

बैंगन (सोलेनम मेलोनजेना ली.) एवं उसके वन्य संबंधियों के मध्य संकरण
योग्यता एवं आनुवंशिक संबंध

**STUDIES ON CROSSABILITY AND GENETIC RELATIONSHIP
AMONG EGGPLANT (*Solanum melongena* L.) AND WILD
RELATIVES**

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AMONG EGGPLANT (*Solanum melongena* L.) AND WILD
RELATIVES**

By

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This is to certify that the thesis entitled “**Studies on crossability and genetic relationship among eggplant (*Solanum melongena* L.) and wild relatives**”, submitted to the Post-Graduate School, Indian Agricultural Research Institute, New Delhi, in partial fulfillment of the requirements for the degree of **Doctor of Philosophy in Horticulture**, embodies the results of bonafide research work carried out by **Ms. Chingakham Premabati Devi (Roll no. 10001)** under my guidance and supervision. No part of the thesis has been submitted for any other degree or diploma.

All the assistance and help received during the course of the investigation have been duly acknowledged by her.

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1. INTRODUCTION

Brinjal (*Solanum melongena* L, $2n=2x=24$), commonly known as eggplant, aubergine or Guinea squash is one of the most popular warm season vegetable crops grown throughout the world. The crop is an integral part of Indian cuisine and purple coloured fruits are mostly preferred. The green and white coloured fruits are also popular due to appealing of colour. It is rich source of vitamins, minerals, fibres and other phytochemicals which have medicinal properties (Gebhardt and Thomas, 2002). Its juice has been used for treatment of asthma, bronchitis, cholera and dysuria and also beneficial in lowering blood cholesterol (Kashyap *et al.*, 2003). Besides these, the fruits contain anthocyanins and highest phenolic compounds (chlorogenic acid) which have antioxidant properties (Stommel and Whitaker, 2003; Mennella *et al.*, 2012; Prohens *et al.*, 2007). Among various vegetables, evaluated for antioxidant activity, eggplant ranked among the top ten for superoxide scavenging activity (Kaur *et al.*, 2013). Because of this, eggplant is considered as a model vegetable crop for the improvement of nutraceutical (Plazas *et al.*, 2013).

Brinjal is a day neutral plant and commercially cultivated as an annual crop. It is cultivated on more than 1.86 million hectares with a production of 49.4 million tonnes in various parts of the world. The maximum share (90%) comes from five countries, of which China shares 58% followed by India (25%), Iran, Egypt and Turkey. At present, the production of eggplant in India is 13.44 million tonnes from 0.72 million hectares (FAO, 2013). It is native to India. China is considered as a secondary centre of origin. *Solanum incanum*, a wild progenitor of *S. melongena* is distributed at least in 10 habitats in India (Lester and Hasan, 1991). Rich diversity exists in different parts of India, viz. Eastern Ghats, North Eastern region, Central, Eastern India particularly in states like Odisha, and West Bengal where there are more than 100 local cultivars grown under different names (Chattopadhyay *et al.*, 2009).

Under *S. melongena* species, there are three main botanical varieties i.e. the common brinjal, to which large, round fruits are grouped under var. *esculentum*. The long, slender types are included under var. *serpentinum* and the dwarf brinjal plants are put under var. *depressum* (Choudhury, 1976). Flowers in brinjal are extra-axillary and borne in three pattern: solitary, cyme (cluster) and mixed (solitary and cyme). There are four types of flowers, depending on the length of style, viz. long style with

big size ovary; medium style with medium size ovary; pseudoshort style with very rudimentary ovary and true short style with very rudimentary ovary (Krishnamurthi and Subramaniam, 1954). The hermaphrodite flowers are large and showy with purple colour corolla. The stigma become receptive and dehiscence of pollen occurs at the same time which results in self-pollination. The extent of cross-pollination by insect has been reported to be 2-48% in India, hence, it is considered as often cross-pollinated crop (Agrawal, 1980). The so called eggplant is due to white coloured and eggshaped fruit is similar to chicken eggs. The colour, size, shape of the eggplant fruit vary significantly with the type of eggplant cultivar. Higher yield with acceptable quality and resistance to biotic and abiotic stresses are the desired traits of breeder in any crop improvement programme. Genetic divergence is one of the important criteria of selection of parents to produce potential hybrid combinations as well as for developing desirable transgressive segregant from hybrids in further filial generation. The analysis of accessions from different geographical areas is important to study the extent of available genetic diversity. It is very difficult to classify morphologically similar and closely related species of brinjal. The relationship between the weedy form, *Solanum insanum* and its wild progenitor *Solanum incanum* were not described clearly (Karihaloo and Gottlieb, 1995; Lester and Hasan, 1990). The confusion in taxonomic classification of eggplant is complex due to the phylogenetic relationships established among taxa are mainly based on morphological features, crossability and F₁ fertility (Baksh and Iqbal, 1979). These parameters are, however, insufficient to establish genetic affinities, because *Solanum melongena* can be crossed not only to putative progenitors but also to more distantly related species (Daunay *et al.*, 1991). Moreover, existence of high level of morphological variability, morphological data can lead to ambiguous interpretations. Therefore, DNA markers are considered superior to morphological and biochemical marker systems because they analyse polymorphism at the DNA level (McDonald, 1995). A number of DNA markers such as RFLP, RAPD, AFLP and SSR etc. are being used for diversity analysis. Among the various DNA markers, SSR has been used widely due to its speed, low cost, and the use of lower quantities of plant DNA.

Wild species of brinjal are reservoir of important genes, e.g. *Solanum aethiopicum* L. (Ethiopian eggplant) resistant to bacterial wilt and rich in β -carotene, vitamin E, folic acid (Collonnier *et al.*, 2001); *S. indicum* L, resistant to little leaf and

shoot and fruit borer and contains more than 0.15% of chlorogenic acids (Bahgat *et al.*, 2008; Patel *et al.*, 2001). *Solanum incanum*, a source of *Verticillium* wilt resistance and considered as a source of variation for high content of phenolic acid conjugates (chlorogenic acid) in breeding programmes aimed at improving the functional quality of eggplant (Prohens *et al.*, 2013; Robinson *et al.*, 2001) and *S. integrifolium* resistant to *Phomopsis* blight, little leaf, bacterial wilt and shoot and fruit borer (Kalloo, 1993). These wild species are used in interspecific hybridization with cultivated eggplant. Interspecific hybridization is one of the most significant approaches for developing genetic stocks, which serve as important sources of genes for quality and resistance traits (Sekara *et al.*, 2007). In interspecific hybridization, the production of hybrid seed is greatly hampered due to certain fertilization barriers. The hybrids obtained between the cultivated eggplant and its wild related species have thrown much light on the cytogenetic relationships of different *Solanum* species besides providing clues to the potential of interspecific hybridization in the development of resistant genotypes.

The crossability and hybridization studies of *Solanum melongena* accessions with its related species have been carried out with inconsistent results (Gowda and Seenappa, 1991; Behera and Singh, 2002). A number of researchers have reported unidirectional crossability, i.e. crossability is feasible only when *S. melongena* genotypes are used as female parents (Chopde and Wanjari, 1974; Rajasekaran 1970a, 1970b; Wanjai 1976). Successful hybridization was reported only when *S. macrocarpon* genotypes were used as the female parent (Omidiji, 1979; Rajasekaran, 1970c). Crossability of *S. melongena* with *S. incanum*, *S. aethiopicum* and *S. torvum* has also been reported (Daunay *et al.*, 1991; Nee, 1999; Kameswara Rao, 2011). The information on both interspecific and intraspecific crossability is important in developing a comprehensive breeding approach. The breeding materials developed through this programme will help in further improvement of brinjal particularly in resistance and quality breeding. The present study was therefore carried out to understand crossability behaviour between cultivated genotypes of *S. melongena* with its wild relatives and to develop breeding lines with desirable traits.

Till date, very limited information is available in the crossability, molecular diversity and phylogenetic relationship of different wild species. Keeping in view the above facts, the present investigation was carried out with following objectives:

- 1 To study the crossability of *Solanum melongena* and its wild relatives.
- 2 To study genetic diversity and phylogenetic relationship of eggplant and its wild relatives based on morphological and molecular markers.
- 3 To characterize the inter-specific hybrids obtained from cross of cultivated and wild species.
- 4 To confirm chromosome number in different related species of *S. melongena* at metaphase of mitosis.

2. REVIEW OF LITERATURE

India is a tropical country and is famous for its diverse geographical and climatic features with large genetic diversity of many crop species. Enormous diversities exist within *Solanum* species, and also in their landraces for many morphological and agronomically important traits (Vageeshbabu, 2011). Interspecific hybridisation is one of the most important methods of creating initial breeding material in eggplant and primitive forms serve as a carrier of resistance genes to biotic, and abiotic stress and also yield and quality fruits (Sekara *et al.*, 2007; Kharkongar *et al.*, 2013). The analysis of accessions derived from different geographical areas is important to study the extent of available genetic diversity. The crossability and hybridization studies of *Solanum melongena* with its related species have been generally inconclusive and the results are often contradictory (Gowda and Seenappa, 1991; Behera and Singh, 2002). Moreover, *Solanum melongena* can be crossed not only to its putative progenitors but also with distantly related species (Daunay *et al.*, 1991). Knowledge of crossability and breeding behaviour of selected interspecific *Solanum* crosses may serve as important aid to plant breeder in the improvement of existing cultivars.

The available literature related to research objective been discussed under the following heads:

Pollen viability:

Anis *et al.* (1994) studied the pollen viability staining with 2% acetocarmine. The fertility ranged from 82-95% in the parents, whereas in F₁hybrids had low fertility of 47.5 % as compare to parents.

Abak and Guler (1994) studied the pollen viability among 14 local and 12 exotic genotypes under low temperature condition in greenhouse. There was significant difference for pollen viability between the genotypes. The highest pollen viabilities during the whole cold period were recorded from vernal (45%), Murena (42%), Baluroi (41%), Mileda (37%) and Prelane (36%) hybrids. When the temperature started to increase, the pollen viability also gradually increased and the difference between genotypes disappeared.

Nascimento *et al.* (2003) studied the pollen viability of eggplant 'Ciça' during storage. Pollen was collected from the male flowers by using a vibrator. Lower fertilization was observed in flowers pollinated with pollen stored for 30 or more days. Pollen stored for 50 and 60 days led to fruits with lower seed quality.

França *et al.* (2009) evaluate the pollen viability of eggplant. The pollen germination was tested in vitro, in different sucrose concentrations (0; 2.5; 5.0; 7.5 and 10.0 g L⁻¹) incubating the pollen during 0.5 and 16 hours. For the in vivo germination test, the pollen was placed during 4 and 24 hours in the flower stigma and after that stained with aniline blue and evaluated in an ultraviolet light microscope. The viability of the pollen grains was also evaluated in tetrazolium solutions (at the concentrations of 1%; 0.75% and 0.5%) and the staining was evaluated after 24 hours. The highest in vitro pollen germination was 10.8%, showing the necessity for a better calibration of the culture medium. The in vivo pollen germination was 66%, showing that this is an adequate methodology to estimate pollen viability in eggplant. The methodologies involving tetrazolium solution weren't efficient to estimate pollen viability evaluation, because of the deficient pollen staining.

Oyelana *et al.* (2009) studied pollen viability of novel hybrid *Solanum melongena* 'Golden' (2n = 2x = 24) x *S. scabrum* 'Scabrum' (2n = 4x = 48). Pollen viability was 38.2% in the hybrid but was 71% and 97.4% in the diploid and tetraploid parents, respectively.

Abdullateef *et al.* (2012) studied the pollen viability among the two varieties of *Solanum melongena* (SM-1, SM-2), three varieties of *S. gilo* (SG-3, SG-4, SG-5) and their F₁ hybrids. The results revealed that the maximum pollen viability in parental line was observed in SM-2 (83.3%) followed by SM-2 (82.3%) and SG-3 (67.0%). In the intervarietal crosses, the maximum viability was observed in SG-4 × SG-5 (76.0%) followed by SM-2 × SM-1 (66.3%), SM-1 × SM-2 (65.90%). while the interspecific crosses the maximum viability was recorded in SM-2 × SG-5 (63.7%) followed by SG-4 × SM-2 (55.5%) and SM-1 × SG-5 (21.2%).

Kumchai *et al.* (2013) studied the pollen viability of parental lines and F₁ hybrids. They found that the parental line Purple Bride (P), PaiChieh (W), and *S. torvum* (T) was almost 100% as revealed by dark staining with round in shape and of

uniform, normal size. The pollen viability of the hybrid progeny (P1×T) strain A-2, (P24×T) strain B-1, (W10×T) strain C-1, (W10×T) strain D-1, and (W10×T) strain G-2 varied between normal, dark stain (0 to 9.8%) and abnormal and light or no stain, which indicated rudimentary (4.5 to 96.2%) and empty pollen (1.3 to 95.5%). Viable pollen counts of the hybrid progeny were low, and (W10×T) strain C-1 showed almost no viable pollen.

Crossability and cytogenetic studies in interspecific hybridization

Sharma *et al.* (1980) studied interspecific hybridization between *Solanum khasianum* and *S. melongena*. The pollen tube growth ceased before penetration of the ovary when *S. melongena* used as pollen parent. In the reciprocal cross, a few ovaries were fertilized but subsequently the embryos degenerated. When excised embryos were cultured in vitro, fertile plants were regenerated successfully. The F₁ generation exhibited the spiny phenotype of *S. khasianum*. Segregates with and without spines were obtained in the F₂.

Rao (1981) studied the cytomorphology of *Solanum incanum*, two varieties of *S. melongena* (Pusa Purple Long and Giant Banaras) and with their hybrids. The hybrids were fertile with mostly normal meiosis indicating a close genetic relationship of *S. incanum* with the varieties of *S. melongena*. The interpretation of cytological data revealed that varieties of *S. melongena* primarily differentiate from *S. incanum* by certain genetic factor.

Rao and Rao (1984) studied the crossability relationships through cytogenetic studies of six species of spinous *Solanum* and interspecific hybrid. The fruit set was not higher than 10%. In crosses *S. indicum* var. multiflora × *S. indicum* or *S. torvum*, fruit set was higher than 30 % although hybrids were not realised. Chromosome pairing was less frequent in hybrids between *S. trilobatum* and *S. suratense*. Higher chromosome association were most common in hybrids between *S. suratense* and *S. melongena* followed by *S. trilobatum* × *S. indicum* var. multiflora.

Patel *et al.* (2001) studied interspecific hybridization to transfer the resistance genes from the wild species. *Solanum indicum* L., a prickly shrub found wild in forests and hilly tracts is reported to be resistant to little leaf and brinjal fruit and shoot borer under field conditions.

Behera and Singh (2002) studied interspecific hybridization between eggplant (*Solanum melongena* L.) and its related species. The degree of crossability was determined by fruit set, number of seedlings germinated and percentage of F₁ with seeded fruit and without seeded fruit. The results revealed that *S. indicum* when used as a pollen parent was crossable with *S. incanum* and *S. melongena* but the reciprocal crosses (*S. indicum* × *S. melongena*) was not successful where F₁ seedlings died after 10–15 days of germination. Similarly, when *S. gilo* was used as a pollen parent crossed with different cultivars of *S. melongena*. The cross *Solanum anomalum* × *S. melongena* cv. Pusa Kranti, produced viable seeds but the hybrid plants were observed to bear small parthenocarpic fruits in clusters.

Gordian *et al.* (2006) studied the cytogenetic behaviour of Nigerian species of *Solanum* L. and attempted induced polyploidy in the species. Colchiploidisation produced tetraploids with 2n = 48 and aneuploids with 2n = 69. The karyotype analysis indicated that the chromosomes were generally very small. There were also slight variations in centromeric positions and arm lengths. Meiotic behaviour of the chromosomes involved a combination of bivalent and multivalent associations especially at the polyploidy levels.

Chattopadhyay *et al.* (2009) studied crossability of three species of brinjal; *Solanum aethiopicum*, *Solanum gilo* and two sets of the different cultivars of *Solanum melongena*. The species *S. aethiopicum* and *S. gilo* were crossable in both ways, although the success was much low, 22.72% in *S. aethiopicum* × *S. gilo* and 26.3% in *S. gilo* × *S. aethiopicum*.

Oyelana and Ugborogho (2009) studied cytomorphological analysis of a novel hybrid *Solanum melongena* 'Golden' (2n = 2x = 24) × *S. scabrum* 'Scabrum' (2n = 4x = 48). The F₁ had fruit eight seeds having 100% germination and chromosome number was 2n = 6x = 72. Meiosis was regular in the hybrid with few univalents and impaired bivalents due to dissimilar parental genomes. Mitotic chromosomes were asymmetrical with various sizes.

Ray (2010) studied chromosome number and karyotype in new cultivars of (*Solanum melongena* var. *esculentum*) cv. Utkal Anushree, cv. Utkal Jyoti, cv. Utkal Madhuri, cv. Utkal Keshari and cv. Utkal Tarini. The somatic chromosome number 2n = 24 was recorded in all the cultivars with significant structural differences in

chromosome complement. Total chromosome length varied from 82.54 μm to 94.24 μm and 42.51 μm^3 to 48.53 μm^3 in cv. Utkal Anushree and cv. Utkal Jyoti respectively. Total F% revealed asymmetric karyotype mostly with median constricted chromosomes. Genome size varied from 7.10 pg to 9.24 pg; having 6958 Mbp to 9055 Mbp in cv. Utkal Anushree and cv. Utkal Tarini and showed significant correlations with chromosome length and chromosome volume.

Montvid (2011) studied the meiotic process in interspecific cross of *Solanum linnaeum* L. $\times$ *Solanum incanum* L. hybrid. The numbers of univalents and tetravalent, as well as the percentage of basic impairments decreased as the age of plants increased and fruit formation occurred at the end of the second year of life.

Morphological characterization

Pramanik *et al.* (1992) studied genetic divergence in brinjal using D^2 statistics for yield and its components in 38 varieties. On the basis of inter and intra cluster distance they group 38 varieties in 9 clusters. The clustering pattern showed that genetic divergence did not match with the geographical distribution.

Sarnaik *et al.* (1998) found genetic diversity in 35 genotypes of brinjal and determined degree of divergence using Mahalanobis D^2 analysis. On the basis of inter and intra cluster distance the genotypes were grouped into five clusters. The lower genetic divergence within the clusters suggested close genetic makeup of the genotype including in them.

Mohanty (2001) studied genetic diversity of 15 brinjal accessions for 5 economically important characters. The accessions were grouped into 5 clusters. The highest inter cluster distance ($D^2=4872.03$) was noticed between cluster IV (KT 4 and BB 4') and V (Pusa Kranti and Bhawanipatna local). They observed that genetic diversity was not parallel to geographic distribution of the accessions.

Patel *et al.* (2001) studied on morphological traits in interspecific hybrids between *Solanum indicum* and *S. melongena*. They found that F_1 's were intermediate in growth habit (semi-spreading) with predominant spines present on stem, petiole, both surface of leaves and on the calyx. The hybrids were taller and profusely branched than their respective parents.

Pradeepa (2002) studied floral morphology in 56 accessions to examine the fruit setting behaviour of eggplants. Most of the accessions produce mixed flower (80.3%) followed by cluster (16%) and solitary flowers (3.6%). The first flower of inflorescence set fruit in all accession, except in accession 02270. The stigma of the first flower was well developed and its position in relation to another tips, varied between accessions, i.e. above (58.9%), on the same level (25%) and below (16.1%) another tips. However, first flowers with stigma that was below anther tips and cluster flowers were aborted. Only the accession 02270 produced fruit in cluster flower which had sigma above anther tips.

Hazra *et al.* (2003) studied the characterization of 70 *Solanum melongena* L. germplasm through 33 morphological, growth, floral and fruit characters. The genotypes showed semi-erect growth habit. Most of the genotype had low to moderate leaf size with shallow lobed margin. Propensity of pigment expression was highest in stem and petiole followed by the fruit, veins, calyx and lamina. Fruits developed from solitary and basal flowers of the cyme were bigger in size compared to those from additional flowers in the cyme. Maximum genotypes had either oval or oblong fruits. All the 26 quantitative characters excepting pollen diameter varied significantly among the genotypes. The plant were dwarf to very tall with few to very high branching habit. Relationship between leaf and fruit size was not convincing. Big fruited genotypes had high moisture, crude protein and sugar and low phenol contents.

Babu and Patil (2004) studied genetic divergence among 90 brinjal genotypes for 20 economic characters. These genotypes were grouped into 7 clusters on the basis of relative magnitude of D^2 values. The maximum contribution towards the total genetic divergence was from yield per plant. There was no close correspondence between geographical distribution and genetic divergence as estimated by D^2 statistics. The maximum inter-cluster distance (2963.86) was observed between clusters IV (DBC-46-HA and OBC-1 04-MH) and VII (OBC-18-AP), while minimum was recorded between clusters III (OBC-14-KA, DBC-19-KA, OBC-68-KA, OBC-80-KA, OBC-115-KA, OBC-13-BI, DBC-34-HA, DBC-38 HA, DBC-43-HA, OBC-66-HA)and IV (417.28).

Mehta *et al.* (2004) reported genetic divergence in 21 genotypes of brinjal using Mahalanobis D^2 analysis. The 21 genotype were group into six clusters on the basis of inter and intra cluster distances. The cluster pattern showed that genetic divergence was not parallel to geographical distribution.

Singh *et al.* (2006) studied genetic divergence among 29 brinjal genotypes. The genotypes were grouped into six clusters irrespective of geographical diversity indicating no parallelism between geographic and genetic diversity. Cluster II topped had maximum fourteen genotypes, while cluster V and VI had only one. The maximum inter-cluster distance was noticed between cluster I and VI. The plant height, number of branches per plant number of fruits per plant, average fruit yield per plant, contributed maximum divergence and had a major role in improvement of fruit yield in brinjal.

Rathi *et al.* (2007) studied the genetic divergence among the 30 genotype of brinjal. The 30 genotypes were group into 5 clusters. The cluster V had 9 genotypes, the cluster IV had 2 genotypes, the cluster III had 6 genotypes, the cluster II had 8 genotypes and the cluster I had 5 genotypes. The maximum (5.788) inter cluster distance was observed between the cluster I and cluster IV followed by cluster II and cluster IV (4.909). The genotype did not cluster according to their geographical distribution.

Kumar *et al.* (2008) studied morphological diversity in a set of 622 accessions, comprising 543 accessions from indigenous sources and 79 accessions of exotic origin. Wide range of variations for 31 descriptors including 13 quantitative and 18 qualitative traits were recorded. The wide regional variations for plant, flower and fruit descriptors revealed enough scope for improvement of yield characters by selection.

Gao *et al.* (2009) studied F₁'Hanhong No. 2' of eggplant developed by crossing E-2 and E-9. The plant grows vigorously and matures early. It took about 50 days from flowering to harvesting. The fruit were long purpled with 30-35 cm in length and 3.5-4.0 cm in diameter. The average fruit weight was about 150 g.

Naujeer (2009) studied the morphological characterization of 27 *S. melongena*, two *S. macrocarpon*, one *S. nigrum*, three *S. violaceum* and one *S.*

torvum. Significant ($p < 0.01$) correlation were observed between several related traits of high agronomic importance and breeding potentials in selection of genetic divergent parents for hybridization. Yield was positively correlated, fruit length and width ($r = 0.5$) fruit weight ($r = 0.8$) but inversely related with number of fruits per plant ($r = -0.6$) and plant height ($r = -0.5$).

Senapati *et al.* (2009) studied genetic diversity among the 32 brinjal genotypes. The analysis of variance showed a wide spectrum of variability among the set of germplasm. High estimates of heritability coupled with higher genetic advance were observed for the characters like number of fruits per plant (96.51, 73.26), fruit weight (96.01, 49.30) and fruit yield per plant (92.76, 75.52). All 32 genotypes were grouped into 8 genetically diverse clusters. The clustering pattern does not bear any relevance with geographical origin of the germplasm. On the basis of clustering mean, the promising genotypes were BBSR-202, BBSR 195-1, IHR-7, 88-7, 88-26 and SM6-6 to be used in improvement programme through selection and hybridization.

Das *et al.* (2010) studied genetic diversity in 40 brinjal genotypes based on 9 traits under eastern Indian conditions. The range of D^2 values varied from 8.13 to 8015.95 which revealed high variability among the genotypes. Based on the degree of divergence, the genotypes were grouped into ten clusters and cluster x had the maximum (22) genotypes. The divergence within the cluster showed medium and consistent level of divergence in all the cluster except cluster x which had highest intra cluster distance. Fruit yield and fruit weight contributed the most towards the genetic divergence.

Polignano *et al.* (2010) studied diversity in 98 accessions of *Solanum melongena* L. and its allied species *S. aethiopicum* L. and *S. macrocarpon* L. for 16 morpho-agronomic and fruit traits and revealed existence of considerable diversity. Plant height, flowering time, flower per inflorescence, fruit length and fruit acidity contributed mostly towards the total divergence. Cluster analysis grouped the accessions into three distinct and significant clusters. No relationship was found between genetic divergence and genetic status of sample.

Sunseri *et al.* (2010) studied diversity analysis among 70 “scarlet eggplant” (*Solanum aethiopicum* L.) entries from different geographical origins. Entries were

first evaluated for morphologic traits and chlorogenic acid content. Differences between entries are highly significant for all traits. Principal component analysis (PCA) revealed that the first three components accounted for 74% of the total variance. Morphologic traits were associated with the first two components, while the third one was moderately correlated with the chlorogenic acid content. The observed similarity allowed to identify only three main groupings. The clusters obtained did not show any relationships with geographic origins and/or botanical groups.

Chattopadhyay *et al.* (2011) studied the genetic diversity among 35 eggplant genotype based on morphological and yield related traits. All the brinjal genotypes under study showed highly significant variations for 12 quantitative traits. Fruit weight, plant height and days to 50% flowering exhibited high heritability and genetic advance indicating additive gene controlling the characters. Among the eleven yield contributing traits, fruit weight and number of marketable fruit per plant showed highly positive effect on marketable fruit yield per plant.

Shinde *et al.* (2012) studied the genetic diversity among 65 brinjal genotypes germplasm based on fourteen characters. The genotypes were grouped into seven clusters and maximum D^2 values (2850.23) was observed between genotypes IAB-104 and Phule Harit, while the lowest D^2 value (6.90) was noted between genotypes Manjari Gota and JBR-1. Cluster A had maximum thirty eight genotypes which was followed by cluster C with ten genotypes, whereas, cluster E, F, G had only one genotypes.

Hurtado *et al.* (2012) studied diversity among 52 accessions of eggplant from three geographically region China, Spain, and Sri Lanka using 28 morphological descriptors. A wide variation was found for most of the morphological traits, and significant differences among the three centers of diversity were detected for 22 of these traits. The PCA analysis showed that eggplants from these three origins were morphologically different and accessions from each of the three secondary centers of diversity presented a typical combination of morphological characteristics.

Fabio *et al.* (2013) studied the diversity of 238 eggplant genotypes collected from Asia and the Mediterranean, with the goal to identify true-breeding line. The phenotypic data were subjected to principal component and hierarchical principal

component analyses. The population structure of the core set of germplasm shows that it can be used as a basis for an association mapping approach.

Begum *et al.* (2013) studied the morphological diversity in 92 eggplant genotypes based on twenty one characters and the genotypes were grouped into ten different clusters. The highest intra-cluster distance was observed in cluster VIII (2.13) containing seven genotypes and the lowest intra-cluster distance (1.18) was observed in cluster IV having four genotypes. The cluster X had the maximum number (17) of genotypes whereas, cluster II and III had minimum number (3) of genotypes. The highest inter-cluster distance was observed between cluster II and VIII (30.86) indicating the genotypes in these clusters were more diverged than those of other clusters. The lowest inter-cluster distance was observed between the clusters V and X (3.72) suggesting a close relationship among the genotypes included within these clusters.

Kumar *et al.* (2013) studied genetic divergence of 14 eggplant genotypes using Mahalanobis's D^2 statistic and six clusters were formed. The maximum number of genotypes (5) was found in cluster III with intra cluster distance of 2597.79. The maximum inter cluster distance was observed between cluster II and cluster V. He suggested that the genotypes belonging to these clusters may be utilized for hybridization programme for crop improvement. The characters *viz.* yield per plant, fruit circumference, little leaf incidence and total phenols content contributed more for genetic divergence.

Ahmed *et al.* (2014) studied genetic diversity in 35 brinjal genotypes using multivariate analysis. The first three principal components accounted (70.33%) of the total variation among eight characters describing 35 genotypes. The genotypes contributed to PC1 were more likely to be associated with higher fruit weight, fruit width and fruit yield whereas the genotypes with higher plant height, plant spread and number of primary branches were contributed to PC2. The maximum inter-cluster distances were recorded between the cluster I and II (278.26) followed by the distance between I and V (245.32). The lowest inter-cluster distance was observed between cluster II and V (35.26) followed by III and V (45.75) suggesting a close relationship among these three clusters.

Sakhanokho *et al.* (2014) studied the intraspecific variability among 12 *Solanum aethiopicum* accessions using 27 morphological traits. The accessions were group into four clusters. The two clusters, each consisting of five accessions and two other clusters, each consisting of only one accession. Variability was high with flower and fruit associated descriptors among the accessions.

Molecular characterization

Aniko *et al.* (2008) developed a set of 39 functional microsatellite (SSR) markers, and used in 44 accessions including 38 cultivated eggplant varieties and six wild *Solanum* species. The set of eggplant EST-SSR markers was informative for phylogenetic analysis and genetic mapping. The EST-SSRs had potentiality to serve as perfect markers for genes determining variation in phenotype. Their high level of transferability to other *Solanaceae* species can be used to provide anchoring points for the integration of genetic maps across species.

Demir *et al.* (2010) studied genetic diversity of eggplant (*Solanum melongena*) germplasm from Turkey by using SSR markers. With amplification of five SSR loci, the number of alleles per microsatellite locus ranged from 2 to 10, with a total of 24 alleles. The locus emf21H22 had the maximum number of 10 alleles followed by emh11O01 and emf21C11 with 5 and 4 alleles, respectively. The average number of alleles per locus was 4.8.

Ali *et al.* (2011) studied molecular diversity analysis of eggplant using inter simple sequence repeat (ISSR) and RAPD to subdivide 143 Chinese cultivated eggplants based on coefficient of parentage, genetic diversity index (GDI) and canonical discriminant analysis. ISSR markers were more effective than RAPD markers for detecting genetic diversity.

Tumbilen *et al.* (2011) studied application of EST-SSRs to examine genetic diversity in 47 accessions of eggplant and its closely relatives species. The markers had very good polymorphism in the 18 species. These markers were found to be valuable resource for studying genetic relationships, fingerprinting, and gene mapping in eggplant.

Adeniji *et al.* (2012) studied the genetic diversity of 39 accessions representing the seven *Solanum* species and a popular tomato variety (LBR 48) using

SSRs markers. A total of 417 alleles were amplified with the number of alleles ranging from 5 (EM 141) to 38 (EM 120 b). Polymorphism was fairly high (0.05 to 0.92) among SSR markers with high number of repeats. Findings indicated that entries originating from different parts of the world did not form a distinct cluster, and there was no association between SSR marker pattern and geographical origin. SSR markers indicated a strong genetic affinity among *S. viarum*, *S. melongena* and *S. aethiopicum* Aculeatum group. Genetic relatedness between *S. dasyphyllum* and *S. macrocarpon* and between *S. aethiopicum* and *S. macrocarpon* were important for breeding.

Hurtado *et al.* (2012) studied genetic diversity among 52 accessions of eggplant from three geographical region using 12 SSRs marker. The SSR characterization identified 110 alleles and allowed a unique genetic fingerprint for each accession. The PCA analysis showed that the genetic differentiation among origins was less clear than for morphological traits, although the analysis of the population structure shows that accessions mostly grouped according to the origin. The genetic diversity (HT) within each origin was high, ranging between 0.5400 (Sri Lanka) and 0.4943 (China), while the standardized genetic differentiation (G'ST) among origins was moderate (0.27).

Verma *et al.* (2012) studied genetic diversity among 29 brinjal varieties using 6 SSRs markers. The markers were polymorphic and detected 25 alleles. The number of alleles per primer ranged from 2 to 10, with a mean of 4.67. UPGMA clustering for SSR markers grouped all the brinjal varieties into two clusters, but grouping patterns were different for each of the marker system. The maximum genetic distance of 1.00 was found between Pusa Bhairav and Green Long, Green Long and KS-224, Green Long and Sl-195, Green Long and KS 331 and between Pusa Kranti and Sl-195 followed by 0.85 between Pusa Kranti and KS-224, and NDB-25 and Pusa Kranti.

Channe *et al.* (2013) studied genetic diversity among 5 brinjal varieties using 11 ISSR primers. 69 scorable bands were generated among 44 comprised polymorphic markers, with an average of 4 polymorphic bands per primer. Through dendrogram the accession were placed in cluster, where cluster A include only one genotype and cluster B is biggest cluster which include three genotypes.

Ge *et al.* (2013) studied 141 eggplants accessions to detect SSR markers associated with nine fruit traits. Population structure analysis was performed with 105 SSR markers which revealed that subgroups were presented in the population. A total of 49 marker associated to eight phenotypic traits were identified although no association was found with the trait of fruit glossiness. The results suggested that the association analysis approach could be a useful alternative to traditional linkage mapping to detect putative QTLs in eggplant.

Haiyan *et al.* (2013) studied genetic diversity among 92 eggplant accessions by using 100 SSRs markers. It revealed a moderate amount of polymorphism with an average polymorphism information content (PIC) value of 0.285. The average value of number of effective loci (N_e), expected heterozygosity (H_e) and Shannon's Information index (I) were 1.631, 0.323 and 0.570, respectively. The levels of genetic diversity observed in the seven areas in China were not evenly distributed and decreased from south to north. The F-statistics for these populations showed medium genetic differentiation ($F_{st} = 0.129$) and considerable gene flow ($N_m = 2.230$). The neighbor-joining (NJ) cluster analysis divided the seven areas into four clades that largely corresponded to geographic divisions.

Vilanova *et al.* (2014) studied the genetic diversity among 30 eggplant accession using 16 SSR markers. 15 SSRs marker were polymorphic with 65 polymorphic alleles, with a range of 2 to 11 alleles per locus. The polymorphism information content (PIC) of SSR markers ranged from 0.07 to 0.77, with an average value of $PIC=0.50$. The mean observed heterozygosity (H_o) presented a very low value $H_o=0.01$, while the mean expected heterozygosity (H_e) had a value of $H_e=0.57$. The principal coordinates analysis (PCoA) confirmed that each of the cultivar groups is genetically diverse and, with the exception of the Round group. Among all accessions, Spanish eggplant landraces present a high degree of homozygosity, considerable intra-cultivar group diversity, and a certain degree of genetic differentiation.

Biochemical

Mitra and Majumdar (1977) studied changes in total phenolic content and polyphenol oxidase activity in four brinjal variety infected with little leaf disease at

different stages of disease development. Both phenol content and polyphenol oxidase activity decreased in the three varieties, at all stages of the disease.

Stommel and whitaker (2003) studied the phenolic acid content in 101 *S. melongena* and 14 accessions representing four related eggplant species, *S. aethiopicum* L., *S. anguivi* L., *S. incanum* L, and *S. macrocarpon* L. Significant differences in phenolic acid content and composition were evident among the five eggplant species and within genotype. Among *S. melongena* accessions, there was a nearly 20 fold range in total hydroxycinnamic acid (HCA) content. The total HCA content among core subset a *S. anguivi* PI 319855 and *S. incanum* PI 500922 , exhibited strikingly different HCA conjugates profiles, which differed from those of all other accessions.

Sadilova *et al.* (2006) studied the acetone extracts from eggplant (*Solanum melongena* L.) peels to characterize with respect to their anthocyanin profiles, colour qualities and antioxidant capacities. According to HPLC-DAD-MS3 analyses the major anthocyanin in eggplant was delphinidin-3-rutinoside. These findings support the relevance of structure related activities of anthocyanins both for understanding food colour and their particular nutritional value.

Bilal *et al.* (2009) studied the total antioxidant activity and total phenolic contents in 22 Turkish eggplant (*Solanum melongena* L.) Total water soluble antioxidant activity of the cultivars varied from 2664 to 8247 mmol Trolox/kg, which is a 3.1-fold difference. Cultivars also showed significant variation for total phenolic contents ranging from 615 to 1376 mg/kg, a 2.2-fold difference. 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.

Hanson *et al.* (2006) studied genetic diversity among 33 eggplant of *Solanum melongena* and two *S. aethiopicum* accessions collected from the AVRDC for superoxide scavenging (SOS) activity with methanol (SOSm) and water (SOSw) extracts, and total phenolics and ascorbic acid. Highly significant differences were detected among accessions for SOS activities with accession means ranging from 26% to 60%. Accessions S00062, S00022 and S00197 displayed high AOA. The SOSm and SOSw were positively correlated with dry matter content and total phenolics content and negatively correlated with fruit weight. There was no

significant linear association between ascorbic acid content and SOSm but found a significant but low correlation between SOSw and ascorbic acid content.

Nisha *et al.* (2009) evaluated the antioxidant potential of four different varieties of eggplant (long green, purple coloured big size, purple coloured moderate size and purple coloured small size) in terms of total phenolic content, DPPH (1,1-diphenyl-2-picrylhydrazyl) total reducing power, superoxide radical scavenging activity, metal chelating activity and total anthocyanin content. Extracts from purple colour small size fruit demonstrated better antioxidant activities than the other samples which may be attributed to the higher phenolic and anthocyanin content.

Singh *et al.* (2009) studied phytochemical investigation of the eggplant extracts and it showed that N-caffeoylputrescine, 5-caffeoylquinic acid, and 3-acetyl-5-caffeoylquinic acid made up the bulk of total eggplant phenolics. The phenolic content of the conventionally grown Blackbell variety was marginally higher or equal to those grown organically. However, the phenolic content of the Millionaire organic variety was much greater than the conventionally grown samples. Eggplant extract inhibition of cupric-ion mediated oxidation of low-density lipoproteins was highly correlated with the content of 5-caffeoylquinic acid ($R^2 = 0.9124$), the most abundant phenolic acid identified.

Eun-Ju *et al.* (2011) examined 70% ethanol (EE) and water extracts (WE) from different parts (calyx, leaf, peel, pulp, and stem) of eggplant and the antioxidant activity of the extracts was evaluated. Total phenolic contents of EE and WE were the highest in peel (55.19 mg/g) and calyx (121.07 mg/g) extracts, respectively. The peel extract showed the highest anthocyanins content (138.05 mg %) followed by calyx (135.94 mg %), stem (110.38 mg %), leaf (97.29 mg %), and pulp (2.29 mg %) extracts. The high SOD-like activity was detected in WE of calyx part ($IC_{50} = 0.39 \pm 0.01 \mu\text{g/ml}$), which is about 1,700 times stronger than WE of pulp part ($IC_{50} = 0.69 \pm 0.01 \text{ mg/ml}$). The results indicate that antioxidant activity of eggplant varied by parts and solvents. This study also shows the calyx part had strong antioxidant activity.

Shaheen *et al.* (2013) studied total phenol content of different varieties of *Solanum melongena* and *Solanum tuberosum* growing in Bangladesh. The total phenol content (TPC) of different varieties of *Solanum melongena* L. varied from

3.16 ± 0.04 -7.86 ± 0.33 mg GAE/g of fresh weight (FW). It also revealed that all varieties of *Solanum tuberosum* L. With peel contained higher TPC than without peel. BARI Begun-8 serves as good sources of polyphenols and therefore may contribute as a source of dietary antioxidant.

Kaur *et al.* (2013) studied thirty four genotypes of eggplant and its wild relatives for their total phenolics, flavonoid content and antioxidant capacity. Free radical scavenging was evaluated using four in-vitro assays, viz. FRAP (Ferric reducing antioxidant power), CUPRAC (cupric reducing antioxidant capacity), TEAC (Trolox equivalent antioxidant capacity) and DPPH (2, 2-diphenylpicrylhydrazyl). Total phenolics in eggplant showed a wide variation, ranging from 22.62 to 234.46 mg gallic acid equivalents (GAE)/100 g fw (244.28 to 2990.64 mg GAE/100 g dw). With the exception of *Solanum aethiopicum* and its accessions (Ac-1, Ac-2 and Ac-3), all wild relatives had significantly ($p = 0.05$) higher total phenolics and flavonoid content than cultivated ones. Total antioxidant capacity (FRAP) in wild genotypes ranged from 1.13 to 8.04 μmol Trolox (TE)/g. In cultivated group, JBR-99 and RCMBL-3 possessed high antioxidant capacity than the rest.

Salerno *et al.* (2014) studied to extract the 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.

Somawathi *et al.* (2014) carried the comparative studied on antioxidant activity and skin colour of brinjal (*Solanum melongena*). They used five different skin colours: purple with no lines (S1), light purple with lines (S2), dark purple with lines (S3), pink coloured (S4) and purple with green lines (S5). There was a significant difference ($p < 0.001$) between the skin colour and antioxidant activity. Total phenolic content (TPC) and FRAP values of brinjal extracts varied from

(48.67±0.27)–(61.11±0.26) (mg GAE/100 g fresh weight) and (4.19±0.11)–(7.46±0.26) (mmol of FeSO₄/g of fresh weight), respectively. Brinjal with S3 skin colour showed the highest TPC and antioxidant activity. S2 showed the least while S1 displayed the highest percentage of DPPH radical scavenging activity with an IC₅₀ value of 3.51±0.62 mg/ml. S3 demonstrated the strongest total antioxidant capacity with an inhibition percentage of 40.45±1.17, while S2 showed the lowest activity (17.78±0.38). All the extracts showed moderate to potent antioxidant activity, among which S3 and S1 demonstrated better antioxidant activity which may be attributed to the higher phenolic content since a linear relation was observed between the TPC and the antioxidant parameters.

Tripathi *et al.* (2014) studied antioxidant activities and biochemical changes in different cultivars of brinjal (*Solanum melongena*). Maximum phenolic content of brinjal fruit in round varieties was obtained in Pusa Purple Round (89.13mg/100g) followed by Pant Rituraj and NDBH-1. Phenolic content was maximum in Pusa Purple Round followed by Pusa Kranti and NB-2 in long varieties. Antioxidant activity of brinjal fruit was noticed between (182.01-234.13 µg) in round varieties and (172.11-219.92 µg) in long varieties. Maximum antioxidant activity of brinjal fruit in round varieties was obtained in Punjab Bahar followed by Pusa Purple Long and NB-1. However in long varieties of brinjal fruit it was maximum in NDBH-2 followed by Pusa Purple Long and NB-1 while, lowest activity was recorded in round variety NDBH-1 and Pant Samrat in long variety.

3. MATERIALS AND METHODS

The present investigation entitled “Studies on crossability and genetic relationship among eggplant (*Solanum melongena* L.) and wild relatives” was carried out from 2012-2015 at the research farm of Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi, located at an elevation of about 228m above MSL, 20°40' north latitude & 77°13' east longitude. The climate of Delhi is semi-arid, sub-tropical with hot summers and cold winters. During crop growing season of 2012-13, the maximum and minimum temperature ranged from June to February were 18 to 42.6°C and 4.7 to 28.9°C respectively, whereas during 2013-14, it ranged from 18.6 to 37.7°C and from 6.8 to 26.7 °C, respectively (Appendix I). The soil of the experimental site was clay-loam. The pollen viability and cytogenetic study was carried out at the Division of Genetics. The molecular analysis was carried out at National Research Centre on Plant Biotechnology. The overall materials and methods used in the experiment are briefly described below.

3.1 Plant materials and raising of crops

The experimental material comprised twenty cultivated *S. melongena* L. genotypes (Pusa Kranti, Pusa Shyamla, NDB-25, Pusa Uttam, Pusa Bindu, DBSR-52, Pusa Ankur, Br-112, DBSR-195, 190-10-12, 129-5, 91-2, G-190, G-129, G-111, Brinjal Var-7, Brinjal Var-3, Arka Shirish, Arka Kusumakar, S-309) and four wild species (*S. indicum*, *S. incanum*, *S. aethiopicum* and *S. integrifolium* showed in Plate 1) and maintained at the Division of Vegetable Science, Indian Agricultural Research Institute, New Delhi, India. Many of the *S. melongena* genotypes are commercially grown in different parts of India. The cultivars/elite lines of *S. melongena* were selected based on their fruit size, colour, shape and cluster bearing behaviour. The cultivated genotypes and four wild species were selfed for three generations before being used in the present study. A standard package of practices was followed for raising the crops during rainy season. Before sowing, the seeds were treated with thiram @2g/kg of seed and sown in plastic trays containing a mixture of sand, topsoil and cowdung in the ratio of 1:3:2. Suitable fungicide and insecticide such as Dithane M-45 @0.25% and Rogoer @0.1% were applied as a foliar spray during growth period against fungal diseases and insects, respectively. The intercultural operations and plant protection measures recommended for the crop were followed as per standard practices and weekly irrigation was given to maintain the proper moisture in the field

for better growth and development of the plants. The experimental field was prepared by one deep ploughing followed by three harrowing followed by clod breaking, hoeing and levelling. After that the whole area was levelled. The bunds and channels were prepared as per the layout. A fertilizer dose of 50 kg N, 80 kg P₂O₅ and 100 kg K₂O per ha was applied before fifteen days of transplanting of seedlings (100 N: 80 P: 100 K kg/ha). The remaining N (50 kg) was applied as top dressing at two split doses, one at 20 days and another at 40 days after transplanting. The Seedlings of 45 days old were transplanted in the main field with a spacing of 75 × 60 cm in 3 replications with 40 plants in each replication. Transplanting of seedlings was done in evening hours and just after transplanting, a light irrigation was given for establishment of the seedlings. The gap filling operation was done after 5 days of transplanting and light irrigation was given to the transplanted plants manually.

3.2 To study the crossability of *Solanum melongena* and its wild relatives

3.2.1 Estimation of pollen viability

For the pollen viability analysis, the mature flower buds were bagged with cotton puff a day prior to anthesis. On the day of anthesis, three flowers were collected at 8 a.m. from three plants of each wild species. The viable pollens were estimated by placing a single anther on glass slide and crushed with forcep followed by staining with 0.5% iodine and 1.1% potassium iodide solution for 15 min. Finally, the pollen grains were collected and counted under microscope (Olympus CH-20i, Japan). Pollen grains with bright red stain were categorized as viable, pink as semi-sterile and unstained as sterile (Prasad *et al.*, 2006).

3.2.2 Interspecific crossing

The interspecific hybridization was carried out in Line x Tester mating design using *S. melongena* genotypes as female parents and wild species as male parents. Forty flower buds of female parent were taken from each *S. melongena* cultivar per cross combination. The mature balloon shaped buds with long style on the female parents were emasculated a day before anthesis and covered with butter paper bags. The leftover buds in the cluster and those naturally pollinated were clipped off. The mature buds in the clusters of male parents were also bagged for collection of uncontaminated pollen. On the day of anthesis of flower in the male parents, the pollen grains were dusted on the stigmatic surface of the emasculated flowers of the

female parents. The flowers were re-bagged thereafter and labelled. The degree of crossability was determined as percentage fruit set, number of seeds per fruit, percentage of F₁ seed germinated and pollen viability in four wild related *Solanum* species.

i) Percentage of fruit set

The fruit set percentage was calculated by following formula:

$$\text{Fruit set (\%)} = \frac{\text{Total numbers of fruit set}}{\text{Total number of female flower bud taken for pollination}} \times 100$$

ii) Number of seeds per fruit

Physiological mature five fruits were selected and their seeds were extracted separately. The total number of seeds per fruits were counted and divided by total number fruits to get average seed number per fruit.

iii) Germination percentage

Germination percentage of F₁ seeds: The germination percentage was calculated as follows:

$$\text{Germination \%} = \frac{\text{Number of seed germinated}}{\text{Number of seed on tray}} \times 100$$

3.3 Morphological diversity

Twenty cultivated parental genotypes of *S. melongena* and four wild species were grown in the field for evaluation of different morphological traits. The observations were taken for the following characters;

3.3.1 Quantitative traits

i) Plant height (cm)

The plant height was measured from the ground level to the tip of the main shoot with the help of a meter scale at the final harvesting stage and the average plant height per plant was calculated.

ii) Number of primary branches per plant

Number of primary branches was counted arising from the main shoot at the time of final harvest and the average number of primary branches per plant was calculated.

iii) Days to first flowering

The number of days, from the date of transplanting to the opening of first flower was recorded on individual plant basis.

iv) Days to first fruit set

The date on which fifty percent of the plants showed first fruit set was recorded and number of days taken on the basis of individual plant.

v) Days to first harvest

The numbers of days taken from date of transplanting to the first fruit harvest was recorded on the basis of individual plant.

vi) Number of flowers per cluster

The total number of flowers was counted from the first five clusters during peak period of flowering in all the tagged plants. The average number of flowers per plant was taken.

vii) Number of fruits per cluster

The first 5 flower clusters per plant were tagged and allowed to develop until fruits were formed during fruiting period and the number of fruits were recorded and then the average was calculated.

viii) Fruit length (cm)

Five fruits were randomly taken and their length from the base of the peduncle to the fruit tip was measured with the help of measuring scale and mean fruit length was calculated.

ix) Fruit diameter (cm)

Five fruits were randomly taken and diameter of fruits was measured with the help of Vernier Callipers and mean fruit diameter was calculated.

x) Fruit shape index

The ratio of polar and equatorial diameter was used to determine the fruit shape index as suggested by Roy and Choudhury (1972).

xi) Number of fruits per plant

The number of fruits harvested from tagged plants in all the picking from each plant was counted. The average number of fruits per plant was calculated.

xii) Average fruit weight (g)

Weight of five randomly selected fruits from a plant was noted. The total weight was then divided by five to get average fruit weight.

xiii) Yield per plant (g)

Total yield per plant (g) was obtained by pooling the harvest over all the picking till the end of the crop season and divided by number of plants to get average yield per plant.

3.4. Qualitative traits:

i) Stem: Anthocyanin colouration

The stem anthocyanin colouration was observed on the basis of the following parameters:

- a. Absent(1)
- b. Present (9)

ii) Stem: Intensity of anthocyanin colouration

The intensity of stem anthocyanin colouration was observed on the basis of the following parameters:

- a. Weak (3)
- b. Medium (5)
- c. Strong (7)
- d. Very strong (9)

iii) Leaf blade colour

The leaf blade colour was observed on the basis of the following parameters:

- a. Green (1)
- b. Purple (2)

iv) Intensity of leaf blade colour

The intensity of leaf blade colour was observed on the basis of the following parameters:

- a. Light (3)
- b. Medium (5)
- c. Dark (7)

v) Colour of leaf vein

The colour of leaf vein was observed on the basis of the following parameters:

- a. Green (1)
- b. Purple (2)

vi) Intensity of colour of leaf vein

The Intensity of colour of leaf vein was observed on the basis of the following parameters:

- a. Light (3)
- b. Medium (5)
- c. Dark (7)

vii) Spines on leaf, viii) Spines on calyx, ix) Spines on stem

The presence of spines on leaf, on calyx and on stem was observed on the basis of the following parameters:

- a. Absent (1)
- b. Present (9)

x) Flower colour

The flower colour was observed on the basis of the following parameters:

- a. Greenish White (1)
- b. Light Purple (2)
- c. Purple (3)
- d. Dark purple (4)

xi) Fruit shape

The fruit shape was observed on the basis of the following parameters:

- a. Globular (1)
- b. Ovoid (2)
- c. Obovate (3)
- d. Pear Shape (4)
- e. Clube Shape (5)
- f. Ellipsoid (6)
- g. Cylindrical (7)

xii) Shape of fruit apex

The shape of fruit apex was observed on the basis of the following parameters:

- a. Indented(1)
- b. Flatterned (2)
- c. Rounded (3)
- d. Pointed (4)

xiii) Colour of fruit skin at commercial harvesting

The colour of fruit skin at commercial harvesting was observed on the basis of the following parameters:

- a. White (1)
- b. Green (2)
- c. Purple (3)

xiv) Intensity of purple colour of skin, xv) Intensity of green colour of skin

The intensity of purple and green colour of skin was observed on the basis of the following parameters

- a. Light (3)
- b. Medium (5)
- c. Dark (7)

xv) Colour of calyx

The colour of calyx was observed on the basis of the following parameters

- a. Green (1)
- b. Purple (2)

xvi) Intensity of colour of calyx

The intensity of colour of calyx was observed on the basis of the following parameters

- a. Weak (3)
- b. Medium (5)
- c. Strong (7)

xvii) Colour of fruit flesh

The colour of fruit flesh was observed on the basis of the following parameters

- a. Whitish (1)
- b. Greenish (2)

xviii) Fruiting pattern

The fruiting habit was observed on the basis of the following parameters

- 1. Solitary (1)
- 2. Cluster (2)
- 3. Mixed (3)

xix) Plant growth habit

Plant growth habit was observed on the basis of the following parameter

- 1. Erect (1)
- 2. Semi spreading(5)
- 3. Spreading (7)
- 4. Horizontal (9)

3.5 Molecular diversity**i) Genomic DNA extraction and marker analysis**

The genomic DNA was extracted from young fresh leaf tissue using cetyltrimethyl ammonium bromide (CTAB) method (Murray and Thompson, 1980).

DNA was purified as per the protocol with minor modifications, that is, 2 µl of RNase (10 mg/ml) was added in the extracted 200µl DNA in microcentrifuge tube and incubated at 37°C for 1 h. Approximately 200 µl of phenol: chloroform :isoamyl alcohol (PCI : 25 : 24 : 1) was added and mixed well by inverting the tubes and centrifuged at 13000 X g for 15 min. The upper aqueous phase was slowly transferred by pipetting to a new microcentrifuge tube. Around 200 µl of chloroform :isoamyl alcohol (C : I: 24 : 1) was added and mixed by inverting the tubes and centrifuged for 15 min. at a speed of 13000 X g. The upper aqueous phase was transferred by pipetting slowly to a new tube and chilled (-20°C) isopropanol was added and tube was inverted gently. To precipitate DNA, tubes were placed at -20°C for 30 min. and centrifuged at 12000 X g for 15 min. DNA pellets were rinsed with 500 µl of chilled 70% ethanol and centrifuged for 5 min. at 13000 X g. The liquid was then pipetted off, and pellets were air-dried, and samples were resuspended in 100 µl of TE buffer and kept at 4°C.

ii) Quantification of DNA and PCR analysis

The purified DNA was quantified by running 2 µl of each DNA sample on 0.8% agarose gel along with the uncut lambda (λ)DNA (100 ng/µl) and in nanodrop. The final concentration was made of 25–50 ng/µl for use in PCR analysis. A set of 39 microsatellite markers were used (Sigma Aldrich, India). Invitro amplification using polymerase chain reaction was performed in an Effendorf Thermo Cycler (Bangalore, Genei) of 25µl of reaction mixture containing 1µl genomic DNA, 19.67µl of nuclease free water, 2.5 µl of DNA polymerase buffer, 0.5 µl dNTP of 10mM, 0.5µl forward primer, 0.5µl reverse primer and 0.33 µl of DNA polymerase II. Amplification of DNA was performed with the following conditions: Initial denaturation at 94°C for 5 min. followed by 35 cycles at denaturation at 94°C for 45 second annealing at 50°C for 45 second, elongation at 72 °C for 1 min. and a final extension at 72°C for 10 min.

iii) Electrophoresis of PCR product

After amplification of DNA sample through PCR, 5µl of 1X loading buffer was added to each of amplification product and mixed thoroughly. From this mixture, 10µl of each sample were loaded in 3.5% metaphor agarose gel prepared in 0.5X TBE buffer. PCR products were resolved by running gel at 80 volt for 5-6

hours. The gels were visualized under UV light and photographed using gel documentation system (Alpha Imager).

3.6 BIOCHEMICAL TRAITS

i) Total phenol content

Phenol content (mg GAE/100g): For extraction of total phenol, 5 g of homogenized samples were extracted twice with 30 ml of ethanol (80%), by stirring and sonicating for 30 min. in dark. The homogenate was then centrifuged for 15 min. at 10000 rpm at 4°C (Eppendorf, Westbury, and U.S.A). The supernatant was then vacuum concentrated at 40°C in a rota-evaporator and stored at -20°C. The concentrated sample was used as sample extract for estimation of total phenol. Total phenols were estimated spectrophotometrically using Foline Ciocalteau reagent (Singleton *et al.*, 1999). To 100 ml of the sample extract (80% ethanol), 2.9 ml of deionized water, 0.5 ml of Folin-ciocalteu reagent and 2.0 ml of 20% Na₂CO₃ solution were added. The mixture was allowed to stand for 60 min and absorption was measured at 750 nm against a reagent blank in U.V spectrophotometer. Results were expressed as gallic acid equivalent (mg GAE/100 g fw).

Total phenolic (mg GAE/100g)

$$= \frac{(O.D. 750 \text{ nm} + 0.22) \times \text{volume (5.5 ml)} \times \text{dilution} \times 10}{0.016 \times \text{weight of sample (g)}}$$

ii) Vitamin C content (mg/100g)

The estimation of ascorbic acid content in fruit juice was described by Rangana (1977).

a) Reagents:

- i) 3% Metaphosphoric acid (HPO₃) (It was prepared by dissolving the 30g of HPO₃ in distilled water and the volume of solution was made up to 1000 ml).
- ii) Standard ascorbic acid : 100 mg of ascorbic acid was dissolved in 3% metaphosphoric acid solution and the volume was made up to 100 ml by adding 3% HPO₃. Then 10ml of this solution was further diluted to 100 ml with 3%HPO₃. This means, 1ml of the final solution contained 0.1mg of ascorbic acid.

- iii) Dye solution : 50 mg of 2, 6 dichlorophenol-indophenol dye and 42 mg of sodium bicarbonate was dissolved in distilled water and the volume was made up to 200 ml. It was stored in refrigerator.

b) Procedure:

- i) Standardization of dye : 5 ml of standard ascorbic acid solution was taken in a beaker and 5 ml of 3% HPO₃ was added to it. The dye was taken in a burette and titrated against standard ascorbic acid solution. The dye factor was determined, using the following formula :

$$\text{Dye factor} = \frac{0.05}{\text{titre value}}$$

- ii) Preparation of sample: 10 ml of brinjal juice was taken from a composite sample of 5 crushed fruits. The final volume was made up to 50 ml with 3% HPO₃.
- iii) Assay of extract : 10 ml aliquot was taken in a conical flask and titrated with the standard dye to a pink end point which persisted for at least 15 seconds.
- iv) Calculation : Calculation of ascorbic acid content of the sample was done using the following formula:

$$\text{Ascorbic acid (mg/100g)} = \frac{\text{Titre} \times \text{Dye factor} \times \text{Final Volume}}{\text{Volume of aliquot taken} \times \text{Volume of sample taken}} \times 100$$

iii) Anthocyanin content (mg/100g)

For extraction of anthocyanin, 5g of homogenised sample were extracted twice with 30 ml of ethanolic HCl (95% ethanol and 1.5 HCl in ratio of 85:15 respectively) by crushing with help of pestle and mortar. The homogenised solution was transferred in 50 ml conical flask and stored overnight at 4°C. In the next day, the solution was filtered through whatman No. 1 paper. The bottle and residue on filter paper were washed repeatedly with ethanolic HCl and finally the volume was made up to 100 ml. The solution was stored in dark place for an hour and absorption was measured at 535 nm O.D. The amount of anthocyanin content is calculated by using the formula, where, (e = 98.2) absorbance of a solution 0.1mg/ml anthocyanin.

$$\text{Total anthocyanin (mg/100 g)} = \frac{\text{O.D.} \times \text{Dilution} \times \text{Final Volume}}{\text{weight of the sample taken} \times e} \times 100$$

iv) Antioxidant (cupric reducing antioxidant capacity)

The method for extraction of antioxidant was recently developed by Apak *et al.* (2004), measures the copper (II) or cupric ion reducing ability of polyphenols. It makes use of the copper (II)-neocuproine [Cu (II)-Nc] reagent as the chromogenic oxidizing agent. For the estimation of antioxidant activity, 5 g of homogenized samples were extracted with 10 ml of ethanol (100 %) with pestle and mortar. The solution was centrifuged at 10000 rpm for 15 min. at 4°C and the supernatant was stored at -20°C. To the 100µl of sample extract (100% ethanol), 1 ml of copper (II) chloride solution, 1 ml of neocuproine alcoholic solution, 1ml of ammonium aqueous buffer at pH 7 and 1ml of distilled water to make the final volume 4.1 ml. The mixture was allowed to stand for 30 min. and absorption was measured at 450 nm against a reagent blank in U.V spectrophotometer and the antioxidant activity was expressed as µmol Trolox g⁻¹.

$$\text{Antioxidant } (\mu \text{ mol/g}) = \frac{\text{trolox}}{\frac{\text{AF}}{\text{ETR}}} \times \frac{\text{VF}}{\text{VS}} \times \frac{\text{Vcup}}{\text{m}} \times r \times 1000$$

Where,

AF = (absorbance, ETR = absolute factor = 1.67×10^4)

VF = Final volume (4.1ml),

VS = sample volume taken (0.01ml)

r = (dilution factor .)if spectrophotometer reading >1, then sample is diluted with distilled water.

Vup = initial volume, m = weight of sample

3.6 Cytological study

i) Confirmation of chromosome number at metaphase of mitosis

The study of chromosome in living conditions is difficult as well as inconvenient. The most suitable method and simpler way to resolve the chromosome is to first fix and then stain the chromosome in the laboratory. The plant cells required more laborious process than the animal cells because of presence of cell wall in the plant cell. Further meiotic chromosome resolution are more easier than the somatic chromosome. Hence, the selection of the cytological techniques schedule

has its own significance in resolving the chromosome. Usually for chromosome analysis particularly somatic chromosomes, certain operation known as pre-treatment is desired before fixation of cell as it helps in getting better resolution of the chromosomes. The various steps involved in the development of a cytological technique for chromosome analysis are as follows by using the methods of Kumar and Lal (2000).

ii) Germination of seeds

The seeds were kept on pre-wetted blotting paper on the petri plate for germination.

iii) Cold water treatment of the cell

One cm length root tip were taken and put inside the glass vial which contain pre-cooled water. This vial is kept on glass containing ice cube and kept at 4°C in refrigerator for 24 hrs.

iv) Fixation of root tip

After the cold water treatment the root tips were transferred into a vial which consist of fixative absolute alcohol : glycerol acidic acid (3:1) for at least 2 days

v) Hydrolysis of the root tip

Fresh root tip were put in a glass vial containing 1-2 ml of 1N HCl and kept for 15 min. at 60°C in hot oven. Then root tips were washed repeatedly with tap water.

vi) Preparation of feulgen

For preparation of feulgen stain, 100 ml of water is taken in a beaker and heat in oven till boiling and poured 0.5g of fuchsin basic powder into it. Finally this solution was filtered in black bottle and then poured 1.5ml 1N HCl and 1.5 g potassium metabisulphide. Sealed the cap in air tied condition and kept in dark place for overnight. The colour solution is in straw colour it signifies ready to use.

vii) Staining of root tip with feulgen

The washed root tips were kept in blotting paper to drain off the water and kept in glass vial containing feulgen for 1-2 hours, to get the stain into the root tip.

viii) Preparation of slide

The stained root tip was cut with the help of forcep and needle and placed on clean slide and drop a small amount of acetocarmine stain. Slowly lower the cover slip to avoid air bubble. Then crush with handle of the needle and kept for few seconds on spirit lamp and pressed hardly with thumb and kept for few min and watch under microscope.

3.7 Statistical analysis

i) Statistical analysis for crossability of *Solanum melongena* and its wild relatives.

The statistical analysis was carried out using SAS 9.4 software package available at Indian Agricultural Statistics Research Institute, New Delhi, India. The percentage data was transformed using arc sine transformation as suggested by Box and Cox (1964). The zero percentage data were first substituted by $0.0025 (1/4n)$, where n is the number of units in which the percentage data were based) before arc sine transformation was made. Subsequently, standard deviation (SD) was also calculated. Pair-wise comparisons on the least squares means (LSMEANS) were performed using the Tukey's Honest Significant Difference (HSD) test and least significant difference (LSD) test was used to describe means with 95% ($p < 0.05$) confidence.

ii) Statistical analysis for the study of morphological and biochemical diversity

The statistical analysis was carried out using SAS 9.4 software package available at Indian Agricultural Statistics Research Institute, New Delhi, India. The Genetic diversity study was carried out using Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Intra as well as inter-cluster distances were calculated by the methods given by Singh and Choudhary (1985). Agglomerative Hierarchical cluster analysis was used to determine differences and similarities among the genotypes and the Euclidean distance measure was used to reflect the best difference existing among the genotypes (Kendall, 1980). Principal factor scores were calculated by using Anderson and Rubin method (1956).

iii) Statistical analysis of molecular diversity

For the molecular analysis, the amplified fragments were scored manually for their presence (denoted as '1') and absence (denoted as '0') for each primer. The similarity matrices were subjected to unweighted pair group method of arithmetic average (UPGMA) for cluster analysis by using Darwin Software 6 version (Posada and Crandall, 2001). For the analysis of SSR marker in Power Maker software version 3.25 (Liu and Muse, 2005) band pattern for each of the microsatellite markers were recorded for each genotypes by assigning a letter to each band for e.g. allele were number as A1, A2 etc. Through this software number of alleles and values of gene diversity and PIC (Botstein, 1980) of each locus from 39 SSR markers were calculated. PIC was calculated by using the formula $PIC = 1 - \sum (P_i)^2$, where P_i is the proportion of the population carrying the i^{th} allele.

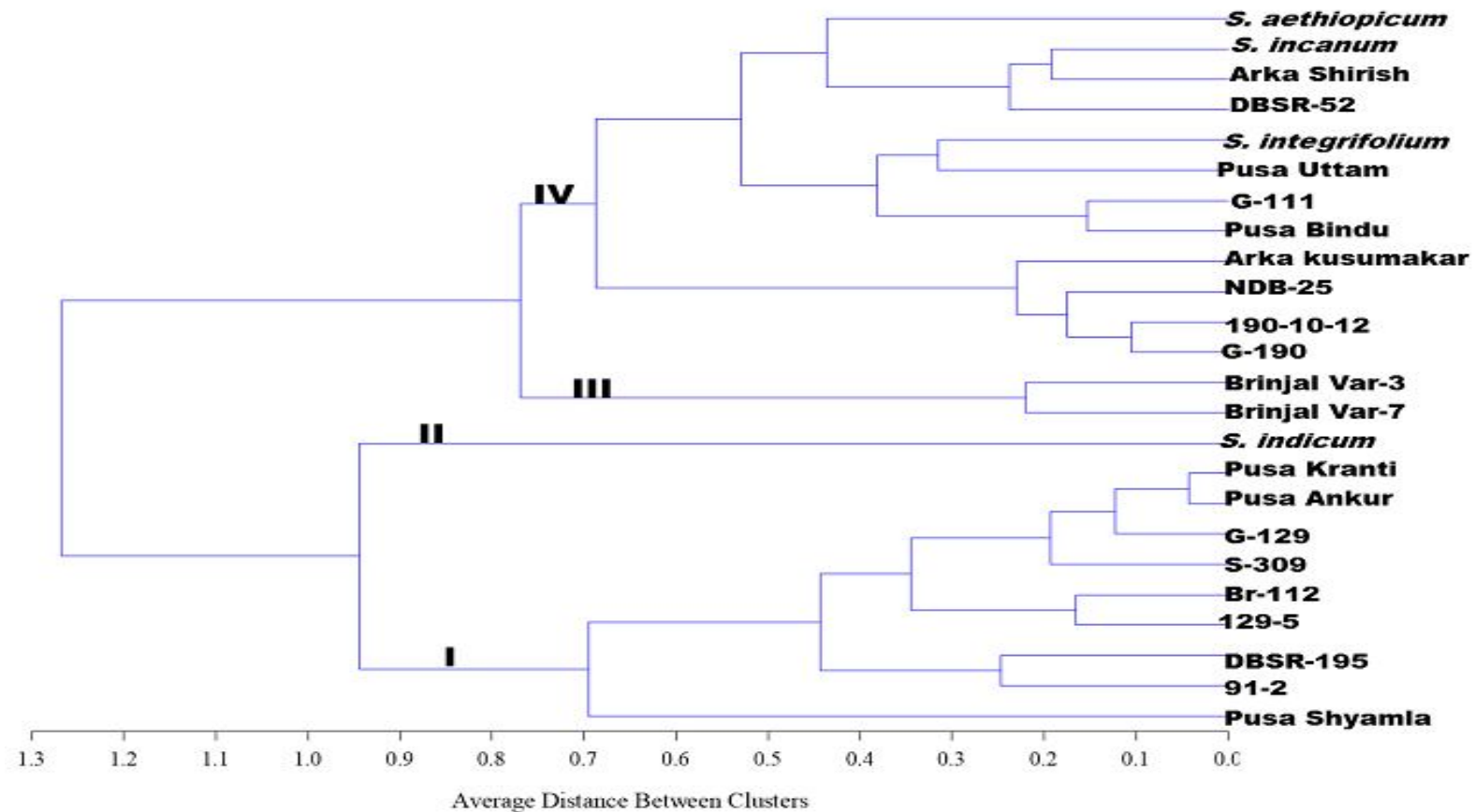


Fig. 1. Dendrogram depicting genetic relationships among 24 genotypes of *S. melongena* and its related wild species based on morphological and biochemical traits produced by complete linkage analysis (scale: Euclidean distance).

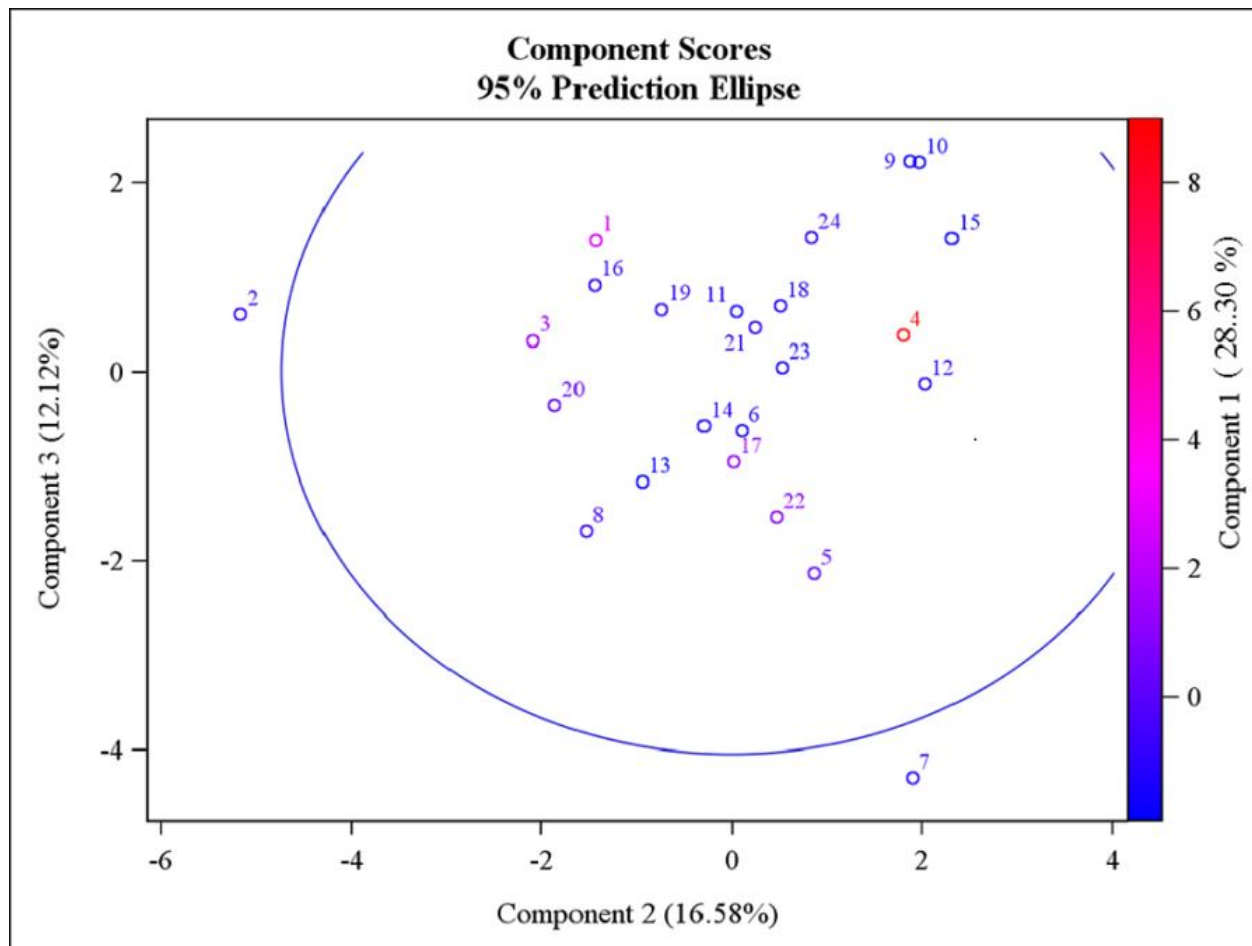


Fig 2. Plot of PF scores based on three factors i.e. PF 1, 2 and 3.

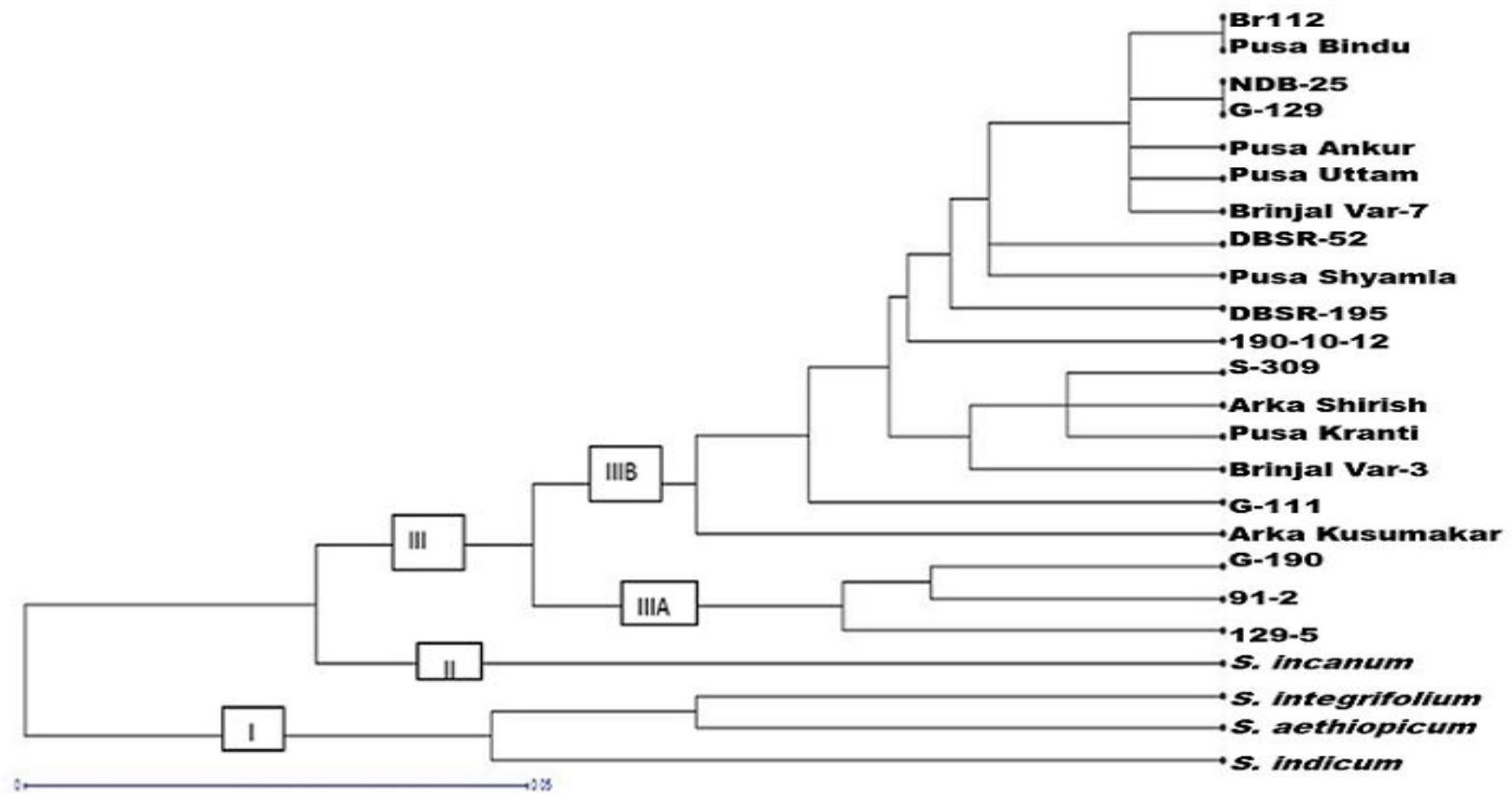


Fig 3. Dendrogram showing Jaccard's dissimilarity produced using UPGMA cluster analysis demonstrating association among 24 genotypes of eggplant

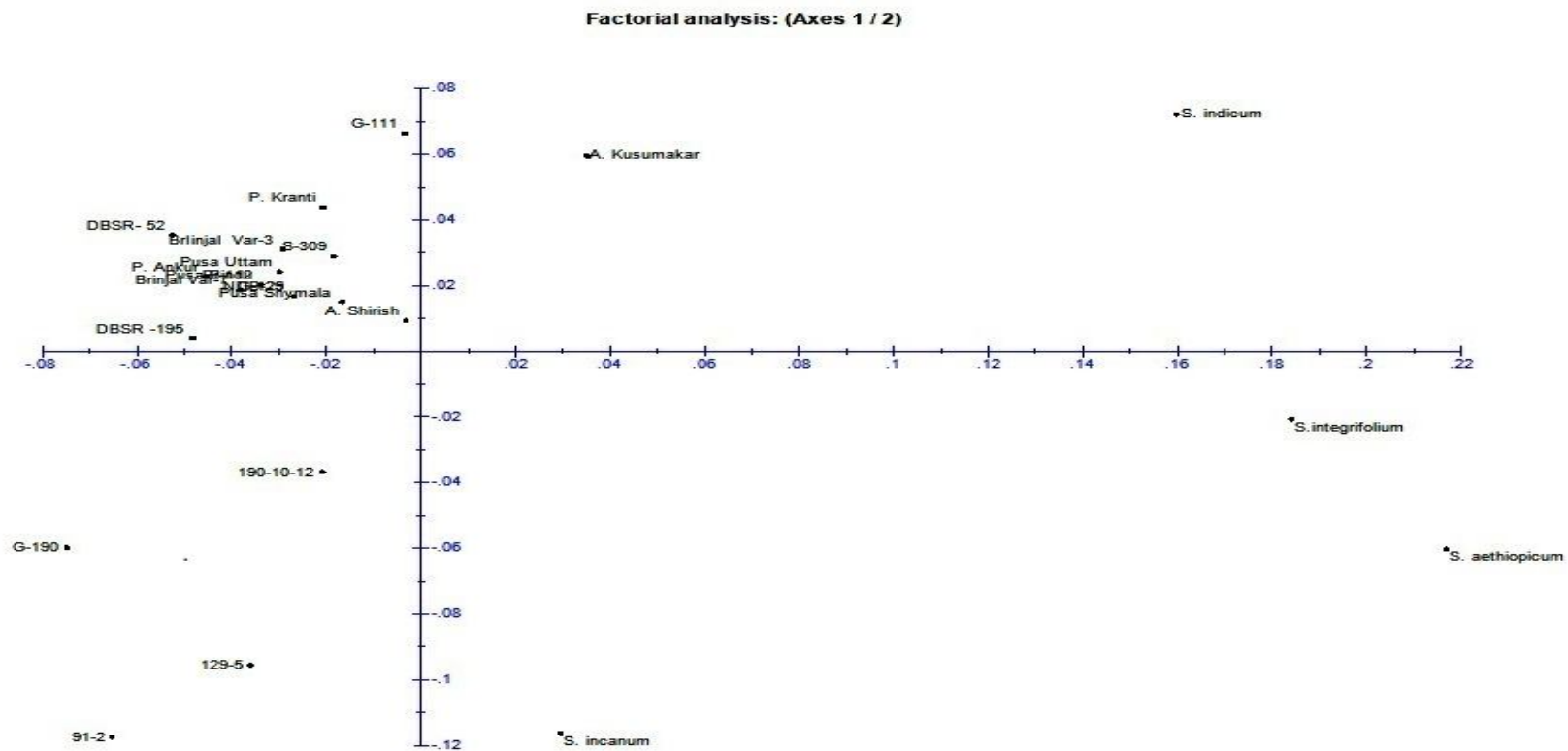


Fig 4. PCA of 24 eggplant genotypes including four wild species using 39 SSR markers.

4. RESULTS

The present study entitled “Studies on crossability and genetic relationship among eggplant (*Solanum melongena* L.) and wild relatives” was conducted during *kharif* seasons of 2012-2015. The results of the present investigation were subjected to appropriate statistical analyses and have been presented under the following headings.

4.1 Studies on crossability between *solanum melongena* and its related wild *Solanum* species

4.1.1 Estimation of pollen viability in four wild *Solanum* species

The pollen viability study was carried out as per the procedure laid out by Prasad *et al.* (2006). The data on pollen viability of the four wild species are presented in Table 1. There was marked variation among the wild species. The maximum (34.78%) fertile pollen was observed in *S. indicum* whereas minimum (11.01%) was in *S. integrifolium*. Among the four wild species, *S. incanum* did not have any sterile pollen. The maximum pollen sterility was observed in the *S. integrifolium* (71.56%) followed by *S. indicum* (15.22%) and *S. aethiopicum* (10.65%) (Plate 2).

4.1.2 Crossability behaviour of each cultivated *S. melongena* genotypes with each of wild *Solanum* species

The hybridization between cultivated *S. melongena* with four wild species revealed three patterns of behaviour of the hybrids *viz.* (a) hybrid, Br-112 $\times$ *S. indicum* died after germination. Hybrids, DBSR-52 $\times$ *S. indicum* (Plate 3a), Pusa Ankur $\times$ *S. aethiopicum* (Plate. 3b), G-190 $\times$ *S. aethiopicum*, 91-2 $\times$ *S. aethiopicum* and 190-10-12 $\times$ *S. aethiopicum* were vigorous in growth, similar to wild parent species, late flowering and fruiting with parthenocarpic fruits. Hybrids, 91-2 $\times$ *S. integrifolium* (Plate.4a), DBSR-52 $\times$ *S. integrifolium*, DBSR-52 $\times$ *S. incanum* (Plate. 4b), Br-112 $\times$ *S. incanum* (Plate.4c), NDB-25 $\times$ *S. incanum* (Plate. 4d) and Pusa Kranti $\times$ *S. incanum* were vigorous in growth development with early flowering and fruiting habit and normal fruits and seed set.

The results on crossability of *S. melongena* genotypes with wild species for fruit set are presented in Table 2. The maximum fruit set (80%) was recorded in

cross Pusa Ankur $\times$ *S. aethiopicum* followed by Pusa Bindu $\times$ *S. aethiopicum* (75%), NDB-25 $\times$ *S. aethiopicum* (75%) and G-190 $\times$ *S. aethiopicum* (63.3%) which were statistically at par. The hybrid combinations Pusa Kranti $\times$ *S. aethiopicum*, Br-112 $\times$ *S. aethiopicum*, DBSR-195 $\times$ *S. aethiopicum*, 129-5 $\times$ *S. aethiopicum*, Pusa Kranti $\times$ *S. integrifolium*, DBSR-195 $\times$ *S. integrifolium*, 190-10-12 $\times$ *S. integrifolium*, Pusa Shymala $\times$ *S. indicum*, 129-5 $\times$ *S. indicum* and 129-5 $\times$ *S. incanum* did not produce any fruit.

The data on number of seeds per fruit and mean germination of F_1 seed in each cross combination are given in Table 3 and Table 4 respectively. The maximum number of seeds per fruit (754.00) were obtained in G-190 $\times$ *S. incanum* followed by DBSR-52 $\times$ *S. incanum* (226.60), G-190 $\times$ *S. aethiopicum* (206.00) and were significantly different from each other. The highest germination of F_1 seeds was noted in Pusa Uttam $\times$ *S. aethiopicum* (71%), 91-2 $\times$ *S. aethiopicum* (71%), G-190 $\times$ *S. aethiopicum* (71%) followed by G-190 $\times$ *S. incanum* (70%) and Br-112 $\times$ *S. incanum* (70%) though these combinations were statistically at par.

4.1.3 Crossability of *S. melongena* genotypes with four wild species

The results of the interspecific hybridization between the cultivated genotypes of *S. melongena* and four wild species (*S. incanum*, *S. aethiopicum*, *S. integrifolium* and *S. indicum*) with respect to mean fruit set (%), number of seeds per fruit and number of F_1 seeds germination (%) are presented in Table 5.

The degree of crossability between the cultivated *S. melongena* genotypes with wild species varied with individual cross combination. The maximum mean fruit set (41.25%) was observed for Pusa Ankur when used as female parent followed by G-190 (37.91%) and NDB-25 (32.08%). The fruit set (%) was statistically at par when genotypes G-190 and Pusa Ankur were used as female parent. The maximum number of seeds per fruit were obtained in G-190 (266.92) followed by Pusa Uttam (101.42) and 91-2 (92.00) which were significantly different. The highest F_1 seed germination (%) was observed for Pusa Ankur (41.58%) followed by Pusa Uttam (40.25%) and 91-2 (35.50%). The genotypes Pusa Ankur and Pusa Uttam were statistically at par while, 91-2 was significantly different from them.

The maximum fruit set (31.73%) was observed when *S. aethiopicum* was used as pollen parent followed by *S. indicum* (22.18%) and *S. incanum* (19.36%) where fruit set was statistically at par in *S. incanum* and *S. indicum*. The maximum number of seeds per fruit (132.44) was obtained in *S. incanum* followed by *S. aethiopicum* (43.72) and *S. integrifolium* (25.10). The mean seed germination was highest (41.25%) when *S. incanum* was used as pollen parent.

4.2 Molecular, morphological, biochemical and diversity analysis

4.2.1 Morphological and biochemical diversity

The data presenting to morphological diversity of cultivated and wild species is given in Table 7. In the present study, the genotypes showed high coefficient of variation for number of fruits per plant (370.47), anthocyanin content (119.46) and ascorbic acid content (80.00) whereas, lowest coefficient of variation observed for days to first harvest (15.21), plant height (15.61) and days to first fruit set (18.58). D^2 statistics for estimating genetic diversity revealed the presence of wide genetic diversity among the 24 genotypes as they formed four gene constellations (Fig. 1). Among the four clusters, cluster IV had maximum (12) genotypes (Arka Shirish, DBSR-52, Pusa Uttam, G-111, Pusa Bindu, Arka Kusumakar, NDB-25, 190-10-12 and G-190) including three wild species (*S. incanum*, *S. aethiopicum* and *S. integrifolium*). Cluster III comprised two cultivated genotypes (BrinjalVar-3 and BrinjalVar-7) belonging to same location. Cluster II had only one wild species (*S. indicum*) whereas, Cluster I comprised nine cultivated genotypes (Pusa Kranti, Pusa Ankur, G-129, S-309, Br-112, 129-5, DBSR-195, 91-2 and Pusa Shyamla).

The average inter and intra-cluster distance of 24 genotypes are presented in Table 6. Among the four clusters, the highest inter cluster distance (90.03) was observed between cluster II and cluster III followed by cluster I and III (73.75), II and IV (73.60). The maximum intra-cluster distance was observed in cluster IV (5.34) having twelve genotypes.

The individual genotype was characterized in respect of their mean values of morphological and biochemical traits presented in Table 7 to find out genotypes having similar characteristics. The cluster I comprised nine genotypes (Pusa Kranti, Pusa Ankur, G-129, S-309, Br-112, 129-5, DBSR-195, 91-2 and Pusa Shyamla) and found to exhibit earliness in flowering (35.03 days), fruiting (49.67 days), harvesting

(73.93), fruit index (2.86) and anthocyanin content (22.67 mg/100g). The cluster II had single wild species (*S. indicum*) having maximum plant height (86.00 cm), number of primary branches per plant (10.00), number of flowers per clusters (7.00), number of fruits per cluster (5.67) and maximum number of fruits per plant (1475.00). The cluster III consisted two genotypes and exhibited maximum fruit length (12.30 cm), fruit diameter (7.80 cm), fruit weight (327.50 g), yield per plant (2560.00 g), total phenol (394.80 mg GAE/100g) and antioxidant activity (5.54 umol/g). The cluster IV had twelve genotypes (*S. aethiopicum*, *S. incanum*, Arka Shirish, DBSR-52, *S. integrifolium*, Pusa Uttam, G-111, Pusa Bindu, Arka Kusumakar, NDB-25, 190-10-12, G-190, Brinjal Var-3, Brinjal Var-7, *S. indicum*, Pusa Kranti, Pusa Ankur, G-129, S-309, Br-112, 129-5, DBSR-195, 91-2, Pusa Shyamla) and showed maximum ascorbic acid (3.58 mg/100g) content.

Eigen value of principle component of total variation obtained from principle component analysis is presented in Table 8. The results revealed that the first principle component (PC1) is largely accounted for the variation among the genotypes with 29.00% followed by second principle component (PC2) (17.00%) and third (PC3) (12.00%). The first three principle components accounted for 57.00% of the total variation among the 24 genotypes describing, seventeen traits. The Eigen vectors of 17 morphological and biochemical traits of 24 *S. melongena* genotypes including four wild species is presented in Table 9. The traits that contributed more positively to PC1 were earliness in flowering, fruiting, number of flowers per cluster, number of fruits per cluster, number of fruits per plant whereas plant height, fruit length, fruit diameter, fruit weight, fruit index, yield per plant, ascorbic acid content and anthocyanin activity were negatively associated. In PC2, the genotypes were positively associated with plant height, days to first fruit harvest, fruit index and yield per plant while the traits like number of primary branches per plant, number of flowers per cluster, number of fruits per cluster, ascorbic acid content and anthocyanin activity were negatively contributed. The genotype in PC3 positively associated with number of primary branches per plant, fruit length and fruit diameter, fruit weight, ascorbic acid, total phenol, antioxidant activity and anthocyanin content whereas number of primary branches, days to first flowering, days to first fruit set, days to first fruit harvest, fruit weight, fruit index, number of

fruits per cluster, yield per plant, phenol and anthocyanin content were negatively associated.

Principal factor scores were utilized in finding genotypes superior for different factors *i.e.* for all the characters cumulatively ascribed to that factor. Principle factor were calculated among 24 genotypes including four wild species for all the 17 morphological and biochemical traits. The genotypes were plotted on graphs utilizing their principal factor scores based on three factors *i.e.* PF 1, 2 and 3 (Fig. 2). The genotypes which found towards high value of the three factors were supposed to be superior for those factors and hence defining the superior of genotype for all traits in those factors. The genotype Pusa Uttam (15) is shown at the extreme right and the wild species, *S. integrifolium* (3) is at extreme left. From this principal factors figure, it was clear that Brinjal Var-7 (10), Brinjal Var-3 (9) and Pusa Uttam (15) may prove better genotypes when the three factors are considered together for diversity. While considering the first 3 components the genotypes *S. incanum* (2) and Arka Shirish (7) are the possible outlier.

4.2.2 Molecular diversity

Genetic diversity was assessed among 24 eggplant *Solanum melongena* L. genotypes including four wild species (*Solanum incanum*, *S. integrifolium*, *S. indicum*, *S. aethiopicum*) presented in (Table 10) using SSR markers. Details of primers with its forward and reverse sequences are presented in Table 11. A total of 39 SSR primers were screened and 30 primers were amplified with scorable polymorphic alleles and these were used for further studies. The number of bands amplified by each of 30 primer ranged from 2.00 to 5.00. The amplification profile for marker EEMS 21, EEMS 42 and EEMS 48 are presented in Plate 5. A total of 86 alleles with an average of 2.39 allele per locus were amplified in 24 *S. melongena* genotypes including four wild species. Heterozygosity for individual loci among 24 genotypes ranged from 0.00 to 0.83. The major allele frequency ranges from 0.56 to 1 (Table 12). Maximum number of alleles (5) were observed for primer EEMS 48 followed by primer EEMS 15 (4). The primer EEMS 7, EEMS 10, EEMS 12, EEMS 18, EEMS 21, EEMS 22, EEMS 24, EEMS 26, EEMS 32, EEMS 33, EEMS 37, EEMS 39, EEMS 42, EEMS 46, EEMS 47, EEMS 49 and EEMS 50 amplified 3 alleles. Two alleles were amplified by EEMS 6, EEMS 13, EEMS 19, EEMS 25 EEMS 29, EEMS 30, EEMS 31, EEMS 35, EEMS 36, EEMS 38, EEMS 45. The

PIC value for 30 polymorphic markers in the present study varied from 0.08 (EEMS 30, EEMS 35, EEMS 45) to 0.57 (EEMS 48), with an average PIC value of 0.24.

Pair-wise dissimilarity index was measured within *S. melongena* genotypes. The minimum dissimilarity index (0.00) was recorded between G-129 and NDB-25, Br-112 and Pusa Bindu genotypes. The maximum dissimilarity index (0.32) was found between wild species *S. aethiopicum* and 91-2 (Table 13)

The UPGMA dendrogram obtained by 30 SSR distributed for 24 genotypes into three major clusters Fig3. The cluster I from bottom predominantly consisted of 3 wild species (*S. indicum*, *S. aethiopicum*, *S. integrifolium*) with small round fruits with hard pulp and the member of this group were less domesticated. The cluster II comprised progenitor, *S. incanum* of the cultivated species, while the cluster III comprised genotypes that have been cultivated extensively. Cluster III was further sub-divided into IIIA comprising G-190, 91-2 and 129-5 genotypes and IIIB comprising remaining 17 genotypes (Br-112, Pusa Bindu, NDB-25, G-129, Pusa Ankur, Pusa Uttam, Brinjal Var-7, DBSR-52, Pusa Shyamla, DBSR-195, 190-10-12, S-309, Arka Shirish, Pusa Kranti, Brinjal Var-3, G-111, Arka Kusumakar. The genotypes Pusa Uttam and Pusa Bindu were grouped under the sub-cluster IIIB and they have one common parent.

4.2.1.1 PCA analysis

The two dimensional PCA is presented in Fig. 4. The PCA plot (Fig4) separated all the accessions into two major clusters. All the accessions belonging to cultivated genotypes appeared in group on the left side of the X-axis. The genotypes (G-111, Pusa Kranti, DBSR-52, Brinjal Var-3, S-309, Pusa Ankur, Pusa Uttam, Pusa Bindu, Br-112, Brinjal Var-7, Pusa Shyamla, Arka Shirish, DBSR-195, NDB-25, G-129) appeared on the left top of the X-axis and the genotypes Br-112 and Pusa Ankur, NDB-25 and g-129 were appeared overlapped to each other. The genotypes 190-10-12, G-190, 129-5, 91-2 were shown at the bottom left of the X-axis. Arka Kusumakar and *S. indicum* appeared on the right tops of the X-axis. The three wild species (*S. incanum*, *S. aethiopicum* and *S. integrifolium*) were presented at right bottom of X- axis.

4.3 Morphological characterization of F₁ hybrids along with parents

4.3.1 Quantitative morphological traits

The comparative detail description of morphological characters of parents and hybrids has been presented in Table 14.

Among the parental genotypes the highest plant height (89.80 cm) was observed in Br-112 followed by NDB-25 (89.20 cm) and Pusa Uttam (89.00 cm) and they were statistically at par. Among F₁, the highest plant height was recorded in DBSR-52 × *S. indicum* (130.67 cm) followed by Pusa Ankur × *S. aethiopicum* (132.00cm) and Pusa Ankur × *S. integrifolium* (126.00 cm). The hybrids Pusa Ankur × *S. aethiopicum* and DBSR-52 × *S. indicum* were found statistically at par while Pusa Ankur × *S. integrifolium* was found to be significantly different from other two crosses.

The mean number of primary branches per plant was found maximum (10.67) in *S. aethiopicum* followed by *S. indicum* (10.00) and Pusa Kranti (9.00). *S. aethiopicum* and *S. indicum* were found to be statistically at par. The hybrids DBSR-52 × *S. indicum* recorded maximum number of primary branches (13.67) followed by NDB-25 × *S. incanum*, (12.67). The hybrid DBSR-52 × *S. indicum* and NDB-25 × *S. incanum* were statistically at par. The minimum primary branches (4.00) was recorded in Arka Shirish which is at par with Arka Kusumakar.

The genotype 91-2 was earliest in flowering (32.33 days) followed by DBSR-195 (33.00 days). The genotype 91-2 and DBSR-195 were found to be statistically at par. Among the F₁, DBSR-195 × *S. incanum* (30.67 days) was earliest in flowering followed by DBSR-52 × *S. integrifolium* (32.67 days) and Br-112 × *S. incanum*, NDB-25 × *S. incanum* (36.67 days). They were found to be significantly different from each others, while the hybrid Pusa Ankur × *S. aethiopicum* took the maximum days (89.00) for flowering.

Amongst the parental genotypes, the earliest fruit set was recorded in *S. incanum* (42.33 days) followed by Pusa Shyamla (45.33 days), DBSR-195 (46.33 days) while *S. incanum* is significantly different from these two. The hybrid DBSR-195 × *S. incanum* showed the earliest fruiting (41.67 days) followed by Br-112 × *S. incanum* (43.00 days) and G-190 × *S. incanum* (44.33 days) and they were found to

be significantly different from each other, while the hybrid Pusa Ankur $\times$ *S. aethiopicum* took maximum days (127.33) to fruit set.

The wild species *S. integrifolium* showed minimum days to first fruit harvest (59.67 days) followed by *S. incanum* (60.33 days) and Pusa Shyamla (61.33 days) and they were found to be statistically at par with each other. The hybrids G-190 $\times$ *S. incanum* reached the earliest in maturity (55.67 days) followed by DBSR-52 $\times$ *S. integrifolium* (62.67 days) and DBSR-195 $\times$ *S. incanum* (66.33 days) and they were found to be significantly different from each other. The hybrid Pusa Ankur $\times$ *S. aethiopicum* took the maximum (160.00 days) to reach harvesting stage

The maximum mean number of flowers per cluster (7.00) was observed in *S. indicum* followed by *S. integrifolium* and DBSR-195 (4.00) in the parental genotypes and *S. indicum* was found significantly different from these two genotypes whereas *S. integrifolium* and DBSR-195 were statistical at par. The hybrid DBSR-52 $\times$ *S. indicum* showed the maximum (10.67) number of flowers per cluster followed by Pusa Ankur $\times$ *S. aethiopicum* (10.33) and they were found statistically at par.

The mean number of fruits per cluster was maximum (5.67) in wild species *S. indicum* followed by *S. integrifolium* (3.33). *S. indicum* and *S. integrifolium* were found to be significantly different. In hybrids, the maximum (7.00) number of fruits per cluster was observed in DBSR-52 $\times$ *S. indicum* followed by Pusa Ankur $\times$ *S. integrifolium* (7.67) and Pusa Ankur $\times$ *S. aethiopicum* (5.67). DBSR-52 $\times$ *S. indicum* and Pusa Ankur $\times$ *S. integrifolium* were statistically at par.

The mean fruit length was highest (16.80 cm) in Pusa Shyamla followed by Pusa Kranti (12.50 cm) and Pusa Uttam (10.30) and they were found to be significantly different. Among the F₁ hybrids, highest fruit length was recorded in 91-2 $\times$ *S. integrifolium* (9.00 cm) followed by Pusa Kranti $\times$ *S. incanum* (8.60 cm) and Pusa Uttam $\times$ *S. integrifolium* (8.50) and they were found to be statistical at par.

The mean fruit diameter was maximum (7.20 cm) in 190-10-12 followed by Pusa Uttam (7.10 cm) and 91-2 (6.30 cm). The genotype 91-2 was found significantly different from these two whereas 190-10-12 and Pusa Uttam were found to be statistically at par. The hybrid Pusa Uttam $\times$ *S. integrifolium* recorded highest (6.50 cm) fruit diameter followed by DBSR-195 (6.20 cm) and Pusa Uttam $\times$ *S. aethiopicum* (4.90) and they were found significantly different from each other.

The mean fruit shape index was maximum (4.71) in Pusa Shyamla followed by Pusa Kranti (2.13) and DBSR-52 (1.85) and they were significantly different from each other. While in the maximum (3.31) fruit index was recorded in DBSR-52 $\times$ *S. integrifolium* followed by 91-2 $\times$ *S. integrifolium* (2.58) and Br-112 $\times$ *S. incanum* (2.51). The hybrid DBSR-52 $\times$ *S. integrifolium* was found significant different from these two, while 91-2 $\times$ *S. integrifolium* and Br-112 $\times$ *S. incanum* were statistically at par.

The mean fruit weight was maximum (230.00 g) in Pusa Uttam followed by 91-2 (222.00g) and Pusa Kranti (208.60 g) and they were found to be statistically significantly different. Among the hybrids, the maximum (75.00g) fruit weight was recorded in NDB-25 $\times$ *S. integrifolium* followed by Pusa Uttam $\times$ *S. incanum* (74.00 g) and they were found statistically at par.

Among the parental genotypes, the highest number of fruits per plant was recorded in *S. indicum* (1573.00) followed by *S. integrifolium* (348.00) and DBSR-195 (71.00) and they were found significantly different from each other. Among the hybrids the highest number of fruits per plant was recorded in by DBSR-52 $\times$ *S. indicum* (322.00) followed by 190-10-12 $\times$ *S. aethiopicum* (319.00) and 91-2 $\times$ *S. aethiopicum* (293.00) and they were found to be significantly different.

Among parental genotypes, the highest mean yield (2850.00 g) was recorded in Pusa Shyamla followed by 91-2 (2664.00 g) and DBSR-195 (2272.00 g) and they were significantly different from each other. Among the hybrids the maximum (1944.00g) mean yield was recorded in Pusa Shyamla $\times$ *S. integrifolium* followed by Pusa Kranti $\times$ *S. incanum* (1653.00 g) and DBSR-195 $\times$ *S. incanum* (1628.00 g) and they were found significantly different from each other. The minimum mean yield was recorded in Br-112 $\times$ *S. incanum* (432.00g).

4.3.2 Qualitative morphological traits

The genotypes were evaluated and characterized for nineteen qualitative morphological traits viz., stem anthocyanin colouration, stem intensity colour, leaf blade colour, intensity of leaf blade colour, leaf vein colour, intensity of leaf vein colour, present of spine on leaf, spine on calyx, spine on stem, flower colour, fruit shape, shape of fruit apex, fruit skin colour at commercial harvesting, intensity of

fruit skin, colour of calyx, intensity of calyx colour, colour of flesh, fruiting pattern and plant growth habit (Table 15).

In the present study, the growth habit of the genotypes has been characterised into three groups. The majority of the genotypes were semi-spreading and covered 80.43% followed by erect (10.87%) and spreading (8.70%). The flower colours were grouped into four different types namely dark purple, purple, light purple and greenish white (Plate 6). Majority of the genotypes showed purple coloured flower (71.74%) followed by greenish white (13.04%) and light purple (10.87%). Dark purple flower were recorded in only two genotypes.

Considering the fruiting habit, the maximum genotypes showed the solitary fruiting habit (60.87%) followed by mixed (22.91%) and cluster (15.22%). The stem anthocyanin colouration was 50% of genotypes were purple colour with medium intensity of colour and remaining stem was green. The leaf blade colour of the maximum number of genotypes was green (95.65%) followed by purple (2%). The maximum number of genotypes (67.39%) showed green vein colour followed by purple vein colour (32.60%) Plate 7(a). The presence of spine on leaf, calyx and stem was considered for characterization of genotypes and it was found that 63.04% genotypes recorded absence of spine on leaf, calyx and stem. The remaining 36.96% genotypes recorded presence of spine on leaf, calyx and stem Plate 7(b).

Fruit colour and shape in brinjal are important characters for consumer's preference. The maximum number of genotypes were recorded for purple colour fruit (47.83%) followed by green colour (39.13%), strip fruits (10.86%) and white colour (4.35%) (Plate 8). For fruit shape, the genotypes have been categorized into six groups viz. globular, ovoid, obovate, pear shape, ellipsoid and cylindrical. There was great variation among the genotypes for fruit shape. The maximum (41.00%) genotypes were recorded as having globular fruit shape followed by ovoid, obovate (15.22%) and (8.70%) of genotypes were cylindrical and ellipsoid. The few number of genotypes was observed to be pear shape (6.52%) and club fruit shape (4.35%). The maximum number of genotypes had round shape apex (47.83%) followed by flattened shape apex (34.78%) and pointed apex (13.04%). Very few genotypes were recorded to have indented apex (4.35%) and it was recorded in wild species of *Solanum aethiopicum* and *S. integrifolium*. The maximum (95.65%) genotypes had greenish flesh colour followed by whitish (4.35%).

4.3.3 Biochemical characterization of interspecific F₁ hybrids along with parents

The biochemical characterization of interspecific F₁ hybrids along with parents has been given in Table 14. The highest (5.77 mg/100g) ascorbic acid content among the parental genotypes was recorded in 91-2 followed by 190-10-12 and *S. aethiopicum* (3.85 mg/100g). The genotype 91-2 was found significant different from these two whereas, 190-10-12 and *S. aethiopicum* were statistically at par. Among the hybrids, the maximum ascorbic acid content was recorded in DBSR-52 × *S. integrifolium* (11.36 mg/100g) followed by 91-2 × *S. incanum* (11.32 mg/100g) and 91-2 × *S. aethiopicum* (5.71 mg/100g). The hybrid 91-2 × *S. aethiopicum* was found significantly different from these two, whereas the hybrid DBSR-52 × *S. integrifolium* and 91-2 × *S. incanum* were found statistically at par.

The highest (4107.81 mg GAE/100g) total phenol content among the parental genotypes was recorded in *S. aethiopicum* followed by *S. integrifolium* (4070.00 mg GAE/100g) and *S. incanum* (3561.25 mg GAE/100g) and they were found statistically at par. In the hybrids, the highest total phenol content was recorded in DBSR-195 × *S. incanum* (414.91 mg GAE acid/100 gfw) followed 91-2 × *S. aethiopicum* (368.16) and 190-10-12 × *S. aethiopicum* (355.44) and they were found to be statistically at par.

Among the parental genotypes, the highest anthocyanin content was recorded in DBSR-52 (80.65 mg/100g) followed by NDB-25 (52.34 mg/100g) and Pusa Shyamla (21.95 mg/100g) and they were found significantly different. Among the F₁ hybrids, the maximum anthocyanin content (62.32 mg/100g) was recorded in Pusa Shymala × *S. integrifolium* followed by Pusa Uttam × *S. incanum* (62.17 mg/100g) and Pusa Ankur × *S. integrifolium* (32.18 mg/100g). The hybrids, Pusa Shymala × *S. integrifolium* and Pusa Uttam × *S. incanum* were found statistically at par but significantly different from Pusa Ankur × *S. integrifolium*.

The highest antioxidant activity (14.58 µmol trolox/g) among the parental genotypes was recorded in *S. incanum* followed by DBSR-195 (6.87µmol trolox/g) and Pusa Shyamla (6.73 µmol trolox/g). *S. incanum* was found significantly different from these two genotypes while *S. incanum* and DBSR-195 were found statistically at par. Among the F₁ hybrids, Br-112 × *S. incanum* had the highest

(63.27 μ moltrolox/g) antioxidant activity followed by DBSR-195 $\times$ *S. incanum* (46.48 μ moltrolox/g) and Pusa Shyamala $\times$ *S. integrifolium* (36.88 μ moltrolox/g) and they were found significantly different from each other.

4.4. Chromosome number study

In the present study, chromosome numbers were counted for four wild species (*Solanum incanum*, *S. aethiopicum*, *S. integrifolium*, *S. indicum*) and one cultivated Pusa Shymala genotype of *S. melongena*. It was found that 24 chromosomes were present in cultivated *S. melongena* cv. Pusa Shyamla and same number was also found in all the four wild species (*S. incanum*, *S. aethiopicum*, *S. integrifolium*, *S. indicum*) with small size of chromosomes in wild species under investigation (Plate 9).



S. indicum



S. integrifolium

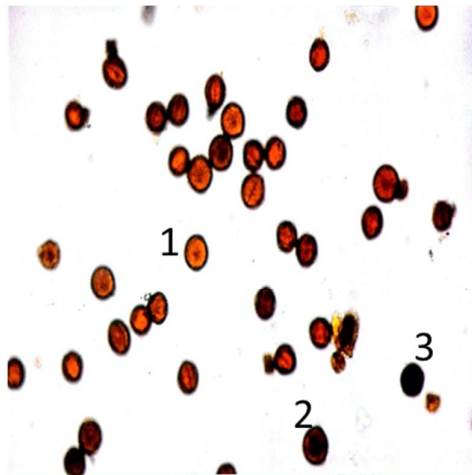


S. aethiopicum

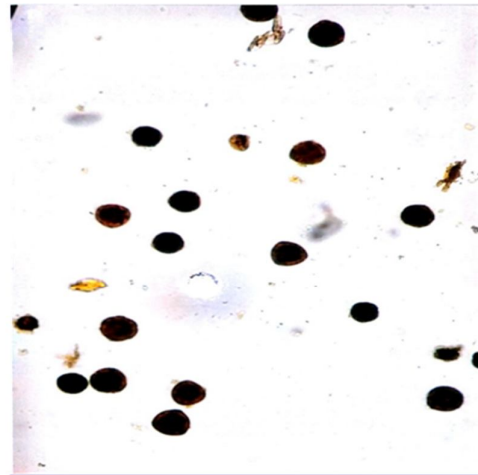


S. incanum

Plate 1 : Wild species of cultivated brinjal (*Solanum melongena*) *S. indicum*, *S. integrifolium*, *S. aethiopicum*, *S. incanum*



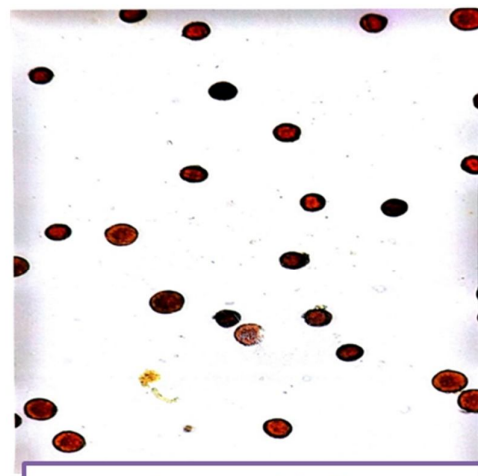
S. indicum



S. incanum



S. aethiopicum



S. integrifolium

Plate 2: Microscopic view of stained pollen of four wild species, 1: unstained (sterile pollen); 2: Pink(Semi-sterile pollen); 3 : Bright red (fertile pollen).



DRSR-52 $\times$ *S. indicum*



Pusa Ankur $\times$ *S. aethiopicum*

Plate 3: Parthenocarpic fruits of interspecific F_1 hybrids :

(a) DRSR-52 $\times$ *S. indicum* and (b) DRSR-91 $\times$ *S. aethiopicum*

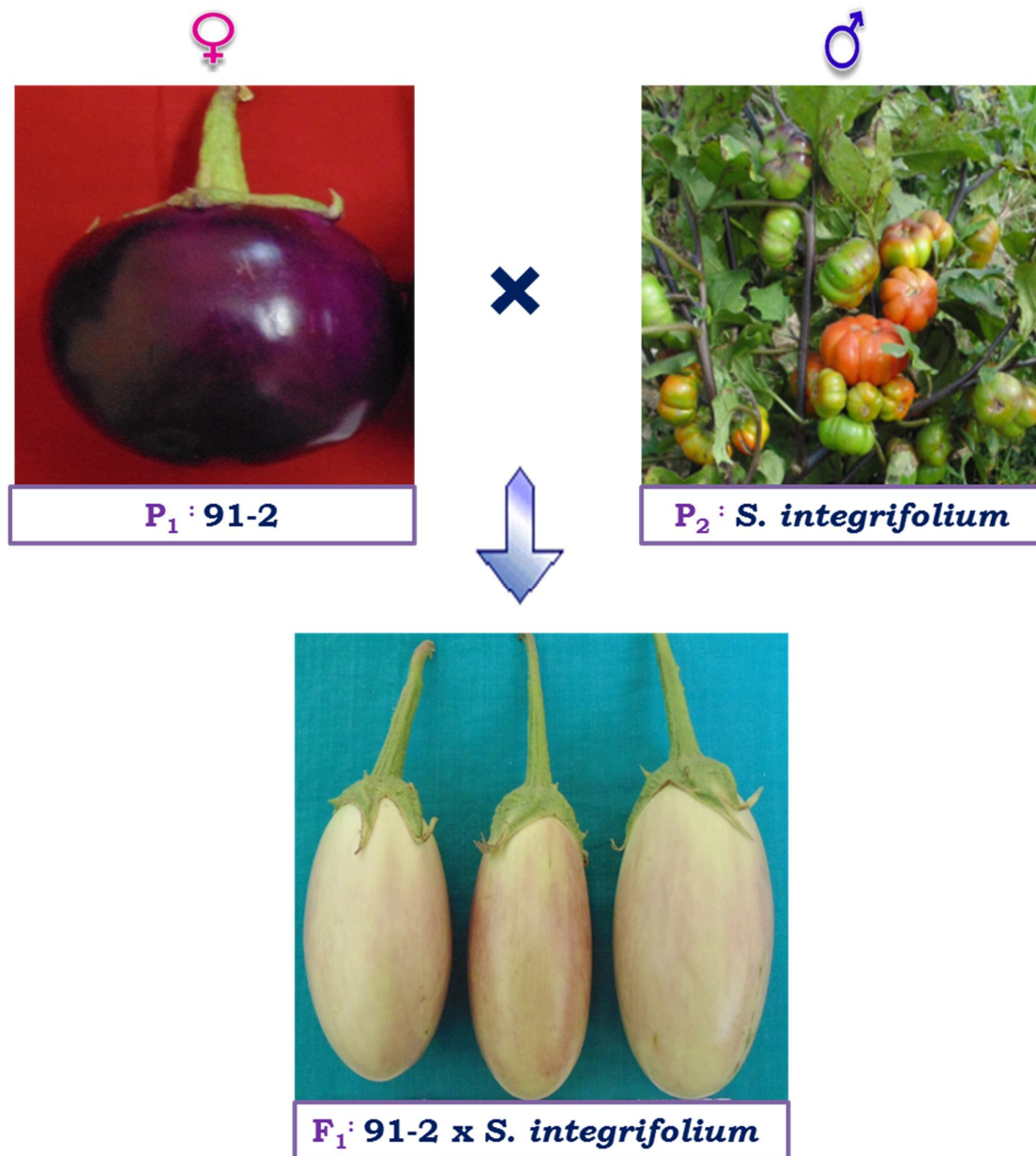


Plate 4 (a): Normal Fruit development of interspecific F₁ hybrid.

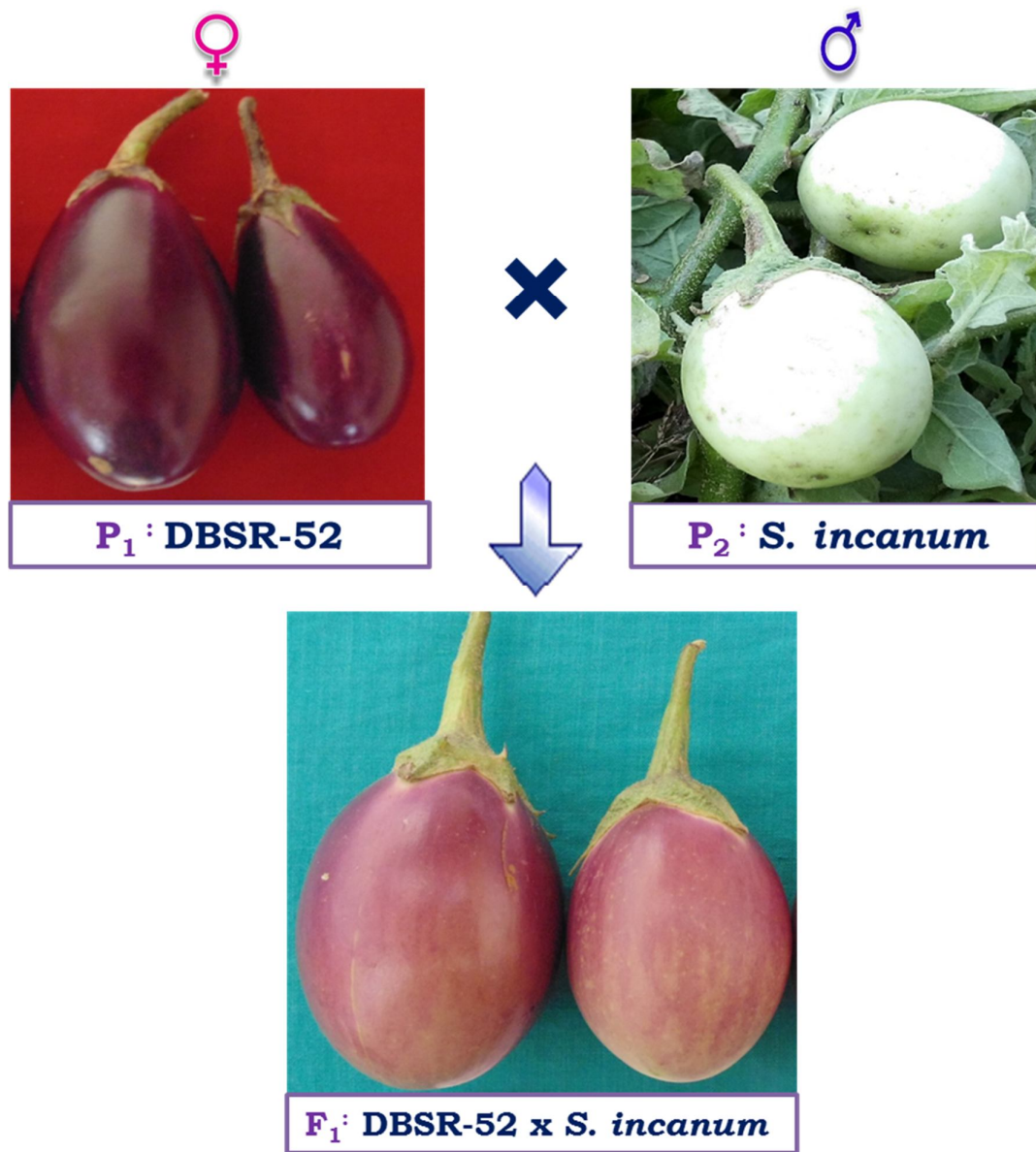


Plate 4 (b) : Normal Fruit development of interspecific F₁ hybrid.

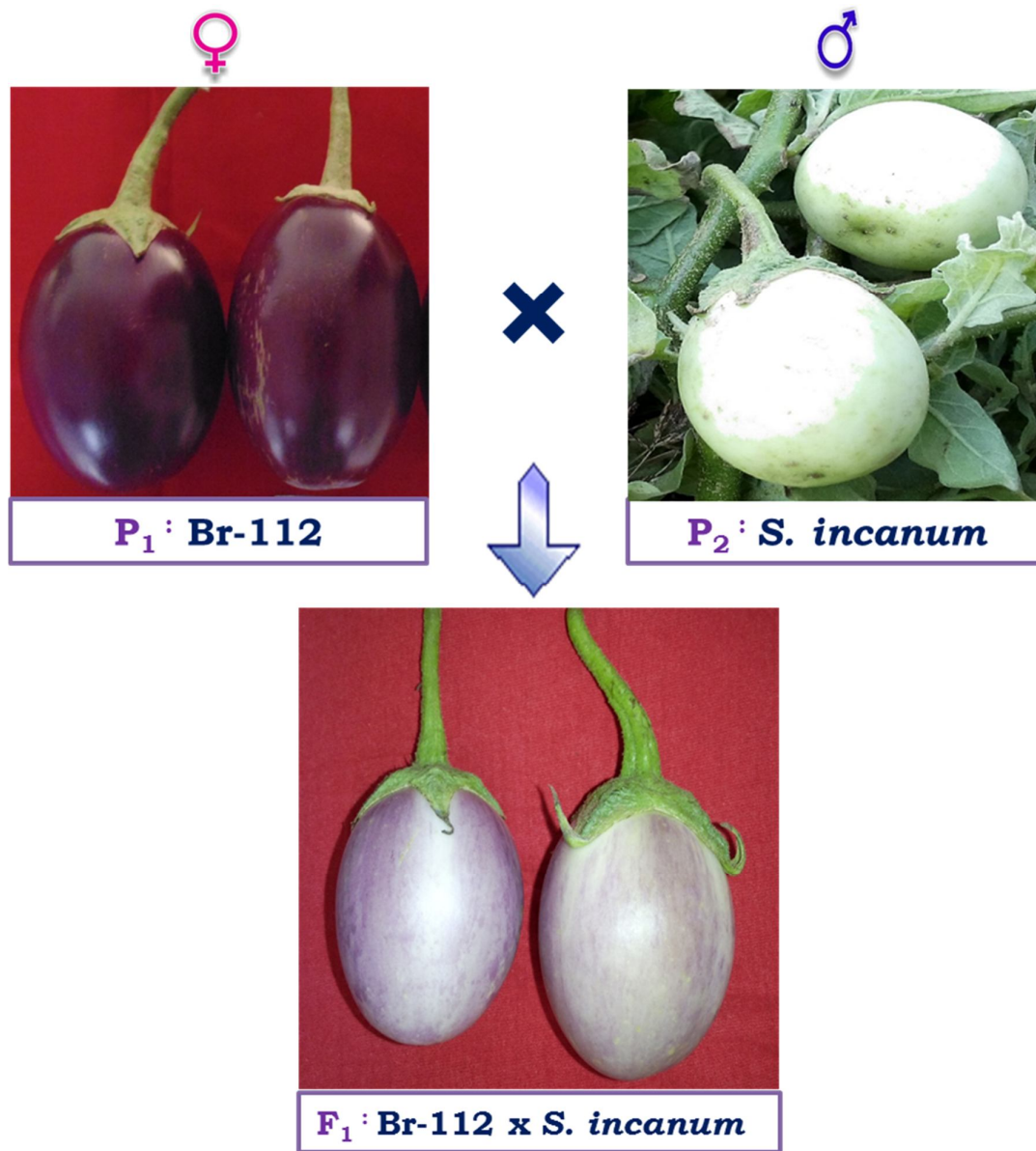


Plate 4 (c) : Normal Fruit development of interspecific F₁ hybrid.

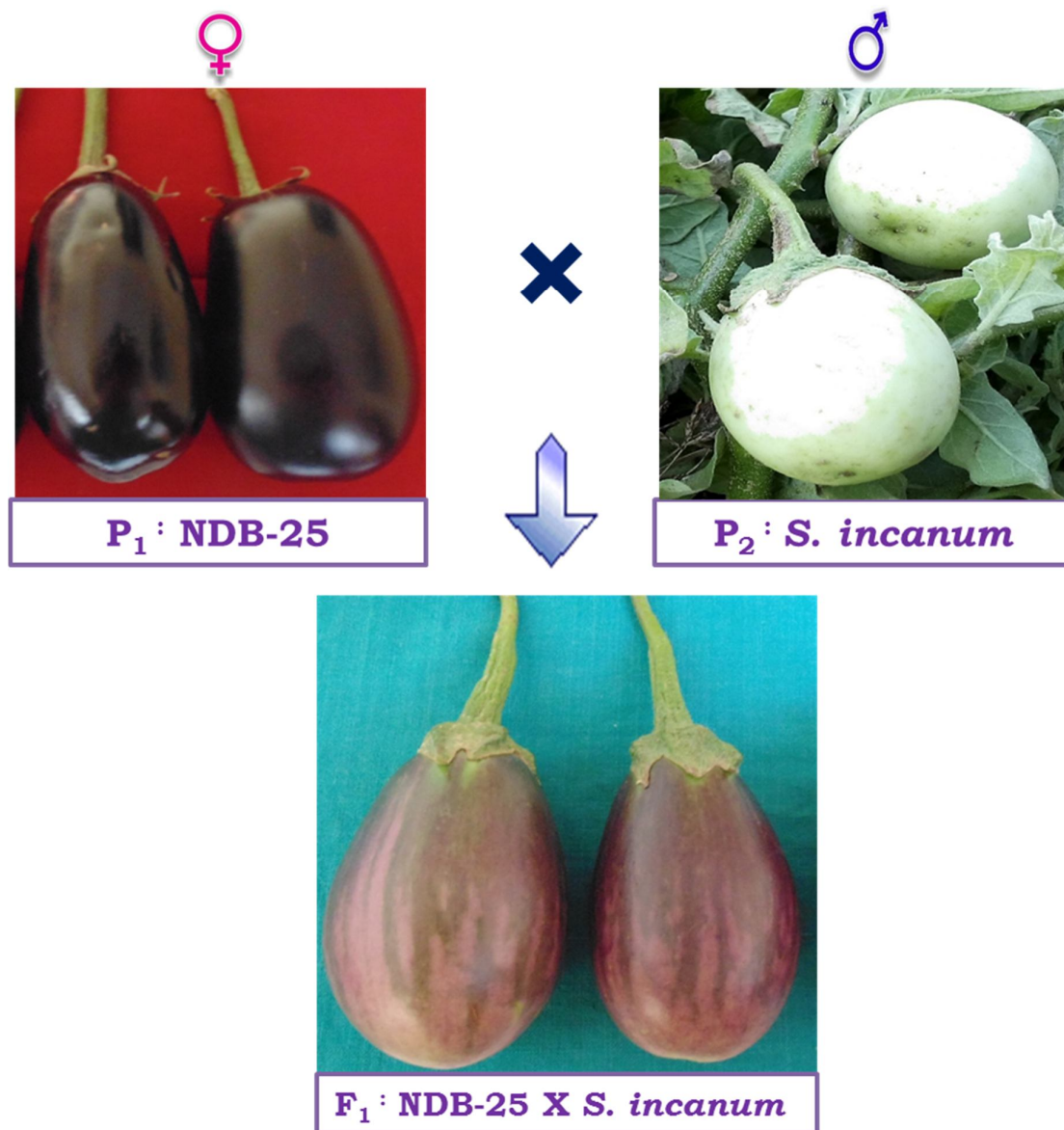


Plate 4 (d) : Normal Fruit development of interspecific F₁ hybrid.

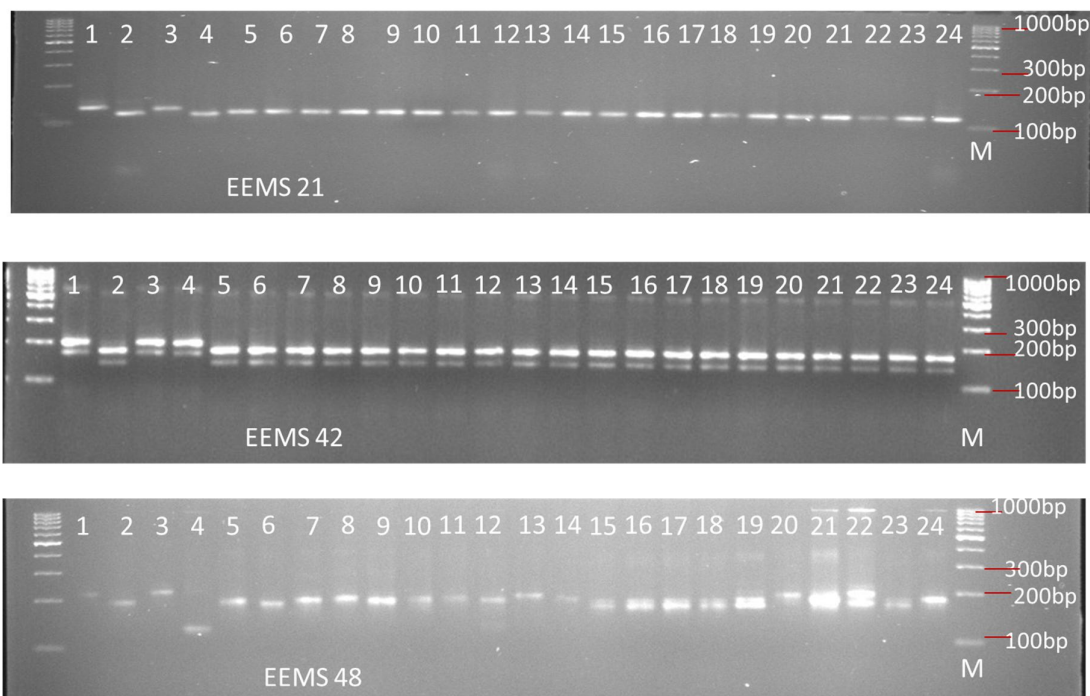


Plate 5 : Profile of DNA amplification of *S. melongena* genotypes including four wild species (metaphor agarose gel 3.5 %, stained with ethidium bromide).

The amplification profile for markers EEMS21, EEMS42 and EEMS48. The marker EEMS 21, EEMS 42 amplified 131 bp and 152 bp respectively. Whereas the marker EEMS 48 expected amplicon was 213 bp but amplified smaller amplicon less than 200 bp in all the genotypes except in *S. aethiopicum* and *S. melongena*.

The identification of each *S. melongena* genotypes including four wild species was shown in Table. 10. The first four lane representing the four wild species of *S. melongena* which showed polymorphism.

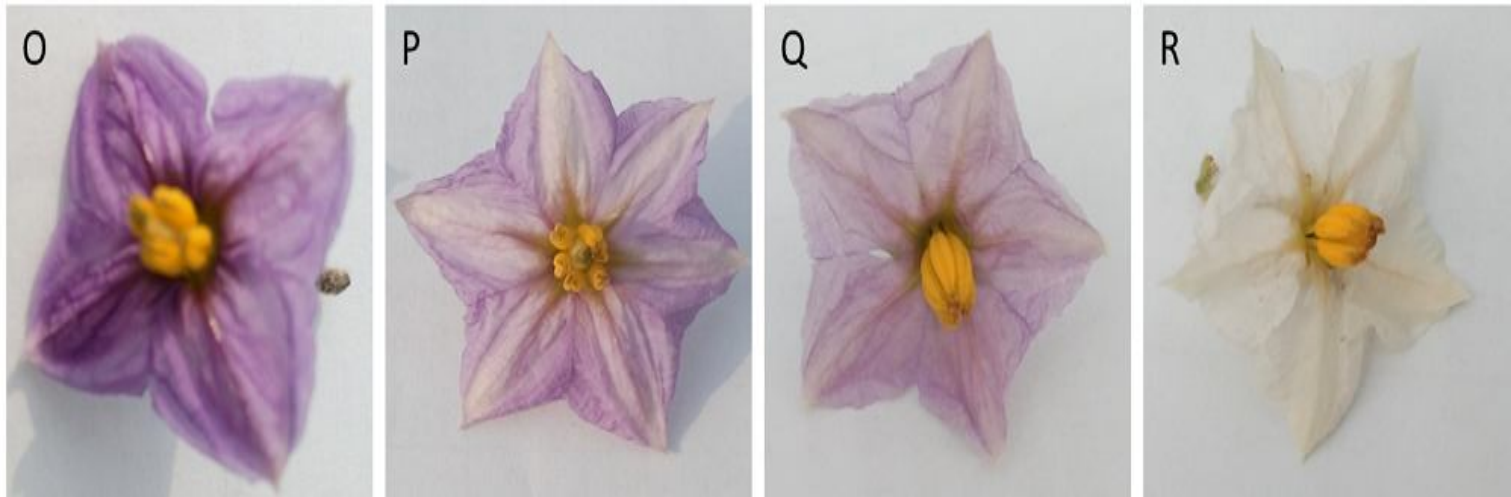


Plate 6 :The different flower colour of the genotypes : PusaBindu (O), DBSR-195 (P), 91-2 X *S.aethiopicum* (Q), Arka Kusumakar (R)



Plate 7 (a): The different leaf blade colour of different genotypes

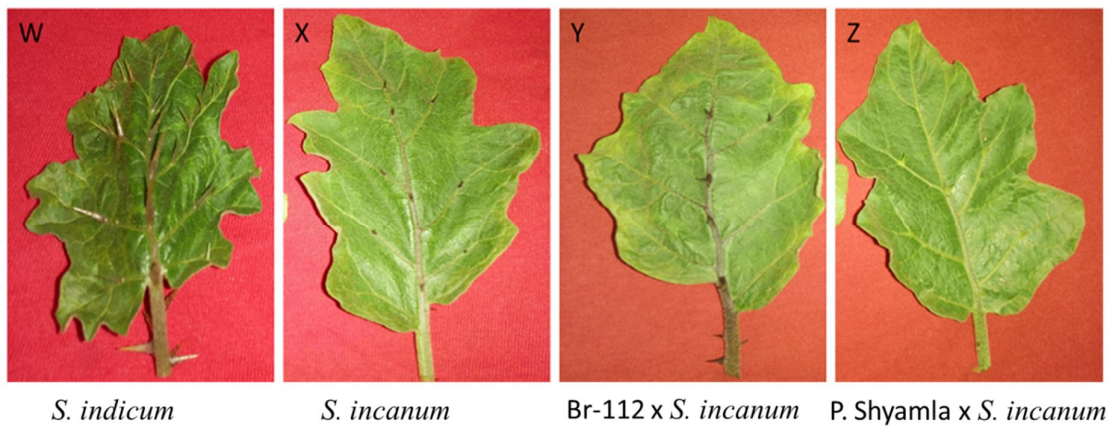


Plate 7(b) : The intensity of spine on leaf of different genotypes :

W : *S. indicum*

X : *S. incanum*

Y : *Br-112* × *S. incanum*

Z : *P. Shyamla* × *S. incanum*



g: (NDB-25)

h:(91-2);

i:(DBSR-52);

j : (DBSR-52 X *S. incanum*)

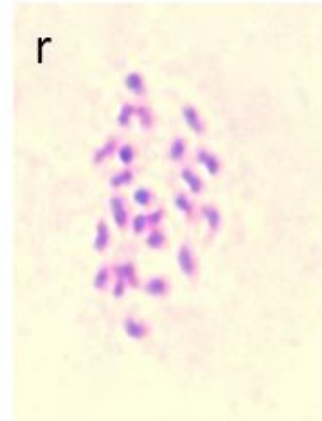
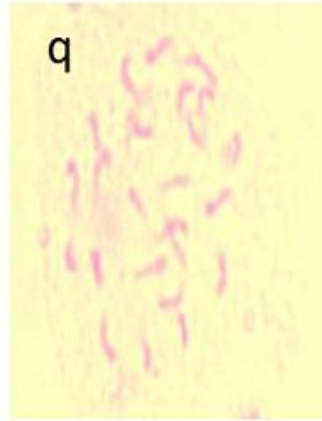
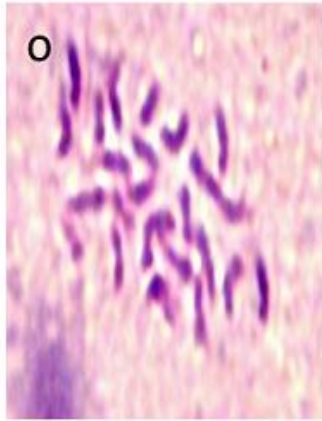
k : (ArkaShirish);

l:(G-190);

m(DBSR-52 x *S. integrifolium*);

n(DBSR-195)

Plate 8 : The different fruit colour intensity of different genotypes



o (*S. incanum*)

p (*S. integrifolium*)

q (*S. indicum*)

r (*S. aethiopicum*)

s (PusaShyamla)

Plate 9 : The chromosome of four wild species and one cultivated genotype

5. DISCUSSION

Brinjal or eggplant is one of the most popular vegetable crop cultivated throughout the country except in higher altitudes. India is the second largest producer of brinjal after China with a 25% share of world production. It is an important cash crop for more than 1.4 million small and marginal farmers (<https://isaaa.org>). However, substantial loss of yield occurs every year due to heavy infestation caused by disease and insect pest. The small and marginal farmers have to spray more than 40 times of pesticides for the management of shoot and fruit borer, which are ineffective (Mohiuddin *et al.*, 2009). Moreover, the application of pesticide by the Indian farmer is not only increasing cost of production but also ultimately causes health hazards. Higher yield with acceptable quality and resistance to biotic and abiotic stresses are the desired traits of breeder in any crop improvement programme. Interspecific hybridization is one of the most significant approaches for developing genetic stocks, which serve as important sources of genes for quality and resistance traits. Desirable traits like resistance against pathogens or abiotic stresses within varying environments, desirable morphological traits are often found only in wild and related species. Through interspecific hybridization, it is possible to use the existing variability of the primary and secondary gene pool. The information on interspecific crossability is important in developing a comprehensive breeding approach. Detail information during the course of investigation obtained on different aspects is being discussed in this chapter under the following sub-headings.

5.1 Studies on crossability between *Solanum melongena* and its wild relatives

5.1.1 Estimation of pollen viability in wild *Solanum* species

Wild relatives have been frequently used in the genetic improvement of many crops, as sources for resistance to biotic and abiotic stresses and quality traits (Zamir, 2001). *Solanum melongena* and *S. aethiopicum*, when crossed produced higher fruit set (Behera and Singh, 2002; Oyelana and Ugborogho, 2008; Khan and Isshiki, 2010). In the present study, maximum viable pollens were observed in *S. indicum*, whereas minimum was observed in *S. integrifolium*. The maximum pollen sterility was shown in *S. integrifolium* followed by *S. indicum*, while sterile pollen was not observed in *S. incanum*. In a previous study, Kumchai *et al.* (2013) also reported

wide ranges of variation for pollen viability in *S. melongena*, *S. torvum* and their hybrid progenies.

5.1.2 Crossability behaviour of each cultivated (*S. melongena*) genotypes with each of wild species

The crossability among the twenty four *S. melongena* genotypes with four wild species showed wide ranges of variation for various characters. The hybrid seed produced by crossing *S. melongena* genotypes and wild species showed variation in the germination of F₁ seed and even complete germination failure was noted in many of the crosses (*G-190* × *S. indicum*, *G-190* × *S. integrifolium*, *Pusa Ankur* × *S. indicum*, *NDB-25* × *S. indicum* and *Pusa Kranti* × *S. indicum*). The failure of pollen germination in some crosses was probably due to the use of different genetic background of the parental lines (Kumchai *et al.*, 2013). When *S. indicum* was used as pollen parent, it was crossable with almost all the *S. melongena* genotypes except *Pusa Shymala* and *129-5*. This study is in conformity with the results of Behera and Singh (2002). Our result contradicts the findings of Rajasekaran (1970a) and Narsimha Rao (1979) who reported incompatibility between *S. melongena* and *S. indicum*.

There was no fruit set in interspecific crosses, viz. *129-5* × *S. incanum*, *Pusa Kranti* × *S. aethiopicum*, *Br-112* × *S. aethiopicum*, *DBSR-195* × *S. aethiopicum*, *129-5* × *S. aethiopicum*, *Pusa Kranti* × *S. integrifolium*, *DBSR-195* × *S. integrifolium*, *190-10-12* × *S. integrifolium*, *Pusa Shymala* × *S. indicum* and *129-5* × *S. indicum*. The genotypes *Brinjal Var-3*, *Brinjal Var-7*, *S-309*, *G-111*, *G129*, *Arka Kusumakar* and *Arka Shirish* did not set any fruits when crossed with any of four wild species. The sterility in these hybrids could be due to irregular chromosome associations at diakinesis and metaphase I and concomitant abnormal disjunction of chromosomes at anaphase of meiosis (Singh and Rao, 1986; Nwofia and Eneoblong, 2001). The normal fruits were borne in clusters (*DBSR-52* × *S. indicum*, *Pusa Ankur* × *S. aethiopicum*, *G-190* × *S. aethiopicum*, *91-2* × *S. aethiopicum*, *190-10-12* × *S. aethiopicum*) but fruits were parthenocarpic with little or devoid of mesocarp. This could be linked to allelic incompatibility at fertilization and the development of normal fruit (Behera and Singh, 2002). Our findings contradict the previous report of Patel *et al.* (2001) where they obtained profuse seeds in the cross of *S. indicum* by using *S. melongena* cvs. *Doli* and *Morbi 4-2*. Such differences observed by different

workers using these *Solanum* species are attributable to the usage of different accessions of *S. indicum*, a species known to be highly polymorphic, and the existence of genotypic variability of different *S. melongena* cultivars used (Rao and Rao, 1984).

Seed of interspecific hybrids, viz. 91-2 $\times$ *S. integrifolium*, DBSR-52 $\times$ *S. integrifolium*, DBSR-52 $\times$ *S. incanum*, Pusa Ankur $\times$ *S. incanum*, NDB-25 $\times$ *S. incanum* and Pusa Kranti $\times$ *S. incanum* were viable and produced highly vigorous plants with earliness in flowering and higher yield. However, Gowda and Seenappa (1991) and Anis *et al.* (1994) reported unilateral hybrids between *S. incanum* and *S. melongena* when *S. incanum* was used as female parent.

The interspecific hybrids, i.e. DBSR-52 $\times$ *S. integrifolium*, 91-2 $\times$ *S. integrifolium*, DBSR-52 $\times$ *S. incanum*, Pusa Ankur $\times$ *S. incanum*, NDB-25 $\times$ *S. incanum*, Pusa Kranti $\times$ *S. incanum*, 91-2 $\times$ *S. incanum*, Br-112 $\times$ *S. incanum*, G-190 $\times$ *S. incanum*, Pusa Shymala $\times$ *S. incanum*, DBSR-52 $\times$ *S. indicum* and Pusa Ankur $\times$ *S. integrifolium* had prickles on stem though these were not present in the female parents. Similarly, Schaff *et al.* (1982) found more prickles than any of the parents in interspecific hybrids between *S. melongena* and *S. macrocarpon*. Among the four wild species, *S. incanum* produced the maximum number of fruits, number of seeds per fruit and maximum F₁ seed germination when used as pollen parent. Previously, fertile hybrids were also obtained in cross of *S. melongena* $\times$ *S. incanum* (Rao *et al.*, 1981; Gowda and Seenappa, 1991; Behera and Singh, 2002). Lester and Hasan (1991), based on phylogenetic analysis, ascertained that Indian putative *S. incanum* is a wild form of *S. melongena* and hence is closely related to it. Hence, interspecific hybridization between these two species attributed to better heterosis. When *S. aethiopicum* was used as pollen parent for Pusa Ankur and G-190, the maximum fruit set was obtained and they were statistically at par. The maximum germination (%) of F₁ seeds was found in the cross Pusa Ankur $\times$ *S. aethiopicum*, but number of seeds per fruit was low. Thus, seed production in interspecific *Solanum* hybrids may be dependent on the compatibility of the parental genomes in the embryo and endosperm; and genetic and biochemical interactions among embryo, endosperm; and maternal sporophytic tissue (Cheng *et al.*, 2004). Earlier, Collonnier *et al.* (2001) found that somatic hybrids between *S. melongena* and *S. aethiopicum* produced plants that were more vigorous than any of the parents. The differences found for

vigour among interspecific hybrids suggests that exploiting variation in combining ability for hybrid vigour will produce superior genotype with desired horticultural value.

5.2 Molecular, morphological and biochemical diversity analysis of *Solanum melongena* genotypes and its related wild species

5.2.1 Morphological and biochemical diversity

Mahalanobis D^2 approach which is based on multivariate analysis serves as good index of genetic diversity analysis. This analysis permits precise comparison among all possible pairs of population in any given group effecting actual crosses (Ahmed *et al.*, 2014; Begum *et al.*, 2013). In the present study, the genotypes showed high coefficient of variation for number of fruits per plant (370.46), anthocyanin content (119.46) and ascorbic acid content (80.00) whereas, low coefficient of variation observed for days to first harvest (15.21), plant height (15.60) and days to first fruit set (17.88). Based on D^2 values, all the 24 genotypes including four wild species were grouped into four highly divergent clusters. The cluster divergence is proved by high inter-cluster and low intra-cluster D^2 values. The wild species *S. aethiopicum* and *S. indicum* were so divergent as they had the maximum distance between them for all the characters that they had to be given the status of separate cluster (Figure 1). These clusters comprising two wild species with specific valuable traits and other genotypes falling in the highly divergent groups will help in broadening the existing genetic base and may produce new genotypes with hitherto unknown combinations. Overall, the clustering pattern revealed that the genotypes were not distributed according to their geographical origin. This is in agreement with the results of Singh *et al.* (2006) and Sunseri *et al.* (2010) of diversity analysis based on the characters used in the present investigation. However, Singh and Prasad (1991) reported that geographical distribution contributed to genetic diversity as estimated by D^2 statistics. Geographic diversity, though appear as an important factor but it is not the only factor in determining the genetic divergence as revealed in our study. It also indicates that the factors other than geographical diversity may be responsible for such grouping of genotypes. One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of genetic material among the crop improvement programmes in the country makes it difficult to maintain the real identity of the

genotypes. Moreover, breeding progenies incorporate genes from varied sources, thus losing the basic geographical origin identity of the genotype. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographical origin such as the germplasm exchange, genetic drift, natural and artificial selections and differential gene expression due to genotype $\times$ environment interactions were mostly responsible for creation of genetic diversity (Murthy and Arunachalam, 1966). Another possibility may be that the estimates might not have been sufficient to account for the variability caused by some other traits of physiological or biochemical nature which might have been important in depicting the total genetic diversity in the population.

Considerable diversity was observed among the genotypes collected from IARI, New Delhi and Uttar Pradesh. This wide diversity can be attributed due to the reason that these regions extend from far west to far east of India and have ecological variable agro-climatic conditions. This is not the case when a plant population is restricted to small geographical areas with identical environmental pressure which help to evolve adaptive gene complexes rather with little diversity.

The inter and intra-cluster D^2 values among 24 genotypes including four wild species presented in Table 6 revealed that maximum inter-cluster distance was observed between the clusters II and III (90.03) followed by cluster I and III (73.75), II and IV (73.60). This indicated that the genotypes included in these clusters were very diverse. Considering group distance and other physical and yield performance, the inter-cluster crosses between the members of cluster II and III were expected to produce new recombinants with desirable traits. The genotypes belonging to clusters I, II, III and IV could have greater genetic divergence and hence, intermating between them may give more transgressive segregates in advanced generations. In group IV three related species (*Solanum aethiopicum*, *S. incanum*, *S. integrifolium*) were clustered with few varieties of *S. melongena*. This may be because of the nearly similar values of the traits of *Solanum* spp. and varieties of *S. melongena* taken for this study except yield per plant. However, *S. incanum* is the most closely related species and had similar flowering traits like that of few varieties of *S. melongena*. The *S. melongena* genotypes belonging to clusters with maximum inter-cluster distance can be utilized as promising parents for hybridization programme to obtain high heterotic response and better segregants for desired traits viz. resistant to biotic

and abiotic stress and higher nutritive value as reported by Babu and Patel (2004) and Mehta *et al.* (2004). Whereas the maximum intra- cluster D^2 value (5.34) was shown by cluster IV indicating that genotypes included in this cluster are very diverse and is due to both natural and artificial selection forces among the genotypes. The intra-cluster distances in all the four clusters were lower than the inter-cluster distances which indicated that the genotypes within the same cluster were closely related.

The individual genotype was characterized in respect of their mean values presented in Table 7 for different traits to find out genotypes having similar characteristics. Depending upon the aim of breeding, the potential genotypes can be selected from different clusters as a parent in hybridization programme. The selection of parents to be included in hybridization programme should be based on genetic distance. From the findings, it is revealed that genotypes of *S. melongena* can be selected from cluster I for earliness in flowering, fruiting, harvesting as the mean values are lower whereas, for fruit index and anthocyanin content had the highest mean values as compared to others clusters. Rahman and Munsur (2009) also indicated that accessions among the clusters separated by high D^2 values could be used in hybridization program for obtaining wide spectrum of variations among the segregates. This revealed that crosses should be made between the genotypes belonging to the distant clusters for high heterotic response and transferring other desired traits *viz.* resistant to biotic and abiotic stresses.

The genotypes were plotted on graphs utilizing their principal factor scores based on three factors i.e. PF 1, 2 and 3 (Fig. 2). The genotypes which found towards high value of the three factors were supposed to be superior for those factors. Hence, the superior genotype able to identify for all considered traits in those factors. From this principal factors figure, it was found that Brinjal Var-7 (10), Brinjal Var-3 (9) and Pusa Uttam (15) may prove better genotypes in hybridization programme when the three factors are considered together. Ahmed *et al.* (2014) used principle component analysis for genetic variability study in large germplasm collection of many species. The present study of genetic diversity provides an insight for genetic inter-relationship among the genotypes of eggplant. The genotypes of highly divergent cluster may also be utilized in a breeding programme for development of high yielding varieties with desirable attribute and they can also be utilized in

heterosis breeding programme for development of F₁ hybrids with superior yield and quality characters.

5.2.2 Molecular diversity

The SSR marker has been found to be useful and robust tool for detecting genetic diversity and determination of genetic relationships within and among a group of *Solanum* species (Munoz-Falcon *et al.*, 2009). The SSR markers are mainly used as compared to the dominantly inherited markers (RAPD, AFLP or ISSR) for assessing diversity within population (Nybom, 2004). SSR markers are highly polymorphic, multi-allelic, co-dominant, polymerase chain reaction (PCR) based easily reproducible and widely distributed among the genome (Powell *et al.*, 1996). The genetic relationship among the different crops including eggplant was reported by many workers. Frary *et al.* (2005) reported that 109 SSRs amplified 172 different alleles in tomatoes with an average of 1.60 allele per locus. Demir *et al.* (2010) screened a set of 19 genotypes of eggplant using 5 SSR primers. The primer amplified 24 alleles and produced an average of 4.80 alleles per locus. Behera *et al.* (2006) assessed the genetic diversity of 96 eggplant and its related species using 23 STMS primer. The number of alleles per primer ranged from 3 to 6 with an average of 4.40. Verma *et al.* (2012) reported 6 polymorphic SSR primer with amplification of total 28 alleles. The number of alleles for each primer ranged from 2-10 with an average of 4.67 per primer. However, in the present study, a total of 86 alleles were amplified with an average of 2.44 allele per locus among the 24 genotypes including four wild species (*Solanum incanum*, *S. aethiopicum*, *S. integrifolium* and *S. indicum*). The results of present finding had the lower average alleles per locus than the result of He *et al.* (2003), when 158 SSR primers were screened, a set of 19 diverse cultivars found with an average of 2.70 alleles per locus. However, Khorsheduzzaman *et al.* (2008) reported an average of 2.20 allele per locus which is lower than the present finding.

The major allele frequency ranged from 0.56 to 1 (Table 12). Maximum number of alleles (5) were observed for primer EEMS 48 followed by 4 alleles in primer EEMS 15. The primer EEMS 7, EEMS 10, EEMS 12, EEMS 18, EEMS 21, EEMS 22, EEMS 24, EEMS 26, EEMS 32, EEMS 33, EEMS 37, EEMS 39, EEMS 42, EEMS 46, EEMS 47, EEMS 49 and EEMS 50 amplified 3 alleles. Two alleles were amplified by EEMS 6, EEMS 13, EEMS 19, EEMS 25 EEMS 29, EEMS 30,

EEMS 31, EEMS 35, EEMS 36, EEMS 38, EEMS 45. Almost all the primer amplified the expected amplicon but only few primers such as EEMS 26, EEMS 31 and EEMS 39 amplified larger than the expected size (355-360 bp) due to insertion of intron. The primer EEMS 48 amplified expected size of amplicon in all the genotypes except in the wild species (*S. indicum*) amplified smaller amplicon (less than 200 bp). This may be due to the deletion of sequence in the genomic region (Stagel *et al.*, 2008).

The UPGMA based cluster analysis (Fig. 3) showed that 24 genotype including four wild species were grouped into three cluster at the dissimilarity coefficient of 0.05. The three wild species (*Solanum indicum*, *S. aethiopicum* and *S. integrifolium*) were universally placed in cluster I, while cluster II had only single wild species (*S. incanum*). The cluster III comprised 20 cultivated genotypes and further divided into sub-cluster IIIA and IIIB. The sub-cluster IIIA comprising G-190, 91-2 and 129-5 genotypes and IIIB comprising remaining 17 genotypes (Br-112, Pusa Bindu, NDB-25, G-129, Pusa Ankur, Pusa Uttam, DBL-7, DBSR-52, Pusa Shyamla, DBSR-195, 190-10-12, S-309, Arka Shirish, Pusa Kranti, DBL-3, G-111, Arka Kusumakar).

The pair wise genetic distance is presented in Table 13. The minimum distance (0.00) was observed between Br-112 and Pusa Bindu, and NDB-25 and G-129 followed by (0.01) between Pusa Bindu and G-129, Pusa Ankur and Brinjal Var-7, Br-112 and G-129, Pusa Bindu and NDB-25. The genotypes Pusa Uttam, Pusa Bindu and Pusa Ankur were grouped under the sub-cluster IIIB. The minimum distance of 0.02 was observed between the genotypes Pusa Bindu and Pusa Ankur. This revealed that they were closely related, which might be due one the parentage was same. Among the four wild species, *S. incanum*, had the minimum (0.18) average distance with the cultivated genotypes as compared to other wild species. This could be due to the fact that *S. incanum* is considered as a progenitor of cultivated genotype of *S. melongena* (Lester and Hasan, 1991).

The maximum distance (0.32) was observed between *S. aethiopicum* and 91-2 followed by 129-5 and *S. aethiopicum* (0.30) and 91-2 and *S. integrifolium*. The minimum distance (00) was observed between Br-112 and Pusa Bindu, NDB-25 and G-129 which is probably due to the presence of same bands at all loci evaluated and

maximum distance (0.32) was observed between *S. aethiopicum* and 91-2 resulted due to non-sharing of band at all loci.

The average PIC is an ideal index to measure polymorphism. A PIC value greater than 0.50 indicates high polymorphism, values between 0.25 and 0.50 indicate loci of intermediate polymorphism and less than 0.25 indicate loci of low polymorphism (Haiyan *et al.*, 2013). In the present study, the maximum (0.57) PIC value was observed in EEMS 48 followed by EEMS 42 (0.50) and EEMS 46(0.48). The minimum PIC (0.00) was recorded in EEMS 14, EEMS 17, EEMS 20, EEMS 23, EEMS 34 and EEMS 44. The average PIC value of 0.24 was recorded for 36 SSR markers which indicate that the loci display low level of polymorphism. The result revealed little genetic polymorphism among the genotypes and existence of a narrow gene pool. This may due to the fact that eggplant and related species belongs to the section *Oliganthes* (Issiki *et al.*, 2003). Moreover, narrow genetic base in Solanaceous plants has been reported by Nunome *et al.* (2003) and Stigel *et al.* (2008) due to its autogamous nature of the crops.

The level of genetic diversity in eggplant varied in different studies. Hurtado *et al.* (2012) observed a high level of genetic diversities among the Chinese accession ($He=0.494$) and for Sri Lankan accession ($He=0.540$). The Nei's genetic diversity of different eggplant groups from Spain varied from 0.20 to 0.44 (Munoz-Falcon *et al.*, 2011). Considerable level of genetic diversity was observed between all the accessions studied. However, in the present study, the genetic diversity was lower ($He=0.073$) than the report of Hurtado *et al.* (2011). The difference report of genetic diversity varies may be due to difference in sample size used and markers. The very low genetic diversity was observed in present investigation. This might be due to very low level of outcrossing in self-pollinated crop like brinjal and other possibilities like inbreeding depression, higher mutation rate, and the presence of heterozygotes (Gowda,1981).

The combined results of molecular and morphological diversity studied revealed different characterization of the genotypes and there was non-significant correlation between them. From the dendrogram based on SSR markers it was found that all the wild species (*S. indicum*, *S. aethiopicum* and *S. integrifolium*) except *S. incanum* were grouped in the same cluster whereas grouping pattern from the dendrogram obtained from morphological traits showed different group of the

genotypes. Dendrogram of SSR markers and quantitative traits showed that genotypes 91-2 and 129-5 grouped under same cluster. It was revealed from the dendrogram of SSR markers and quantitative traits that the genotypes Br-112 and Pusa Bindu, and NDB-25 and G-129 were not able to get distinguished by SSR markers but these genotypes were separated based on the dendrogram for quantitative traits. Further, since sufficient morphological data based on quantitative traits was not taken into consideration in the present study, probably that might be the reason the wild species showing different clustering pattern and placed in different cluster along with other cultivars. However, molecular diversity revealed that wild species were uniquely place in a same cluster and diverse from the cultivated *S. melongena* genotype.

Comparison of 4 clusters obtained by D^2 statistic based on 17 morphological and biochemical traits with the dendrogram based on SSR markers revealed that 14 genotypes including four wild species developed at IARI, New Delhi fall under different cluster in both the analysis. The possible reason for this observation could be that these varieties were developed either through selection or hybridization from local collections collected from different geographical regions of India. For example 129-5, 91-2 and S-309 were developed by single plant selection from indigenous or local collections collected from different regions of India. Pusa Ankur and Pusa Bindu were developed by hybridization and selection from the advance generation of the cross of Gujarat Round and Sel-91-1.

Among various genetic markers, SSR are the most desirable because they are crop specific, though their genome coverage is less and little genetic polymorphism was found among the genotypes due to existence of a narrow gene pool. Morphological markers, although most important as they cover more genome and are the result of expressed genes and their interactions, are highly influenced by environment. However, prior knowledge of the structure of the genetic diversity within collection of genotype may be of great help to make decisions on breeding strategies and to use in current and future breeding programs. In order to effectively utilize the genetic variability for crop improvement, both morphological and molecular SSR markers were used to enhance the diversity among genotypes.

5.3 Morphological characterization of F₁ hybrids along with parents

5.3.1. Quantitative morphological traits

The systematic characterization of available genotypes using different morphological traits is needed for identification and delimitation among the eggplant genotypes. The parental genotypes and F₁ hybrids varied significantly for plant characters viz., plant height, number of primary branches per plant, days to first flowering, days to first fruit set, days to first fruit harvest, number of flowers per cluster, number of fruits per cluster, fruit length, fruit diameter, fruit shape index, number of fruits per plant and yield per plant. In the present study, the plant height for parental genotypes ranged from 42.00 to 89.80 cm with a mean of 77.52 cm. In the F₁ hybrids plant height ranged from 50.80 cm to 130.67 cm with a mean of 81.18 cm. It was found that some of the hybrids were taller and produced more branches as compared to their respective parents. Similarly, Patel *et al.* (2001) observed that hybrids were taller and profusely branched than their respective parents, which suggested that these traits are governed by over dominance gene action. There was a great variation in number of primary branches per plant among parental genotypes which ranged from 5.67 to 10.67 with an average of 7.89. For the F₁ hybrids, it ranged from 6.33 to 13.67 with an average of 10.15. There is a positive correlation between number of branches and yield as reported earlier by Chen and Li (1994).

The parental genotypes and F₁ hybrids showed lots of variation for days to first flowering, days to first fruit setting and days to first harvesting. Among the parental genotypes, days to first flowering ranged from 32.67 to 89.00 days with an average of 39.64 days, while in the F₁ hybrids, it ranged from 30.67 to 89 with an average of 43.88. Days to first fruit set among the parental genotypes ranged from 42.33 to 89.33 days with an average of 51.53 days, while in the F₁ it ranged from 41.67 to 127 days with an average of 67.91 days. Days to first harvest among the parental genotypes ranged from 59.67 to 103.33 days with an average 74.18 days, while in F₁ hybrids it ranged from 55.67 to 160.00 days with an average of 89.03 days. The genotypes and F₁ hybrids which showed earliness in flowering and fruiting were considered as desirable traits since eggplant is comparatively long duration crop. Therefore, it reduces the duration of cropping period as well as biotic and abiotic stresses. Moreover, these genotypes will be appropriate for the multiple cropping systems. Kamalakaran *et al.* (2007) opined that earliness has main role in

multiple cropping systems. This trait can be introgressed into the commercial varieties through future breeding.

Among the genotypes, variation was found for the number of flowers per cluster, number of fruits per cluster and number of fruits per plant and yield per plant. The number of flowers per cluster among the parental genotypes ranged from 1 to 7 with average of 2.16 whereas, in F₁ hybrids, it ranged from 1.00 to 10.67 with an average of 3.53. The number of fruits per cluster in parental genotypes ranged from 1.00 to 5.67 with an average of 1.98 whereas, in F₁ hybrids, it ranged from 1.00 to 7.00 with average 2.35. The number of fruits per plant ranged from 6.00 to 1475.00 with average of 141.93 but in F₁ hybrids ranged from 7.00 to 322.00 with an average of 77.41. Among the parental genotypes, yield per plant ranged from 249.00g to 2850.00g with an average of 1451.11g while in the F₁ hybrids, it ranged from 432.00g to 1628.00g with an average of 1108.70 g. Some of the F₁ hybrids produced more number of fruits per plant than either of the parents. Such findings have been reported earlier by Nalini *et al.* (2011), Reddy *et al.* (2011) and Gowda *et al.* (1990) in the interspecific hybrids of *Solanum melongena* and *S. macrocarpon*, whereas, Patel *et al.* (2001) found that solitary and cluster fruiting habit was observed in the interspecific hybridization between *S. melongena* and *S. indicum*.

A great variation was observed in fruit length, fruit diameter, fruit shape index and fruit weight. The parental genotype for fruit length ranged from 0.80 cm to 16.50 cm with an average of 7.10 cm whereas in F₁ it ranged from 2.00cm to 9.00 cm with an average of 6.13cm. The parental genotype for fruit diameter ranged from 0.70 cm to 7.20 cm with an average of 4.72 cm whereas in F₁ it ranged from 1.70 cm to 6.5 cm with an average of 3.64 cm. The parental genotype for fruit shape index ranged from 1.03 cm to 4.71 cm with an average of 1.66 cm whereas in F₁ it ranged from 0.83 cm to 3.31 cm with an average of 1.71 cm. The parental genotype for fruit weight ranged from 0.30 to 230.00g with an average of 101.89 whereas in F₁ it ranged from 2.40 to 75.00 g with an average of 46.6 g. The maximum number of fruits was found in the F₁ hybrid and the number of fruit was more than the parental genotypes but the size of the fruit was small. Smaller size of fruit is not considered as undesirable, in some part of India region particularly in southern part of Gujarat where consumers prefer smaller fruit size with more number of fruits having round to oval fruit shape (Reddy and Patel, 2014).

5.3.2 Qualitative morphological characters

The comparative study of different morphological characters and sorting out the similarity and difference among various varieties of species and it makes possible to categorize varieties in a specific group. Through this characterization, it make clear to understand the interrelationship among different groups of a species and it is possible to study wide varieties of species at a time. In the present study, 24 genotypes of brinjal including four species and F₁ were classified using 19 morphological qualitative characters.

The plant growth habit was categorized into different group suggested by different workers (Tambe *et al.*, 1992; Hazra *et al.*, 2003). The classification is based on the strong and stiffness of the stem such as *viz.* erect (strong and stiffness), semi-erect (strong but not so much stiff), semi-spreading (weak stem with profuse branching habit), spreading (very weak stem revealing somewhat decumbent habit and dwarf and bushy (strong and stiff but short stem with profuse branching habit). In the present study, the maximum genotypes were semi-spreading and less number of genotypes had erect growth habit. The results of present findings were similar with reports of Hazra *et al.* (2003) and Shinde *et al.* (2012).

Flowering in brinjal was extra-axillary and borne in three patterns: solitary, cyme (cluster) and mixed (both solitary and cyme). Solitary flowers and the basal flowers of the cyme were long styled with plump ovary or medium styled with developed ovary and were functionally fertile. However, fruit setting was higher in the long styled flower as compared to medium styled flower. The maximum number of genotypes showed solitary fruiting habit and minimum number of genotypes were found to have cluster fruiting habit. The present study supported with the findings of Shinde *et al.* (2012) as they also found solitary fruiting habit in most of the genotypes. Hazra *et al.* (2003) reported that maximum genotypes showed mixed fruiting and least number of genotypes were found to have solitary flower and fruiting habits in their population.

Anthocyanin is the main pigment of brinjal producing mainly purple and violet colour in different plant parts and chlorophyll content has darkening effect on colour (Nothmann *et al.*, 1976). Pigment production and expression could be regarded as a common feature in brinjal. In fact, pigmentation of brinjal is under dominant genetic control (Patil and More, 1989), expression of pigment in different

plant parts was not same. Out of the 46 genotypes, 24 genotypes showed purple colour stem. The flower colour was grouped in four different groups namely dark purple, purple, light purple and greenish white. Maximum genotypes had showed the purple colour. This finding was in conformity with the results of Shinde *et al.* (2012) as maximum genotypes showed the purple flower colour.

Colour of the fruits is one of the important traits in brinjal. The genotypes fell into fruit colour groups namely dark purple, medium purple, light purple, dark green, medium green, light green, purple with green stripes, purple with violet stripes, green with purple stripes. In the present study, the maximum genotypes were found to have purple fruits (47.83%). This result was similar to the finding of Shinde *et al.* (2012) as they found maximum number of genotypes were purple fruit colour. Besides these, purple striped genotypes were found in less number and some of the genotypes had pigmented fruits with green calyx. Similar finding was reported by Hazra *et al.* (2003) and concluded that pigmentation in brinjal was complex in nature and its expression indicated the involvement of different gene groups for the conditioning in different plant part. Intensity of the basic purple fruit colour varied with the genotypes presumably due to different final anthocyanin and chlorophyll content in the fruits.

Development of spine in different plant parts was a predominant character of brinjal. However, in present study, in maximum number of genotypes spine were absent on stem, leaf and calyx. Similar finding of non-spiny fruits was reported by Shinde *et al.* (2012) as majority of genotypes showed non-spiny. In the present study, hybrids produced spine on their stem, leaf and calyx, when crossed with spiny male parent, though the female parent has no spine. Similarly, Schaff *et al.* (1982) found that interspecific hybrids between *S. melongena* and *S. macrocarpon* had more prickles than any of the parents. Lester (1986) also reported that when non-spiny parents *S. macrocarpon* and *S. aethiopicum* were used in hybridization and produce F₁ hybrids with present of prickles.

5.3.3 Biochemical characterization of interspecific F₁ hybrids along with parents

Phytochemicals such as phenol, ascorbic acid, antioxidant and anthocyanin are naturally found in plant of brinjal. These phytochemicals play an important role in good health as they are biologically active and function to protect plant against invasion, disease and infection. In the present study, the content of ascorbic acid

varied among the genotypes. In parents, ascorbic acid content ranged from 1.28 to 12.82 mg /100g with an average of 2.29 mg/100g, whereas, in F₁s it ranged from 0.91 to 11.36 mg /100g with an average of 3.13 mg/100g. The total phenols in the parental genotypes ranged from 95.22 mg GAE/100g to 414.91 mg GAE/100g with an average of 245.37 mg GAE/100g, whereas in F₁ hybrids, it ranged from 96.25 to 414.91 mg GAE/100g with an average of 237.35 mg GAE/100g. Hanson *et al.* (2006) reported the ascorbic acid content of 50.00 to 129±9 g/100g and phenol content 0.74±0.17 to 1.43±0.45 g/100g in 33 *S. melongena* accessions. Phenol content is one of the most important characters to reduce shoot and fruit borer incidence. If the phenol content is high, borer infestation will be less (Patel and Reddy, 2014). The content of anthocyanin among the parental genotypes ranged from 0.23 to 80.65 mg/100g with an average of 16.81, whereas in F₁ hybrids it ranged from 0.71 to 62.17 mg/100g with an average of 16.09. Nisha *et al.* (2009) reported in brinjal that the total phenol content ranged from 83.31 to 106.98 mg/100g and for anthocyanin it ranged from 0.53 to 0.76 mg/100g.

The antioxidant activity ranging from 0.98 to 14.58 µmol/g was found in parental genotypes with an average of 4.44, while in the F₁ hybrids, it ranged from 2.01 to 63.27 µmol/g with an average of 13.52 µmol/g. Milan *et al.* 2010 reported that antioxidant activity ranged from 1.20 to 113.00 µmol TE/g and 0.0 to 68.10 µmol TE/g using ORAC assay and TRAP assay respectively. They also found that total polyphenol content ranged from 605.60 to 20.00 mg GAE/100g fresh weight.

5.4. Chromosome number study

Cytological studies in eggplant have been contributory in classification of plant. Continuing survey of chromosome number in eggplant furnishes additional evidences on the significance of polyploidy and accompanying hybridization in forming the complex patterns of variation that cause taxonomic perplexities in the genus. The differences in basic number of chromosomes may occur due to successive unequal translocations which finally remove all the essential genetic material from a chromosome, permitting its loss without penalty to the organism. In the present investigation, attempt has been made to confirm the chromosome number of four wild different species (*S. incanum*, *S. integrifolium*, *S. aethiopicum* and *S. indicum*) and one cultivated genotype (Pusa Shymala). It was found that the cultivated *S. melogena* cv. Pusa Shyamla and all the four wild species (*S. incanum*, *S.*

aethiopicum, *S. integrifolium*, *S. indicum*) had same chromosome number ($2n=2x=24$) with small varied size of chromosome under investigation (Plate 9). Similar finding had been reported by Choudhari, 1981; Ray, 2010 as they found that chromosome number $2n=2x=24$, in *S. melongena*. The results are also in conformity with the findings of Roxas *et al.* (1995) in *S. melongena* and *S. aethiopicum*, Wamotair *et al.* (2007) in *S. integrifolium* and Olatunji (2005) in *Solanum indicum* as all of them reported same i.e. $2n = 2x = 24$ chromosome number in these wild species. Based on the present study, it is confirmed that all 4 species taken have same chromosome numbers i.e. $2n = 2x = 24$.

Table 1: Pollen viability of four wild *Solanum* species used as pollen donor parents.

Category	<i>S. incanum</i>	<i>S. indicum</i>	<i>S. aethiopicum</i>	<i>S. integrifolium</i>	LSD (p=0.05)
Fertile %	21.57 (3.76 ^c)	34.78 (4.24 ^a)	27.63 (4.01 ^b)	11.01 (3.09 ^d)	0.07
Semi-sterile %	78.43 (5.05 ^a)	50.01 (4.60 ^c)	61.73 (4.81 ^b)	17.43 (3.55 ^d)	0.04
Sterile %	0.00 (0.00 ^d)	15.22 (3.41 ^b)	10.61 (3.05 ^c)	71.56 (4.96 ^a)	0.06

The category is based on the report of Prasad *et al.* (2006)

Mean with the same letter are not significantly different according to Tukey's Honest Significant Difference Test.

Data in the parentheses : Arc Sine transformed values.

Table 2: The fruit set (%) in each cross combination of 20 cultivated genotypes of *S. melongena* with four wild species.

Eggplant genotypes	<i>S. incanum</i>	<i>S. aethiopicum</i>	<i>S. integrifolium</i>	<i>S. indicum</i>
Pusa Kranti	24.17(3.87 ^{fghijk})	0.00 ^r	0.00 ^r	20.83(3.70 ^{Ijkl})
Pusa Shyamala	15.00(3.38 ^{lm})	19.17 (3.61 ^{klm})	23.33 (3.84 ^{ghIjk})	0.00 ^r
NDB-25	15.00 (3.38 ^{lm})	75.00 (5.01 ^a)	13.33 (3.28 ^{mn})	25.00(3.89 ^{fghIjk})
Pusa Uttam	45.00 (4.50 ^{bcd})	27.50 (4.00 ^{fghIj})	6.39 (2.54 ^p)	4.17(2.09 ^q)
Pusa Bindu	6.67 (2.54 ^p)	75.00 (5.01 ^a)	9.17 (2.84 ^{op})	22.50(3.79 ^{hIjk})
DBSR-52	15.00 (3.38 ^{lm})	27.50 (3.99 ^{fghij})	25.28 (3.92 ^{fghij})	29.17 (4.04 ^{efghi})
Pusa Ankur	27.50 (4.00 ^{fghij})	80.00(5.07 ^a)	9.17 (2.84 ^{op})	48.33(4.56 ^{bcd})
BR-112	40.00 (4.38 ^{cde})	0.00 ^r	18.06 (3.59 ^{klm})	33.33 (4.19 ^{defg})
DBSR-195	20.00 (3.66 ^{ijklm})	0.00 ^r	0.00 ^r	31.67 (4.13 ^{defgh})
190-10-12	4.17 (2.09 ^q)	35.00 (4.24 ^{cdef})	0.00 ^r	21.67 (3.75 ^{Ijkl})
129-5	0.00 ^r	0.00 ^r	4.17 (2.09 ^q)	0.00 ^r
91-2	20.00 (3.68 ^{ijkl})	10.00 (2.98 ^{no})	7.22 (2.64 ^{op})	8.33(2.75 ^{op})
G-190	19.17 (3.61 ^{klm})	63.33 (4.84 ^{ab})	25.83 (3.94 ^{fghIjk})	43.33 (4.46 ^{cd})
Arka Shirish	No fruit set	No fruit set	No fruit set	No fruit set
Arka Kusumakar	No fruit set	No fruit set	No fruit set	No fruit set
Brinjal Var-3	No fruit set	No fruit set	No fruit set	No fruit set
Brinjal Var-7	No fruit set	No fruit set	No fruit set	No fruit set
S-309	No fruit set	No fruit set	No fruit set	No fruit set
G-111	No fruit set	No fruit set	No fruit set	No fruit set
G-129	No fruit set	No fruit set	No fruit set	No fruit set
S.Em.±= 0.22				
CD (P=0.05) = 0.51				

Data in the parentheses : Arc Sine transformed values.

Mean with the same letter are not significantly different according to Tukey's Honest Significant Difference Test

Table 3: The number of seeds per fruits in each cross combination of 20 cultivated genotypes of *S. melongena* with four wild species.

Genotypes	<i>S. incanum</i>	<i>S. aethiopicum</i>	<i>S. integrifolium</i>	<i>S. indicum</i>
Pusa Kranti	24.67 ^l	0.00 ^q	0.00 ^q	10.00 ^{nop}
Pusa Shyamala	25.67 ^l	0.00 ^q	11.67 ^{no}	0.00 ^q
NDB-25	48.67 ^j	0.00 ^q	46.00 ^{ik}	95.33 ^g
Pusa Uttam	176.00 ^e	183.67 ^{de}	46.00 ^{ik}	0.00 ^q
Pusa Bindu	0.00 ^q	0.00 ^q	2.00 ^{pq}	6.00 ^{opq}
DBSR-52	226.67 ^b	0.00 ^q	23.00 ^{lm}	39.00 ^k
Pusa Ankur	23.67 ^l	6.33 ^{opq}	15.00 ^{mn}	2.00 ^{pq}
BR-112	68.33 ^{hi}	0.00 ^q	0.00 ^q	26.00 ^l
DBSR-195	189.00 ^d	0.00 ^q	0.00 ^q	0.00 ^q
190-10-12	0.00 ^q	65.33 ⁱ	0.00 ^q	0.00 ^q
129-5	0.00 ^q	0.00 ^q	0.00 ^q	0.00 ^q
91-2	185.00 ^d	107.00 ^f	76.00 ^h	0.00 ^q
G-190	754.00 ^a	206.00 ^c	106.67 ^f	1.00 ^q
Arka Shirish	No fruit set	No fruit set	No fruit set	No fruit set
Arka Kusumakar	No fruit set	No fruit set	No fruit set	No fruit set
Brinjal Var-3	No fruit set	No fruit set	No fruit set	No fruit set
Brinjal Var-7	No fruit set	No fruit set	No fruit set	No fruit set
S-309	No fruit set	No fruit set	No fruit set	No fruit set
G-111	No fruit set	No fruit set	No fruit set	No fruit set
G-129	No fruit set	No fruit set	No fruit set	No fruit set
S.Em.± = 16.30				
CD (P=0.05) = 17.01				

Table 4: The germination (%) of F₁ in each cross combination of 20 cultivated genotypes of *S. melongena* with four wild species.

Genotypes	<i>S. incanum</i>	<i>S. aethiopicum</i>	<i>S. integrifolium</i>	<i>S. indicum</i>
Pusa Kranti	58.67 (4.76 ^c)	0.00 ⁱ	0.00 ⁱ	0.00 ⁱ
Pusa Shyamala	66.00 (4.88 ^{ab})	0.00 ⁱ	58.00 (4.75 ^c)	0.00 ⁱ
NDB-25	33.33 (4.2 ^{fg})	0.00 ⁱ	57.00 (4.74 ^c)	0.00 ⁱ
Pusa Uttam	40.00 (4.37 ^c)	71.00 (4.96 ^a)	50.00 (4.60 ^d)	0.00 ⁱ
Pusa Bindu	0.00 ⁱ	0.00 ⁱ	0.00 ⁱ	0.00 ⁱ
DBSR-52	35.66 (4.25 ^f)	0.00 ⁱ	47.00 (4.54 ^d)	30.00 (4.09 ^g)
Pusa Ankur	61.67 (4.81 ^{bc})	58.67 (4.76 ^c)	46.00 (4.52 ^d)	0.00 ⁱ
BR-112	70.00 (4.94 ^a)	0.00 ⁱ	0.00 ⁱ	3.00 (1.79 ^h)
DBSR-195	67.00 (4.90 ^{ab})	0.00 ⁱ	0.00 ⁱ	0.00 ⁱ
190-10-12	0.00 ⁱ	60.00 (4.79 ^{bc})	0.00 ⁱ	0.00 ⁱ
129-5	0.00 ⁱ	0.00 ⁱ	0.00 ⁱ	0.00 ⁱ
91-2	34.00 (4.22 ^f)	71.00 (4.96 ^a)	3.00 (4.30 ^{e f})	0.00 ⁱ
G-190	70.00 (4.94 ^a)	71.00 (4.96 ^a)	0.00 ⁱ	0.00 ⁱ
Arka Shirish	No fruit set	No fruit set	No fruit set	No fruit set
Arka Kusumakar	No fruit set	No fruit set	No fruit set	No fruit set
Brinjal Var-3	No fruit set	No fruit set	No fruit set	No fruit set
Brinjal Var-7	No fruit set	No fruit set	No fruit set	No fruit set
S-309	No fruit set	No fruit set	No fruit set	No fruit set
G-111	No fruit set	No fruit set	No fruit set	No fruit set
G-129	No fruit set	No fruit set	No fruit set	No fruit set
S.Em.± = 0.32				
CD (P=0.05) = 0.14				

Data in the parentheses : Arc Sine transformed values.

Table 5 : The mean value of fruit set (%), number of seeds per fruit and germination (%) of F₁ seeds in the cross of 20 *S. melongena* genotypes with four wild species.

Genotypes	Fruit set % (x)	No. of seeds/fruit (y)	Germination % of F ₁ seeds (z)
Pusa Kranti	11.25 (1.89 ^h)	8.67 ^{hi}	14.67 (1.19 ^g)
Pusa Shyamala	14.38 (2.71 ^{fg})	9.33 ^h	31.00 (2.410 ^d)
NDB-25	32.08 (3.89 ^b)	47.50 ^e	22.58 (2.23 ^e)
Pusa Uttam	20.76 (3.28 ^{de})	101.42 ^b	40.25 (3.48 ^a)
Pusa Bindu	28.33 (3.55 ^{cd})	2.00 ⁱ	0 (0.00 ^h)
DBSR-52	24.24 (3.83 ^{bc})	72.17 ^d	28.17 (3.22 ^c)
Pusa Ankur	41.25 (4.12 ^{ab})	11.75 ^{gh}	41.58 (3.53 ^a)
BR-112	22.85 (3.04 ^e)	23.58 ^f	18.25 (1.68 ^f)
DBSR-195	12.92 (1.95 ^h)	47.25 ^e	16.75 (1.23 ^g)
190-10-12	15.21 (2.52 ^g)	16.33 ^g	15.00 (1.20 ^g)
129-5	1.04 (0.53 ⁱ)	0.00 ^j	0 (0.00 ^h)
91-2	11.39(3.01 ^{ef})	92.00 ^c	35.50 (3.37 ^b)
G-190	37.91(4.21 ^a)	266.92 ^a	35.25 (2.48 ^d)
Arka Shirish	No fruit set	No fruit set	No fruit set

Arka Kusumakar	No fruit set	No fruit set	No fruit set
Brinjal Var-3	No fruit set	No fruit set	No fruit set
Brinjal Var-7	No fruit set	No fruit set	No fruit set
S-309	No fruit set	No fruit set	No fruit set
G-111	No fruit set	No fruit set	No fruit set
G-129	No fruit set	No fruit set	No fruit set

Cont.

S.Em.±	0.29	20.13	0.34
LSD (P=0.05)	0.32	6.91	0.10

<i>S. incanum</i> with cultivated genotype	*19.36 (3.66 ^b)	**132.44 ^a	***41.25(3.56 ^a)
<i>S. aethiopicum</i> with cultivated genotype	*31.73 (4.15 ^a)	**43.72 ^b	***25.5 (1.89 ^c)
<i>S. integrifolium</i> with cultivated genotype	*10.92 (3.09 ^c)	**25.10 ^c	***22.69(2.11 ^b)
<i>S. indicum</i> with	*22.18 (3.79 ^b)	**13.80 ^d	***2.54 (0.45 ^d)

cultivated genotype

S.Em.±	0.19	26.94	0.64
LSD (P=0.05)	0.14	2.95	0.04

x: mean value of fruit set (%) in crossing of each cultivated genotypes with all four wild species.

y: mean value of the seeds per fruit in crossing of each cultivated genotypes with all four wild species.

z: mean value of the germination % of F₁ seeds in crossing of each cultivated genotypes with all four wild species

* mean value of fruit set (1%) in crossing of 13 genotypes with each wild species.

** mean value of the seeds per fruit in crossing of 13 genotypes with each wild species.

*** mean value of the germination % of F₁ seeds in crossing of 13 genotypes with each wild species.

Mean with the same letter are not significantly different according to Tukey's Honest Significant Difference Test.
Data in the parentheses : Arc Sine transformed values.

Table 6: Average inter and intra cluster distance (D^2) for 24 *S. melongena* genotypes

Traits	I	II	III	IV
I	3.11	66.36	73.75	59.98
II	66.36	0	90.03	73.60
III	73.75	90.03	4.54	52.98
IV	59.98	73.60	52.98	5.34

Table 7. Cluster means for seventeen characters in 24 brinjal genotypes.

Traits		I	II	III	IV
Number of genotypes and percentage CV		9	1	2	12
	CV	37.50%	4.17%	8.33%	50.00%
Plant height (cm)	15.61	79.13	86.00	76.80	76. 56
Number of primary branches per plant	23.82	7.81	10.00	7.00	6. 67
Days to first flower opening	20.81	35.034	72.33	45.33	39.50
Days to first fruit set	18.58	49.67	89.33	58.50	50.61
Days to first harvest	15.21	73.93	103.33	90.50	75. 67
Number of flower per cluster	75.86	1.74	7.00	1.00	2.00
Number of fruit per cluster	70.52	1. 56	5. 67	1.00	1.97
Fruit length (cm)	50.57	10.63	0.78	12.30	9.70
Fruit shape index (Length/Breadth)	76.56	2.86	1.14	1.57	2.67
Fruit diameter (cm)	42.57	4.64	0.68	7.80	4.24
Fruit weight (g)	69.17	131.33	0.60	327.50	120.29
Number of fruit per plant	370.47	20. 67	1573.00	8.50	20.67
Yield per plant (g)	37.47	1745.67	944.00	2560.00	1419.00
Ascorbic acid (mg/100g)	80.00	2.22	1.92	2.86	3.58
Total phenol (mg GAE/100g)	47.84	118.79	174.97	394.80	337.54
Anthocyanin (mg/100g)	119.46	22.67	0.89	7.37	18.33
Antioxidant (μmol trolox/g)	60.29	4.78	3.22	5.54	4.44

Table 8: Eigen values and proportion of variance explained by 17 principle components.

Traits	Eigen value	Variability (%)	Cumulative %
P1	5.16	0.29	0.29
P2	2.98	0.17	0.45
P3	2.18	0.12	0.57
P4	1.98	0.11	0.68
P5	1.53	0.08	0.77
P6	1.12	0.06	0.83
P7	0.85	0.05	0.88
P8	0.72	0.04	0.92
P9	0.52	0.03	0.95
P10	0.38	0.02	0.97
P11	0.27	0.02	0.98
P12	0.12	0.01	0.99
P13	0.08	0.00	0.99
P14	0.05	0.00	1.00
P15	0.03	0.00	1.00
P16	0.02	0.00	1.00
P17	0.01	0.00	1.00

Table 9. Eigen Vectors for seventeen traits of 24 *S. melongena* genotype

Traits	F1	F2	F3	F4	F5	F6	F7	F8	F9	F10	F11	F12	F13	F14	F15	F16	F17
Plant height (cm)	-0.08	0.27	0.22	-0.25	-0.09	0.18	0.73	-0.09	0.37	0.08	0.07	0.06	0.06	-0.18	-0.13	-0.11	0.03
Number of primary branches per plant	0.18	-0.08	-0.26	-0.44	0.05	0.07	-0.33	0.22	0.57	0.34	0.12	0.25	0.08	0.04	0.10	0.08	0.02
Days to first flower opening	0.33	0.29	-0.12	-0.04	0.23	-0.07	0.02	-0.02	-0.20	-0.23	0.27	0.53	-0.07	0.28	-0.40	-0.19	0.09
Days to first fruit set	0.33	0.34	-0.07	-0.09	-0.05	-0.12	-0.16	0.12	-0.06	-0.14	0.14	-0.43	0.61	-0.30	-0.13	-0.08	-0.01
Days to first harvest	0.14	0.52	-0.03	-0.01	-0.05	-0.13	-0.15	0.15	0.19	-0.13	-0.56	-0.03	-0.46	-0.18	-0.08	0.11	-0.08
Number of flower per cluster	0.39	-0.05	0.10	0.18	-0.04	0.17	0.11	0.07	-0.17	0.32	-0.29	0.07	0.11	-0.02	0.03	0.19	0.69
Number of fruit per cluster	0.37	-0.06	0.12	0.27	-0.12	0.13	0.13	0.15	-0.07	0.30	-0.25	0.20	0.21	0.13	0.03	-0.14	-0.65
Fruit length (cm)	-0.26	0.28	0.39	-0.09	0.13	-0.10	-0.20	0.15	-0.13	0.09	-0.07	0.26	0.14	-0.06	0.48	-0.49	0.14
Fruit diameter (cm)	-0.10	0.16	0.60	-0.06	0.18	-0.12	-0.14	0.01	0.00	0.07	0.12	0.08	0.15	0.15	-0.14	0.65	-0.12
Fruit weight (g)	-0.28	0.15	-0.43	0.01	-0.14	0.01	0.13	-0.08	-0.09	-0.24	-0.25	0.42	0.43	-0.04	0.23	0.36	-0.02
Fruit shape index (L/B)	-0.28	0.38	-0.23	0.05	0.04	0.10	0.05	0.13	0.00	0.29	-0.06	-0.36	0.08	0.68	-0.07	-0.06	0.06
Number of fruit per plant	0.38	0.20	-0.02	-0.11	0.02	0.22	0.16	-0.02	-0.12	-0.20	0.30	-0.15	-0.23	0.15	0.66	0.21	-0.08
Yield per plant (g)	-0.24	0.23	-0.13	0.20	-0.01	0.54	-0.15	0.26	-0.24	0.25	0.32	0.09	-0.16	-0.41	-0.14	0.10	-0.08
Ascorbic acid (mg/100g)	-0.01	-0.01	0.09	0.61	0.20	0.23	-0.06	0.16	0.55	-0.39	0.07	0.02	0.13	0.08	0.06	-0.04	0.11
Total phenol(mg GAE/100g)	0.00	0.05	-0.23	0.32	0.29	-0.63	0.30	0.22	0.04	0.31	0.23	0.01	-0.09	-0.19	0.15	0.10	-0.01
Anthocyanin (mg/100g)	-0.04	-0.07	0.12	0.01	-0.71	-0.20	0.05	0.55	-0.01	-0.17	0.20	0.09	-0.08	0.16	-0.03	0.03	0.11
Antioxidant (umol trolox/g)	-0.05	-0.27	-0.01	-0.30	0.46	0.14	0.24	0.62	-0.18	-0.25	-0.23	-0.10	0.03	-0.01	-0.06	0.03	-0.04

Table 10: *Solanum* wild species and cultivated (*Solanum melongena*) genotypes assayed (shape and skin colour are indicated in bracket).

Code	Wild species	Parentage/Source	Salient characteristic
1	<i>Solanum aethiopicum</i>	IARI, New Delhi	Resistant to Root knot nematode
2	<i>Solanum incanum</i>	IARI, New Delhi	Resistant to Little leaf, fusarium wilt
3	<i>Solanum integrifolium</i>	IARI, New Delhi	Resistant to Bacterial wilt, phomopsis blight, little leaf, shoot and fruit borer
4	<i>Solanum indicum</i>	IARI, New Delhi	Resistant to Fusarium wilt
Cultivated genotype			
5	Arka Kusumakar	IIHR, Bangalore	Long green, cluster bearing
6	Pusa Kranti	PPLX Hydepur X Wynad Giant, IARI, New Delhi	Oblong, dark purple
7	Arka Shirish	IIHR, Bangalore	Long green
8	Selection-309	IARI, New Delhi	Long white
9	Brinjal Var-3	IIVR, Varanasi	Round purplish strip
10	Brinjal Var-7	IIVR, Varanasi	Oblong greenish strip
11	G-129	MPKV, RahuriMaharashtra	Spiny, long dark purple
12	G-111	MPKV, RahuriMaharashtra	Spiny , round Purple
13	Pusa Shymala	Sel NDB 25-11 X Sel HE-12-2 IARI, New Delhi	Long purple
14	NDB-25	NDUAT, Faizabad(UP)	Long purple
15	Pusa Uttam	GR X Pant Rituraj, IARI, New Delhi	round purple
16	Pusa Bindu	GR X Pant Rituraj, IARI, New Delhi	small round purple
17	DBSR- 52	IARI, New Delhi	small round purple
18	Pusa Ankur	GR X 91-1, IARI, New Delhi	small round purple
19	Br-112	HAU, Hisar	round purple
20	DBSR -195	IARI, New Delhi	small white oval
21	190-10-12	Panipat, Hyderabad	round Purple
22	129-5	IARI, New Delhi	Long purple
23	91-2	Pantnagar, Uttarakhand	Long purple
24	G-190	IARI, New Delhi	Round green

Table 11: Allelic variation in 39 SSR loci.

Code	repeat	forward primer(5'-3')	reverse primer (5'-3)
EEMS06	(T)14	TCATGCGAAGATTAATTAATGTGA	GAGTGGATGATCAAGAATGG C
EEMS07	(T)13	CCATGCCAGAATGGAAACTT	AACGAAAACACGATCAACCC
EEMS10	(A)20	TCAAGCAGAACGAAGATGGA	GTAGGGGACGTGGATTGAGA
EEMS12	(A)16	CGGGCAACTCTTCACATTTT	ATTGGTTTGCTATCGAATTTCT
EEMS13	(A)14	TGAGATACGCGTACAATGACTTC	GGGGTTTTGCTGCTGTTATC
EEMS14	(A)13	GGAATGGACCAAACCCCTAA	AGAGCTTCGTTGCTTGGTGT
EEMS15	(C)12	GGGACAAATCTGACCTTTGG	CTGGTGGCAAATTCCTCGAT
EEMS16	(AC)7	CAATTTTTCGGTTCCTAATCAAG	CTTCAAGGAAAAAGGAGGCC
EEMS17	(CA)8	TGACATGTAGCTGGGCAGAG	TGGAGTGTGCATCCCAAATA
EEMS18	(AG)7	GGAGAACTGAAAAATTTGTAGAGAG	GAGGAGTTTCCGACATGAGC
EEMS19	(AT)9	GGCATGACAAAATCATACAAACA	TGTTGGTTAAGTCCATGGGAA
EEMS20	(AT)8	AACATCAGCCAGGGTGTTC	TGCTGAAAATTACAAGCCAAA
EEMS21	(AGA)5	TGATGTTGAACCGACACAAGA	CGTCTTCATCTTCCTCCTCG
EEMS22	(AAG)5	GAAGGACGTTGGTCCTGGTA	CTGTTCAATTATCCCCATCGC
EEMS23	(TTC)5	CACCAATTTCCCCCTTCTTT	CGGTTGGTAAAGAAAACCCA
EEMS24	(CTT)5	CACCTGTTTGAGCACCTTGA	CACCGAAGGCAGAGAAGAAG
EEMS25	(CTT)5	CCCATAGCTTTGCTCGAGAT	GCACCAAAGGCAGAGAAGAA
EEMS26	(CTT)5	GACACTCCCCTACTTCCACCT	CGCTTAGCAGAAGCCGATAA
EEMS28	(TAA)21	GACGATGACGACGACGATAA	TGGACTCACAACCTCAGCCAG
EEMS29	(ATG)5	TCAGTCAACTGCATCACCAGA	ATTCCCATTATTGGCTGCTG
EEMS30	(TAC)5	TTTACATGACAGCACCAGGC	ATTTTATGGGAATGGGGTCC
EEMS31	(TGG)5	GAGAAGTTGGCTTCAGTGCC	TAAACTCAAGGGATGCTGGG
EEMS32	(TCA)5	TAAGGAGTCTGATGCCGCTT	GTAATGCTCCTCCACGGCTA
EEMS33	(TCA)5	CTATCTCCTTTTCCCCGACC	ATGAATAAGCTGCCACCACC
EEMS34	(TCA)5	GCTTGATTCCCCACAAAGAA	GTTTCATCGCCCTCATCATT
EEMS35	(TCA)5	ATGGCTTCTGATGGACCAAG	CACCTGATGAACGTGGATGG
EEMS36	(TGT)5	TCTATCATCCCCAGATCCCA	AAGGTCGCATGGACATTAGG
EEMS37	(TCC)5	CCCTTCCACCCACACTTCA	GTTTTGCACCTTTCCATCGT
EEMS38	(CAC)5	TTCAATCGAACTTCGGAACC	ATGACGGTGGATCTCGCTAC
EEMS39	(CTG)5	GGAGAGATGGATGCCGAATA	TCTCGACCTTAGCCTGCATT
EEMS41	(GCA)5	ATTCTGCATTTCATCGGAAGG	GGATTGCTTGTGGGAATATCA
EEMS42	(GCA)6	GCTCAGCAACCACAGTACCA	GTCCGGACTTCATCAGCATT
EEMS44	(GCC)5	CCTCAAACCCCTCTCCCTTC	GTGAAACGTGGTGGAGGTCT
EEMS45	(AGAACC)4	AGCGCTTGTCAGGCTATAA	TTTCCACCATGAGCAAATGA
EEMS46	(ACCAGC)6	ACCAAACGTGCATGAAACAA	GGAAATGTTGGTGGGAATTGG
EEMS47	(GCT)5..(TTC)5	CGAACACATTCGCAAATCAC	GCATCACAAGGATGGAAAGG
EEMS48	(TAA)20(CGA)8	CAATGCAAACAATTATCATTTTCG	TCGATGTTGTTGTGCTCGTT
EEMS49	(TA)12(GA)7	TGAAATTGATCAATACCTATAAATTTAG	GAAAGCCAGGATAGCATTCG
EEMS50	(TA)9(GA)8	AAATCCGGCCATTCTGTGTA	ACATCGTTCCGCCTCTATTG

Table 12: Primers, Major allele frequency, Allele no., Gene diversity, Heterozygosity, PIC values of markers used.

Code	Major Allele Frquency	Allele No	Gene Diversity	Heterozygosity	PIC
EEMS06 (T)14	0.83	2.00	0.28	0.00	0.24
EEMS07 (T)13	0.63	3.00	0.53	0.00	0.47
EEMS10 (A)20	0.83	3.00	0.29	0.00	0.26
EEMS12 (A)16	0.83	3.00	0.29	0.00	0.27
EEMS13 (A)14	0.88	2.00	0.22	0.00	0.19
EEMS14 (A)13	1.00	1.00	0.00	0.00	0.00
EEMS15 (C)12	0.75	4.00	0.41	0.00	0.39
EEMS17 (CA)8	1.00	1.00	0.00	0.00	0.00
EEMS18 (AG)7	0.83	3.00	0.29	0.00	0.27
EEMS19 (AT)9	0.71	2.00	0.41	0.00	0.33
EEMS20 (AT)8	1.00	1.00	0.00	0.00	0.00
EEMS21 (AGA)5	0.83	3.00	0.29	0.00	0.27
EEMS22 (AAG)5	0.71	3.00	0.45	0.00	0.40
EEMS23 (TTC)5	1.00	1.00	0.00	0.00	0.00
EEMS24 (CTT)5	0.58	3.00	0.50	0.83	0.40
EEMS25 (CTT)5	0.94	2.00	0.12	0.13	0.11
EEMS26 (CTT)5	0.75	3.00	0.39	0.00	0.34
EEMS29 (ATG)5	0.88	2.00	0.22	0.00	0.19
EEMS30 (TAC)5	0.96	2.00	0.08	0.00	0.08
EEMS31 (TGG)5	0.83	2.00	0.28	0.00	0.24
EEMS32 (TCA)5	0.81	3.00	0.32	0.04	0.29
EEMS33 (TCA)5	0.83	3.00	0.29	0.00	0.26
EEMS34 (TCA)5	1.00	1.00	0.00	0.00	0.00
EEMS35 (TCA)5	0.96	2.00	0.08	0.00	0.08
EEMS36 (TGT)5	0.79	2.00	0.33	0.00	0.28
EEMS37 (TCC)5	0.83	3.00	0.29	0.00	0.26
EEMS38 (CAC)5	0.92	2.00	0.15	0.00	0.14
EEMS39 (CTG)5	0.58	3.00	0.54	0.67	0.46
EEMS42 (GCA)6	0.56	3.00	0.57	0.63	0.50
EEMS44 (GCC)5	1.00	1.00	0.00	0.00	0.00
EEMS45 (AGAACC)4	0.96	2.00	0.08	0.00	0.08
EEMS46 (ACCAGC)6	0.63	3.00	0.54	0.00	0.48
EEMS47(GCT)5..(TTC)5	0.63	3.00	0.5313	0.00	0.47
EEMS48(TAA)20(CGA)8	0.56	5.00	0.62	0.33	0.57
EEMS49 (TA)12(GA)7	0.83	3.00	0.29	0.00	0.27
EEMS50 (TA)9(GA)8	0.92	3.00	0.16	0.00	0.15
Mean	0.82	2.44	0.27	0.07	0.24

Table 13. Genetic distance (GD) among 24 pairs genotypes based on SSR

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
1																								
2	0.27																							
3	0.10	0.23																						
4	0.16	0.22	0.13																					
5	0.23	0.15	0.20	0.19																				
6	0.27	0.19	0.24	0.22	0.12																			
7	0.24	0.15	0.20	0.19	0.09	0.05																		
8	0.26	0.18	0.23	0.21	0.11	0.02	0.04																	
9	0.27	0.19	0.24	0.23	0.13	0.05	0.05	0.04																
10	0.26	0.17	0.22	0.21	0.11	0.07	0.04	0.06	0.08															
11	0.25	0.16	0.22	0.20	0.10	0.07	0.03	0.05	0.07	0.02														
12	0.28	0.20	0.25	0.24	0.14	0.07	0.06	0.06	0.07	0.08	0.08													
13	0.27	0.18	0.24	0.22	0.12	0.09	0.05	0.07	0.09	0.03	0.03	0.10												
14	0.25	0.16	0.22	0.20	0.10	0.07	0.03	0.05	0.07	0.02	0.00	0.08	0.03											
15	0.26	0.18	0.23	0.22	0.12	0.08	0.05	0.07	0.08	0.02	0.03	0.09	0.02	0.03										
16	0.25	0.17	0.22	0.20	0.10	0.07	0.04	0.06	0.07	0.02	0.01	0.08	0.03	0.01	0.03									
17	0.27	0.19	0.24	0.23	0.13	0.09	0.06	0.08	0.09	0.05	0.03	0.10	0.06	0.03	0.05	0.02								
18	0.25	0.17	0.22	0.21	0.11	0.07	0.04	0.06	0.08	0.01	0.02	0.08	0.03	0.02	0.02	0.02	0.05							
19	0.25	0.17	0.22	0.20	0.10	0.07	0.04	0.06	0.07	0.02	0.01	0.08	0.03	0.01	0.03	0.00	0.02	0.02						
20	0.26	0.18	0.23	0.21	0.11	0.08	0.04	0.07	0.08	0.05	0.05	0.09	0.07	0.05	0.06	0.05	0.07	0.05	0.05					
21	0.24	0.16	0.21	0.20	0.09	0.09	0.05	0.07	0.09	0.07	0.06	0.10	0.08	0.06	0.08	0.07	0.09	0.07	0.07	0.07				
22	0.30	0.22	0.27	0.25	0.15	0.14	0.11	0.13	0.15	0.13	0.12	0.16	0.14	0.12	0.14	0.13	0.15	0.13	0.13	0.13	0.09			
23	0.32	0.23	0.29	0.27	0.17	0.16	0.13	0.15	0.16	0.15	0.14	0.17	0.16	0.14	0.15	0.14	0.17	0.15	0.14	0.15	0.10	0.07		
24	0.29	0.20	0.26	0.24	0.14	0.13	0.10	0.12	0.13	0.12	0.11	0.14	0.13	0.11	0.12	0.11	0.14	0.12	0.11	0.12	0.08	0.06	0.08	

1. *Solanum aethiopicum*, 2. *Solanum incanum*, 3. *Solanum integrifolium*, 4. *Solanum indicum*, 5. Arka Kusumakar, 6. Pusa Kranti, 7. Arka Shirish, 8. Selection-309, 9. Brinjal Var-3, 10. Brinjal Var-7, 11. G-129, 12. G-111, 13. Pusa Shyamal, 14. NDB-25, 15. Pusa Uttam, 16. Pusa Bindu, 17. DBSR- 52, 18. Pusa Ankur, 19. Br-112, 20. DBSR -195, 21. G-190-10-12, 22. 129-5, 23. 91-2, 24. G-190

Table 14: Quantitative morphological characterization of interspecific F₁ hybrids along with parents

Name of the genotypes	Plant height (cm)	Number of primary branches per plant	Days to first flowering	Days to first fruit set
<i>S. aethiopicum</i>	42.00 ^w	10.67 ^{dc}	47.67 ^c	61.67 ^{gh}
<i>S. incanum</i>	71.20 ^{pq}	8.67 ^{fg}	37.67 ^{kl}	42.33 ^{vwx}
<i>S. integrifolium</i>	64.20 ^r	7.33 ^{hij}	38.67 ^{jkl}	49.67 ^{opqr}
<i>S. indicum</i>	86.00 ^{ef}	10.00 ^{de}	72.33 ^b	89.33 ^e
Pusa Kranti	86.20 ^{ef}	9.00 ^{ef}	33.67 ^{opqr}	48.33 ^{pqrs}
Pusa Shymala	73.60 ^{nop}	9.00 ^{ef}	35.33 ^{mno}	45.33 ^{tu}
NDB-25	89.20 ^d	6.00 ^{kl}	34.67 ^{nopq}	49.67 ^{opqr}
Pusa Uttam	89.00 ^d	7.00 ^{ijk}	37.00 ^{lm}	50.33 ^{mnop}
DBSR- 52	72.20 ^{pq}	5.67 ^l	35.00 ^{mnop}	52.00 ^{lmn}
Pusa Ankur	74.00 ^{no}	6.67 ^{ijkl}	37.67 ^{kl}	47.33 st
Br-112	89.80 ^d	9.00 ^{ef}	33.00 ^{pqr}	50.00 ^{nopq}
DBSR -195	83.40 ^{fgh}	7.67 ^{ghi}	33.00 ^{pqr}	46.33 ^{stu}
190-10-12	78.80 ^{jkl}	7.33 ^{hij}	40.33 ^{ij}	40.33 ^x
91-2	85.40 ^{fg}	6.67 ^{ijkl}	32.33 ^{rs}	48.00 ^{qrs}
G-190	77.80 ^{klm}	7.67 ^{ghi}	46.33 ^{cd}	52.33 ^{lm}
Pusa Kranti × <i>S. incanum</i>	88.40 ^{de}	6.67 ^{ijkl}	41.00 ^{hi}	53.67 ^{kl}
Pusa Shymala × <i>S. incanum</i>	72.80 ^{op}	10.33 ^d	38.67 ^{jkl}	50.67 ^{mno}
Pusa Shymala × <i>S. integrifolium</i>	64.80 ^r	7.67 ^{ghi}	37.67 ^{kl}	55.67 ^{jk}
NDB-25 × <i>S. incanum</i>	81.20 ^{ij}	12.67 ^{ab}	36.67 ^{lmn}	57.67 ^{ij}
NDB-25 × <i>S. integrifolium</i>	79.80 ^{jk}	10.67 ^{dc}	38.67 ^{jkl}	56.67 ^{ij}

Cont.

Pusa Uttam × <i>S. aethiopicum</i>	69.60 ^q	8.33 ^{fgh}	37.67 ^{kl}	63.67 ^g
Pusa Uttam × <i>S. incanum</i>	77.00 ^{lm}	10.33 ^d	41.67 ^{ghi}	58.67 ⁱ
Pusa Uttam × <i>S. integrifolium</i>	50.80 ^v	6.33 ^{jkl}	43.00 ^{fgh}	63.67 ^g
DBSR- 52 × <i>S. incanum</i>	76.60 ^{lm}	10.33 ^d	37.67 ^{kl}	53.00 ^l
DBSR- 52 × <i>S. integrifolium</i>	76.00 ^{mn}	12.67 ^{ab}	32.67 ^{qrs}	46.33 ^{stu}
DBSR- 52 × <i>S. indicum</i>	130.67 ^a	13.67 ^a	72.67 ^b	88.00 ^c
Pusa Ankur × <i>S. aethiopicum</i>	132.00 ^a	7.67 ^{ghi}	89.00 ^a	127.33 ^a
Pusa Ankur × <i>S. incanum</i>	71.20 ^{pq}	10.33 ^d	44.33 ^{def}	61.33 ^h
Pusa Ankur × <i>S. integrifolium</i>	126.00 ^b	12.33 ^b	45.67 ^{cde}	70.33 ^f
Br-112 × <i>S. incanum</i>	60.20 ^s	8.67 ^{fg}	36.67 ^{lmn}	43.00 ^{vw}
DBSR -195 x <i>S. incanum</i>	69.20 ^q	6.33 ^{jkl}	30.67 ^s	41.67 ^x
190-10-12 × <i>S. aethiopicum</i>	84.80 ^{fgh}	12.67 ^{ab}	46.33 ^{cd}	121.33 ^b
91-2 × <i>S. aethiopicum</i>	83.80 ^{fgh}	12.33 ^b	44.33 ^{def}	118.67 ^c
91-2 × <i>S. incanum</i>	54.00 ^u	8.33 ^{fgh}	39.67 ^{ijk}	47.67 ^{rs}
91-2 × <i>S. integrifolium</i>	82.60 ^{hi}	11.67 ^{bc}	43.67 ^{efg}	58.00 ⁱ
G-190 × <i>S. aethiopicum</i>	97.60 ^c	12.67 ^{ab}	47.33 ^c	112.67 ^d
G-190 × <i>S. incanum</i>	56.80 ^v	10.67 ^{dc}	39.67 ^{ijk}	44.33 ^{uv}
S.Em.±	2.33	0.49	1.58	1.95
LSD (p=0.005)	2.48	1.14	2.04	2.27

Table 14: Quantitative morphological characterization of interspecific F₁ hybrids along with parents

Name of the genotypes	Days to first harvest	Number of flower per cluster	Number of fruit per cluster	Fruit length (cm)
<i>S. aethiopicum</i>	74.33 ^l	2.67 ^g	2.33 ^{ef}	3.0 ^m
<i>S. incanum</i>	60.33 ^t	1.00 ⁱ	1.00 ^g	5.5 ^l
<i>S. integrifolium</i>	59.67 ^t	4.00 ^f	3.33 ^d	3.5 ^m
<i>S. indicum</i>	103.33 ^d	7.00 ^d	5.67 ^b	0.8 ^o
Pusa Kranti	75.00 ^l	1.00 ⁱ	1.00 ^g	12.5 ^b
Pusa Shymala	61.33 st	1.00 ⁱ	1.00 ^g	16.5 ^a
NDB-25	68.33 ^{no}	1.00 ⁱ	1.00 ^g	8.5 ^{ef}
Pusa Uttam	82.33 ^{ij}	1.00 ⁱ	1.00 ^g	10.3 ^c
DBSR- 52	73.67 ^l	3.67 ^f	3.33 ^d	6.5 ^{ijk}
Pusa Ankur	73.33 ^l	1.00 ⁱ	1.00 ^g	8.0 ^{fg}
Br-112	74.33 ^l	1.00 ⁱ	1.00 ^g	8.0 ^{fg}
DBSR -195	65.67 ^q	4.00 ^f	3.33 ^d	6.0 ^{kl}
190-10-12	86.00 ^{fg}	2.00 ^{gh}	1.67 ^{fg}	9.5 ^d
91-2	73.67 ^l	1.00 ⁱ	1.00 ^g	6.5 ^{ijk}
G-190	81.33 ^j	1.00 ⁱ	1.00 ^g	9.0 ^{de}
Pusa Kranti × <i>S. incanum</i>	63.33 ^r	1.00 ⁱ	1.00 ^g	8.6 ^{ef}
Pusa Shymala × <i>S. incanum</i>	66.33 ^r	2.67 ^g	1.00 ^g	7.5 ^{gh}
Pusa Shymala × <i>S. integrifolium</i>	67.67 ^{opq}	1.67 ^{hi}	1.33 ^g	7.2 ^{hi}

Cont.

Name of the genotypes	Days to first harvest	Number of flower per cluster	Number of fruit per cluster	Fruit length (cm)
NDB-25 × <i>S. incanum</i>	71.33 ^m	1.00 ⁱ	1.00 ^g	7.50 ^{gh}
NDB-25 × <i>S. integrifolium</i>	73.67 ^l	1.00 ⁱ	1.00 ^g	7.30 ^{gh}
Pusa Uttam × <i>S. aethiopicum</i>	96.67 ^e	1.00 ⁱ	1.00 ^g	7.50 ^{gh}
Pusa Uttam × <i>S. incanum</i>	83.33 ^{hi}	1.00 ⁱ	1.00 ^g	7.60 ^{gh}
Pusa Uttam × <i>S. integrifolium</i>	87.33 ^f	1.00 ⁱ	1.00 ^g	8.50 ^{ef}
DBSR- 52 × <i>S. incanum</i>	66.67 ^{opq}	1.00 ⁱ	1.00 ^g	7.20 ^{hi}
DBSR- 52 × <i>S. integrifolium</i>	62.67 ^{rs}	1.00 ⁱ	1.00 ^g	6.90 ^{hij}
DBSR- 52 × <i>S. indicum</i>	101.67 ^d	10.67 ^a	7.00 ^a	3.2. ^m
Pusa Ankur × <i>S. aethiopicum</i>	160.00 ^a	10.33 ^{ab}	5.67 ^b	2.10 ⁿ
Pusa Ankur × <i>S. incanum</i>	78.67 ^k	1.00 ⁱ	1.00 ^g	7.20 ^{hi}
Pusa Ankur × <i>S. integrifolium</i>	84.67 ^{gh}	10.33 ^{ab}	7.67 ^a	3.70 ^m
Br-112 × <i>S. incanum</i>	68.67 ⁿ	1.00 ⁱ	1.00 ^g	6.00 ^{kl}
DBSR -195 × <i>S. incanum</i>	66.33 ^{pq}	4.33 ^f	2.67 ^{de}	6.20 ^{jkl}
190-10-12 × <i>S. aethiopicum</i>	156.33 ^b	9.67 ^b	4.33 ^c	2.0 ⁿ
91-2 × <i>S. aethiopicum</i>	153.33 ^c	8.33 ^c	5.67 ^b	3.10 ^m
91-2 × <i>S. incanum</i>	68.67 ⁿ	1.00 ⁱ	1.00 ^g	5.50 ^l
91-2 × <i>S. integrifolium</i>	66.67 ^{opq}	1.00 ⁱ	1.00 ^g	9.00 ^{de}
G-190 × <i>S. aethiopicum</i>	159.00 ^a	5.67 ^e	3.33 ^d	3.50 ^m
G-190 × <i>S. incanum</i>	55.67 ^u	1.67 ^{hi}	1.00 ^g	7.50 ^{gh}
S.Em.±	1.38	0.28	0.18	0.19
LSD (P=0.005)	1.92	0.88	0.68	0.71

Table 14: Quantitative morphological characterization of interspecific F₁ hybrids long with parents

Name of the genotypes	Fruit diameter (cm)	Fruit index (cm)	Fruit weight (g)	Number of fruit per plant
<i>S. aethiopicum</i>	2.50 ^o	1.20 ^{mnop}	2.60 ^{yzaa}	96.00 ^h
<i>S. incanum</i>	3.40 ^{jk}	1.62 ^{ghi}	24.00 ^{yzaa}	14.00 ^{tu}
<i>S. integrifolium</i>	3.00 ^m	1.17 ^{mnop}	3.80 ^{yza}	348.00 ^b
<i>S. indicum</i>	0.70 ^r	1.15 ^{mnop}	0.30 ^{yzab}	1475.00 ^a
Pusa Kranti	5.90 ^d	2.13 ^d	208.60 ^c	9.00 ^{wx}
Pusa Shymala	3.50 ^j	4.71 ^a	150.00 ^e	19.00 ^{pqr}
NDB-25	5.70 ^d	1.49 ^{hijk}	102.60 ^f	17.00 ^{rs}
Pusa Uttam	7.10 ^a	1.45 ^{ijkl}	230.00 ^a	6.00 ^y
DBSR- 52	3.50 ^j	1.85 ^{ef}	43.00 ^t	21.00 ^{nop}
Pusa Ankur	6.20 ^c	1.29 ^{klmn}	94.00 ^g	6.00 ^y
Br-112	6.20 ^c	1.29 ^{klmn}	89.00 ^h	13.00 ^{tu}
DBSR -195	3.50 ^j	1.72 ^{fgh}	32.00 ^w	71.00 ⁱ
190-10-12	7.20 ^a	1.32 ^{jklm}	149.00 ^e	12.00 ^{uv}
91-2	6.30 ^c	1.03 ^{opqr}	222.00 ^b	12.00 ^{uv}
G-190	6.20 ^c	1.45 ^{ijkl}	177.40 ^d	10.00 ^{vw}
Pusa Kranti × <i>S. incanum</i>	3.80 ⁱ	2.26 ^d	57.00 ^{no}	29.00 ^j
Pusa Shymala × <i>S. incanum</i>	4.20 ^h	1.80 ^{fg}	38.00 ^v	20.00 ^{opq}
Pusa Shymala × <i>S. integrifolium</i>	3.50 ^j	2.05 ^{de}	72.00 ^j	27.00 ^{jk}
NDB-25 × <i>S. incanum</i>	2.80 ⁿ	2.68 ^c	41.00 ^u	22.0 ^{mno}
NDB-25 × <i>S. integrifolium</i>	3.40 ^{jk}	2.16 ^d	75.00 ⁱ	15.0 st
Pusa Uttam × <i>S. aethiopicum</i>	4.90 ^e	1.53 ^{hij}	62.00 ^m	10.0 ^{vw}
Pusa Uttam × <i>S. incanum</i>	4.60 ^f	1.65 ^{fghi}	74.00 ⁱ	9.0 ^{wx}

Cont.

Pusa Uttam $\times$ <i>S. integrifolium</i>	6.50 ^b	1.31 ^{ijklm}	67.00 ^l	7.0 ^{xy}
DBSR- 52 $\times$ <i>S. incanum</i>	3.30 ^{jk}	2.18 ^d	55.00 ^p	27.0 ^{jk}
DBSR- 52 $\times$ <i>S. integrifolium</i>	2.10 ^p	3.31 ^b	58.00 ⁿ	24.0 ^{lm}
DBSR- 52 $\times$ <i>S. indicum</i>	3.00 ^m	1.07 ^{nopq}	4.40 ^{yz}	322.0 ^c
Pusa Ankur $\times$ <i>S. aethiopicum</i>	1.70 ^q	1.231 ^{mnp}	3.70 ^{yza}	225.0 ^f
Pusa Ankur $\times$ <i>S. incanum</i>	4.60 ^f	1.57 ^{ghi}	52.00 ^q	25.0 ^{kl}
Pusa Ankur $\times$ <i>S. integrifolium</i>	4.40 ^g	0.84 ^{qr}	70.00 ^k	23.0 ^{lmn}
Br-112 $\times$ <i>S. incanum</i>	2.40 ^o	2.51 ^c	48.00 ^r	9.0 ^{wx}
DBSR -195 $\times$ <i>S. incanum</i>	6.20 ^c	1.00 ^{pqr}	74.00 ⁱ	22.0 ^{mno}
190-10-12 $\times$ <i>S. aethiopicum</i>	2.4 ^o	0.83 ^r	3.80 ^{yza}	319.0 ^d
91-2 $\times$ <i>S. aethiopicum</i>	2.40 ^o	1.29 ^{klmn}	2.40 ^{yzaa}	293.0 ^e
91-2 $\times$ <i>S. incanum</i>	3.20 ^l	1.72 ^{fgh}	45.00 ^s	17.0 ^{rs}
91-2 $\times$ <i>S. integrifolium</i>	3.50 ^j	2.58 ^c	56.0 ^{op}	18.0 ^{qr}
G-190 $\times$ <i>S. aethiopicum</i>	2.80 ⁿ	1.25 ^{lmno}	4.80 ^y	217.0 ^g
G-190 $\times$ <i>S. incanum</i>	4.40 ^g	1.71 ^{fgh}	62.0 ^m	23.0 ^{lmn}
S.Em. $\pm$	0.01	0.02	1.33	3.12
LSD (P=0.005)	0.18	0.23	1.88	2.88

Table 14: Quantitative morphological characterization of interspecific F₁ hybrids along with parents

Name of the genotypes	Yield per plant (g)	Ascorbic acid (mg/100g)	Total phenol (mg GAE/100g)	Anthocyanin (mg/100g)	Antioxidant (μ mol trolox/g)
<i>S. aethiopicum</i>	249.60 ^{zj}	3.85 ^d	410.78 ^a	0.23 ^u	2.75 ^{nop}
<i>S. incanum</i>	336.00 ^{zi}	3.20 ^e	356.13 ^{abcde}	9.78 ^k	14.58 ^g
<i>S. integrifolium</i>	1322.40 ^q	1.92 ⁱ	407.00 ^{abc}	0.99 ^{stu}	4.37 ^l
<i>S. indicum</i>	885.00 ^y	1.92 ⁱ	174.97 ^{jkl}	0.89 ^{tu}	3.22 ^{mno}
Pusa Kranti	1877.40 ^e	1.92 ⁱ	95.22 ^m	4.81 ^o	4.27 ^l
Pusa Shymala	2850.00 ^a	2.56 ^g	95.56 ^m	21.95 ^f	6.73 ^j
NDB-25	1744.20 ^g	3.20 ^e	259.53 ^{ghi}	52.34 ^c	4.48 ^l
Pusa Uttam	1380.00 ^p	3.21 ^e	414.91 ^a	21.59 ^{fg}	0.98 ^t
DBSR- 52	903.00 ^x	2.56 ^g	342.72 ^{abcdef}	80.65 ^a	1.33 st
Pusa Ankur	564.00 ^{z^f}	1.28 ^k	98.66 ^{lm}	19.50 ^h	1.74 ^{rs}
Br-112	1157.00 ^t	1.28 ^k	98.31 ^{lm}	3.07 ^q	4.57 ^l
DBSR -195	2272.00 ^c	1.92 ⁱ	152.23 ^{klm}	9.78 ^k	6.87 ^j
190-10-12	1788.00 ^f	3.85 ^d	299.75 ^{defg}	3.37 ^{pq}	4.54 ^l
91-2	2664.00 ^b	5.77 ^b	194.22 ^{hij}	21.74 ^{fg}	2.69 ^{opq}
G-190	1774.00 ^g	1.92 ⁱ	280.50 ^{efg}	1.47 st	3.50 ^m
Pusa Kranti × <i>S. incanum</i>	1653.00 ⁱ	1.13 ^l	283.25 ^{efg}	5.23 ^o	3.42 ^{mn}
Pusa Shymala × <i>S. incanum</i>	760.00 ^{zb}	2.86 ^f	185.97 ^{ijk}	19.65 ^h	27.84 ^d
Pusa Shymala × <i>S. integrifolium</i>	1944.00 ^d	3.33 ^e	163.63 ^{klm}	62.32 ^b	36.88 ^c
NDB-25 × <i>S. incanum</i>	902.00 ^x	1.88 ⁱ	103.81 ^{lm}	5.29 ^o	4.34 ^l
NDB-25 × <i>S. integrifolium</i>	1125.00 ^u	1.90 ⁱ	334.47 ^{bcdefg}	42.26 ^d	14.98 ^g
Pusa Uttam × <i>S. aethiopicum</i>	620.00 ^{ze}	1.11 ^l	336.88 ^{abcdefg}	8.65 ^{lm}	5.49 ^k
Pusa Uttam × <i>S. incanum</i>	666.00 ^{zd}	1.99 ⁱ	104.50 ^{lm}	62.17 ^b	2.14 ^{pqr}
Pusa Uttam × <i>S. integrifolium</i>	469.00 ^{zg}	1.10 ^l	262.97 ^{ghi}	8.95 ^{kl}	2.01 ^{qrs}

Cont.

DBSR- 52 × <i>S. incanum</i>	1485.00 ^l	1.14 ^l	330.00 ^{cdefg}	2.82 ^{qr}	2.55 ^{opq}
DBSR- 52 × <i>S. integrifolium</i>	1392.00 ^o	11.36 ^a	107.94 ^{klm}	0.71 ^{tu}	4.52 ^l
DBSR- 52 × <i>S. indicum</i>	1416.80 ⁿ	2.86 ^f	196.63 ^{hij}	20.77 ^g	3.24 ^{mno}
Pusa Ankur × <i>S. aethiopicum</i>	832.50 ^z	2.61 ^g	133.38 ^{jklm}	6.82 ⁿ	7.78 ⁱ
Pusa Ankur × <i>S. incanum</i>	1300.00 ^r	0.91 ⁱ	96.25 ^{lm}	0.85 ^{tu}	8.13 ⁱ
Pusa Ankur × <i>S. integrifolium</i>	1610.00 ^k	1.90 ⁱ	194.91 ^{hij}	32.18 ^e	10.09 ^h
Br-112 × <i>S. incanum</i>	432.00 ^{zh}	2.86 ^f	192.84 ^{hij}	12.86 ^j	63.27 ^a
DBSR -195 x <i>S. incanum</i>	1628.00 ^j	1.43 ^j	414.91 ^a	8.89 ^{kl}	46.47 ^b
190-10-12 × <i>S. aethiopicum</i>	1212.20 ^s	1.90 ⁱ	355.44 ^{abcdef}	7.75 ^{mn}	19.74 ^e
91-2 × <i>S. aethiopicum</i>	703.20 ^{zc}	5.71 ^b	368.16 ^{abcd}	1.93 ^{rs}	16.44 ^f
91-2 × <i>S. incanum</i>	765.00 ^{za}	11.32 ^a	122.72 ^{jklm}	16.34 ⁱ	3.88 ^{lm}
91-2 × <i>S. integrifolium</i>	1008.00 ^w	1.99 ⁱ	268.81 ^{fgh}	0.91 ^{tu}	2.36 ^{pqr}
G-190 × <i>S. aethiopicum</i>	1041.60 ^v	2.38 ^h	345.81 ^{abcdef}	4.29 ^{op}	3.46 ^m
G-190 × <i>S. incanum</i>	1426.00 ^m	5.24 ^c	318.31 ^{defg}	22.25 ^f	8.37 ⁱ
S.Em.±	1.99	0.39	2352.41	0.39	0.19
LSD (P=0.005)	1.75	0.14	78.4	1.02	0.71

Table 15. Quantitative morphological characterization of interspecific F₁ hybrids along with parents

Name of genotype	Stem antho- cyanin colouratio n	Stem (intensity)	Leaf blade colour	Leaf blade (intensity)	Leaf colour vein	Colour of vein intensity	Spine on leaf	Spine on calyx	Spine on stem	Flower colour
<i>S. aethiopicum</i>	A (1)	St (7)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	GW (1)
<i>S. incanum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	GW (1)
<i>S. integrifolium</i>	P (9)	St (7)	G (1)	M (5)	P (2)	L (3)	Pr (9)	Pr (9)	Pr (9)	GW (1)
<i>S. indicum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)
Arka Kusumaka	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	GW (1)
Pusa Kranti	A (1)	M (5)	G (1)	M (5)	P (2)	L (3)	A (1)	A (1)	A (1)	P (3)
Arka Shirish	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	GW (1)
S-309	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
Brinjal Var-3	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
Brinjal Var-7	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	GW (1)
G-129	P (9)	St (7)	G (1)	M (5)	P (2)	D (7)	A (1)	A (1)	A (1)	P (3)
G-111	A (1)	W (3)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)
Pusa Shymala	P (9)	M (5)	G (1)	D (7)	P (2)	M (5)	A (1)	A (1)	A (1)	P (3)
NDB-25	P (9)	M (5)	G (1)	M (5)	P (2)	M (5)	A (1)	A (1)	A (1)	P (3)
Pusa Uttam	P (9)	M (5)	G (1)	M (5)	P (2)	M (5)	A (1)	A (1)	A (1)	P (3)
Pusa Bindu	P (9)	St (7)	P (2)	D (7)	P (2)	D (7)	A (1)	A (1)	A (1)	P (3)
DBSR- 52	P (9)	W (3)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
Pusa Ankur	P (9)	W (3)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
Br-112	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
DBSR -195	A (1)	M (5)	G (1)	L (3)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
190-10-12	P (9)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
129-5	A (1)	M (5)	G (1)	M (5)	P (2)	L (3)	A (1)	A (1)	A (1)	P (3)
91-2	P (9)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
G-190	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	P (3)
Pusa Kranti × <i>S. incanum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)

Name of genotype	Stem antho- cyanin colouration	Stem (intensity)	Leaf blade colour	Leaf blade (intensity)	Leaf colour vein	Colour of vein intensity	Spine on leaf	Spine on calyx	Spine on stem	Flower colour
Pusa Shymala $\times$ <i>S. incanum</i>	P (9)	W (3)	G (1)	M (5)	P (2)	M (5)	Pr (9)	Pr (9)	Pr (9)	P (3)
Pusa Shymala $\times$ <i>S. integrifolium</i>	P (9)	W (3)	G (1)	M (5)	G (1)	L (3)	A (1)	A (1)	A (1)	D P (4)
NDB-25 $\times$ <i>S. incanum</i>	G (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)
NDB-25 $\times$ <i>S. integrifolium</i>	P (9)	M (5)	G (1)	L (3)	P (2)	D (7)	A (1)	A (1)	A (1)	D P (4)
Pusa Uttam $\times$ <i>S. aethiopicum</i>	P (9)	M (5)	G (1)	M (5)	P (2)	M (5)	A (1)	A (1)	A (1)	P (3)
Pusa Uttam $\times$ <i>S. incanum</i>	P (9)	M (5)	G (1)	M (5)	P (2)	M (5)	A (1)	A (1)	A (1)	P (3)
Pusa Uttam $\times$ <i>S. integrifolium</i>	P (9)	M (5)	G (1)	M (5)	P (2)	M (5)	A (1)	A (1)	A (1)	P (3)
DBSR- 52 $\times$ <i>S. incanum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)
DBSR- 52 $\times$ <i>S. integrifolium</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)
DBSR- 52 $\times$ <i>S. indicum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)
Pusa Ankur $\times$ <i>S. aethiopicum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	L P (2)
Pusa Ankur $\times$ <i>S. incanum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)
Pusa Ankur $\times$ <i>S. integrifolium</i>	P (9)	St (7)	P (2)	M (5)	P (2)	D (7)	Pr (9)	Pr (9)	Pr (9)	L P (2)
Br-112 $\times$ <i>S. incanum</i>	P (9)	W (3)	G (1)	M (5)	G (1)	M (5)	Pr (9)	Pr (9)	Pr (9)	P (3)
DBSR -195 $\times$ <i>S. incanum</i>	A (1)	M (5)	G (1)	M (5)	G (1)	M (5)	A (1)	A (1)	A (1)	P (3)
190-10-12 $\times$ <i>S. aethiopicum</i>	P (9)	W (3)	G (1)	M (5)	G (1)	M (5)	A (1)	A (1)	A (1)	L P (2)
91-2 $\times$ <i>S. aethiopicum</i>	P (9)	W (3)	G (1)	M (5)	G (1)	M (5)	A (1)	A (1)	A (1)	L P (2)
91-2 $\times$ <i>S. incanum</i>	P (9)	M (5)	G (1)	M (5)	P (2)	M (5)	Pr (9)	Pr (9)	Pr (9)	P (3)
91-2 $\times$ <i>S. integrifolium</i>	A (1)	M (5)	G (1)	M (5)	G (1)	M (5)	Pr (9)	Pr (9)	Pr (9)	P (3)
G-190 $\times$ <i>S. aethiopicum</i>	P (9)	W (3)	G (1)	D (7)	G (1)	L (3)	A (1)	A (1)	A (1)	L P (2)
G-190 $\times$ <i>S. incanum</i>	P (9)	M (5)	G (1)	D (7)	G (1)	L (3)	Pr (9)	Pr (9)	Pr (9)	P (3)

Name of genotype	Fruit shape	Fruit shape of apex	Fruit skin colour at commercial harvesting	Intensity of fruit colour	Colour of calyx	Intensity of calyx colour	Colour of flesh	Fruiting pattern	Plant growth
<i>S. aethiopicum</i>	Glo (1)	I (1)	G (2)	D (7)	G (1)	St (7)	G (2)	Mx (3)	SSpr (5)
<i>S. incanum</i>	Ovo (2)	R (3)	G (2)	M (5)	G (1)	M (5)	G (2)	Sol (1)	Spr (7)
<i>S. integrifolium</i>	Glo (1)	I (1)	G (2)	M (5)	P (2)	M (5)	G (2)	Mx (3)	SSpr (5)
<i>S. indicum</i>	Glo (1)	R (3)	GGs (9)	D (7)	G (1)	W (3)	G (2)	Clu(2)	Er (1)
Arka Kusumaka	Cyl (7)	Po (4)	G (2)	L (3)	G (1)	W (3)	G (2)	Mx (3)	Spr (7)
Pusa Kranti	Ell (6)	R (3)	P (3)	D (7)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
Arka Shirish	Cyl (7)	Po (4)	G (2)	D (3)	G (1)	W (3)	G (2)	Sol (1)	SSpr (5)
S-309	Club (5)	Po (4)	W (1)	W (1)	G (1)	M (5)	Wh (1)	Mx (3)	SSpr (5)
Brinjal Var-3	Glo (1)	F (2)	P (3)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
Brinjal Var-7	Pear (4)	F (2)	G (2)	L (3)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
G-129	Cyl (7)	R (3)	P (3)	D (7)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
G-111	Glo (1)	R (3)	P (3)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
Pusa Shymala	Club (5)	R (3)	P (3)	D (7)	G (1)	M (5)	G (2)	Mx (3)	SSpr (5)
NDB-25	Pear (4)	F (2)	P (3)	D (7)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
Pusa Uttam	Glo (1)	F (2)	P (3)	D (7)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
Pusa Bindu	Glo (1)	F (2)	P (3)	D (7)	G (1)	W (3)	G (2)	Clu(2)	SSpr (5)
DBSR- 52	Obo (3)	R (3)	P (3)	M (5)	G (1)	M (5)	G (2)	Mx (3)	SSpr (5)
Pusa Ankur	Ovo (2)	R (3)	P (3)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
Br-112	Glo (1)	R (3)	P (3)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
DBSR -195	Obo (3)	R (3)	W (1)	W (1)	G (1)	W (3)	Wh (1)	Mx (3)	SSpr (5)
190-10-12	Ovo(2)	F (2)	P (3)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
129-5	Ell (6)	R (3)	P (3)	M (5)	G (1)	M (5)	G (2)	Mx (3)	SSpr (5)
91-2	Glo (1)	R (3)	P (3)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
G-190	Ovo (2)	F (2)	G (2)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
Pusa Kranti × <i>S. incanum</i>	Obo (3)	R (3)	PVS (9)	-	G (1)	W (3)	G (2)	Sol (1)	SSpr (5)

Name of genotype	Fruit shape	Fruit shape of apex	Fruit skin colour at commercial harvesting	Intensity of fruit colour	Colour of calyx	Intensity of calyx colour	Colour of flesh	Fruiting pattern	Plant growth
PusaShymala × <i>S. incanum</i>	Cyl (7)	Po (4)	G (2)	D (7)	G (1)	W (3)	G (2)	Sol (1)	SSpr (5)
PusaShymala × <i>S. integrifolium</i>	Ell (6)	Po (4)	P (3)	D (7)	P (2)	St (7)	G (2)	Mx (3)	SSpr (5)
NDB-25 × <i>S. incanum</i>	Ell (6)	R (3)	PGS (9)	-	G (1)	W (3)	G (2)	Sol (1)	SSpr (5)
NDB-25 × <i>S. integrifolium</i>	Pear (4)	F (2)	P (3)	D (7)	P (2)	St (7)	G (2)	Sol (1)	Spr (7)
PusaUttam × <i>S. aethiopicum</i>	Glo (1)	F (2)	P (3)	D (7)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
PusaUttam × <i>S. incanum</i>	Glo (1)	F (2)	P (3)	D (7)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
PusaUttam × <i>S. integrifolium</i>	Glo (1)	F (2)	P (3)	D (7)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
DBSR- 52 × <i>S. incanum</i>	Obo (3)	R (3)	P (3)	M (5)	P (2)	W (3)	G (2)	Sol (1)	SSpr (5)
DBSR- 52 × <i>S. integrifolium</i>	Obo (3)	R (3)	PGS (9)	-	P (2)	W (3)	G (2)	Sol (1)	SSpr (5)
DBSR- 52 × <i>S. indicum</i>	Glo (1)	F (2)	G (2)	M (5)	G (1)	M (5)	G (2)	Clu(2)	Spr (7)
PusaAnkur × <i>S. aethiopicum</i>	Glo (1)	F (2)	G (2)	M (5)	G (1)	M (5)	G (2)	Clu(2)	Er (1)
PusaAnkur × <i>S. incanum</i>	Ovo (2)	R (3)	GPS (9)	-	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
PusaAnkur × <i>S. integrifolium</i>	Glo (1)	R (3)	G (2)	M (5)	P (2)	M (5)	G (2)	Clu(2)	SSpr (5)
Br-112 × <i>S. incanum</i>	Ovo (2)	R (3)	P (3)	M (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
DBSR -195 x <i>S. incanum</i>	Obo (3)	R (3)	P (3)	M (5)	G (1)	W (3)	G (2)	Mx (3)	SSpr (5)
190-10-12 × <i>S. aethiopicum</i>	Glo (1)	R (3)	G (2)	M (5)	G (1)	M (5)	G (2)	Clu(2)	Er (1)
91-2 × <i>S. aethiopicum</i>	Glo (1)	Po (4)	G (2)	M (5)	G (1)	M (5)	G (2)	Clu(2)	Er (1)
91-2 × <i>S. incanum</i>	Glo (1)	F (2)	G (2)	M (5)	G (1)	W (3)	G (2)	Sol (1)	SSpr (5)
91-2 × <i>S. integrifolium</i>	Obo (3)	R (3)	G (2)	L (5)	G (1)	M (5)	G (2)	Sol (1)	SSpr (5)
G-190 × <i>S. aethiopicum</i>	Glo (1)	F (2)	G (2)	M (5)	G (1)	W (3)	G (2)	Mx (3)	Er (1)
G-190 × <i>S. incanum</i>	Ovo (2)	F (2)	G (2)	D (7)	G (1)	W (3)	G (2)	Sol (1)	SSpr (5)

P = Purple, LP = Light purple, DP = Dark purple, G = Green, GW = Greenish white, W = Weak, M = Medium, St = Strong, L = Light, D = Dark, A = Absent, Pr = Present, Cy l = Cylindrical, Ell = Ellipsoid, Glo = Globular, Obo = Obovate, Ovo = Ovoid, Po = Pointed, R = Round, F = Flattened, I= Indented, Wh= White, Sol= Solitary, Mx=Mixed, Clu= Cluster, SSpr= Semi-Spreading, Spr= Sprading, Er= Erect, PGS= Purple with green strips, PVS= Purple with violet strips, GPS= Green with purple strips, GGS= Green with green strips

6. SUMMARY AND CONCLUSION

Brinjal is one of the most important solanaceous vegetable crops grown commercially throughout the world. Brinjal is known by different vernacular names across the continent such as eggplant in United States, aubergine in France, melongena in Italy and brinjal in India. Its popularity is universal and is an integral part of Indian cuisine and have immense important due to its array of medicinal properties. White varieties are said to be good for diabetic patients while roots are credited with anti-asthmatic properties. The crop is native to India and it is endowed with wide diversity of eggplant although limited work has been undertaken to utilize its genetic resources. Interspecific hybridization is one of the most significant approaches for developing genetic stocks, which serve as important sources of genes for quality and resistance traits (Sekara *et al.*, 2007).

The present investigation entitled “Studies on crossability and genetic relationship among eggplant (*Solanum melongena* L.) and wild relatives” was undertaken at the research farm of Division of Vegetable Science, IARI, New Delhi during 2012 to 2015. Twenty four genotypes of brinjal including four wild species (*Solanum incanum*, *S. aethiopicum*, *S. integrifolium* and *S. indicum*) collected from all over India were used for present investigation viz., interspecific hybridization, morphological and biochemical diversity (D²) analysis of parental genotypes with respect to 17 important quantitative characters. Molecular diversity, was also carried out by using PCR based 39 SSR markers. Quantitative and qualitative morphological characterization of F₁ hybrids along with their parental genotypes was also done. The chromosome study was done in four wild species and one cultivated genotype.

The interspecific hybridization was carried out involving twenty cultivated genotypes and four wild *Solanum* species. The cultivated genotypes were used as female parents and wild species as pollen parents in all possible combinations without reciprocals. The crossability relationship of *S. melongena* genotypes with the wild species was determined by occurrence of pollen viability of four wild species, fruit set (%), number of seeds per fruit and germination (%) of F₁ seed. There was marked variation among the four wild species for pollen viability. The maximum (34.78%) fertile pollens were observed in *S. indicum*, whereas minimum (11.01%) was in *S. integrifolium*. The maximum pollen sterility was shown in the *S. integrifolium* (71.56%) and minimum in *S. aethiopicum* (13.2%). The mean fruit set

was maximum for DBSR-91 (41.25%) followed by DBR-G-190 (37.91%) and NDB-25 (32.08%). The maximum number of seeds per fruit (266.92) were obtained in DBR-G-190 followed by Pusa Uttam (101.42) and Sel-91-2 (92.00). The mean value of highest germination (%) of F₁ seed was observed for DBSR-91 (41.58%) followed by Pusa Uttam (40.25%) and Sel-91-2 (35.50%) when crossed with wild species. The maximum fruit set (80%) was recorded in cross DBSR-91 × *S. aethiopicum*. The highest germination of F₁ seed (71%) was recorded in three cross combinations, Pusa Uttam × *S. aethiopicum*, Sel-91-2 × *S. aethiopicum*, DBR-G-190 × *S. aethiopicum*. The highest number of seeds per fruit (754) were recorded in DBR-G-190 × *S. incanum*.

All the twenty four parental genotypes were subject to morphological and biochemical diversity analysis with respect to 17 important quantitative traits by using Mahalanobis D² statistics. The 24 parental genotypes were grouped into 4 clusters based on D² values. Among the four clusters, cluster IV had maximum (12) genotypes including three wild species (*S. incanum*, *S. aethiopicum* and *S. integrifolium*). Cluster III comprised two cultivated genotypes belonging to same location. Cluster II had only one wild species (*S. indicum*) whereas, Cluster I comprised nine cultivated genotypes.

The highest inter cluster distance (90.03) was observed between cluster II and cluster III and minimum distance in (52.98) III and IV. The maximum intra-cluster distance was observed in cluster IV (5.34). On the basis of mean performance of different clusters, genotypes having high yield along with fruit weight, fruit diameter, fruit length, total phenol and antioxidant activity were observed in cluster III. The clustering pattern revealed that the genotypes were not distributed according to their geographical origin.

For better understanding of diversity among the genotypes, diversity at molecular level was also carried out by using SSR markers. For molecular analysis, 39 SSR primers were screened and 30 SSR primers showed polymorphism and amplified band ranged from 2 to 5. A total of 86 alleles were amplified with an average of 2.39 allele per locus. Morphological diversity based on quantitative traits and SSR markers was not similar and grouping pattern was different from one another.

There was a great variation observed on characterization of parental genotypes and F₁ hybrids through 17 quantitative traits including biochemical traits. In the present study, the plant height ranges from 42 to 130.67 cm and number of primary branches per plant recorded 5.67 to 13.67. The days to first flowering ranges 32.67 to 89 days, days to first fruit set (42.33 to 127 days) and days to first harvest 59.67 to 160 days. The number of flowers per cluster ranges from 1 to 10.67, number of fruit per cluster 1 to 7, number of fruits per plant (6 to 1475) and yield per plant (249 g to 2850 g). For fruit length it ranges from (0.8 cm to 16.5 cm), fruit diameter (0.70 cm to 7.20 cm), fruit shape index it ranges from 0.83 to 4.71 cm and fruit weight (0.30 to 230g). The ascorbic acid content ranges from 1.28 to 12.82 mg /100g, total phenol content (95.22 mg GAE/100g to 414.91 mg GAE/100g), anthocyanin content (0.98 to 63.27 µmol/g), the antioxidant activity (0.98 to 14.58 µmol trolox/g).

The qualitative characterization of F₁ along with the parents has been carried out. It was found that the majority of the genotypes come under semi-spreading (80.43%) growth habits and 50% of genotypes had purple colour stem with medium intensity of colour. Maximum number of genotypes had purple colour flower (71.74%) with solitary fruiting habit (60.87%). Most of the genotypes (95.65%) showed green leaf blade colour with (67.39%) green vein colour. The genotypes (36.96%) were found to have spine on leaf, calyx and stem. The maximum number of genotypes were recorded for purple colour fruit (47.83%) with (41.0%) globular shape and (47.83%) round shape apex with greenish flesh (95.65%) colour.

Cytological studied on four wild species and one commercial variety Pusa Shyamla of *S. melongena*. It was found that the same chromosome number (2n=2x=24) that existed in cultivated *S. melongena* cv. Pusa Shyamla was also confirmed in all the four wild species (*S. incanum*, *S. aethiopicum*, *S. integrifolium*, *S. indicum*) under investigation. Interspecific crosses reported in this study will be used in transferring desirable traits in different genetic backgrounds of cultivated *S. melongena*. Through crossability study *S. incanum* was found highly crossable with the cultivated *S. melongena* genotypes.

Through morphological characterization and D² analysis, a wide range of variation for almost all the economically important traits was present in this crop so there is a vast scope for improvement through different breeding procedure, though

less diversity was observed at molecular level. The molecular diversity is not in consonance with morphological diversity but for effectively utilize the genetic variability for crop improvement both morphological and molecular SSR markers were used to enhanced the diversity among genotypes. The genetic distance observed among the varieties/ breeding lines would play a major role for making hybrid combinations and/or selection of transgressive segregants for further improvement in brinjal.

STUDIES ON CROSSABILITY AND GENETIC RELATIONSHIP AMONG EGGPLANT (*Solanum melongena* L.) AND WILD RELATIVES

ABSTRACT

The present investigation entitled, “Studies on crossability and genetic relationship among eggplant (*Solanum melongena* L.) and wild relatives” was undertaken at the research farm of Division of Vegetable Science, IARI, New Delhi during 2012-2015. Interspecific hybridization was carried out involving twenty cultivated genotypes of brinjal and four wild *Solanum* species (*Solanum incanum*, *S. aethiopicum*, *S. integrifolium* and *S. indicum*). The cultivated genotypes were used as female parents and wild species as pollen parents in all possible combinations without reciprocal. The crossability relationship of *S. melongena* genotypes with the wild species was determined by fruit set (%), number of seeds per fruit and germination (%) of F₁ seed and pollen viability in four wild related *Solanum* species. The mean fruit set was maximum for DBSR-91 (41.25%) followed by DBR-G-190 (37.91%) and NDB-25 (32.08%). The maximum number of seeds per fruit (266.92) was obtained in DBR-G-190 followed by Pusa Uttam (101.42) and Sel-91-2 (92.00). The highest germination (%) of F₁ seeds was observed in DBSR-91 (41.58%) followed by Pusa Uttam (40.25%) and Sel-91-2 (35.50%) when species were used as male parents. The maximum fruit set (80%) was recorded in cross DBSR-91 × *S. aethiopicum* followed by Pusa Bindu × *S. aethiopicum* (75%) and NDB-25 × *S. aethiopicum* (75%). The highest germination of F₁ seeds (71%) was recorded in three cross-combinations viz. Pusa Uttam × *S. aethiopicum*, Sel-91-2 × *S. aethiopicum* and DBR-G-190 × *S. aethiopicum*. The highest number of seeds per fruit (754) was recorded in DBR-G-190 × *S. incanum* followed by DBSR-52 × *S. incanum* (226.6), DBR-G-190 × *S. aethiopicum* (206). The maximum (34.78%) fertile pollens were observed in *S. indicum*, whereas minimum (11.01%) was in *S. integrifolium*. The maximum pollen sterility was shown in the *S. integrifolium* (71.56%) followed by *S. indicum* (15.2%) and *S. aethiopicum* (13.2%). All the twenty four parental genotypes including cultivated *S. melongena* and four wild species were subjected to morphological and biochemical diversity analysis with respect to 17 important quantitative traits by using Mahalanobis D² statistics. The twenty four parental genotypes were grouped into 4 clusters based on D² values which exhibited no association between geographical distance and genetic divergence.

Molecular diversity was also studied by using 39 SSR markers of which 30 SSR markers showed polymorphism. The UPGMA dendrogram obtained by 30 SSR markers classified 24 genotypes in 3 clusters. Morphological diversity based on 17 quantitative traits and molecular diversity based on 30 SSR markers were not similar with respect to clustering of genotypes

There was a great variation observed on characterization of parental genotypes and F_{1s} through 17 quantitative traits including biochemical traits. In the present study, among the parental genotypes and F_1 hybrids, it has been observed that plants height ranged from 42 to 130.67 cm and number of primary branches per plant from 5.67 to 13.67. The days for first flowering ranged from 32.67 to 89 days and days to first harvest from 59.67 to 160 days. The number of fruits per plant ranges from 6 to 1475 and yield per plant from 249 g to 2850 g. For fruit length, it ranged from 0.8 cm to 16.5 cm, fruit diameter from 0.70 cm to 7.20 cm, and fruit weight from 0.30 to 230 g. The ascorbic acid content ranged from 1.28 to 12.82 mg /100g, total phenol content from 95.22 mg GAE/100g to 414.91 mg GAE/100g and the antioxidant activity from 0.98 to 14.58 μ mol trolox/g.

Based on cytological study, it was found that all the wild species had similar chromosome number i.e. $2n=2x=24$.

बैंगन (*सोलेनम मेलोनजेना* ली.) एवं उसके वन्य संबंधियों के मध्य संकरण योग्यता एवं आनुवंशिक संबंध

सार

सन् 2012–2015 के दौरान भा. कृ. अ. संस्थान, नई दिल्ली के शाक विज्ञान संभाग के अनुसंधान प्रक्षेत्र पर, "बैंगन (*सोलेनम मेलोनजेना* ली.) एवं उसके वन्य संबंधियों के मध्य संकरण योग्यता एवं आनुवंशिक संबंध", नामक प्रस्तुत अध्ययन किया गया। बैंगन के बीस कृष्य जीनप्ररूपों एवं चार जंगली *सोलेनम* प्रजातियों (*सोलेनम इनकानम*, *सो. इंटैग्रीफोलियम* एवं *सो. इंडिकम*) का समावेश कर अंतरप्रजातीय संकरण किया गया। बिना किसी व्युत्क्रमी संयोजन के सभी संभव संयोजनों में मादा जनकों के रूप में कृष्य जीनप्ररूपों तथा पराग जनकों के रूप में वन्य प्रजातियों तथा परग जनकों के रूप में वन्य प्रजातियों का उपयोग किया गया। वन्य प्रजातियों के साथ *सो. मेलोनजेला* जीनप्ररूपों की संकरणयोग्यता का चार वन्य संबंधी *सोलेनम* प्रजातियों के फल बनने (%), प्रति फल बीजों की संख्या तथा एफ₁ संतति के अंकुरण (%) एवं पराग जीवनक्षमता के आधार पर निर्धारण किया गया। औसत फ्रूट सैट डी बी एस आर – 91 में अधिकतम (41.25%) था जिसके पश्चात डी बी आर – जी – 190 (37.91%) एवं एन डी बी – 25 (32.08%) का स्थान रहा। प्रति फल अधिकतम बीजों की संख्या (266.92) डी बी आर – जी – 190 में प्राप्त हुई जिसके पश्चात पूसा उत्तम (101.42) एवं सेल-91-2 (92.00) का स्थान रहा। एफ₁ बीजों का अधिकतम अंकुरण (%) डी बी एस आर – 91 (41.58%) में देखा गया जिसके पश्चात पूसा उत्तम (40.25%) एवं सेल-91-2 (35.50%) का स्थान रहा जब ये प्रजातियाँ नर जनकों के रूप में उपयोग की गईं। अधिकतम फल निर्माण (80%), क्रॉस डी बी एस आर-91 × *सो. एइथियोपिकम* में रेकार्ड किया गया जिसके पश्चात पूसा बिन्दु × *सो. एइथियोपिकम* (75.00%) एवं ए डी बी – 25 × *सो. एइथियोपिकम* (75.00%) का स्थान रहा। तीन क्रॉस संयोजनों अर्थात्, पूसा उत्तम × *सो. एइथियोपिकम*, सेल-91-2 × *सो. एइथियोपिकम* एवं डी बी आर – जी – 19 × *सो. एइथियोपिकम* में एफ₁ बीजों का अधिकतम अंकुरण (71.00%) रेकार्ड किया गया। प्रतिफल बीजों का अधिकतम संख्या (754.00), डी बी आर – जी – 190 × *सो. इनकानम* में रेकार्ड की गई जिसके पश्चात डी बी एस आर-52- × *सो. इनकानम* (226.60) एवं डी बी आर-जी-190 × *सो. एइथियोपिकम* (206.00) का स्थान रहा। *सो. इंडिकम* में अधिकतम उर्वर पराग कण देखे गए जबकि *सो. इंटैग्रीफोलियम* में न्यूनतम (11.01%) देखे गए। अधिकतम पराग बंध्यता *सो. इंटैग्रीफोलियम* (71.56%) ने दर्शायी जिसके पश्चात *सो. इंडिकम* (15.20%) एवं *सो. एइथियोपिकम* (13.20%) का स्थान रहा। चार वन्य प्रजातियों एवं कृष्य *सो. मेलोनजेना* सहित सभी चौबीस जनक-जीनप्ररूपों का महालोनाबिस डी² साँख्यिकी का उपयोग कर, 17 महत्वपूर्ण प्रमात्रात्मक गुणों के सन्दर्भ में आकारिकीय एवं जैवरासायनिक विविधता विश्लेषण किया गया। डी² के आधार पर इन चौबीस जनक-जीनप्ररूपों का 4 समुच्चयों में समूहन किया गया जिसने भौगोलिक दूरी एवं आनुवंशिक अपसरण के बीच कोई संबंध नहीं दर्शाया। 39 एस एस आर चिह्नों का उपयोग कर आणविक विविधता का भी अध्ययन जिनमें से 30 एस एस आर ने बहुरूपता दर्शायी। 30 एस एस आर चिह्नों से प्राप्त यू पी जी एम ए डेंड्रोग्राम ने इन चौबीस जीनप्ररूपों को 3 समुच्चयों में वर्गीकृत किया। 17 मात्रात्मक गुणों पर आधारित आकारिकीय विविधता एवं 30 एस एस आर चिह्नों पर आधारित आणविक विविधता, जीनप्ररूपों के समुच्चयों के संदर्भ में एक समान नहीं थीं।

जैवरासायनिक गुणों सहित 17 मात्रात्मक गुणों के द्वारा जनक जीनप्ररूपों एवं एफ1 का अभिलक्षणन करने पर बहुत अधिक विभिन्नता देखी गई। प्रस्तुत अध्ययन में, जनक जीनप्ररूपों एवं एफ1 संकरों में यह देखा गया कि पौधों की ऊँचाई 42.00 से 130.67 से मी की सीमा में तथा प्रति पौधा प्राथमिक शाखाओं की संख्या 5.67 से 13.67 की सीमा में थे। प्रथम पुष्पन हेतु दिन 32.67 से 89 दिन एवं प्रथम तुड़ाई हेतु दिन 59.67 से 160 दिन की सीमा में थे। प्रति पौधा फलों की संख्या 6.00 से 1475.00 एवं प्रति पौधा उपज 249.00 ग्रा से 2850.00 ग्रा की सीमा में पाए गए। फल-लम्बाई 0.80 से मी से 16.50 से मी, फल-व्यास 0.70 से मी से 7.20 से मी एवं फल-भार 0.30 से 230 ग्रा की सीमा में पाए गए। एस्कोर्बिक अम्ल अंश 1.28 से 12.85 मि ग्रा/100 ग्रा, कुल फीनोल अंश 95.22 मि ग्रा जी ए ई / 100 ग्रा से 414.91 मि ग्रा जी ए ई / 100 ग्रा एवं प्रति ऑक्सीकारक सक्रियता 0.98 से 14.58 माइक्रोमोल ट्रोलोक्स/ग्रा की सीमा में थी। कोशिकाविज्ञान संबंधी अध्ययन के आधार पर यह पाया गया कि सभी वन्य प्रजातियों की गुणसूत्र संख्या $2n = 2x = 24$ थी।

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Appendix I: Meteorological data recorded at IARI, New Delhi.

Latitude: 28.40°N; longitude: 77.13°E, Height above mean sea level: 228.00 m

2012-2013

Date	Fortnight/Month		Temperature°c		Relative humidity (%)	Rainfall (mm)
			Max	Min		
1-15	I/June	summer	42.53	28.11	34.13	2.07
16-30	II/June		42.65	28.97	35.97	2.07
1-15	I/July	Rainy season	36.70	26.97	70.47	21.88
16-31	II/July		36.53	27.26	69.76	20.21
1-15	I/August		33	26.05	75.67	9.975
16-31	II/August		32.49	25.71	79.11	14.95
1-15	I/September	Autumn	33.63	25.8	76.4	9.6
16-30	II/September		33.13	22.23	70.6	0.00
1-15	I/October		34.72	18.09	63.2	0.00
16-31	II/October		30.52	14.23	62.56	0.00
1-15	I/November	Winter	28.17	12.11	65.73	0.00
16-30	II/November		26.35	7.75	58.00	0.00
1-15	I/December		23.61	7.55	58.67	3.50
16-31	II/December		19.83	7.45	72.31	0.00
1-15	I/January	Spring	15.9	4.3	91.87	0
16-30	II/January		19.99	5.15	92.19	2.55
1-15	I/February		21.91	8.94	90.53	4.55
16-28	II/February		22.21	10.42	93	3.17
1-15	I/March	Spring	28.81	11.96	87.67	0
16-31	II/March		30.83	15.24	86.56	0.79

2013-2014

1-15	I/June	38.79	27.43	76.80	0.72
16-30	II/June	36.53	25.87	83.40	9.35
1-15	I/July	35.53	25.94	88.53	11.81
16-31	II/July	34.07	25.48	94.00	17.66
1-15	I/August	32.42	25.60	95.92	12.89
16-31	II/August	33.14	24.68	93.19	21.28
1-15	I/September	35.10	24.47	83.07	0.41
16-30	II/September	33.85	23.59	90.07	6.65
1-15	I/October	31.55	22.30	92.20	7.27
16-31	II/October	31.46	16.32	94.94	0.00
1-15	I/November	26.65	11.33	91.13	0.03
16-30	II/November	27.10	8.53	90.67	0.00
1-15	I/December	25.27	7.42	93.47	0.00
16-31	II/December	19.63	6.76	94.06	0.12
1-15	I/January	18.85	4.87	96.27	0.00
16-30	II/January	18.36	8.68	97.00	1.16
1-15	I/February	21.06	7.09	96.33	3.64
16-28	II/February	24.24	10.47	92.47	3.14
1-15	I/March	24.24	10.47	92.47	3.14
16-31	II/March	29.31	14.84	87.75	1.03

Appendix II: Analysis of variance for various quantitative characters of F₁ hybrid and along with parents.

S No.	Character	Replication			Genotype			Error	
		DF	MSS	F	DF	MSS	F	DF	MSS
1	Plant height (cm)	2	14.11	6.06	36	1098.52	471.72	72	2.32
2	Number of primary branches per plant	2	18.71	38.23	36	15.65	31.96	72	0.48
3	Days to first flower opening	2	18.24	11.57	36	425.53	269.91	72	1.57
4	Days to first fruit set	2	8.78	4.50	36	1644.33	843.05	72	1.95
5	Days to first harvest	2	13.14	9.49	36	2421.81	1748.74	72	1.38
6	Number of flower per cluster	2	0.01	0.03	36	29.61	106.68	72	0.28
7	Number of fruit per cluster	2	0.01	0.05	36	11.36	64.67	72	0.17
8	Fruit length (cm)	2	0.95	4.95	36	27.47	142.76	72	0.19
9	Fruit shape index (Length/Breadth)	2	0.01	0.67	36	1.68	83.52	72	0.02
10	Fruit diameter (cm)	2	0.45	36.80	36	8.04	652.84	72	0.01

S No.	Character	Replication			Genotype			Error	
		DF	MSS	F	DF	MSS	F	DF	MSS
10	Fruit diameter (cm)	2	0.45	36.80	36	8.04	652.84	72	0.01
11	Fruit weight (g)	2	155.91	116.92	36	11521.49	8640.24	72	1.33
12	Number of fruit per plant	2	276.65	88.64	36	192682.92	61740.10	72	3.12
13	Yield per plant (g)	2	431.01	372.59	36	1137981.93	983757	72	1.16
14	Ascorbic acid (mg/100g)	2	0.15	21.75	36	16.78	2386.92	72	0.01
15	Total phenol (mg GAE/100g)	2	2261.81	0.96	36	36290.66	15.43	72	2352.41
16	Anthocyanin (mg/100g)	2	20.72	53.22	36	1175.08	3018.12	72	0.39
17	Antioxidant (μ mol trolox /g)	2	3.13	16.56	36	540.50	2858.64	72	0.19