0.0767), number of flowers attained the fruit (-0.0052), plant spread (-0.0039) and Days to 50% flowering (-0.0025).

Days to 50% flowering had direct and positive effect of (0.0102) on fruit yield per plant via plant height (0.0936), flower per plant (0.0827), fruit index (0.0324), primary branches per plant (0.0324), stem diameter (0.0027), Negative indirect effect was observed by average fruit weight (0.629), fruit diameter (0.0394), plant spread (-0.0304),), fruits per plant (-0.0285), fruit length (-0.0186) and), number of flower attained the fruit (-0.0098).

Number of flowers per plant had direct and negative effect of (-0.7466) on fruit yield per plant via fruits per plant (1.4902), number of flowers attained the fruit (0.3636), fruits diameter (0.2222), plant spread (0.0259), stem diameter (0.0257), plant height

(0.0203) and branches per plant (0.0122). Negative indirect effect was observed by average fruit weight (-0.6257), fruit length (-0.1636), fruit index (-0.0721) and Days to 50% flowering (-0.0011).

Number of flowers attained the fruit had direct and positive effect of (0.3609) on fruit yield per plant via fruits per plant (1.5030), stem diameter (0.0265), plant spread (0.0253), plant height (0.0244) and primary branches per plant (0.0019). Negative indirect effect was observed by flower per plant (-0.7520), average fruit weight (-0.6042), fruit length (-0.1511), fruit index (-0.0782) and Days to 50% flowering (-0.0003).

Plant spread had direct and negative effect of (-0.1326) on fruit yield per plant via flower per plant (0.1460), average fruit weight (0.1345), plant height (0.1228), fruit index (0.0313), stem diameter (0.0051), Days to 50% flowering (0.0023) and fruit length (0.0018). Negative indirect effect was observed by fruit per plant (-0.3263), Number of flowers attained the fruit (-0.0688), fruits diameter (-0.0306) and primary branches per plant (-0.0039).

Fruit length had direct and negative effect of (-0.5051) on fruit yield per plant via fruit per plant (0.5462), fruit per plant (0.2305), fruit index (0.1501), Number of flowers attained the fruit (0.1079), plant height (0.0822), primary branches per plant (0.0156) plant spread (0.0005) and Days to 50% flowering (0.0004). Negative indirect effect was observed by flower per plant (-0.2418), average fruit weight (-0.2311) and stem diameter (-0.0029).

Fruit diameter had direct and negative effect of (-0.4177) on fruit yield per plant via average fruit weight (0.7192), flower per plant (0.3972), fruit length (0.2787), fruit index (0.1713), stem diameter (0.0098), Days to 50% flowering (0.0010). Negative indirect effect

was observed by fruit per plant (-0.8570), Number of flowers attained the fruit (-0.1899), plant height (-0.0586), primary branches per plant (-0.0325) and plant spread (-0.0097).

Stem diameter had direct and negative effect of (-0.0709) on fruit yield per plant via flower per plant (0.2710), fruit diameter (0.0578), primary branches per plant (0.0444) and plant spread (0.0966). Negative indirect effect was observed by fruit per plant (-0.4897), fruit index (-0.0412), Number of flowers attained the fruit (-0.1347), average fruit weight (-0.1337), plant height (-0.0127), fruit length (-0.0209) and Days to 50% flowering (-0.0004).

Average fruit weight had direct and positive effect of (1.0308) on fruit yield per plant via flower per plant (0.4532), fruit index (0.1816), fruit length (0.1132) and stem diameter (0.0092). Negative indirect effect was observed by fruit per plant (-0.8948), fruit diameter (-0.2914), Number of flowers attained the fruit (-0.2116), primary branches per plant (-0.0764), plant spread (-0.0173), plant height (-0.0101) and Days to 50% flowering (-0.0006).

Number of fruits per plant had direct and positive effect of (1.4975) on fruit yield per plant via Number of flowers attained the fruit (0.3622), fruit diameter (0.2390), plant spread (0.0289) stem diameter (0.0232), plant height (0.0175) and primary branches per plant (0.0088). Negative indirect effect was observed by flower per plant (-0.7429), average fruit weight (-0.6160), fruit length (-0.1842), fruit index (-0.0732) and Days to 50% flowering (-0.0002).

Fruit index had direct and positive effect of (0.3415) on fruit yield per plant via (0.3622), Average fruit weight (0.5481), flower per plant (0.1576), plant height (0.0163), stem diameter (0.0085) and Days to 50% flowering (0.0010). Negative indirect effect was

observed by fruit per plant (-0.3211), fruit length (-0.2219), fruit diameter (-0.2095), Number of flowers attained the fruit (-0.0826), primary branches per plant (-0.0239) and plant spread (-0.0122).

Phenotypic path coefficient analysis.

Direct effect

The direct and indirect effect of different characters on fruit yield at phenotypic level is presented in Table 4.10. The highest positive direct effect on fruit yield per plant was observed by fruits per plant (1.1092) via average fruit weight (1.0902), fruit diameter (0.2459), fruit length (0.2259), plant height (0.1270), Days to 50% flowering (0.1144) and flower per plant (0.1116). Negative direct effect was exerted by fruit index (-0.3779), plant spread (-0.0766), primary branches per plant (-0.0750) and Number of flowers attained the fruit (-0.0546).

Indirect effect

Plant height had direct and positive effect of (0.1270) on fruit yield per plant via fruits per plant (0.0889), fruit length (0.0672), Days to 50% flowering (0.0376), primary branches per plant (0.0166), flower per plant (0.0134) and stem diameter (0.0021). Negative indirect effect was observed in fruit diameter (-0.0472), average fruit weight (-0.0382), plant spread (-0.0356), fruit index (-0.0308) and Number of flowers attained the fruit (-0.0049).

Number of primary branches per plant had direct and negative effect of (-0.0750) on fruit yield per plant via average fruit weight (0.5753), fruit diameter (0.0552), stem diameter (0.0053) and Number of flowers attained the fruit (0.0007). While negative indirect effect observed in fruit per plant (-0.0726), fruit index (-0.0696), plant height (-

0.0281), Days to 50% flowering (-0.0261), fruit length (-0.0232) Number of flowers attained the fruit (-0.0079) and plant spread (-0.0020).

Days to 50% flowering had direct and positive effect of (0.1144) on fruit yield per plant via plant height (0.0417), fruit diameter (0.0215), primary branches per plant (0.0171), fruit length (0.0083), Number of flowers attained the fruit (0.0033), and stem diameter (0.0007). While negative indirect effect observed in average fruit weight (-0.0620), fruit per plant (-0.0416), fruit index (-0.0358), plant spread (-0.0168) and flower per plant (-0.0118).

Number of flowers per plant had direct and positive effect of (0.1116) on fruit yield per plant via fruit per plant (1.0206), fruit index (0.0702), fruit length (0.0697), plant height (0.0153), plant spread (0.0148), stem diameter (0.0068) and primary branches per plant (0.0053). While negative indirect effect observed in average fruit weight (-0.6275), fruit diameter (-0.1209), Number of flowers attained the fruit (-0.0506) and Days to 50% flowering (-0.0121).

Number of flowers attained the fruit had direct and negative effect of (-0.0546) on fruit yield per plant via average fruit per plant (1.0637), flower per plant (0.1034), fruit index (0.0853), fruit length (0.0614), plant spread (0.0128), Plant height (0.0114), stem diameter (0.0063) and primary branches per plant (0.0010). While negative indirect effect observed in average fruit weight (-0.6082), fruit diameter (-0.1213), and Days to 50% flowering (-0.0068).

Plant spread had direct and negative effect of (-0.0766) on fruit yield per plant via average fruit weight (0.1405), plant height (0.0591), Days to 50% flowering (0.0249), fruit diameter (0.0178), Number of flowers attained the fruit (0.0091), stem diameter (0.0009)

and fruit length (0.0003). However, negative indirect effect observed in fruit per plant (-0.2289), fruit index (-0.0364) flower per plant (-0.0216), and primary branches per plant (-0.0019).

Fruit length had direct and positive effect of (0.2259) on fruit yield per plant via fruit per plant (0.3881), plant height (0.0378), flower per plant (0.0344), primary branches per plant (0.0077) and Days to 50% flowering (0.0042). However, negative indirect effect observed in average fruit weight (-0.2392), fruit index (-0.1706), fruit diameter (-0.1273), Number of flowers attained the fruit (-0.0148), stem diameter (-0.0011) and plant spread (-0.0001).

Fruit diameter had direct and positive effect of (0.2429) on fruit yield per plant via average fruit weight (0.7465), Number of flowers attained the fruit (0.0273), Days to 50% flowering (0.0101) and stem diameter (0.0025). However, negative indirect effect observed in fruit per plant (-0.6065), fruit index (-0.1931), fruit length (-0.1184), flower per plant (-0.0555), plant height (-0.0247), primary branches per plant (-0.0171) and plant spread (-0.0056).

Stem diameter had direct and negative effect of (-0.0190) on fruit yield per plant via average fruit index (0.0362), primary branches per plant (0.0209), Number of flowers attained the fruit (0.0181), fruit length (0.0133) and plant spread (0.0037). However, negative indirect effect observed in fruit per plant (-0.3397), average fruit weight (-0.1293), flower per plant (-0.0402), fruit diameter (-0.0312), Plant height (-0.0137) and Days to 50% flowering (-0.0041).

Average fruit weight had direct and positive effect of (1.0902) on fruit yield per plant via fruit diameter (0.1663), Number of flowers attained the fruit (0.0305) and Stem

diameter (0.0023). However, negative indirect effect observed in fruit per plant (-0.6443), fruit index (-0.1945), flower per plant (-0.0642), fruit length (-0.0496), primary branches per plant (-0.0396), plant spread (-0.0099), Days to 50% flowering (-0.0065) and Plant height (-0.0045).

Number of fruits per plant had direct and positive effect of (1.1092) on fruit yield per plant via flower per plant (0.1027), fruit length (0.0791), fruit index (0.0761), plant spread (0.0158), Plant height (0.0102) Stem diameter (0.0058) and primary branches per plant (0.0049). However, negative indirect effect observed in Average fruit weight (-0.6333), fruit diameter (-0.1328) Number of flowers attained the fruit (-0.0524) and Days to 50% flowering (-0.0043).

Fruit index had direct and negative effect of (-0.3779) on fruit yield per plant via Average fruit weight (0.5612), fruit diameter (0.1241), fruit length (0.1020), Number of flowers attained the fruit (0.0123), Days to 50% flowering (0.0109), Plant height (0.0104) and Stem diameter (0.0018). However, negative indirect effect observed in fruit per plant (-0.2232), flower per plant (-0.0207), primary branches per plant (-0.0138) and plant spread (-0.0074).

Genetic divergence

The studies of genetic divergence among the twenty genotypes of brinjal were carried out by using Mahalanobis (D^2) statistical and as described by **Rao (1952).**

Cluster mean

The cluster mean calculated for thirteen characters under study is presented in Table 4.11. It shows plant height exerts highest mean for cluster IV (92.19) followed by cluster II (88.02), cluster V (83.27), cluster III (77.13) and minimum recorded with cluster I (74.15).

Number of primary branches per plant shows highest mean with cluster III (7.71) followed by cluster IV (6.23), cluster I (5.79), cluster V (5.45) and lowest for cluster II (5.40).

Days to 50% flowering exhibits highest mean with cluster II (68.39) followed by cluster IV (59.43), cluster V (58.88), cluster (54.56) and lowest mean obtained with cluster I (53.60).

Number of flowers per plant gives highest mean with cluster I (57.45) followed by cluster IV (56.14), cluster II (44.31), cluster V (38.28) and lowest was recorded with cluster III (32.88).

Among the clusters Number of flower attained the fruit shows highest mean with cluster IV (26.53) followed by cluster I (26.35), cluster II (20.65), cluster V (17.51) and the lowest mean was found with cluster III (14.98).

Plant spread exhibits highest mean with cluster II (83.72) followed by cluster III (83.13), cluster IV (77.70), cluster V (72.83) and minimum mean was recorded with cluster I (63.32).

Fruit length shows highest mean with cluster IV (15.83) followed by cluster I (13.40), cluster III (11.81), cluster V (10.54) and lowest mean among the clusters was recorded with cluster II (10.15).

Fruit diameter shows highest mean with cluster III (9.29) followed by cluster II (6.79), cluster V (5.79), cluster I (5.13) and lowest mean among the clusters was recorded with cluster IV (4.69).

Stem diameter shows highest mean with cluster V (1.85) followed by cluster I (1.75), cluster II (1.69), cluster III (1.68) and lowest mean among the clusters was recorded with cluster IV (1.63).

Average fruit weight shows highest mean with cluster III (153.04) followed by cluster II (96.96), cluster IV (92.98), cluster V (92.02) and lowest mean among the clusters was recorded with cluster I (75.51).

Number of fruits per plant exhibits highest mean with cluster I (23.50) followed by cluster IV (23.41), cluster II (17.70), cluster V (14.96) and minimum mean was recorded with cluster III (11.40).

Fruit index exhibits highest mean with cluster III (109.70) followed by cluster IV (74.16), cluster II (66.57), cluster I (66.11) and minimum mean was recorded with cluster V (57.57).

Average yield per plant exhibits highest mean with cluster IV (2117.25) followed by cluster I (1766.56), cluster III (1740.42), cluster II (1715.50) and minimum mean was recorded with cluster V (1306.23).

Inter and Intra-cluster distance

The average intra and inter cluster D^2 values and average intra and inter cluster distance values are presented in Table 4.12. The intra cluster distance were observed minimum (2.064) in cluster III and maximum (2.464) in cluster II followed by cluster V (2.361), cluster IV (2.347) and cluster I (2.110).

Cluster I shows the maximum inter cluster distance with Cluster III (6.613) followed by cluster II (4.146), cluster V (4.021) and minimum with cluster IV (3.184). Cluster II have maximum inter cluster distance with cluster III (5.026) followed by cluster

IV (3.410) and minimum with cluster V (2.755). Cluster III shows maximum inter cluster distance for cluster IV (6.326) and minimum with cluster V (5.141). Among all 5 clusters, cluster IV shows inter cluster distance with cluster (4.720).

Clustering pattern of 20 genotypes of brinjal on the basis of Mahalanobis D^2statistics.

Twenty genotypes were analyzed and grouped into 5 clusters. The clustering pattern of these genotypes is presented in Table 4.13. Cluster II have maximum 6 genotypes namely SVT-4, SVT-11, KS-224, SVT-6, Pant Samrat, Pant Rituraj followed by cluster V have 5 genotypes namely B-3-L, PR-5, Pusa Ankur, Swamani, SVT-2, cluster VI also consist 4 genotypes namely SVT-9, Azad Kranti, SVT-3, Kashi Taru, cluster I have 3 genotypes namely ABH-1, EG-01-03-02, Pusa Shyamla and cluster III have 2 genotypes namely SVT-1, SVT-12.

Antioxidant properties of different Brinjal Genotypes: -

The present study was conducted on the brinjal genotypes for their phenolic compounds, and antioxidant activities. A significant difference was found among the 20 different genotypes in terms of Total phenol, anthocyanin content, polyphenol oxidase and Total ascorbic acid content the result so obtained are presented is Table 4.14 and Figure 4.4 as well as described under this section as follow: -

Total phenol content: -

The different genotypes of brinjal were evaluated in terms of total phenol content present in their fruit. Data revels the genotypes were found statistically significant in terms of total phenol content.

Among the genotypes the highest content of total phenol was found under T_7 (B-3-L) 120.20±6.00 mg/100g followed by T_1 (SVT-9) where 117.31±5.87 mg/100 g of total phenol was found. While there was minimum Total phenol was observed under T_{18} (SVT-12) in which 69.23±4.15 mg/100g of Phenol was present.

Anthocyanin content: -

Anthocyanin is the naturally occurring water soluble pigment belongs to the flavonoid group which is a subclass of polyphenol family; they are responsible for the red, purple and blue colors found in many fruits, vegetables, cereal grains and flowers and have a strong antioxidant capacity. The anthocyanin investigation carried out under the present study has been discussed under this section: -

Data presented in Table and figure shows the variable result for the Anthocyanin content evaluated in 20 different genotypes of Brinjal. Highest content of Anthocyanin was found under T_{19} (Kashi Taru) which was 73.24±4.39 mg/100 g, it was followed by T_{12} (PR-5). However, the lowest content was observed under T_1 (SVT-9) in which only 0.68±0.03 mg/100 g of Anthocyanin was found.

Polyphenol oxidase: -

Antioxidant studies in terms of polyphenol oxidase under 20 different germplasm of brinjal are presented in table and figure. The data reveals the Polyphenol oxidase content was found statistically significant. The maximum Polyphenol oxidase was recorded under T_{19} (Kashi Taru) in which 1.61±0.10 mg/100g PPO was observed it was followed by T_{17} (SVT-2) where 1.55±0.09 mg/100g of PPO was recorded. Whereas, minimum (0.50±0.03 mg/100g) PPO was found in T_1 (SVT-9).

Ascorbic acid content: -

The present investigation was carried out for the estimation of total ascorbic acid content in 20 different genotypes of brinjal, each variety selected in the study shows significant difference in the Ascorbic acid content. Data presented in Table 4.14 and Figure 4.4.

It is evident from the table 4.14 and figure 4.4 among the genotypes highest amount of ascorbic acid was detected under T_{13} (Pant Samrat) in which 7.90±0.70 mg/100g Ascorbic acid was detected, followed by T_{14} (Pusa Ankur) in which 7.73±0.45 mg/100g. However, minimum amount was found under T_4 (SVT-11) with 1.89±0.15 mg/100g Ascorbic acid.

Molecular characterization:

In the present study twenty genotypes of brinjal were characterized using sixteen SSR markers. The result obtained through molecular analysis has been explained in this part. The total genomic DNA was extracted and purified in all the twenty germplasm of brinjal was checked for quality and quantity using DNA and subjected to SSR markers analysis. Out of a total sixteen primers are used, three primers have not showed any amplification (CSM44, CSM48, and CSM49) and the eleven primers (CSM4, CSM9, CSM15, CSM16, CSM25, CSM26, CSM27, CSM36, CSM42, CSM43, CSM65) were found polymorphic and two primers (CSM41, CSM54) were fond monomorphic (Table 4.15). The diversity or similarities between genotypes were given in the form of a dendrogram Figure 4.5. The clustering pattern based on the matrix was obtained by using Un Weight Pair Group Method Analysis (UPGMA) program.

Gel electrophoresis and molecular diversity analysis Primer's analysis

Total number of bands, number of polymorphic bands, number of monomorphic bands, the average number of polymorphic bands per primer, the average number of monomorphic bands per primers, percent polymorphism, polymorphic information content (PIC) and resolving power (RP) were obtained from thirteen SSR primers are show in plate 4.1-4.14 and Table 4.15 Total numbers of bands 215 were obtained with an average of 16.54 bands per primer. Out of 215 bands, 175 bands were obtained polymorphic and 40 monomorphic bands. Eleven primers showed a 100% polymorphic (CSM4, CSM9, CSM15, CSM16, CSM25, CSM26, CSM27, CSM36, CSM42, CSM43 and CSM65) and two primers showed a 100% monomorphic (CSM41 and CSM54). The number of polymorphic alleles ranged from 8-19. The highest numbers of bands (19) were found in CSM27 and the lowest numbers of bands (8) were found in CSM9. Two monomorphic alleles were also produced 20-20 bands in CSM41 and CSM54.

PIC values

The PIC values derived from the allelic diversity and frequency among the genotypes were not uniform for all the SSR loci tasted. The PIC values for SSR loci ranged from 0.09 (CSM27) to 0.364 (CSM9) with the average PIC values of 0.20 (Table 4.15). The analysis given the highest PIC value was exhibited in primer CSM9 (0.364) followed by CSM25 (0.351), CSM26 (0.304), CSM4 and CSM64 (0.268), CSM16, CSM36, CSM43 (0.222), CSM15, CSM42 (0.163). The minimum PIC values were show in CSM27 (0.09).

Resolving power

The significant values of RP indicate the ability of primers to resolve the different closely related genotypes of brinjal. The resolving power of thirteen SSR primers ranged

from 0.1 (CSM27) to 1.0 (CSM25) with the average RP of 0.35 (Table 4.15). The highest RP were exhibited in CSM25 (1.0) followed by CSM9 (0.8), CSM26 (0.5), CSM4 (0.4), CSM65 (0.4), CSM16 (0.3), CSM36 (0.3), CSM43 (0.3), CSM15 (0.2), CSM42 (0.2) and minimum RP was found in CSM27 (0.1).

Cluster analysis of dendrogram

Cluster analysis based on SSR molecular markers can be presented in a dendrogram to indicate the estimated relation between different genotypes. The UPGMA- based cluster shows (Table 4.16) that all the genotypes are interlinked with each other to a greater degree and recorded high genetic similarities. Thirteen SSR primers were used for the classification of cultivars and based on clustering, 20 brinjal genotype were clustered into three main groups Group I, Group II and Group III (Table 4.16). Group 1 includes 5 genotypes and was further keep in one cluster (GI-C1). Whereas, Group II includes 11 genotype and which was further sub-divided into 2 clusters (GII-C1, GII-C2). While Group III includes 4 genotypes and was further keep in one cluster (GIII-C1).

Jaccard coefficient of similarity

The band information of SSR primers were scored for the presence (number) and absence (zero) in all the brinjal studies here for each primer. The statistical analysis was carried out NTSYSpc- 2.02 software. To make a group genotype into a separate cluster, a dendrogram was prepared using the UPGMA method.

Genetic similarities were calculated using Jaccard similarities co-efficient. Significant genetic variation was found among all brinjal genotypes ranged from 0.462 to 1.00 (Table 4.17) the genotype Azad Kranti and SVT-1 were found maximum similarity (1.00) and minimum similarity (0.462) were found in Pusa Shyamla and Swamani variety.

Table 4.4 Analysis of variance (ANOVA) mean sum square for thirteen characters of brinjal

Source of variation	DF	Plant Height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of flowers per plant	Number of flowers attained the fruit	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	Stem diameter (cm)	Average fruit weight (gm)	Number of fruits per plant	Fruit index	Average yield (g/plant)
Replication	2	9.98	0.09	0.77	4.14	2.40	2.01	0.12	0.14	0.002	1.76	0.28	11.93	10515.8
Treatment	19	205.22**	3.65**	176.54**	299.43**	76.23**	344.31**	43.85**	10.10**	0.046*	1934.8**	73.35**	1229.9**	424356.4**
Error	38	16.82	0.21	3.60	10.06	2.63	4.01	0.52	0.12	0.002	2.73	1.34	30.47	9984.4
Total	59	77.26	1.31	59.20	103.05	26.32	113.53	14.46	3.34	0.016	624.89	24.49	416.11	143444.3

*, ** significant at 5% and 1% level, respectively

Table 4.5 Mean performance of the brinjal genotypes for thirteen characters

Sr. no.	Genotypes	Plant Height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of flowers per plant	Number of flowers attained the fruit	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	Stem diameter (cm)	Average fruit weight (gm)	Number of fruits per plant	Fruit index	Average yield (g/plant)
1	**SVT-9**	88.34	7.25	60.38	56.54	26.54	69.17	12.60	4.03	1.52	91.82	22.96	50.67	2107.50
2	**Azad Kranti**	87.73	6.38	56.63	60.29	29.75	81.62	17.31	4.61	1.63	65.56	26.46	79.98	1725.17
3	**SVT-4**	102.70	4.63	64.75	47.63	21.09	92.61	10.11	7.75	1.62	95.52	16.63	78.18	1604.17
4	**SVT-11**	86.66	5.42	64.17	45.63	23.21	81.69	9.51	5.50	1.75	91.89	21.17	52.36	1942.83
5	**SVT-3**	92.88	5.88	65.13	62.88	30.30	80.85	13.56	5.56	1.66	94.47	26.21	75.42	2477.50
6	**SVT-1**	78.79	9.29	56.88	30.71	15.09	89.66	11.58	8.88	1.78	170.40	11.63	102.78	1948.00
7	**B-3-L**	87.65	5.79	60.63	46.34	21.21	67.48	12.58	4.30	1.86	95.92	18.09	53.97	1700.83
8	**KS-224**	80.59	4.96	74.08	41.84	18.84	79.85	9.33	8.14	1.86	95.42	16.54	76.30	1562.33
9	**SVT-6**	84.38	6.21	76.50	43.50	21.29	63.50	9.58	9.27	1.54	118.85	18.09	88.94	2146.67
10	**ABH-1**	71.32	7.54	50.34	56.67	26.21	66.90	8.33	6.14	1.66	82.17	22.17	51.13	1823.17
11	**EG-01-03-02**	71.55	4.83	53.29	61.13	28.63	63.99	13.95	4.58	1.70	69.21	26.25	63.87	1815.83
12	**PR-5**	83.66	5.29	55.04	30.71	14.29	69.19	7.99	6.99	1.89	104.28	10.46	55.80	1089.50
13	**Pant Samrat**	87.36	5.59	69.33	42.96	19.55	95.33	14.50	3.60	1.63	73.08	16.84	52.26	1228.83
14	**Pusa Ankur**	82.68	5.25	50.88	44.67	19.71	83.64	7.56	6.24	1.86	77.01	16.21	47.17	1245.50
15	**Swamani**	74.42	5.92	56.42	33.88	15.54	63.67	7.28	6.66	1.72	109.50	13.21	48.36	1444.83
16	**Pusa Shyamla**	79.58	5.00	57.17	54.54	24.21	59.07	17.91	4.67	1.89	75.16	22.08	83.33	1660.67
17	**SVT-2**	87.92	5.00	71.46	35.79	16.79	80.19	17.30	4.76	1.94	73.37	14.34	82.55	1050.50
18	**SVT-12**	75.46	6.13	52.25	35.05	13.88	76.61	12.04	9.70	1.58	135.69	11.17	116.62	1532.83
19	**Kashi Taru**	99.81	5.42	55.58	44.84	19.54	79.17	19.86	4.56	1.73	120.07	18.00	90.59	2158.83
20	**Pant Rituraj**	86.41	5.58	61.50	44.29	19.92	89.31	7.86	6.51	1.71	107.02	16.92	51.35	1808.17
	Mean	**84.49**	**5.87**	**60.62**	**45.99**	**21.28**	**76.67**	**12.04**	**6.12**	**1.73**	**97.32**	**18.27**	**70.08**	**1703.68**
	Min	71.32	4.63	50.34	30.71	13.88	59.07	7.28	3.60	1.52	65.56	10.46	47.17	1050.50
	Max	102.70	9.29	76.50	62.88	30.30	95.33	19.86	9.70	1.94	170.40	26.46	116.62	2477.50
	SE(d)	3.35	0.37	1.55	2.59	1.33	1.63	0.59	0.29	0.04	1.35	0.95	4.51	81.59
	C.D.	6.80	0.76	3.15	5.26	2.69	3.32	1.19	0.58	0.08	2.74	1.92	9.16	165.80
	C.V.	4.85	7.80	3.13	6.90	7.63	2.61	5.97	5.72	2.70	1.70	6.33	7.88	5.87

Table 4.6 Estimation of variability (GCV & PCV), Heritability, Genetic Advance and Genetic Advance as percent of man

Genotypes	**Heritability (%)**	**GA**	**GA% mean**	**GCV (%)**	**PCV (%)**	**ECV (%)**	**% contribution**
Plant Height (cm)	78.88	14.50	17.16	9.38	10.56	4.85	10.98
Number of primary branches per plant	84.53	2.03	34.54	18.24	19.84	7.80	10.53
Days to 50% flowering	94.11	15.17	25.03	12.52	12.91	3.13	7.99
Number of flowers per plant	90.56	19.25	41.86	21.35	22.44	6.90	9.22
Number of flowers attained the fruit	90.31	9.70	45.56	23.28	24.49	7.63	8.62
Plant spread (cm)	96.59	21.56	28.12	13.89	14.13	2.61	6.79
Fruit length (cm)	96.55	7.69	63.91	31.57	32.13	5.97	6.51
Fruit diameter (cm)	96.44	3.69	60.27	29.79	30.34	5.72	6.18
Stem diameter (cm)	87.23	0.23	13.53	7.03	7.53	2.69	8.40
Average fruit weight (gm)	99.58	52.17	53.60	26.08	26.13	1.70	3.35
Number of fruits per plant	94.72	9.82	53.76	26.81	27.55	6.33	7.52
Fruit index	92.92	39.71	56.66	28.53	29.60	7.88	7.51
Average yield (g/plant)	93.26	739.34	43.40	21.81	22.59	5.87	6.41

Table 4.7. Estimation of correlation coefficient for phenotypic (PC) levels among different characters in brinjal: -

Characters	Plant Height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of flowers per plant	Number of flowers attained the fruit	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	Stem diameter (cm)	Average fruit weight (gm)	Number of fruits per plant	Fruit index	Average yield (g/plant)
Plant Height (cm)	1.000	-0.221	0.329*	0.120	0.090	0.465**	0.297*	-0.194	-0.108	-0.035	0.080	0.082	0.196
Number of primary branches per plant			-0.228	-0.071	-0.014	0.026	-0.103	0.227	-0.278*	0.528**	-0.065	0.184	0.332**
Days to 50% flowering				-0.105	-0.060	0.218	0.037	0.089	-0.036	-0.057	-0.037	0.095	0.039
Number of flowers per plant					0.927**	-0.193	0.309*	-0.498**	-0.361**	-0.576**	0.920**	-0.186	0.503**
Number of flowers attained the fruit						-0.167	0.272*	-0.499**	-0.331**	-0.558**	0.959**	-0.226	0.554**
Plant spread (cm)							0.001	0.073	-0.049	0.129	-0.206	0.096	-0.113
Fruit length (cm)								-0.524**	0.059	-0.219	0.350**	0.451**	0.145
Fruit diameter (cm)									-0.129	0.685**	-0.547**	0.511**	0.008
Stem diameter (cm)										-0.119	-0.306*	-0.096	-0.485**
Average fruit weight (gm)											-0.581**	0.515**	0.276*
Number of fruits per plant												-0.201	0.581**
Fruit index													0.180
Average yield (g/plant)													1.000

Table 4.8 Estimation of correlation coefficient for genotypic (GC) levels among different characters in brinjal

Characters	Plant Height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of flowers per plant	Number of flowers attained the fruit	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	Stem diameter (cm)	Average fruit weight (gm)	Number of fruits per plant	Fruit index	Average yield (g/plant)
Plant Height (cm)	1.000	-0.326*	0.397**	0.086	0.104	0.521**	0.349**	-0.249	-0.092	-0.043	0.074	0.069	0.212
Number of primary branches per plant			-0.244	-0.092	-0.014	0.029	-0.117	0.244	-0.334**	0.575**	-0.066	0.180	0.383**
Days to 50% flowering				-0.111	-0.027	0.229	0.037	0.094	-0.038	-0.061	-0.019	0.095	0.064
Number of flowers per plant					1.007**	-0.196	0.324*	-0.532**	-0.363**	-0.607**	0.995**	-0.211	0.551**
Number of flowers attained the fruit						-0.191	0.299*	-0.526**	-0.373**	-0.586**	1.004**	-0.229	0.576**
Plant spread (cm)							-0.004	0.073	-0.072	0.131	-0.218	0.092	-0.118
Fruit length (cm)								-0.552**	0.041	-0.224	0.365**	0.439**	0.152
Fruit diameter (cm)									-0.138	0.698**	-0.572**	0.502**	0.012
Stem diameter (cm)										-0.130	-0.327*	-0.121	-0.531**
Average fruit weight (gm)											-0.598**	0.532**	0.286*
Number of fruits per plant												-0.214	0.561**
Fruit index													0.202
Average yield (g/plant)													1.000

Table 4.9 Direct and Indirect effect of thirteen characters with fruit yield per plant at Genotypic (GC) levels of brinjal

Characters	Plant Height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of flowers per plant	Number of flowers attained the fruit	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	Stem diameter (cm)	Average fruit weight (gm)	Number of fruits per plant	Fruit index	Average yield (g/plant)
Plant Height (cm)	**0.2357**	0.0433	0.0040	-0.0643	0.0374	-0.0691	-0.1761	0.1039	0.0065	-0.0440	0.1109	0.0236	0.212
Number of primary branches per plant	-0.0767	**-0.1328**	-0.0025	0.0684	-0.0052	-0.0039	0.0592	-0.1021	0.0237	0.5927	-0.0990	0.0615	0.383**
Days to 50% flowering	0.0936	0.0324	**0.0102**	0.0827	-0.0098	-0.0304	-0.0186	-0.0394	0.0027	-0.0629	-0.0285	0.0324	0.064
Number of flowers per plant	0.0203	0.0122	-0.0011	**-0.7466**	0.3636	0.0259	-0.1636	0.2222	0.0257	-0.6257	1.4902	-0.0721	0.551**
Number of flowers attained the fruit	0.0244	0.0019	-0.0003	-0.7520	**0.3609**	0.0253	-0.1511	0.2198	0.0265	-0.6042	1.5030	-0.0782	0.576**
Plant spread (cm)	0.1228	-0.0039	0.0023	0.1460	-0.0688	**-0.1326**	0.0018	-0.0306	0.0051	0.1345	-0.3263	0.0313	-0.118
Fruit length (cm)	0.0822	0.0156	0.0004	-0.2418	0.1079	0.0005	**-0.5051**	0.2305	-0.0029	-0.2311	0.5462	0.1501	0.152
Fruit diameter (cm)	-0.0586	-0.0325	0.0010	0.3972	-0.1899	-0.0097	0.2787	**-0.4177**	0.0098	0.7192	-0.8570	0.1713	0.012
Stem diameter (cm)	-0.0217	0.0444	-0.0004	0.2710	-0.1347	0.0096	-0.0209	0.0578	**-0.0709**	-0.1337	-0.4897	-0.0412	-0.531**
Average fruit weight (gm)	-0.0101	-0.0764	-0.0006	0.4532	-0.2116	-0.0173	0.1132	-0.2914	0.0092	**1.0308**	-0.8948	0.1816	0.286*
Number of fruit per plant	0.0175	0.0088	-0.0002	-0.7429	0.3622	0.0289	-0.1842	0.2390	0.0232	-0.6160	**1.4975**	-0.0732	0.561**
Fruit index	0.0163	-0.0239	0.0010	0.1576	-0.0826	-0.0122	-0.2219	-0.2095	0.0085	0.5481	-0.3211	**0.3415**	0.202

Table 4.10 Direct and Indirect effect of thirteen characters with fruit yield per plant at phenotypic (PC) levels in brinjal

Characters	Plant Height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of flowers per plant	Number of flowers attained the fruit	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	Stem diameter (cm)	Average fruit weight (gm)	Number of fruits per plant	Fruit index	Average yield (g/plant)
Plant Height (cm)	**0.1270**	0.0166	0.0376	0.0134	-0.0049	-0.0356	0.0672	-0.0472	0.0021	-0.0382	0.0889	-0.0308	0.196
Number of primary branches per plant	-0.0281	**-0.0750**	-0.0261	-0.0079	0.0007	-0.0020	-0.0232	0.0552	0.0053	0.5753	-0.0726	-0.0696	0.332**
Days to 50% flowering	0.0417	0.0171	**0.1144**	-0.0118	0.0033	-0.0167	0.0083	0.0215	0.0007	-0.0620	-0.0416	-0.0358	0.039
Number of flowers per plant	0.0153	0.0053	-0.0121	**0.1116**	-0.0506	0.0148	0.0697	-0.1209	0.0069	-0.6275	1.0206	0.0702	0.503**
Number of flowers attained the fruit	0.0114	0.0010	-0.0068	0.1034	**-0.0546**	0.0128	0.0614	-0.1213	0.0063	-0.6082	1.0637	0.0853	0.554**
Plant spread (cm)	0.0591	-0.0019	0.0249	-0.0216	0.0091	**-0.0766**	0.0003	0.0178	0.0009	0.1405	-0.2289	-0.0364	-0.113
Fruit length (cm)	0.0378	0.0077	0.0042	0.0344	-0.0148	-0.0001	**0.2259**	-0.1273	-0.0011	-0.2392	0.3881	-0.1706	0.145
Fruit diameter (cm)	-0.0247	-0.0171	0.0101	-0.0555	0.0273	-0.0056	-0.1184	**0.2429**	0.0025	0.7465	-0.6065	-0.1931	0.008
Stem diameter (cm)	-0.0137	0.0209	-0.0041	-0.0402	0.0181	0.0037	0.0133	-0.0312	**-0.0190**	-0.1293	-0.3397	0.0362	-0.485**
Average fruit weight (gm)	-0.0045	-0.0396	-0.0065	-0.0642	0.0305	-0.0099	-0.0496	0.1663	0.0023	**1.0902**	-0.6443	-0.1945	0.276*
Number of fruits per plant	0.0102	0.0049	-0.0043	0.1027	-0.0524	0.0158	0.0791	-0.1328	0.0058	-0.6333	**1.1092**	0.0761	0.581**
Fruit index	0.0104	-0.0138	0.0109	-0.0207	0.0123	-0.0074	0.1020	0.1241	0.0018	0.5612	-0.2232	**-0.3779**	0.180

Table 4.11 Cluster mean of different genotype of brinjal

Clusters		Plant Height (cm)	Number of primary branches per plant	Days to 50% flowering	Number of flowers per plant	Number of flowers attained the fruit	Plant spread (cm)	Fruit length (cm)	Fruit diameter (cm)	Stem diameter (cm)	Average fruit weight (gm)	Number of fruit per plant	Fruit index	Average yield (g/plant)
I	**Mean**	74.15	5.79	53.60	57.45	26.35	63.32	13.40	5.13	1.75	75.51	23.50	66.11	1766.56
	SE ±	4.70	1.52	3.43	3.36	2.21	3.96	4.81	0.88	0.12	6.49	2.38	16.21	91.78
II	**Mean**	88.02	5.40	68.39	44.31	20.65	83.72	10.15	6.79	1.69	96.96	17.70	66.57	1715.50
	SE ±	7.60	0.55	5.96	2.07	1.56	11.60	2.26	2.04	0.11	15.37	1.79	16.54	322.14
III	**Mean**	77.13	7.71	54.56	32.88	14.48	83.13	11.81	9.29	1.68	153.04	11.40	109.70	1740.42
	SE ±	2.35	2.24	3.27	3.07	0.86	9.23	0.33	0.58	0.15	24.54	0.32	9.79	293.57
IV	**Mean**	92.19	6.23	59.43	56.14	26.53	77.70	15.83	4.69	1.63	92.98	23.41	74.16	2117.25
	SE ±	5.57	0.79	4.32	7.97	4.95	5.78	3.36	0.64	0.09	22.28	3.94	16.90	308.40
V	**Mean**	83.27	5.45	58.88	38.28	17.51	72.83	10.54	5.79	1.85	92.02	14.46	57.57	1306.23
	SE ±	5.47	0.39	7.84	6.87	2.88	8.61	4.36	1.19	0.08	16.16	2.91	14.43	269.71

Table 4.12 Average intra and inter cluster (D^2 value) distance in twenty genotypes of brinjal.

Clusters	I	II	III	IV	V
I	**2.110**				
II	4.146	**2.464**			
III	6.613	5.026	**2.064**		
IV	3.184	3.410	6.326	**2.347**	
V	4.021	2.755	5.141	4.720	**2.361**

Table 4.13 Clustering pattern of 20 genotypes of brinjal on the basis of Mahalanobis D^2 statistics.

Clusters	No of genotypes	Genotypes
I	**3**	ABH-1, EG-01-03-02, Pusa Shyamla
II	**6**	SVT-4, SVT-11, KS-224, SVT-6, Pant Samrat, Pant Rituraj
III	**2**	SVT-1, SVT-12
IV	**4**	SVT-9, Azad Kranti, SVT-3, Kashi Taru,
V	**5**	B-3-L, PR-5, Pusa Ankur, Swamani, SVT-2,

Table 4.16 Clustering pattern of 20 brinjal genotype on the basis of genetic divergence by SSR

Grouping of clusters	No. of sub clades	clusters	No. of genotypes	Genotypes
I	1	GI-C1	5	**SVT-9** **SVT-4** **SVT-2** **Pusa Ankur** **EG-01-03-02**
II	2	GII-C1	6	**Azad Kranti** **ABH-1** **SVT-6** **SVT-11** **KS-224** **Pant Rituraj**
		GII-C2	5	**SVT-1** **PR-5** **Swamani** **Pant Samrat** **Pusa Shyamla**
III	3	GIII-C1	4	**SVT-3** **Kashi Taru** **B-3-L** **SVT-12**

4.14 Antioxidant properties of different Brinjal Genotypes

Treatment	Total Phenol	Anthocyanin	Polyphenol oxidase	Vitamin C
T1	117.31±5.87ij	0.68±0.03a	0.50±0.03a	2.41±0.12ab
T2	92.49±3.70bcdef	51.24±2.05ghi	0.75±0.03abc	2.01±0.08a
T3	77.21±4.63abc	36.47±2.19cde	0.97±0.06bcde	3.11±0.19bc
T4	85.58±6.85abcde	39.58±3.17def	1.11±0.09cdefg	1.89±0.15a
T5	71.89±2.16a	47.33±1.42fgh	0.95±0.03abcde	3.85±0.12cde
T6	102.10±4.10efghij	57.40±2.30jk	1.07±0.06bcdef	4.80±0.20ef
T7	120.20±6.00j	62.20±3.10jkl	1.22±0.24defgh	5.90±0.30g
T8	107.63±6.45fghij	55.20±3.3ijk	1.30±0.20efgh	4.17±0.25de
T9	115.17±8.05hij	27.30±1.90bc	1.30±0.10efgh	6.27±0.45g
T10	97.50±7.80defgh	67.44±5.34klm	0.97±0.38bcde	6.57±0.55gh
T11	93.37±3.75bcdef	38.17±1.55def	1.14±0.20cdefg	3.57±0.15cd
T12	104.27±8.35fghij	71.33±5.75lk	1.43±0.21fgh	6.17±0.45g
T13	81.10±7.30abcd	40.50±3.60def	1.23±0.15defgh	7.90±0.70i
T14	75.20±4.50ab	35.57±2.15cde	0.80±0.10abcd	7.73±0.45i
T15	99.17±4.95defghi	31.33±1.55cd	0.63±0.06ab	4.83±0.25ef
T16	105.30±6.10fghij	42.30±2.50efg	1.27±0.15efgh	5.60±0.30fg
T17	114.11±6.85hij	21.43±1.29b	1.55±0.09gh	4.25±0.24de
T18	69.23±4.15a	61.70±3.70jk	0.73±0.06abc	7.33±0.45hi
T19	112.31±6.74ghij	73.24±4.39m	1.61±0.10h	3.44±0.21bcd
T20	94.12±5.65cdefg	49.93±3.00ghi	0.99±0.06bcdef	5.68±0.34fg
SE (m)	**2.11**	**2.31**	**0.04**	**0.24**

Table 4.1 Days to 50% flowering

Sr. no.	Genotypes	2020-21		2021-22	
		Control	Treatments GA_3 50ppm + Nitrobenzene 150ppm	Control	Treatments GA_3 50ppm + Nitrobenzene 150ppm
1	SVT-9	61.75	55.42	59.00	54.75
2	Azad Kranti	56.58	50.92	56.67	50.67
3	SVT-4	65.08	58.58	64.42	57.58
4	SVT-11	64.92	59.25	63.42	59.17
5	SVT-3	65.00	59.33	65.25	60.33
6	SVT-1	57.42	52.75	56.33	52.00
7	B-3-L	60.92	55.58	60.33	54.92
8	KS-224	74.58	67.25	73.58	64.42
9	SVT-6	76.83	70.17	76.17	72.58
10	ABH-1	50.33	46.00	50.33	46.42
11	EG-01-03-02	53.75	49.08	52.83	48.25
12	PR-5	55.25	50.25	54.83	47.42
13	Pant Samrat	69.58	62.58	69.08	62.58
14	Pusa Ankur	51.75	47.08	50.00	46.83
15	Swamani	57.42	52.08	55.42	51.75
16	Pusa Shyamla	57.08	52.75	57.25	53.92
17	SVT-2	72.25	66.92	70.67	66.50
18	SVT-12	53.75	49.75	50.75	47.67
19	Kashi Taru	56.25	50.92	54.92	50.00
20	Pant Rituraj	61.83	56.17	61.17	53.50
	Mean	61.12	55.64	60.12	55.06
	SE(m) ±	0.87	0.28	0.88	0.28
	C.D. at 5%	2.45	0.78	2.47	0.78

Table 4.2 Number of flowers per plant

Sr. no.	Genotypes	2020-21		2021-22	
		Control	Treatments GA_3 50ppm + Nitrobenzene 150ppm	Control	Treatments GA_3 50ppm + Nitrobenzene 150ppm
1	SVT-9	57.00	61.83	56.08	60.42
2	Azad Kranti	61.17	67.08	59.42	64.50
3	SVT-4	48.33	53.25	46.92	53.00
4	SVT-11	46.50	51.00	44.75	50.08
5	SVT-3	64.17	70.08	61.58	65.42
6	SVT-1	29.33	33.92	32.08	34.75
7	B-3-L	46.42	50.75	46.25	48.92
8	KS-224	41.83	46.83	41.83	46.17
9	SVT-6	43.67	49.17	43.33	48.00
10	ABH-1	57.33	61.92	56.00	58.83
11	EG-01-03-02	59.33	65.83	62.92	65.25
12	PR-5	30.00	36.75	31.42	36.58
13	Pant Samrat	41.83	47.33	44.08	48.08
14	Pusa Ankur	45.17	51.17	44.17	51.58
15	Swamani	33.00	39.25	34.75	38.58
16	Pusa Shyamla	54.75	60.67	54.33	59.33
17	SVT-2	34.75	41.67	36.83	40.83
18	SVT-12	34.25	41.91	35.83	40.42
19	Kashi Taru	43.58	49.08	46.08	49.17
20	Pant Rituraj	45.00	51.08	43.58	48.42
	Mean	45.87	51.53	46.11	50.42
	SE(m) ±	1.37	0.44	1.35	0.43
	C.D. at 5%	3.88	1.23	3.81	1.21

Table 4.3 Number of Flowers attained the fruits

Sr. no.	Genotypes	2020-21		2021-22	
		Control	Treatments GA_3 50ppm + Nitrobenzene 150ppm	Control	Treatments GA_3 50ppm + Nitrobenzene 150ppm
1	SVT-9	26.50	29.58	26.58	29.42
2	Azad Kranti	29.50	33.08	30.00	32.42
3	SVT-4	20.92	24.08	21.25	24.42
4	SVT-11	23.50	27.00	22.92	26.83
5	SVT-3	30.58	34.17	30.00	33.75
6	SVT-1	14.17	17.50	16.00	19.75
7	B-3-L	20.67	24.42	21.75	24.75
8	KS-224	18.67	23.17	19.00	23.58
9	SVT-6	20.50	23.75	22.08	25.00
10	ABH-1	25.50	28.83	26.92	29.42
11	EG-01-03-02	29.33	32.92	27.92	32.08
12	PR-5	13.67	17.42	14.92	18.75
13	Pant Samrat	18.83	22.50	20.25	23.08
14	Pusa Ankur	18.83	22.42	20.58	23.17
15	Swamani	14.50	18.33	16.58	20.00
16	Pusa Shyamla	24.83	28.42	23.58	26.83
17	SVT-2	16.00	19.83	17.58	21.17
18	SVT-12	13.33	17.08	14.42	19.33
19	Kashi Taru	19.25	23.33	19.83	24.50
20	Pant Rituraj	19.42	22.92	20.42	23.00
	Mean	20.93	24.54	26.58	29.42
	SE(m) ±	0.75	0.24	0.72	0.23
	C.D. at 5%	2.12	0.67	2.02	0.64

Table 4.15 Primer name, total bands, polymorphic bands, monomorphic bands, PIC and RP of SSR primers

Sr. no.	Primers	Total alleles	Polymorphic Bands	Monomorphic Bands	PIC	RP
1	**CSM4**	16	16	0	0.268	0.4
2	**CSM9**	8	8	0	0.364	0.8
3	**CSM15**	18	18	0	0.163	0.2
4	**CSM 16**	17	17	0	0.222	0.3
5	**CSM 25**	14	14	0	0.351	1
6	**CSM 26**	15	15	0	0.304	0.5
7	**CSM 27**	19	19	0	0.09	0.1
8	**CSM 36**	17	17	0	0.222	0.3
9	**CSM 41**	20	0	20	0	0
10	**CSM 42**	18	18	0	0.163	0.2
11	**CSM 43**	17	17	0	0.222	0.3
12	**CSM 54**	20	0	20	0	0
13	**CSM 65**	16	16	0	0.268	0.4
Total		**215**	**175**	**40**	**2.637**	**4.5**
Average		**16.54**	**13.46**	**3.08**	**0.20**	**0.35**

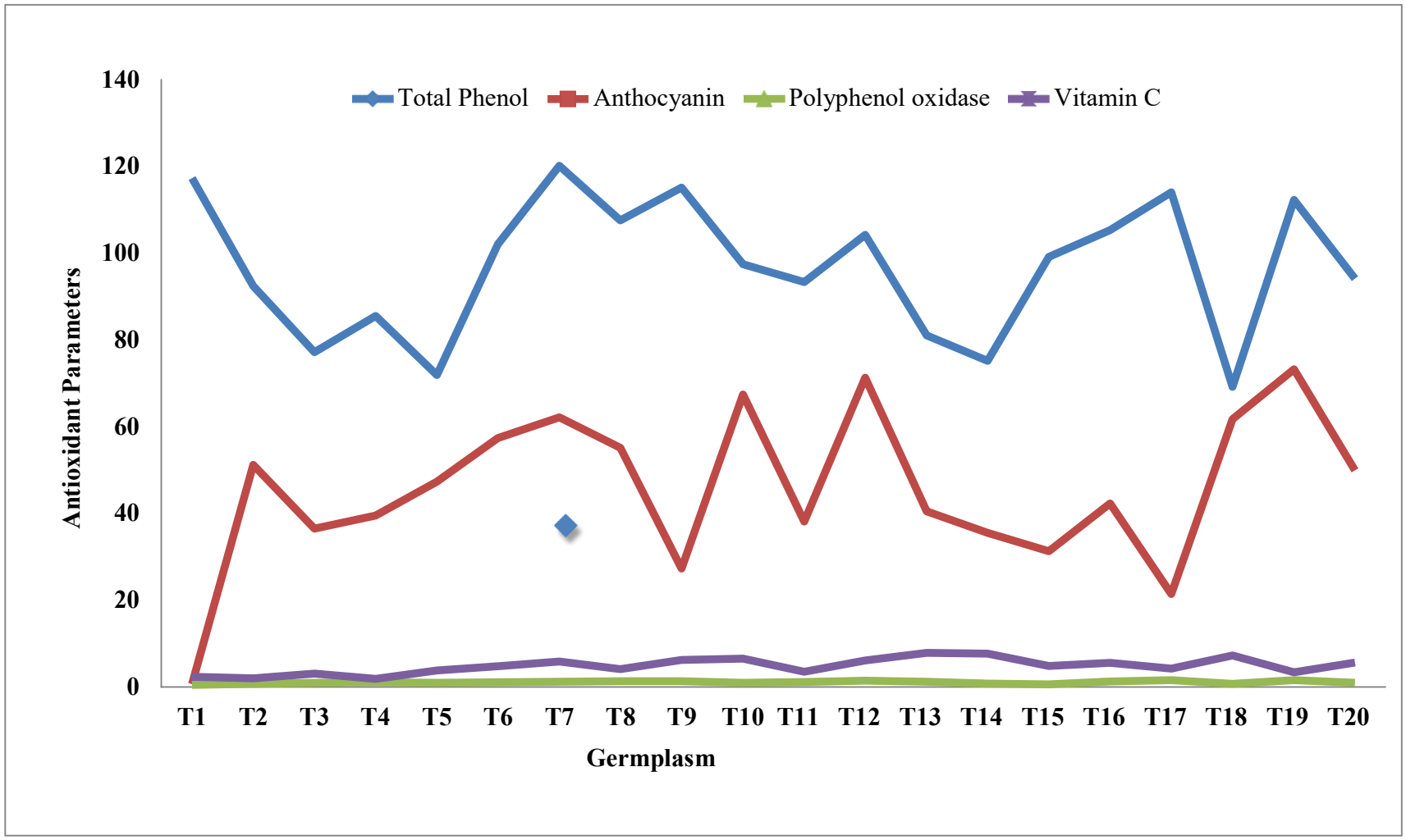


Fig. 4.4. properties of different Brinjal Genotypes

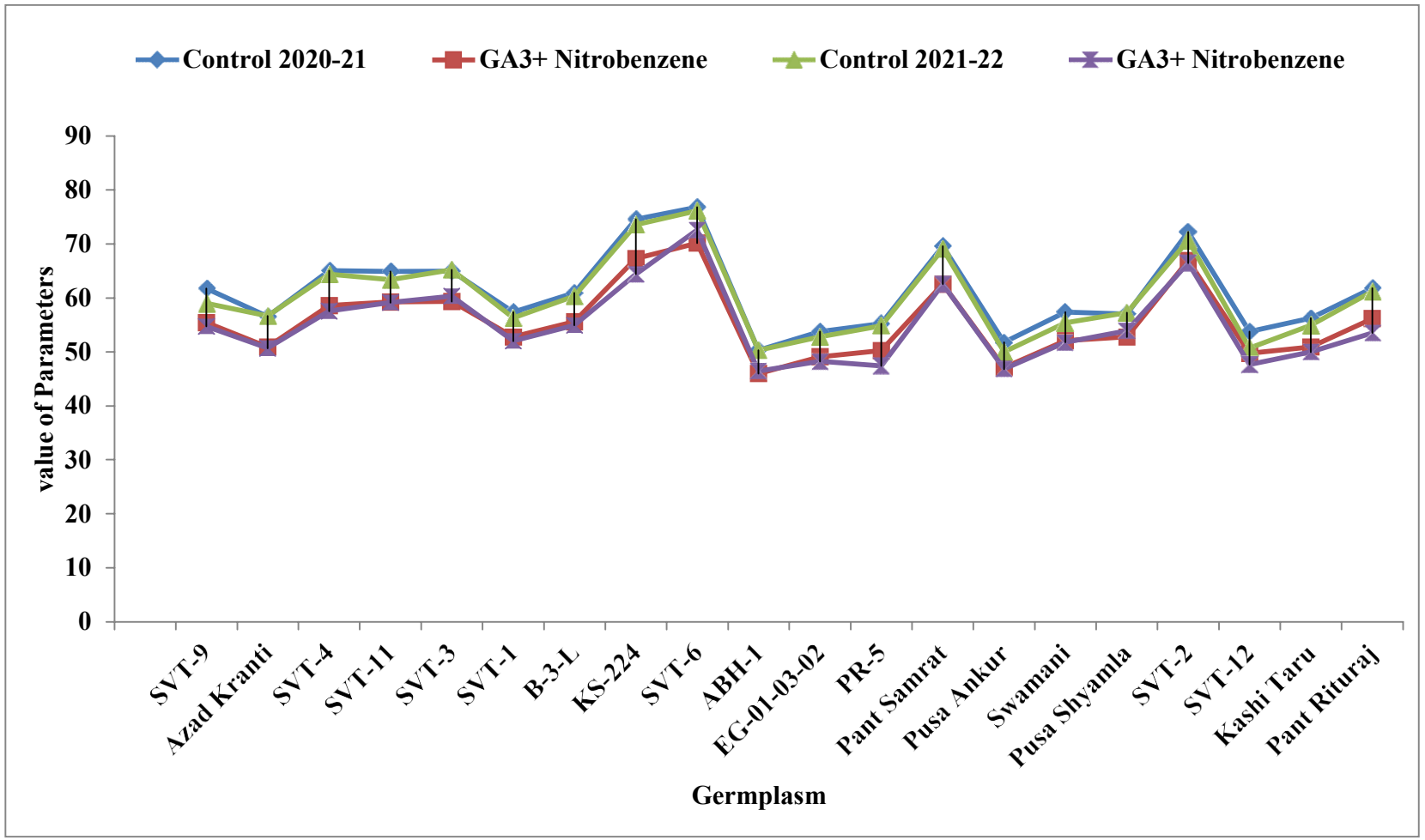


Fig.4.1. Days to 50% flowering

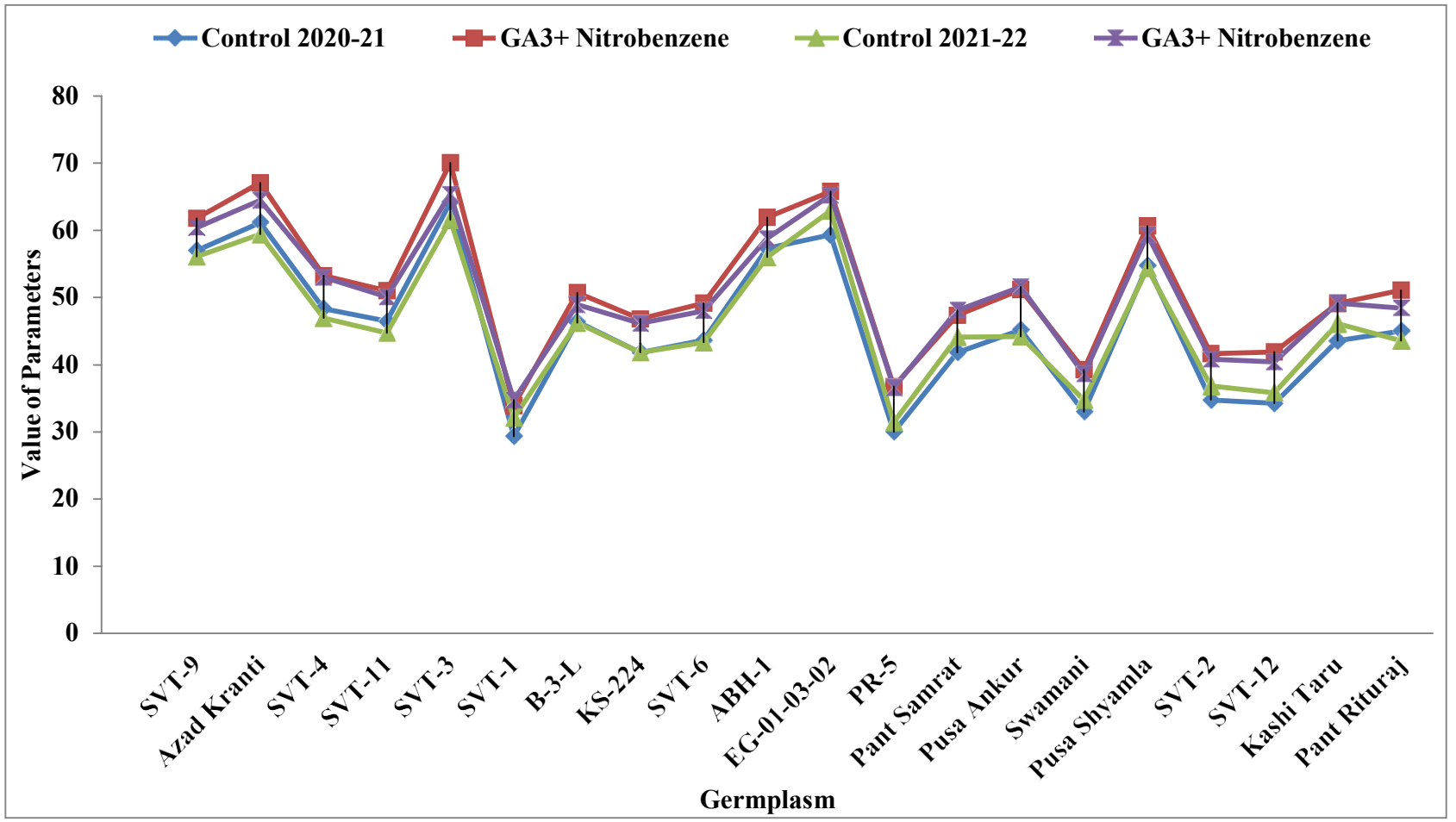


Fig. 4.2. Number of flowers per plant

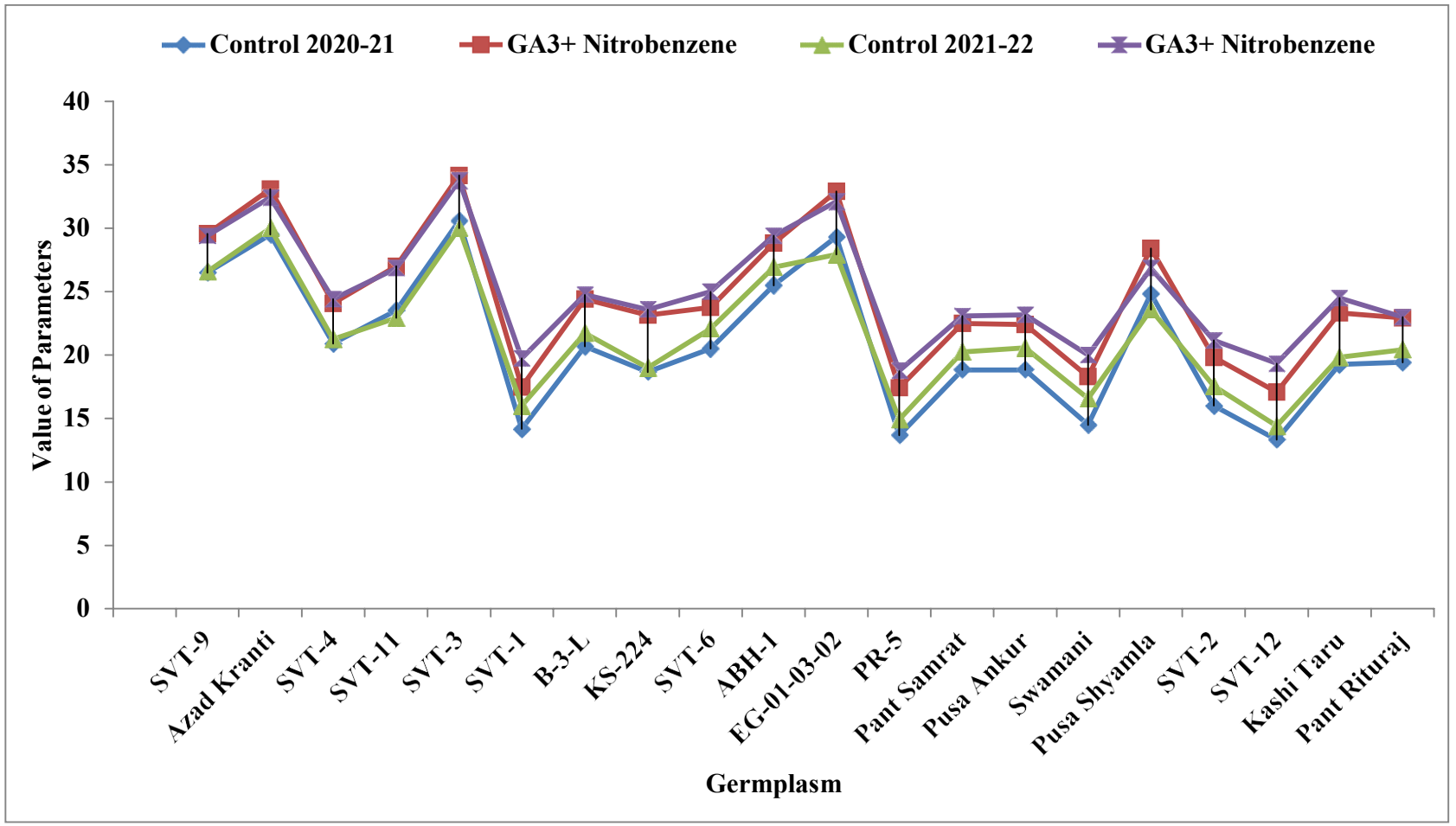


Fig. 4.3. Number of flowers attained the fruit

Fig. 4.5. PIC value of SSR primers

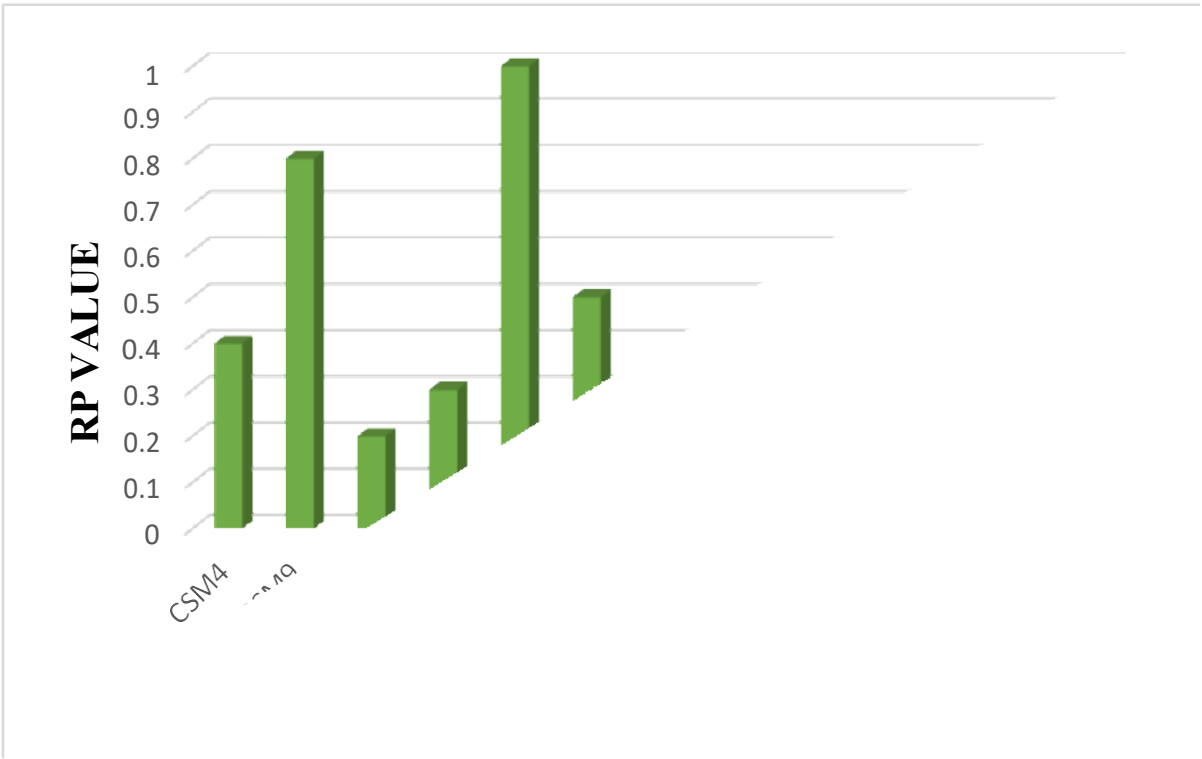


Fig. 4.6. Resolving power (RP) value of SSR primers

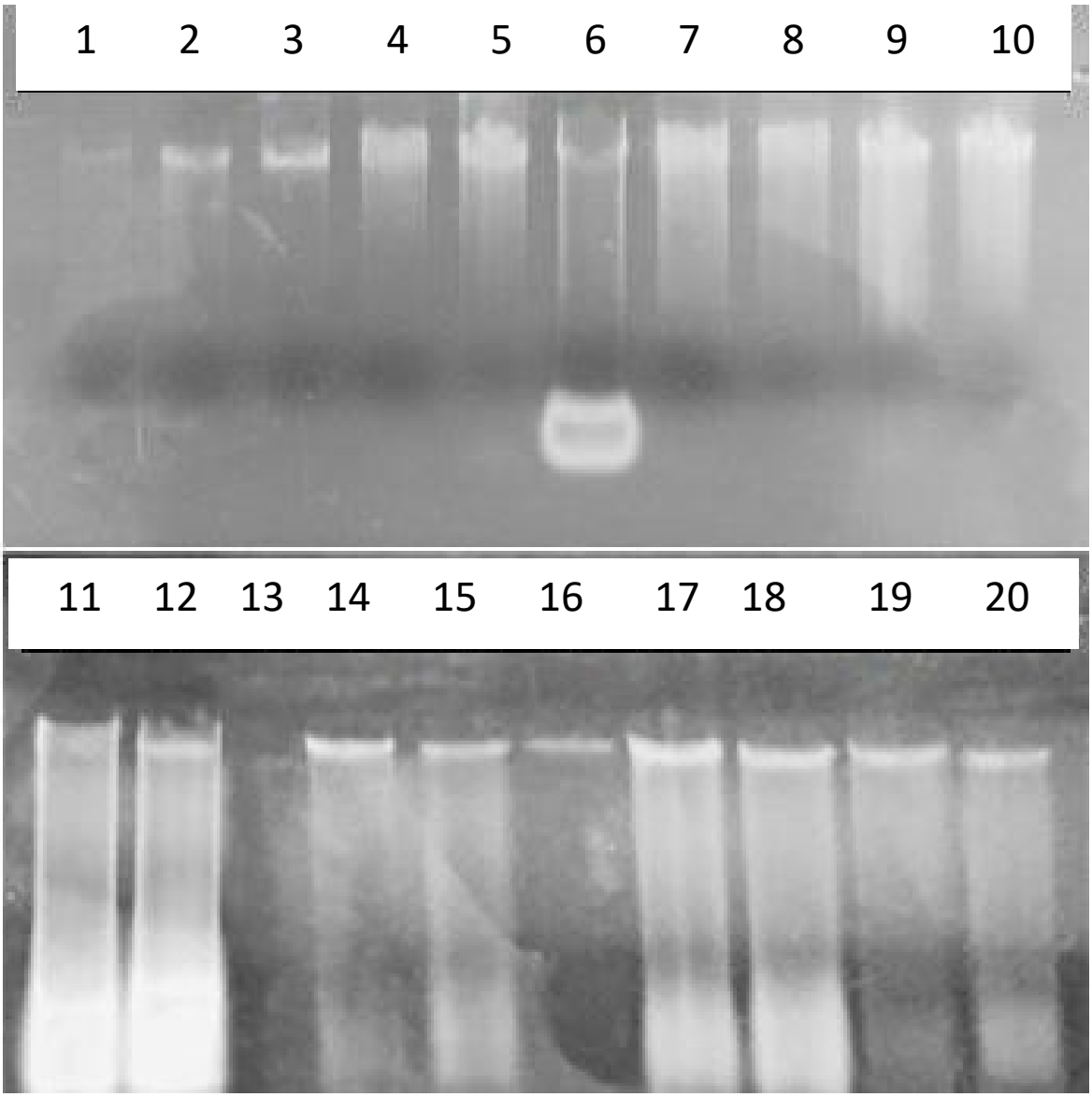
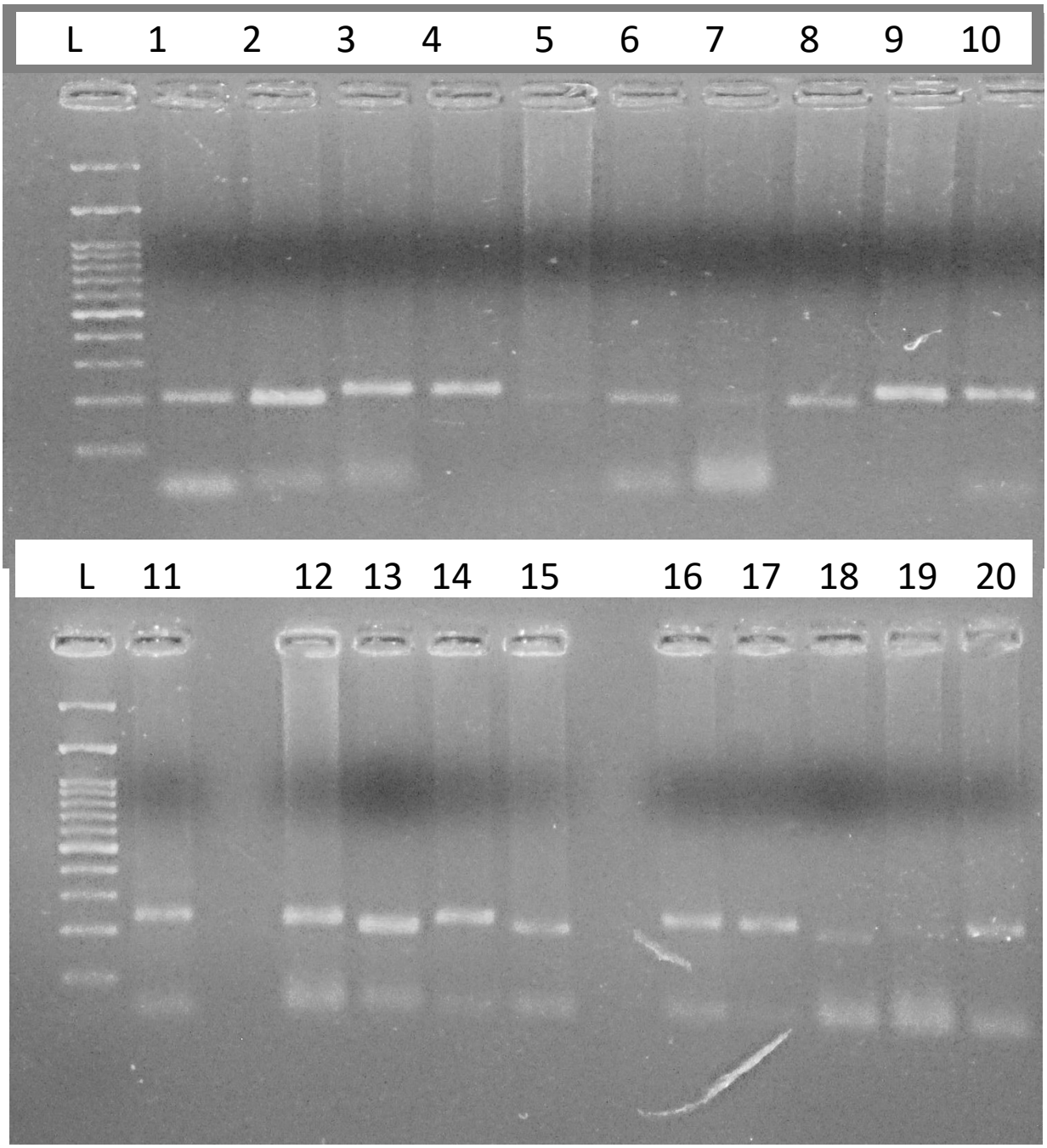


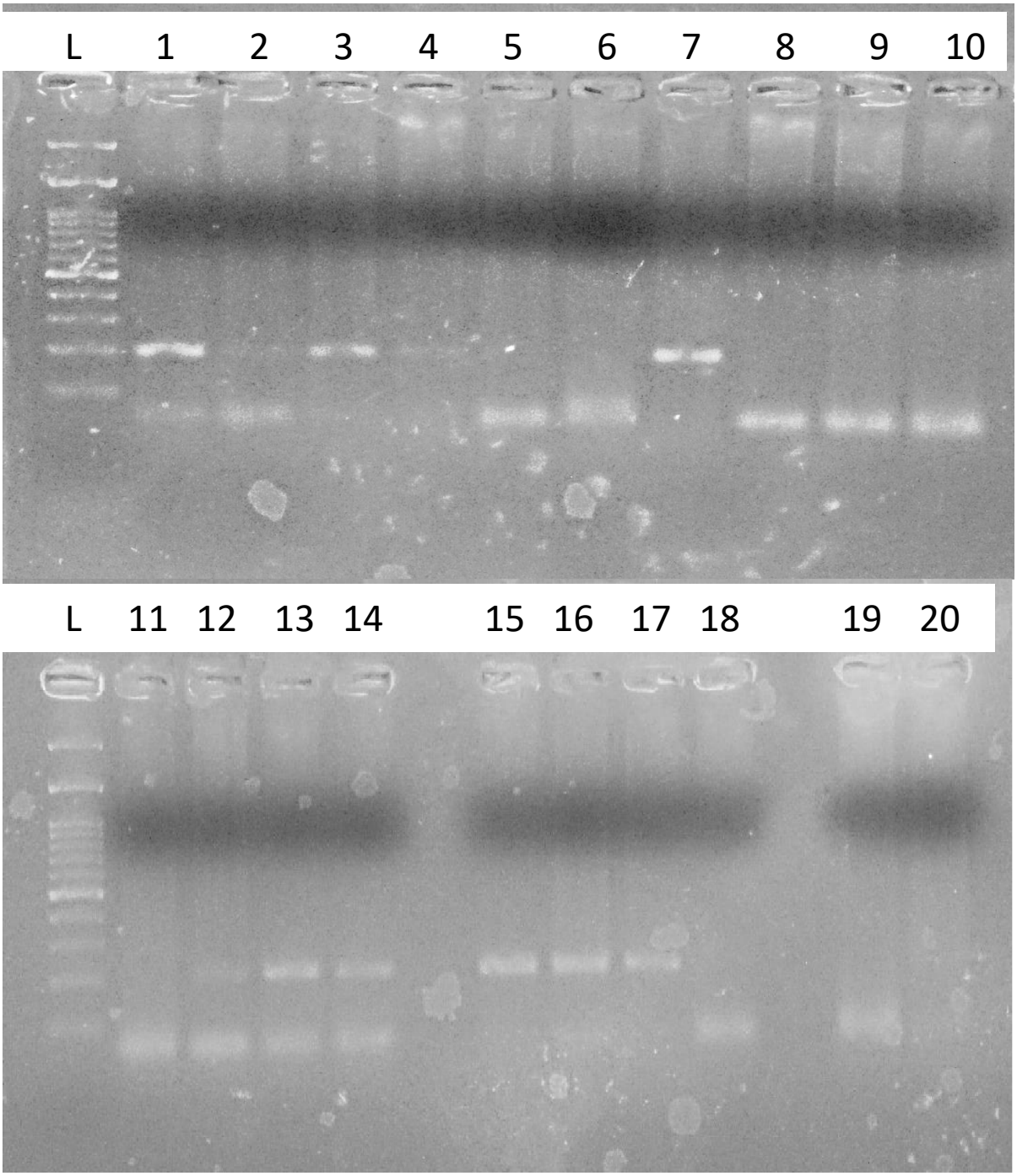
Plate 4.1 Genomic pattern of 20 brinjal genotype

L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj



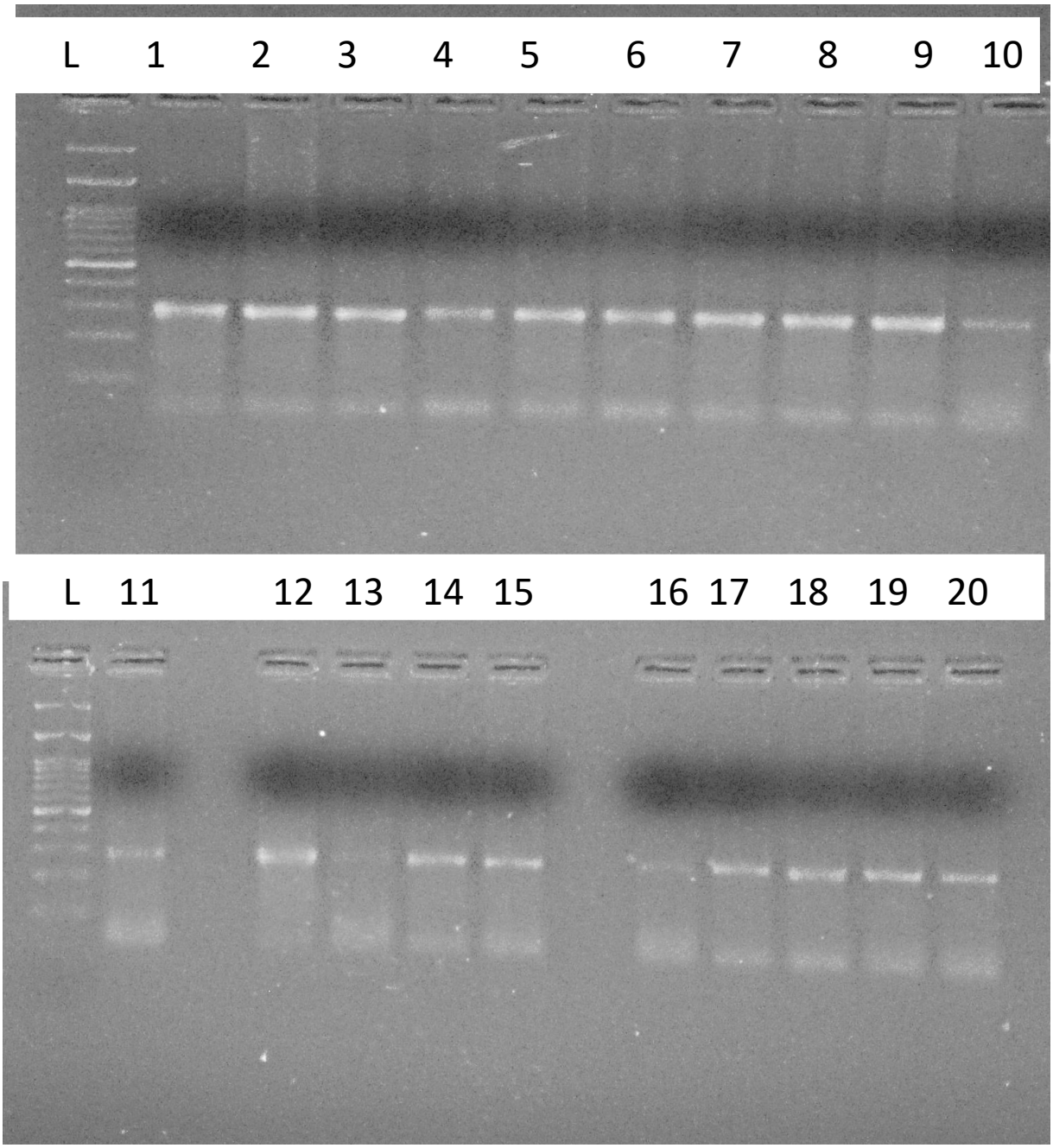
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.2. SSR profiling pattern of 20 brinjal genotype with CSM 4 primer



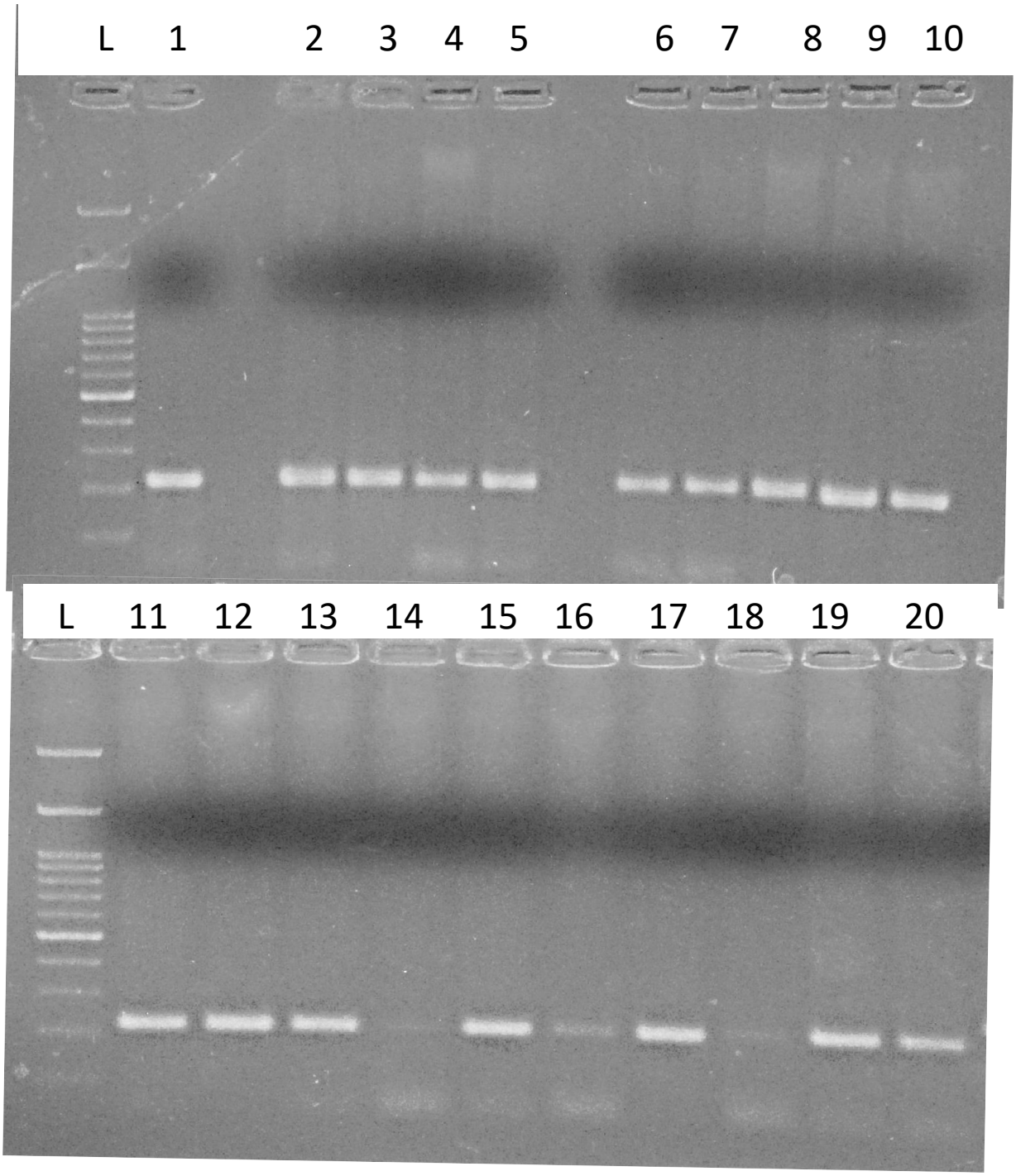
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Ritura

Plate 4.3. SSR profiling pattern of 20 brinjal genotype with CSM 16 primer



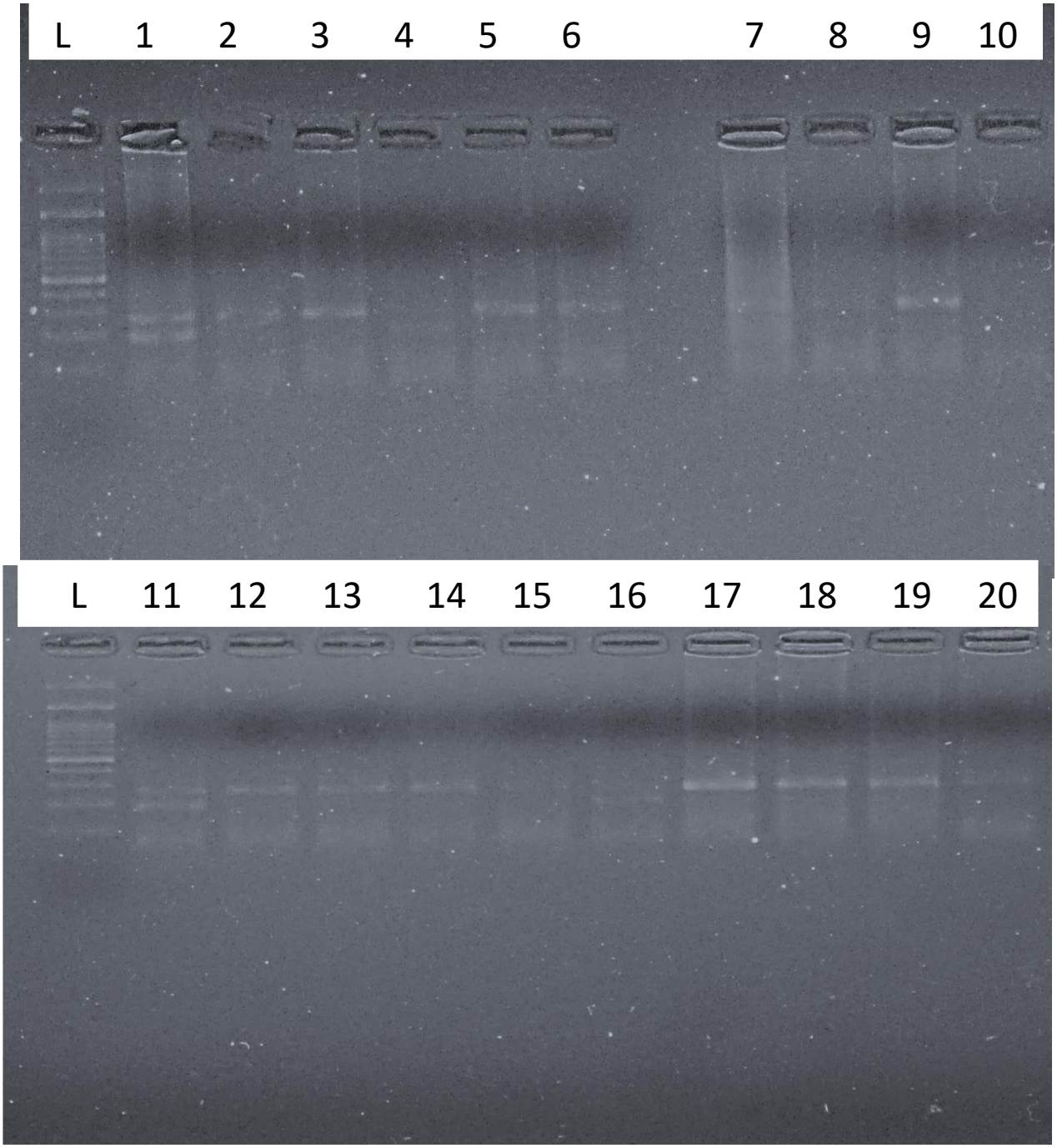
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Ritura

Plate 4.4. SSR profiling pattern of 20 brinjal genotype with CSM 16 primer



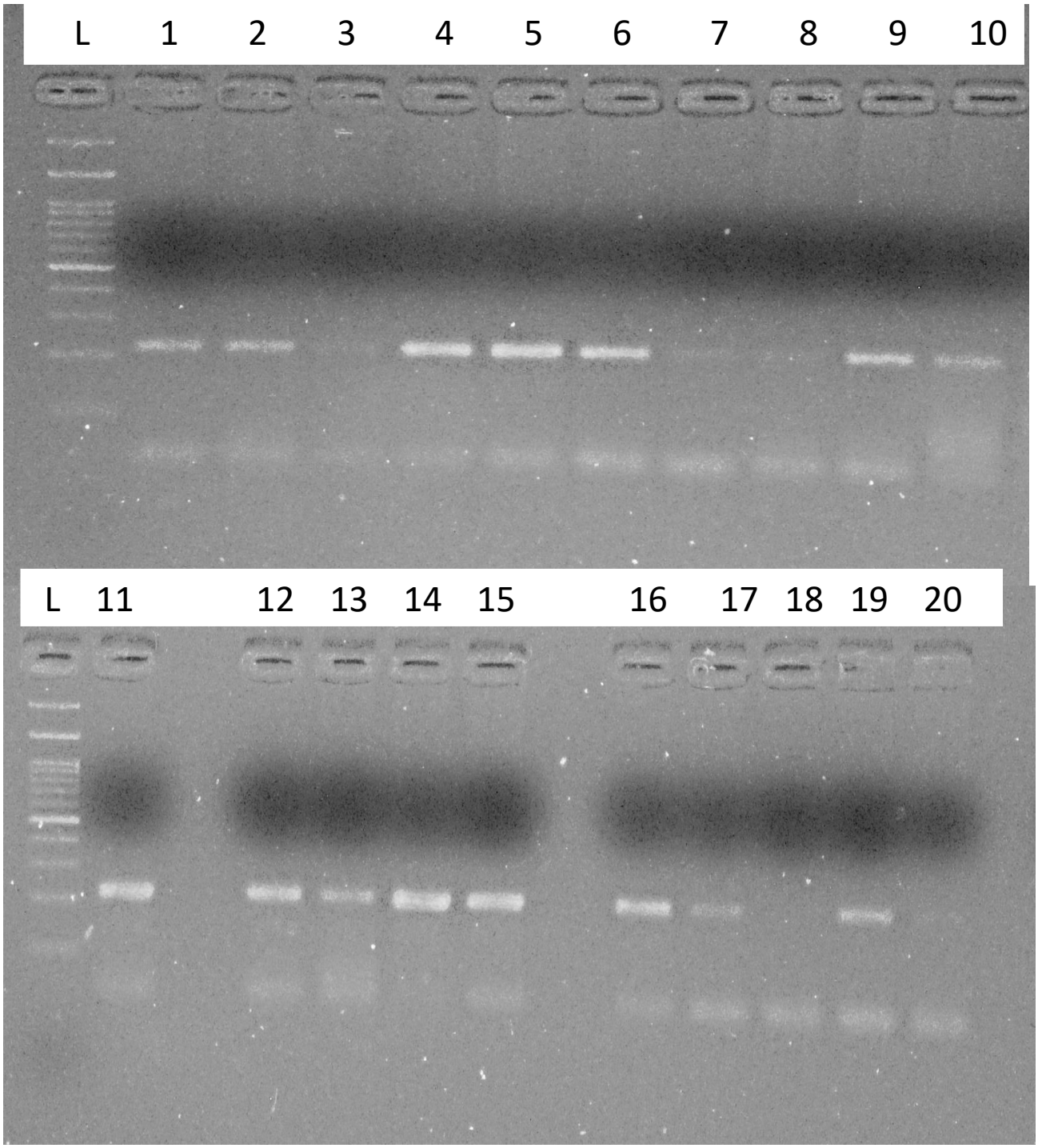
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Ritura

Plate 4.5. SSR profiling pattern of 20 brinjal genotype with CSM 16 primer



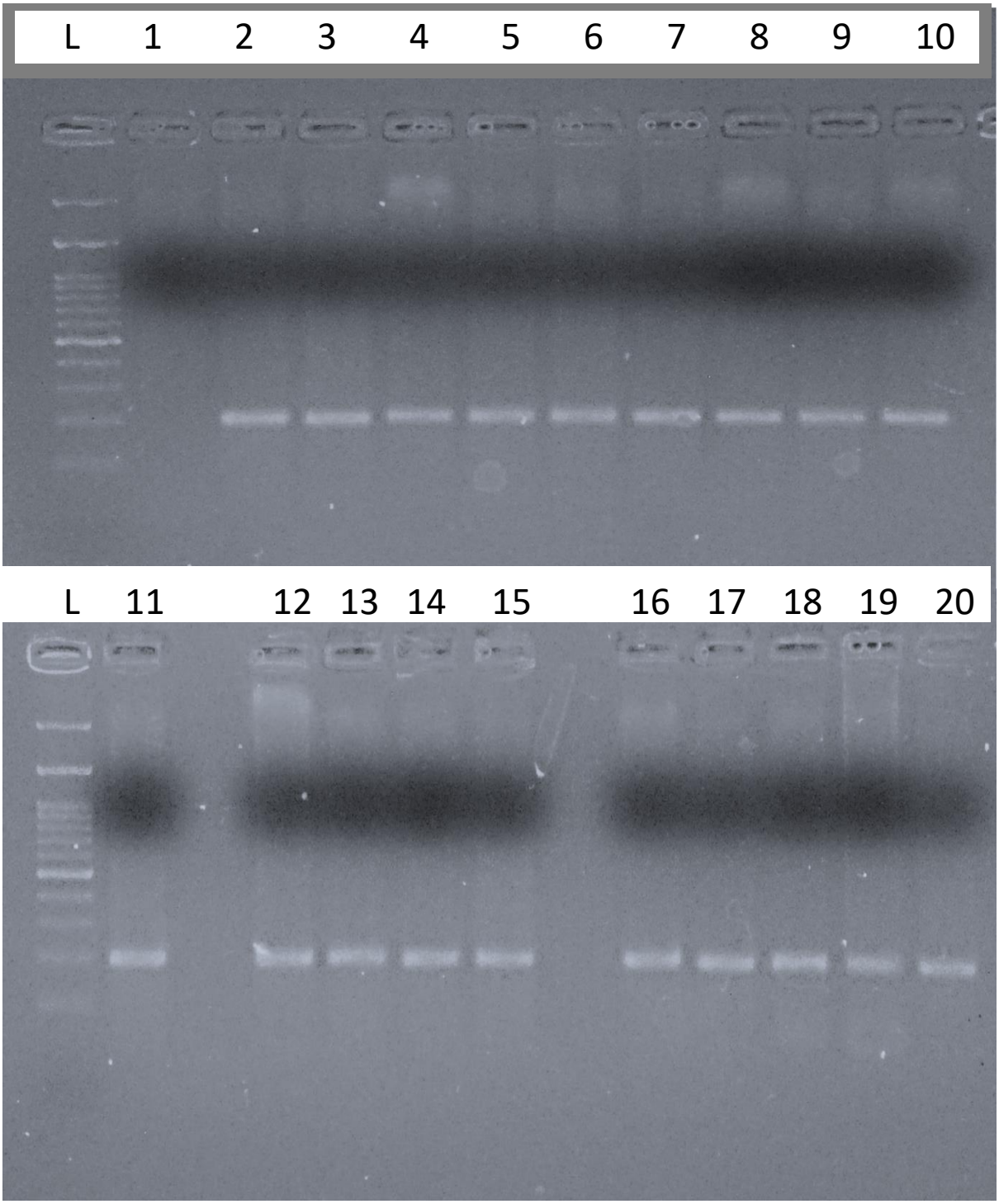
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Ritura

Plate 4.6. SSR profiling pattern of 20 brinjal genotype with CSM 25 primer



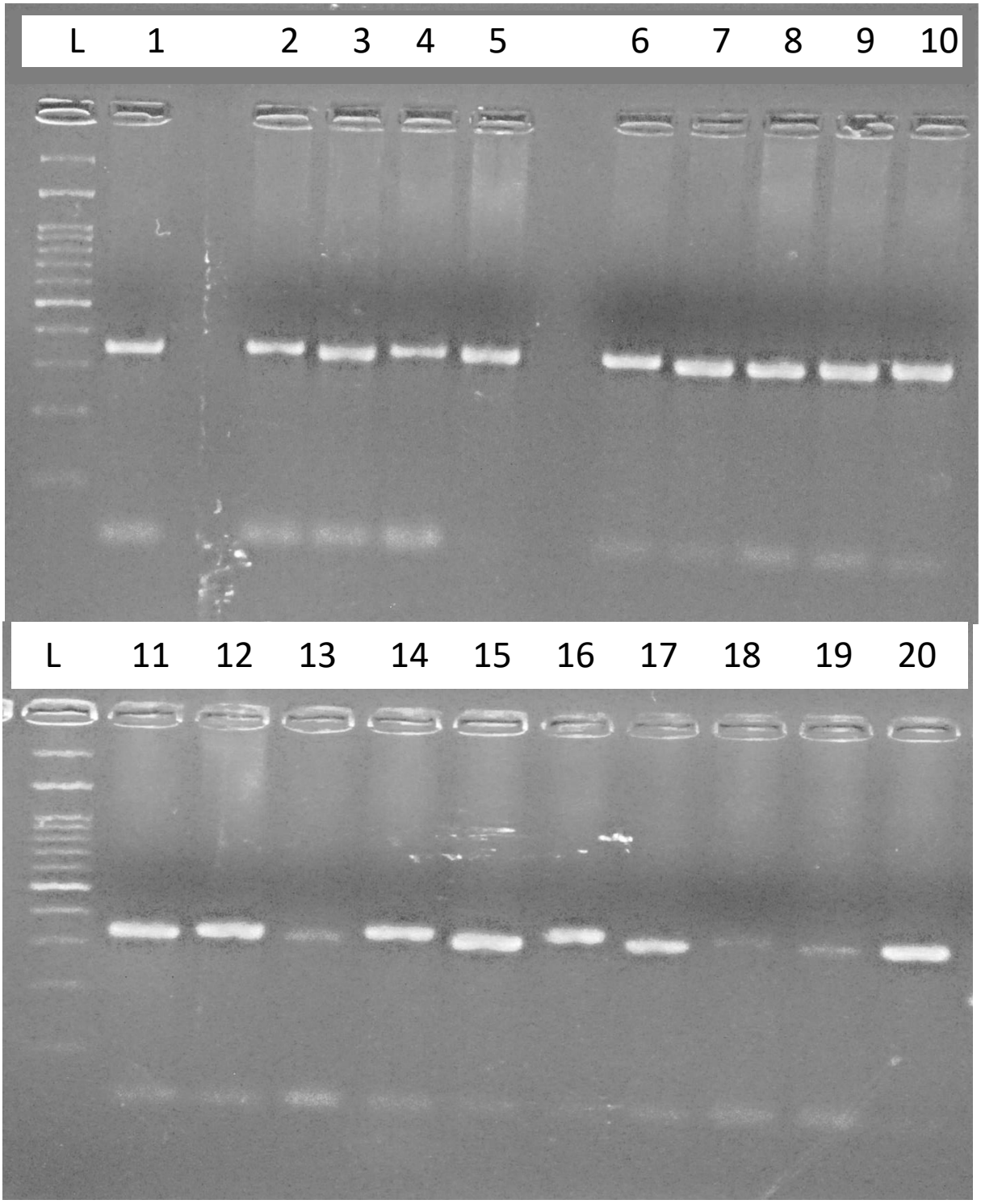
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Ritura

Plate 4.7. SSR profiling pattern of 20 brinjal genotype with CSM 26 primer



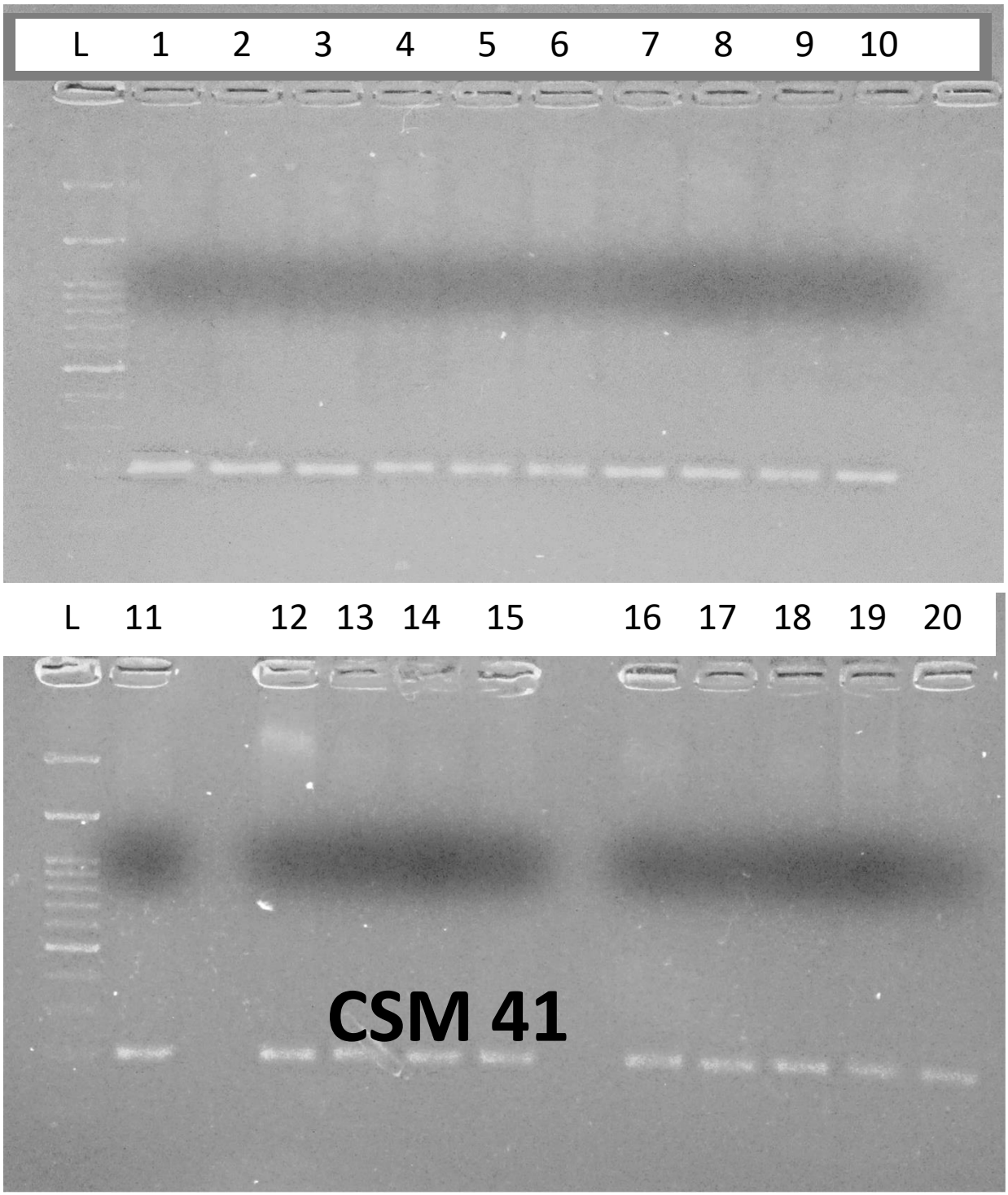
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.8. SSR profiling pattern of 20 brinjal genotype with CSM 27 primer



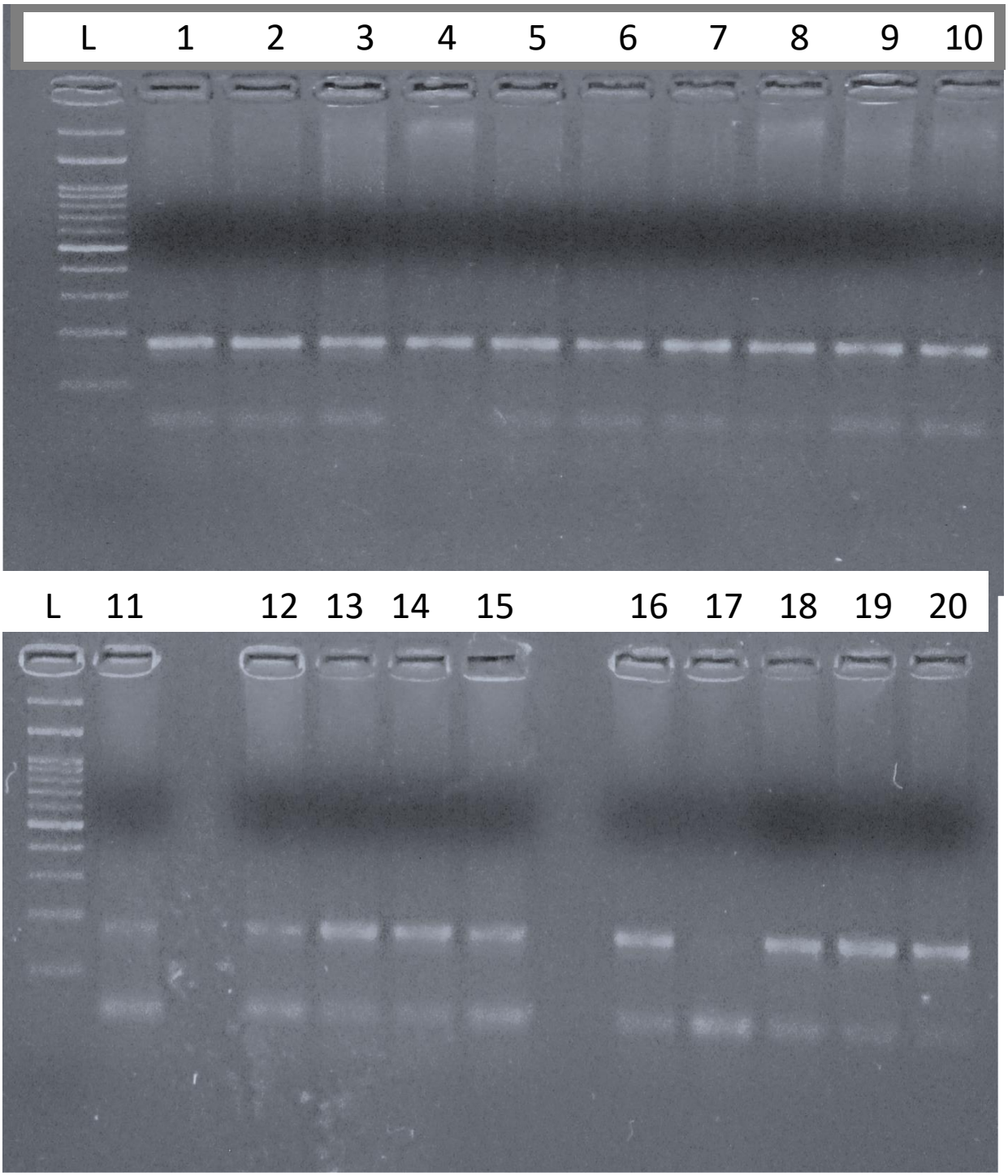
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.9. SSR profiling pattern of 20 brinjal genotype with CSM 36 primer



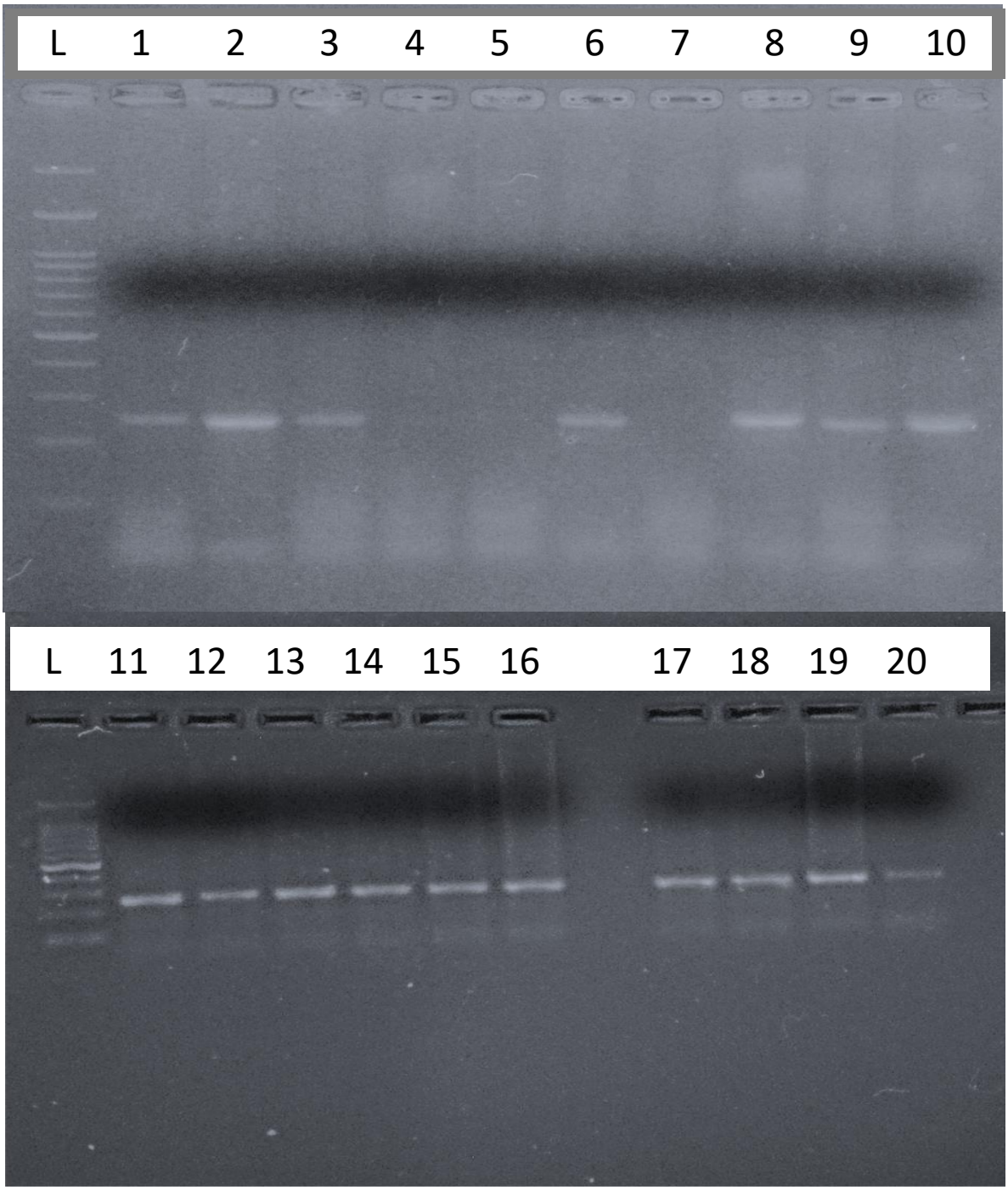
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.10. SSR profiling pattern of 20 brinjal genotype with CSM 41 primer



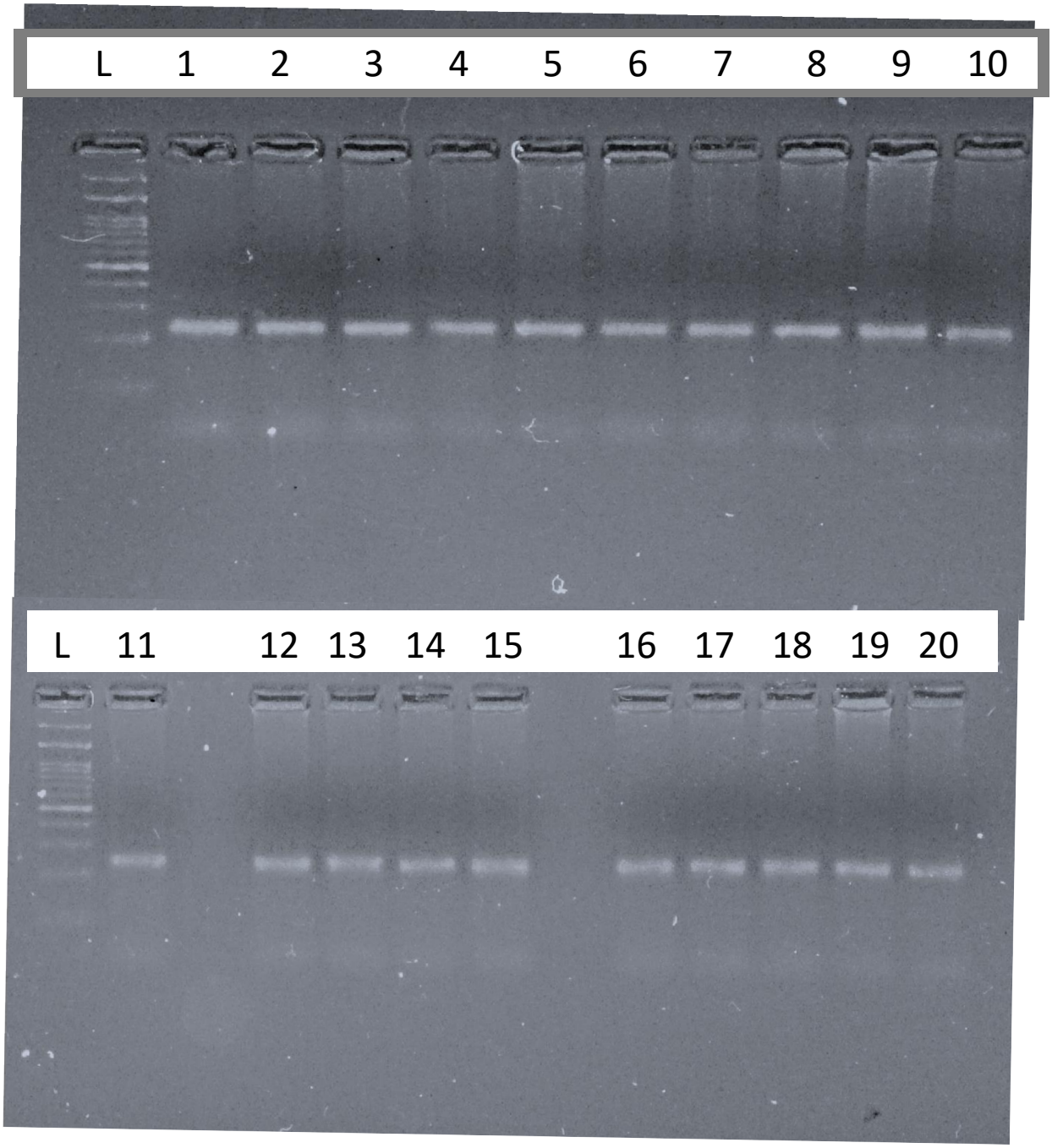
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.11. SSR profiling pattern of 20 brinjal genotype with CSM 42 primer



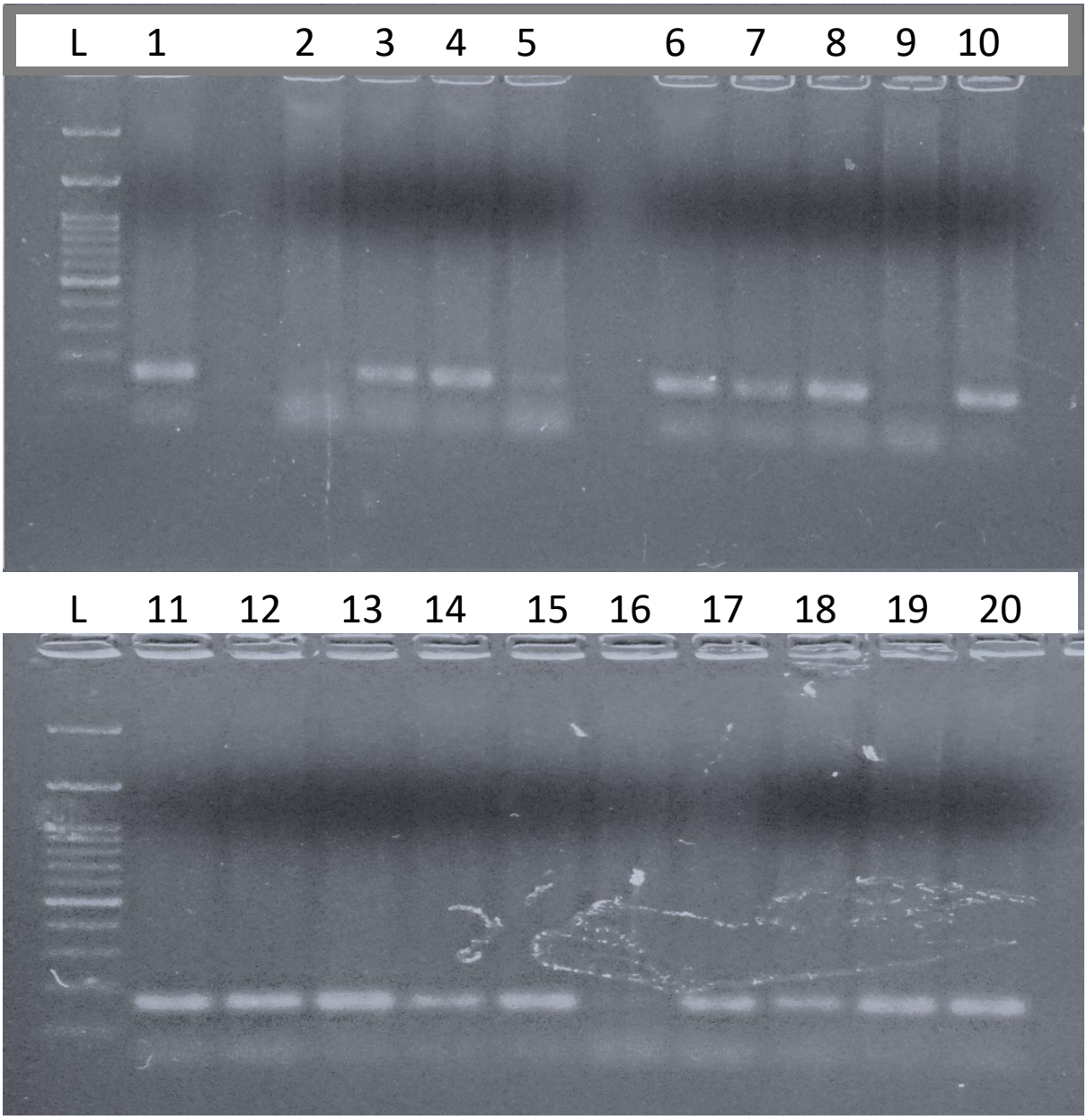
L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.12. SSR profiling pattern of 20 brinjal genotype with CSM 43 primer



L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.13. SSR profiling pattern of 20 brinjal genotype with CSM 43 primer



L- Ladder, 1-SVT-9, 2- Azad Karanti, 3- SVT-4, 4- SVT-11, 5- SVT-3, 6- SVT-1, 7- B-3-L, 8- KS-224, 9- SVT-6, 10- ABH-1, 11- EG-01-03-02, 12- PR-5, 13- Pant Samrat, 14- Pusa Ankur, 15- Swamani, 16- Pusa Shyamla, 17- SVT-2, 18- SVT-12, 19- Kashi Taru, 20- Pant Rituraj

Plate 4.14. SSR profiling pattern of 20 brinjal genotype with CSM 65 primer

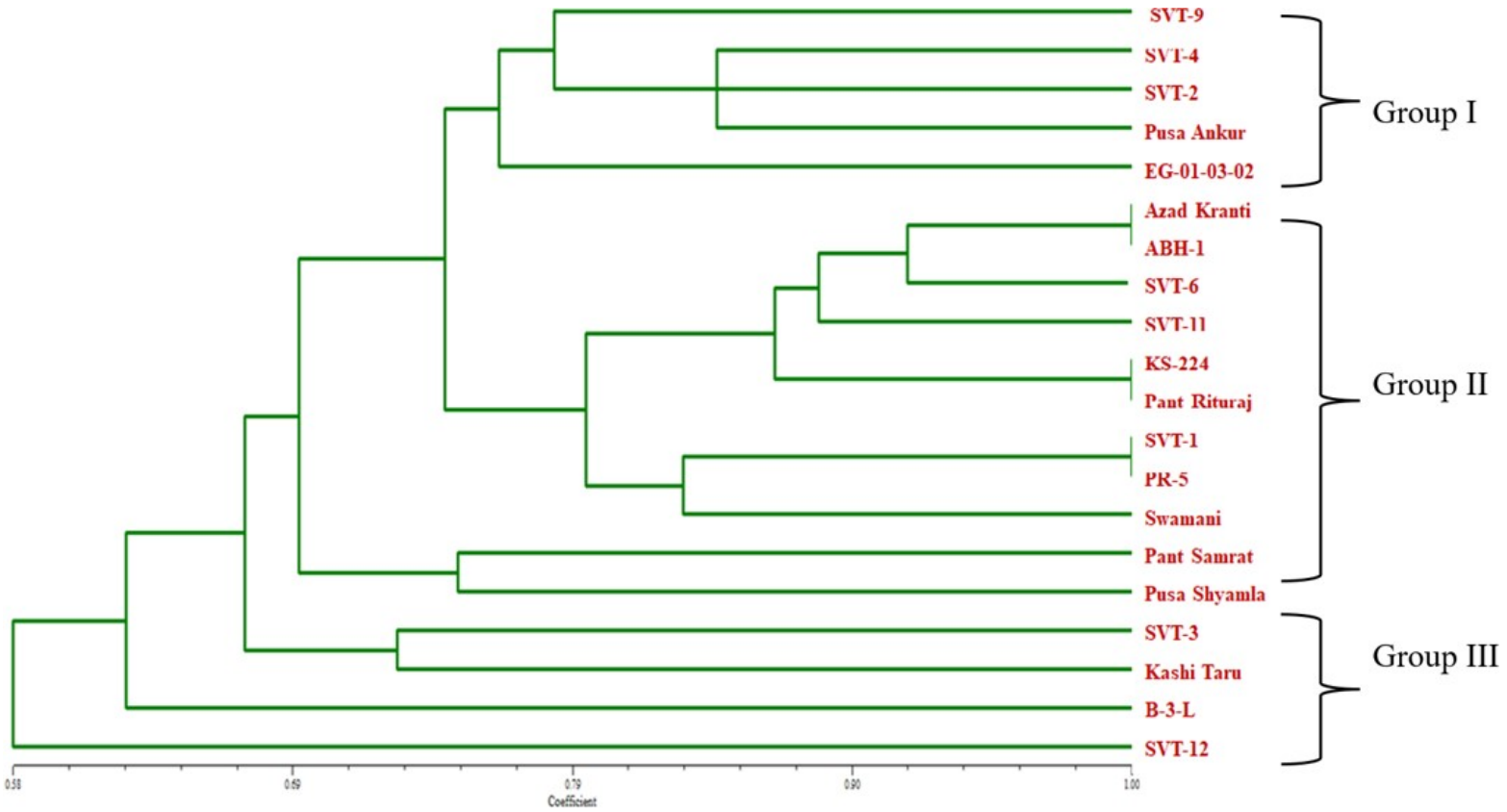


Fig. 4.7 Dendogram showing clustering pattern of 20 brinjal genotypes constructed using UPGMA based on Jaccard's similarity coefficient obtained from SSR analysis

The present investigation entitled "**Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in brinjal (*Solanum melangena* L.)"** was carried out during the *Rabi* season of year 2020-21 and 2021-22 at Horticulture Research Center department of Horticulture, college of Agriculture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram Meerut.

Brinjal is considered as one of the top ten vegetables in terms of scavenging capacity as well as one of the most consumed vegetables in the world. It has three main cultivated species and a large number of verities which have been cultivated over the globe. A wide range of variation present in any crop always provides the better chances of selecting desired type and it is important to investigate the extent of available genetic diversity in order to maintain, evaluate and utilize germplasm effectively. The major consideration for a superior variety is high economic yield, desirable maturity duration and quality trait. Information on nature and magnitude of genetic variability is of immense value for starting any systematic breeding programme in crops.

In the present investigation the genetic variability among the 20 germplasm of brinjal have been carried out using morpho-physiological and molecular tools and the results from the investigation have been discussed under the following sections: -

Effect of Gibberellic acid and Nitrobenzene on flowering characters of brinjalgenotypes

Effect of GA_3 and Nitrobenzene on flower attributing characters was carried out in the present investigation. GA_3 regulates flower initiation and its development and it is essential for male and female fertility not for differentiation of floral organs **Griffiths (2006),** GA-deficient mutants in *Arabidopsis* and tomato showed abnormal stamen

development **Griffiths (2006), Hu (2008), Rieu (2008).** While extreme GA deficiency revealed female sterility. **Nester (1988), Goto (1999),** No viable pollen develops in severe GA-deficient mutants, and sepals, petals, and pistils are underdeveloped, leading in some cases even to premature abortion of the flower. **Nester (1988), Goto (1999), Koornneef (1980).**

Nitrobenzene is an organic compound with chemical formula $C_6H_5NO_2$. Nitrobenzene is quickly absorbed into the plants. Its influences the bio- chemical pathway of the plants to uptake more nutrients from the soil. It also increases the nutrient use efficiency thus improves the vegetative growth. Induces profuse flowering and helps in the retention of the flowers and fruits.

The effect of nitrobenzene in combination of GA_3 was tested for flowering characters among the 20 different germplasm of brinjal. A significant difference among the genotypes has been evaluated in terms of Days to 50% flowering, number of flowers per plant and number of flowers attained the fruit. A significant different was observed in all the characters which was in accordance with the study of **Mithila *et al.* 2012** who observed the capacity of Nitrobenzene in improving flowering as well as the fruit setting percentage. Furthermore, observed the stimulation in growth of flower parts and promotion in early fruit setting. **Nuruzzamani *et al.* (2015)** observed the reduction in fruit drop. The results obtained from the present study might be due to Nitrobenzene transport to the axillary buds would have resulted in a better sink for the mobilization of photo assimilates at a faster rate.

Analysis of Variance (ANOVA)

The data collected on different parameters under study was subjected to the analysis of variance was done for all the characters to test the significance among the genotypes under study. The sum squares due to genotypes were further partitioned in to

Replication, Genotypes and Error or highly significance variance was observed for all thirteen characters under study. This analysis revealed that significant differences exist among the material used in the present investigation for all the thirteen characters studied viz., Plant height (cm), Number of primary branches per plant, Days to 50% flowering, Number of flowers per plant, Number of flowers attained the fruit, Plant spread (cm), Length of fruit (cm), Diameter of fruit (cm), Average fruit weight (gm), Number of fruits per plant, Fruit index, Average yield (g/plant), Stem diameter at harvesting(cm). Similar results shown by **Lenuta and Nedelea (2010), Nayak *et al.* (2014), Janaki *et al.* (2015) and Patel *et al.* (2015).**

Mean Performance of Genotypes

The study of mean performance among the genotypes for all thirteen characters viz Plant height (cm), Number of primary branches per plant, Days to 50% flowering, Number of flowers per plant, Number of flowers attained the fruit, Plant spread (cm), Length of fruit (cm), Diameter of fruit (cm), Average fruit weight (gm), Number of fruits per plant, Fruit index, Average yield (g/plant), Stem diameter at harvesting(cm) significant difference indicating sufficient genetic variability. The mean for fruit yield per plant was higher in the genotypes SVT-3 (2477.50 g) eleven genotypes recorded higher fruit yield than general mean (1703.68 g) revealed by **Chinthagunti *et al.* (2018).** Similar differences shown by **Dhameliya *et al.* (2007) and Dhaka *et al.* (2012).**

Genetic variability, heritability and genetic advance

Genetic variability is considered as an important factor which is essential requirement for crop improvement programme for obtaining high yielding progenies. Differences always exist among individuals in a population and assessing the origin and magnitude of variability is the key to success phenotypic variability is observable and includes both genotypic and environmental variations and therefore, also called total

variation. Genotypic variation refers to genetic or inherent variability, which remains unchanged by environmental conditions. The estimates of genotypic and phenotypic coefficient of variation for thirteen characters of brinjal genotypes showed that magnitude of phenotypic coefficients of variation PCV (32.13) were higher than genotypic coefficient of variation GCV (31.57) for all thirteen characters studied. Similar results shown by **Golany *et al.* (2007), Madhavi *et al.* (2015), Rad *et al.* (2015) and Pujer *et al*. (2017).**

The higher the heritable variation, the greater will be the possibility of fixing the character by selection methods. Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. The estimated values of heritability in broad sense were classified as high (more than 70%), medium (50-70%) and low (less than 50%). The results showed that the magnitude of heritability was higher than the genetic advance**.** Similar results shown by **Karak *et al.* (2012), Shekar *et al.* (2012), Patel *et al.* (2013), Mili *et al.* (2014), Madhavi *et al.* (2015) and Jirankali *et al*. (2019).**

Correlation coefficient analysis

Correlation analysis for various parameters of growth and yield components in response to plant population. Most of the parameters resulted in highly significant positive and negative correlations with brinjal yield. The interdependency of various morphological characters viz., Plant height (cm), Number of primary branches per plant, Days to 50% flowering, Number of flowers per plant, Number of flower attained

the fruit, Plant spread (cm), Length of fruit (cm), Diameter of fruit (cm), Average fruit weight (gm), Number of fruit per plant, Fruit index, Average yield (g/plant), Stem diameter at harvesting (cm) of 20 brinjal genotypes was evaluated. Variation was observed in all 20 cultivars for all characters studied. Correlation coefficients between characters were significantly negative, indicating that an increase in one variable reduces the other variable.

The most important trait, yield per plant had exhibited highly significant and positive phenotypic correlation with number of fruits per plant (0.561). While negative but non-significant correlation was exhibited between yield per plant and plant spread (-0.118). Similar results shown by **Ahmed (2013), Rajya Lakshmi (2014), Shende (2014), Angadi *et al.* (2017) and Koundinya *et al.* (2017).**

Path coefficients analysis

Path coefficient analysis is a standardized partial regression coefficient, which splits the correlation coefficient into direct and indirect effects and also measures the direct and indirect contribution of various independent variables on dependent variable. Correlation in combination with path analysis would give better insight into cause-and-effect relationship between different pairs of characters. **Dewey and Lu (1959)** for the first time applied the technique of path coefficient to plant breeding and reported that it provides important information about the specific forces acting to produce a particular correlation. In the present study, the highest positive direct effect on fruit yield per plant was observed by number of fruits per plant (1.4975), followed by average fruit weight (1.0308), number of flower attained the fruit (0.3609), fruit index (0.3415), plant height (0.2357) and Days to 50% flowering (0.0102). Negative direct effect was exerted by number of flowers per plant (-0.7466) followed by fruit length (-0.5051), fruit diameter (-0.4177), number of primary branches per plant (-0.1328), plant spread (-0.1326) and

stem diameter (-0.0709). Similar results shown by **Naliyadhara (2007), Jadhao *et al.* (2009), Mangi *et al.* (2017) and Neha *et al.* (2017).**

Genetic divergence

Mahalanobis D^2 statistics was used to measure the degree of diversification among the lines. Using this technique, grouping of lines was done in five clusters where brinjal germplasm grouped together were less divergent than the ones placed indifferent clusters based on yield performance. The clusters separated by greatest statistical distance exhibited maximum divergence. Cluster II was the largest cluster comprising of 6 genotypes (SVT-4, SVT-11, KS-224, SVT-6, Pant Samrat, Pant Rituraj) followed by cluster V with 5 genotypes (B-3-L, PR-5, Pusa Ankur, Swamani, SVT-2), cluster IV also contains 4 genotypes (SVT-9, Azad Kranti, SVT-3, Kashi Taru), cluster I contains 3 genotypes (ABH-1, EG-01-03-02, Pusa Shyamla) and cluster III contains 2 genotypes (SVT-1, SVT-12). The results showed that the inter-cluster distances between the different clusters of brinjal genotypes differed widely. The inter-cluster distances were larger than the intra-cluster distance suggesting wider genetic diversity among the brinjal genotypes of different groups. Similar results also shown by **Bansal and Mehta (2007), Mehta and Sahu (2009), Rahamn *et al.* (2014), Kumar *et al.* (2016), Ravali *et al*. (2017) and Nand *et al.* (2018).**

Antioxidant properties of different Brinjal Genotypes

Brinjal is most widely grown important vegetables with low calorie and many health benefits. It is popularity among the growers is increasing rapidly because of its richness in antioxidants like anthocyanin and phenolic acids **(Gajewski *et al.* 2009).** The chlorogenic acid is the predominant phenolic compound in all varieties tested, which is one of the most potent free radical scavengers found in plant tissues. Eggplant is a good source of dietary fiber (USDA, 2014), vitamins (vitamins B1 and B6),

minerals like potassium, magnesium, calcium, sodium and iron **(Raigon *et al.* 2008)** and has varieties of bioactive compounds, like phenolic, carotenoids and alkaloids. The cooking of eggplant enhances phenolic content and antioxidant activity as compared to raw fruits **(Kalkan and Yücecan, 2013).**

In the present investigation 20 different genotypes of brinjal were selected and comparison of their antioxidant properties was studied and discussed as follow: -

Total phenol content

Phenolic compounds have received a great deal of attention in recent years due to their powerful antioxidant properties. Eggplant fruit is a very rich source of phenolic compounds having antioxidant properties. The quantity and quality of phenols present in fruit and vegetables may be significantly influenced by cultivar, environment, soil type, growing condition, storage conditions, and cooking

Total phenol of all the cultivar used in the study was estimated on dry weight basis and a wide variation (69.23±4.15 to 120.20±6.00) was observed among the result obtained in terms of total phenol content. These findings are also in agreement with **Kaur *et al.* (2014)** who had reported the Variation in total phenols in a single species. In the present study the highest total phenol content (120.20±6.00 mg/100g) was examined in B-3-L this result was consistent to previous study reporting total phenol content in the variety GBL-1 as 39.12 mg/100g. **Kandoliya *et al.* (2015). Ahmed *et al.* (2016)** reported the phenolic content of seven eggplant varieties in the range 608.2 to 929.2 mgGAE/100g. **Uthumporn *et al.* (2016)** reported that the total phenolic content shown by Indian type dried at 40°C is 3545.8 mgGAE/100g while the lowest was shown by Thailand eggplant type dried at 50°C is 1184.3 mgGAE/100g. The observed variation in the total phenol content may be attributed to the varietal difference along with the stages of fruit at the time of harvest.

Ascorbic acid content

As per the present investigation the estimation of ascorbic acid was done on dry weight basis. It is an essential nutrient of brinjal, which helps in repairing of the tissues and in production of neurotransmitter enzyme. Being a good antioxidant, it helps in functioning of several enzymes. It is also necessary for the growth, formation of collagen, absorption of iron, boost immunity, and wound healing, maintenance of cartilage, bones, and teeth for overall development of the body.

The results so obtained from the study in terms of ascorbic acid content were found in range of 1.89±0.15 - 7.90±0.70 mg/100g. Ascorbic acid was detected in each germplasm with an average of 4.87 mg/100g. These findings are also in agreement with **Bor *et al.* (2006)** who worked with the water extract of brinjal and reported 2.25 mg/100g. **Hanson *et al.* (2006)** reported ascorbic acid content in the range of 56.00-129.00 mg/100 g on a dry mass basis. **San Jose *et al.* (2013)** reported Vitamin C content of seven eggplant cultivars of Occidental type in the range of 1.02-2.20 mg/100g. The results obtained in the present investigation are similar to the findings of **Medina *et al.* (2014)**, who has reported the content in range of 7.40-22.00 mg/100g on fresh weight basis. The variation in the reported result may be due to varietal differences or due to the differences in the harvesting time.

Anthocyanin content

Brinjal exhibits a good amount of anthocyanin which varies significantly among the varieties as each variety has distinct color resulted in variation in anthocyanin content in them. Anthocyanin rises serum antioxidant volume, prevent heart diseases and hyperlipidemia by decreasing LDL (low-density lipoprotein) oxidation. It is helpful in reducing the weight by plummeting serum triglyceride and cholesterol and increasing

high-density lipoprotein (HDL) cholesterol and decreasing serum triglyceride level **(Seeram *et al.* 2001).**

Antioxidant study in terms of anthocyanin was carried out in the present research. The anthocyanin content of all 20 genotypes varied significantly and was estimated in a range varied from 0.68±0.03 mg/100g in T1 (SVT-9) to 73.24±4.39m T19 (Kashi Taru). The results obtained from the present investigation are in accordance with the various earlier researchers. **Eun-Ju *et al.* (2011)** reported that the highest anthocyanin content was in peel (138.05 mg/100g) whereas the pulp contains 2.29 mg/100g. **Li *et al.* (2012)** reported that the anthocyanin content was found to be 29.55 mgCya-3-glu/100g on a dry weight basis. **Boulekbache-Makhlouf *et al.* (2013)** reported that the anthocyanin content of the three different extracts were about 51.56 and 82.83 mgDGE/100g DP for acetone and methanolic extracts, respectively. **Medina *et al.* (2014)** reported the highest anthocyanin content in the Philippine variety was to be 161.00 mgC3GE/100g. **Lo Scalzo *et al.* (2016)** reported much higher anthocyanin contents in three genotypes 'Tunisina', 'Buia' and 'L305' as 41.00, 155.00 and 96.00 mgDel-3-glu/100g respectively. Such variation in the anthocyanin content might be due to varietal difference, stage of harvest and different nutrient status of the soil.

Polyphenol oxidase content

Polyphenol oxidase investigation for 20 germplasm was carried out in sequence of antioxidant study of brinjal. Polyphenol oxidase responsible for browning reaction and a important constituent for quality parameter in the vegetable. The enzyme catalyses the o- hydroxylation of monophenol (Phenol molecules in which the benzene ring contains a single hydroxyl substituent) to o-diphenols (phenol molecules containing two hydroxyl substituent's). They can also further catalyze the oxidation of o-diphenols to produce o-quinines. It is the rapid polymerization of o-quinones to

produce black, brown or red pigments (polyphenol) that is the cause of fruit browning. The PPO activity for brinjal fruit of different variety studied in present investigation varied from 0.50±0.03 mg/100g to 1.61±0.10 mg/100g. The study was also in accordance with the findings of **Kandoliya *et al.* (2015) and Neves *et al.* (2009).**

5.9 Molecular characterization

The variability among germplasm can be assessed by using different morphological and molecular markers. In brinjal, morphological variability had been assessed by several researchers **(Demir *et al. (*2010) and Verma *et al.* (2012)).** Despite, broad genetic base within *S. melongena* L**. (Khan *et al.* 2013)** it is still difficult to discriminate genotypes based on their phenotype. Moreover, phenotypic based selection and genetic analysis, which does not reliably reflect true genetic diversity, are highly affected by environment, quantitative inheritance of traits, partial and dominance trait expression. Many of these complications associated with phenotype-based assay can be easily overcome through DNA based molecular markers. With the advent of recent methods in molecular biology, different molecular markers have been applied for the study of molecular diversity in brinjal.

SSR primers analysis

In the present study 16 SSR primers was screened, out of which thirteen primers produces amplification and over used for the genetic diversity among twenty germplasm. Three primers (CSM44, CSM48 and CSM49) have not given amplification and the rest of the eleven primers give polymorphic bands. Total 175 bands were produced by eleven primers with an average of 13.46 bands per primer showing 100% polymorphism. However, two primers show monomorphic with total 40 bands with an average of 3.08 bands per primer. Similar result was reported by **Ansari *et al.* (2015) and Kaur *et al.* (2020).** The PIC value in the present investigation ranged from 0.09

(CSM27) to 0.364 (CSM9) with an average value of 0.20. PIC is a parameter associated with discrimination power of markers, depending upon the number of detectable alleles and distribution of their frequency. The result shows that primer CSM9 illustrates maximum value of PIC (0.364). In addition, the value of resolving power (RP) ranged from 0.1 (CSM27) to 1.00 (CSM25). Maximum RP showed by primer CSM25 (1.00). Cluster analysis based on untended paired group method of arithmetic means 20 brinjal genotype was clustered into three main groups Group I, Group II and Group III. Group 1 includes 5 genotypes and was further keep in one cluster, Whereas Group II includes 11 genotype and which was further sub-divided into 2 clusters and Group III includes 4 genotypes and was further keep in one cluster. Similar results were shown by **Rongali *et al.* (2017), Sharmin *et al.* (2018), Ahmed *et al.* (2019) and TG *et al.* (2020).**

CHAPTER-6 SUMMARY AND CONCLUSION

The present study entitled **"Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in brinjal (*Solanum melangena* L.)"** was carried out Horticulture Research Center department of Horticulture, college of Agriculture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Modipuram Meerut during Rabi 2020-21 & 2021-22. Twenty genotypes of brinjal were evaluated for flower induction through PGRs, genetic diversity and yield related traits. Thirteen quantitative traits were considered to obtain information on the nature and magnitude of genetic variability, degree of association among different yield contributing traits with yield and related traits and the degree of genetic divergence. The study was conducted based on morphological characterization and molecular markers (SSR).

Finding of the present study are summarized in the following heads: -

Flower induction through growth regulators

Since fruit setting in brinjal is hinders due to different lengths of style, application of GA_3 and Nitrobenzene improved significantly in days to 50% flowering by 4-7 days during 2020-21 and 3.08-7.67during 2021-22, number of flowers per plant by 4.33-7.66 during 2020-21 and 2.33-7.41 during 2021-22 and number of flowers attained the fruit 3.08-4.5 during 2020-21 and 2.42-4.67 during 2021-22 among all the germplasm studied.

Morphological characterization

The data collected on different parameters under study was subjected to the standard statistical analysis describe in the previous chapter the analysis of variance was

done for all the characters to test the significance among the genotypes under study. This analysis revealed that significant differences exist among the material used in the present investigation for all the thirteen characters.

In mean performance of twenty genotypes of brinjal, the highest days of 50% flowering (76.50) was observed in SVT- 6, while the lowest days (50.34) was recorded in ABH-1. The highest plant height (102.70 cm) was observed in SVT-4, while the lowest plant height (71.32 cm) was recorded in ABH-1. The maximum number of primary branches per plant (9.29) was recorded in SVT -1, whereas, the minimum number of primary branches per plant (4.63) was found in SVT-4. The maximum number of flowers per plant (62.88) was recorded in SVT-3, whereas, the minimum number of flowers per plant (30.71) per plant was recorded in PR-5. The highest number of successful fruit attainment was recorded in SVT-3 in which 30.30 fruit was counted out of the total flowers on the plant in the entire season, while the minimum number of flower (13.88) attained the fruit found in SVT-12. Maximum Plant spread (95.33cm) was recorded in Pant Samrat, whereas minimum plant spread (59.07 cm) was found in Pusa Shyamla. The maximum fruit length (19.86 cm) was recorded in Kashi Taru, However the minimum length (7.28 cm) was observed in Swamani. The maximum diameter of fruit recorded in SVT-12 which was 9.70 cm and the minimum diameter was found in Pant Samrat (3.60cm). The maximum stem diameter was recorded in SVT-2 which was 1.94 cm and the minimum (1.52 cm) was found in SVT-9. The Maximum number of fruits per plant (26.46) was recorded in Azad Kranti, while the minimum number of fruits per plant (10.46) was found in PR-5. The highest fruit weight (170.40 g) was found in SVT-1, while the lowest fruit weight (65.56 g) was recorded in Azad Kranti. The maximum fruit index (116.62) was

found in SVT-12, whereas, the minimum (47.17) was observed in Pusa Ankur. The highest yield per plant (2477.50 g) was observed in SVT-3 and the lowest (1050.50 g) was recorded in SVT-2.

Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits. The estimates revealed that the stem diameter showed minimum phenotypic variation (7.53) as well as genotypic variation (7.03), and Fruit length showed maximum phenotypic variation (32.13) as well as genotypic variation (31.57).

Estimates of heritability and genetic advance for different characters revealed the minimum heritability was found in minimum heritability was found plant height (78.88) and the maximum heritability was found in average fruit weight (99.58) among thirteen characters of brinjal. Expected genetic advance (GA) as percentage of mean was observed minimum in stem diameter (13.53) and maximum in fruit length (63.91).

The path coefficient analysis revealed that the significant positive direct effect on yield per plant was observed by Number of fruits per plant (1.4975), average fruit weight (1.0308), number of flowers attained the fruit (0.3609), plant height (0.2357) and Days to 50% flowering (0.0102) indicating that these traits will be considered as main component of selection in a breeding programme for higher seed yield. While, negative direct effect was exerted by flower per plant (-0.7466) followed by fruit length (-0.5051), fruit diameter (-0.4177), primary branches per plant (-0.1238), plant spread (-0.1236) and stem diameter (-0.0709) at both genotypic and phenotypic level.

Cluster mean shows that days of plant height exerts highest mean for cluster IV (92.19) and minimum recorded with cluster I (74.15). Number of primary branches per

plant shows highest mean with cluster III (7.71) and lowest for cluster II (5.40). The maximum mean value for days of 50% flowering exerts highest mean for cluster II (68.39) and lowest for cluster I (53.60). Number of flowers per plant gives highest mean with cluster IV (56.14) and lowest was recorded with cluster III (32.88). Number of flowers attained the fruit shows highest mean with cluster IV (26.53) and lowest mean was found with cluster III (14.98).

Plant spread shows maximum (83.72) mean value for cluster II and minimum (63.32) for cluster I. Fruit length shows maximum (15.83) mean value for cluster IV and minimum (10.15) for cluster II. Fruit diameter shows maximum (9.29) mean value for cluster III and minimum (4.69) for cluster IV. Stem diameter shows highest (1.85) mean value for cluster V and lowest (1.63) for cluster IV. Number of fruits per plant shows maximum (23.50) mean value for cluster I and minimum (11.40) for cluster III. Average fruit weight shows maximum (153.04) mean value for cluster III and minimum (75.51) for cluster I. Fruit index shows maximum (109.70) mean value for cluster III and minimum (57.57) for cluster V. Yield per plant shows maximum (2117.25) mean value for cluster IV and minimum (1306.23) for cluster V.

The value of intra cluster distance was observed maximum (2.464) in cluster II and minimum (2.064) in cluster III. Whereas, Cluster IV shows the maximum (6.613) inter cluster distance with Cluster I and minimum (2.755) inter cluster distance observed between clusters V with cluster II.

Twenty genotypes were analyzed and grouped into 5 clusters. Cluster II had maximum 6 genotypes, cluster V had 5 genotypes and cluster VI also consist 4 genotypes, cluster I have 3 genotypes and minimum in cluster III have 2 genotypes. These results revealed that the

selections grouped within a particular cluster were more or less genetically similar to each other.

Antioxidant properties

Among the genotypes the highest content of total phenol was found under T7 (B-3-L) 120.20±6.00 mg/100g and lowest T1 (SVT-12) in which 69.23±4.15 mg/100g.

Highest content of Anthocyanin was found under T19 (Kashi Taru) which was 73.24±4.39 mg/100 g and minimum content was observed under T1 (SVT-9) in which only 0.68±0.03 mg/100 g.

The maximum Polyphenol oxidase was recorded under T19 (Kashi Taru) in which 1.61±0.10 mg/100g and minimum (0.50±0.03 mg/100g) PPO was found in T1 (SVT-9).

The maximum amount of ascorbic acid was detected under Treatnet13 (Pant Samrat) in which 7.90±0.70 mg/100g and minimum amount was found under T4 (SVT-11) with 1.89±0.15 mg/100g.

Molecular characterization

Cluster analysis based on SSR analysis of 20 brinjal genotypes were grouped into three main cluster like Group I, Group II and Group III. Group I include 5 genotypes and was further keeping in clusters (GI-C1) which comprises five genotypes. Whereas, Group II includes 11 genotypes, subdivided into 2 clusters (GII-C1, GII-C2), which comprises eight, six and five genotypes respectively. While Group III includes 4 genotypes and was further keep in one cluster (GIII-C1). PIC values for SSR loci ranged from 0.09 (CSM27) to 0.364 (CSM9) with an average value of 0.20. Primer CSM9 showed maximum PIC value (0.364). In addition, the value of resolving power ranged from 0.1 (CSM27) to 1.0 (CSM25). Maximum resolving power showed by primer CSM25 (1.0).

Conclusion

- Based on the present investigation, it is observed that GA_3 and Nitrobenzene can be utilized for more flowers in short duration for obtaining higher yield.
- Generally, substantial variability in the considered traits among the brinjal genotypes was observed and this might be used as important input for the future breeding programme. It is expected that from these results new brinjal varieties can be obtained to increase the production and productivity to the crop substantially.
- On the basis of mean performance of genotypes, it can be concluded that genotypes SVT-3, Kashi Taru and SVT-6 performed best for fruit yield per plant in the present investigation.
- The present investigation showed significant phenotypic and genotypic variation between genotypes for the traits considered. Improvement in fruit or yield could be achieved by direct indirect selection for high yielding genotypes or for yield components positively associated to yield.
- The correlation studies conclude that the, traits number of fruits per plant, fruit index, average fruit weight, fruit diameter, plant spread were correlated to each other and will have great influence in increasing the fruit yield of the studied crop.
- The path coefficient analysis concludes that characters Number of fruit per plant on fruit yield via average fruit yield, number of flowers attained the fruit, plant height and days to 50% flowering fruits per plant, had highest significant positive direct effect on fruit yield per plant. Thus, selection of these traits can be considered as guidelines for further breeding work.

- High heritability coupled with high genetic advance as percentage of mean were observed by the characters viz., fruit length showing the influence of additive gene action on the characters hence, may be useful for effective and modified selection.
- Antioxidant study in brinjal can further be utilized for selecting the promising germplasm.
- Based on molecular analysis of SSR was extremely useful for studying the genetic relationship between brinjal genotypes.
- Finally, these studies have given important clues in understanding genotypes relationship, which may further assist in developing and planning breeding strategies.
- Genotypes falls in cluster IV may be selected as a parent for further breeding program for getting higher yield.
- PIC value in UPGMA dendrogram shows the wide variation among genotypes studied and the most diverse genotypes such as SVT-12 and B-3-L may be used as parent material.

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ABSTRACT

Name: Kaushelendra Pratap Singh **Id. No. :** 3674
Major: Horticulture **Degree:** Ph.D (Horticulture)
Minor: Ag. Biotechnology **Department:** Horticulture
Advisor: Dr. Bijendra Singh

Thesis title: "Studies on induction of flower through growth regulators and genetic diversity analysis by molecular markers in brinjal (*Solanum melangena* L.)"

The present study was conducted at Horticultural Research Center of SVP University of Agriculture & Technology, Meerut during *Rabi* 2020-21 and 2021-22. 20 genotypes of brinjal were evaluated for genetic diversity analysis and yield related traits in randomized block design (RBD) with three replications. Thirteen quantitative traits were considered to obtain information on the nature and magnitude of genetic variability, degree of association among different yield contributing traits and the degree of genetic divergence and molecular analysis. Analysis of variance revealed substantial amount of variability among the genotypes for all the characters, under study, indicated wide spectrum of variability among the genotypes. High genotypic and phenotypic coefficient of variation was observed for fruit index (31.57, 32.13), moderate PCV and GCV was recorded for fruit diameter (30.34, 29.79), fruit index (29.60, 28.53), number of fruit per plant (27.55, 26.81), average fruit weight (26.13, 26.08). High heritability coupled with high genetic advance was observed for average fruit weight (99.58, 53.60), Plant spread (96.59, 28.12), fruit length (96.55, 63.91), fruits diameter (96.44, 29.79). Fruit yield per plant exhibited highly significant and positive correlation with average fruit weight (0.685, 0.698) both genotypic and phenotypic level. Path coefficient analysis showed that numbers of fruit per plant (1.4975) have direct positive effect on genotypic level and fruits per plant (1.1092) have direct positive effect at phenotypic level. Mahalanobis (D^2) static revealed considerable genetic diversity among the genotypes. Genotypes were grouped into 5 clusters. Cluster II had maximum 6 genotypes. In the present study, the maximum intra cluster distance was observed for cluster III, the maximum inter cluster distance was revealed between Cluster I & III. At molecular level 13 SSR primers produced 215 alleles. PIC values ranges from 0.09 to 0.364 with the average value 0.20 for SSR markers. Average resolving power is 0.35 for SSR primers. Unweighted pair-group method arithmetic average cluster analysis and principal coordinate analysis on the marker-based GS grouped the cultivated varieties separately from whole accessions into different clusters. On the basis of theses range of PIC value, the genotypes SVT-12 and B-3-L may be considered as parents for further breeding program for different traits.

(Dr. Bijendra Singh)
Advisor

(Kaushelendra Pratap Singh)
Author

CURRICULUM VITAE

Name :Kaushelendra Pratap Singh
Date of Birth :10.02.1993
Place of Birth :Lakhimpur Kheri,U.P.

ACADEMIC QUALIFICATIONS:

- 2009: Passedhigh school examination from Kisan Inter College Lakhimpur Kheri(U.P.)
- 2011 : PassedIntermediate Examination fromShri Laxman PrasdaRaj Inter College Lakhimpur Kheri (U.P.)
- 2016 : Completed Bachelor of Science in Agriculture (B.Sc.Ag.) from Narendra Deva University of Agriculture & Technology Faizabad (U.P.).
- 2018:Completed M.Sc. (Ag.) Horticulture from Sardar Vallabhbhai Patel University of Agriculture & Technology, Meerut. 250110 (U.P.).

RESIDENTIAL ADDRESS:

- Name :Kaushelendra Pratap Singh
- S/O :Saranam Singh
- Address :Village Daudapur,Post Bhoolanpur, Lakhimpur Kheri (U.P.).
- Pin: 261501
- Mobile No. :9648121414
- E-mail :*kpsingh6444@gmail.com*