STUDIES ON COMBINING ABILITY, MOLECULAR DIVERSITY AND RESPONSE TO LATE BLIGHT (*Phytophthora infestans* (Mont.) de Bary) IN TOMATO (*Solanum lycopersicum* L.) UNDER POLYHOUSE CONDITION

Thesis

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By

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August, 2018
Pantnagar

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CERTIFICATE

This is to certify that the thesis entitled **"STUDIES ON COMBINING ABILITY, MOLECULAR DIVERSITY AND RESPONSE TO LATE BLIGHT (*Phytophthora infestans* (Mont.) de Bary) IN TOMATO (*Solanum lycopersicum* L.) UNDER POLYHOUSE CONDITION"** submitted in partial fulfillment of the requirements for the degree of **Doctor of Philosophy** with major in **Horticulture (Vegetable Science)** and minor in **Genetics and Plant Breeding**, of the College of Post Graduate Studies, G.B. Pant University of Agriculture and Technology, Pantnagar, is a record of *bona-fide* research carried out by **Mr. Ankit Panchbhaiya, Id. No. 38423,** under my supervision and no part of the thesis has been submitted for any other degree or diploma.

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August, 2018

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We, the undersigned, members of the Advisory Committee of **Mr. Ankit Panchbhaiya, Id. No. 38423,** a candidate for the degree of **Doctor of Philosophy** with major in **Horticulture (Vegetable Science)** and minor in **Genetics and Plant Breeding** agree that the thesis entitled **"STUDIES ON COMBINING ABILITY, MOLECULAR DIVERSITY AND RESPONSE TO LATE BLIGHT (*Phytophthora infestans* (Mont.) de Bary) IN TOMATO (*Solanum lycopersicum* L.) UNDER POLYHOUSE CONDITION"** may be submitted in partial fulfilment of the requirements for the degree.

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Introduction

Chapter 1 INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is an important vegetable of Solanaceae family having chromosome number 2n=2x=24. It has originated from wild form in the Peru-Equador-Bolivia region of the Andes, South America (Rick, 1969) and is grown in almost every corner of the world (Roberston and Labate, 2007). It is one of the most popular and widely grown vegetables in the world ranking second in importance to potato in many countries. In England, it is popularly known as 'Love of Apple' (Shanmugavelu, 1989) while, in India it is commonly referred as 'Poor man's orange' (Tewari, 1996). The fruits are eaten as raw or cooked form. Large quantities of tomato are used to produce soup, juice, ketchup, puree, paste and powder. Green tomatoes are also used for pickles and preserves. Tomato universally treated as 'Protective Food' and is being extensively grown as annual plant all over the world. It is an excellent source of income to small and marginal farmers and contributes to the nutrition of the consumers.

Tomato is one of the most highly praised vegetables consumed widely. It is a major source of vitamins, minerals and organic acids. Although, the vitamins only account for a small proportion of the total dry matter but they are highly significant from the nutritional point of view. There are various types of flavouring compounds found in the fruits, which enrich the taste. The total sugar content is 2.5 per cent in ripe fruit and amount of ascorbic acid varies from 16-65mg/100g of fruit weight. Total amino acid is 100-350mg/100g. Tomato is also rich in medicinal values. The pulp and juice are digestible mid aperients, a promoter of gastric secretion and blood purifier. It is also considered to be intestinal antiseptic. It is said to be useful in cancer of the mouth, sore mouth, *etc*. Dried tomato juice retains vitamin C. It stimulates torpid liver and is good in chronic dyspepsia. It is one of the richest vegetables which keep our stomach and intestine in good condition. Tomato, a primary source of lycopene, showed significant association with low prostate cancer risk. Tomato juice has become an exceedingly popular appetizer and beverage.

India ranks second in tomato producing country followed by China in the world. The National production of tomato in 2016-17 is estimated at 197 lakh tonnes with an area of 8.1 lakh hectare and the average productivity of tomato is 24 MT/ha (Anonymous, 2017). In India, tomato has wider coverage in comparison to other vegetables. The major tomato producing states are Andhra Pradesh, Madhya Pradesh, Karnataka Utter Pradesh, Maharashtra, West Bengal, Orissa and Bihar. Andhra Pradesh is leading state in area as well as in production of tomato in India.

Tomato is typical day neutral plant and mainly self-pollinated, but a certain percentage of cross-pollination (1% to 47%) also occurs (Rick, 1949). It is a perennial, often grown outdoors in temperate climates as an annual. *S. lycopersicum* and near relatives are self fertile but the former is outcrossed to a considerable extent in certain part of subtropical areas and its native region. Three different types of tomato plants can be distinguished: (i) tall or indeterminate type, (ii) semi-bush or semi-determinate type and (iii) bush or determinate type. In 'indeterminate' cultivars of tomato, once flower initiation started it continues through the life of the plant and it is unlikely that the total yield of fruits will be limited by the number of flowers initiated (Hurd and Cooper, 1967). Determinate types stop growing after flowering. They require less labour, so they are popular for commercial cultivation. They have a comparatively concentrated fruiting and the fruits ripen much faster than those from indeterminate types. 'Determinate' cultivars of tomato have prolific flowering followed by a period when fruit growth is dominant. With synchronization of fruiting, once-over harvesting by machines becomes possible (Gould, 1983) and if this is the objective it is important that flowering of the main shoot and of the branches should be concentrated into as short a period as possible.

India have diverse agroclimatic conditions, the protected vegetable cultivation technology can be utilized for year round and off-season production of high value low volume vegetable crops, production of virus free high quality seedlings and quality hybrid seed production. Among vegetables, tomato is the first crop grown in polyhouse worldwide. Demand for tomatoes is usually strong due to the vine-ripe nature and general overall high level of eating quality.

Selection of the most suitable cultivar is a pre-requisite for successful tomato cultivation in a greenhouse. The important characteristics related to cultivars include high fruit yield, high number of fruits, good shelf life, high TSS, disease resistance and freedom from cracking and green shoulder. Consumer's preference with respect to size, shape and colour of the variety also plays an important role in varietal selection. Although yield and adaptability are the primary concerns of most tomato breeding programmes, there have been several instances of considerable effort to develop cultivars with improved fruit quality. Serious attempts have been made to increase fruit solids content and to alter fruit acid content. Intense effort has been applied for breeding cultivars with improved colour and there have been limited attempts to manipulate genetically the volatile compounds. These efforts have met with varying degree of success; many have had limited success because of the complex interactions between the various components of tomato fruits and between plant and fruit characteristics and fruit composition. The effort needed to screen for fruit composition has been a deterrent to progress on quality.

Open field and protected tomato production differs in their disease problems. Protected cropping is characterized by an extreme monoculture, heavy reliance on chemicals for disease control, a long cropping season and constant handling of the plants. Economic pressures may lead to serious problems involving pH balance, fertility, soil sterilization and general sanitation with concomitant effects on disease development. Covered production, whether under glass or plastic, is typified by such environmental conditions as high humidity, poor circulation and low light intensity. Diseases which are common in tomato are leaf mould, grey mould, late blight, powdery mildew and pith necrosis. Late blight caused by *Phytophthora infestans* attacks both tomato and potato crops. The fungus generally survives on living plant material from potato cull piles, previously diseased crops or wild solanaceous weeds. The disease is most destructive on outdoor tomato crops during warm humid periods. Entire fields can be blighted in a few days. Occasionally covered unheated plantings can also be affected (Jones, 1978). Foliage and fruits appear blighted as though damaged by frost. Affected leaves have irregular dark lesions around which a fine white mould ring develops during wet weather. Brown streaks may occur on stems and petioles. Affected fruit have firm large irregular brownish-green

blotches. The fruit surfaces appear greasy and rough. In warm areas the fungus can survive on volunteer tomatoes, potatoes or solanaceous weeds. In cooler areas tomato transplants or infected potato tubers in cull piles can serve as inoculum sources. Fungal spores can be airborne for up to 30 km. Cool (15-20^{o}C) wet periods are most conductive for late blight infection. Foggy, misty weather or overhead irrigation can provide these conditions. Later the disease develops rapidly during warm humid periods resulting in a severe blighting of the crop in a few days. Rotting of the fruit and foliage can occur quickly with an accompanying foul smell. Resistance to late blight is reported in *Solanum peruvianum* and *S. hirsutum* and is inherited multigenically (Gallegly, 1960). However, resistance to tomato race 0 is conferred by the single dominant gene '*Ph*' (Walter, 1967).

In spite of India's strong quarantine measures, a new insect has entered in India. It has been identified as *Tuta absoluta* (Meyrick) (order Lepidoptera and family Gelechiidae), a native of South America. It has several common names like tomato borer, South American tomato moth, tomato leaf miner and South American tomato pinworm. Outside South America, this pest was reported first in Spain during 2006 (Desneux *et al*., 2011). Since then, it has spread to some European and North African Mediterranean countries, where it has become a serious threat to tomato production in both greenhouse and outdoor conditions (Desneux *et al*. 2010). In India, it was first reported in October, 2014 in Maharashtra (Shashank *et al*., 2015). Subsequently pest was recorded from Karnataka, Tamil Nadu, Andhra Pradesh and Gujarat by different scientists (Sridhar *et al*., 2014; Ballal *et al*., 2016; Kumari *et al*., 2015 and Ballal *et al*., 2016, respectively). Since then alert notice was issued by the Indian Council of Agricultural Research to keep vigil on the incidence of *T. absoluta* in different states. Recently *T. absoluta* was first time reported under polyhouse condition in Uttarakhand by Singh and Panchbhaiya (2018). The pest can produce 10 to 12 generations a year and can lay 250 to 300 eggs by each female in her lifetime. Eggs are cylindrical and creamy white in colour and are laid singly or in small groups on the surface of the leaves, buds, stems and calyx of young fruits. Incubation period is around seven days. Freshly hatched larvae are light yellow to green in colour. As the larvae mature, they turn dark green in colour. The characteristic dark band posterior to the head capsule of the larva help in identifying this pest. There are four larval instars and

the larval period is completed in eight days; the first two instars mine the leaves by feeding on the mesophyll and leaving the epidermis intact, thus creating tunnels on the leaf commonly known as "mines". These mines reduce the photosynthetic surface of the leaves and result in early drying and eventual death of the plant. Later the third and fourth instar larvae leave the mines and bore into stalks, apical buds and fruits. Fruits infested by *T. absoluta* could be identified by presence of characteristic pin holes. The damage generally attracts secondary pathogens leading to fruit rot. Pupation occurs in a silken cocoon, either in the soil or on the leaf surface, within mines or among plant debris. Pupal period lasts for ten days. Adults are silvery brown with black spots on the fore wings. It causes 50 to 100 per cent reduction in yield and fruit quality in greenhouses and fields (EPPO, 2005).

The efficiency of selection largely depends upon the magnitude of variability present in the breeding population. Hence, knowledge of variability present in the gene pool of a crop species is essential to start a judicious breeding programme. Selection is also effective when there is genetic variability among the individuals in population. Earlier variability used to be assessed by visual observation. Now biometrical methods are available for systematic assessment of genetic variability. A quantitative measures which provides information about the correspondence between genotypic variance and phenotypic variance is heritability. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1981). It is the ratio of variance due to hereditary differences to the total phenotypic variance. This ratio is expressed in percentage. If the percentage is large, character is regarded as highly heritable. On the other hand, if it is smaller, environmental agency is considered as mostly responsible for phenotypic manifestation of the character.

Heterosis term was coined by Shull in 1914. Heterosis refers to the superiority of F_1 hybrid in one or more characters over its parents. In other words, heterosis refers to increase of F_1 in fitness and vigour over the parental values. In current usage heterosis and hybrid vigour are used as synonyms and interchangeable. Heterosis can be estimated over mid-parent value (relative heterosis), better parent value (heterobeltiosis) and check parent

(standard heterosis). Generally, positive heterosis is considered as desirable, but in some cases negative heterosis is also desirable (such as earliness, days to first flowering, days from flowering to first fruit setting, days from fruit setting to maturity). Heterosis is confined only to the F_1 generation of a cross and it declines in F_2 and subsequent generations. The first incidence of heterosis in tomato was observed by Hedrick and Booth (1907) for increased yield and number of fruits in tomato. To obtain a high heterotic result, it is important that the parental lines should be genetically diverse.

The concept of general and specific combining ability is of practical importance to the breeders. It is therefore, in the interest of breeders to know how the two combining abilities are related to various components of heritable variations. It helps in the selection of suitable parents for hybridization and in identification of superior cross combinations. Average performance of a genotype in series of hybrid combination is the general combining ability (GCA), whereas average performance of a parent in specific cross combination is the specific combining ability (SCA).

Diallel cross refers to all possible crosses among 'n' lines and the analysis based on the estimation of such a set of crosses is known as diallel analysis. It is extensively used for the evaluation of varieties or strains in terms of their genetic makeup. Diallel analysis provides a sensitive approach for large scale studies of quantitative characters. It yields reliable information on the components of variance and on GCA and SCA variances and effects. Thus it helps in the selection of suitable parents for hybridization as well as in the choice of appropriate breeding procedures. The mating among selected parents may include reciprocal crosses also.

Keeping all above facts in consideration, the present investigation entitled **"Studies on combining ability, molecular diversity and response to late blight (*Phytophthora infestans* (Mont.) de Bary) in tomato (*Solanum lycopersicum* L.) under polyhouse condition"** was taken with following objectives.

1. To estimate the extent of genetic variability for different yield related and quality traits.
2. To assess the molecular diversity of parental lines.

3. To estimate the extent of heterosis over its parents *i.e*. relative heterosis, heterobeltiosis and standard heterosis.
4. To study the combining ability, nature and magnitude of gene action.
5. To screen the parents and F_1 hybrids against late blight (*Phytophthora infestans*).
6. To estimate the percentage fruit damage due to new invasive pest American pin worm (*Tuta absoluta* (Meyrick)) for parents and hybrids.

Review of Literature

Chapter 2 REVIEW OF LITERATURE

In this chapter, an attempt has been made to review the relevant literature of present study **"Studies on combining ability, molecular diversity and response to late blight (*Phytophthora infestans* (Mont.) de Bary) in tomato (*Solanum lycopersicum* L.) under polyhouse condition"** under the following sub-heads:

2.1 Genetic variability for different yield related and quality traits

2.2 Molecular markers for studying the genetic diversity

3.3 Heterosis studies

3.4 Combining ability and gene action studies

3.5 Screening of parents and F_1 against late blight (*Phytophthora infestans*)

3.6 Screening of tomato genotypes against new invasive pest *Tuta absoluta*

2.1. Genetic variability for different yield related and quality traits

As early as 1889, Galton observed that a part of continuous variation is due to heredity. Genetic variability is an obvious feature of considerable importance in crop improvement. It is the basic necessity for any breeding programme to be successful. Vavilov (1951) for the first time perceived the importance of genetic variability and advocate that the wide range of variability provides better scope of selecting desired genotypes.

The degree to which the variability of quantitative character is transmitted to the progeny is referred as heritability. Genetic advance is the product of heritability and infers the potentiality of selection intensity. Genetic advance, when considered along with heritability gives reasonable assessment of the resultant effects of selection in breeding populations (Johnson *et al*., 1955).

Bernousi *et al*. (2011) assessed twenty five tomato genotypes for yield and important morphological traits. Analysis of variance on the studied traits revealed significant differences among genotypes for all the characters except for total soluble solids, titratable acidity and fruit yield. Mean data revealed wide range was present for most of studied traits. Maximum and minimum variability were observed for number of fruits per plant and pH of fruits respectively.

Dar *et al*. (2012) evaluated 60 diverse genotypes of tomato collected from various places. Analysis of coefficient of variation revealed that the magnitude of the phenotypic coefficient of variation was higher than that of the genotypic coefficient of variation for all the seven characters under study. The highest values of the phenotypic coefficient of variation (PCV) were recorded for fruit yield, number of locules per fruit and pericarp thickness. High genotypic coefficients of variation (GCV) were recorded for yield and pericarp thickness. High heritability was recorded for most of the characters.

Islam *et al*. (2012) conducted experiment on 11 cherry tomato inbred lines and observed that nine traits exhibited a wide range of genetic variability. High genotypic and phenotypic coefficients of variation were obtained for individual fruit weight (68.16 and 74.23%, respectively) followed by number of fruits per plant (58.8 and 68.34%, respectively). High estimates of heritability, genetic advance and genotypic coefficient of variation were observed for the traits of individual fruit weight and number of fruits per plant. Fruit yield per plant showed low heritability along with low genetic advance. Among the lines, CH154 produced the highest number of fruits per plant (291) and highest fruit yield (1.89 kg/plant and 63.4 t/ha).

Narolia *et al*. (2012) studied genetic variability, heritability and genetic advance for thirteen quantitative characters in 55 genotypes of tomato. The analysis of variance indicated significant differences among the genotypes for all characters. Variability was high for all the characters studied except days to 50 per cent flowering for which variability was low. High heritability coupled with high genetic advance as per cent of mean was observed for all the characters except days to 50 per cent flowering. High estimates of genotypic coefficient of variation, heritability and genetic advance were recorded for plant height, days to 50 per cent flowering, number of flowers per cluster, number of fruits per plant, average fruit weight, number of locules per fruit, acidity, total soluble solids, ascorbic acid content and fruit yield per plant.

Kumar *et al*. (2013) assessed twenty-six genotypes of tomato to determine the nature and magnitude of variability for yield and yield-contributing characters. The analysis of variance revealed highly significant differences among all genotypes for the characters. The genotype 'EC-357838' had the highest mean value for number of fruit per plant, total soluble solids and yield per plant. High phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and heritability estimates,

coupled with high genetic gain were observed for plant height, number of fruit per plant, yield per plant and fruit weight.

Patil *et al*. (2013) observed significant differences among the progenies of tomato for all the traits under study. The high values of genotypic coefficient of variability and heritability estimates associated with greater values of genetic advance were observed for fruit yield per plant, average fruit weight, number of locules per fruit and height of plants.

Saleem *et al*. (2013) generated twenty-five F_1 hybrids of tomato from 5×5 diallel crosses, were evaluated to study the quantitative genetics of yield and some yield related traits and recorded highest estimates of genotypic and phenotypic coefficients of variability for number of fruits per plant while fruit width was the most heritable trait.

Shankar *et al.* (2013) estimated the genetic variability among tomato genotypes and observed high estimates of PCV and GCV for plant height, number of fruits per cluster, average fruit weight, yield per plant, titratable acidity, ascorbic acid and lycopene. High heritability assisted with high genetic advance as per cent of mean was observed for plant height, number of fruits per cluster, fruit length, fruit width, average fruit weight, number of locules per fruit, pericarp thickness, titratable acidity, ascorbic acid and lycopene.

Agarwal *et al*. (2014) conducted experiment on tomato and found that significant variations for all the traits under study. High estimates of heritability, genetic coefficient of variation and genetic advance were observed for number of fruits per plant and average fruit weight.

Khapte and Jansirani (2014) conducted the experiment with different tomato genotypes to study the genetic variability for yield and yield-contributing traits and observed high heritability for plant height, number of flowers per truss, fruit length, fruit diameter, fruit shape index, pericarp thickness, total soluble solids, average fruit weight, fruit firmness, number of fruits per plant and yield per plant.

Meitei *et al*. (2014) carried out the experiment to study the genetic variability for yield and yield attributes trait in tomato. The pooled analysis of variance revealed significant variation among the genotypes studied for all the characters. High GCV were observed for number of fruit fruits per plant, single fruit weight, fruit yield per

plant and fruit yield per hectare. High heritability coupled with high genetic advance was observed for number of fruits per plant, single fruit weight, fruit yield per plant and fruit yield per hectare. High heritability with moderate to low genetic advance was observed for days to 50 per cent flowering and fruiting, first and last picking, plant height and fruit diameter.

Mukul *et al*. (2014) carried out an investigation to study genetic variability among 16 yield related traits including 30 genotypes of tomato. Genotypic coefficient of variation ranged from 9.35 to 42.02 per cent and highest GCV was observed in fruit yield per plant (42.02%). Heritability in broad sense ranged from 66.00 (number of primary branches) to 90.10 (number of fruits per plant) per cent. High genetic advance was observed for fruit yield per plant (81.95%) coupled with high heritability (89.60%).

Premalakshmi *et al*. (2014) conducted the investigation with fourteen genotypes of tomato to find out the variability for different quantitative traits. The accessions revealed wide variability for all characters evaluated. Phenotypic variances were higher than their respective genotypic variances. High estimates of heritability, genetic advance and genotypic coefficient of variation for the traits of average fruit weight and number of fruits per plant.

Reddy *et al*. (2014) studied variability in 56 exotic lines and 3 check varieties of tomato. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes for all the quantitative characters studied. High phenotypic coefficient of variation and genotypic coefficient of variation were observed for plant height, number of flowers per cluster, number of fruits per cluster, fruit weight and fruit yield. High heritability coupled with high genetic advance were observed for the characters plant height, number of flowers per cluster, number of fruits per cluster, fruit length and fruit weight while, medium heritability coupled with high genetic advance was observed for the trait fruit yield per plant.

Sherpa *et al*. (2014) evaluated seventeen exotic genotypes of tomato and found significant differences among genotypes for all studied properties. Three (CLN2777-E, CLN2777-F and CLN2777-A) high yielding and two (Alisha Craig O gc and Feb-2) having better processing quality genotypes identified in the present study. High heritability coupled with high genetic advance were observed for number of fruits per

cluster, plant height, polar diameter, number of fruits per plant, fruit weight, pericarp thickness, total soluble solids, titratable acidity, ascorbic acid content, lycopene content and fruit yield per plant.

Sharma and Jaipaul (2014) worked out heritability and genetic advance for yield and its components in tomato. Heritability estimates and expected genetic advance were found to be high for plant height, fruit weight, number of fruits per cluster and fruit yield per plant.

Singh *et al*. (2014) evaluated sixteen diverse genotypes of tomato to study the genetic variability, heritability and genetic advance. The analysis of variance revealed significant differences among genotypes for all the traits. Both genotypic as well as phenotypic coefficients of variations were observed high for number of flowers per plant, fruit weight per cluster and number of fruits per plant. Heritability in broad sense was high for plant height, number of flowers per plant, number of locules per fruit and pericarp thickness. Genetic advance in per cent of mean was maximum for number of cluster per plant followed by number of flowers per plant, fruit weight per cluster and number of fruits per plant.

Kumar *et al*. (2015) evaluated twenty genotypes of tomato for study of genetic variability and obtained high estimates of PCV and GCV for number of fruits per plant, plant height, total fruits yield, average fruit weight, number of fruits per cluster and number of locules per fruit. High heritability assisted with high genetic advance as per cent of mean was observed for fruit length, plant height, number of fruits per plant, number of fruits per cluster, number of locules per fruit and 100 seed weight.

Meena *et al*. (2015) found highly significant differences among all tomato genotypes for the characters. Analysis of coefficient of variation revealed that the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits under study. Ascorbic acid recorded highest genotypic and phenotypic coefficients of variation, indicating higher magnitude of variability. High heritability accompanied with high genetic advance was noted for fruit yield per plant, plant height, number of flowers per plant and ascorbic acid.

Prajapati *et al.* (2015) showed significant variation among the genotypes of tomato for all evaluated traits. Number of fruits per plant showed the highest genotypic

and phenotypic variance (1282.0 and 1287.6%) whereas, test weight showed the lowest (0.03 and 0.08%). Genotypic coefficients of variations (GCV) and phenotypic coefficient of variation (PCV) were highest for average fruit weight (48.85 and 48.87%) whereas, the lowest were recorded for days to 50 per cent fruit setting (1.984 and 2.81%). The highest heritability estimates were observed for average fruit weight (99.92%) while, the lowest was for the test weight (45.29%). Highest genetic advance as per cent of mean was recorded for average fruit weight (100.59%) and lowest for days to 50 per cent fruit setting (2.89%).

Pujer *et al.* (2015) evaluated twelve traits of 7 cherry tomato lines. These lines exhibited a wide range of genetic variability. High genotypic and phenotypic coefficients of variation were obtained for average fruit weight (67.76 and 67.90%, respectively) followed by number of fruits per plant (56.45 and 57.28%, respectively). High estimates of heritability, genetic advance and genotypic coefficient of variation for the traits of average fruit weight and number of fruits per plant. Fruit yield per plant showed high heritability along with low genetic advance. Among the lines, L 03686 produced the highest number of fruits per plant (450) and maximum fruit yield (2.2 kg/plant).

Shokat *et al.* (2015) evaluated twenty varieties/hybrids of tomato for genetic heritability and different reproductive traits. Analysis of variance showed significant differences for all the parameters in the tomato germplasm. Estimates of broad sense heritability were found higher for all the characters under study while, expected genetic advance in response to selection was high for days to 50 per cent flowering (19.80%) and fruit setting (25.62%).

Singh *et al.* (2015) assessed the genetic variability among the tomato genotypes and observed high magnitude of phenotypic as well as genotypic coefficients of variation in case of fruit yield per plant followed by average fruit weight, number of locules per fruit, number of fruits per plant and plant height. High amount of GCV and PCV were observed for all the traits except days to 50 per cent flowering, which showed very low variability. High heritability along with high genetic advance in per cent of mean was estimated for all the traits except days to 50 per cent flowering. Fruit yield per plant followed by average fruit weight, number of locules per fruit, number of

fruits per plant and plant height were the top five traits which showed high level of genetic advance.

Ullah *et al.* (2015) observed twenty parental genotypes of tomato for yield and yield attributing traits to measure genetic variability analysis. Analysis of variance for each trait showed significant differences among the genotypes. High genotypic and phenotypic coefficients of variation were recorded for number of fruits per plant, number of locules per fruit and fruit yield per plant. Heritability was observed high for number of flowers per cluster, number of fruits per plant, fruit weight and fruit length. High heritability associated with high genetic advance was observed for number of fruits per plant, fruit weight and number of flowers per cluster.

Ahmad *et al.* (2016) evaluated different tomato genotypes to assess the genetic variability and found that for all the traits PCV value was higher than GCV. Little difference was found among GCV and PCV for the traits like plant height, fruit diameter, fruit size and fruit weight. There is high difference between GCV and PCV for the parameters like number fruit per clusters, number of flowers per cluster and fruit yield per plant. High value of heritability percentage was noted in parameters like plant height (91.34%), fruit diameter (90.22%), fruit size (93.53%), number of fruits per plant (83.69%) and fruit weight (83.69%). Low value of heritability was noted for number of fruits per cluster, number of flowers per clusters and fruit yield per plant. Highest genetic advance (91.94%) was noted for the trait, number of fruits per plant which is coupled with high heritability.

Hasan *et al*. (2016) conducted the experiment with 30 different tomato genotypes to study the genetic variability for yield and yield-contributing traits along with quality traits. Analysis of variances showed high degree of variation existed among the genotypes of the studied traits. Yield contributing traits showed higher phenotypic coefficient of variation as compared to their corresponding genotypic coefficient of variation. Individual fruit weight showed high heritability (99.71%) with high genetic advance (85.4%) followed by number of fruits per plant (99.65 and 81.26%). High heritability but low genetic advance showed in fruit diameter (98.83 and 5.59%), total soluble solid (80.51 and 1.85%) and ascorbic acid content (90.75 and 9.52%).

Kumar and Singh (2016) carried out research work to analyse the variability parameters in twenty five tomato genotypes. Analysis of variation revealed significant differences between the genotypes for all the traits. High genotypic and phenotypic coefficient variation was observed for average fruit weight followed by number of fruits per plant and lowest for days taken to first fruit harvest. High genetic advance was obtained for fruit yield per plant, fruit yield per hectare and plant height.

Kumar *et al*. (2016) carried out experiment with eighteen tomato genotypes including seven cultivars of cultivated tomato, five wild species, three inter specific hybrids and three back cross progenies. The characters that exhibited higher GCV and PCV values for number of fruits per plant, polar diameter, fruit weight, test weight, plant height, number of fruits per cluster, number of locules per fruit, number of flowers per cluster and equatorial diameter. High heritability along with high genetic advance as per cent of mean was observed for the traits like number of fruits per plant, fruit weight and test weight.

Nalla *et al.* (2016) conducted a field experiment on tomato to study the genetic variability, heritability and genetic advance for quantitative and qualitative traits in 27 genotypes including two checks. A high degree of significant variation was observed for all the characters studied except for ascorbic acid and equatorial diameter of fruit. Moderate to high GCV and PCV, high heritability with high genetic advance observed for most of the yield attributing characters. High estimate GCV and PCV was recorded for number of locules per fruit, number of fruits per truss and plant height. High heritability was noticed in characters like total soluble solids, fruit yield per plant and number of fruits per plant. Genetic advance as per cent of mean were recorded very high for number of locules per fruit followed by number of fruits per truss.

Rai *et al.* (2016) carried out experiment and estimated genetic variability among 56 genotypes of tomato. Analysis of coefficient of variation revealed that, the magnitude of phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the studied traits. Further, high estimates of heritability and genetic gain were recorded for number of fruits per plant, average fruit weight, fruit yield per plant and lycopene content.

Kumar *et al*. (2017a) evaluated twenty one diverse thermo tolerant tomato genotypes. Analysis of variance revealed highly significant mean sum of square due to treatment for all the traits. Phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) in all the morphological traits under study and the GCV was very close to PCV for most of the characters. High heritability in combination with high genetic advance as per cent over mean was recorded in fruit yield per plant, fruit pericarp thickness and fruit equatorial diameter.

Kumar *et al*. (2017b) observed wide range of variation for fruit yield and related constituents in tomato. The high PCV, GCV, ECV, heritability (broad sense) and genetic advance over percentage of mean were recorded for fruit yield per plant.

Kumar *et al*. (2017c) evaluated twenty one thermo tolerant tomato genotypes for physiological and biochemical traits. Analysis of variance indicated highly significant mean sum of square due to treatment for all the traits and there was a sufficient amount of genetic variation in all the genotypes under study. Phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) in most of the traits under the experiment. High PCV was observed in the characters *viz*., fruit yield per plant (39.15%) and lycopene content (22.46%) whereas, high GCV was recorded for fruit yield per plant (38.79%) and lycopene content (20.99%). Fruit yield per plant recorded maximum heritability (98.84%) followed by TSS (98%). High heritability coupled with high genetic advance was recorded in fruit yield per plant.

Kaushal *et al*. (2017) revealed significant variation among tomato germplasm for all the characters. Higher phenotypic and genotypic coefficients of variation (PCV and GCV) were observed for average fruit weight, number of fruits per plant and percentage acidity. High heritability coupled with high genetic advance as per cent of mean were estimated for average fruit weight, number of fruits per plant, percentage acidity, pericarp thickness and number of locules per fruit.

Lekshmi and Celine (2017) evaluated fourty tomato genotypes under polyhouse condition and observed wide range of variability among the characters studied for effective selection of superior genotypes. The present appraisal uncovered that PCV and GCV were higher for plant height, number of truss per plant, fruit weight, number

of fruits per plant and fruit yield per plant. High heritability was observed for plant height, fruit weight, fruit girth, number of fruits per truss, number of fruits per plant, lycopene and fruit yield per plant.

2.2. Molecular markers for studying the genetic diversity

Molecular marker technology provides information that can help to define the distinctiveness of germplasm and their ranking according to their close relativeness and their phylogenetic position. It is a complementary approach for genetic characterization.

Benor *et al*. (2008) conducted an experiment to determine the genetic diversity of 39 determinate and indeterminate tomato inbred lines. Using 35 SSR polymorphic markers, a total of 150 alleles were found with moderate levels of diversity and a high number of unique alleles existing in these tomato lines. The mean number of alleles per locus was 4.3 and the average polymorphism information content (PIC) was 0.31. UPGMA clustering at genetic similarity value of 0.85 grouped the inbred lines into four groups.

Kwon *et al*. (2009) investigated genetic characterization of 63 commercial tomato varieties using 33 SSR markers. A total of 132 polymorphic amplified fragments were obtained by using 33 SSR markers. The average polymorphism information content (PIC) was 0.628 ranging from 0.210 to 0.880. One hundred thirty two SSR loci were used to calculate Jaccard's distance coefficients for UPGMA cluster analysis. A clustering group of varieties based on the results of SSR analysis were categorized into cherry and classic fruit type varieties. Almost all of the varieties were discriminated by SSR marker genotypes.

Meng *et al*. (2010) used RAPD and SSR to assess genetic diversity in 61 tomato varieties from different species. 2062 and 869 clear fragments were amplified by RAPD and SSR, respectively. On the other hand, more polymorphic products were found by SSR as compared to RAPD, *i.e*., 100 and 43.84 per cent, respectively. In addition, a higher value of the average similarity coefficient and lower PIC value were reflected in RAPD (0.79, 0.407) compared to SSR (0.56, 0.687).

El-Awady *et al*. (2012) screened ten cultivars of tomato with 20 simple sequence repeat (SSR) primers in order to determine genetic identities, genetic diversity and genetic relationships among these cultivars. On an average, 38 alleles were amplified

using SSR primers with scorable fragment sizes ranging from approximately 75 to 275bp. 23 alleles were polymorphic thus revealing 60.5 per cent of polymorphism. The genetic similarity estimated according to SSR data was scaled between 17.6 and 93.2 per cent. Unweighted pair group method with arithmetic mean (UPGMA) clustering grouped the cultivars into two groups where the two Egyptian cultivars Edkawy and Giza 80 were clustered in different group.

Glogovac *et al*. (2013) assessed genetic diversity using eight microsatellite markers in 30 tomato genotypes. Markers SSR248, TMS9, TMS42 and SSR111 had very high PIC (Polymorphism information content) values.

Sanghani and Mavia (2013) carried out molecular characterization of ten tomato genotypes using SSR markers. From the SSR data it was found that the primer LETTC 002 was the best primer showing good amplification with maximum PIC value (0.749). Jaccard's similarity coefficient ranged from 0.519 to 0.846 and revealed that HADT-145 and NDT-9 showed maximum variability compared to other eight genotypes. The SSR analysis revealed that out of ten genotypes HADT-145 and NDT-9 showed maximum similarity (73.7%). The lowest similarity of 58.1 per cent was found between GT-1 and JTL-04-108.

Sardaro *et al*. (2013) measured genetic diversity present in 47 most common tomato varieties using 11 micro-satellite markers. Among the markers used, a total of 48 alleles were detected. A dendrogram based on total microsatellite polymorphism grouped 47 varieties into three major clusters at 0.75 similarity coefficient.

Korir *et al*. (2014) examined the genetic diversity and relationship of 42 tomato varieties with EST-SSR markers. The genetic diversity was between 0.18 and 0.77 with a mean of 0.49 and polymorphic information content ranged from 0.17 to 0.74 with a mean of 0.45. Based on the cluster analysis using unweighted pair-group method with arithmetic average (UPGMA), all the tomato varieties fell into 5 groups.

Singh and Goswami (2014) carried out molecular diversity in all 24 genotypes landrace collections of tomato and genotypes were screened with twenty SSR primers. On the basis of resolving power, primer A-8, A-13 and A-19 were most significant as they are able to recognize all 24 genotypes. The gene diversity was varied from 0.65 to 0.97 values with a mean diversity of 0.84. On an average, 54 scorable and reproducible

alleles were amplified using all primers. Cluster analysis clearly showed the genetic diversity among the genotypes under study.

Singh *et al*. (2015) carried out studies on molecular diversity in 24 genotypes of tomato. Sixteen SSR primers were used to identify the genetic diversity. On an average, 52 scorable and reproducible alleles were amplified using all primers. Cluster analysis clearly showed the genetic diversity among the genotypes under study.

Zhou *et al*. (2015) used molecular markers to assess the genetic diversity of 29 cultivated tomatoes, 14 wild tomatoes and seven introgression lines. Fifteen polymorphic genomic simple sequence repeat (genomic-SSR) and 13 polymorphic expressed sequence tag-derived SSR (EST-SSR) markers amplified 1115 and 780 clear fragments, respectively. Genomic-SSRs detected a total of 64 alleles, with a mean of 4 alleles per primer while, EST-SSRs detected 52 alleles with a mean of 4 alleles per primer. The polymorphism information content was slightly higher in genomic-SSRs (0.49) than in EST-SSRs (0.45). The mean similarity coefficient among the wild tomatoes was lower than the mean similarity coefficient among the cultivated tomatoes. The dendrogram based on genetic distance divided the 50 tomato genotypes into eight clusters..

Gharsallah *et al.* (2016) evaluated tomato genotypes and observed that genotyping cultivars using 19 polymorphic SSRs out of 25 tested produced a total of 70 alleles with an average of 3.68 alleles per locus and PIC values ranging from 0.22 (SSR26, SSR92, SSR66 and TG35) to 0.82 (SSR 356).

Gongolee *et al.* (2016) studied molecular diversity in five tomato varieties and genetic characterization of introduced tomato varieties were investigated using 15 SSR markers. Out of 15 markers, 14 gave polymorphic bands. The number of alleles ranged from 2.00 (SSR2), (SSR3) to 6.00 (SSR9 and SSR11) alleles per locus with a mean value of 4.07 alleles per locus. The average Polymorphic Information Content (PIC) value was 0.59 ranging from 0.31 (SSR2) to 0.77 (SSR9). The most polymorphic primers were SSR9, SSR11 and SSR4 based on PIC values. The Agglomerative hierarchical clustering grouped the tomato varieties into two (A & B) clusters. At a coefficient of 0.88, cluster B had three sub-clusters BI (Heinz), BII (Shasta) and BIII (OP-B155 and CRI-P00). At a coefficient of 0.90 varieties OP-B155 and CRI-P00 were identified as the most genetically related varieties.

Kumar *et al.* (2016a) conducting the experiment to study the genetic variation of 15 cherry tomato genotypes started with the screening of polymorphic microsatellite markers. From the identified 10 polymorphic SSR markers, a total of 142 polymorphic amplified fragments were obtained. The average polymorphism information content (PIC) was 0.987 and ranging from 0.958 (SSR-47) to 0.996 (SLM6-18). One hundred fourty two SSR loci were used to calculate Jaccard's distance coefficients for UPGMA cluster analysis. The generated dendrogram of 15 cherry tomato genotypes showed low level of similarity among these genotypes. Two major clusters were generated at 23 per cent level of similarity level. The major cluster A consists of five genotypes whereas major cluster B consists of rest of 10 genotypes. The result also showed that, maximum, 89 per cent of similarity was found between Cherry T-1×Co-3-2 and Cherry T-4 × Pant T-3 genotypes.

Kumar *et al.* (2016b) studied genetic variation of 19 genotypes of tomato started with the screening of polymorphic microsatellite markers. From the identified 11 polymorphic SSR markers, a total of 261 polymorphic amplified fragments were obtained. The average polymorphism information content (PIC) was 0.990 ranging from 0.979 (SSR-110) to 0.995 (SSR-253). Two hundred sixty one SSR loci were used to calculate Jaccard's distance coefficients for UPGMA cluster analysis. The generated dendrogram of 19 tomato genotypes showed low level of similarity among these genotypes. Two major clusters were generated at 43 per cent level of similarity. The cluster A consists of two genotypes whereas cluster B consist of rest of 17 genotypes. The results also showed that the genotypes Arka Vikas and 2012TODVAR-2 were 100 per cent similar.

Raveendar *et al.* (2016) determine the genetic diversity and population structure of 355 tomato accessions from Asia using 18 simple-sequence repeats (SSRs). A total of 176 alleles were detected at an average of ten alleles per SSR locus. The average major allele frequency and polymorphic information content were 0.69 and 0.39, respectively.

Aguirre *et al.* (2017) assessed the genetic diversity of 30 introductions of cherry tomato with 36 microsatellite molecular markers. A dendrogram was built using the Dice-Nei and Li similarity index and the UPGMA clustering method. A coefficient of genetic differentiation was found (Fst = 0.3474), showing a high genetic differentiation

of the introductions; those from Brazil, Ecuador, and Peru were the most genetically diverse, presenting 100 per cent of polymorphic loci. The molecular variance analysis indicated a variation of 11 per cent between the groups and 89 per cent within the same.

Kanjariya *et al*. (2017) assessed genetic variability in 15 germplasm (seven different species) of tomato using a combination of qualitative and molecular data. The joint dissimilarity matrix showed moderate correlation with the original matrices of quality and molecular data. However, the correlation between the qualitative dissimilarity matrix and the genotypic dissimilarity matrix was low. Diversity varied from 0 to 1.43 among the 15 germplasm, with an average dissimilarity among genotypes of 0.62. Joint analysis of qualitative and molecular diversity indicated that the genetic diversity of the tomato germplasm was 174 per cent and 69 per cent higher than the diversity estimated from qualitative and molecular data, respectively.

Rosy *et al.* (2018) analysed molecular diversity among 21 genotypes of tomato using nine SSR primers and total number of amplicons obtained was 33 with three unique bands. Total polymorphism across genotypes was 100 per cent. Genetic similarity matrix, based on Jaccard's coefficients, ranged from 3.85 per cent to 73.17 per cent indicating a wide genetic base.

Choudhary *et al.* (2018) evaluated the genetic diversity of 24 genotypes of tomato using 25 simple-sequence repeats (SSRs). A total of 64 alleles were detected at an average of 2.720 alleles per SSR locus. The average major allele frequency and polymorphic information content were 0.6622 and 0.3875, respectively. The UPGMA cluster analysis induced by SSRs data grouped 24 tomato genotypes into 3 main clusters. Cluster I and II comprised 15 and 8 genotypes respectively and a single tomato genotype CO-3 was grouped in cluster III.

2.3 Heterosis Studies

The term heterosis refers to the natural phenomenon in which F_1 hybrid obtained from crossing of genetically diverse individuals out-perform over their parents in multiple traits including better adaptability, yield and resistances to biotic and abiotic stresses (Fu *et al.*, 2015 and Shull, 1948). Heterosis in crop species can be seen in terms of decrease in growth rate, total biomass, stress resistances, seed yield and population fitness (Kalloo *et al*., 2006).

The exploitation of hybrid vigour in tomato has received greater importance on account of several advantages of hybrids over pure line varieties with response to better adaptability, marketable fruit yield and resistance to biotic and abiotic stresses.

Hedrick and Booth (1907) were the first to notice heterosis in tomato. But, the use of F_1 hybrids for boosting tomato production was first advocated by Wellington (1912) and Daskaloff (1932). In Bulgaria heterosis breeding work was started and developed the first F_1 hybrid in tomato which quickly became popular because of earliness and higher yield. After Second World War popularity of tomato F_1 hybrids extended quickly to the European countries, USA and Japan (Yordanov, 1983). In India, 1973 first release of tomato hybrid namely 'Karnataka' was introduced by Indo-American Hybrid Seeds (IAHS), Bangalore for commercial cultivation (Anonymous, 2000).

Kurian *et al.* (2001) studied heterosis for yield components and fruit characters for different tomato varieties. Heterotic hybrids were identified for average fruit weight (Sakthi x Fresh Market 9 and Sakthi x HW 208F), fruit yield per plant (Sakthi x TH 318 and Sakthi x Fresh Market 9), number of locules per fruit (LE 206 x Ohio 8129 and LE 214 x St 64) and pericarp thickness (Sakthi x St 64, LE 206 x 64 and LE 214 x St 64).

Joshi *et al.* (2005) estimated extent of heterosis in tomato and revealed that amongst crosses, H-711492 x 101 and 260 x V-16 exhibited the maximum heterosis over better parent for whole fruit firmness and pericarp thickness, respectively.

Hannan *et al.* (2007) conducted study on a 10×10 diallel set of tomato excluding reciprocals to find out the extent of heterosis for yield with important quality traits. Positive high significant heterosis was found for fruit yield (211.00, 232.00 and 298.00%), for brix % (61.04, 106.70 and 37.76%) and for days to first flowering (8.92, 9.33 and 6.07%) over the mid, better and standard parent, respectively.

Rao *et al.* (2007) conducted study for estimation of heterosis in tomato. Based on the heterotic performance in desirable direction for yield and its related attributes, Feb-2 x Pusa Sheetal and Feb-2 x Pusa Gaurav were found to be the best in terms of yield potential. Further, these hybrids being determinate and early in nature are suitable under short season conditions.

Gul *et al.* (2010) conducted a study in tomato using an 8 × 8 diallel set excluding reciprocals to quantify the magnitude of heterosis for yield and its five yield

components. Highly significant relative heterosis and heterobeltiosis of positive nature was found for number of flowers per cluster, number of fruits per cluster, fruit length, fruit weight and fruit yield per plant. Positive significant relative heterosis and heterobeltiosis was observed for number of flowers per cluster, number of fruits per cluster, fruit length, fruit width, fruit weight and fruit yield per plant. Four hybrids possessed significantly useful heterobeltiosis for fruit weight.

Shalaby (2012) studied heterosis in tomato. Analysis of variance revealed highly significant differences among all the F_1 hybrid means and their respective six parental values for all examined traits. Positive heterosis over better parent was observed in some crosses for most of studied characters except average fruit weight, which had negative values. Heterosis over better parent ranged from 12.7 to 66.2 per cent for total fruit yield.

Farzane *et al.* (2013) examine the extent of heterosis in a complete diallel crosses design (9×9) of nine tomato lines. The crosses Sps×Mb3, Vfj×Pte12 and Prg ×Supc were the earliest hybrids among 72 hybrids studied. The heterosis showed a good response to number of days to 50 per cent, seed emergence and days to first inflorescence.

Narasimhamurthy *et al.* (2013) crossed ripening tomato mutants with commercially grown varieties such as 'Pusa Ruby', 'Sankranti' and 'Vaibhav'. The highest heterotic effect over better parent was exhibited by the crosses 'alc × Vaibhav' for fruit keeping quality and 'rin × Vaibhav' for fruit yield per plant.

Yadav *et al.* (2013) estimated magnitude of heterosis and its variances in tomato. The most promising crosses showing significantly standard heterosis for maximum yield were CO-3 × Arka Vikas, CO-3 × NDT-5, NDTVR-60 × NDT-5 and RCMT-1 × NDT-5.

Agarwal *et al.* (2014) crossed eight parental lines of diverse origin of tomato in 8 × 8 diallel mating design excluding reciprocals. The highest significant heterosis over better and standard parent was recorded for average fruit weight (74.69 and 117.27%) followed by total soluble solids for better parent heterosis. The range of heterosis for fruit yield over better parent was 6.63-35.90 per cent and cross between CLN 5915-206 × CLN 1314G recorded the maximum heterosis over both better (35.90%) and standard parent (56.32%) for the trait.

Amaefula *et al.* (2014) estimated heterobeltiosis for the hybrids and showed that the Wild × Petomech cross had the highest positive heterobeltiosis of 358.36 per cent in fruit yield. The highest negative heterosis of -95.59 per cent was recorded for the hybrid Wild × Grosso in average fruit weight while, the hybrid Insulata × Grosso had the lowest negative heterosis of -16.27 per cent in average fruit weight.

Chauhan *et al.* (2014) developed twenty eight hybrids of tomato using eight parents in half diallel fashion for estimation of heterosis for yield and its attributing traits. Hybrids Pusa Gaurav x Taiwan, Pusa Rohini x Pusa Gaurav and Pusa Rohini x Roma were found most promising for yield and its contributing traits. These hybrid exhibited heterosis to the tune of 48.14 per cent, 44.47 per cent and 73.41 per cent over better parents and 83.43 per cent, 76.78 per cent and 74.24 per cent, respectively over the check cultivar for fruit yield per plant. The cross combination Pusa Gaurav x Taiwan expressed highest significant standard parent heterosis and SCA estimates for yield and its attributing traits.

Cheema *et al.* (2014) carried out investigation in tomato using ten lines, 45 crosses and hybrid check TH-1. Heterosis was observed for almost all the characters. The best performing crosses were Acc.No.2 x Acc.No.3 for total yield, number of fruit per plant, fruit weight, harvesting span, titratable acidity and lycopene content and Acc.No.2 x Acc.No.5 for total yield, number of fruits per plant, harvesting span, TSS, titratable acidity and lycopene content. Acc.No.2 x Acc.No.8 for total yield, number of fruits per plant, titratable acidity and lycopene content and Acc.No.6 x Acc.No.10 for total yield, number of fruits per plant, TSS and lycopene content. All these crosses also expressed maximum heterosis over respective better parent for these traits. The combination Acc.No.1 x Acc.No.9 and Acc.No.4 x Acc.No.6 had maximum fruit yield of 2.97 kg and 2.93 kg per plant and it showed 63.19 and 85.44 per cent increase over better parent, 67.80 and 65.54 per cent respectively increase over the standard check.

Mali and Patel (2014) conducted experiment on diallel analysis in tomato to study the magnitude of heterosis in tomato for fourteen characters including fruit yield and its related components. The experimental material comprising of five genetically diverse parental lines and their twenty hybrids (including reciprocals). Significant differences among genotypes were obtained for all the traits. In order of merit, the five promising hybrids *viz.,* NTE 2 x NTE 3, NTE 2 x NTE 4, NTE 2 x NTE 1, NTE 1 x

NTE 5 and NTE 1 x NTE 2 exhibited standard heterosis range of 104.40 to 201.19 per cent and 90.15 to180.20 per cent over commercial checks, GT 2 and JT 3, respectively.

Shankar *et al.* (2014) studied heterosis for yield and quality in tomato of 24 F_1 hybrids. The resultant 24 F_1s were evaluated along with their parents and two standard checks for yield and quality characters. The hybrids exhibited high *per se* performance and also showed high standard heterosis. The cross LE-62 × Arka Vikas registered high negative standard heterosis for days to 50 per cent flowering. The potential crosses like LE-64 × Arka Vikas, LE-53 × Arka Alok, LE-53 × Arka Meghali, LE-64 × Arka Meghali and LE-62 × Arka Alok exhibited high standard heterosis and high *per se* performance for yield per plant. Among promising hybrids for yield per plant the crosses LE-53 × Arka Alok for TSS and titratable acidity, LE-53 × Arka Meghali for titrable acidity and lycopene content and LE-64 × Arka Meghali for titratable acidity and ascorbic acid showed significant standard heterosis.

Sherpa *et al.* (2014) studied the extent of heterosis and dominance behaviour of fifteen yield components and post harvest quality traits in tomato. All 9 F_1 hybrids had significantly higher number of fruits per cluster over both mid-and better-parental values while, for the other traits, hybrids expressed average heterosis in both directions. The maximum extent of heterobeltiosis (53.56%) was found in lycopene content of fruit followed by number of fruits per cluster (32.59%) and fruit yield per plant (31.77%).

Dagade *et al.* (2015) generated a set of 28 crosses by crossing eight inbred lines of tomato. Significant genetic differences were observed among the parents, F_1 hybrids and F_2 populations for all the characters under study. The cross GT 1 x H 24 exhibited higher heterobeltiosis as well as standard heterosis. The cross, Pusa Ruby x Arka Vikas had stable performance in both generations.

Figueiredo *et al.* (2015) estimated the heterosis in industrial tomato genotypes for the identification of those with good potential for breeding programs. Ten lines of industrial tomato, 45 hybrids derived from a complete diallel and two commercial check cultivars were evaluated. The parent lines RVTD-04, RVTD-10 and RVTD-08 had an exceptionally high presence of favorable alleles for most traits. High genetic divergence between the parents was observed, contributing positively to significant heterosis values.

Pandey and Mall (2015) carried out heterotic performance of 44 hybrids and their parents including check in tomato. The most worthy common crosses selected on the basis of *per se* performance, heterobeltiosis and standard heterosis for different traits in Bilahi-2 x H-86 and Himlata x H-86 for total yield, MM x H-88 and KS-60 x H-24 for number of fruits per plant in E2, MM x H-86 and MM x H-88 for average fruit weight in E1 and EC 168282 x H-24 in E2 for length of fruits, Himlata x H-88 in both experiment and NDT-2 x H-88 in E2 for diameter of fruits and Himlata x H-86 in E1 and NDT-2 x H-86 in E2 for early yield per plant. However, for agronomical traits, Bilahi-2xH-86 in both environments for plant height as well as number of primary branches per plant was observed as valuable cross combination. Promising hybrid identified for the characters important to processing and quality point of view, were MM x H-88 in both environments for total soluble solids; EC 2291-2 x H-88 in both environments for ascorbic acid content and EC 7343 x H-24 in E1 and Bilahi-2 x H-88 in E2 for pericarp thickness. However, none of the crosses were common for titratable acidity in both the environments in relation to above three parameters *i.e. per se* performance, standard heterosis and heterobeltiosis.

Samiyoddin *et al.* (2015) studied heterosis in genotypes of tomato for number of locules, pericarp thickness, total soluble solids, pH of fruit juice, lycopene and ascorbic acid. AR 21 x Arka Vikas, AR 29 x PKM 1, AR 56 x PKM 1 and Podlandt Pink x Arka Alok are good cross combinations for fruit yield per plant. Tommy Toe x Arka Vikas and AR 29 x Arka Vikas are early to flower and the crosses AR 4 x PKM 1 and AR 21 x PKM 1 are good hybrids for lycopene whereas, AR 56 x PKM 1 and AR 21 x Arka Vikas are good hybrids for TSS.

Savita and Singh (2015) evaluated fourty three entries consisting of thirteen diversified genotypes of tomato along with their thirty F_1 hybrids. Highest significant heterobeltiosis was expressed by the F_1 hybrids Selection 06-01 × Punjab Chhuhara (for TSS at immature and turning stage), Selection 06-01 x PT-3 (for TSS at red ripe stage), CLN2070A × PT-3 (for number of locules per fruit) and CLN2070A × Sweet-72 (for pericarp thickness).

Vilas and Rana (2015) studied the impact of heterosis on yield components and quality characters of 50 F_1 hybrids of tomato. In this study, among crosses, the best cross combinations in favourable direction were observed for EC 620383 x Punjab

Chhuhara. The line, Punjab Varkha Bahar-2 and cross EC 620533 x Arka Vikas recorded significantly maximum heterosis for number of fruits per truss. The cross BBWR-11-1 x Palam Pink recorded higher number of fruits per plant and the cross EC 620391 x Punjab Chhuhara, the line Punjab Varkha Bahar-2 and tester Arka Meghali recorded the maximum total fruit yield per plant compared to standard checks. The highest TSS was noted in line EC 620445 and tester Hisar Meghali had more TSS than the check variety Hisar Arun. Among crosses, the cross EC 620534 x Arka Vikas recorded the highest TSS manifesting higher heterosis for TSS.

Bharathkumar *et al.* (2016) revealed that the tomato hybrids IIHR977 × IIHR2890 and IIHR2891 × IIHR2853 were best heterotic hybrids for early fruit maturity over both the commercial checks in tomato genotypes whereas, hybrids namely IIHR1816 × IIHR2852, IIHR1816 × IIHR2890, IIHR2848 × IIHR2853, IIHR2850 × IIHR2852, IIHR2891 × IIHR2852 and IIHR2892 × IIHR2890 exhibited significant heterosis for early blight resistance and yield per hectare over Abhinav. IIHR1816 × IIHR2853 and IIHR1816 × IIHR2852 that exhibited highest significant heterosis of 68.96 and 52.93 per cent, respectively over check Abhinav.

Biswas *et al.* (2016) developed ten tomato hybrids from half diallel crossing fashion among five parental lines of tomato. Significant better parent heterosis was found for all characters except days to first harvest. The maximum better parent heterosis for number of fruits per plant was observed for the cross combination of C51 × C71 (85.12%) followed by C41 × C11 (67.10%). The highest heterosis for individual fruit weight was recorded (69.31%) from FP5 × C71. The highest positive significant heterosis for pericarp thickness was found for the cross combination of C41 × C71 (60%) followed by C11 × C71 (46.25%). Positive and significant heterosis for TSS (%) was estimated from the cross C11 × FP5 (8.7%). All the cross combinations showed positive and significant heterobeltiotic effect for fruit yield per plant of which C41 × FP5 exhibited the highest heterosis (203.22%) closely followed by C41 × C51 (183.33%).

Jose *et al.* (2016) estimated magnitude of heterosis including 21 F_1 cross combinations in tomato. The most promising crosses showing significantly standard heterosis for maximum yield were AVTO-9 x GT-2, AVTO-1 x JT-3, AVTO-6 x AT-3, AVTO-9 x AT-3 and AVTO-9 x JT-3. The results suggest a high degree of variability and heterosis in positive direction among the crosses.

Kumar *et al.* (2016) crossed six diverse parental lines of tomato in a 6 × 6 diallel mating design excluding reciprocals. Significant positive heterosis over mid parent, heterobeltiosis including standard heterosis for both the check was observed in desirable direction for most of the traits. Seven cross combination over the mid parent, five crosses over better parent, two cross over commercial check (HYB-Roop-666) and six crosses over the commercial check (TS-15) exhibited positive and significant heterosis for fruit yield per plant. The cross Punjab Chhuhara x Best of All exhibited maximum heterosis over the mid parent (34.73%), better parent (31.82%), the cross Arka Abha x Punjab Chhuhara over commercial check HYB-Roop-666 (19.03%) and over commercial check TS-15 (34.44%) for fruit yield per plant.

Kumar and Gowda (2016) studied the extent of heterosis in tomato. The highest heterotic effect over mid parent was exhibited by the cross Vaibhav x RIL-160, Arka Alok x RIL-160 and Arka Alok x RIL-108 for both characters.

Marbhal *et al.* (2016) evaluated twenty one F_1s of tomato, their seven parents and a commercial hybrid *viz*., Suncherry Extra Sweet. Significantly highest positive heterosis was recorded for height of plant by the hybrid 4 x 6 (24.74 %) over better parent, number of fruits per cluster by 3 x 6 (25.00%) over better and top parent, number of clusters per plant by 3 x 6 (24.91%, 22.82%, 101.10%) over better, top parent and commercial hybrid, respectively and fruit yield by 2 x 6 (46.52%) and 1 x 3 (38.25%) over better and top parent, respectively.

Sahu *et al.* (2016) determined heterotic cross combinations in tomato and obtained heterobeltiosis and standard heterosis for fruit yield and its components. Hybrid RCMT-1/DVRT-2 and JTP-02-07/DVRT-2 for days to 50 per cent flowering, RCMT-1/CO-3 for number of fruits per plant, Pant T-8/ DVRT-2 and JTP-02-07/DVRT-2 for average fruit weight (g) and Local-2/DVRT-2 for total fruit yield per plant (kg) were reported promising on the basis of all types of heterosis. However the highest heterobeltiosis was observed in Improved Shalimar/CO-3, Local-2/DVRT-2 and Pant T-8/DVRT-2 and standard heterosis in Local-2/DVRT-2 and Pant T-8/DVRT-2 for total fruit yield per plant. A high degree of heterosis for other traits in desired direction was also observed.

Sankhla *et al.* (2016) conducted the study on diallel analysis in tomato to study the magnitude of heterosis for twenty characters including fruit yield and its related

components. The experimental material comprised six genetically diverse parental lines and their thirty hybrids (including reciprocals). Significant difference among genotypes was obtained for all the traits. In order of merit, the promising hybrids *viz.*, AVTO-2 x JTL-08-15, NTL-1 x JTL-08-15, NTL1 x AVTO-2 and AVTO-2x NTL-50 exhibited standard heterosis range of 23.79 to 68.62 per cent over commercial check, Abhinav.

Amin *et al.* (2017) estimated heterosis in tomato among 45 F_1 hybrids for yield and related traits. The most desirable cross combination *viz.*, KS-227 x Roma for fruit yield per plant also showed desirable better parent heterosis for days to first picking and fruit size. The cross combinations DVRT-1 x S-II (average fruit weight), Arka Vikas x KS-227 (plant height), Marglobe x Roma (flesh thickness), KS-227 x Roma (number of fruits per plant), VLT-32 x Roma (total soluble solids) and VLT-32 x Shalimar-I (vitamin C) showed highest better parent heterosis. These cross combinations also revealed high *per se* performance.

Kumar *et al.* (2017a) studied heterosis for yield components and yield per plant using 8 x 8 half diallel cross in tomato. Heterosis for yield per plant ranged from -25.57 (P7 x P8) to 43.81 (P6 x P8) per cent over better parent and heterosis over standard variety NDTP-4 (SV-1) varied from -52.19 (P1 x P6) to 60.80 (P4 x P7) per cent and heterosis over standard variety NDTP-7 (SV-2) varied from -59.23 (P1 x P6) to 37.13 (P4 x P7) per cent respectively. Significant heterosis over better and standard varieties was observed for all the traits. Five crosses P4 x P7, P5 x P7, P1 x P7, P2 x P7 and P3 x P7 showed standard heterosis for fruit yield per plant, also found significant over better parents with the different magnitude. Out of top three heterotic F_1 with the attractive fruit shape crosses P4 x P7, P1 x P7 and P5 x P7 which also found maximum fruit weight and high number of fruits per plant and also identified for developing high-yielding F_1 hybrids of tomato.

Panchal *et al.* (2017) evaluated fourty tomato genotypes (11 parental genotypes, 28 F_1 hybrids and one commercial check- Abhinav) in order to estimate the extent of heterosis and quality traits. In which, significant differences among genotypes were obtained for all the traits. In the present investigation, mid parent heterosis ranged from -45.31 to 182.20 per cent, better parent ranged from -53.23 to 127.18 per cent and standard heterosis -0.79 to 295.83 per cent for fruit yield. The maximum standard heterosis recorded by cross JTL-12-12× JT-3 was 295.83 per cent, followed by NTL-1

× AT-3 (273.39%), JTL12-12 × GT-2 (196.52%), JTL-12-12 × AT-3 (177.53%), NTL-1 × JT-3 (160.31%), JTL-12-10 × GT-2 (156.80%) and JTL-12-11 × GT-2 (155.55%). Positive significant heterosis was found for all the traits.

Gautam *et al.* (2018) evaluated 6 x 6 diallel cross excluding reciprocal of tomato with parents for heterotic manifestation of yield and yield attributing characters. The heterosis over better parent to the extent of -14.64, -7.70, 15.84, 21.29, 15.30 and 38.91 per cent was recorded for days to first flowering, days to marketable maturity, average fruit weight, number of fruits per plant, harvest duration, fruit yield per hectare and plant height, respectively. Three promising crosses *viz*., UHFT-9 x Solan Lalima, UHFT-10 x Solan Lalima and UHFT-22 x Solan Lalima were identified for developing high yielding F_1 hybrids of tomato with many desirable horticultural traits.

2.4 Combining ability and gene action studies

Combining ability studies provide more reliable useful information for the selection of parents in terms of performance of the hybrids and elucidate the nature and magnitude of various types of gene actions involved in the expression of quantitative traits. The information obtained from general combining ability of parents and specific combining ability of crosses helps us to select the suitable parents and related cross combinations, respectively.

In general combining ability (GCA), genes with additive effects are most important while, specific combining ability (SCA) is more dependent on genes with dominance and epistatic effects. Allard (1960) stressed the need of studying the combining ability in case of self pollinated crops by stating that phenotypically equal promising parents do not always produce superior progenies in segregating generations while, certain combinations mix well and give superior segregants. The information on the nature and magnitude of gene action is of vital importance in breeding a better type.

Joshi *et al.* (2005) conducted an experiment on tomato to estimate the combining ability for different traits and revealed that FT-5, 102, Magna and Cal-ace were good general combiners for fruit firmness, number of locules per fruit and pericarp thickness while, V-16 was good general combiner for all the characters except number of locules per fruit. The ratio of GCA/SCA variances observed less than unity for all the characters, depicting the predominance of non additive genetic variance.

Joshi and Kohli (2006) obtained 45 cross combinations from crossing 10 diverse lines of tomato in half-diallel fashion. Line EC-401927 appeared to be good general combiner for ascorbic acid content. The crosses UHF-II x EC-401927 and CLN5915-206D4-2-2-0 x FT-5 exhibited highest SCA estimates for total soluble solids and number of locules, respectively. However, the combination CLN1462A x FT-5 gave significant SCA estimates in desirable direction for ascorbic acid contents and stem end scar size in tomato. Heritability estimates in narrow sense was observed low for total soluble solids, ascorbic acid content, fruit shape index and stem end scar size.

Mondal *et al.* (2009) estimated combining ability in tomato for fruit yield, yield components and fruit quality traits. Involvement of both additive and non additive gene action was operative for the control of number of fruits per plant, fruit weight, number of locules per fruit and equatorial diameter of fruit. All the fruit quality characters like, TSS and lycopene contents of the fruit were governed by non additive gene action. Taking into consideration the *per se* performance, heterosis and SCA effect in the hybrid, H-24 × NF-31 and H-24 × Hissar Arun were the best hybrids.

Farzane *et al.* (2012) conducted experiment on a 10 × 10 diallel cross set of tomato including reciprocals to find out the combining ability for fruit yield per plant, yield components and number of locules per fruit. Significant differences among genotypes were obtained for all of traits. The variances for general combining ability (GCA) and specific combining ability (SCA) were highly significant indicating the presence of additive as well as non-additive gene effects except the number of fruits per plant and relative magnitude of these variances indicated that additive gene effects were more prominent for all of the traits. The tomato genotype Mb3 proved to be the best general combiner for fruit yield and number of fruits per plant.

Shalaby (2012) studied combining ability in tomato. The mean squares due to general combining ability (GCA) and specific combining ability (SCA) were also highly significant. Among parents, Peto86 and CLN2498E proved the best combiners for plant height. The parents Peto86 and CLN2400A were the best combiners for earliness and total fruit yield while, CastleRock cv. was the best combiner for average fruit weight and fruit firmness. The best specific cross combinations were CastleRock x CLN 2123, CastleRock x CLN2400B, Peto 86 x CLN2400A and Peto 86 x CLN2498E for total yield per plant.

Narasimhamurthy *et al.* (2013) crossed ripening tomato mutants with commercially grown varieties such as 'Pusa Ruby', 'Sankranti' and 'Vaibhav'. The analysis of variance revealed the predominance of non-additive gene action for all the traits. In respect of both GCA and SCA effects, the parents and hybrids differed significantly. Among the parents, 'Alcobaca' and 'Vaibhav' were the best general combiners for fruit keeping quality. Between the crosses, 'Alc × Vaibhav' is a valuable combiner for fruit keeping quality and yield characters under study.

Nadeem *et al.* (2013) evaluated twenty one genotypes of tomato. All traits showed considerable genetic variation with variable environmental influence. Additive gene action was involved in expression of days to 50 per cent flowering, vine length, number of fruits per plant and fruit weight. Dominance played major role for lycopene contents.

Shankar *et al.* (2013) studied combining ability effects and gene action in tomato for yield and yield contributing traits. The analysis of variance revealed that the variance were highly significant for all the traits under study. The magnitude of SCA variance was greater than GCA variance suggesting the predominance of non additive gene action for number of fruits per cluster and yield per plant. Based on GCA effects of parents, the line LE-53, LE-64 and the tester Arka Alok were found to be good general combiners for most of the traits. The crosses EC-157568 x Arka Vikas, EC-163611 x Arka Alok, LE- 62 x Arka Alok and LE-64 x Arka Vikas were found to be superior specific combinations on the basis of yield per plant performance.

Yadav *et al.* (2013) estimated magnitude of combining ability effects and its variances in tomato. Ratio of general combining ability (GCA) and specific combining ability (SCA) variance revealed preponderance of non-additive genetic variances for all studied traits. On the basis of GCA effects across ten traits, Potato Leaf, Pant T-7, IC-177371 and NDTVR-60 were identified as most promising parental lines for inclusion in hybridization programmes. Outstanding crosses based on SCA effect across ten traits were RCMT-2 × VR-20, LCT-6 × VR-20 and Azad T-5 × VR-20.

Agarwal *et al.* (2014) crossed eight parental lines of diverse origin of tomato in 8 × 8 diallel mating design excluding reciprocals. Significant and highest general combining ability effect for fruit yield and average fruit weight was recorded in CLN

5915-206 (49.06 and 8.23 respectively), for total soluble solids in CLN 2264H (0.18) and for dry matter content in Best of All (0.32). Genotype with positive and moderately high GCA for dry matter (Pith Sel, DARL-1 and Best of All) and TSS (CLN 2264H and DARL-1) exhibited good specific combining ability for exploiting hybrid vigour for these traits.

Cheema *et al.* (2014) carried out investigation in tomato using ten lines, 45 crosses and hybrid check TH-1. Analysis of variance for combining ability revealed that mean squares due to general and specific combining ability were highly significant for all the characters studied. Parents Acc.No.4, Acc.No.9, Acc.No.5 and Acc.No.1 were best general combiners for most of the traits. The crosses Acc.No.2 x Acc.No.8, Acc.No.2 x Acc.No.5 and Acc.No.7 x Acc.No.10 were best specific combiner for fruit weight, total yield, lycopene content, titratable acidity and TSS.

Rattan and Bindal (2014) studied combining ability in indeterminate tomato. Analysis of variance for combining ability exhibited significance of females and males for yield, number of fruits per plant, fruit weight and pericarp thickness. It was significant for females × males for number of fruits per plant, fruit yield per plant and fruit weight.

Saeed *et al.* (2014) showed that parents and F_1 hybrids of tomato differed significantly for general combining ability and specific combining ability effects. The values of general combining ability (GCA) and specific combining ability (SCA) variances depicted non-additive and additive gene action with predominance of non-additive gene action in the genetic determination for all characters except fruit yield per plant. Parent lines LA-2662 and CLN-2418A provided the best general combining ability effects in more than one yield contributing traits. Specific combining ability effects in desired direction were recorded in two crosses *viz*., LA-2662 × CLN-2418A and LA-2662 × BL-1078.

Sherpa *et al.* (2014) studied the genetic control of fifteen yield components and post harvest quality traits in tomato. Among parental lines, CLN2777-G and FEB-2 were the best general combiners for yield and processing traits. Crosses (CLN2768-A x A.C.AFT and CLN2777-G x FEB-2) showing high specific combining ability and yield involved parents showing high general combining ability for fruit yield per plant and

other horticultural traits. The performances of the hybrids illustrated the presence of various degrees of dominance effects *i.e*., partial to over dominance or no dominance.

Aminu and Mala (2015) evaluated nineteen entries of tomato consisting of seven parental lines plus twelve F_1 hybrids. The estimates of variance components in all the combining ability analyses exhibited that the ratio of GCA to SCA variance indicated greater importance of non-additive genes action for the characters except plant height. The study revealed the significant differences of general combining ability (GCA) effects of parents and that of specific combining ability (SCA) effects of the hybrids. The parents Nematex, Atkinson, Rossol, Danbaga and Dansyria were identified as the best general combiners for plant height, weight of fruits per plant and weight of fruits per plot. The hybrids Nematex x ExGashu'a, Nematex x Roma VF, Atkinson x Ex-Gashu'a, Atkinson x Dansyria, Rossol x Dansyria and Rossol x Roma VF recorded the highest SCA effects for number of fruits per plant, weight of fruits per plant and weight of fruits per plot.

Dagade *et al.* (2015) examined combining abilities for nutritional quality content in tomato and indicated that most of the traits were governed by additive gene action however non additive gene action was also important. The parent Pusa Ruby was found to be good general combiners for yield and nutritional traits. The cross Pusa Ruby x Arka Vikas was desirable for fruit yield as well as nutritional characters since it inherited all nutritional traits except TSS content in F_1 generation and carotene content in F_2 generation in desired direction.

Enang *et al.* (2015) estimated heterosis and general combining ability on tomato. Significant difference was observed in the combining ability analysis of variance in all the agronomic characters under study. The cultivars, Cherry, Currant, UC28B and Roma VF were identified as the best general combiners and the best yielders in terms of number of fruits per plant.

Kumar *et al.* (2015) estimated general and specific combining abilities (GCA and SCA) in tomato and found that LBR-12 was good general combiner for total fruit yield, pericarp thickness, polar equatorial (P/E) ratio, TSS and lycopene content, LBR-13 for pericarp thickness, lycopene content, titratable acidity and carotenoids; LBR-19 for fruit yield, pericarp thickness, lycopene content and titratable acidity. 8-2-

1-2-5 was found to be good combiner for average fruit weight, total fruit yield, number of locules per fruit and lycopene content, EC-119197 for average fruit weight, P/E ratio, TSS and carotenoids. F_1 hybrids from cross combinations, LBR-7 × 8-2-1-2-5 were recorded with good specific combiner for average fruit weight, polar dia/equatorial dia ratio, lycopene and carotenoids, LBR-15 × EC-119197 for total fruit yield, number of locules per fruit, P/E ratio, LBR-13 × EC-119197 for average fruit weight, number of locules per fruit, pericarp thickness, P/E ratio, titratable acidity and carotenoids.

Renuka *et al.* (2015) carried out a study on tomato to know the combining ability effects for growth, yield and quality traits in a 7 x 7 diallel analysis excluding reciprocals by using 7 parents. Parents IIHR-2754(P1) and IIHR-2864(P5) exhibited high general combining ability effect for most of the characters. Genotypes IIHR-2754(P1) and IIHR-2864(P5) was good general combiner for yield. The crosses IIHR-2754 X IIHR-2864 and IIHR-2754 X IIHR-2866 showed high specific combining ability and *per se* performance for fruit yield per plant.

Vilas *et al.* (2015) conducted an experiment on combining ability for yield and yield related traits of 50 F_1 hybrids of tomato. The analysis of genetic variance for yield components showed that the main part of genetic variance was due to additive effect. EC 620533 was the promising line, EC 620534 the better general combiner and EC 620391, BBWR-10-3-17 and BBWR-11-1 the good general combiner. Punjab Chhuhara was better general combiner for and total number of fruits per plant followed by Arka Meghali and Palam Pink, which showed significant GCA effect. Among crosses, BBWR-11-1 x Palam Pink was the better general combiner for the above traits.

Aisyah *et al.* (2016) conducted experiment in a 6 × 6 full diallel cross set of tomato including reciprocals to estimate the general combining ability and specific combining ability for yield per plant and yield components. Significant differences among genotypes were obtained for all the traits. The variances for general combining ability (GCA) and specific combining ability (SCA) were highly significant indicating the presence of additive as well as non-additive gene effects except the fruit thickness. The tomato genotype IPB 78 was the best general combiner for fruit yield per plant, individual fruit weight, fruit length and fruit thickness. The tomato genotype IPB T73 x IPB T3 proved to be the best specific combiner for yield and number of fruits per plant.

Basavaraj *et al.* (2016) carried out the investigation to study the combining ability of parents and crosses for fruit yield and quality components in tomato using 45 hybrids. The present study revealed that none of the parent was good general combiner for all the traits as combining ability effects were not consistent for yield and its components. The analysis of variance for combining ability showed the existence of significant variation for seven characters. T-26, T-36, Swarna Naveen, Vaibhav, DMT-1, DMT-5, S-22, HUB-18, Arka Abha and DMT-2 were identified as good combiners over all characters. Similarly the crosses, S-22 x Arka Abha, DMT-5 x Arka Alok, DMT-5 x Arka Abha and T-26 x DMT-2 were identified as the good specific combiner for fruit yield per plant and the crosses Swarna Naveen x Arka Alok and T-36 x Arka Alok were found to be superior for processing qualities.

Figueiredo *et al.* (2016) used a complete diallel among 10 tomato lines for processing traits. Non-additive effects prevailed over the expression of total fruit yield, commercial production and TSS whereas, additive effects prevailed for average fruit mass. Lines RVT-08, RVT-05 and RVT-10 were most appropriate for intra-population breeding. Experimental hybrids RVT-08 x RVT-09, RVT-07 x RVT-10 and RVT-08 x RVT-10 were pointed as the experimental genotypes with the best performance, surpassing the commercial genotypes for the traits evaluated.

Habu *et al.* (2016) crossed two heat tolerant and four susceptible tomato genotypes in a half diallel mating design. The results of combining ability analysis indicated that, both additive and non-additive actions were important for the inheritance of the traits. However, SCA variance components were higher than GCA variance components, indicating preponderance of dominance gene action for genetic control of the majority traits. The parent Icrixina was the best general combiner for the majority of the traits among the parents while, Petomech × Roma Savana and Icrixina × Rio Grande were the most desirable cross combinations for fruit yield per plant.

Hamada *et al.* (2016) crossed five tomato varieties by using complete diallel crosses mating design, in order to produce 20 hybrids and showed that additive genetic variances were higher than their corresponding values of dominance genetic variances for plant height. On the other hand, values of dominance genetic variances were higher than their corresponding values of additive genetic variances for fruit characters and chemical traits.

Kumar and Gowda (2016) studied combining ability effects in tomato. In respect of GCA effects, L121 was found best general combiner for total yield per plant. Among the crosses, Vaibhav x RIL-160 and L121 x RIL-108 were the most valuable combiners for total yield per plant.

Kumar *et al.* (2016) conducted combining ability studies using a diallel set of ten varieties of tomato (excluding reciprocal) revealed highly significant GCA and SCA effects for all characters studied. This showed that both additive and non-additive gene action were involved in the inheritance of these characters. The parental line P10 (H-29), P5 (Angoor Lata), P1 (Pusa Bahar) and P7 (Kalyanpur Tuape-1) were the best general combiners and top performing hybrids were P9 x P10 (KS-16 x KS-29), P7 x P10 (Kalyanpur Type-1 x KS-29) and P1 x P9 (Pant Bahar x KS-16) for most of the economic characters including yield.

Louis *et al.* (2016) conducted field experiments to estimate the combining ability in tomato. Result of the analysis of variance indicated highly significant difference for all characters among entries except weight of fruits per plant. The result suggested the presence of genetic variability among the tomato genotypes under study. Significant difference was observed in the combining ability analysis of variance in all the agronomic characters under study suggesting both additive and non-additive genetic effects were important in governing this character under study with more preponderance of additive effects. The cultivars, Cherry, Currant, UC28B, and Roma VF were identified as the best general combiners and the best yielders in terms of number of fruits per plant.

Sikder *et al.* (2016) studied the gene action and combining ability for yield and quality traits in tomato. Result revealed that there was highly significant variance among the genotypes for different traits and non-additive gene effect was predominant for the inheritance of those traits. Among the parents, Alisa Craig Aft and Alisa Craig were considered as best general combiner. Cross combination Alisa Craig Aft x BCT-53 showed the superior specific combining ability at desired direction for maximum number of traits. Considering the mean performance and SCA effects together, Alisa Craig dg x CLNB, Alisa Craig dg x BCT53, Alisa Craig Aft x Patharkutchi and Alisa Craig Aft x BCT-53 were superior for yield and quality traits.

Agarwal *et al.* (2017) studied combining ability effects in tomato. Analysis of variance for combining ability indicated variation for all traits under study due to lines. Crosses for all traits indicated availability of sufficient diversity to choose the best crosses for yield, quality and yield-attributing traits. EC95 and CLN 2264F exhibited desirable general combining ability effects for yield, quality and yield-attributing traits. Cross-combinations EC93 × CLN 2264F and EC95 × CO3 exhibited higher specific combining ability for yield and yield-attributing traits, crosses EC86 × CO3, EC89 × CLN 2264H and EC95 × Punjab Chhuhara were good for quality attributing traits and crosses EC86 × CO3, EC88 × Punjab Chhuhara, EC89 × Punjab Chhuhara, EC93 × CLN 2264H and EC94 × CO3 were good specific combiner for earliness.

Kattegoudar *et al.* (2017) studied combining ability in tomato for yield and quality traits by using full diallel analysis. The results revealed highly significant differences among tomato genotypes and crosses for all observed characters. Significant mean squares for general combining ability (GCA), specific combining ability (SCA) and reciprocal combining ability indicated joint role of additive, non-additive and maternal effects for the expression of plant height, days to 50 per cent flowering, number of flowers per clusters, average fruit weight, yield per plant, number of locules per fruit and TSS. PKM-1 and Anagha showed superiority for most of the yield attributing traits. Anagha has shown superiority for yield. For number of locules and total soluble solids, the hybrid Arka Saurabh x Anagha showed the highest positive significant SCA effect. PKM-1 x Utkal Raja for pericarp thickness, showed positive significant SCA effects.

Raj *et al.* (2017) conducted an experiment to find out the general and specific combining abilities in tomato. EC-620410 was found good general combiner for days to 50 per cent flowering and fruit shape index (P/E), BT-1-1 had maximum GCA for number of fruits per cluster, average fruit weight, fruit yield per plant, harvest duration, total soluble solids and ascorbic acid content, FT-5 was good general combiner for most of the traits except for average fruit weight, number of locules per fruits and plant height. F_1 hybrid from cross combinations, EC-191535 × Solan Lalima was good in terms of earliness, better fruit shape and fruit yield per plant. Hybrids of BT-1-1 × FT-5 were superior in terms of number of fruits per cluster and number of fruits per plant whereas, hybrids of BT-1-1 × Solan Lalima were found promising for average fruit weight.

Savale and Patel (2017) estimated combining ability in tomato for fruit yield, yield components and fruit quality traits. Combining ability analysis revealed that both additive and non additive gene actions were important for fruit yield and its related traits. None of the parents exhibited desirable GCA effects for all the traits in individual as well as in pooled over environments. However, overall ranking of genotypes revealed that the parents *viz*., AVTO-7, AVTO-5, JTL-12-12, GT-2 and JT-3 were good general combiners for fruit yield and its contributing characters. The cross AVTO-5 x GT-2 having the maximum SCA effect for fruit yield also had high SCA effect for titratable acidity and non-reducing sugar per cent.

Triveni *et al.* (2017) carried out the experiment to study the combining ability of the parents and crosses for yield and yield contributing traits in tomato. The present study revealed that none of the parent was best combiner for all the traits. Combining ability analysis revealed that magnitude of specific combining ability variance was greater than general combining ability variance suggesting the predominance of non-additive gene action for all the characters studied. The GCA effects of the parents revealed that EC 620494, EC 654289, Arka Meghali and Pusa Ruby were found to be promising general combiners for growth and quality traits. Based on significant SCA effects three hybrids *viz*., LA 3667 x Arka Vikas, EC 631407 x Pusa Ruby and EC 654289 x Pusa Ruby were identified as promising for growth and quality characters.

2.5 Screening of parents and F_1 against late blight (*Phytophthora infestans*)

Late blight is a destructive disease of the cultivated tomato, with the potential to quickly destroy all plant organs. If crops are unprotected, late blight can destroy an entire tomato crop within 7 to 10 days (Foolad *et al*., 2008 and Nowicki *et al*., 2012). Economic losses due to late blight can include reduced yield, lower fruit quality, diminished storability and costs associated with fungicide application (Nowicki *et al*., 2012). Most commercial cultivars of tomato are susceptible to late blight and the disease is currently controlled mainly by cultural practices and frequent use of fungicides. Recently, there have been intense efforts to develop tomato cultivars with improved resistance to late blight and few resistant cultivars have been released (Gardner and Panthee, 2010). Islam *et al.* (2001) assessed fifteen advanced lines of tomato including two check cvs. ‘Manik’ and ‘Bari-10’ under natural epiphytotics for their performance to late blight disease. The highest late blight disease incidence was

found in V-52 and V-215 and the lowest in V-378. Two lines were found resistant (V-426 and V-259), two moderately resistant (V-187 and V-385), two were tolerant (V-282 and V-422), four moderately susceptible (V-378, V-138, V-258 and BARI-10), three were susceptible (V-330, V-201 and Manik) and two highly susceptible (V-52 and V-215), but none was found highly resistant. Baliyan *et al.* (2013) evaluated six varieties of tomato for late blight resistance. Heinz 1370 was the highest severely affected tomato variety by late blight disease and thus produced the lowest marketable fruit percentage. On an average, FA 593 was the least affected variety by late blight. Nowakowska *et al.* (2014) compared the 5-year field performance of late blight resistance in several tomato cultigens. In the field trials, LA 1033, L 3707 and L 3708 displayed the highest resistance for late blight disease. Kumar *et al.* (2015) evaluated fifty-six accessions of tomato (10 lines, 4 testers, 40 F_1 hybrids, 1 standard check and 1 susceptible check) and observed that out of 40 hybrids, 4 namely, LBR-19 × 8-2-1-2-5, LBR-12 × EC-119197, LBR-13 x 1-6-1-4 and LBR-6 × 1-6-1-4 were observed with high disease resistance to late blight and root knot nematodes vis-à-vis appropriate heterosis for desirable traits; particularly fruit yield, fruit weight, pericarp thickness, TSS and dry matter. Meya *et al.* (2015) observed significant differences in diseases incidence and severity among three tomato varieties: Cal J, Meru and Tanya whereby Cal J and Tanya were susceptible to tomato late blight and Septoria leaf spot while, tomato variety Meru was resistant to the former two diseases.

Various researchers also include wild species for screening against late blight disease. Arellano-Rodríguez *et al.* (2011) worked with wild species of cherry tomato and materials generated through crosses and backcrosses between wild materials and open pollinated cultivars and selected 9 breeding lines which were tested under natural infection of *P. infestans* both in field and greenhouse. Breeding lines have proven resistant, statistically equal or superior to the 'LA 2533' in field and laboratory tests using highly virulent strains of *P. infestans.* Akhtar *et al.* (2016) screened 285 tomato genotypes of diverse genetic pool using a low tunnel assay. Results over the multiyear (2013-2015) elucidated one resistant genotype LO6122 (*Solanum arcanum*) and 31 moderately resistant genotypes (one of *S. arcanum* and 30 of *S. lycopersicum*) to late blight resistant of the genotypes. Strong resistance conferred by LO6122 points out the presence of an alternate source of genes resistant to late blight. Arafa *et al.* (2017) assessed the resistance level of four tomato genotypes and 48 wild relatives of

cultivated tomato to *P. infestans*. The highest late blight resistance was detected in *S. habrochaites* accessions LA1777, LA1352, LA2855, LA1347, LA1718 and LA1295, with disease severities ranging from 4.5 to 13.5 per cent. The overall results demonstrate that LA1777 had a high level of resistance against all isolates of *P. infestans*. Solankey *et al.* (2017) determined the reaction of 152 tomato genotypes including 4 wild relatives, *i.e*., *Solanum chilense*, *S. pimpenellifolium*, *S. cheesmaniae, S. peruvianum*, against late blight using whole-plant scoring. These genotypes were screened and evaluated in two different conditions (open field and side open poly house). Of the 152 genotypes, none of the test genotypes showed immune reaction. Moreover, the genotypes Arka Rakshak, Arka Alok, BRDT-1, Kashi Anupam, Arka Ananya, Azad T-5, C 6 T and Kashi Vishesh showed high yield potential and lower incidence for late blight. Moreover, wild species *S. chilense*, *S. pimpenellifolium*, *S. cheesmaniae* and *S. peruvianum* showed resistance reaction for late blight. The genotype EC 538380 showed highly resistant disease reaction against late blight besides bearing more fruits. Ray *et al.* (2018) screened one hundred genotypes of tomato during winter season under field condition and data was recorded on 0-5 scale at 30, 60 and 90 days in which eleven genotypes were highly resistant, seventeen genotypes were resistant, nineteen genotypes were moderately resistant, twenty four genotypes were susceptible and twenty nine genotypes were highly susceptible. Fourty eight F_1s were screened along with their parents during rainy season under field condition. Out of fourty eight F_1s, eighteen cross combinations were highly resistant and others were resistant, moderately resistant, susceptible and highly susceptible. The parents namely *Solanum peruvianum* and Pusa Rohini showed highly resistant and other parents were either resistant, moderately resistant, susceptible or highly susceptible in respect of disease reaction.

2.6 Screening of tomato genotypes against new invasive pest *Tuta absoluta*

Tuta absoluta has a great potential to cause yield losses in the major tomato-producing areas. Cost-benefit analysis showed that *T. aboluta* significantly increased costs of pest management, primarily as a result of increased use of insecticides (Thomas, 1999 and Lietti *et al.*, 2005). The rapid growth, potential natural dispersal and resistance to insecticides render this pest as the most serious threat for tomato production systems worldwide (Desneux *et al*., 2010). Oliveira *et al.* (2009) evaluated resistance to *Tuta*

absoluta on 57 tomato accessions by the three commercial cultivars (Santa Clara, Moneymaker and TOM-601) under greenhouse conditions. Based on these data it was concluded that only accessions HGB-674 and HGB1497 appeared to be the most promising. Sobreira *et al.* (2009) evaluated the injury caused by *Tuta absoluta* (Meyrick) in the leaves and plant of 15 cherry tomato accessions. In general, the accession CCAUFES 40 was the most resistant to *T. absoluta*. Oliveira *et al.* (2012) examined the resistance of improved tomato strains to the tomato moth, *Tuta absoluta*. TOM-584 and TOM-679 strains were used as susceptible controls. The improved strain TOM-687 has a widely documented resistance and was used as a standard resistant strain. The wild strain PI134417, which is resistant, was also used as a standard resistant strain. The experiment was installed in a greenhouse with a completely randomized design. The wild strain PI 134417 was confirmed as being highly resistant. TOM-622 and TOM-687 showed significant reductions in the oviposition rate of the tomato moth, damage to the plants, injury to the leaflets and the percentage of leaflets attacked in comparison with the control strains (TOM-584 and TOM-679). The levels of resistance to the moth for the TOM-622, ZGB-703 and TOM-687 strains were similar.

Gharekhani and Salek-Ebrahimi (2013) evaluated the damage of *T. absoluta* on eleven tomato cultivars under greenhouse condition. Larval mines on the leaves as well as the terminal bud damage were considered. Damaged leaves, active mines and damaged terminal buds were significantly different among the cultivars. Sridhar *et al.* (2014) observed the infestation of *T. absoluta* ranged from low to high (up to 15 mines/plant) in different tomato fields surveyed. In some of the fields up to 87 per cent of the tomato plants were infested by *T. abosoluta*. Kalleshwaraswamy *et al.* (2015) observed damage of *T. absoluta* on both leaves and fruits of tomato. Results showed that on the leaves, the damage was confined mainly to the top portion of the plant. On average, 2.7 to 60.7 leaves per plant showed symptoms. Furthermore, 1.2 to 12.6 fruits per plant showed pinhole symptoms and also observed an average density of 0.8 to 8.8 larvae per plant. Shanmugam *et al.* (2016) first noticed the occurrence of *T. absoluta* in Karimangalam block in the tomato hybrid Sivam. The widely cultivated tomato hybrids Sivam and Sagar were equally susceptible to the *T. absoluta* with 20-32 per cent leaf damage and 28-53 per cent fruit damage. The damage was mostly found in the middle and lower leaves and half ripened and ripened fruits. In a single fruit 8-12 holes were

noticed during the survey. Ghaderi *et al.* (2017) evaluated seven tomato cultivars to *T. absoluta* and indicated that Cal JN3 was the most susceptible to infestation and Primo Early and Early Urbana Y were the most resistant to *T. absoluta* among the tomato cultivars tested. Singh and Panchbhaiya (2018) first time reported the occurrence of *Tuta absoluta* (Meyrick) in tomato from Uttarakhand state of India under polyhouse condition and found that at final harvesting stage, 80 to 90 per cent incidence was observed in PPT-2, PBT-5, PBT-13, PBT-4 and PBT-10, while 70 to 75 per cent incidence was observed in PBT-9 and PBT-10. In same polyhouse cherry tomato variety Pant Cherry Tomato-1 (PCT-1) showed moderate resistance (30% incidence) against this new devastating pest.

Materials and Methods

Chapter 3 MATERIALS AND METHODS

The details of material used and methodology followed during the present investigation **"Studies on combining ability, molecular diversity and response to late blight (*Phytophthora infestans* (Mont.) de Bary) in tomato (*Solanum lycopersicum* L.) under polyhouse condition"** have been describe in this chapter.

3.1 EXPERIMENTAL SITE

3.1.1 Location

The experiment was conducted at Vegetable Research Centre (V.R.C.), Govind Ballabh Pant University of Agriculture & Technology, Pantnagar, Uttarakhand during the year 2016 to 2018. This university is situated in the foot hills of Shivalik range of Himalayas in the narrow belt called '*Tarai*'. Geographically, it is situated at an altitude of 243.84m above mean sea level, and between 29.50° North latitude and 79.30° East longitude. The molecular experiment was carried out at the National Agricultural Innovation Project (NAIP) laboratory, Department of Vegetable Science and biochemical analysis was conducted at Horticultural laboratory, Department of Horticulture, Pantnagar.

3.1.2 Agroclimatic condition

The climate of the region is broadly humid subtropical with cool winter and hot dry summer. During hot summer, maximum temperature exceeds 40^{o}C while, in winters the minimum temperature occasionally touches 0^{o}C. The monsoon generally starts from the third week of June and recedes by the end of September. Occasional light rains are expected during winter months also, frost is expected from late December to February. The mean relative humidity remains almost 80-90 per cent from mid-June to end of February and then it steadily decreases to 50 per cent by the first week of May and remains so till mid-June.

The weekly average of various weather parameters that prevailed during the course of investigation are presented in Appendix I.

3.1.3 Soil condition

The soil at Pantnagar comes under the category of mollisoils. The soil of experimental field was sandy-loam with adequate drainage and optimum water holding capacity.

3.2 EXPERIMENTAL MATERIAL

The experimental material for this study consists of 8 genotypes which were selected based on their diversity for various traits (Plate 1). From these 8 genotypes, 28 crosses were evolved in a half diallel mating design. The parents and their F_1's are presented in Table 3.1 and 3.2, respectively.

3.1 List of parents used for study

S. No.	Parent line	Source
1	Pant Cherry Tomato-1 (PCT-1) – Resistant check for late blight disease	New Delhi
2	Pant Polyhouse Tomato -2 (PPT-2) – Standard check for evaluation	G.B.P.U.A. & T., Pantnagar
3	PBT-2	Rehovot Agriculture Campus, Israel
4	PBT-4	Rehovot Agriculture Campus, Israel
5	PBT-5	Rehovot Agriculture Campus, Israel
6	PBT-9	Rehovot Agriculture Campus, Israel
7	PBT-10	Rehovot Agriculture Campus, Israel
8	PBT-13	Rehovot Agriculture Campus, Israel

3.2 List of F_1 hybrids developed through diallel mating design

S. No.	F_1 hybrids
1	PCT-1 x PPT-2
2	PCT-1 x PBT-9
3	PCT-1 x PBT-5
4	PCT-1 x PBT-2
5	PCT-1 x PBT-13
6	PCT-1 x PBT-10
7	PCT-1 x PBT-4
8	PPT-2 x PBT-9
9	PPT-2 x PBT-5
10	PPT-2 x PBT-2
11	PPT-2 x PBT-13
12	PPT-2 x PBT-10
13	PPT-2 x PBT-4
14	PBT-9 x PBT-5

S. No.	F_1 hybrids
15	PBT-9 x PBT-2
16	PBT-9 x PBT-13
17	PBT-9 x PBT-10
18	PBT-9 x PBT-4
19	PBT-5 x PBT-2
20	PBT-5 x PBT-13
21	PBT-5 x PBT-10
22	PBT-5 x PBT-4
23	PBT-2 x PBT-13
24	PBT-2 x PBT-10
25	PBT-2 x PBT-4
26	PBT-13 x PBT-10
27	PBT-13 x PBT-4
28	PBT-10 x PBT-4

PCT-1

PPT-2

PBT-9

PBT-5

PBT-2

PBT-13

PBT-10

PBT-4

Plate 1 Eight parents used for study

3.3 CROSSING PROGRAMME

Crossing programme was carried out to generate 28 single cross hybrids from eight parents. Crossing programme was started at flowering stage and continued till sufficient number of fruit set and seeds availability was ensured.

The number of flowers per cluster varies from three to several. The early flowers that open in the cluster are large-sized as in a typical cyme. The plant produces bright yellow flowers. The flowers are pentamerous, bisexual, regular, complete ebracteate and hypogynous. The lateral section of the flower shows the details of sepals, petals, stamens, style, ovary and ovules. The pistil has two or several carpels. The anther connate appearing in the throat of the corolla and they dehisce through the pericidal dehiscence. Usually, the style is shorter has anther cone which cause high degree of self pollination.

The anthesis of flower starts in the morning at about 6 AM with maximum flower opening in the late morning. The maximum amount of anther dehiscence takes place from 8 to 11 AM depending upon the season. The stigma becomes receptive 16 hr before anthesis axis. Stigma is ready to receive pollen grains and remains this for five days after anthesis. Pollen grain germination takes place approximately two hrs after pollen has been applied on the stigma. Ovules ripen over two days. Pollen can be stored upto three days under ordinary conditions. Pollen from one day stored flower provides best seed set. At 0^{o}C, it can be stored for 2-3 months. While, it remains viable for six months at 5^{o}C in a dessicator. The optimum temperature for pollen germination is 18-25^{o}C. Tomato pollen germinates best in a liquid solution of 20 per cent sucrose and 10ppm boron.

Emasculation was done in afternoon one day prior to anthesis. At this stage, the sepals have started to separate and the anthers and corolla is beginning to change from light to dark yellow. The stigma is fully receptive at this stage allowing for pollination even immediately after emasculation. Anthers are removed as a group with or without the surrounding corolla, by inserting forceps between the sepals to grip the base of the anthers and/or petals which are then removed by a firm but steady pull. Pollen next day forenoon is best applied in experimental crosses by slitting the inside of the anthers of mature flowers of the male parent with the forceps in such a way that a small amount of pollen is collected at the tip of the forceps. This can then be lightly applied to the stigmatic surface and should be visible as a white covering.

3.4 CULTURAL OPERATIONS

3.4.1 Nursery raising and transplanting

The seeds were sown in plastic pro trays by using artificial soilless media inside the naturally ventilated polyhouse for raising healthy and vigorous seedlings of tomato. Combinations of three ingredients *viz*., cocopeat, vermiculite and perlite are used as rooting medium for raising the nursery. These ingredients are mixed in 3:1:1 (V/V) ratio. The seedlings were ready for transplanting after one month of sowing and were subsequently transplanted inside the naturally ventilated polyhouse equipped with drip irrigation system for efficient use of water and fertilizers for long duration cultivation of tomato crop. Healthy seedlings are transplanted at a planting distance of 60 x 45cm. Before transplanting of seedlings, soil is thoroughly prepared and beds are made with the help of tractor rotavator.

3.4.2 Pruning and training

The tomato plants were pruned to two branches per plant. Starting from 15 to 25 days after transplanting and pruning was done at weekly intervals. The main stem of tomato plant branches into two branches into two after the first flower cluster and only these two branches were maintained and other branches were removed. Any branch developing at the bottom was also pruned. Training is done with the support of wire, string and stakes. Each branch tied with separate plastic twine to train along it. The branches were tied to the plastic twines. Tying of plants to the plastic twine starts from 4^{th} week after planting and tying was usually done at weekly interval along with the pruning operation simultaneously.

3.5 EXPERIMENTAL DESIGN AND LAYOUT PLAN

All 8 parents and 28 F_1 hybrids were evaluated for late blight during 2016-17 whereas, for *Tuta absoluta* and different yield related traits during 2017-18 under three different polyhouses. The details of experimental plan are given below:

Experimental site	:	Vegetable Research Centre, Pantnagar
Design	:	Randomized Block Design (RBD)
Replication	:	3
Treatments	:	36
Spacing	:	60 cm x 45 cm

3.6 OBSERVATIONS RECORDED

Five competitive plants from each entry in each replication were randomly selected before flowering and tagged for the purpose of recording observations on different quantitative traits and their average values were used in the statistical analysis. The observations were recorded for the following traits:

A. Flowering and maturity characters

1. Days to 50 per cent flowering

This was determined by counting the number of days from transplanting until 50 per cent of the tagged plants per genotype had flowered.

2. Days to first fruit set

The numbers of days were counted from the date of transplanting to first fruit set and expressed in term of number of days, when first fruit setting occur.

3. Days to first fruit ripening

The period from the fruit setting to the date of fruit ripening was recorded and expressed in term of number of days, when first red ripen fruit occur.

B. Plant architectural characters

1. Plant height (cm)

Plant height of five randomly selected plants was recorded with the help of a meter scale from the base of the plant to the shoot tip at the final picking and the average height (cm) per plant was calculated.

2. Internodal length (cm)

Internodal length of five randomly selected plants was recorded with the help of a meter scale at the final picking and the average internodal length (cm) per plant was calculated.

C. Yield and yield contributing characters

1. Number of flowers per cluster

Number of flowers per cluster was recorded as average of five random clusters at flowering stage and the average was calculated.

2. Number of fruits per cluster

Number of fruits per cluster was counted at the time of first harvesting on 5 random plants from each plant five clusters were taken and means was computed for each variety per replication and the mean of five clusters was computed.

3. Number of fruits per plant

The number of fruits counted at each harvest and cumulative total of all the harvest were known as number of fruits per plant. The data were recorded on 5 randomly selected plants in a replication and averaged.

4. Average fruit weight (g)

Average fruit weight was measured in gram. The data were recorded on five randomly selected fruits in a replication and averaged.

5. Fruit length (cm)

Fruit length was recorded from five randomly selected fruits in all the accessions using vernier calliper and was expressed in centimeters and averaged.

6. Fruit width (cm)

Fruit width was measured in centimeter by the help of vernier calliper. The data were recorded on five randomly selected fruits in a replication and averaged.

7. Fruit shape index (FSI)

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

Ratio (Fruit shape index)	Shape
>1.00	Oval
0.86 – 0.99	Spherical
0.71 – 0.85	Intermediate (Flat round)
≤ 0.70	Flat

Polar and equatorial diameters were measured in each case on five randomly taken fruits with the help of vernier calliper after cutting the fruits longitudinally and mean value was worked out.

8. Fruit yield per plant (kg)

The weight of fruits of five selected plants was recorded at each picking and the total weight of fruits was calculated by cumulative harvest in kilograms, which was averaged over replications.

9. Fruit yield per hectare (q/ha)

The total yield obtained from the five plants was recorded and average fruit yield per hectare was calculated.

D. Seed yield characters

1. 100 seed weight (g)

100 well-developed seeds were collected from the bulk of five selected plants and weight was recorded with the help of electronic balance and expressed in gram (g).

E. Fruit quality related traits

1. Number of locules per fruit

Number of locules was recorded for five random fruits in all the accessions, the fruits were cut opened horizontally and the number of locules per fruit was counted.

2. Pericarp thickness (cm)

Five fruits were selected randomly from each genotype and cut transversely into two halves. Then pericarp thickness (cm) was measured with the help of vernier callipers and the average was calculated. The same fruits which were cut to the count number of locules were used to measure pericarp thickness.

3. Diameter of stalk scar (cm)

Five fruits were selected randomly from each genotype and diameter of stalk scar (cm) was measured with the help of scale and the average was calculated.

4. Fruit firmness

This was determined shortly after harvest using a hand held penetrometer. Readings (kg/cm^2) were recorded on 3 fruits per genotype per replication and the mean value determined.

5. Total soluble solids (^{o} Brix)

Five fruits from each genotype were randomly taken from the harvested lot and thoroughly washed under tap water. The fruits were cut into small pieces and squeezed to obtain the juice and with the help of Erga hand refractometer under room temperature conditions (20^{o}C) by putting 2-3 drop of juice on the prism and taking the reading in ^{o}Brix. Then average was calculated and was expressed as per cent soluble solids in juice.

6. pH of fruit juice

Sample juice extracted from five blended fruits per each genotype was poured into separate beakers. A digital pH of fruit juice meter was then used for the pH readings. The readings were taken in triplicates and the average for each replication determined.

7. Titratable acidity

10g of macerated fruit pulp was thoroughly mixed with distilled water and volume made up to 100ml and filtered through a muslin cloth. 10ml of this solution was titrated against 0.1N NaOH solution using phenolphthalein as indicator. The total titratable acidity was calculated in terms of citric acid on the basis of 1ml sodium hydroxide equivalent to 0.0064g of anhydrous citric acid. The titrable acidity was estimated by using the formula:

$$\text{Titratable acidity (\%)} = \frac{1 \times \text{Titre value} \times \text{N. of NaOH} \times \text{equivalent weight of acid} \times 10}{10 \times \text{Wt. of sample}} \times 100$$

8. Ascorbic acid (mg/100g)

Composite flesh with peel of 3 randomly sampled fruits per replication at edible maturity were used to estimate ascorbic acid content in the fresh fruits by volumetric method as suggested by AOAC (2001).

Materials

(i) Metaphosphoric acid 3%

(ii) Dye solution: 42mg sodium bicarbonate was taken into a small volume of distilled water and 50mg of 2, 6-dichlorophenol indophenol was dissolved in it. Volume was made upto 200ml with distilled water.

(iii) Stock standard solution: 100mg ascorbic acid was dissolved in 100ml of 3% metaphosphoric acid solution in a standard flask (1mg/ml).

(iv) Working Standard: 10ml of the stock solution was diluted to 100ml with 3% metaphosphoric acid.

Procedure

(i) Pipette out 5 ml of the working standard solution into a 100 ml conical flask and then 10 ml metaphosphoric acid was added in it and titrated against the dye solution (V1ml). End point was the appearance of pink colour which persists for a few minutes. The amount of the dye consumed was equivalent to the amount of ascorbic acid.

(ii) 2g of fruit sample was crushed and extracted in 3% metaphosphoric acid. Volume was made upto 100ml and centrifuged for 20 minutes.

(iii) 5 ml of this supernatant was pipetted out and added into the 10 ml of 3% metaphosphoric acid.

(iv) It was titrated against the dye (V2 ml).

Calculation:

$$\text{Ascorbic acid(mg/100g)} = \frac{\text{Titre value} \times \text{Dye factor} \times \text{Vol. of made up}}{\text{Aliquot of extract taken for estimation} \times \text{weight of sample taken for estimation}} \times 100$$

Where, Dye factor = 0.5/titre value

9. Lycopene (mg/100g)

Lycopene is responsible for red color of tomato, its content varies depending on the potential of the accession to accumulate the same and hence the lycopene content was estimated using the protocol proposed by Ranganna (1976). Carotenoids in the sample were extracted in acetone and then taken up in petroleum ether. Lycopene has absorption maxima at 473nm and 503nm. One mole of lycopene when dissolved in one liter light petroleum (40-60^{o}C) and measured in a spectrophotometer at 503nm in 1cm light path gives an absorbance of 17.2X 104. Therefore, a concentration of 3.1206µg lycopene/ml gives unit absorbance.

Materials

i. Acetone (AR grade)

ii. Petroleum ether 40-60 (AR)

iii. Anhydrous sodium sulphate

iv. 5% sodium sulphate

Procedure

Three to four tomato fruits were taken in a waring blender and pulped it well to a smooth consistency. 5-10g of this pulp was weighed. Extracted the pulp repeatedly with acetone using pestle and mortar or a waring blender until the residue was colourless. Pooled the acetone extracts and transferred to a separating funnel containing about 20ml petroleum ether and mixed it gently. Added 20ml of 5% sodium sulphate solution and shaked the separating funnel gently. Volume of petroleum ether might be reduced during these processes because of its evaporation. So added 20ml more of petroleum ether to the separating funnel for clear separation of two layers. Most of the colour was noticed in the upper petroleum ether layer. Separated the two phases and re-extracted the lower aqueous phase with additional 20ml petroleum ether until the aqueous phase was colorless. Pooled the petroleum ether extracts and washed once with a little distilled water.

Poured the washed petroleum ether extract containing carotenoids into a brown bottle containing about 10g anhydrous sodium sulphate. Kept it aside for 30 min or longer. Decanted the petroleum ether extract into a 100ml volumetric flask through a funnel containing cotton wool. Washed sodium sulphate slurry with petroleum ether until it was colorless and transferred the washings to the volumetric flask. Made up the volume and measured the absorbance in a spectrophotometer at 503nm using petroleum ether as blank.

Calculation

Absorbance (1 unit) = 3.1206µg lycopene/ml.

$$\text{mg lycopene in 100g sample} = \frac{31.206 \text{ x Absorbance}}{\text{Wt. of sample (g)}}$$

10. Total carotenoids (mg/100 g)

Analysis of total carotenoids is based on the extraction of crude pigment mixture in a lipid solvent and measurement of its optical density at 440nm. The sample is extracted in acetone which dissolves both the fat and water soluble pigments. The acetone extract is then taken in petroleum ether layer. The fat soluble carotenoids pass from acetone to the petroleum ether leaving all the rest of the pigments in the acetone.

Reagents

1. Acetone
2. Petroleum ether (b.p. 65-70^{o}C)
3. Granular anhydrous sodium sulphate (Na_2SO_4)

Procedure

Take 1 to 2 grams of fresh ripe tomato sample and grind it with acetone using acid and alkali washed sand in a pestle and mortar. The extract is decanted into a conical flask. Continue the extraction till the residue is colourless. Combine the extracts and transfer into a separating funnel. Add 10-15ml of petroleum ether. Add about 25ml of 5% sodium sulphate solution. Shake it and keep it for sometime and yellow pigment is transferred into the petroleum ether later. Now collect the layer in a volumetric flask and separate acetone layer containing 5% sodium sulphate. Keep on adding 15ml petroleum ether to the acetone layer containing Na_2SO_4 until all the colour gets transferred into the petroleum ether layer. Make the volume with petroleum ether and measure the colour intensity at 452nm in a spectrophotometer.

Calculation

$$\text{Total carotenoids (mg/100g)} = \frac{3.857 \text{ x O. D. x Volume made up x dilution x } 100}{\text{Wt. of sample x } 1000}$$

F. Plant protection

1. Late blight of tomato

All eight parents (PCT-1 as a resistant check) and twenty eight F_1 hybrids were evaluated during 2016-17 in three replication. In each replication, disease incidence for late blight was recorded for all twelve plants and five plants were randomly selected for disease severity. Spores suspension was prepared in water by using infected leaves of

tomato. The suspension was sprayed on healthy tomato plants using a hand sprayer until complete leaf coverage and excess runoff was observed. Following observations were recorded for late blight disease in polyhouse experiment:

i. Disease incidence:

Data of different parents and F_1 hybrids against late blight incidence in present experiment taken at 15, 30, 45, 60, 75 and 90 days after initiation (DAI) of disease. Disease incidence was calculated for late blight disease under polyhouse conditions using the given formula:

$$\text{Disease Incidence} = \frac{\text{Number of plants infected}}{\text{Total Number of plants}} \times 100$$

ii. Disease severity:

Data of disease reactions of different parents and F_1 hybrids against late blight severity in present experiment recorded at 10, 20, 30, 40, 50, 60, 70, 80, 90 and 100 days after initiation (DAI) of disease. On the basis of infection on leaves, branches and fruits of each plant, disease severity was estimated on 0-5 scale (Table 3.3) described by Akhtar *et al*. (2012). Percent Disease Index (PDI) was calculated by given formula.

$$\text{PDI} = \frac{\text{Sum of all the disease ratings}}{\text{No. of Plant observed} \times \text{Maximum disease grade}} \times 100$$

Table 3.3: Disease scale for rating of tomato late blight

Disease Rating	Symptoms severity for whole plant assay	Infection %	Disease reaction
0	No visible symptoms apparent	0	Immune
1	A few minute lesions to about 10% of the total leaf area is blighted and usually confined to the 2 bottom leaves.	0.01 - 10	Highly resistant
2	Leaves on about 25% of the total plant area are infected.	10.01 - 25	Resistant
3	Leaves on about 50% of the total plant area are infected.	25.01 - 40	Moderately resistant
4	Leaves on about 75% of the total plant area are infected.	40.01 - 60	Susceptible
5	Leaves on whole plant are blighted and plant is dead.	>60.01	Highly susceptible

2. Infestation of *Tuta absoluta*

Five harvesting of tomato fruits were performed for evaluations of the damage caused by the *Tuta absoluta* insect and percentage of fruit damage (PFD) was recorded for all parents and their F_1 hybrids. Percentage of fruits damage was estimated using the following formula:

$$\text{Percentage of fruits damage} = \frac{\text{Number of infected fruits}}{\text{Total number of fruits}} \times 100$$

3.7 ASSESSMENT OF GENETIC DIVERSITY USING SSR MARKERS

For the study of genetic divergence DNA from selected eight genotypes of tomato was extracted from two to three week old seedlings at National Agricultural Innovation Project (NAIP) laboratory, Department of Vegetable Science, G. B. Pant University of Agriculture and Technology, Pantnagar. The detailed procedure for DNA extraction is given below:

The genomic DNA was extracted by CTAB (Cetyl tri-methyl ammonium bromide) method as described by Doyle and Doyle (1990) with some modifications.

3.7.1 Collection of experimental tissues

The genotypes were grown at Vegetable Research Center, Pantnagar, Udham Singh Nagar. 2-3 weeks old fresh leaves were taken for genomic DNA extraction from all the eight genotypes and wrapped in aluminium foil. Samples were placed in an ice box and brought to laboratory. One gram of leaf sample was weighed with electronic balance and placed in -20^{o}C refrigerator.

3.7.2 Isolation of genomic DNA

Total genomic DNA was isolated using the CTAB method. The list of buffers and stock solutions is given in Appendix-II. Pre-heat CTAB buffer at 60^{o}C for thirty minutes in a water bath. Take 2.0ml centrifuge tube and mark them from 1 to 8. In each centrifuge tube add 1ml of extraction buffer (2 percent CTAB). Grind the leaf sample to a fine powder in a pre-cooled mortar and pestle using liquid nitrogen. Mix extraction buffer and powdered sample thoroughly. Incubate at 65^{o}C for one hour (cap should be slightly loose). Mix it intermittently at almost 10 minutes interval. After taking tubes out from the water bath, allow it to come to room temperature and add 10ml of

chloroform and isoamyl alcohol (24:1) mixture. Swirl the tube gently by moving wrist in the shape of 8 for approximately 10 minutes. Centrifuge at 15,000 rpm for 15 minutes. Transfer the aqueous phase to a fresh centrifuge tube. Add double amount of iso-propanol. Mix the contents very gently by inverting the tube 10-15 times. Keep the tubes overnight at -20^{o}C. Spool out the DNA thread using a wide-bore tip into a micro-centrifuge tube.

3.7.3 Determination of quality and quantity of isolated DNA

3.7.3.1 Qualitative analysis "agarose gel electrophoresis"

Electrophoresis through Agarose is the standard method used to check the quality of DNA fragments. The technique is simple, rapid to perform and capable of resolving fragments of DNA. Submerged gel electrophoresis unit was used for fractionating genomic DNA on agarose gel.

Procedure

1. The open end of a clean, dry plastic tray supplied with the electrophoresis apparatus was sealed with tape so as to form mold.
2. Agarose gel was prepared by dissolving (boiling) appropriate amount of agarose in 0.5 X TBE buffer (0.8% for genomic DNA). Cool it down to approximately 50^{o}C. 8µl of ethidium bromide was added in this agarose solution and poured it in gel casting plate with already adjusted gel comb.
3. The agarose solution was left to solidify at room temperature for 30-40 minutes.
4. After complete setting of gel the comb was removed carefully with the tape and the gel was mounted in an electrophoresis tank filled with 0.5 X TBE buffer.
5. The DNA loading dye was mixed with DNA sample in 1:6 ratio and loaded in gel along with one sample of known quantity of DNA.
6. Electrophoresis was done by running the gel at 80 volts for 45 minutes.
7. The gel was then visualized on an UV trans illuminator.
8. The photograph of gel was taken in a gel documentation unit.

3.7.3.2 Quantification of genomic DNA

The purified genomic DNA, dissolved in TE buffer was taken for quantification by UV absorbance at 260 nm in a UV spectrophotometer.

To measure the concentration of DNA by using UV spectrophotometer, the blank is set against TE buffer and then after proper rinsing of Quartz cuvette, the sample with appropriate dilution was loaded in cuvette. The optical density (O.D.) was measured at 260nm for estimating the concentration of DNA. The O.D. was also recorded at 280nm to determine protein contamination. The concentration of DNA was calculated by using following equation:

Concentration of DNA (µg/µl) = O.D. x 50 x dilution factor/1000

The ratio of $O.D._{260/280}$ gives the amount of RNA or protein contamination in the preparation. A value of 1.8 is optimum for best DNA preparation. A value of ratio below 1.8 indicates the presence of protein in the preparation and a value above 1.8 indicates RNA contamination in the isolated DNA.

3.7.4 PCR amplification

The polymerase chain reaction (PCR) is a powerful, extremely sensitive technique with application in the field of molecular biology, agricultural diagnostics, forensic analysis and population genetics. It is based on the enzymatic amplification of DNA fragments that are flanked by oligo-nucleotide primer hybridizing to opposite strands of the target sequence. The PCR involves three basic steps which constitute a single cycle:

(i) Denaturation of the target DNA at 92-94 ^{o}C

(ii) Annealing of the primers to the template DNA

(iii) Primer extension by addition of nucleotides to the 3' end of the primers by the enzyme DNA polymerase.

As the number of PCR cycle increases, the amount of target DNA synthesized increases exponentially. Availability of thermostable DNA polymerase Taq (from the bacteria *Thermus aquaticus*) has facilitated automation of the PCR (Saiki *et al.,* 1988).

Primer annealing temperature depends on its T_m value which is calculated from the following equation. T_m (^{o}C) = 4 (G+C) + 2 (A+T) ± 3. Where A, T, G and C stand

for the number of corresponding nucleotides in the primer. Annealing may fail at a temperature much higher than T_m whereas annealing temperature much below T_m may lead to non-specific amplification. Annealing temperature gradient of range 30-38^oC was applied in case of decamer primers.

3.7.4.1 PCR ingredients

A. Design of primers

The most essential requirement of PCR is the availability of short oligonucleotides called primers having sequence complementary to either end of the target DNA segment called template DNA to be synthesized on large amount. List of primers used is given in Table 3.4.

Table 3.4 List of SSR primers used for DNA amplification

S. No.	Primer code	Forward primer (5´→ 3´)	Reverse primer (5´→ 3´)
1.	SSR20	GAGGACGACAACAACAACGA	GACATGCCACTTAGATCCACAA
2.	SSR43	CTCCAAATTGGGCAATAACA	TTAGGAAGTTGCATTAGGCCA
3.	SSR47	TCCTCAAGAAATGAAGCTCTGA	CCTTGGAGATAACAACCACAA
4.	SSR63	CCACAAACAATTCCATCTCA	GCTTCCGCCATACTGATACG
5.	SSR65	GGCAGGAGATTGGTTGCTTA	TTCCTCCTGTTTCATGCATTC
6.	SSR74	ACTCACCATGGCTGCTTCTT	TTTCTTGAAGGGTCTTTCCC
7.	SSR86	AGGGCAACAAATCCCTCTTT	GGAGACGAGGCTGCTTACAC
8.	SSR92	AAGAAGAAGGATCGATCGAAGA	TCATGACCACGATACTACATGTTTC
9.	SSR99	GCCTCGGATTCAATAGCATTA	CACAAAGAAGCAAACAACTCCA
10.	SSR110	TGTAACGTCAAACTTCAGGTG	CTCCGCAATGTGTTGTATGG
11.	SSR111	TTCTTCCCTTCCATCAGTTCT	TTTGCTGCTATACTGCTGACA
12.	SSR136	GAAACCGCCTCTTTCACTTG	CAGCAATGATTCCAGCGATA
13.	SSR248	GCATTCGCTCTAGCTCGTTT	GGGAGCTTCATCATAGTAACG
14.	SSR253	CCACAAACAATTCCATCTCA	GCT'TCCGCCATACTGATACG
15.	SSR255	TGTGAATACAATTTGCACCC	GGGTTACTAATGCACAAGCGA
16.	SSR268	CTGAAGCTGAGAAAGGCGAC	CTGGCATTTAAGGCAAAGAA
17.	SLM6-5	ATGCACGCAAAGGTTATTCC	AGTCGAAGTTGGCTTGACCA
18.	SLM6-7	CAATTGAAGATTGGGGCTTT	AGCAGCTCACCTCACGTTTT
19.	SLM6-12	GAGATCACGTTTTTCCTTCCA	GATGGACTATGAAGGAGACTTCG
20.	SLM6-14	TCCGTAATAAGTTGAGGAACCA	TCACAAGAATATTTGCCGTCAT

B. Template DNA: The genomic DNA isolated from eight samples was suitably diluted and its 100 ng per PCR tube was used as a template in PCR amplification.

C. Taq DNA polymerase: Taq DNA polymerase is a 94 kD thermostable enzyme which has 5'→3' polymerase activity and 3'→5' exonuclease activity. It is highly active at temperature around 72°C. The enzyme used in the reaction was obtained from Himedia.

The concentration of enzyme was 3 Unit per µl. One unit of Taq DNA polymerase is defined as the amount of enzyme which incorporates 10nm of total deoxyribo nucleoside triphosphate into acid precipitable DNA in 30 minutes at 75°C under optimal assay conditions.

D. dNTPs

The dNTPs used in this reaction was obtained from Himedia as 2.5 mM each (dATP, dGTP, dCTP, dTTP).

E. Taq assay buffer (10X) A

The 10X assay buffer for the enzyme was also obtained from Himedia. Assay buffers contained 100mM Tris-HCl (pH 9.0), 15mM $MgCl_2$, 500mM KCl and 0.1% gelatin. One vial of 25mM $MgCl_2$ was also supplied along with Taq polymerase for making $MgCl_2$ gradient.

F. Molecular biology grade water:

Molecular biology grade water obtained from Himedia was used in master-mix.

3.7.4.2 Standardization of the polymerase chain reaction (PCR conditions)

There are number of variables in a PCR which have to be optimized to give the target amplification. These parameters are:

- Denaturation temperature and time
- Annealing temperature and time
- Amounts of template and primer
- Concentration of $MgCl_2$ in the assay buffer
- The number of cycles

After repeated PCR reactions a reaction mixture was standardized for eight tomato genotypes which gave strong amplifications. The reaction mixture is presented in Table 3.5. Gradient PCR was used for standardizing the PCR reactions for 20 primers with all the eight genotypes. Final reaction that gave good result and clear bands are presented in Table 3.6.

PCR procedure:

(i) 1µl of the sample (50ng/µl) was added to the master- mixture (Table 3.5) given above from different tomato samples which would act as template.

(ii) The tubes were vortexed for proper mixing of template in the cocktail.

(iii) Tubes were placed in a thermal cycler (Eppendorf Master Cycler Gradient).

(iv) The cycler was programmed to perform the temperature shift as given in Table 3.6.

(v) After completion of PCR cycles, sub-samples of the amplicons were analyzed by agarose gel electrophoresis just to check PCR amplification.

3.7.4.3 SSR PCR amplification

PCR amplification was undertaken by the procedure as given below. Amplifications were performed in 20 µl volume containing the following components:

Table 3.5 Reagents with their concentration and quantity used for single PCR reaction

S. No.	Reagent	Single tube (µl)
1	DNA template (50ng/µl)	4.0
2	Primer Forward (50ng/µl)	1.0
3	Primer Reverse (50ng/µl)	1.0
4	dNTPs mix (2.5mM each)	0.8
5	Taq buffer A (10X)	4.0
6	Taq polymerase (3U/µl)	0.6
7	Triple distilled water	8.6
	Total	**20 µl**

Table 3.6 PCR amplification protocol for SSR primers

Cycles	Denaturation		Annealing		Polymerization	
	Temp.	Time	Temp.	Time	Temp.	Time
First cycle	94^0C	5 min	-	-	-	-
35 cycles	94^0C	1 min	48-59^0C	1 min	72^0C	1 min
Last cycle	-	-	-	-	72^0C	7 min

3.7.5 Analysis of amplicons (PCR products): Agarose gel electrophoresis

Horizontal electrophoresis assembly was used for fractioning amplified product on agarose gel. Agarose gel (2.5%) was prepared in 100ml of 0.5 X TBE buffer dissolving 1.5g and 2.5g agarose, respectively. For each well, DNA sample and DNA loading dye were mixed in 10:1 ratio and loaded with a micropipette. Electrophoresis was done at 80 V for 2.5 hrs in 0.5X TBE electrophoresis buffer. The gel was then visualized on an UV transilluminator. The photograph of gel was taken in a gel documentation unit and saved.

3.7.6 Scoring of Bands

The SSR-PCR bands were examined under ultra violet transilluminator and photographed under gel documentation unit. The SSR bands were counted and scored as 1 for their presence or 0 for their absence. The sizes of the bands were estimated by using 100bp standard marker. The presence and absence of bands in all genotypes for 20 primers were used to generate Bi-nomial data using excel sheet. Bands were marked as present only if the DNA amplification produced the fragment of a particular sequence and absent if the DNA amplification lacked that fragment. The banding patterns of all genotypes against each primer were compared. Bands present in one genotype and absent in another genotype were regarded as variable and used to score for polymorphism. In order to check the informativeness and discriminatory power of SSR primers utilized in this study, certain parameters like polymorphism percentage, polymorphic information content and number of alleles were calculated.

(a) Percentage Polymorphism

It was calculated by dividing the polymorphic bands by the total number of scored bands:

$$\frac{\text{Number of polymorphic bands}}{\text{Total number of bands}} \times 100$$

(b) Polymorphism Information Content (PIC value)

The markers with more alleles have larger polymorphism information content. It was calculated as proposed by Roldan-Ruiz *et al*., (2000).

$$PIC = 2fi\ (1\text{-}fi)$$

where,

fi = frequency of bands present

1-fi = frequency of bands absent

3.7.7 Diversity Analysis

The collected data were aligned for the construction of cluster analysis and similarity matrix. The cluster analysis of 8 genotypes was constructed with the help of NTSYS software based on Unweighted paired group of arithmetic mean average (UPGMA). A tree like dendrogram was constructed using NTSYS software. Genotypes were divided in various clusters, sub-cluster and sub-sub clusters based on genetic diversity among them and linkage distance was calculated.

3.8 STATISTICAL ANALYSIS

3.8.1 Simple analysis of variance

The analysis of variance for design of experiment was done for partitioning the variance into treatments and replications according to procedure given by Panse and Sukhatme (1967) and the software used for analysis was STPR-3 in the following manner.

Table-3.7: Analysis of variance

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	'F' values
Replications	r - 1	RSS	RSS/r - 1= Mr	Mr/Me
Treatments	t – 1	TSS	TSS/t - 1= Mt	Mt/Me
Error	(r - 1) (t - 1)	ESS	ESS/(r-1)(t-1) = Me	
Total	rt-1			

Where,

r = number of replications

t = number of treatments (genotypes, including parents)

Mr = mean sum of square due to replications

Mt = mean sum of square due to treatments

Me = mean sum of square due to error

σ^2_g = genotypic variance

σ^2_e = error variance

The value of critical difference (CD) was used for testing the significance of means between any two treatments as follows:

CD = S Ed x 't' at error degree of freedom

Where,

S Ed = standard error of difference between two treatment means

$$\text{S Ed} = \sqrt{\frac{2\text{EMS}}{\text{r}}}$$

Where,

EMS is mean sum of square due to error and r is number of replications.

Range

This was estimated as the difference between the least and the greatest value of series of observations of accessions.

Coefficient of variance (C.V.)

Standard deviation expressed as percentage of mean is known as coefficient of variation (CV). It was calculated as:

$$\text{CV (\%)} = \frac{\text{SD}}{\bar{\text{X}}} \times 100$$

Where,

$\overline{X}$ = mean of character

SD = standard deviation

This statistic is generally used to judge the precision of the experiment.

3.8.2. Estimation of genotypic, phenotypic and environmental variances

The variance due to genotype, phenotype and environment were computed as follows.

$$\text{Genotypic variance } (\sigma g^2) = \frac{\text{MS due to genotypes (adj)} - \text{MS due to error (intra block)}}{\text{r (replication)}}$$

Environmental variance (σe^2) = Error mean sum of squares

Phenotypic variance (σp^2) = $\sigma g^2 + \sigma e^2$ (MS due to error)

Where, 'r' is number of replications.

Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variance were estimated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

Genotypic coefficient of variation (GCV)

$$\text{GCV } (\%) = \frac{Genotypic\ standard\ deviation}{Mean} \times 100$$

Phenotypic coefficient of variation (PCV)

$$\text{PCV } (\%) = \frac{Phenotypic\ standard\ deviation}{Mean} \times 100$$

Environment co-efficient of variation (ECV)

$$\text{ECV } (\%) = \frac{Environmental\ standard\ deviation}{Mean} \times 100$$

Where,

$\overline{X}$ = General mean

σ g = Genotypic standard deviation

σ p = Phenotypic standard deviation

GCV and PCV were classified as suggested by Burton and Devane (1953)

<10% : Low

10-20% : Moderate

>20% : High

3.8.3. Estimation of heritability

The broad sense heritability (h^2bs) was estimated by following the procedure suggested by Weber and Moorthy (1952) as indicated here below.

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

Where,

h^2 (%) = Heritability (Broad sense)

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

Heritability (h^2) in broad sense was categorized as suggested by Hanson *et al.*, 1956 and the same is given below.

< 50% - Low

50-75% - Moderate

> 75% - High

3.8.4. Genetic advance (GA)

Expected genetic advance was estimated by the method proposed by Johnson *et al.* (1955).

$GA = h^2 . K.\sigma p$

Where,

h^2 = Heritability in broad sense

σp = Phenotypic standard deviation of given character

K = Selection differential at 5% selection intensity (2.06).

3.8.5. Genetic advance as per cent of mean ($\overline{GA}$%)

$$G.A.(\%) = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

Genetic advance as per cent of mean was categorized as low, moderate and high as given by Johnson *et al.* (1955). It is as follows:

<10% - Low

10-20% - Moderate

>20% - High

3.8.6 Estimation of heterosis

The magnitude of heterosis was estimated in relation to mid-parent, better parent and standard parent. They were thus, calculated as percentage increase or decrease of F_1s over the mid-parent (MP), better parent (BP) and standard parent (SP) using the methods of Turner (1953) and Hayes *et al*. (1956). The formula used for estimation of heterosis given by Fonseca and Patterson (1968) was used.

For the characters like days to 50% flowering, first flower producing node, first fruit producing node and inter-nodal length, low scoring parent was considered as better parent in the estimation of heterobeltiosis. Whereas, high scoring parent was considered as a better parent for the rest of the traits.

Heterosis for each trait was computed and the significance of F_1 heterosis values were tested by comparing them with critical difference (CD) values obtained separately for MP and BP employing the formulae given below.

3.8.6.1 For mid-parent heterosis

$$\text{Per cent heterosis over mid-parent (MP)} = \frac{F1 - MP}{MP} \times 100$$

$$\text{Where, mid-parent} = \frac{P1+P2}{2}$$

Where, P_1 and P_2 are parents of a hybrid combination.

The deviations for heterosis were tested for their significance by the following standard errors.

$$SE = \sqrt{\frac{3}{2}\frac{MSE}{r}}$$

Where,

MSE = Mean sum of square due to error obtained from general analysis of variance

r = Number of replications

C.D. = S.E.(d) x 't' value at error df (P = 0.05 and P 0.01 levels of significance)

Significance of heterosis values was tested using 't' test:

$$t = \frac{\overline{F_1} - \overline{MP}}{S.E.\ of\ heterosis\ over\ \overline{MP}}$$

Calculated 't' value was compared with table value at error degrees of freedom for significance.

3.8.6.2 For better parents heterosis

Per cent heterosis over better parent (BP) = $\frac{F1 - BP}{BP} x\ 100$

Per cent heterosis over better parent is also called as heterobeltiosis (BH).

CD for better parents heterosis = SE x 't' value.

$$SE = \sqrt{\frac{2MSE}{r}}$$

Where,

MSE = Mean sum of square due to error obtained from general analysis of variance

r = Number of replications

t = Table 't' value at error degrees of freedom

Significance of heterosis values was tested using 't' test:

$$t = \frac{\overline{F_1} - \overline{BP}}{S.E.\ of\ heterosis\ over\ BP}$$

Calculated 't' value was compared with table value at error degrees of freedom for significance.

3.8.6.3 For standard parents heterosis

$$\text{Per cent heterosis over standard parent (SP)} = \frac{F1 - SP}{SP} \times 100$$

Per cent heterosis over standard parent is also called as standard heterosis.

CD for standard parents heterosis = SE x 't' value.

$$SE = \sqrt{\frac{2MSE}{r}}$$

Where,

MSE = Mean sum of square due to error obtained from general analysis of variance

r = Number of replications

t = Table 't' value at error degrees of freedom

Significance of heterosis values was tested using 't' test:

$$t = \frac{\overline{F_1} - \overline{SP}}{\text{S.E. of heterosis over SP}}$$

Calculated 't' value was compared with table value at error degrees of freedom for significance.

The analysis for estimation of heterosis was done through STPR-11 (G.B.P.U.A. & T., Pantnagar) software.

3.8.7 Combining ability analysis

The combining ability analysis for different characters was carried out following the method 2 model 1 of Griffing (1956), where parents and F_1's were included but not the reciprocals. Thus the experimental material for this method comprises of n(n+1)/2 genotypes.

The mathematical model for the combining ability analysis is assumed to be:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{bc} \sum_k \sum_l e_{ijkl}$$

Where,

ij = 1, 2,----------, p (p = number of parents involved in diallel)

k = 1, 2, ----------, r (r = number of replications)

l = 1, 2, ----------, c (c = number of observations taken in each plot)

μ = the population mean

g_i, g_j = GCA effect of i^{th} and j^{th} parents, respectively

Sij = the interaction, *i.e.* the specific combining ability (SCA) for the cross between i^{th} and j^{th} parents such that Sij = Sji.

e_{ijkl} = environmental effect associated with $ijkl^{th}$ observation

The restriction imposed on this mathematical model is:

(i) $\sum_i g_i = 0$

(ii) $\sum_j s_{ij} = 0$

The orthogonal partitioning of the variety sum of squares in the ANOVA is as follows:

Table 3.8: Analysis of variance for method 2, model 1 with expectations of mean squares

Sources	**d.f.**	**Sum of square**	**Mean sum of square**	**Expectations of mean squares**
G.C.A.	p-1	S_g	M_g	$\sigma_e^2 + (p+2)\left[\frac{1}{p-1}\right]\sum_{x=1}^{p} g_i^2$
S.C.A.	p(p-1)/2	S_s	M_s	$\sigma_e^2 + \frac{2}{p(p-1)}\sum_{i=1}^{p}\sum_{j=1}^{p} s_{ij}^2$
Error	(r-1) (t-1)	S_e	M_e	σ_e^2

Where,

P = number of parents

$$S_g = \frac{1}{P+2}\left[\sum_{i=1}^{} (Yi + Yii)^2 - \frac{4}{p} Y_{..}^2\right]$$

$$S_s = \sum_i \leq \sum_j Y_{ij}^2 - \frac{1}{P+2} \sum_{i=l} (Yi + Yii)^2 + \frac{2}{(P+1)(P+2)} Y_{..}^2$$

Y_i = total of the array involving of i^{th} parent

Y_{ii} = mean value of the i^{th} parent of the array

Y_{ij} = mean value of i x j^{th} cross

Y.. = total of all the elements in the diallel table without

$$\text{Reciprocals} \left[\frac{P\,(P-1)}{2} \text{ progenies and P parental lines} \right]$$

Me = error mean square

Mg, Ms and Me were obtained by dividing each sum of squares by the corresponding degree of freedom. The following 'F' ratios were used for testing the significance of GCA and SCA effects.

(i) To test significance of differences among GCA variance of character.

$$F = \frac{M_g}{M_e}$$

The calculated F-value is tested against table F-value at (P-1) vs. error degree of freedom.

(ii) To test the significance of differences among sca variance of a character,

$$F = \frac{M_s}{M_e}$$

The calculated F-value is tested against table F-value at [P(P-1)/2] vs. error degree of freedom.

The software used for analysis of combining ability (GCA and SCA) was OPSTAT (HAU, Hisar)

3.8.8 Estimation of combining ability effects

When MS_g and MS_s both are significant, they justify the adequacy of calculating general combining ability or GCA (g_i) and specific combining ability or

SCA (S_{ij}) effects for each parent and cross, respectively. These were obtained by using the following formulae:

(a) Estimation of GCA effects

$$g_i = \frac{1}{P+2}\left[\sum (Y_i + Y_{ii}) - \frac{2}{P} Y..\right]$$

(b) Estimation of SCA effects

$$s_{ij} = Y_{ij} \frac{1}{(P+2)} (Y_i + Y_{ii} + Y_j + Y_{ij}) + \frac{2}{(P+1)(P+2)} Y..$$

Where,

Y_j = total of the array involving j^{th} parent

Standard errors

The standard errors, which are necessary in connection with testing the significance of GCA and SCA effects and differences between various GCA as well as SCA effects were calculated as:

Standard error of combining ability effects

$$SE(g_i) = \left[\frac{P-1}{P(P+2)} \sigma_e^2\right]^{\frac{1}{2}}$$

$$SE(s_{ij}) = \left[\frac{P(P-1)}{(P+1)(P+2)} \sigma_e^2\right]^{\frac{1}{2}}$$

To test the significance of each g_i and S_{ij},'t' values are calculated as follows:

For GCA effect

$$t(g_i) = \frac{g_i}{SE(g_i)}$$

For SCA effect

$$t(S_{ij}) = \frac{s_{ij}}{SE(s_{ij})}$$

The calculated value of ratio is referred to the 't' table for error degree of freedom.

3.8.9 Estimation of genetic components and other genetic parameters for method 2 model I of Griffing (1956).

The genetic variance parameters were estimated as given below:

i. $\sigma^2 g = (MS_g - MSe)/(p+2)$

ii. $\sigma^2 s = MS_s - MS_e$

iii. $\sigma^2 e = MS_e$

iv. $\sigma^2 A = 2\sigma^2 g$

v. $\sigma^2 D = \sigma^2 s$

Degree of dominance

The additive ('D') and dominance ('H') genetic variance were used to estimate dominance ratio.

Degree of dominance (dominance ratio) = $\sqrt{(\sigma^2 D/\sigma^2 A)}$

If dominance ratio is:

a. 1 show complete dominance

b. >1 show over dominance

c. <1 show partial dominance

Results and Discussion

Chapter 4 RESULTS AND DISCUSSION

The present investigation on **"Studies on combining ability, molecular diversity and response to late blight (*Phytophthora infestans* (Mont.) de Bary) in tomato (*Solanum lycopersicum* L.) under polyhouse condition"** was carried out at V.R.C., Pantnagar (Uttarakhand). The results obtained in respect of various aspects of the present investigation are described in this chapter under following heads:-

4.1 Analysis of Variance (ANOVA)

4.2 Genetic variability for different yield related and quality traits

4.3 To assess the molecular diversity of parental lines

4.4 To estimate the extent of heterosis over its parents

4.5 To study the combining ability, nature and magnitude of gene action

4.6 To screen the parents and F_1 hybrids of tomato against late blight (*Phytophthora infestans*)

4.7 To estimate the percentage fruit damage due to new invasive pest American pin worm (*Tuta absoluta*) for parents and hybrids

4.1 Analysis of Variance (ANOVA)

Mean data of fifteen yield related and ten quality traits were subjected to Analysis of variance (ANOVA) for Randomized Block Design (RBD) is presented in Table 4.1 and Table 4.2. The mean sum of square due to treatments was found highly significant for yield related and quality traits under study at 1% and 5% level of significance, which indicated that considerable amount of variability were present in the genotypes included in the study. Hence, there is ample scope for selection of promising genotypes in breeding programme for yield related and quality traits. Similar results with respect to analysis of variance also reported by Narolia *et al*. (2012), Kumar *et al*. (2013), Agarwal *et al*. (2014), Meiti *et al*. (2014), Reddy *et al*. (2014), Singh *et al*. (2014), Meena *et al*. (2015), Prajapati *et al*. (2015), Shokat *et al*. (2015), Ullah *et al*. (2015), Hasan *et al*. (2016), Kumar and Singh (2016), Kumar *et al*. (2017a) and Kumar *et al.* (2017c).

Table 4.1: Analysis of variance for fifteen yield related traits in tomato

S. N.	Characters	df	Mean sum of squares		
			Replication	Genotype	Error
			2	35	70
1	Days to 50 per cent flowering		24.482	40.012**	5.415
2	Days to first fruit set		25.817	48.642**	4.732
3	Days to first fruit ripening		0.190	96.107**	2.882
4	Number of flowers per cluster		0.889	44.451**	0.775
5	Number of fruits per cluster		0.073	12.547**	0.268
6	Number of fruits per plant		60.911	8,771.391**	79.967
7	Internodal length (cm)		0.126	7.068**	0.821
8	Average fruit weight (g)		168.874	3,880.309**	42.306
9	Fruit length (cm)		0.108	2.774**	0.069
10	Fruit width (cm)		0.116	2.490**	0.131
11	Fruit shape index		0.021	0.089**	0.012
12	Plant height (cm)		577.632	8,026.012**	1,646.279
13	100 seed weight (g)		0.0005	0.0076**	0.0004
14	Fruit yield per plant (kg)		0.0005	5.051**	0.181
15	Fruit yield per hectare (t/ha)		0.833	6,255.634**	224.116

* Significant at 5% level of probability
** Significant at 1% level of probability

Table 4.2: Analysis of variance for ten quality traits in tomato

S. N.	Characters	df	Mean sum of squares		
			Replication	Genotype	Error
			2	35	70
1	Number of locules per fruit		0.028	1.505**	0.085
2	Pericarp thickness (cm)		0.031	0.110**	0.009
3	Diameter of stalk scar (cm)		0.045	0.403**	0.012
4	Fruit firmness (kg/cm^2)		0.200	1.112**	0.042
5	Total soluble solids (%)		0.146	2.053**	0.109
6	pH of fruit juice		0.016	0.103**	0.018
7	Titratable acidity (%)		0.0005	0.022**	0.001
8	Ascorbic acid (mg/100g)		4.455	24.184**	3.904
9	Lycopene (mg/100g)		0.922	10.655**	0.638
10	Total carotenoids (mg/100g)		0.305	31.571**	1.161

* Significant at 5% level of probability
** Significant at 1% level of probability

4.2 Genetic variability for different yield related and quality traits

4.2.1 Mean performance of parents and F_1 hybrids

4.2.1.1 Yield related traits

The *per se* performance of parents and F_1 hybrids for yield related traits were computed and have been given in Table 4.3. The character wise description of yield related parameters are as follows:

4.2.1.1.1 Days to 50 per cent flowering

Mean values for days to 50 per cent flowering ranged between 30.33 to 43.67 days with an average value 35.43 days. Among the parents, PCT-1 (31.67) and PBT-2 (32.67) were recorded the minimum days to 50 per cent flowering. However, maximum days to 50 per cent flowering were observed in PBT-13 (43.00) and PBT-4 (38.67). Among the crosses, minimum days to 50 per cent flowering was observed in PCT-1 x PBT-4 (30.33), PBT-9 x PBT-2 (30.33) and PBT-13 x PBT-10 (30.33). Whereas, maximum values for same character were noticed in PPT-2 x PBT-13 (43.67), PPT-2 x PBT-5 (39.67) and PBT-9 x PBT-10 (39.67).

4.2.1.1.2 Days to first fruit set

Perusal of data revealed that mean values for days to first fruit set ranged from 43.00 to 57.47 days with an average of 49.03 days. Among the parents, PCT-1 (43.50) and PBT-2 (44.20) recorded minimum mean values for days to first fruit set whereas, maximum values were recorded in PBT-13 (56.27) and PBT-4 (51.60). Among the crosses, minimum values for same character was noticed in PCT-1 x PBT-4 (43.00), PCT-1 x PBT-5 (43.33) and PBT-9 x PBT-2 (43.53). However, maximum mean values were recorded in PPT-2 x PBT-13 (57.47), PPT-2 x PBT-5 (54.40) and PPT-2 x PBT-9 (54.27).

4.2.1.1.3 Days to first fruit ripening

Mean values for days to first fruit ripening ranged from 68.20 to 95.13 days and the mean value for same trait was 84.01 days. Among the parents, minimum days to first fruit ripening were recorded in PCT-1 (68.20) and PBT-10 (74.40) whereas, maximum days to first fruit ripening were observed in PBT-13 (95.13) and PBT-4 (88.80). Among the hybrids generated, PCT-1 x PBT-5 (75.93), PBT-9 x PBT-5

(76.27) and PBT-9 x PBT-2 (77.53) recorded minimum days to first fruit ripening. However, maximum days to first fruit ripening were noticed in PPT-2 x PBT-13 (92.93), PPT-2 x PBT-2 (92.27) and PPT-2 x PBT-5 (90.67).

4.2.1.1.4 Number of flowers per cluster

Perusal of data revealed that mean values for number of flowers per cluster ranged from 7.67 to 26.40 with the mean value 12.56. Among the parents, maximum values for number of flowers per cluster was noticed in PCT-1 (22.00) and PPT-2 (13.73) whereas, minimum values were recorded in PBT-2 (7.67) and PBT-4 (8.47). Among the 28 F_1s, PCT-1 x PBT-5 (26.40), PBT-5 x PBT-4 (17.93) and PCT-1 x PBT-13 (15.87) recorded maximum number of flowers per cluster. However, cross combination PBT-10 x PBT-4 (8.93), PPT-2 x PBT-9 (9.47), PPT-2 x PBT-5 (9.80) and PPT-2 x PBT-4 (9.80) recorded minimum number of flowers per cluster.

4.2.1.1.5 Number of fruits per cluster

Number of fruits per cluster ranged from 5.47 to 14.80 with an average value 7.57. Among the parents, maximum values for this trait were recorded in PCT-1 (12.87) and PPT-2 (8.33) whereas, PBT-13 (5.47), PBT-9 (5.67) and PBT-4 (5.67) recorded minimum values for same trait. Among the 28 F_1s, maximum values for number of fruits per cluster were recorded in PCT-1 x PBT-5 (14.80), PCT-1 x PPT-2 (10.40) and PBT-5 x PBT-4 (9.93), albeit minimum values were recorded in PBT-10 x PBT-4 (5.73), PBT-5 x PBT-10 (5.80), PPT-2 x PBT-13 (5.87) and PBT-9 x PBT-10 (5.87).

4.2.1.1.6 Number of fruits per plant

Perusal of data revealed that mean values for number of fruits per plant ranged from 27.39 to 355.73 with an estimated mean value 55.12. Among the parents, maximum values for number of fruits per plant were noticed in PCT-1 (355.73) and PPT-2 (54.93) whereas, minimum values were recorded in PBT-2 (27.39) and PBT-4 (30.25). Among the 28 F_1s, PCT-1 x PBT-5 (94.78), PBT-5 x PBT-4 (84.81) and PCT-1 x PPT-2 (78.73) recorded maximum number of fruits per plant. However, cross combination PBT-9 x PBT-10 (32.09), PBT-9 x PBT-2 (33.27) and PPT-2 x PBT-13 (33.50) recorded minimum number of fruits per plant.

Table 4.3: Mean performance of tomato genotypes for different yield related traits

S.N.	Genotypes	Days to 50% flowering	Days to first fruit set	Days to first fruit ripening	No. of flowers/ cluster	No. of fruits/ cluster	No. of fruits/ plant	Internodal length (cm)	Avg. fruit wt. (g)
1	PCT-1	31.67	43.50	68.20	22.00	12.87	355.73	10.00	9.90
2	PPT-2	37.67	50.33	82.40	13.73	8.33	54.93	10.27	77.00
3	PBT-9	36.00	49.20	83.13	9.13	5.67	30.37	11.00	109.60
4	PBT-5	36.67	48.73	81.93	10.00	7.13	40.67	9.27	89.07
5	PBT-2	32.67	44.20	81.40	7.67	5.87	27.39	13.07	119.27
6	PBT-13	43.00	56.27	95.13	9.20	5.47	31.89	13.07	69.80
7	PBT-10	35.00	47.07	74.40	10.67	7.93	47.19	10.27	76.27
8	PBT-4	38.67	51.60	88.80	8.47	5.67	30.25	12.80	91.53
9	PCT-1 x PPT-2	33.00	47.67	84.13	15.13	10.40	78.73	10.53	77.00
10	PCT-1 x PBT-9	36.33	49.27	82.93	13.33	9.20	70.99	10.93	31.73
11	PCT-1 x PBT-5	31.00	43.33	75.93	26.40	14.80	94.78	11.20	71.73
12	PCT-1 x PBT-2	35.67	49.47	81.53	14.27	8.60	49.74	9.13	34.80
13	PCT-1 x PBT-13	38.00	52.07	86.20	15.87	8.13	56.60	9.67	43.40
14	PCT-1 x PBT-10	35.00	49.93	81.80	12.87	7.13	41.47	11.80	29.20
15	PCT-1 x PBT-4	30.33	43.00	79.93	15.47	9.33	75.11	11.00	69.07
16	PPT-2 x PBT-9	39.33	54.27	88.67	9.47	6.33	41.12	10.40	139.20
17	PPT-2 x PBT-5	39.67	54.40	90.67	9.80	6.40	38.38	8.53	107.60
18	PPT-2 x PBT-2	38.33	53.40	92.27	10.40	6.47	37.27	9.00	133.93
19	PPT-2 x PBT-13	43.67	57.47	92.93	10.13	5.87	33.50	11.20	121.27

20	PPT-2 x PBT-10	38.67	53.00	88.93	9.93	6.27	42.24	10.27	93.33
21	PPT-2 x PBT-4	39.00	52.53	86.60	9.80	6.47	34.03	9.40	125.93
22	PBT-9 x PBT-5	31.00	44.87	76.27	12.53	6.27	35.27	8.07	141.53
23	PBT-9 x PBT-2	30.33	43.53	77.53	11.33	6.53	33.27	8.87	68.47
24	PBT-9 x PBT-13	39.00	53.27	88.67	10.33	6.67	35.59	9.20	103.73
25	PBT-9 x PBT-10	39.67	54.00	90.20	11.27	5.87	32.09	11.27	109.07
26	PBT-9 x PBT-4	36.67	50.53	89.73	15.47	8.07	60.74	7.80	95.40
27	PBT-5 x PBT-2	32.67	46.00	81.73	11.20	6.73	41.49	9.07	64.00
28	PBT-5 x PBT-13	32.00	45.47	82.40	15.07	7.60	48.65	10.47	31.33
29	PBT-5 x PBT-10	31.67	44.40	81.73	9.87	5.80	35.75	8.80	106.27
30	PBT-5 x PBT-4	31.67	45.47	83.60	17.93	9.93	84.81	13.40	120.27
31	PBT-2 x PBT-13	33.67	46.67	79.47	13.00	9.60	51.33	12.40	123.80
32	PBT-2 x PBT-10	33.33	46.80	83.40	10.73	6.87	38.21	12.53	61.80
33	PBT-2 x PBT-4	32.33	48.00	82.33	11.07	6.60	48.96	12.93	91.87
34	PBT-13 x PBT-10	30.33	44.27	83.80	15.13	7.87	50.94	11.93	159.93
35	PBT-13 x PBT-4	38.00	52.27	90.40	14.67	7.93	39.65	11.60	106.40
36	PBT-10 x PBT-4	33.67	48.67	85.33	8.93	5.73	35.31	9.73	63.60
GM		**35.43**	**49.03**	**84.01**	**12.56**	**7.57**	**55.12**	**10.58**	**88.00**
Sem		1.34	1.27	0.98	0.508	0.299	5.17	0.52	3.76
C.D. (1%)		5.03	4.70	3.67	1.90	1.12	19.33	1.96	14.06
C.D. (5%)		3.79	3.54	2.77	1.44	0.85	14.56	1.48	10.59
C.V.		6.57	4.44	2.02	7.01	6.84	16.22	8.57	7.39

S.N.	Genotypes	Fruit length (cm)	Fruit width (cm)	Fruit shape index	Plant height (cm)	100 seed wt. (g)	Fruit yield/plant (kg)	Fruit yield/ha (t/ha)
1	PCT-1	2.11	1.83	1.17	409.07	0.13	3.71	130.44
2	PPT-2	5.37	5.04	1.07	403.20	0.35	4.06	142.97
3	PBT-9	5.41	4.96	1.09	316.47	0.38	3.28	115.31
4	PBT-5	4.46	5.07	0.89	338.13	0.36	3.20	112.50
5	PBT-2	4.62	5.40	0.86	411.67	0.40	3.10	108.97
6	PBT-13	5.15	4.40	1.18	351.93	0.37	1.34	47.27
7	PBT-10	5.01	5.62	0.89	330.40	0.38	3.59	126.30
8	PBT-4	6.55	4.14	1.59	236.87	0.29	2.48	87.15
9	PCT-1 x PPT-2	4.07	3.62	1.13	401.40	0.39	3.06	107.75
10	PCT-1 x PBT-9	3.14	3.44	0.92	438.33	0.33	2.04	71.71
11	PCT-1 x PBT-5	3.76	3.81	0.99	431.67	0.30	6.83	240.37
12	PCT-1 x PBT-2	3.21	3.24	0.99	405.73	0.39	2.46	86.46
13	PCT-1 x PBT-13	3.99	3.82	1.05	423.33	0.40	2.19	76.89
14	PCT-1 x PBT-10	3.65	3.76	0.97	411.40	0.36	2.08	73.11
15	PCT-1 x PBT-4	5.11	4.09	1.25	447.53	0.31	3.41	119.98
16	PPT-2 x PBT-9	6.10	5.42	1.13	372.07	0.37	5.45	191.93
17	PPT-2 x PBT-5	5.21	4.99	1.05	332.40	0.36	4.13	145.32
18	PPT-2 x PBT-2	5.46	5.31	1.03	397.87	0.36	4.93	173.34
19	PPT-2 x PBT-13	5.36	4.72	1.14	420.00	0.38	4.02	141.33
20	PPT-2 x PBT-10	4.38	4.03	1.09	434.40	0.35	3.85	135.53

21	PPT-2 x PBT-4	5.82	4.47	1.30	430.00	0.36	4.04	142.06
22	PBT-9 x PBT-5	5.73	6.28	0.92	355.87	0.36	4.83	169.97
23	PBT-9 x PBT-2	3.89	4.39	0.89	236.13	0.42	2.41	84.70
24	PBT-9 x PBT-13	4.41	4.77	0.93	427.33	0.34	3.47	122.21
25	PBT-9 x PBT-10	4.93	4.71	1.05	330.53	0.38	2.90	102.15
26	PBT-9 x PBT-4	5.15	4.43	1.17	381.73	0.35	5.72	201.31
27	PBT-5 x PBT-2	4.19	4.38	0.96	346.67	0.39	2.49	87.61
28	PBT-5 x PBT-13	3.17	3.26	0.98	373.20	0.33	2.29	80.53
29	PBT-5 x PBT-10	5.26	4.85	1.09	427.60	0.33	3.89	136.77
30	PBT-5 x PBT-4	5.30	5.06	1.05	361.00	0.32	5.71	200.79
31	PBT-2 x PBT-13	5.05	5.43	0.93	368.40	0.39	6.19	217.82
32	PBT-2 x PBT-10	4.23	4.14	1.03	406.53	0.39	2.92	102.90
33	PBT-2 x PBT-4	5.68	3.46	1.66	411.27	0.28	3.06	107.57
34	PBT-13 x PBT-10	6.05	6.35	0.95	448.67	0.39	5.52	194.33
35	PBT-13 x PBT-4	5.18	5.47	0.95	420.87	0.36	4.26	149.89
36	PBT-10 x PBT-4	4.89	4.67	1.05	386.13	0.39	3.09	108.68
GM		**4.75**	**4.52**	**1.07**	**384.05**	**0.35**	**3.67**	**129.00**
Sem		0.15	0.21	0.06	23.43	0.01	0.25	8.64
C.D. (1%)		0.57	0.78	0.23	87.73	0.04	0.92	32.67
C.D. (5%)		0.43	0.59	0.18	66.08	0.03	0.69	24.38
C.V.		5.52	7.99	10.18	10.56	5.78	11.60	11.61

4.2.1.1.7 Internodal length (cm)

Mean values for internodal length ranged from 7.80 to 13.40 cm with an average of 10.58 cm. Among the parents, PBT-5 (9.27) and PCT-1 (10.00) recorded minimum internodal length while, parents namely PBT-2 (13.07) and PBT-13 (13.07) recorded maximum internodal length. Among the 28 cross combinations, PBT-9 x PBT-4 (7.80), PBT-9 x PBT-5 (8.07) and PPT-2 x PBT-5 (8.53) recorded minimum internodal length whereas, maximum mean values were recorded in PBT-5 x PBT-4 (13.40), PBT-2 x PBT-4 (12.93) and PBT-2 x PBT-10 (12.53).

4.2.1.1.8 Average fruit weight (g)

Average fruit weight exhibited variation among thirty six treatments which ranged from 9.90 to 159.93g with an average of 88.00g. Among the parents, PBT-2 (119.27) and PBT-9 (109.60) recorded maximum average fruit weight while, minimum average fruit weight was recorded in PCT-1 (9.90) and PBT-13 (69.80). Among the F_1 hybrids generated, maximum average fruit weight was recorded in PBT-13 x PBT-10 (159.93), PBT-9 x PBT-5 (141.53) and PPT-2 x PBT-9 (139.20). The minimum values for the same characters were recorded in PCT-1 x PBT-10 (29.20), PBT-5 x PBT-13 (31.33) and PCT-1 x PBT-9 (31.73).

4.2.1.1.9 Fruit length (cm)

Mean values for fruit length ranged from 2.11 to 6.55 cm and the average value was 4.75 cm. Among the parents, PBT-4 (6.55) and PBT-9 (5.41) recorded maximum values for this trait, although minimum values were recorded in PCT-1 (2.11) and PBT-5 (4.46). Among the 28 cross combinations, maximum values for fruit length were recorded in PPT-2 x PBT-9 (6.10), PBT-13 x PBT-10 (6.05) and PPT-2 x PBT-4 (5.82) while, PCT-1 x PBT-9 (3.14), PBT-5 x PBT-13 (3.17) and PCT-1 x PBT-2 (3.21) recorded minimum values for the same trait.

4.2.1.1.10 Fruit width (cm)

Fruit width ranged from 1.83 cm to 6.35 cm with an average value 4.52 cm. Among the parents, maximum values for this trait were recorded in PBT-10 (5.62) and PBT-2 (5.40) whereas, PCT-1 (1.83) and PBT-4 (4.14) recorded minimum values for same trait. Among the 28 F_1s, maximum values for fruit width were recorded in PBT-

13 x PBT-10 (6.35), PBT-9 x PBT-5 (6.28) and PBT-13 x PBT-4 (5.47), albeit minimum values were recorded in PCT-1 x PBT-2 (3.24), PBT-5 x PBT-13 (3.26) and PCT-1 x PBT-9 (3.44).

4.2.1.1.11 Fruit shape index

Mean values for fruit shape index ranged from 0.86 to 1.66 and the average value was 1.07. PBT-4 (1.59) and PBT-13 (1.18) recorded maximum values among the parents whereas, minimum values were found in PBT-2 (0.86), PBT-5 (0.89) and PBT-10 (0.89). Among the F_1s, maximum values for fruit shape index were recorded in PBT-2 x PBT-4 (1.66), PPT-2 x PBT-4 (1.30) and PCT-1 x PBT-4 (1.25) while, PBT-9 x PBT-2 (0.89), PCT-1 x PBT-9 (0.92) and PBT-9 x PBT-5 (0.92) recorded minimum values for the same trait.

4.2.1.1.12 Plant height (cm)

Plant height exhibited variation among 36 treatments which ranged from 236.13 to 448.67 cm with a mean value 384.05 cm. Among the parents, maximum mean values for plant height were recorded in PBT-2 (411.67) and PCT-1 (409.07) whereas, minimum values observed in PBT-4 (236.87) and PBT-9 (316.47). Among 28 F_1s, PBT-13 x PBT-10 (448.67), PCT-1 x PBT-4 (447.53) and PCT-1 x PBT-9 (438.33) have maximum values for plant height while, the cross combination PBT-9 x PBT-2 (236.13), PBT-9 x PBT-10 (330.53) and PPT-2 x PBT-5 (332.40) recorded minimum mean values for plant height.

4.2.1.1.13 100 seed weight (g)

Perusal of data revealed that mean values for 100 seed weight ranged from 0.13 to 0.42g and average value was 0.35g. Among the parents, maximum 100 seed weight was recorded in PBT-2 (0.40), PBT-9 (0.38) and PBT-10 (0.38) whereas, PCT-1 (0.13) and PBT-4 (0.29) recorded minimum 100 seed weight. Among the 28 cross combinations, PBT-9 x PBT-2 (0.42), PCT-1 x PBT-13 (0.40) and seven crosses with 0.39g of 100 seed weight had maximum mean values for the trait while, cross combinations *viz*., PBT-2 x PBT-4 (0.28), PCT-1 x PBT-5 (0.30) and PCT-1 x PBT-4 (0.31) recorded minimum 100 seed weight.

4.2.1.1.14 Fruit yield per plant (kg)

Mean values for fruit yield per plant was ranged between 1.34 to 6.83 kg and the average value was 3.67 kg. Among the parents, maximum values for the same trait were observed in PPT-2 (4.06) and PCT-1 (3.71) whereas, minimum values were observed in PBT-13 (1.34) and PBT-4 (2.48). Among the 28 cross combinations, PCT-1 x PBT-5 (6.83), PBT-2 x PBT-13 (6.19) and PBT-9 x PBT-4 (5.72) showed maximum values for fruit yield per plant. However, minimum values for same trait was observed in PCT-1 x PBT-9 (2.04), PCT-1 x PBT-10 (2.08) and PCT-1 x PBT-13 (2.19).

4.2.1.1.15 Fruit yield per hectare (t/ha)

Perusal of data revealed that mean values for fruit yield per hectare ranged from 47.27 to 240.37 t/ha with an average 129.00 t/ha. Among the parents, PPT-2 (142.97) and PCT-1 (130.44) recorded the highest fruit yield per hectare while, lowest fruit yield per hectare was recorded in PBT-13 (47.27) and PBT-4 (87.15). Among the 28 F_1s, PCT-1 x PBT-5 (240.37), PBT-2 x PBT-13 (217.82) and PBT-9 x PBT-4 (201.31) exhibited highest fruit yield per hectare while, PCT-1 x PBT-9 (71.71), PCT-1 x PBT-10 (73.11) and PCT-1 x PBT-13 (76.89) recorded lowest fruit yield per hectare.

4.2.1.2 Quality traits

4.2.1.2.1 Number of locules per fruit

Mean values for number of locules per fruit was ranged from 1.67 to 5.00 and the average value was 2.56. Among the parents, maximum values for the same trait were observed in PBT-2 (3.00) and PBT-13 (3.00) whereas, minimum values were observed in PPT-2 (2.00), PBT-9 (2.00) and PBT-10 (2.00). Among the 28 cross combinations, PBT-2 x PBT-10 (5.00), PBT-2 x PBT-13 (4.33) and PBT-9 x PBT-5 (3.33) recorded maximum values for number of locules per fruit. However, minimum values for same trait were observed in PPT-2 x PBT-9 (1.67) and twelve other crosses showed 2.00 number of locules per fruit (Table 4.4).

4.2.1.2.2 Pericarp thickness (cm)

Perusal of data revealed that mean values for pericarp thickness ranged from 0.35 to 1.21 cm with an average value 0.83 cm. Among the parents, PBT-10 (0.92) and PBT-5 (0.90) recorded the highest pericarp thickness while, lowest pericarp thickness

recorded in PCT-1 (0.35) and PPT-2 (0.69). Among the 28 F_1s, PBT-9 x PBT-2 (1.21), PBT-2 x PBT-4 (1.14) and PPT-2 x PBT-4 (1.13) exhibited highest pericarp thickness while, PCT-1 x PBT-13 (0.51), PBT-5 x PBT-13 (0.56) and PCT-1 x PBT-2 (0.57) recorded lowest pericarp thickness.

4.2.1.2.3 Diameter of stalk scar (cm)

Diameter of stalk scar exhibited variation among 36 treatments which ranged from 0.31 to 2.17 cm and the estimated mean value was 1.11 cm. Among the parents, minimum mean values for diameter of stalk scar were recorded in PCT-1 (0.31) and PBT-10 (0.73) whereas, maximum values observed in PBT-13 (1.19), PBT-2 (0.91) and PBT-4 (0.91). Among the 28 F_1s, PBT-5 x PBT-13 (0.72), PCT-1 x PBT-2 (0.73) and PCT-1 x PBT-13 (0.74) recorded minimum values for diameter of stalk scar while, the cross combination PBT-13 x PBT-10 (2.17), PPT-2 x PBT-10 (1.62) and PBT-5 x PBT-10 (1.58) recorded maximum mean values for diameter of stalk scar.

4.2.1.2.4 Fruit firmness (kg/cm^2)

Perusal of data revealed that mean values for fruit firmness ranged from 3.62 to 5.81 kg/cm^2 with an average value 4.54 kg/cm^2. Among the parents, PBT-4 (5.36) and PBT-5 (5.22) recorded maximum mean values for fruit firmness whereas, minimum values were recorded in PBT-9 (3.63) and PCT-1 (3.68). Among the crosses, maximum values for same character was noticed in PBT-9 x PBT-5 (5.81), PBT-2 x PBT-13 (5.42), PPT-2 x PBT-13 (5.38) and PBT-9 x PBT-13 (5.38). However, minimum mean values were recorded in PBT-5 x PBT-2 (3.62), PCT-1 x PBT-13 (3.78) and PCT-1 x PBT-2 (3.83).

4.2.1.2.5 TSS (%)

TSS (%) exhibited variation among 36 treatments which ranged from 4.37 to 8.07 per cent and the mean value was 6.20 per cent. Among the parents, maximum mean values for TSS (%) were recorded in PCT-1 (8.07) and PPT-2 (6.97) whereas, minimum values were found in PBT-9 (4.80) and PBT-4 (5.37). Among the 28 F_1s, PCT-1 x PPT-2 (7.43), PCT-1 x PBT-10 (7.33), PCT-1 x PBT-5 (7.20) and PCT-1 x PBT-2 (7.20) recorded maximum values for TSS while, among the cross combination, PBT-5 x PBT-4 (4.37), PCT-1 x PBT-4 (5.03) and PBT-13 x PBT-10 (5.03) recorded minimum mean values for TSS.

Table 4.4: Mean performance of tomato genotypes for different quality traits

S.N.	Genotypes	No. of locules/fruit	Pericarp thickness (cm)	Dia. of stalk scar (cm)	Fruit firmness (kg/cm^2)	TSS (%)	pH of fruit juice	Titratable acidity (%)	Ascorbic acid (mg/100 g)	Lycopene (mg/100g)	Total carotenoids (mg/100g)
1	PCT-1	2.33	0.35	0.31	3.68	8.07	4.72	0.46	40.11	7.81	13.56
2	PPT-2	2.00	0.69	0.79	4.34	6.97	4.64	0.28	30.00	13.14	21.50
3	PBT-9	2.00	0.79	0.80	3.63	4.80	4.66	0.27	25.72	9.63	14.77
4	PBT-5	2.33	0.90	0.87	5.22	5.40	4.78	0.22	26.17	10.31	15.17
5	PBT-2	3.00	0.82	0.91	3.75	5.87	4.91	0.25	25.33	9.45	14.45
6	PBT-13	3.00	0.83	1.19	5.04	6.70	4.78	0.44	26.83	10.53	17.18
7	PBT-10	2.00	0.92	0.73	4.10	6.50	4.77	0.37	28.33	12.93	20.27
8	PBT-4	2.67	0.74	0.91	5.36	5.37	4.67	0.35	27.11	7.19	12.33
9	PCT-1 x PPT-2	2.00	0.94	1.17	4.19	7.43	4.26	0.63	33.06	11.19	18.46
10	PCT-1 x PBT-9	3.00	0.81	1.46	4.40	7.03	4.32	0.42	28.67	9.00	14.19
11	PCT-1 x PBT-5	2.00	1.01	1.51	4.63	7.20	4.46	0.49	31.44	11.20	18.57
12	PCT-1 x PBT-2	2.33	0.57	0.73	3.83	7.20	4.28	0.34	28.72	9.26	14.49
13	PCT-1 x PBT-13	2.00	0.51	0.74	3.78	6.77	4.38	0.45	31.61	10.56	15.57
14	PCT-1 x PBT-10	3.00	0.73	0.83	4.20	7.33	4.46	0.47	32.28	11.57	18.93
15	PCT-1 x PBT-4	2.00	0.82	1.19	4.51	5.03	4.35	0.38	28.55	9.46	14.49
16	PPT-2 x PBT-9	1.67	0.80	0.87	4.35	6.43	4.46	0.30	30.78	8.99	14.56
17	PPT-2 x PBT-5	2.00	0.95	1.27	4.00	5.77	4.54	0.34	31.28	11.82	18.72
18	PPT-2 x PBT-2	2.00	0.89	1.53	4.48	6.80	4.67	0.42	28.33	10.26	17.24
19	PPT-2 x PBT-13	3.00	0.73	0.85	5.38	7.13	4.44	0.38	28.22	13.15	22.43
20	PPT-2 x PBT-10	3.00	1.06	1.62	3.99	6.53	4.54	0.44	30.77	15.04	24.76

21	PPT-2 x PBT-4	2.00	1.13	1.21	4.86	6.20	4.64	0.36	33.39	13.35	22.53
22	PBT-9 x PBT-5	3.33	0.93	1.47	5.81	5.63	4.57	0.27	30.28	11.32	18.16
23	PBT-9 x PBT-2	2.00	1.21	0.77	4.79	6.07	4.87	0.27	27.61	8.08	13.74
24	PBT-9 x PBT-13	2.00	0.77	0.98	5.38	6.20	4.77	0.32	30.22	8.58	15.45
25	PBT-9 x PBT-10	3.00	0.62	1.01	3.98	6.20	4.68	0.34	31.17	11.62	19.90
26	PBT-9 x PBT-4	2.00	1.09	1.23	5.23	5.30	4.75	0.35	28.50	10.82	18.35
27	PBT-5 x PBT-2	3.00	0.79	1.41	3.62	5.87	4.52	0.36	26.83	9.41	14.80
28	PBT-5 x PBT-13	2.00	0.56	0.72	4.99	6.27	4.47	0.43	28.39	12.96	20.05
29	PBT-5 x PBT-10	2.33	0.93	1.58	4.01	6.03	4.56	0.29	30.72	12.68	21.74
30	PBT-5 x PBT-4	2.00	0.90	1.57	4.80	4.37	4.88	0.24	27.39	9.23	14.60
31	PBT-2 x PBT-13	4.33	0.79	1.10	5.42	6.60	4.25	0.43	30.95	10.35	14.67
32	PBT-2 x PBT-10	5.00	0.58	1.14	4.02	6.07	4.40	0.31	26.45	9.03	14.43
33	PBT-2 x PBT-4	3.00	1.14	0.89	4.98	5.73	4.33	0.42	28.11	6.93	10.87
34	PBT-13 x PBT-10	3.00	1.07	2.17	4.73	5.03	4.66	0.31	26.50	9.69	15.79
35	PBT-13 x PBT-4	2.67	0.79	1.48	5.27	5.90	4.76	0.29	26.33	11.85	20.27
36	PBT-10 x PBT-4	3.00	0.67	0.90	4.65	5.27	4.53	0.33	27.55	9.09	17.64
GM		**2.56**	**0.83**	**1.11**	**4.54**	**6.20**	**4.58**	**0.36**	**29.27**	**10.49**	**17.07**
Sem		0.17	0.05	0.06	0.12	0.19	0.08	0.02	1.14	0.46	0.62
C.D. (1%)		0.63	0.20	0.24	0.45	0.71	0.29	0.07	4.27	1.73	2.33
C.D. (5%)		0.47	0.15	0.18	0.34	0.54	0.22	0.05	3.22	1.30	1.75
C.V.		11.40	11.32	9.90	4.53	5.32	2.93	9.09	6.75	7.62	6.31

4.2.1.2.6 pH of fruit juice

Perusal of data revealed that mean values for pH of fruit juice ranged from 4.25 to 4.91 and the average value was 4.58. Among the parents, PPT-2 (4.64) and PBT-9 (4.66) recorded minimum mean values for pH of fruit juice whereas, maximum values were recorded in PBT-2 (4.91), PBT-5 (4.78) and PBT-13 (4.78). Among the crosses, minimum values for same character were noticed in PBT-2 x PBT-13 (4.25), PCT-1 x PPT-2 (4.26) and PCT-1 x PBT-2 (4.28). However, maximum mean values were recorded in PBT-5 x PBT-4 (4.88), PBT-9 x PBT-2 (4.87) and PBT-9 x PBT-13 (4.77) for pH of fruit juice.

4.2.1.2.7 Titratable acidity (%)

Mean values for titratable acidity was ranged from 0.22 to 0.63 per cent and the average value was 0.36 per cent. Among the parents, maximum values for the same trait were observed in PCT-1 (0.46) and PBT-13 (0.44) whereas, minimum values were observed in PBT-5 (0.22) and PBT-2 (0.25). Among the 28 cross combinations, PCT-1 x PPT-2 (0.63), PCT-1 x PBT-5 (0.49) and PCT-1 x PBT-10 (0.47) recorded maximum values for titratable acidity. However, minimum values for same trait were observed in PBT-5 x PBT-4 (0.24), PBT-9 x PBT-5 (0.27) and PBT-9 x PBT-2 (0.27).

4.2.1.2.8 Ascorbic acid (mg/100g)

Mean values for ascorbic acid was ranged between 25.33 to 40.11 mg/100g and the mean value was 29.27 mg/100g. Among the parents, maximum values for the same trait were observed in PCT-1 (40.11) and PPT-2 (30.00) whereas, minimum values were observed in PBT-2 (25.33) and PBT-9 (25.72). Among the 28 cross combinations, PPT-2 x PBT-4 (33.39), PCT-1 x PPT-2 (33.06) and PCT-1 x PBT-10 (32.28) recorded maximum values for ascorbic acid. However, minimum values for same trait were observed in PBT-13 x PBT-4 (26.33), PBT-2 x PBT-10 (26.45) and PBT-13 x PBT-10 (26.50).

4.2.1.2.9 Lycopene (mg/100g)

Perusal of data revealed that mean values for lycopene content in fruits ranged from 6.93 to 15.04 mg/100g and the average value for the trait was 10.49 mg/100g. Among the parents, PPT-2 (13.14) and PBT-10 (12.93) recorded maximum mean values for lycopene whereas, minimum values were recorded in PCT-1 (7.81) and PBT-4 (7.19). Among the crosses, maximum values for same character was noticed in

PPT-2 x PBT-10 (15.04), PPT-2 x PBT-4 (13.35) and PPT-2 x PBT-13 (13.15). However, minimum mean values were recorded in PBT-2 xPBT-4 (6.93), PBT-9 x PBT-2 (8.08) and PBT-9 x PBT-13 (8.58).

4.2.1.2.10 Total carotenoids (mg/100g)

Mean values for total carotenoids ranged between 10.87 to 24.76 mg/100g and the average value was 17.07 mg/100g. Among the parents, PPT-2 (21.50) and PBT-10 (20.27) were recorded the maximum total carotenoids. However, minimum total carotenoids were observed in PBT-4 (12.33) and PCT-1 (13.56). Among the crosses, maximum total carotenoids were observed in PPT-2 x PBT-10 (24.76), PPT-2 x PBT-4 (22.53) and PPT-2 x PBT-13 (22.43) whereas, minimum values for same character were noticed in PBT-2 x PBT-4 (10.87), PBT-9 x PBT-2 (13.74) and PCT-1 x PBT-9 (14.19).

4.2.2 Genetic components and other genetic parameters

Effectiveness of any selection programme depends upon the existence of genetic variability present within the population. The assessment of genetic variability present in a given crop population can be determined by using the biometrical components such as range, variance, coefficient of variation, standard error and heritability.

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are the best criteria to measure available variability. Heritability of a character is important in determining its response to selection. Genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an effective breeding program. The broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect (Allard, 1960). It is generally expressed in percentage.

Assessment of variability parameters revealed that there is lot of variation present among the genotypes studied. In general, the value of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters studied in the present findings, indicating the considerable influence of environmental factors on the performance of genotypes for different characters. Similar results were also reported in tomato by Dar *et al*. (2012), Premalakshmi *et al*. (2014), Meena *et al*. (2015), Ahmad *et al*. (2016), Hasan *et al*. (2016), Rai *et al*. (2016), Kumar *et al*. (2017a) and Kumar *et al*. (2017c).

4.2.2.1 Yield related traits

Data presented in Table 4.5 revealed that high GCV and PCV estimates were observed for many traits *viz.*, number of fruits per plant (97.64 and 98.98%), average fruit weight (40.64 and 41.31%), fruit yield per hectare (34.76 and 36.65%), fruit yield per plant (34.75 and 36.64%), number of flowers per cluster (30.37 and 31.17%) and number of fruits per cluster (26.74 and 27.60%). Moderate to high GCV and PCV was observed in fruit length (19.99 and 20.74%) and fruit width (19.60 and 21.17%). Moderate to high GCV and PCV for these traits clearly indicate ample scope for yield improvement in tomato through selection due to the presence of sufficient variability genotypes studied. The GCV and PCV were low for days to first fruit ripening (6.64 and 6.94%), days to first fruit set (7.80 and 8.98%) and days to 50 per cent flowering (9.59 and 11.62%) whereas, moderate for fruit shape index (15.02 and 18.20%), 100 seed weight (13.82 and 14.97%) internodal length (13.64 and 16.11%) and plant height (12.01 and 15.99%).

The results of the present investigation agreed with the finding of Dar *et al.* (2012), Islam *et al.* (2012), Saleem *et al*. (2013), Meiti *et al*. (2014), Singh *et al*. (2014), Pujer *et al*. (2015), Ullah *et al*. (2015), Ahmad *et al*. (2016), Kumar and Singh (2016), Kumar *et al*. (2017b) and Kaushal *et al*. (2017).

Broad sense heritability estimates ranged from 56.37 per cent (Plant height) to 97.31 per cent (Number of fruits per plant) (Table 4.5). Number of fruits per plant recorded maximum heritability (97.31%) followed by average fruit weight (96.80%), number of flowers per cluster (94.95%), number of fruits per cluster (93.86%), fruit length (92.89%), days to first fruit ripening (91.51%), fruit yield per plant (89.97%), fruit yield per hectare (89.97%), fruit width (85.72%), 100 seed weight (85.26%) and days to first fruit set (75.57%). The heritability estimates for these traits indicate that these characters are least influenced by the environment.

Internodal length (71.72%), fruit shape index (68.14%), days to 50 per cent flowering (68.05%) and plant height (56.37%) exhibited moderate level of heritability. However, low heritability (<50%) was not observed for any character. Low to moderate estimates of broad sense heritability indicates that these characters are highly influenced by environmental effects and the genetic improvement through selection in these traits is difficult due to masking effect of environment on the genotypic effects.

Table 4.5: Estimation of coefficient of variance and other genetic parameters for different yield related traits in tomato

S.N.	Characters	Range	General Mean	GCV (%)	PCV (%)	ECV (%)	Heritability (%)	GA as % of mean
1	**Days to 50 per cent flowering**	30.33-43.67	35.43	9.59	11.62	6.57	68.05	16.29
2	**Days to first fruit set**	43.00-57.47	49.03	7.80	8.98	4.44	75.57	13.97
3	**Days to first fruit ripening**	68.20-95.13	84.01	6.64	6.94	2.02	91.51	13.08
4	**Number of flowers per cluster**	7.67-26.40	12.56	30.37	31.17	7.01	94.95	60.96
5	**Number of fruits per cluster**	5.47-14.80	7.57	26.74	27.60	6.84	93.86	53.36
6	**Number of fruits per plant**	27.39-355.73	55.12	97.64	98.98	16.22	97.31	198.43
7	**Internodal length (cm)**	7.80-13.40	10.58	13.64	16.11	8.56	71.72	23.80
8	**Average fruit weight (g)**	9.90-159.93	88.00	40.64	41.31	7.39	96.80	82.38
9	**Fruit length (cm)**	2.11-6.55	4.75	19.99	20.74	5.53	92.89	39.68
10	**Fruit width (cm)**	1.83-6.35	4.52	19.60	21.17	8.00	85.72	37.39
11	**Fruit shape index**	0.86-1.66	1.07	15.02	18.20	10.27	68.14	25.55
12	**Plant height (cm)**	236.13-448.67	384.05	12.01	15.99	10.56	56.37	18.57
13	**100 seed weight (g)**	0.13-0.42	0.35	13.82	14.97	5.75	85.26	26.29
14	**Fruit yield per plant (kg)**	1.34-6.83	3.67	34.75	36.64	11.60	89.97	67.90
15	**Fruit yield per hectare (t/ha)**	47.27-240.37	129.00	34.76	36.65	11.61	89.97	67.92

High estimates of genetic advance as percentage of mean (>20%) was observed for most of the characters under study *viz.*, number of fruits per plant (198.43%), average fruit weight (82.38%), fruit yield per hectare (67.92%), fruit yield per plant (67.90), number of flowers per cluster (60.96%), number of fruits per cluster (53.36%), fruit length (39.68%), fruit width (37.39%), 100 seed weight (26.29%), fruit shape index (25.55%) and internodal length (23.80%). High estimates of genetic advance as percentage of mean indicated that selection for these characters in segregating generations based on phenotypic performance would likely be more effective.

Moderate level of genetic advance as percentage of mean (10-20%) were observed for plant height (18.57%), days to 50 per cent flowering (16.29%), days to first fruit set (13.97%) and days to first fruit ripening (13.08%).

For efficient selection we cannot solely rely on heritability. The combination of high heritability along with high genetic advance will provide a clear base on the reliability of that particular trait in the selection of variable entries. Based on the underlying facts, the traits under study were categorized into four different groups as per the analysis: First group included majority of the characters under study exhibited high estimates of broad sense heritability and high estimates of genetic advance as percentage of mean *viz.* number of flowers per cluster, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit length, fruit width, 100 seed weight, fruit yield per plant and fruit yield per hectare. High heritability and high genetic advance estimates for these characters indicated that these traits were less affected by environmental factors and hence, there exists an ample scope for the improvement of concerned traits through direct selection. The second group of traits included days to first fruit set and days to first fruit ripening, which had high heritability estimates coupled with moderate genetic advance as per cent of mean. The third group consisted internodal length and fruit shape index which had moderate heritability coupled with high genetic advance. The fourth group included days to 50 per cent flowering and plant height which had moderate heritability estimates coupled with moderate genetic advance as per cent of mean.

For different characters, similar results were also observed by various researchers like Agarwal *et al*. (2014), Meiti *et al*. (2014), Mukul *et al*. (2014),

Premalakshmi *et al*. (2014), Ullah *et al*. (2015), Kumar *et al*. (2016), Nalla *et al*. (2016), Rai *et al*. (2016), Kumar *et al*. (2017a) and Kaushal *et al*. (2017).

4.2.2.2 Quality traits

The read through data presented in Table 4.6 revealed that high GCV and PCV estimates were observed for many traits *viz.*, diameter of stalk scar (32.59 and 34.06%), number of locules per fruit (26.92 and 29.24%), titratable acidity (23.20 and 24.80%) and pericarp thickness (22.14 and 24.92%). Moderate GCV and PCV were observed in total carotenoids (18.65 and 19.69%), lycopene (17.43 and 19.02%), fruit firmness (13.16 and 13.91%) and TSS (12.99 and 14.04%). Moderate to high GCV and PCV for these traits clearly indicate ample scope for yield improvement in tomato through selection due to the presence of sufficient variability genotypes studied. The GCV and PCV were low for pH of fruit juice (3.68 and 4.70%) and ascorbic acid (8.88 and 11.16%).

The results of the present investigation agreed with the finding of Dar *et al.* (2012), Patil *et al*. (2013), Kumar *et al*. (2015), Singh *et al*. (2015), Ullah *et al*. (2015), Kumar *et al*. (2016), Nalla *et al*. (2016) and Kaushal *et al*. (2017).

Broad sense heritability estimates ranged from 61.15 per cent (pH of fruit juice) to 91.57 per cent (diameter of stalk scar) (Table 4.6). Diameter of stalk scar recorded maximum heritability (91.57%) followed by total carotenoids (89.72%), fruit firmness (89.46%), titratable acidity (87.50%), TSS (85.60%), number of locules per fruit (84.78%), lycopene (83.96%) and pericarp thickness (78.91%). Ascorbic acid (63.39%) and pH of fruit juice (61.15%) exhibited moderate level of heritability. However, low heritability (<50%) was not observed for any character.

High estimates of genetic advance as percentage of mean (>20%) was observed for most of the characters under study *viz.*, diameter if stalk scar (64.24%), number of locules per fruit (51.06%), titratable acidity (44.70%), pericarp thickness (40.51%), total carotenoids (36.39%), lycopene (32.89%), fruit firmness (25.63%) and TSS (24.76%). Moderate level of genetic advance as percentage of mean (10-20%) were observed only for ascorbic acid (14.57%) and low level was also observed for single character pH of fruit juice (5.93%).

Table 4.6: Estimation of coefficient of variance and other genetic parameters for different quality traits in tomato

S.N.	Characters	Range	General Mean	GCV (%)	PCV (%)	ECV (%)	Heritability (%)	GA as % of mean
1	**Number of locules per fruit**	1.67-5.00	2.56	26.92	29.24	11.41	84.78	51.06
2	**Pericarp thickness (cm)**	0.35-1.21	0.83	22.14	24.92	11.45	78.91	40.51
3	**Diameter of stalk scar (cm)**	0.31-2.17	1.11	32.59	34.06	9.89	91.57	64.24
4	**Fruit firmness (kg/cm^2)**	3.62-5.81	4.54	13.16	13.91	4.51	89.46	25.63
5	**Total soluble solids (%)**	4.37-8.07	6.20	12.99	14.04	5.33	85.60	24.76
6	**pH of fruit juice**	4.25-4.91	4.58	3.68	4.70	2.93	61.15	5.93
7	**Titratable acidity (%)**	0.22-0.63	0.36	23.20	24.80	8.77	87.50	44.70
8	**Ascorbic acid (mg/100g)**	25.33-40.11	29.27	8.88	11.16	6.75	63.39	14.57
9	**Lycopene (mg/100g)**	6.93-15.04	10.49	17.43	19.02	7.62	83.96	32.89
10	**Total carotenoids (mg/100g)**	10.87-24.76	17.07	18.65	19.69	6.31	89.72	36.39

The traits under study were categorized into three different groups as per the analysis: First group included majority of the characters under study showed high estimates of broad sense heritability and high estimates of genetic advance as percentage of mean *viz.*, number of locules per fruit, pericarp thickness, diameter of stalk scar, TSS, titratable acidity, fruit firmness, lycopene and total carotenoids. The second group of traits included single character ascorbic acid, which had medium heritability estimates coupled with moderate genetic advance as per cent of mean. The third group included pH of fruit juice which had moderate heritability coupled with low genetic advance.

For different quality traits, similar results were also observed by various researchers like Dar *et al*. (2012), Patil *et al*. (2013), Singh *et al*. (2014), Kumar *et al*. (2015), Singh *et al*. (2015), Nalla *et al.* (2016), Rai *et al.* (2016), Kumar *et al.* (2017a), Kaushal *et al.* (2017) and Lekshmi and Celine (2017).

4.3 Analysis of molecular diversity in tomato

Molecular marker technology provides information that can help to define the distinctiveness of germplasm and their ranking according to the number of close relatives and their polygenetic position. It is a complementary approach for genetic characterization. The present study was aimed to analyze diversity among eight parental lines using SSR molecular marker.

4.3.1 PCR optimization and primer screening

The polymerase chain reaction (PCR) amplification procedure was optimized by determining the most appropriate concentration of DNA template, Taq DNA polymerase and Mg^{++} ion required to generate repeatable PCR amplification profiles. The random primers suitable for generation of polymorphic amplification profile among the genotypes of tomato were identified by the screening of twenty SSR primers. All eight genotypes were scored manually. Bands were recorded as present (1) or absent (0) across the lane. Very thin or faint bands were not considered for final scoring as these were inconsistent.

4.3.2 SSR amplification

SSR amplification of DNA extracted from eight genotypes was done with twenty SSR primers for their molecular marker characterization and to establish distinctiveness

among them. The PCR products run on agrose gel were scored manually. The amplification profile generated by each primer was compared and the relative molecular size of each band was examined by comparing with DNA size marker.

Twenty SSR primers used for study and out of twenty primers, sixteen primers generated polymorphic bands. Total 46 bands amplified by 16 SSR primers in the eight tomato germplasm of which polymorphic and monomorphic bands were 43 and 3, respectively. Primer SLM6-5 gave one unique band. The range of amplified products was 100-700bp approximately (Table 4.7). Benor *et al*. (2008) studied the genetic diversity of 39 determinate and indeterminate tomato lines and also reported the range amplified products of 100-400bp.

The number of SSR alleles scored, polymorphic information content observed for each primer in eight genotypes are presented in Table 4.8. The number of alleles per locus varied from two (SSR43, SSR47, SSR65, SSR92, SSR110, SSR111, SSR253 and SLM6-12) to six (SLM6-7). Average number of bands per primer was 2.86. A range of polymorphism was observed from 50 per cent (SSR47) to 100 per cent (SSR20, SSR43, SSR63, SSR65, SSR92, SSR110, SSR111, SSR248, SSR253, SLM6-5, SLM6-7, SLM6-12 and SLM6-14) with an average of 93.23 per cent. The PIC value ranged from 0.117 (SSR47) to 0.891 (SLM6-5) with an average 0.596 (Table 4.8). Benor *et al*. (2008) observed the mean number of alleles per locus 4.3 and the average PIC 0.31 among the tomato genotypes. Glocovac *et al*. (2013) also found polymorphism in tomato genotypes with primers SSR111 and SSR248. Kwon *et al*. (2009) found average PIC 0.628 ranging from 0.210 to 0.880 in tomato. Similar results was also reported by Korir *et al*. (2014), Gongolee *et al*. (2016), Kumar *et al*. (2016a), Kumar *et al*. (2016b), Raveendar *et al*. (2016) and Choudhary *et al*. (2018).

A total of twenty SSR primers were used in diversity analysis of eight genotypes of tomato. The primer which showed polymorphism was used for characterization of germplasm. The amplification results in tomato germplasm with individual primers are given below.

SSR 20

This primer paired revealed four amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-400bp. This primer pair gave PIC value of 0.422 and per cent polymorphism was 100 per cent (Plate 2).

Table 4.7: Summary of SSR amplified products

S. N.	Specification	Particular
1	Total number of primer tested	20
2	Number of polymorphic primers	16
3	Number of monomorphic primers	04
4	Total number of unique bands	01
5	Number of primers that gave unique bands	01
6	Total number of polymorphic bands identified	43
7	Total number of monomorphic bands	03
8	Total number of bands	46
9	Size range of amplified products (bp)	100-700bp
10	Percent polymorphism	50-100%
11	PIC value	0.117-0.891

SSR43

This primer paired gave two amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 200-300bp. The primer pair gave PIC value of 0.609 and showed 100 per cent polymorphism (Plate 2).

SSR 47

Primer generated two amplified loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-200bp. The primer pair revealed PIC value of 0.117 and 50 per cent polymorphism (Plate 2).

SSR63

This primer generated three amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-300bp. This primer pair gave PIC value of 0.484 and per cent polymorphism was 100 per cent (Plate 2).

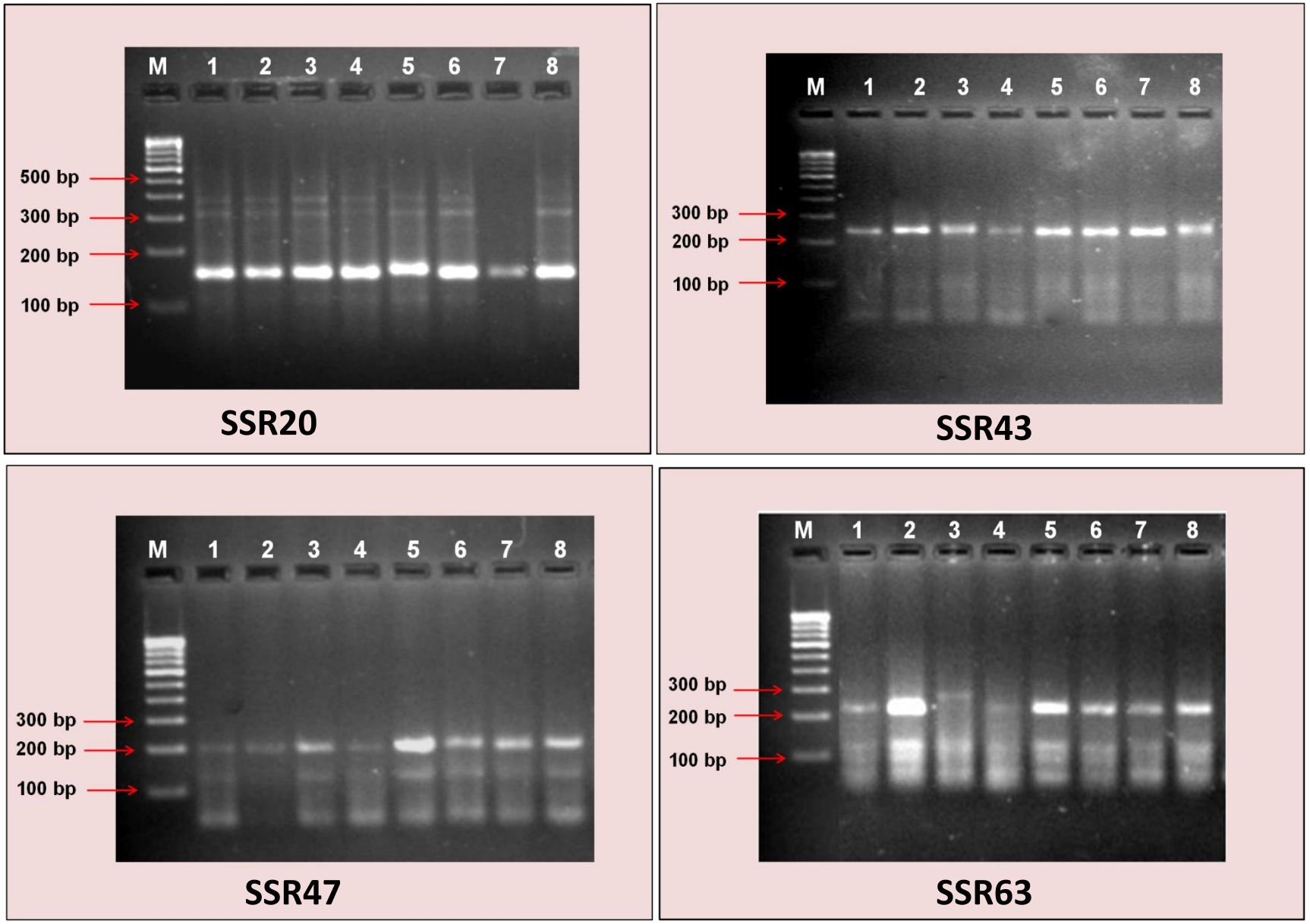

Plate 2 PCR amplification of 8 tomato genotypes by SSR primer SSR20, SSR43, SSR47 and SSR63

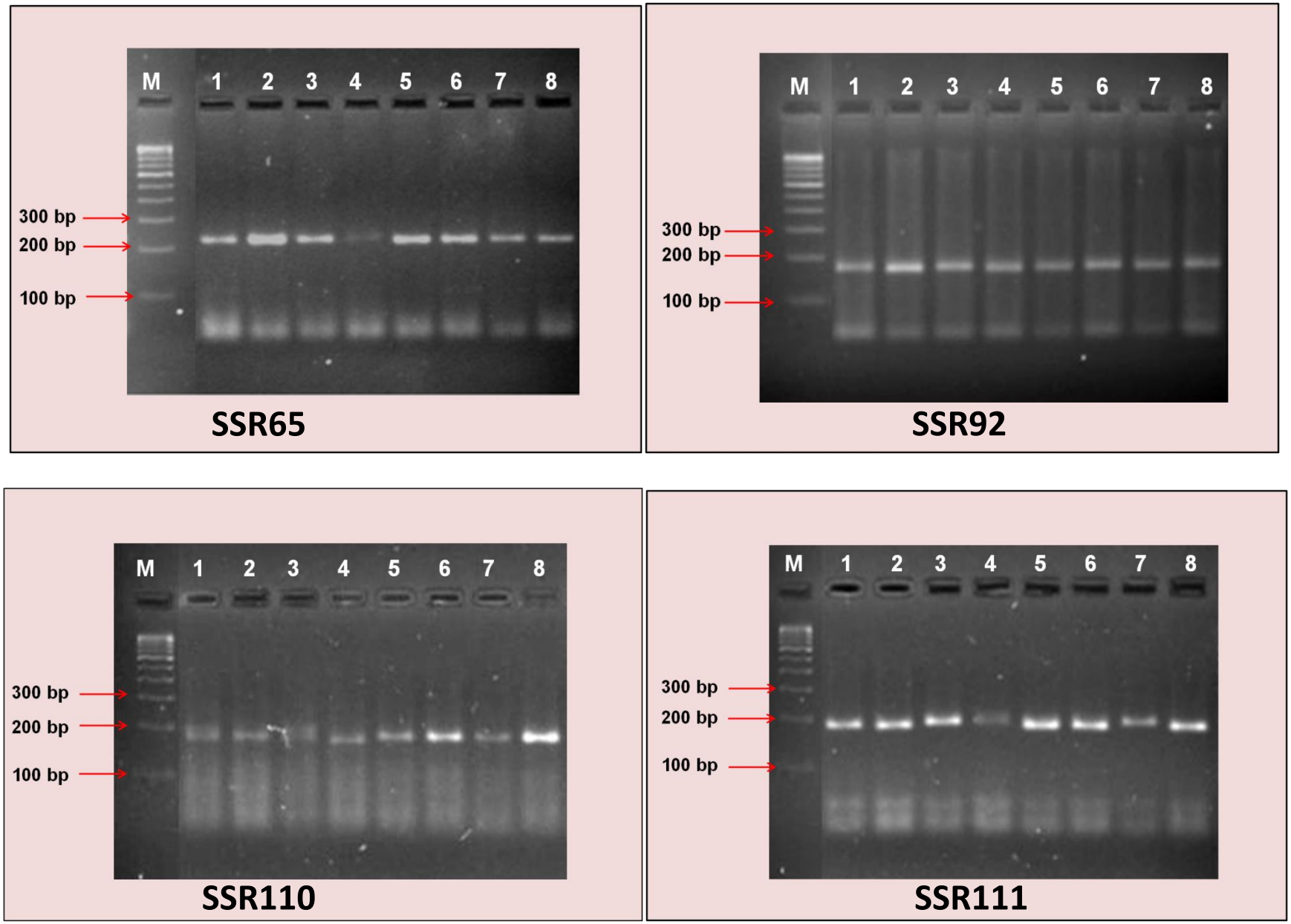

Plate 3 PCR amplification of 8 tomato genotypes by SSR primer SSR65, SSR92, SSR110 and SSR111

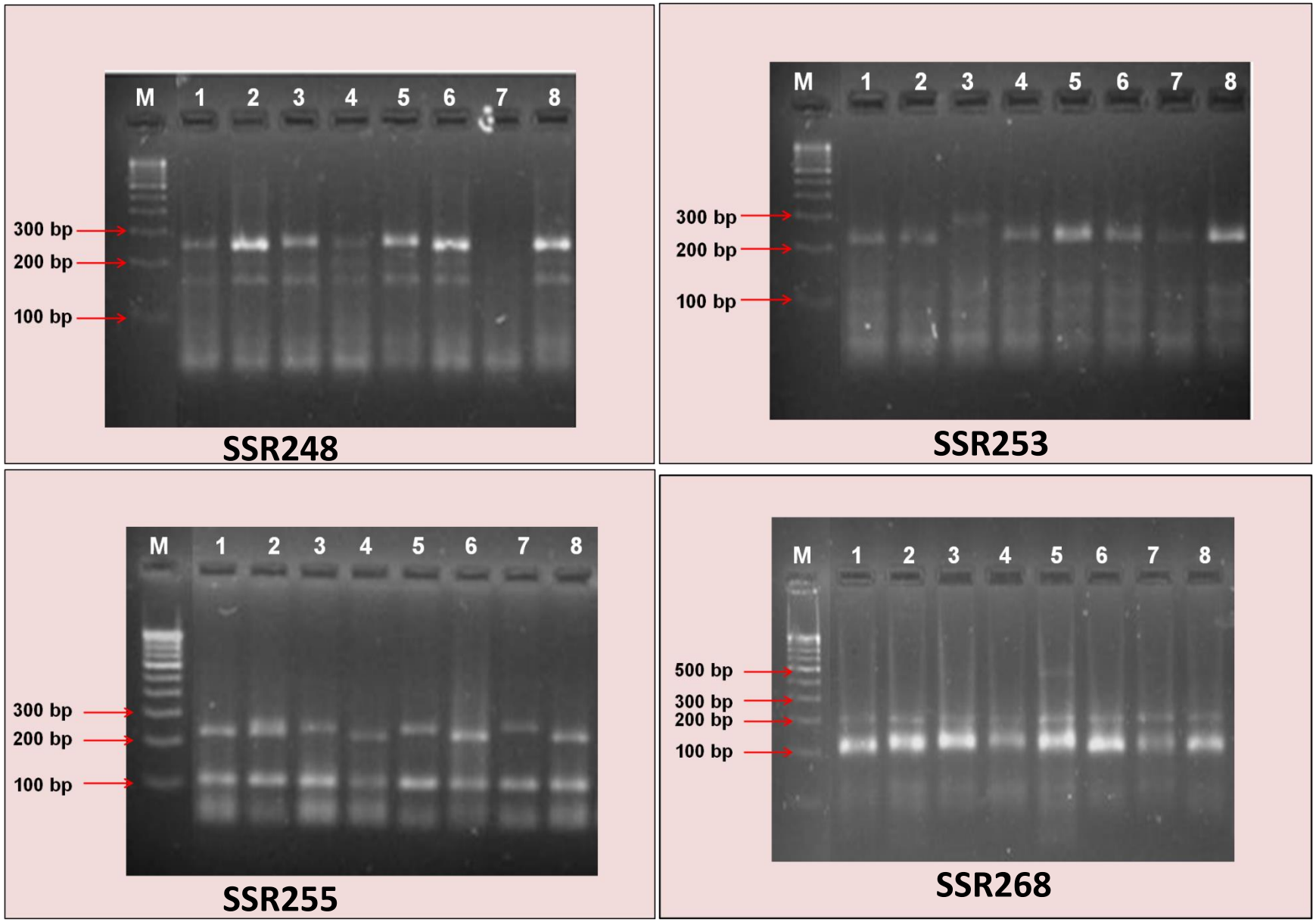

Plate 4 PCR amplification of 8 tomato genotypes by SSR primer SSR248, SSR253, SSR255 and SSR268

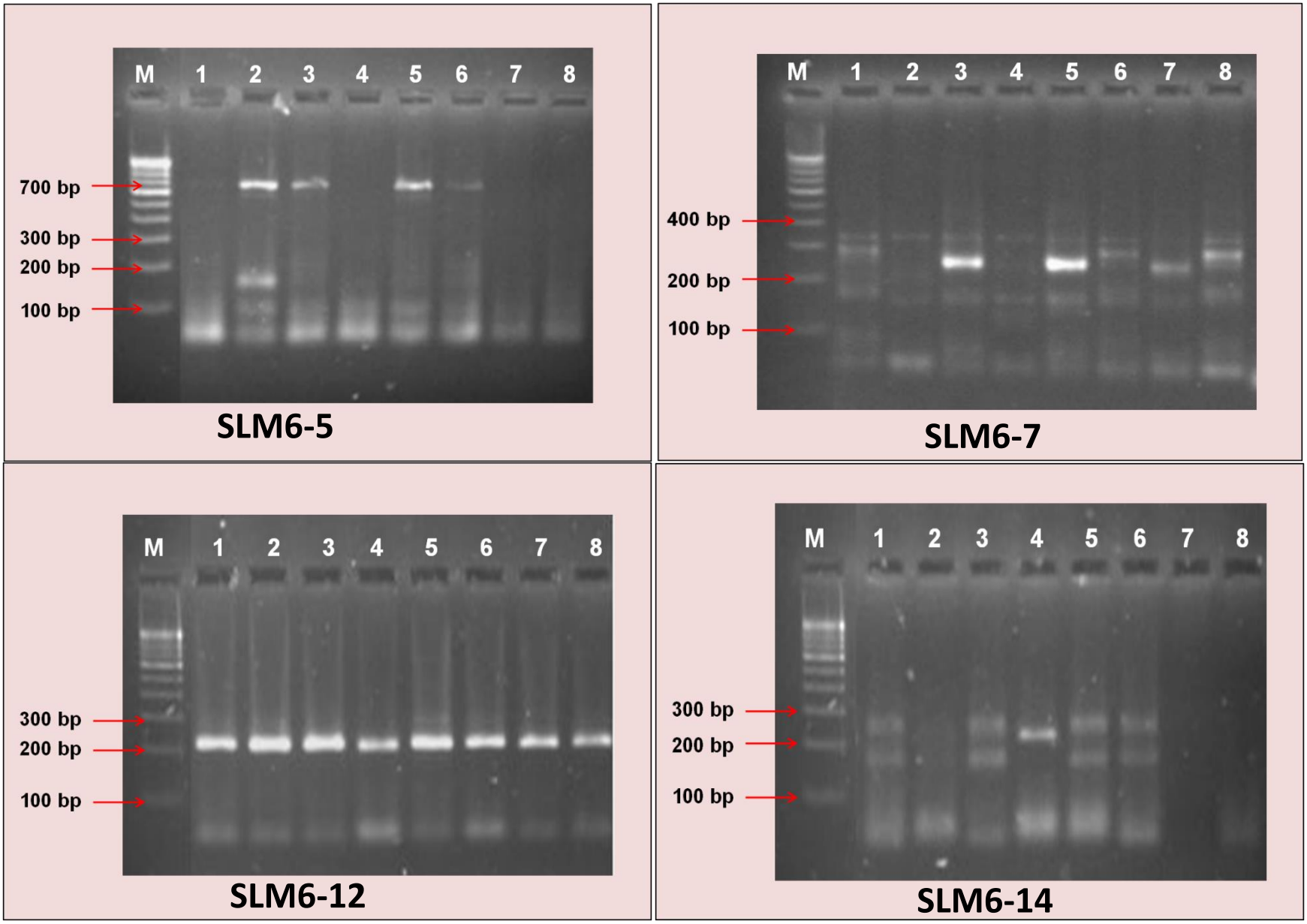

Plate 5 PCR amplification of 8 tomato genotypes by SSR primer SLM6-5, SLM6-7, SLM6-12 and SLM6-14

SSR65

Primer SSR65 amplified two amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 200-300bp. This primer pair showed PIC value of 0.609 and revealed 100 per cent polymorphism (Plate 3).

SSR92

This primer paired revealed two amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-200bp. The primer pair gave PIC value of 0.688 and per cent polymorphism was 100 per cent (Plate 3).

SSR110

Primer generated two amplified loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-200bp. The primer pair gave PIC value of 0.609 and 100 per cent polymorphism (Plate 3).

SSR111

In tomato germplasm, two alleles were amplified by primer SSR111 and produced 100 per cent polymorphic band. PIC of the primer was 0.734 and size of SSR amplicons ranged from 190-210bp (Plate 3).

SSR248

This primer generated four amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-300bp. This primer pair gave PIC value of 0.504 exhibited 100 per cent polymorphism (Plate 4).

SSR253

Primer generated two amplified loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 200-300bp. The primer pair gave PIC value of 0.609 and per cent polymorphism was 100 per cent (Plate 4).

SSR255

This primer paired revealed three amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-300bp. The primer pair gave PIC value of 0.490 and showed 66.67 per cent polymorphism (Plate 4).

Table 4.8: Level of polymorphism revealed by twenty SSR primers in eight genotypes of tomato

S. N.	Primer	Amplified product	No. of amplified alleles	Polymorphic band (s)	Monomorphic band (s)	Percent (%) polymorphism	PIC value
1	SSR20	100-400bp	4	4	0	100.00	0.422
2	SSR43	200-300bp	2	2	0	100.00	0.609
3	SSR47	100-200bp	2	1	1	50.00	0.117
4	SSR63	100-300bp	3	3	0	100.00	0.484
5	SSR65	200-300bp	2	2	0	100.00	0.609
6	SSR92	100-200bp	2	2	0	100.00	0.688
7	SSR110	100-200bp	2	2	0	100.00	0.609
8	SSR111	190-210bp	2	2	0	100.00	0.734
9	SSR248	100-300bp	4	4	0	100.00	0.504
10	SSR253	200-300bp	2	2	0	100.00	0.609
11	SSR255	100-300bp	3	2	1	66.67	0.490
12	SSR268	200-500bp	4	3	1	75.00	0.590
13	SLM6-5	100-700bp	3	3	0	100.00	0.891
14	SLM6-7	100-400bp	6	6	0	100.00	0.747
15	SLM6-12	200-300bp	2	2	0	100.00	0.609
16	SLM6-14	100-300bp	3	3	0	100.00	0.828
Total			**46**	**43**	**3**		
Average			**2.86**	**2.69**	**0.19**	**93.23**	**0.596**

SSR268

Primer SSR268 revealed four amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 200-500bp. The primer pair gave PIC value of 0.590 and 75.00 per cent polymorphism (Plate 4).

SLM6-5

Primer generated three amplified loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-700bp. The primer pair gave PIC value of 0.891 and revealed 100 per cent polymorphism (Plate 5).

SLM6-7

Primer generated six amplified loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-400bp. The primer pair gave PIC value of 0.747 and per cent polymorphism was 100 per cent (Plate 5).

SLM6-12

In tomato germplasm, two alleles were amplified by primer SLM6-12 on agrose gel electrophoresis. The size of SSR amplicons ranged from 200-300bp.The primer pair gave PIC value of 0.609 and showed 100 per cent polymorphism (Plate 5).

SLM6-14

This primer generated three amplified SSR loci on agrose gel electrophoresis. The size of SSR amplicons ranged from 100-300bp. This primer pair gave PIC value of 0.828 and per cent polymorphism was 100 per cent (Plate 5).

4.3.3 Genetic diversity analysis using SSR primers

Data scored on eight tomato germplasm with twenty microsatellite (SSR) primers were used to generate Jaccard's similarity coefficient presented in Table 4.9. In tomato germplasm, Jaccard's similarity coefficient varied from 0.52 to 0.94 with an average value of 0.70. PBT-9 and PBT-13 (0.94) were found to be the most similar genotypes among the eight genotypes studied followed by PBT-10 and PBT-13 (0.90). Minimum Jaccard's similarity coefficient was found in PCT-1 with PBT-2 and PBT-5 (0.52). Similar findings were also reported by many researchers in different tomato genotypes, El-Awady *et al*. (2012), Sanghani and Mavia (2013), Singh and Goswami (2014), Singh *et al*. (2014) and Rosy *et al*. (2018).

Table 4.9: Pair wise Jaccard's similarity coefficient among eight genotypes of tomato

Genotypes	PBT-13	PPT-2	PBT-5	PCT-1	PBT-2	PBT-9	PBT-4	PBT-10
PBT-13	1.00							
PPT-2	0.78	1.00						
PBT-5	0.70	0.64	1.00					
PCT-1	0.62	0.68	0.52	1.00				
PBT-2	0.70	0.68	0.76	0.52	1.00			
PBT-9	0.94	0.84	0.76	0.64	0.76	1.00		
PBT-4	0.70	0.64	0.68	0.56	0.60	0.68	1.00	
PBT-10	0.90	0.76	0.64	0.60	0.64	0.84	0.68	1.00

4.3.4 Cluster analysis based on SSR markers

The phylogenetic tree was constructed through NTSYSpc cluster analysis software using UPGMA (Un-weighted pair group method with arithmetic mean). All eight germplasm were demarcated into two major clusters A and B (Fig. 4.1) at 59 per cent similarity.

Eight genotypes of tomato were separated into major cluster I and II. Cluster I comprised most diverse germplasm (PCT-1) and rest of seven genotypes retained in cluster II. Cluster II was again bifurcated into two sub clusters namely cluster IIA and IIB at 67 per cent similarity. Cluster IIA consisted of six genotypes namely PBT-13, PBT-9, PBT-10, PPT-2, PBT-5 and PBT-2 while, cluster IIB containing the single germplasm PBT-4. Cluster IIA was further subdivided into two small clusters IIA1 and IIA2 at 70 per cent similarity. Cluster IIA1 consisted four genotypes namely PBT-13, PBT-9, PBT-10 and PPT-2 while cluster IIA2 comprised two genotypes *i.e.*, PBT-5 and PBT-2 (76% similarity). Cluster IIA1 was again divided into two super small cluster a and b at 79 per cent similarity. Cluster a consisted three genotypes namely PBT-13, PBT-9 and PBT-10, whereas cluster B retained single genotype PPT-2.

The germplasm which showed similar morphological and genetic trends were more or less together in both these cases. Morphological characteristics of all eight genotypes were given in Appendix III. PCT-1, a cherry tomato line showed deviation from existing cluster was also diverse with respect to their genetic makeup and morphological traits

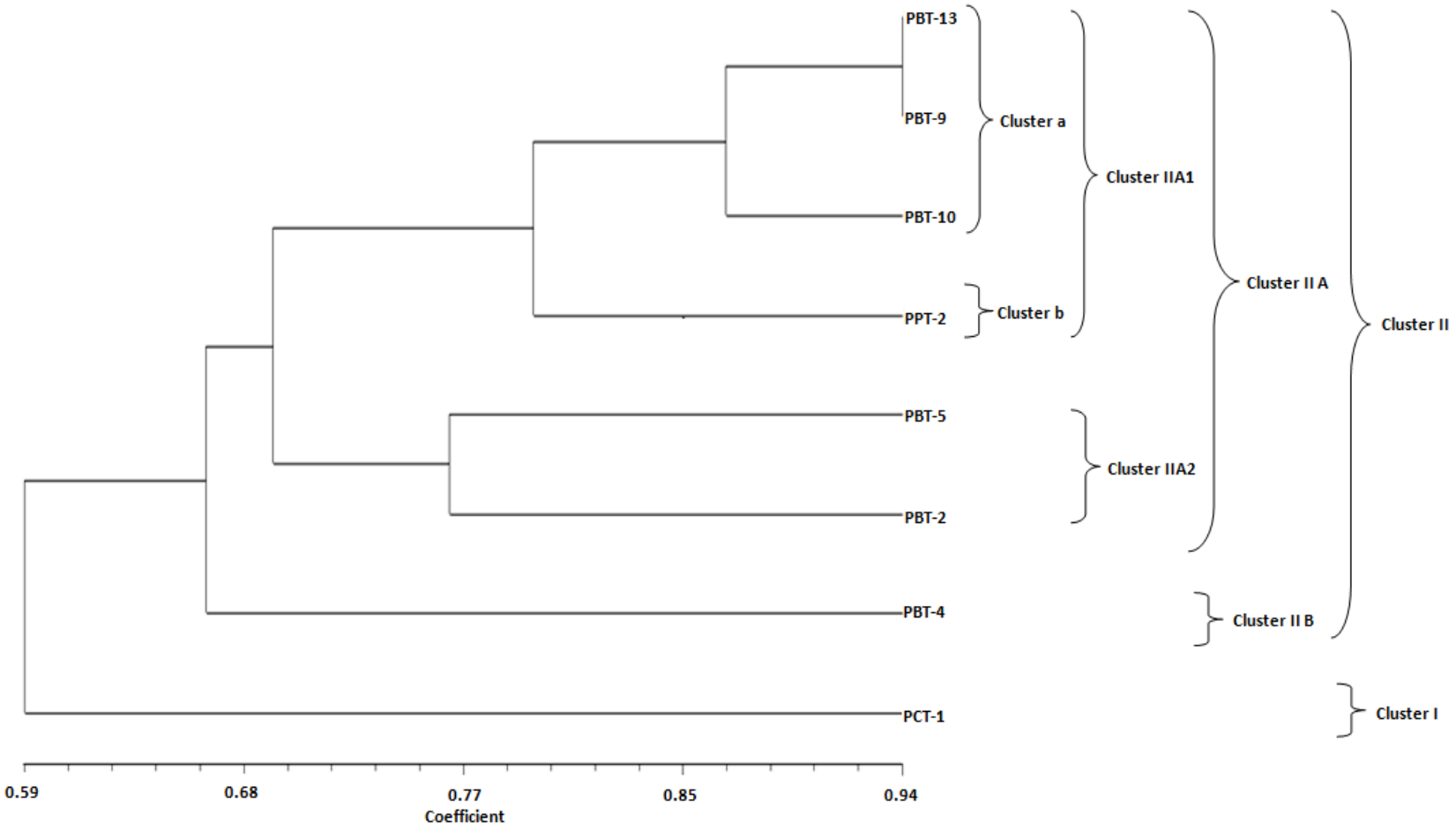

Fig. 4.1: Dendrogram depicting the classification of eight genotypes of tomato constructed using UPGMA method based on SSR

(small size of fruits and more number of fruits per cluster). Similar case was also found in PBT-4, this was also exhibited deviation from other cluster because of different type of foliage *i.e.*, potato leaf type and also semi determinate in growth habit compare to others which are indeterminate types.

4.4 Estimation of Heterosis

Hedrick and Booth (1907) were the first to report the presence of heterosis in tomato. Commercial cultivation of hybrids in tomato was started around late 1930's or early 1940's (Riggs 1988). In India, Indo-American Hybrid Seed Company launched its first hybrid of tomato 'Karnataka' for commercial cultivation. Of late, the farmers prefer hybrid cultivars on account of their superiority over the open pollinated cultivars in terms of yield, uniformity and quality attributes.

The estimation of heterosis was done for fifteen yield related and ten quality traits under polyhouse condition. The types of heterosis *viz.,* heterosis over mid-parent or relative heterosis, heterosis over better parent or heterobeltiosis and heterosis over check or standard heterosis estimated. Performance of F_1 hybrids and per cent increase/decrease over mid-parent, better parent and standard check for different characters are presented and discussed below.

4.4.1 Heterosis for yield related traits

4.4.1.1 Days to 50 per cent flowering

For earliness which is a desirable character, parents and hybrids with negative heterosis are preferred. The estimates of relative heterosis, heterobeltiosis and standard heterosis for days to 50 per cent flowering are presented in Table 4.10. Data revealed that heterosis over mid parent, better parent and over check parent value ranged from -22.231 to 11.746 per cent, -13.889 to 19.987 and -19.485 to 15.928 per cent, respectively. Out of twenty eight crosses, eight hybrids exhibited significant relative heterosis, nine hybrids showed significant heterobeltiosis and twelve hybrids showed significant standard heterosis for days to 50 per cent flowering.

For relative heterosis, seven cross combinations exhibited significant desirable negative relative heterosis. Among them top five crosses were PBT-13 x PBT-10 (-22.231%), PBT-5 x PBT-13 (-19.669%), PBT-5 x PBT-4 (-15.928%), PBT-9 x PBT-5

(-14.683%) and PCT-1 x PBT-4 (-13.762%). However, out of all crosses, four crosses showed significant negative heterobeltiosis namely PBT-9 x PBT-5 (-13.889%), PBT-5 x PBT-4 (-13.635%), PBT-13 x PBT-10 (-13.343%) and PBT-5 x PBT-13 (-12.735%). Looking to standard heterosis, among the crosses, eleven cross combinations exhibited significant negative standard heterosis in desirable direction for this particular trait. Top five crosses which showed maximum negative heterosis over check parents for days to 50 per cent flowering were PCT-1 x PBT-4 (-19.485%), PBT-9 x PBT-2 (-19.485%), PBT-13 x PBT-10 (-19.485), PCT-1 x PBT-5 (-17.706%) and PBT-9 x PBT-5 (-17.706%). This result is counteracting with Mali and Patel (2014), Reddy *et al*. (2014), Sherpa *et al.* (2014), Dagade *et al*. (2015), Sahu *et al*. (2016), Bharathkumar *et al.* (2016), Marbhal *et al*. (2016) and Kumar *et al*. (2017a).

4.4.1.2 Days to first fruit set

Days to first fruit set is also an earliness character, so their negative heterosis over mid parent, better parent and over check parent is desirable. Data presented in Table 4.11 revealed that relative heterosis, heterobeltiosis and standard heterosis ranged from -14.322 to 12.980 per cent, -7.921 to 20.814 per cent and -14.564 to 14.186 per cent, respectively. For days to first fruit set out of 28 cross combinations, 13 crosses showed significant relative heterosis, 10 crosses exhibited significant heterobeltiosis and 10 crosses showed significant standard heterosis.

Out of twenty eight cross combinations, five crosses showed desirable significant negative relative heterosis for days to first fruit set were PBT-13 x PBT-10 (-14.322%), PBT-5 x PBT-13 (-13.390%), PCT-1 x PBT-4 (-9.569%), PBT-5 x PBT-4 (-9.359%) and PBT-9 x PBT-5 (-8.363%). Out of all crosses, none of them showed significant negative heterobeltiosis for days to first fruit set and out of twenty eight cross combinations, nine crosses showed significant desirable negative standard heterosis for days to first fruit set and among them top five cross combinations were PCT-1 x PBT-4 (-14.564%), PCT-1 x PBT-5 (-13.908%), PBT-9 x PBT-2 (-13.511%), PBT-13 x PBT-10 (-12.041%) and PBT-5 x PBT-10 (-11.782%). Significant negative heterosis for days to first fruit set in tomato was also reported by Amin *et al*. (2017).

Table 4.10: Heterosis for days to 50 per cent flowering

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	33.00	-4.817	4.200	-12.397*
2	PCT-1 x PBT-9	36.33	7.374	14.714*	-3.557
3	PCT-1 x PBT-5	31.00	-9.277	-2.116	-17.706**
4	PCT-1 x PBT-2	35.67	10.880	12.630	-5.309
5	PCT-1 x PBT-13	38.00	1.781	19.987**	0.876
6	PCT-1 x PBT-10	35.00	4.995	10.515	-7.088
7	PCT-1 x PBT-4	30.33	-13.762*	-4.231	-19.485**
8	PPT-2 x PBT-9	39.33	6.773	9.250	4.407
9	PPT-2 x PBT-5	39.67	6.726	8.181	5.309
10	PPT-2 x PBT-2	38.33	8.985	17.325*	1.752
11	PPT-2 x PBT-13	43.67	8.268	15.928*	15.928*
12	PPT-2 x PBT-10	38.67	6.426	10.486	2.655
13	PPT-2 x PBT-4	39.00	2.174	3.531	3.531
14	PBT-9 x PBT-5	31.00	-14.683**	-13.889*	-17.706**
15	PBT-9 x PBT-2	30.33	-11.664	-7.163	-19.485**
16	PBT-9 x PBT-13	39.00	-1.266	8.333	3.531
17	PBT-9 x PBT-10	39.67	11.746*	13.343*	5.309
18	PBT-9 x PBT-4	36.67	-1.781	1.861	-2.655
19	PBT-5 x PBT-2	32.67	-5.769	0.000	-13.273*
20	PBT-5 x PBT-13	32.00	-19.669**	-12.735*	-15.052*
21	PBT-5 x PBT-10	31.67	-11.623*	-9.514	-15.928*
22	PBT-5 x PBT-4	31.67	-15.928**	-13.635*	-15.928*
23	PBT-2 x PBT-13	33.67	-11.008*	3.061	-10.619
24	PBT-2 x PBT-10	33.33	-1.493	2.020	-11.521
25	PBT-2 x PBT-4	32.33	-9.364	-1.041	-14.176*
26	PBT-13 x PBT-10	30.33	-22.231**	-13.343*	-19.485**
27	PBT-13 x PBT-4	38.00	-6.943	-1.733	0.876
28	PBT-10 x PBT-4	33.67	-8.592	-3.800	-10.619
Range	**Minimum**	**30.33**	**-22.231**	**-13.889**	**-19.485**
	Maximum	**43.67**	**11.746**	**19.987**	**15.928**

Table 4.11: Heterosis for days to first fruit set

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	47.67	1.609	9.586	-5.285
2	PCT-1 x PBT-9	49.27	6.300	13.264**	-2.106
3	PCT-1 x PBT-5	43.33	-6.039	-0.391	-13.908**
4	PCT-1 x PBT-2	49.47	12.816**	13.724**	-1.709
5	PCT-1 x PBT-13	52.07	4.380	19.701**	3.457
6	PCT-1 x PBT-10	49.93	10.257*	14.782**	-0.795
7	PCT-1 x PBT-4	43.00	-9.569*	-1.149	-14.564**
8	PPT-2 x PBT-9	54.27	9.053*	10.305*	7.828
9	PPT-2 x PBT-5	54.40	9.832*	11.636*	8.087
10	PPT-2 x PBT-2	53.40	12.980**	20.814**	6.100
11	PPT-2 x PBT-13	57.47	7.824*	14.186**	14.186**
12	PPT-2 x PBT-10	53.00	8.830*	12.598**	5.305
13	PPT-2 x PBT-4	52.53	3.071	4.371	4.371
14	PBT-9 x PBT-5	44.87	-8.363*	-7.921	-10.848*
15	PBT-9 x PBT-2	43.53	-6.788	-1.516	-13.511**
16	PBT-9 x PBT-13	53.27	1.015	8.272	5.841
17	PBT-9 x PBT-10	54.00	12.184**	14.723**	7.292
18	PBT-9 x PBT-4	50.53	0.258	2.703	0.397
19	PBT-5 x PBT-2	46.00	-1.001	4.072	-8.603*
20	PBT-5 x PBT-13	45.47	-13.390**	-6.690	-9.656*
21	PBT-5 x PBT-10	44.40	-7.307	-5.672	-11.782**
22	PBT-5 x PBT-4	45.47	-9.359*	-6.690	-9.656*
23	PBT-2 x PBT-13	46.67	-7.097	5.588	-7.272
24	PBT-2 x PBT-10	46.80	2.553	5.882	-7.014
25	PBT-2 x PBT-4	48.00	0.209	8.597	-4.629
26	PBT-13 x PBT-10	44.27	-14.322**	-5.949	-12.041**
27	PBT-13 x PBT-4	52.27	-3.087	1.298	3.855
28	PBT-10 x PBT-4	48.67	-1.348	3.399	-3.298
Range	**Minimum**	**43.00**	**-14.322**	**-7.921**	**-14.564**
	Maximum	**57.47**	**12.980**	**20.814**	**14.186**

4.4.1.3 Days to first fruit ripening

Days to first fruit ripening is an important character as it also leads to earliness of crop. Thus, in tomato high negative value of heterosis for days to first fruit ripening was established to earliness. Data presented in Table 4.12 revealed that the range of heterosis for days to first fruit ripening was -9.964 to 14.727 per cent for relative heterosis, -6.908 to 26.393 per cent for heterobeltiosis and -7.852 to 12.779 per cent for standard heterosis. Among all crosses, 19 hybrids showed significant relative heterosis, 22 hybrids showed significant heterobeltiosis and 14 hybrids exhibited significant standard heterosis for days to first fruit ripening.

Out of twenty eight crosses, four cross combinations showed significant negative relative heterosis namely PBT-2 x PBT-13 (-9.964%), PBT-9 x PBT-5 (-7.585%), PBT-5 x PBT-13 (-6.924%) and PBT-9 x PBT-2 (-5.756%). For heterobeltiosis two cross combinations *viz*., PBT-9 x PBT-5 (-6.908%) and PBT-9 x PBT-2 (-4.754%) showed significant negative heterosis over better parent. Out of all cross combinations, three crosses *i.e*., PCT-1 x PBT-5 (-7.852%), PBT-9 x PBT-5 (-7.439%) and PBT-9 x PBT-2 (-5.910%) showed negative standard heterosis over check parent for days to first fruit ripening.

Significant negative heterosis for days to first fruit ripening was also reported by Hannan *et al*. (2007) in tomato.

4.4.1.4 Number of flowers per cluster

The read-through of data presented in the Table 4.13 revealed that heterosis over mid parent, better parent and over check parent for number of flowers per cluster ranged from -21.212 to 94.153 per cent, -41.500 to 79.300 per cent and -34.960 to 92.280 per cent, respectively. For number of flowers per cluster out of all cross combinations, 18 crosses showed significant relative heterosis, 21 hybrids showed significant heterobeltiosis and 17 hybrids exhibited significant standard heterosis.

Out of twenty eight cross combinations, twelve crosses showed desirable significant positive relative heterosis for number of flowers per cluster and among them top five were PBT-5 x PBT-4 (94.153%), PBT-9 x PBT-4 (75.795%), PBT-13 x PBT-4 (66.044%), PCT-1 x PBT-5 (65.000%) and PBT-5 x PBT-13 (56.979%) while, ten

cross combinations showed significant positive heterosis over better parent for same traits. Top five cross combinations which showed desirable significant heterosis over better parents were PBT-5 x PBT-4 (79.300%), PBT-9 x PBT-4 (69.441%), PBT-13 x PBT-4 (59.457%), PBT-5 x PBT-13 (50.700%) and PBT-13 x PBT-10 (41.799%). In case of standard heterosis out of 28 cross combinations, three crosses showed significant positive heterosis over standard checks namely PCT-1 x PBT-5 (92.280%), PBT-5 x PBT-4 (30.590%) and PCT-1 x PBT-13 (15.586%). Heterosis for number of flowers per cluster in desirable positive direction was also reported by Gul *et al*. (2010).

4.4.1.5 Number of fruits per cluster

The perusal of data presented in Table 4.14 revealed that range of heterosis for number of fruits per cluster was -31.442 to 69.312 per cent for relative heterosis, -44.600 to 65.543 per cent for heterobeltiosis and -31.212 to 77.671 per cent for standard heterosis. Among 28 cross combinations, 16 hybrids exhibited significant heterosis over mid parent, 21 hybrids showed significant heterosis over better parent and 20 hybrids showed significant heterosis over standard check parent for number of fruits per cluster.

Among all crosses, eight crosses exhibited desirable significant positive relative heterosis for same traits. Top five cross combinations which showed significant positive relative heterosis were PBT-2 x PBT-13 (69.312%), PBT-5 x PBT-4 (55.156%), PCT-1 x PBT-5 (48.000%), PBT-13 x PBT-4 (42.370%) and PBT-9 x PBT-4 (42.328%). In case of heterobeltiosis among all crosses five cross combinations exhibited desirable significant positive heterosis over better parent namely PBT-2 x PBT-13 (63.543%), PBT-9 x PBT-4 (42.328%), PBT-13 x PBT-4 (39.859%), PBT-5 x PBT-4 (39.271%) and PCT-1 x PBT-5 (14.996%). Out of all crosses four cross combinations showed significant positive standard heterosis which were PCT-1 x PBT-5 (77.671%), PCT-1 x PPT-2 (24.850%), PBT-5 x PBT-4 (19.208%) and PBT-2 x PBT-13 (15.246%). Desirable significant positive heterosis for number of fruits per cluster in tomato was also reported by Gul *et al*. (2010), Narasimhamurthy *et al*. (2013), Sherpa *et al*. (2014), Vilas and Rana (2015) and Marbhal *et al*. (2016).

Table 4.12: Heterosis for days to first fruit ripening

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	84.13	11.726**	23.358**	2.100
2	PCT-1 x PBT-9	82.93	9.602**	21.598**	0.643
3	PCT-1 x PBT-5	75.93	1.152	11.334**	-7.852**
4	PCT-1 x PBT-2	81.53	8.997**	19.545**	-1.056
5	PCT-1 x PBT-13	86.20	5.553**	26.393**	4.612*
6	PCT-1 x PBT-10	81.80	14.727**	19.941**	-0.728
7	PCT-1 x PBT-4	79.93	1.822	17.199**	-2.998
8	PPT-2 x PBT-9	88.67	7.135**	7.609**	7.609**
9	PPT-2 x PBT-5	90.67	10.351**	10.668**	10.036**
10	PPT-2 x PBT-2	92.27	12.662**	13.354**	11.978**
11	PPT-2 x PBT-13	92.93	4.692**	12.779**	12.779**
12	PPT-2 x PBT-10	88.93	13.431**	19.530**	7.925**
13	PPT-2 x PBT-4	86.60	1.168	5.097*	5.097*
14	PBT-9 x PBT-5	76.27	-7.585**	-6.908**	-7.439**
15	PBT-9 x PBT-2	77.53	-5.756**	-4.754*	-5.910**
16	PBT-9 x PBT-13	88.67	-0.516	6.664**	7.609**
17	PBT-9 x PBT-10	90.20	14.518**	21.237**	9.466**
18	PBT-9 x PBT-4	89.73	4.380*	7.939**	8.896**
19	PBT-5 x PBT-2	81.73	0.080	0.405	-0.813
20	PBT-5 x PBT-13	82.40	-6.924**	0.574	0.000
21	PBT-5 x PBT-10	81.73	4.561*	9.852**	-0.813
22	PBT-5 x PBT-4	83.60	-2.068	2.038	1.456
23	PBT-2 x PBT-13	79.47	-9.964**	-2.371	-3.556
24	PBT-2 x PBT-10	83.40	7.060**	12.097**	1.214
25	PBT-2 x PBT-4	82.33	-3.255	1.143	-0.085
26	PBT-13 x PBT-10	83.80	-1.138	12.634**	1.699
27	PBT-13 x PBT-4	90.40	-1.702	1.802	9.709**
28	PBT-10 x PBT-4	85.33	4.571*	14.691**	3.556
Range	**Minimum**	**75.93**	**-9.964**	**-6.908**	**-7.852**
	Maximum	**92.93**	**14.727**	**26.393**	**12.779**

Table 4.13: Heterosis for number of flowers per cluster

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	15.13	-15.309**	-31.227**	10.197
2	PCT-1 x PBT-9	13.33	-14.359**	-39.409**	-2.913
3	PCT-1 x PBT-5	26.40	65.000**	20.000**	92.280**
4	PCT-1 x PBT-2	14.27	-3.809	-35.136**	3.933
5	PCT-1 x PBT-13	15.87	1.731	-27.864**	15.586*
6	PCT-1 x PBT-10	12.87	-21.212**	-41.500**	-6.264
7	PCT-1 x PBT-4	15.47	1.543	-29.682**	12.673
8	PPT-2 x PBT-9	9.47	-17.148*	-31.027**	-31.027**
9	PPT-2 x PBT-5	9.80	-17.404**	-28.623**	-28.623**
10	PPT-2 x PBT-2	10.40	-2.804	-24.253	-24.253**
11	PPT-2 x PBT-13	10.13	-11.644	-26.220**	-26.220**
12	PPT-2 x PBT-10	9.93	-18.607**	-27.677**	-27.677**
13	PPT-2 x PBT-4	9.80	-11.712	-28.623**	-28.623**
14	PBT-9 x PBT-5	12.53	30.998**	25.300**	-8.740
15	PBT-9 x PBT-2	11.33	34.881**	24.096*	-17.480**
16	PBT-9 x PBT-13	10.33	12.711	12.283	-24.763**
17	PBT-9 x PBT-10	11.27	13.838	5.623	-17.917**
18	PBT-9 x PBT-4	15.47	75.795**	69.441**	12.673
19	PBT-5 x PBT-2	11.20	26.769**	12.000	-18.427**
20	PBT-5 x PBT-13	15.07	56.979**	50.700**	9.760
21	PBT-5 x PBT-10	9.87	-4.499	-7.498	-28.114**
22	PBT-5 x PBT-4	17.93	94.153**	79.300**	30.590**
23	PBT-2 x PBT-13	13.00	54.120**	41.304**	-5.317
24	PBT-2 x PBT-10	10.73	17.012*	0.562	-21.850**
25	PBT-2 x PBT-4	11.07	37.175**	30.697**	-19.374**
26	PBT-13 x PBT-10	15.13	52.290**	41.799**	10.197
27	PBT-13 x PBT-4	14.67	66.044**	59.457**	6.846
28	PBT-10 x PBT-4	8.93	-6.688	-16.307	-34.960**
Range	**Minimum**	**8.93**	**-21.212**	**-41.500**	**-34.960**
	Maximum	**26.40**	**94.153**	**79.300**	**92.280**

Table 4.14: Heterosis for number of fruits per cluster

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	10.40	-1.887	-19.192**	24.850**
2	PCT-1 x PBT-9	9.20	-0.755	-28.516**	10.444
3	PCT-1 x PBT-5	14.80	48.000**	14.996**	77.671**
4	PCT-1 x PBT-2	8.60	-8.218	-33.178**	3.241
5	PCT-1 x PBT-13	8.13	-11.341*	-36.830**	-2.401
6	PCT-1 x PBT-10	7.13	-31.442**	-44.600**	-14.406*
7	PCT-1 x PBT-4	9.33	0.647	-27.506**	12.005
8	PPT-2 x PBT-9	6.33	-9.571	-24.010**	-24.010**
9	PPT-2 x PBT-5	6.40	-17.206**	-23.169**	-23.169**
10	PPT-2 x PBT-2	6.47	-8.873	-22.329**	-22.329**
11	PPT-2 x PBT-13	5.87	-14.928*	-29.532**	-29.532**
12	PPT-2 x PBT-10	6.27	-22.878**	-24.730**	-24.730**
13	PPT-2 x PBT-4	6.47	-7.571	-22.329**	-22.329**
14	PBT-9 x PBT-5	6.27	-2.031	-12.062	-24.730**
15	PBT-9 x PBT-2	6.53	13.172	11.244	-21.609**
16	PBT-9 x PBT-13	6.67	19.749*	17.637	-19.928**
17	PBT-9 x PBT-10	5.87	-13.676*	-25.977**	-29.532**
18	PBT-9 x PBT-4	8.07	42.328**	42.328**	-3.121
19	PBT-5 x PBT-2	6.73	3.538	-5.610	-19.208**
20	PBT-5 x PBT-13	7.60	20.635**	6.592	-8.764
21	PBT-5 x PBT-10	5.80	-22.975**	-26.860**	-30.372**
22	PBT-5 x PBT-4	9.93	55.156**	39.271**	19.208**
23	PBT-2 x PBT-13	9.60	69.312**	63.543**	15.246*
24	PBT-2 x PBT-10	6.87	-0.435	-13.367*	-17.527**
25	PBT-2 x PBT-4	6.60	14.385	12.436	-20.768**
26	PBT-13 x PBT-10	7.87	17.463*	-0.757	-5.522
27	PBT-13 x PBT-4	7.93	42.370**	39.859**	-4.802
28	PBT-10 x PBT-4	5.73	-15.735*	-27.743**	-31.212**
Range	**Minimum**	**5.73**	**-31.442**	**-44.600**	**-31.212**
	Maximum	**14.80**	**69.312**	**65.543**	**77.671**

4.4.1.6 Number of fruits per plant

The read-through of data presented in the Table 4.15 revealed that heterosis over mid parent, better parent and over check parent for number of fruits per plant ranged from -79.415 to 139.171 per cent, -88.342 to 108.532 per cent and -41.580 to 72.547 per cent, respectively. For number of fruits per plant out of all cross combinations, 11 crosses showed significant relative heterosis, 13 hybrids showed significant heterobeltiosis and 12 hybrids exhibited significant standard heterosis.

Out of 28 crosses four hybrids namely PBT-5 x PBT-4 (139.171%), PBT-9 x PBT-4 (100.396%), PBT-2 x PBT-13 (73.178%) and PBT-2 x PBT-4 (69.882%) exhibited significant positive heterosis over mid parent while, four hybrids showed significant positive heterosis over better parent which were PBT-5 x PBT-4 (108.532%), PBT-9 x PBT-4 (100.00%), PBT-2 x PBT-4 (61.851%) and PBT-2 x PBT-13 (60.960%). In case of heterosis over check parent out of all cross combinations, four hybrids showed significant positive standard heterosis *i.e*., PCT-1 x PBT-5 (72.547%), PBT-5 x PBT-4 (54.397%), PCT-1 x PPT-2 (43.328%) and PCT-1 x PBT-4 (36.738%). Similar findings for number of fruits per plant were reported by Cheema *et al*. (2014), Chauhan *et al*. (2014), Pandey and Mall (2015), Vilas and Rana (2015), Biswas *et al*. (2016), Sahu *et al*. (2016), Kumar *et al.* (2017b) and Gautam *et al*. (2018).

4.4.1.7 Internodal length (cm)

Data presented in Table 4.16 revealed that the range of heterosis for internodal length was -34.454 to 21.432 per cent for relative heterosis, -29.091 to 44.542 per cent for heterobeltiosis and -24.051 to 30.477 per cent for standard heterosis. Among 28 crosses, 13 hybrids showed significant relative heterosis, 5 hybrids showed significant heterobeltiosis and 6 hybrids exhibited significant standard heterosis for internodal length.

For internodal length, out of twenty eight cross combinations, ten hybrids exhibited desirable significant negative heterosis over mid parent. Top five cross combinations which showed significant negative relative heterosis were PBT-9 x PBT-4 (-34.454%), PBT-9 x PBT-2 (-26.298%), PBT-9 x PBT-13 (-23.556%), PPT-2 x PBT-2 (-22.879%) and PCT-1 x PBT-2 (-20.850%) and two crosses *i.e*., PBT-9 x

PBT-4 (-29.091%) and PBT-9 x PBT-2 (-19.364%) showed significant negative heterosis over better parent for the same trait. In case of standard heterosis out of all crosses, two cross combination exhibited significant negative heterosis for internodal length which were PBT-9 x PBT-4 (-24.051%) and PBT-9 x PBT-5 (-21.422%).

4.4.1.8 Average fruit weight (g)

The perusal of data presented in Table 4.17 revealed that range of heterosis for average fruit weight was -60.559 to 118.977 per cent for relative heterosis, -71.049 to 109.689 per cent for heterobeltiosis and -62.078 to 107.701 per cent for standard heterosis. Among 28 cross combinations, 26 hybrids exhibited significant heterosis over mid parent, 24 hybrids showed significant heterosis over better parent and 24 hybrids showed significant heterosis over standard check parent for average fruit weight.

Among all crosses, seventeen crosses exhibited desirable significant positive relative heterosis for same traits. Top five cross combinations which showed significant positive relative heterosis were PBT-13 x PBT-10 (118.977%), PCT-1 x PPT-2 (77.215%), PPT-2 x PBT-13 (65.218%), PPT-2 x PBT-4 (49.445%) and PPT-2 x PBT-9 (49.196%). In case of heterobeltiosis among all crosses, eleven crosses exhibited significant positive heterosis over better parent and five cross combinations exhibited desirable significant positive heterobeltiosis were PBT-13 x PBT-10 (109.689%), PPT-2 x PBT-13 (57.494%), PPT-2 x PBT-4 (37.583%), PBT-5 x PBT-4 (31.400%) and PBT-9 x PBT-5 (29.133%). Out of all crosses sixteen cross combinations showed desirable positive standard heterosis for average fruit weight and among them top five crosses were PBT-13 x PBT-10 (107.701%), PBT-9 x PBT-5 (83.805%), PPT-2 x PBT-9 (80.779%), PPT-2 x PBT-2 (73.935%) and PPT-2 x PBT-4 (63.545%). Similar findings for average fruit weight were reported by Gul *et al*. (2010), Agarwal *et al*. (2014), Cheema *et al*. (2014), Chauhan *et al*. (2014), Pandey and Mall (2015), Biswas *et al*. (2016), Sahu *et al*. (2016), Amin *et al*. (2017), Kumar *et al.* (2017a) and Gautam *et al*. (2018).

4.4.1.9 Fruit length (cm)

The read-through of data presented in the Table 4.18 revealed that heterosis over mid parent, better parent and over check parent for fruit length ranged -34.027 to 19.094 per cent, -41.959 to 12.754 per cent and -41.527 to 13.594 per cent,

respectively. For fruit length, out of all cross combinations, 16 crosses showed significant relative heterosis, 20 hybrids showed significant heterobeltiosis and 14 hybrids exhibited significant standard heterosis.

Out of 28 crosses, seven cross combinations exhibited significant positive heterosis over mid parent and among them top five crosses were PBT-13 x PBT-10 (19.094%), PCT-1 x PBT-4 (18.014%), PBT-9 x PBT-5 (16.109%), PCT-1 x PBT-5 (14.460%) and PPT-2 x PBT-9 (13.173%) whereas, for heterobeltiosis two hybrids *i.e*., PBT-13 x PBT-10 (17.476%) and PPT-2 x PBT-9 (12.754%) showed desirable significant positive heterosis for fruit length. In case of heterosis over check parent out of all cross combinations two hybrids showed significant positive standard heterosis *i.e*., PPT-2 x PBT-9 (13.594%) and PBT-13 x PBT-10 (12.663%) for same character. Similar findings for fruit length were reported by Gul *et al*. (2010), Chauhan *et al*. (2014), Mali and Patel (2014), Reddy *et al*. (2014), Biswas *et al*. (2016), Kumar *et al.* (2016) and Kumar *et al*. (2017b).

4.4.1.10 Fruit width (cm)

Data presented in Table 4.19 revealed that the range of heterosis for fruit width was -31.151 to 37.018 per cent for relative heterosis, -40.000 to 24.318 per cent for heterobeltiosis and -35.714 to 25.992 per cent for standard heterosis. Among 28 crosses, 11 hybrids showed significant relative heterosis, 17 hybrids showed significant heterobeltiosis and 13 hybrids exhibited significant standard heterosis for fruit width.

For fruit width out of twenty eight cross combinations, five hybrids *i.e*., PCT-1 x PBT-4 (37.018%), PBT-13 x PBT-4 (28.103%), PBT-13 x PBT-10 (26.747%), PBT-9 x PBT-5 (25.224%) and PCT-1 x PBT-13 (22.632%) exhibited significant positive heterosis over mid parent and three hybrids *i.e*., PBT-13 x PBT-4 (24.318%), PBT-9 x PBT-5 (23.866%) and PBT-13 x PBT-10 (12.989%) showed significant positive heterosis over better parent for the same trait. In case of standard heterosis out of all crosses, two cross combinations exhibited significant positive heterosis for fruit width which were PBT-13 x PBT-10 (25.992%) and PBT-9 x PBT-5 (24.603%). The results are in close agreement with the findings of Chauhan *et al*. (2014), Mali and Patel (2014), Reddy *et al*. (2014), Biswas *et al*. (2016) and Kumar *et al.* (2016).

Table 4.15: Heterosis for number of fruits per plant

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	78.73	-61.657**	-77.868**	43.328**
2	PCT-1 x PBT-9	70.99	-63.227**	-80.044**	29.237
3	PCT-1 x PBT-5	94.78	-52.180**	-73.356**	72.547**
4	PCT-1 x PBT-2	49.74	-74.034**	-86.017**	-9.448
5	PCT-1 x PBT-13	56.60	-70.796**	-84.089**	3.040
6	PCT-1 x PBT-10	41.47	-79.415**	-88.342**	-24.504
7	PCT-1 x PBT-4	75.11	-61.081**	-78.886**	36.738*
8	PPT-2 x PBT-9	41.12	-3.587	-25.141	-25.141
9	PPT-2 x PBT-5	38.38	-19.707	-30.129	-30.129
10	PPT-2 x PBT-2	37.27	-9.451	-32.150	-32.150
11	PPT-2 x PBT-13	33.50	-22.829	-39.013*	-39.013*
12	PPT-2 x PBT-10	42.24	-17.274	-23.102	-23.102
13	PPT-2 x PBT-4	34.03	-20.099	-38.048*	-38.048*
14	PBT-9 x PBT-5	35.27	-0.704	-13.278	-35.791*
15	PBT-9 x PBT-2	33.27	15.201	9.549	-39.432*
16	PBT-9 x PBT-13	35.59	14.327	11.602	-35.208*
17	PBT-9 x PBT-10	32.09	-17.251	-31.998	-41.580*
18	PBT-9 x PBT-4	60.74	100.396**	100.000**	10.577
19	PBT-5 x PBT-2	41.49	21.922	2.016	-24.468
20	PBT-5 x PBT-13	48.65	34.096	19.621	-11.433
21	PBT-5 x PBT-10	35.75	-18.621	-24.242	-34.917*
22	PBT-5 x PBT-4	84.81	139.171**	108.532**	54.397**
23	PBT-2 x PBT-13	51.33	73.178**	60.960*	-6.554
24	PBT-2 x PBT-10	38.21	2.467	-19.029	-30.439
25	PBT-2 x PBT-4	48.96	69.882*	61.851*	-10.868
26	PBT-13 x PBT-10	50.94	28.832	7.947	-7.264
27	PBT-13 x PBT-4	39.65	27.615	24.334	-27.817
28	PBT-10 x PBT-4	35.31	-8.807	-25.175	-35.718*
Range	**Minimum**	**32.09**	**-79.415**	**-88.342**	**-41.580**
	Maximum	**94.78**	**139.171**	**108.532**	**72.547**

Table 4.16: Heterosis for internodal length

S. N.	F_1 hybrid	*Per se* performance (cm)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	10.53	3.897	5.300	2.532
2	PCT-1 x PBT-9	10.93	4.095	9.300	6.426
3	PCT-1 x PBT-5	11.20	16.243*	20.820*	9.056
4	PCT-1 x PBT-2	9.13	-20.850**	-8.700	-11.100
5	PCT-1 x PBT-13	9.67	-16.168*	-3.300	-5.842
6	PCT-1 x PBT-10	11.80	16.428*	18.000	14.898
7	PCT-1 x PBT-4	11.00	-3.509	10.000	7.108
8	PPT-2 x PBT-9	10.40	-2.210	1.266	1.266
9	PPT-2 x PBT-5	8.53	-12.692	-7.983	-16.943
10	PPT-2 x PBT-2	9.00	-22.879**	-12.366	-12.366
11	PPT-2 x PBT-13	11.20	-4.027	9.055	9.056
12	PPT-2 x PBT-10	10.27	0.000	0.000	0.000
13	PPT-2 x PBT-4	9.40	-18.509**	-8.471	-8.471
14	PBT-9 x PBT-5	8.07	-20.375*	-12.945	-21.422*
15	PBT-9 x PBT-2	8.87	-26.298**	-19.364*	-13.632
16	PBT-9 x PBT-13	9.20	-23.556**	-16.364	-10.419
17	PBT-9 x PBT-10	11.27	5.971	9.737	9.737
18	PBT-9 x PBT-4	7.80	-34.454**	-29.091**	-24.051**
19	PBT-5 x PBT-2	9.07	-18.800**	-2.158	-11.685
20	PBT-5 x PBT-13	10.47	-6.267	12.945	1.947
21	PBT-5 x PBT-10	8.80	-9.928	-5.070	-14.314
22	PBT-5 x PBT-4	13.40	21.432**	44.542**	30.477**
23	PBT-2 x PBT-13	12.40	-5.126	-5.126	20.740*
24	PBT-2 x PBT-10	12.53	7.369	22.006*	22.006*
25	PBT-2 x PBT-4	12.93	-0.039	1.016	25.901**
26	PBT-13 x PBT-10	11.93	2.228	16.164	16.164
27	PBT-13 x PBT-4	11.60	-10.321	-9.375	12.950
28	PBT-10 x PBT-4	9.73	-15.648*	-5.258	-5.258
Range	**Minimum**	**7.80**	**-34.454**	**-29.091**	**-24.051**
	Maximum	**13.40**	**21.432**	**44.542**	**30.477**

Table 4.17: Heterosis for average fruit weight

S. N.	F_1 hybrid	*Per se* performance (g)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	77.00	77.215**	0.000	0.000
2	PCT-1 x PBT-9	31.73	-46.895**	-71.049**	-58.792**
3	PCT-1 x PBT-5	71.73	44.953**	-19.468**	-6.844
4	PCT-1 x PBT-2	34.80	-46.118**	-70.823**	-54.805**
5	PCT-1 x PBT-13	43.40	8.908	-37.822**	-43.636**
6	PCT-1 x PBT-10	29.20	-32.227*	-61.715**	-62.078**
7	PCT-1 x PBT-4	69.07	36.192**	-24.538**	-10.299
8	PPT-2 x PBT-9	139.20	49.196**	27.007**	80.779**
9	PPT-2 x PBT-5	107.60	29.584**	20.804**	39.740**
10	PPT-2 x PBT-2	133.93	36.475**	12.291*	73.935**
11	PPT-2 x PBT-13	121.27	65.218**	57.494**	57.494**
12	PPT-2 x PBT-10	93.33	21.785**	21.208*	21.208*
13	PPT-2 x PBT-4	125.93	49.445**	37.583**	63.545**
14	PBT-9 x PBT-5	141.53	42.477**	29.133**	83.805**
15	PBT-9 x PBT-2	68.47	-40.167**	-42.592**	-11.078
16	PBT-9 x PBT-13	103.73	15.641*	-5.356	34.714**
17	PBT-9 x PBT-10	109.07	17.362**	-0.484	41.649**
18	PBT-9 x PBT-4	95.40	-5.136	-12.956*	23.896**
19	PBT-5 x PBT-2	64.00	-38.562**	-46.340**	-16.883*
20	PBT-5 x PBT-13	31.33	-60.559**	-64.825**	-59.312**
21	PBT-5 x PBT-10	106.27	28.547**	19.311**	38.013**
22	PBT-5 x PBT-4	120.27	33.189**	31.400**	56.195**
23	PBT-2 x PBT-13	123.80	30.957**	3.798	60.779**
24	PBT-2 x PBT-10	61.80	-36.790**	-48.185**	-19.740*
25	PBT-2 x PBT-4	91.87	-12.837*	-22.973**	19.312*
26	PBT-13 x PBT-10	159.93	118.977**	109.689**	107.701**
27	PBT-13 x PBT-4	106.40	31.904**	16.246*	38.182**
28	PBT-10 x PBT-4	63.60	-24.195**	-30.515**	-17.403*
Range	**Minimum**	**29.20**	**-60.559**	**-71.049**	**-62.078**
	Maximum	**159.93**	**118.977**	**109.689**	**107.701**

Table 4.18: Heterosis for fruit length

S. N.	F_1 hybrid	*Per se* performance (cm)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	4.07	8.824	-24.209**	-24.209**
2	PCT-1 x PBT-9	3.14	-16.489**	-41.959**	-41.527**
3	PCT-1 x PBT-5	3.76	14.460*	-15.695**	-29.981**
4	PCT-1 x PBT-2	3.21	-4.606	-30.519**	-40.223**
5	PCT-1 x PBT-13	3.99	9.917	-22.524**	-25.698**
6	PCT-1 x PBT-10	3.65	2.528	-27.146**	-32.030**
7	PCT-1 x PBT-4	5.11	18.014**	-21.985**	-4.842
8	PPT-2 x PBT-9	6.10	13.173**	12.754*	13.594**
9	PPT-2 x PBT-5	5.21	6.002	-2.980	-2.980
10	PPT-2 x PBT-2	5.46	9.309*	1.676	1.676
11	PPT-2 x PBT-13	5.36	1.901	-0.186	-0.186
12	PPT-2 x PBT-10	4.38	-15.607**	-18.436**	-18.436**
13	PPT-2 x PBT-4	5.82	-2.349	-11.145**	8.380
14	PBT-9 x PBT-5	5.73	16.109**	5.915	6.704
15	PBT-9 x PBT-2	3.89	-22.433**	-28.096**	-27.561**
16	PBT-9 x PBT-13	4.41	-16.477**	-18.484**	-17.877**
17	PBT-9 x PBT-10	4.93	-5.374	-8.872	-8.194
18	PBT-9 x PBT-4	5.15	-13.880**	-21.374**	-4.097
19	PBT-5 x PBT-2	4.19	-7.709	-9.307	-21.974**
20	PBT-5 x PBT-13	3.17	-34.027**	-38.447**	-40.968**
21	PBT-5 x PBT-10	5.26	11.088*	4.990	-2.048
22	PBT-5 x PBT-4	5.30	-3.724	-19.084**	-1.304
23	PBT-2 x PBT-13	5.05	3.378	-1.942	-5.959
24	PBT-2 x PBT-10	4.23	-12.150*	-15.569**	-21.229**
25	PBT-2 x PBT-4	5.68	1.701	-13.282**	5.773
26	PBT-13 x PBT-10	6.05	19.094**	17.476**	12.663*
27	PBT-13 x PBT-4	5.18	-11.453**	-20.916**	-3.538
28	PBT-10 x PBT-4	4.89	-15.398**	-25.344**	-8.939
Range	**Minimum**	**3.14**	**-34.027**	**-41.959**	**-41.527**
	Maximum	**6.10**	**19.094**	**12.754**	**13.594**

Table 4.19: Heterosis for fruit width

S. N.	F_1 hybrid	*Per se* performance (cm)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	3.62	5.386	-28.175**	-28.175**
2	PCT-1 x PBT-9	3.44	1.325	-30.645**	-31.746**
3	PCT-1 x PBT-5	3.81	10.435	-24.852**	-24.405**
4	PCT-1 x PBT-2	3.24	-10.373	-40.000**	-35.714**
5	PCT-1 x PBT-13	3.82	22.632*	-13.182	-24.206**
6	PCT-1 x PBT-10	3.76	0.940	-33.096**	-25.397**
7	PCT-1 x PBT-4	4.09	37.018**	-1.208	-18.849*
8	PPT-2 x PBT-9	5.42	8.400	7.540	7.540
9	PPT-2 x PBT-5	4.99	-1.286	-1.578	-0.992
10	PPT-2 x PBT-2	5.31	1.724	-1.667	5.357
11	PPT-2 x PBT-13	4.72	0.000	-6.349	-6.349
12	PPT-2 x PBT-10	4.03	-24.390**	-28.292**	-20.040**
13	PPT-2 x PBT-4	4.47	-2.614	-11.310	-11.310
14	PBT-9 x PBT-5	6.28	25.224**	23.866**	24.603**
15	PBT-9 x PBT-2	4.39	-15.251*	-18.704**	-12.897
16	PBT-9 x PBT-13	4.77	1.923	-3.831	-5.357
17	PBT-9 x PBT-10	4.71	-10.964	-16.192*	-6.548
18	PBT-9 x PBT-4	4.43	-2.637	-10.685	-12.103
19	PBT-5 x PBT-2	4.38	-16.332**	-18.889**	-13.095
20	PBT-5 x PBT-13	3.26	-31.151**	-35.700**	-35.317**
21	PBT-5 x PBT-10	4.85	-9.261	-13.701*	-3.770
22	PBT-5 x PBT-4	5.06	9.881	-0.197	0.397
23	PBT-2 x PBT-13	5.43	10.816	0.556	7.738
24	PBT-2 x PBT-10	4.14	-24.864**	-26.335**	-17.857*
25	PBT-2 x PBT-4	3.46	-27.463**	-35.926**	-31.349**
26	PBT-13 x PBT-10	6.35	26.747**	12.989*	25.992**
27	PBT-13 x PBT-4	5.47	28.103**	24.318**	8.532
28	PBT-10 x PBT-4	4.67	-4.303	-16.904*	-7.341
Range	**Minimum**	**3.24**	**-31.151**	**-40.000**	**-35.714**
	Maximum	**6.35**	**37.018**	**24.318**	**25.992**

4.4.1.11 Fruit shape index

The perusal of data presented in Table 4.20 revealed that range of heterosis for fruit shape index was -31.408 to 35.510 per cent for relative heterosis, -40.252 to 22.472 per cent for heterobeltiosis and -16.822 to 55.140 per cent for standard heterosis. Among 28 cross combinations, seven hybrids exhibited significant heterosis over mid parent, ten hybrids showed significant heterosis over better parent and two hybrids showed significant heterosis over standard check parent for fruit shape index.

Among all crosses, two crosses *viz*., PBT-2 x PBT-4 (35.510%) and PBT-5 x PBT-10 (22.472%) exhibited desirable significant positive relative heterosis for same traits. In case of heterobeltiosis among all crosses, none of them exhibited desirable significant heterosis over better parent. Out of all crosses two cross combinations showed significant positive standard heterosis which were PBT-2 x PBT-4 (55.140%) and PPT-2 x PBT-4 (21.495%) for fruit shape index. Desirable significant heterosis for fruit shape index in tomato was also reported by Kurian *et al*. (2001).

4.4.1.12 Plant height (cm)

Data presented in Table 4.21 revealed that the range of heterosis for plant height was -35.140 to 42.957 per cent for relative heterosis, -42.640 to 27.486 per cent for heterobeltiosis and -41.435 to 11.276 per cent for standard heterosis. Among twenty eight crosses, twelve hybrids showed significant relative heterosis, three hybrids showed significant heterobeltiosis and one hybrid exhibited significant standard heterosis for plant height.

For plant height, out of twenty eight cross combinations, eleven hybrids exhibited significant positive heterosis over mid parent. Top five cross combinations which showed significant positive relative heterosis were PBT-13 x PBT-4 (42.957%), PCT-1 x PBT-4 (38.570%), PBT-9 x PBT-4 (37.976%), PBT-10 x PBT-4 (36.138%) and PPT-2 x PBT-4 (34.361%). Among all crosses two hybrids, namely PBT-13 x PBT-10 (27.486%) and PBT-5 x PBT-10 (26.459%) exhibited significant positive heterosis over better parent. In case of heterosis over check parent none of cross combinations showed desirable significant positive standard heterosis for plant height. Desirable significant positive heterosis for plant height was also reported by Narasimhamurthy *et al*. (2013), Dagade *et al*. (2015), Pandey and Mall (2015), Marbhal *et al*. (2016), Amin *et al*. (2017), Kumar *et al*. (2017a) and Gautam *et al*. (2018).

Table 4.20: Heterosis for fruit shape index

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	1.13	0.893	-3.419	5.607
2	PCT-1 x PBT-9	0.92	-18.584*	-21.368*	-14.019
3	PCT-1 x PBT-5	0.99	-3.883	-15.385	-7.477
4	PCT-1 x PBT-2	0.99	-2.463	-15.385	-7.477
5	PCT-1 x PBT-13	1.05	-10.638	-11.017	-1.869
6	PCT-1 x PBT-10	0.97	-5.825	-17.094	-9.346
7	PCT-1 x PBT-4	1.25	-9.420	-21.384**	16.822
8	PPT-2 x PBT-9	1.13	4.630	3.670	5.607
9	PPT-2 x PBT-5	1.05	7.143	-1.869	-1.869
10	PPT-2 x PBT-2	1.03	6.736	-3.738	-3.738
11	PPT-2 x PBT-13	1.14	1.333	-3.390	6.542
12	PPT-2 x PBT-10	1.09	11.224	1.869	1.869
13	PPT-2 x PBT-4	1.30	-2.256	-18.239**	21.495*
14	PBT-9 x PBT-5	0.92	-7.071	-15.596	-14.019
15	PBT-9 x PBT-2	0.89	-8.718	-18.349	-16.822
16	PBT-9 x PBT-13	0.93	-18.062*	-21.186**	-13.084
17	PBT-9 x PBT-10	1.05	6.061	-3.670	-1.869
18	PBT-9 x PBT-4	1.17	-12.687	-26.415**	9.346
19	PBT-5 x PBT-2	0.96	9.714	7.865	-10.280
20	PBT-5 x PBT-13	0.98	-5.314	-16.949	-8.411
21	PBT-5 x PBT-10	1.09	22.472*	22.472	1.869
22	PBT-5 x PBT-4	1.05	-15.323*	-33.962**	-1.869
23	PBT-2 x PBT-13	0.93	-8.824	-21.186*	-13.084
24	PBT-2 x PBT-10	1.03	17.714	15.730	-3.738
25	PBT-2 x PBT-4	1.66	35.510**	4.403	55.140**
26	PBT-13 x PBT-10	0.95	-8.213	-19.492*	-11.215
27	PBT-13 x PBT-4	0.95	-31.408**	-40.252**	-11.215
28	PBT-10 x PBT-4	1.05	-15.323*	-33.962**	-1.869
Range	**Minimum**	**0.89**	**-31.408**	**-40.252**	**-16.822**
	Maximum	**1.66**	**35.510**	**22.472**	**55.140**

Table 4.21: Heterosis for plant height

S. N.	F_1 hybrid	*Per se* performance (cm)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	401.40	-1.165	-1.874	-0.446
2	PCT-1 x PBT-9	438.33	20.831*	7.154	8.714
3	PCT-1 x PBT-5	431.67	15.542	5.525	7.060
4	PCT-1 x PBT-2	405.73	-1.129	-1.441	0.628
5	PCT-1 x PBT-13	423.33	11.257	3.488	4.993
6	PCT-1 x PBT-10	411.40	11.269	0.570	2.034
7	PCT-1 x PBT-4	447.53	38.570**	9.404	10.995
8	PPT-2 x PBT-9	372.07	3.400	-7.722	-7.722
9	PPT-2 x PBT-5	332.40	-10.324	-17.560	-17.560
10	PPT-2 x PBT-2	397.87	-2.348	-3.352	-1.323
11	PPT-2 x PBT-13	420.00	11.239	4.167	4.167
12	PPT-2 x PBT-10	434.40	18.430	7.738	7.738
13	PPT-2 x PBT-4	430.00	34.361**	6.647	6.647
14	PBT-9 x PBT-5	355.87	8.728	5.244	-11.739
15	PBT-9 x PBT-2	236.13	-35.140**	-42.640**	-41.435**
16	PBT-9 x PBT-13	427.33	27.868**	21.425	5.985
17	PBT-9 x PBT-10	330.53	2.195	0.040	-18.022
18	PBT-9 x PBT-4	381.73	37.976**	20.624	-5.324
19	PBT-5 x PBT-2	346.67	-7.531	-15.789	-14.021
20	PBT-5 x PBT-13	373.20	8.163	6.043	-7.440
21	PBT-5 x PBT-10	427.60	27.922**	26.459*	6.052
22	PBT-5 x PBT-4	361.00	25.565*	6.763	-10.466
23	PBT-2 x PBT-13	368.40	-3.510	-10.510	-8.631
24	PBT-2 x PBT-10	406.53	9.568	-1.247	0.827
25	PBT-2 x PBT-4	411.27	26.830*	-0.097	2.001
26	PBT-13 x PBT-10	448.67	31.510**	27.486**	11.276
27	PBT-13 x PBT-4	420.87	42.957**	19.587	4.382
28	PBT-10 x PBT-4	386.13	36.138**	16.868	-4.233
Range	**Minimum**	**236.13**	**-35.140**	**-42.640**	**-41.435**
	Maximum	**448.67**	**42.957**	**27.486**	**11.276**

4.4.1.13 100 seed weight (g)

Date presented in Table 4.22 revealed that range of heterosis for 100 seed weight was -18.841 to 62.500 per cent for relative heterosis, -30.000 to 11.429 per cent for heterobeltiosis and -20.000 to 20.000 per cent for standard heterosis. Among all crosses, thirteen hybrids showed significant relative heterosis, nine hybrids showed significant heterobeltiosis and twelve hybrids exhibited significant standard heterosis for 100 seed weight.

Out of twenty eight crosses, nine cross combinations showed significant positive relative heterosis and among them top five crosses were PCT-1 x PPT-2 (62.500%), PCT-1 x PBT-13 (60.000%), PCT-1 x PBT-4 (47.619%), PCT-1 x PBT-2 (47.170%) and PCT-1 x PBT-10 (41.176%). For heterobeltiosis only one cross combination *viz*., PCT-1 x PPT-2 (11.429%) showed significant positive heterosis over better parent. Out of all cross combinations, nine crosses namely PBT-9 x PBT-2 (20.000%), PCT-1 x PBT-13 (14.286%), PCT-1 x PPT-2 (11.429%), PCT-1 x PBT-2 (11.429%), PBT-5 x PBT-2 (11.429%), PBT-2 x PBT-13 (11.429%), PBT-2 x PBT-10 (11.429%), PBT-13 x PBT-10 (11.429%) and PBT-10 x PBT-4 (11.429%) showed significant positive standard heterosis over check parent for 100 seed weight.

4.4.1.14 Fruit yield per plant (kg)

The perusal of data presented in Table 4.23 revealed that range of heterosis for fruit yield per plant was -41.631 to 178.829 per cent for relative heterosis, -45.013 to 99.677 per cent for heterobeltiosis and -49.754 to 68.227 per cent for standard heterosis. Among 28 cross combinations, 17 hybrids exhibited significant heterosis over mid parent, 16 hybrids showed significant heterosis over better parent and 19 hybrids showed significant heterosis over standard check parent for fruit yield per plant.

Among all crosses, twelve crosses exhibited desirable significant positive relative heterosis for same traits. Top five cross combinations which showed desirable significant positive relative heterosis were PBT-2 x PBT-13 (178.829%), PBT-13 x PBT-10 (123.935%), PBT-13 x PBT-4 (123.037%), PBT-5 x PBT-4 (101.056%) and PBT-9 x PBT-4 (98.611%). In case of heterobeltiosis among all crosses, nine cross combinations exhibited desirable significant positive heterosis over better parent and among them top five crosses were PBT-2 x PBT-13 (99.677%), PCT-1 x PBT-5 (84.013%), PBT-5 x PBT-4 (78.438%), PBT-9 x PBT-4 (74.390%) and PBT-13 x PBT-4 (71.774%). Out of

all crosses, seven cross combinations showed significant positive standard heterosis for fruit yield per plant and top five hybrids which exhibited significant positive standard heterosis were PCT-1 x PBT-5 (68.227%), PBT-2 x PBT-13 (52.463%), PBT-9 x PBT-4 (40.887%), PBT-5 x PBT-4 (40.640%) and PBT-13 x PBT-10 (35.961%). Significant positive heterosis for fruit yield per plant has been reported by many researchers, some of them are Sherpa *et al*. (2005), Gul *et al*. (2010), Agarwal *et al*. (2014), Chauhan *et al*. (2014), Reddy *et al*. (2014), Samiyoddin *et al.* (2015), Vilas and Rana (2015), Biswas *et al*. (2016), Jose *et al*. (2016), Kumar *et al*. (2016), Marbhal *et al*. (2016), Sahu *et al*. (2016), Amin *et al*. (2017) and Kumar *et al.* (2017a).

4.4.1.15 Fruit yield per hectare (t/ha)

The read-through of data presented in the Table 4.24 revealed that heterosis over mid parent, better parent and over check parent for fruit yield per hectare ranged -43.047 to 178.827 per cent, -45.025 to 99.890 per cent and -49.843 to 68.126 per cent, respectively. For fruit yield per hectare, out of all cross combinations, 17 crosses showed significant relative heterosis, 16 hybrids showed significant heterobeltiosis and 19 hybrids exhibited significant standard heterosis.

Out of 28 crosses, 12 cross combinations exhibited significant positive heterosis over mid parent for same character and among them top five crosses were PBT-2 x PBT-13 (178.827%), PBT-13 x PBT-10 (123.921%), PBT-13 x PBT-4 (123.017%), PBT-5 x PBT-4 (101.142%) and PBT-9 x PBT-4 (98.864%). For heterobeltiosis nine cross combinations showed significant positive heterosis for fruit yield per hectare and among them top five crosses were PBT-2 x PBT-13 (99.890%), PCT-1 x PBT-5 (84.276%), PBT-5 x PBT-4 (78.480%), PBT-9 x PBT-4 (74.582%) and PBT-13 x PBT-4 (71.991%). Out of all crosses seven cross combinations showed significant positive standard heterosis for fruit yield per hectare and top five hybrids which exhibited significant positive standard heterosis for the same trait were PCT-1 x PBT-5 (68.126%), PBT-2 x PBT-13 (52.354%), PBT-9 x PBT-4 (40.806%), PBT-5 x PBT-4 (40.442%) and PBT-13 x PBT-10 (35.924%). Significant positive heterosis for fruit yield per hectare was also reported by Hannan *et al*. (2007), Amaefula *et al*. (2014), Cheema *et al*. (2014), Pandey and Mall (2015), Bharathkumar *et al.* (2016), Panchal *et al*. (2017) and Gautam *et al*. (2018).\

Table 4.22: Heterosis for 100 seed weight

S. N.	F_1 hybrid	*Per se* performance (g)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	0.39	62.500**	11.429*	11.429*
2	PCT-1 x PBT-9	0.33	29.412**	-13.158*	-5.714
3	PCT-1 x PBT-5	0.30	22.449**	-16.667**	-14.286*
4	PCT-1 x PBT-2	0.39	47.170**	-2.500	11.429*
5	PCT-1 x PBT-13	0.40	60.000**	8.108	14.286*
6	PCT-1 x PBT-10	0.36	41.176**	-5.263	2.857
7	PCT-1 x PBT-4	0.31	47.619**	6.897	-11.429*
8	PPT-2 x PBT-9	0.37	1.370	-2.632	5.714
9	PPT-2 x PBT-5	0.36	1.408	0.000	2.857
10	PPT-2 x PBT-2	0.36	-4.000	-10.000*	2.857
11	PPT-2 x PBT-13	0.38	5.556	2.703	8.571
12	PPT-2 x PBT-10	0.35	-4.110	-7.895	0.000
13	PPT-2 x PBT-4	0.36	12.500*	2.857	2.857
14	PBT-9 x PBT-5	0.36	-2.703	-5.263	2.857
15	PBT-9 x PBT-2	0.42	7.692	5.000	20.000**
16	PBT-9 x PBT-13	0.34	-9.333*	-10.526*	-2.857
17	PBT-9 x PBT-10	0.38	0.000	0.000	8.571
18	PBT-9 x PBT-4	0.35	4.478	-7.895	0.000
19	PBT-5 x PBT-2	0.39	2.632	-2.500	11.429*
20	PBT-5 x PBT-13	0.33	-9.589*	-10.811*	-5.714
21	PBT-5 x PBT-10	0.33	-10.811*	-13.158*	-5.714
22	PBT-5 x PBT-4	0.32	-1.538	-11.111*	-8.571
23	PBT-2 x PBT-13	0.39	1.299	-2.500	11.429*
24	PBT-2 x PBT-10	0.39	0.000	-2.500	11.429*
25	PBT-2 x PBT-4	0.28	-18.841**	-30.000**	-20.000**
26	PBT-13 x PBT-10	0.39	4.000	2.632	11.429*
27	PBT-13 x PBT-4	0.36	9.091	-2.703	2.857
28	PBT-10 x PBT-4	0.39	16.418**	2.632	11.429*
Range	**Minimum**	**0.28**	**-18.841**	**-30.000**	**-20.000**
	Maximum	**0.42**	**62.500**	**11.429**	**20.000**

Table 4.23: Heterosis for fruit yield per plant

S. N.	F_1 hybrid	*Per se* performance (kg)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	3.06	-21.236*	-24.631*	-24.631*
2	PCT-1 x PBT-9	2.04	-41.631**	-45.013**	-49.754**
3	PCT-1 x PBT-5	6.83	97.685**	84.097**	68.227**
4	PCT-1 x PBT-2	2.46	-27.753*	-33.693**	-39.409**
5	PCT-1 x PBT-13	2.19	-13.267	-40.970**	-46.059**
6	PCT-1 x PBT-10	2.08	-43.014**	-43.935**	-48.768**
7	PCT-1 x PBT-4	3.41	10.178	-8.086	-16.010
8	PPT-2 x PBT-9	5.45	48.501**	34.236**	34.236**
9	PPT-2 x PBT-5	4.13	13.774	1.724	1.724
10	PPT-2 x PBT-2	4.93	37.709**	21.429*	21.429*
11	PPT-2 x PBT-13	4.02	48.889**	-0.985	-0.985
12	PPT-2 x PBT-10	3.85	0.654	-5.172	-5.172
13	PPT-2 x PBT-4	4.04	23.547*	-0.493	-0.493
14	PBT-9 x PBT-5	4.83	49.074**	47.256**	18.966
15	PBT-9 x PBT-2	2.41	-24.451*	-26.524*	-40.640**
16	PBT-9 x PBT-13	3.47	50.216**	5.793	-14.532
17	PBT-9 x PBT-10	2.90	-15.575	-19.220	-28.571**
18	PBT-9 x PBT-4	5.72	98.611**	74.390**	40.887**
19	PBT-5 x PBT-2	2.49	-20.952	-22.188	-38.670**
20	PBT-5 x PBT-13	2.29	0.881	-28.438*	-43.596**
21	PBT-5 x PBT-10	3.89	14.580	8.357	-4.187
22	PBT-5 x PBT-4	5.71	101.056**	78.438**	40.640**
23	PBT-2 x PBT-13	6.19	178.829**	99.677**	52.463**
24	PBT-2 x PBT-10	2.92	-12.706	-18.663	-28.079**
25	PBT-2 x PBT-4	3.06	9.677	-1.290	-24.631*
26	PBT-13 x PBT-10	5.52	123.935**	53.760**	35.961**
27	PBT-13 x PBT-4	4.26	123.037**	71.774**	4.926
28	PBT-10 x PBT-4	3.09	1.812	-13.928	-23.892*
Range	**Minimum**	**2.04**	**-41.631**	**-45.013**	**-49.754**
	Maximum	**6.83**	**178.829**	**99.677**	**68.227**

Table 4.24: Heterosis for fruit yield per hectare

S. N.	F_1 hybrid	*Per se* performance (t/ha)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	107.75	-21.181*	-24.635*	-24.635*
2	PCT-1 x PBT-9	71.71	-41.640**	-45.025**	-49.843**
3	PCT-1 x PBT-5	240.37	97.884**	84.276**	68.126**
4	PCT-1 x PBT-2	86.46	-27.772*	-33.717**	-39.526**
5	PCT-1 x PBT-13	76.89	-13.466	-41.053**	-46.219**
6	PCT-1 x PBT-10	73.11	-43.047**	-43.951**	-48.863**
7	PCT-1 x PBT-4	119.98	10.281	-8.019	-16.080
8	PPT-2 x PBT-9	191.93	48.622**	34.245**	34.245**
9	PPT-2 x PBT-5	145.32	13.767	1.644	1.644
10	PPT-2 x PBT-2	173.34	37.604**	21.242*	21.242*
11	PPT-2 x PBT-13	141.33	48.581**	-1.147	-1.147
12	PPT-2 x PBT-10	135.53	0.665	-5.204	-5.204
13	PPT-2 x PBT-4	142.06	23.466*	-0.636	-0.636
14	PBT-9 x PBT-5	169.97	49.221**	47.403**	18.885
15	PBT-9 x PBT-2	84.70	-24.469*	-26.546*	-40.757**
16	PBT-9 x PBT-13	122.21	50.338**	5.984	-14.521
17	PBT-9 x PBT-10	102.15	-15.442	-19.121	-28.551**
18	PBT-9 x PBT-4	201.31	98.864**	74.582**	40.806**
19	PBT-5 x PBT-2	87.61	-20.883	-22.124	-38.721**
20	PBT-5 x PBT-13	80.53	0.807	-28.418*	-43.673**
21	PBT-5 x PBT-10	136.77	14.548	8.290	-4.337
22	PBT-5 x PBT-4	200.79	101.142**	78.480**	40.442**
23	PBT-2 x PBT-13	217.82	178.827**	99.890**	52.354**
24	PBT-2 x PBT-10	102.90	-12.526	-18.527	-28.027**
25	PBT-2 x PBT-4	107.57	9.698	-1.285	-24.760*
26	PBT-13 x PBT-10	194.33	123.921**	53.864**	35.924**
27	PBT-13 x PBT-4	149.89	123.017**	71.991**	4.840
28	PBT-10 x PBT-4	108.68	1.832	-13.951	-23.984*
Range	**Minimum**	**71.71**	**-43.047**	**-45.025**	**-49.843**
	Maximum	**240.37**	**178.827**	**99.890**	**68.126**

4.4.2 Heterosis for quality traits

4.4.2.1 Number of locules per fruit

The perusal of data presented in Table 4.25 revealed that range of heterosis for number of locules per fruit was -24.953 to 100.00 per cent for relative heterosis, -33.333 to 66.667 per cent for heterobeltiosis and -16.500 to 150.00 per cent for standard heterosis. Among 28 cross combinations, 10 hybrids exhibited significant heterosis over mid parent, 16 hybrids showed significant heterosis over better parent and 13 hybrids showed significant heterosis over standard check parent for number of locules per fruit.

Among all crosses, eight crosses exhibited desirable significant positive relative heterosis for same traits. Top five cross combinations which showed desirable significant positive relative heterosis were PBT-2 x PBT-10 (100.000%), PBT-9 x PBT-5 (53.811%), PPT-2 x PBT-10 (50.000%), PBT-9 x PBT-10 (50.000%) and PBT-2 x PBT-13 (44.333%). In case of heterobeltiosis among all crosses, seven cross combinations exhibited desirable significant positive heterosis over better parent and among them top five crosses were PBT-2 x PBT-10 (66.667%), PBT-9 x PBT-10 (50.000%), PPT-2 x PBT-10 (50.000%), PBT-2 x PBT-13 (44.333%) and PBT-9 x PBT-5 (42.918%). Out of all crosses, thirteen cross combinations showed significant positive standard heterosis for number of locules per fruit and top hybrids which exhibited significant positive standard heterosis were PBT-2 x PBT-10 (150.00%), PBT-2 x PBT-13 (116.500%), PBT-9 x PBT-5 (66.500%) and nine cross combinations showed 50.000% heterosis over check parent for same character. Similar findings for number of locules per fruit were also reported by Kurian *et al*. (2001), Joshi *et al*. (2005), Mali and Patel (2014), Sherpa *et al.* (2014), Savita and Singh (2015), Biswas *et al.* (2016), Amin *et al*. (2017) and Kumar *et al*. (2017c).

4.4.2.2 Pericarp thickness (cm)

Date presented in Table 4.26 revealed that range of heterosis for pericarp thickness was -35.260 to 80.769 per cent for relative heterosis, -38.554 to 52.703 per cent for heterobeltiosis and -26.087 to 75.362 per cent for standard heterosis. Among all crosses, 13 hybrids showed significant relative heterosis, 12 hybrids showed significant heterobeltiosis and 13 hybrids exhibited significant standard heterosis for pericarp thickness.

Table 4.25: Heterosis for number of locules per fruit

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	2.00	-7.621	-14.163	0.000
2	PCT-1 x PBT-9	3.00	38.568**	28.755*	50.000**
3	PCT-1 x PBT-5	2.00	-14.163	-14.163	0.000
4	PCT-1 x PBT-2	2.33	-12.570	-22.333*	16.500
5	PCT-1 x PBT-13	2.00	-24.953*	-33.333**	0.000
6	PCT-1 x PBT-10	3.00	38.568**	28.755*	50.000**
7	PCT-1 x PBT-4	2.00	-20.000	-25.094*	0.000
8	PPT-2 x PBT-9	1.67	-16.500	-16.500	-16.500
9	PPT-2 x PBT-5	2.00	-7.621	-14.163	0.000
10	PPT-2 x PBT-2	2.00	-20.000	-33.333**	0.000
11	PPT-2 x PBT-13	3.00	20.000	0.000	50.000**
12	PPT-2 x PBT-10	3.00	50.000**	50.000**	50.000**
13	PPT-2 x PBT-4	2.00	-14.347	-25.094*	0.000
14	PBT-9 x PBT-5	3.33	53.811**	42.918**	66.500**
15	PBT-9 x PBT-2	2.00	-20.000	-33.333**	0.000
16	PBT-9 x PBT-13	2.00	-20.000	-33.333**	0.000
17	PBT-9 x PBT-10	3.00	50.000**	50.000**	50.000**
18	PBT-9 x PBT-4	2.00	-14.347	-25.094*	0.000
19	PBT-5 x PBT-2	3.00	12.570	0.000	50.000**
20	PBT-5 x PBT-13	2.00	-24.953*	-33.333	0.000
21	PBT-5 x PBT-10	2.33	7.621	0.000	16.500
22	PBT-5 x PBT-4	2.00	-20.000	-25.094*	0.000
23	PBT-2 x PBT-13	4.33	44.333**	44.333**	116.500**
24	PBT-2 x PBT-10	5.00	100.000**	66.667**	150.000**
25	PBT-2 x PBT-4	3.00	5.820	0.000	50.000**
26	PBT-13 x PBT-10	3.00	20.000	0.000	50.000**
27	PBT-13 x PBT-4	2.67	-5.820	-11.000	33.500*
28	PBT-10 x PBT-4	3.00	28.480*	12.360	50.000**
Range	**Minimum**	**1.67**	**-24.953**	**-33.333**	**-16.500**
	Maximum	**5.00**	**100.00**	**66.667**	**150.00**

Table 4.26: Heterosis for pericarp thickness

S. N.	F_1 hybrid	*Per se* performance (cm)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	0.94	80.769**	36.232*	36.232*
2	PCT-1 x PBT-9	0.81	42.105**	2.532	17.391
3	PCT-1 x PBT-5	1.01	61.600**	12.222	46.377**
4	PCT-1 x PBT-2	0.57	-2.564	-30.488*	-17.391
5	PCT-1 x PBT-13	0.51	-13.559	-38.554**	-26.087
6	PCT-1 x PBT-10	0.73	14.961	-20.652*	5.797
7	PCT-1 x PBT-4	0.82	50.459**	10.811	18.841
8	PPT-2 x PBT-9	0.80	8.108	1.266	15.942
9	PPT-2 x PBT-5	0.95	19.497	5.556	37.681**
10	PPT-2 x PBT-2	0.89	17.881	8.537	28.986*
11	PPT-2 x PBT-13	0.73	-3.947	-12.048	5.797
12	PPT-2 x PBT-10	1.06	31.677**	15.217	53.623**
13	PPT-2 x PBT-4	1.13	58.042**	52.703**	63.768**
14	PBT-9 x PBT-5	0.93	10.059	3.333	34.783*
15	PBT-9 x PBT-2	1.21	50.311**	47.561**	75.362**
16	PBT-9 x PBT-13	0.77	-4.938	-7.229	11.594
17	PBT-9 x PBT-10	0.62	-27.485**	-32.609**	-10.145
18	PBT-9 x PBT-4	1.09	42.484**	37.975**	57.971**
19	PBT-5 x PBT-2	0.79	-8.140	-12.222	14.493
20	PBT-5 x PBT-13	0.56	-35.260**	-37.778**	-18.841
21	PBT-5 x PBT-10	0.93	2.198	1.087	34.783*
22	PBT-5 x PBT-4	0.90	9.756	0.000	30.435*
23	PBT-2 x PBT-13	0.79	-4.242	-4.819	14.493
24	PBT-2 x PBT-10	0.58	-33.333**	-36.957**	-15.942
25	PBT-2 x PBT-4	1.14	46.154**	39.024**	65.217**
26	PBT-13 x PBT-10	1.07	22.286*	16.304	55.072**
27	PBT-13 x PBT-4	0.79	0.637	-4.819	14.493
28	PBT-10 x PBT-4	0.67	-19.277	-27.174*	-2.899
Range	**Minimum**	**0.51**	**-35.260**	**-38.554**	**-26.087**
	Maximum	**1.21**	**80.769**	**52.703**	**75.362**

Out of twenty eight crosses, ten cross combinations showed significant positive relative heterosis and among them top five crosses were PCT-1 x PPT-2 (80.769%), PCT-1 x PBT-5 (61.600%), PPT-2 x PBT-4 (58.042%), PCT-1 x PBT-4 (50.459%) and PBT-9 x PBT-2 (50.311%). For heterobeltiosis five cross combinations *viz*., PPT-2 x PBT-4 (52.703%), PBT-9 x PBT-2 (47.561%), PBT-2 x PBT-4 (39.024%), PBT-9 x PBT-4 (37.975%) and PCT-1 x PPT-2 (36.232%) showed significant positive heterosis over better parent. Out of all cross combinations, thirteen crosses showed significant positive standard heterosis over check parent for pericarp thickness and top five crosses exhibited significant standard heterosis for same trait were PBT-9 x PBT-2 (75.362%), PBT-2 x PBT-4 (65.217%), PPT-2 x PBT-4 (63.768%), PBT-9 x PBT-4 (57.971%) and PBT-13 x PBT-10 (55.072%). Significant positive heterosis for pericarp thickness was also reported by Kurian *et al*. (2001), Joshi *et al*. (2005), Sherpa *et al.* (2014), Pandey and Mall (2015), Savita and Singh (2015), Biswas *et al*. (2016) and Kumar *et al*. (2017c).

4.4.2.3 Diameter of stalk scar (cm)

The read-through of data presented in the Table 4.27 revealed that heterosis over mid parent, better parent and over check parent for diameter of stalk scar ranged -30.097 to 163.063 per cent, -17.241 to 387.097 per cent and -8.861 to 174.684 per cent, respectively. For diameter of stalk scar, out of all cross combinations, 19 crosses showed significant relative heterosis, 21 hybrids showed significant heterobeltiosis and 18 hybrids exhibited significant standard heterosis.

Out of 28 crosses, only one cross combination *viz*., PBT-5 x PBT-13 (-30.097%) exhibited desirable significant negative heterosis over mid parent for same character. For heterobeltiosis also one hybrid *i.e*., PBT-5 x PBT-13 (-17.241%) exhibited significant negative heterosis for diameter of stalk scar. Out of all crosses, no cross combinations showed significant negative standard heterosis for diameter of stalk scar.

4.4.2.4 Fruit firmness (kg/cm^2)

Data presented in Table 4.28 revealed that the range of heterosis for fruit firmness was -19.287 to 31.299 per cent for relative heterosis, -30.651 to 27.733 per cent for heterobeltiosis and -16.590 to 33.871 per cent for standard heterosis. Among twenty eight crosses, 15 hybrids showed significant relative heterosis, 12 hybrids showed significant heterobeltiosis and 14 hybrids exhibited significant standard heterosis for fruit firmness.

Table 4.27: Heterosis for diameter of stalk scar

S. N.	F_1 hybrid	*Per se* performance (cm)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	1.17	112.727**	277.419**	48.101**
2	PCT-1 x PBT-9	1.46	163.063**	370.968**	84.810**
3	PCT-1 x PBT-5	1.51	155.932**	387.097**	91.139**
4	PCT-1 x PBT-2	0.73	19.672	135.484**	-7.595
5	PCT-1 x PBT-13	0.74	-1.333	138.710**	-6.329
6	PCT-1 x PBT-10	0.83	59.615**	167.742**	5.063
7	PCT-1 x PBT-4	1.19	95.082**	283.871**	50.633**
8	PPT-2 x PBT-9	0.87	9.434	10.127	10.127
9	PPT-2 x PBT-5	1.27	53.012**	60.759**	60.759**
10	PPT-2 x PBT-2	1.53	80.000**	93.671**	93.671**
11	PPT-2 x PBT-13	0.85	-14.141	7.595	7.595
12	PPT-2 x PBT-10	1.62	113.158**	121.918**	105.063**
13	PPT-2 x PBT-4	1.21	42.353**	53.165**	53.165**
14	PBT-9 x PBT-5	1.47	76.048**	83.750**	86.076**
15	PBT-9 x PBT-2	0.77	-9.942	-3.750	-2.532
16	PBT-9 x PBT-13	0.98	-1.508	22.500	24.051
17	PBT-9 x PBT-10	1.01	32.026*	38.356*	27.848*
18	PBT-9 x PBT-4	1.23	43.860**	53.750**	55.696**
19	PBT-5 x PBT-2	1.41	58.427**	62.069**	78.481**
20	PBT-5 x PBT-13	0.72	-30.097**	-17.241**	-8.861
21	PBT-5 x PBT-10	1.58	97.500**	116.438**	100.000**
22	PBT-5 x PBT-4	1.57	76.404**	80.460**	98.734**
23	PBT-2 x PBT-13	1.10	4.762	20.879	39.241**
24	PBT-2 x PBT-10	1.14	39.024**	56.164**	44.304**
25	PBT-2 x PBT-4	0.89	-2.198	-2.198	12.658
26	PBT-13 x PBT-10	2.17	126.042**	197.260**	174.684**
27	PBT-13 x PBT-4	1.48	40.952**	62.637**	87.342**
28	PBT-10 x PBT-4	0.90	9.756	23.288	13.924
Range	**Minimum**	**0.72**	**-30.097**	**-17.241**	**-8.861**
	Maximum	**2.17**	**163.063**	**387.097**	**174.684**

Table 4.28: Heterosis for fruit firmness

S. N.	F_1 hybrid	*Per se* performance (kg/cm^2)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	4.19	4.489	-3.456	-3.456
2	PCT-1 x PBT-9	4.40	20.383**	19.565**	1.382
3	PCT-1 x PBT-5	4.63	4.045	-11.303**	6.682
4	PCT-1 x PBT-2	3.83	3.096	2.133	-11.751*
5	PCT-1 x PBT-13	3.78	-13.303**	-25.000**	-12.903**
6	PCT-1 x PBT-10	4.20	7.969	2.439	-3.226
7	PCT-1 x PBT-4	4.51	-0.221	-15.858**	3.917
8	PPT-2 x PBT-9	4.35	9.159*	0.230	0.230
9	PPT-2 x PBT-5	4.00	-16.318**	-23.372**	-7.834
10	PPT-2 x PBT-2	4.48	10.754*	3.226	3.226
11	PPT-2 x PBT-13	5.38	14.712**	6.746	23.963**
12	PPT-2 x PBT-10	3.99	-5.450	-8.065	-8.065
13	PPT-2 x PBT-4	4.86	0.206	-9.328*	11.982*
14	PBT-9 x PBT-5	5.81	31.299**	11.303**	33.871**
15	PBT-9 x PBT-2	4.79	29.810**	27.733**	10.369*
16	PBT-9 x PBT-13	5.38	24.106**	6.746	23.963**
17	PBT-9 x PBT-10	3.98	2.975	-2.927	-8.295
18	PBT-9 x PBT-4	5.23	16.352**	-2.425	20.507**
19	PBT-5 x PBT-2	3.62	-19.287**	-30.651**	-16.590**
20	PBT-5 x PBT-13	4.99	-2.729	-4.406	14.977**
21	PBT-5 x PBT-10	4.01	-13.948**	-23.180**	-7.604
22	PBT-5 x PBT-4	4.80	-9.263**	-10.448**	10.599*
23	PBT-2 x PBT-13	5.42	23.322**	7.540	24.885**
24	PBT-2 x PBT-10	4.02	2.420	-1.951	-7.373
25	PBT-2 x PBT-4	4.98	9.330*	-7.090	14.747**
26	PBT-13 x PBT-10	4.73	3.501	-6.151	8.986
27	PBT-13 x PBT-4	5.27	1.346	-1.679	21.429**
28	PBT-10 x PBT-4	4.65	-1.691	-13.246**	7.143
Range	**Minimum**	**3.62**	**-19.287**	**-30.651**	**-16.590**
	Maximum	**5.81**	**31.299**	**27.733**	**33.871**

For fruit firmness, out of twenty eight cross combinations, ten hybrids exhibited significant positive heterosis over mid parent. Top five cross combinations which showed significant positive relative heterosis were PBT-9 x PBT-5 (31.299%), PBT-9 x PBT-2 (29.810%), PBT-9 x PBT-13 (24.106%), PBT-2 x PBT-13 (23.322%) and PCT-1 x PBT-9 (20.383%). Among all crosses three hybrids namely PBT-9 x PBT-2 (27.733%), PCT-1 x PBT-9 (19.565%) and PBT-9 x PBT-5 (11.303) exhibited significant positive heterosis over better parent. In case of heterosis over check parent, eleven cross combinations showed desirable significant positive standard heterosis and the top five hybrids showed significant positive standard heterosis were PBT-9 x PBT-5 (33.871%), PBT-2 x PBT-13 (24.885%), PBT-9 x PBT-13 (23.963%), PPT-2 x PBT-13 (23.963%) and PBT-13 x PBT-4 (21.429%). Significant positive heterosis for fruit firmness was also reported by Joshi *et al*. (2005), Shalaby (2012) and Narasimhamurthy *et al*. (2013).

4.4.2.5 TSS (%)

Data presented in Table 4.29 revealed that the range of heterosis for TSS was -25.149 to 9.246 per cent for relative heterosis, -37.670 to 4.259 per cent for heterobeltiosis and -37.303 to 6.600 per cent for standard heterosis. Among 28 crosses, 7 hybrids showed significant relative heterosis, 12 hybrids showed significant heterobeltiosis and 17 hybrids exhibited significant standard heterosis for TSS.

For TSS, out of twenty eight cross combinations, two hybrids *i.e.,* PBT-9 x PBT-2 (13.777%), PCT-1 x PBT-9 (9.246%) exhibited significant positive heterosis over mid parent. Out of all crosses, none of them showed significant positive heterobeltiosis and standard heterosis for TSS. Significant positive heterosis for TSS has been reported by many researchers, some of them are Hannan *et al*. (2007), Agarwal *et al*. (2014), Narasimhamurthy *et al*. (2013), Pandey and Mall (2015), Samiyoddin *et al.* (2015), Savita and Singh (2015), Vilas and Rana (2015), Biswas *et al*. (2016), Amin *et al*. (2017) and Panchal *et al*. (2017).

4.4.2.6 pH of fruit juice

The read-through of data presented in the Table 4.30 revealed that heterosis over mid parent, better parent and over check parent for pH of fruit juice ranged

-12.281 to 1.822 per cent, -11.088 to 4.506 per cent and -8.405 to 5.172 per cent, respectively. For pH of fruit juice, out of all cross combinations, 13 crosses showed significant relative heterosis, 9 hybrids showed significant heterobeltiosis and 6 hybrids exhibited significant standard heterosis.

For relative heterosis, thirteen cross combinations exhibited significant desirable negative relative heterosis. Among them top five crosses were PBT-2 x PBT-13 (-12.281%), PCT-1 x PBT-2 (-11.111%), PBT-2 x PBT-4 (-9.603%), PBT-2 x PBT-10 (-9.091%) and PCT-1 x PPT-2 (-8.974%). However, out of all crosses, nine crosses showed significant negative heterobeltiosis and among them top five crosses were PBT-2 x PBT-13 (-11.088%), PCT-1 x PBT-2 (-9.332%), PCT-1 x PPT-2 (-8.190%), PBT-2 x PBT-10 (-7.757%) and PCT-1 x PBT-9 (-7.296%). Looking to standard heterosis, among the crosses, six cross combinations exhibited significant negative standard heterosis in desirable direction for this particular trait. Top five crosses which showed maximum negative heterosis over check parents for pH of fruit juice were PBT-2 x PBT-13 (-8.405%), PCT-1 x PPT-2 (-8.190%), PCT-1 x PBT-2 (-7.759%), PCT-1 x PBT-9 (-6.897%) and PBT-2 x PBT-4 (-6.681%).

4.4.2.7 Titratable acidity (%)

The read-through of data presented in the Table 4.31 revealed that heterosis over mid parent, better parent and over check parent for titratable acidity ranged -26.582 to 70.270 per cent, -34.091 to 50.000 per cent and -14.286 to 125.000 per cent, respectively. For titratable acidity, out of all cross combinations, 13 crosses showed significant relative heterosis, 12 hybrids showed significant heterobeltiosis and 15 hybrids exhibited significant standard heterosis.

Out of 28 crosses, 11 cross combinations exhibited significant positive heterosis over mid parent for same character and among them top five crosses were PCT-1 x PPT-2 (70.270%), PPT-2 x PBT-2 (58.491%), PBT-5 x PBT-2 (53.191%), PCT-1 x PBT-5 (44.118%) and PBT-2 x PBT-4 (40.000%). For heterobeltiosis five cross combinations showed significant positive heterosis for titratable acidity namely PPT-2 x PBT-2 (50.000%), PBT-5 x PBT-2 (44.000%), PCT-1 x PPT-2 (36.957%), PBT-2 x PBT-4 (20.000%) and PPT-2 x PBT-10 (18.919%). Out of all crosses, 15 cross combinations showed significant positive standard heterosis for titratable acidity and

top five hybrids which exhibited significant positive standard heterosis for the same trait were PCT-1 x PPT-2 (125.000%), PCT-1 x PBT-5 (75.000%), PCT-1 x PBT-10 (67.857%), PCT-1 x PBT-13 (60.714%) and PPT-2 x PBT-10 (57.143%). Desirable significant positive heterosis for titratable acidity was also reported by Cheema *et al*. (2014), Reddy *et al*. (2014), Mali and Patel (2014), Figueiredo *et al*. (2015), Pandey and Mall (2015) and Panchal *et al*. (2017).

4.4.2.8 Ascorbic acid (mg/100g)

The perusal of data presented in Table 4.32 revealed that range of heterosis for ascorbic acid was -15.055 to 18.673 per cent for relative heterosis, -28.821 to 15.705 per cent for heterobeltiosis and -12.233 to 11.300 per cent for standard heterosis. Among 28 cross combinations, nine hybrids exhibited significant heterosis over mid parent, nine hybrids showed significant heterosis over better parent and no hybrids showed significant heterosis over standard check parent for ascorbic acid.

Among all crosses, six crosses exhibited desirable significant positive relative heterosis for same traits. Top five cross combinations which showed desirable significant positive relative heterosis were PBT-2 x PBT-13 (18.673%), PPT-2 x PBT-4 (16.932%), PBT-9 x PBT-5 (16.708%), PBT-9 x PBT-10 (15.338%) and PBT-9 x PBT-13 (15.014%). In case of heterobeltiosis among all crosses, two cross combinations *viz*., PBT-9 x PBT-5 (15.705%) and PBT-2 x PBT-13 (15.356%) exhibited desirable significant positive heterosis over better parent. Out of all crosses no cross combination showed significant positive standard heterosis for ascorbic acid. Significant positive heterosis for ascorbic acid was also reported by Reddy *et al*. (2014), Mali and Patel (2014), Pandey and Mall (2015), Amin *et al*. (2017) and Panchal *et al*. (2017).

4.4.2.9 Lycopene (mg/100g)

The read-through of data presented in the Table 4.33 revealed that heterosis over mid parent, better parent and over check parent for lycopene ranged -21.036 to 33.747 per cent, -31.583 to 23.077 per cent and -47.260 to 14.460 per cent, respectively. For lycopene, out of all cross combinations, 14 crosses showed significant relative heterosis, 11 hybrids showed significant heterobeltiosis and 20 hybrids exhibited significant standard heterosis.

Table 4.29: Heterosis for TSS

S. N.	F_1 hybrid	*Per se* performance (%)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	7.43	-1.197	-7.931	6.600
2	PCT-1 x PBT-9	7.03	9.246*	-12.887**	0.861
3	PCT-1 x PBT-5	7.20	6.904	-10.781**	3.300
4	PCT-1 x PBT-2	7.20	3.300	-10.781**	3.300
5	PCT-1 x PBT-13	6.77	-8.328*	-16.109**	-2.869
6	PCT-1 x PBT-10	7.33	0.618	-9.170*	5.165
7	PCT-1 x PBT-4	5.03	-25.149**	-37.670**	-27.834**
8	PPT-2 x PBT-9	6.43	9.261	-7.747	-7.747
9	PPT-2 x PBT-5	5.77	-6.710	-17.217**	-17.217**
10	PPT-2 x PBT-2	6.80	5.919	-2.439	-2.439
11	PPT-2 x PBT-13	7.13	4.316	2.296	2.296
12	PPT-2 x PBT-10	6.53	-3.044	-6.313	-6.313
13	PPT-2 x PBT-4	6.20	0.486	-11.047*	-11.047*
14	PBT-9 x PBT-5	5.63	10.392	4.259	-19.225**
15	PBT-9 x PBT-2	6.07	13.777*	3.407	-12.912**
16	PBT-9 x PBT-13	6.20	7.826	-7.463	-11.047*
17	PBT-9 x PBT-10	6.20	9.735	-4.615	-11.047*
18	PBT-9 x PBT-4	5.30	4.228	-1.304	-23.960**
19	PBT-5 x PBT-2	5.87	4.170	0.000	-15.782**
20	PBT-5 x PBT-13	6.27	3.636	-6.418	-10.043*
21	PBT-5 x PBT-10	6.03	1.345	-7.231	-13.486**
22	PBT-5 x PBT-4	4.37	-18.849**	-19.074**	-37.303**
23	PBT-2 x PBT-13	6.60	5.012	-1.493	-5.308
24	PBT-2 x PBT-10	6.07	-1.859	-6.615	-12.912**
25	PBT-2 x PBT-4	5.73	1.957	-2.385	-17.791**
26	PBT-13 x PBT-10	5.03	-23.788**	-24.925**	-27.834**
27	PBT-13 x PBT-4	5.90	-2.237	-11.940*	-15.352**
28	PBT-10 x PBT-4	5.27	-11.205*	-18.923**	-24.390**
Range	**Minimum**	**4.37**	**-25.149**	**-37.670**	**-37.303**
	Maximum	**7.43**	**9.246**	**4.259**	**6.600**

Table 4.30: Heterosis for pH of fruit juice

S. N.	F_1 hybrid	*Per se* performance	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	4.26	-8.974**	-8.190**	-8.190**
2	PCT-1 x PBT-9	4.32	-7.889**	-7.296*	-6.897*
3	PCT-1 x PBT-5	4.46	-6.105*	-5.508	-3.879
4	PCT-1 x PBT-2	4.28	-11.111**	-9.322**	-7.759**
5	PCT-1 x PBT-13	4.38	-7.789**	-7.203*	-5.603
6	PCT-1 x PBT-10	4.46	-6.006*	-5.508	-3.879
7	PCT-1 x PBT-4	4.35	-7.348**	-6.852*	-6.250*
8	PPT-2 x PBT-9	4.46	-4.086	-3.879	-3.879
9	PPT-2 x PBT-5	4.54	-3.609	-2.155	-2.155
10	PPT-2 x PBT-2	4.67	-2.199	0.647	0.647
11	PPT-2 x PBT-13	4.44	-5.732*	-4.310	-4.310
12	PPT-2 x PBT-10	4.54	-3.507	-2.155	-2.155
13	PPT-2 x PBT-4	4.64	-0.322	0.000	0.000
14	PBT-9 x PBT-5	4.57	-3.178	-1.931	-1.509
15	PBT-9 x PBT-2	4.87	1.776	4.506	4.957
16	PBT-9 x PBT-13	4.77	1.059	2.361	2.802
17	PBT-9 x PBT-10	4.68	-0.742	0.429	0.862
18	PBT-9 x PBT-4	4.75	1.822	1.931	2.371
19	PBT-5 x PBT-2	4.52	-6.708**	-5.439	-2.586
20	PBT-5 x PBT-13	4.47	-6.485**	-6.485*	-3.664
21	PBT-5 x PBT-10	4.56	-4.503	-4.403	-1.724
22	PBT-5 x PBT-4	4.88	3.280	4.497	5.172
23	PBT-2 x PBT-13	4.25	-12.281**	-11.088**	-8.405**
24	PBT-2 x PBT-10	4.40	-9.091**	-7.757**	-5.172
25	PBT-2 x PBT-4	4.33	-9.603**	-7.281*	-6.681*
26	PBT-13 x PBT-10	4.66	-2.408	-2.306	0.431
27	PBT-13 x PBT-4	4.76	0.741	1.927	2.586
28	PBT-10 x PBT-4	4.53	-4.025	-2.998	-2.371
Range	**Minimum**	**4.25**	**-12.281**	**-11.088**	**-8.405**
	Maximum	**4.88**	**1.822**	**4.506**	**5.172**

Table 4.31: Heterosis for titratable acidity

S. N.	F_1 hybrid	*Per se* performance (%)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	0.63	70.270**	36.957**	125.000**
2	PCT-1 x PBT-9	0.42	15.068*	-8.696	50.000**
3	PCT-1 x PBT-5	0.49	44.118**	6.522	75.000**
4	PCT-1 x PBT-2	0.34	-4.225	-26.087**	21.429
5	PCT-1 x PBT-13	0.45	0.000	-2.174	60.714**
6	PCT-1 x PBT-10	0.47	13.253*	2.174	67.857**
7	PCT-1 x PBT-4	0.38	-6.173	-17.391*	35.714**
8	PPT-2 x PBT-9	0.30	9.091	7.143	7.143
9	PPT-2 x PBT-5	0.34	36.000**	21.429	21.429
10	PPT-2 x PBT-2	0.42	58.491**	50.000**	50.000**
11	PPT-2 x PBT-13	0.38	5.556	-13.636	35.714**
12	PPT-2 x PBT-10	0.44	35.385**	18.919*	57.143**
13	PPT-2 x PBT-4	0.36	14.286	2.857	28.571*
14	PBT-9 x PBT-5	0.27	10.204	0.000	-3.571
15	PBT-9 x PBT-2	0.27	3.846	0.000	-3.571
16	PBT-9 x PBT-13	0.32	-9.859	-27.273**	14.286
17	PBT-9 x PBT-10	0.34	6.250	-8.108	21.429
18	PBT-9 x PBT-4	0.35	12.903	0.000	25.000*
19	PBT-5 x PBT-2	0.36	53.191**	44.000**	28.571*
20	PBT-5 x PBT-13	0.43	30.303**	-2.273	53.571**
21	PBT-5 x PBT-10	0.29	-1.695	-21.622*	3.571
22	PBT-5 x PBT-4	0.24	-15.789	-31.429**	-14.286
23	PBT-2 x PBT-13	0.43	24.638**	-2.273	53.571**
24	PBT-2 x PBT-10	0.31	0.000	-16.216	10.714
25	PBT-2 x PBT-4	0.42	40.000**	20.000*	50.000**
26	PBT-13 x PBT-10	0.31	-23.457**	-29.545**	10.714
27	PBT-13 x PBT-4	0.29	-26.582**	-34.091**	3.571
28	PBT-10 x PBT-4	0.33	-8.333	-10.811	17.857
Range	**Minimum**	**0.24**	**-26.582**	**-34.091**	**-14.286**
	Maximum	**0.63**	**70.270**	**50.000**	**125.000**

Table 4.32: Heterosis for ascorbic acid

S. N.	F_1 hybrid	*Per se* performance (mg/100g)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	33.06	-5.691	-17.577**	10.200
2	PCT-1 x PBT-9	28.67	-12.897*	-28.522**	-4.433
3	PCT-1 x PBT-5	31.44	-5.130	-21.616**	4.800
4	PCT-1 x PBT-2	28.72	-12.225*	-28.397**	-4.267
5	PCT-1 x PBT-13	31.61	-5.557	-21.192**	5.367
6	PCT-1 x PBT-10	32.28	-5.669	-19.521**	7.600
7	PCT-1 x PBT-4	28.55	-15.055**	-28.821**	-4.833
8	PPT-2 x PBT-9	30.78	10.481	2.600	2.600
9	PPT-2 x PBT-5	31.28	11.376	4.267	4.267
10	PPT-2 x PBT-2	28.33	2.404	-5.567	-5.567
11	PPT-2 x PBT-13	28.22	-0.686	-5.933	-5.933
12	PPT-2 x PBT-10	30.77	5.503	2.567	2.567
13	PPT-2 x PBT-4	33.39	16.932**	11.300	11.300
14	PBT-9 x PBT-5	30.28	16.708*	15.705*	0.933
15	PBT-9 x PBT-2	27.61	8.168	7.348	-7.967
16	PBT-9 x PBT-13	30.22	15.014*	12.635	0.733
17	PBT-9 x PBT-10	31.17	15.338*	10.025	3.900
18	PBT-9 x PBT-4	28.50	7.893	5.127	-5.000
19	PBT-5 x PBT-2	26.83	4.194	2.522	-10.567
20	PBT-5 x PBT-13	28.39	7.132	5.814	-5.367
21	PBT-5 x PBT-10	30.72	12.734*	8.436	2.400
22	PBT-5 x PBT-4	27.39	2.815	1.033	-8.700
23	PBT-2 x PBT-13	30.95	18.673**	15.356*	3.167
24	PBT-2 x PBT-10	26.45	-1.416	-6.636	-11.833
25	PBT-2 x PBT-4	28.11	7.208	3.689	-6.300
26	PBT-13 x PBT-10	26.50	-3.916	-6.460	-11.667
27	PBT-13 x PBT-4	26.33	-2.373	-2.877	-12.233
28	PBT-10 x PBT-4	27.55	-0.613	-2.753	-8.167
Range	**Minimum**	**26.33**	**-15.055**	**-28.821**	**-12.233**
	Maximum	**33.39**	**18.673**	**15.705**	**11.300**

Table 4.33: Heterosis for lycopene

S. N.	F_1 hybrid	*Per se* performance (mg/100g)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	11.19	6.826	-14.840*	-14.840*
2	PCT-1 x PBT-9	9.00	3.211	-6.542	-31.507**
3	PCT-1 x PBT-5	11.20	23.620**	8.632	-14.764*
4	PCT-1 x PBT-2	9.26	7.300	-2.011	-29.528**
5	PCT-1 x PBT-13	10.56	15.158*	0.285	-19.635**
6	PCT-1 x PBT-10	11.57	11.572	-10.518	-11.948
7	PCT-1 x PBT-4	9.46	26.133**	21.127*	-28.006**
8	PPT-2 x PBT-9	8.99	-21.036**	-31.583**	-31.583**
9	PPT-2 x PBT-5	11.82	0.810	-10.046	-10.046
10	PPT-2 x PBT-2	10.26	-9.163	-21.918**	-21.918**
11	PPT-2 x PBT-13	13.15	11.111	0.076	0.076
12	PPT-2 x PBT-10	15.04	15.382**	14.460*	14.460*
13	PPT-2 x PBT-4	13.35	31.333**	1.598	1.598
14	PBT-9 x PBT-5	11.32	13.541	9.796	-13.851*
15	PBT-9 x PBT-2	8.08	-15.304*	-16.096	-38.508**
16	PBT-9 x PBT-13	8.58	-14.881*	-18.519*	-34.703**
17	PBT-9 x PBT-10	11.62	3.014	-10.131	-11.568
18	PBT-9 x PBT-4	10.82	28.656**	12.357	-17.656**
19	PBT-5 x PBT-2	9.41	-4.757	-8.729	-28.387**
20	PBT-5 x PBT-13	12.96	24.376**	23.077**	-1.370
21	PBT-5 x PBT-10	12.68	9.122	-1.933	-3.501
22	PBT-5 x PBT-4	9.23	5.486	-10.475	-29.756**
23	PBT-2 x PBT-13	10.35	3.604	-1.709	-21.233**
24	PBT-2 x PBT-10	9.03	-19.303**	-30.162**	-31.279**
25	PBT-2 x PBT-4	6.93	-16.707*	-26.667**	-47.260**
26	PBT-13 x PBT-10	9.69	-17.391**	-25.058**	-26.256**
27	PBT-13 x PBT-4	11.85	33.747**	12.536	-9.817
28	PBT-10 x PBT-4	9.09	-9.642	-29.698**	-30.822**
Range	**Minimum**	**6.93**	**-21.036**	**-31.583**	**-47.260**
	Maximum	**15.04**	**33.747**	**23.077**	**14.460**

Out of 28 crosses, eight cross combinations exhibited significant positive heterosis over mid parent for same character and among them top five crosses were PBT-13 x PBT-4 (33.747%), PPT-2 x PBT-4 (31.333%), PBT-9 x PBT-4 (28.565%), PCT-1 x PBT-4 (26.133%) and PBT-5 x PBT-13 (24.376%). For heterobeltiosis, three cross combinations showed positive significant heterosis for lycopene namely PBT-5 x PBT-13 (23.077%), PCT-1 x PBT-4 (21.127%) and PPT-2 x PBT-10 (14.460%). Out of all crosses, only one cross combination *i.e*., PPT-2 x PBT-10 (14.460%) showed significant positive standard heterosis for lycopene. Similar findings for lycopene content were reported by Sherpa *et al*. (2014), Cheema *et al*. (2014), Reddy *et al*. (2014), Narasimhamurthy *et al*. (2013), Figueiredo *et al*. (2015), Samiyoddin *et al.* (2015) and Panchal *et al*. (2017).

4.4.2.10 Total carotenoids (mg/100g)

Data presented in Table 4.34 revealed that the range of heterosis for total carotenoids was -19.713 to 37.377 per cent for relative heterosis, -32.279 to 24.238 per cent for heterobeltiosis and -49.442 to 15.163 per cent for standard heterosis. Among twenty eight crosses, 15 hybrids showed significant relative heterosis, 15 hybrids showed significant heterobeltiosis and 22 hybrids exhibited significant standard heterosis for total carotenoids.

For total carotenoids, out of twenty eight cross combinations, eleven hybrids exhibited significant positive heterosis over mid parent. Top five cross combinations which showed significant positive relative heterosis were PBT-13 x PBT-4 (37.377%), PBT-9 x PBT-4 (35.424%), PPT-2 x PBT-4 (33.195%), PCT-1 x PBT-5 (29.273%) and PBT-5 x PBT-13 (23.957%). Among all crosses, six hybrids exhibited significant positive heterosis over better parent and top five cross combination for the same trait were PBT-9 x PBT-4 (24.238%), PCT-1 x PBT-5 (22.413%), PBT-9 x PBT-5 (19.710%), PBT-13 x PBT-4 (17.986%) and PBT-5 x PBT-13 (16.705%). In case of heterosis over check parent only one cross combination *i.e*., PPT-2 x PBT-10 (15.163%) showed desirable significant positive standard heterosis for total carotenoids.

Table 4.34: Heterosis for total carotenoids

S. N.	F_1 hybrid	*Per se* performance (mg/100g)	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	PCT-1 x PPT-2	18.46	5.305	-14.140**	-14.140**
2	PCT-1 x PBT-9	14.19	0.176	-3.927	-34.000**
3	PCT-1 x PBT-5	18.57	29.273**	22.413**	-13.628**
4	PCT-1 x PBT-2	14.49	3.463	0.277	-32.605**
5	PCT-1 x PBT-13	15.57	1.301	-9.371	-27.581**
6	PCT-1 x PBT-10	18.93	11.913*	-6.611	-11.953*
7	PCT-1 x PBT-4	14.49	11.935	6.858	-32.605**
8	PPT-2 x PBT-9	14.56	-19.713**	-32.279**	-32.279**
9	PPT-2 x PBT-5	18.72	2.100	-12.930*	-12.930*
10	PPT-2 x PBT-2	17.24	-4.089	-19.814**	-19.814**
11	PPT-2 x PBT-13	22.43	15.977**	4.326	4.326
12	PPT-2 x PBT-10	24.76	18.554**	15.163**	15.163**
13	PPT-2 x PBT-4	22.53	33.195**	4.791	4.791
14	PBT-9 x PBT-5	18.16	21.309**	19.710**	-15.535**
15	PBT-9 x PBT-2	13.74	-5.955	-6.974	-36.093**
16	PBT-9 x PBT-13	15.45	-3.286	-10.070	-28.140**
17	PBT-9 x PBT-10	19.90	13.584*	-1.825	-7.442
18	PBT-9 x PBT-4	18.35	35.424**	24.238**	-14.651**
19	PBT-5 x PBT-2	14.80	-0.068	-2.439	-31.163**
20	PBT-5 x PBT-13	20.05	23.957**	16.705**	-6.744
21	PBT-5 x PBT-10	21.74	22.686**	7.252	1.116
22	PBT-5 x PBT-4	14.60	6.182	-3.757	-32.093**
23	PBT-2 x PBT-13	14.67	-7.240	-14.610*	-31.767**
24	PBT-2 x PBT-10	14.43	-16.878**	-28.811**	-32.884**
25	PBT-2 x PBT-4	10.87	-18.820**	-24.775**	-49.442**
26	PBT-13 x PBT-10	15.79	-15.674**	-22.102**	-26.558**
27	PBT-13 x PBT-4	20.27	37.377**	17.986**	-5.721
28	PBT-10 x PBT-4	17.64	8.221	-12.975*	-17.953**
Range	**Minimum**	**10.87**	**-19.713**	**-32.279**	**-49.442**
	Maximum	**24.76**	**37.377**	**24.238**	**15.163**

For yield related and quality traits most promising heterotic crosses with respect to each character in desired direction are presented in Table 4.35 and 4.36, respectively based on the significance test of relative heterosis, heterobeltiosis and standard heterosis as well as the *per se* performance of the cross combinations, the most promising heterotic hybrids are identified and depicted in tabular form with respect to each character.

For days to 50 per cent flowering, cross PBT-13 x PBT-10 showed desirable significant negative heterosis over mid parent, better parent and standard parent while, PBT-5 x PBT-4 showed desirable significant negative heterosis over mid parent and better parent. In case of days to first fruit ripening PCT-1 x PBT-4 exhibited desirable significant negative heterosis over mid parent and check parent. PBT-9 x PBT-5 showed desirable significant negative heterosis over mid parent, better parent and standard parent for days to first fruit ripening whereas, PBT-9 x PBT-2 exhibited desirable significant negative heterobeltiosis and standard heterosis. For number of flowers per cluster cross PBT-5 x PBT-4 exhibited desirable significant positive heterosis over all three cases while, PBT-9 x PBT-4 and PBT-13 x PBT-4 showed significant positive relative heterosis and heterobeltiosis. For number of fruits per cluster cross PBT-2 x PBT-13 showed desirable significant positive heterosis over mid parent and better parent. For number of fruits per plant PBT-5 x PBT-4 exhibited desirable significant positive heterosis over all three cases while, PBT-9 x PBT-4 showed significant positive relative heterosis and heterobeltiosis.

For internodal length PBT-9 x PBT-4 revealed desirable significant negative heterosis over mid parent, better parent and standard parent while, PBT-9 x PBT-2 showed significant negative heterosis over mid parent and better parent. PBT-13 x PBT-10 exhibited desirable significant positive heterosis over mid parent, better parent and standard parent whereas, PPT-2 x PBT-13 showed significant positive heterosis for relative heterosis and heterobeltiosis for average fruit weight. PBT-13 x PBT-10 showed desirable significant heterosis over mid parent, better parent and standard parent for fruit length and cross PPT-2 x PBT-9 exhibited significant positive heterosis over better parent and standard parent. For fruit width PBT-13 x PBT-4 showed desirable significant relative heterosis and heterobeltiosis while, PBT-13 x PBT-10

exhibited significant relative and standard heterosis. PBT-9 x PBT-5 revealed significant heterosis over better parent and check parent for fruit width. PBT-2 x PBT-4 showed desirable significant heterosis over mid parent and check parent for fruit shape index. For 100 seed weight PCT-1 x PPT-2 showed desirable significant heterosis over mid parent, better parent and standard parent while, PCT-1 x PBT-13 showed desirable heterosis over mid parent and standard parent. For fruit yield per plant and fruit yield per hectare cross PBT-2 x PBT-13 showed desirable significant positive heterosis in all three cases while, PCT-1 x PBT-5 showed positive significant heterosis for heterobeltiosis and standard heterosis.

Among quality traits, for number of locules per fruit PBT-2 x PBT-10 showed desirable significant heterosis in all three cases while, PBT-9 x PBT-5 exhibited significant relative and standard heterosis. For pericarp thickness PPT-2 x PBT-4 exhibited desirable significant positive heterosis in all three cases whereas, crosses PBT-9 x PBT-2 and PBT-2 x PBT-4 showed significant heterobeltiosis and standard heterosis. PBT-5 x PBT-13 showed desirable significant negative heterosis over mid and better parent for diameter of stalk scar. For fruit firmness desirable significant positive heterosis over all three cases was observed in PBT-9 x PBT-5 while, PBT-9 x PBT-2 showed significant positive relative heterosis and heterobeltiosis and PBT-9 x PBT-13 exhibited desirable significant heterosis over mid parent and standard parent. For pH of fruit juice desirable significant negative heterosis was reported in PBT-2 x PBT-13 for all three cases while, PCT-1 x PBT-2 showed desirable significant heterosis in all three cases and PCT-1 x PPT-2 showed desirable significant heterobeltiosis and standard heterosis. For titratable acidity PCT-1 x PPT-2 exhibited desirable significant positive heterosis over all three cases whereas, PPT-2 x PBT-2 and PBT-5 x PBT-2 showed desirable significant heterosis over relative heterosis and heterobeltiosis. Crosses PBT-2 x PBT-13 and PBT-9 x PBT-5 showed desirable significant positive heterosis over mid and better parent for ascorbic acid. For lycopene content PPT-2 x PBT-10 showed desirable significant heterosis over better parent and check parent. For total carotenoids PBT-9 x PBT-4 showed desirable significant positive relative heterosis and heterobeltiosis.

Table 4.35: Summary table showing top three promising heterotic crosses with respect to each yield related traits in desired direction

S.N.	Characters	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	**Days to 50% flowering**	PBT-13 x PBT-10 PBT-5 x PBT-13 PBT-5 x PBT-4	PBT-9 x PBT-5 PBT-5 x PBT-4 PBT-13 x PBT-10	PCT-1 x PBT-4 PBT-9 x PBT-2 PBT-13 x PBT-10
2	**Days to first fruit set**	PBT-13 x PBT-10 PBT-5 x PBT-13 PCT-1 x PBT-4	–	PCT-1 x PBT-4 PCT-1 x PBT-5 PBT-9 x PBT-2
3	**Days to first fruit ripening**	PBT-2 x PBT-13 PBT-9 x PBT-5 PBT-5 x PBT-13	PBT-9 x PBT-5 PBT-9 x PBT-2	PCT-1 x PBT-5 PBT-9 x PBT-5 PBT-9 x PBT-2
4	**No. of flowers/cluster**	PBT-5 x PBT-4 PBT-9 x PBT-4 PBT-13 x PBT-4	PBT-5 x PBT-4 PBT-9 x PBT-4 PBT-13 x PBT-4	PCT-1 x PBT-5 PBT-5 x PBT-4 PCT-1 x PBT-13
5	**No. of fruits/cluster**	PBT-2 x PBT-13 PBT-5 x PBT-4 PCT-1 x PBT-5	PBT-2 x PBT-13 PBT-9 x PBT-4 PBT-13 x PBT-4	PCT-1 x PBT-5 PCT-1 x PPT-2 PBT-5 x PBT-4
6	**No. of fruits/plant**	PBT-5 x PBT-4 PBT-9 x PBT-4 PBT-2 x PBT-13	PBT-5 x PBT-4 PBT-9 x PBT-4 PBT-2 x PBT-4	PCT-1 x PBT-5 PBT-5 x PBT-4 PCT-1 x PPT-2
7	**Internodal length**	PBT-9 x PBT-4 PBT-9 x PBT-2 PBT-9 x PBT-13	PBT-9 x PBT-4 PBT-9 x PBT-2	PBT-9 x PBT-4 PBT-9 x PBT-5
8	**Avg. fruit wt.**	PBT-13 x PBT-10 PCT-1 x PPT-2 PPT-2 x PBT-13	PBT-13 x PBT-10 PPT-2 x PBT-13 PPT-2 x PBT-4	PBT-13 x PBT-10 PBT-9 x PBT-5 PPT-2 x PBT-9
9	**Fruit length**	PBT-13 x PBT-10 PCT-1 x PBT-4 PBT-9 x PBT-5	PBT-13 x PBT-10 PPT-2 x PBT-9	PPT-2 x PBT-9 PBT-13 x PBT-10
10	**Fruit width**	PCT-1 x PBT-4 PBT-13 x PBT-4 PBT-13 x PBT-10	PBT-13 x PBT-4 PBT-9 x PBT-5	PBT-13 x PBT-10 PBT-9 x PBT-5
11	**Fruit shape index**	PBT-2 x PBT-4 PBT-5 x PBT-10	–	PBT-2 x PBT-4 PPT-2 x PBT-4
12	**Plant height**	PBT-13 x PBT-4 PCT-1 x PBT-4 PBT-9 x PBT-4	PBT-13 x PBT-10 PBT-5 x PBT-10	–
13	**100 seed wt.**	PCT-1 x PPT-2 PCT-1 x PBT-13 PCT-1 x PBT-4	PCT-1 x PPT-2	PBT-9 x PBT-2 PCT-1 x PBT-13 PCT-1 x PPT-2
14	**Fruit yield/plant**	PBT-2 x PBT-13 PBT-13 x PBT-10 PBT-13 x PBT-4	PBT-2 x PBT-13 PCT-1 x PBT-5 PBT-5 x PBT-4	PCT-1 x PBT-5 PBT-2 x PBT-13 PBT-9 x PBT-4
15	**Fruit yield/ha**	PBT-2 x PBT-13 PBT-13 x PBT-10 PBT-13 x PBT-4	PBT-2 x PBT-13 PCT-1 x PBT-5 PBT-5 x PBT-4	PCT-1 x PBT-5 PBT-2 x PBT-13 PBT-9 x PBT-4

Table 4.36: Summary table showing top three promising heterotic crosses with respect to each quality traits in desired direction

S.N.	Characters	Relative heterosis (%)	Heterobeltiosis (%)	Standard heterosis (%)
1	**No. of locules/fruit**	PBT-2 x PBT-10 PBT-9 x PBT-5 PPT-2 x PBT-10	PBT-2 x PBT-10 PBT-9 x PBT-10 PPT-2 x PBT-10	PBT-2 x PBT-10 PBT-2 x PBT-13 PBT-9 x PBT-5
2	**Pericarp thickness**	PCT-1 x PPT-2 PCT-1 x PBT-5 PPT-2 x PBT-4	PPT-2 x PBT-4 PBT-9 x PBT-2 PBT-2 x PBT-4	PBT-9 x PBT-2 PBT-2 x PBT-4 PPT-2 x PBT-4
3	**Diameter of stalk scar**	PBT-5 x PBT-13	PBT-5 x PBT-13	–
4	**Fruit firmness**	PBT-9 x PBT-5 PBT-9 x PBT-2 PBT-9 x PBT-13	PBT-9 x PBT-2 PCT-1 x PBT-9 PBT-9 x PBT-5	PBT-9 x PBT-5 PBT-2 x PBT-13 PBT-9 x PBT-13
5	**TSS**	PBT-9 x PBT-2 PCT-1 x PBT-9	–	–
6	**pH of fruit juice**	PBT-2 x PBT-13 PCT-1 x PBT-2 PBT-2 x PBT-4	PBT-2 x PBT-13 PCT-1 x PBT-2 PCT-1 x PPT-2	PBT-2 x PBT-13 PCT-1 x PPT-2 PCT-1 x PBT-2
7	**Titratable acidity**	PCT-1 x PPT-2 PPT-2 x PBT-2 PBT-5 x PBT-2	PPT-2 x PBT-2 PBT-5 x PBT-2 PCT-1 x PPT-2	PCT-1 x PPT-2 PCT-1 x PBT-5 PCT-1 x PBT-10
8	**Ascorbic acid**	PBT-2 x PBT-13 PPT-2 x PBT-4 PBT-9 x PBT-5	PBT-9 x PBT-5 PBT-2 x PBT-13	–
9	**Lycopene**	PBT-13 x PBT-4 PPT-2 x PBT-4 PBT-9 x PBT-4	PBT-5 x PBT-13 PCT-1 x PBT-4 PPT-2 x PBT-10	PPT-2 x PBT-10
10	**Total carotenoids**	PBT-13 x PBT-4 PBT-9 x PBT-4 PPT-2 x PBT-4	PBT-9 x PBT-4 PCT-1 x PBT-5 PBT-9 x PBT-5	PPT-2 x PBT-10

4.5 Estimation of combining ability and gene action

4.5.1 Analysis of variance for combining ability

Analysis of variance for combining ability with respect to different yield related and quality traits are presented in Table 4.37 and 4.38, respectively.

The total variability among F_1 hybrids was further partitioned into different components and their significance was tested. It is evident from the table that the mean sum of squares due to parents and crosses was significant for all fifteen yield related and ten quality traits studied.

4.5.2 Estimates of combining ability effects

The success of a breeding programme depends upon the choice of suitable parents and their utilization by adopting an appropriate breeding method. The combining ability analysis has been used extensively to identify potential parents either to be used in the development of hybrids or recombinant breeding for getting elite pure parents. This analysis facilitates the partitioning of genotypic variation of crosses into variation due to general combining ability (GCA) and specific combining ability (SCA). GCA effects are the measure of additive gene action which represent the fixable components of genetic variance and are used to classify the parents for the breeding behavior in hybrid combinations. On the other hand, SCA effects are the measure of non-additive gene action which is related to non-fixable component of genetic variance (Sprague 1966). The common approach of choosing the parents on the basis of performance, adaptation and genetic variability does not necessarily lead to useful results because of the differential ability of the parents. This ability of the parents depends upon the complex interaction among the genes and hence cannot be judged by *per se* performance alone (Allard 1960). Therefore, it is important to assess the general and specific combining ability effects in the selection of the parents and the formulation of an appropriate crossing plan. Among the various breeding methods, diallel mating design (method 2) excluding reciprocals (Griffing 1956) has been used in the present study to evaluate 8 parents and their 28 crosses. The results are presented and discussed as follows:

Table 4.37: Analysis of variance for combining ability in tomato genotypes for yield related traits

S. N.	Characters		Mean sum of squares		
			GCA	SCA	Error
		df	7	28	70
1	Days to 50 per cent flowering		92.114**	26.986**	5.415
2	Days to first fruit set		118.989**	31.054**	4.732
3	Days to first fruit ripening		253.784**	56.682**	2.889
4	Number of flowers per cluster		116.609**	26.411**	0.775
5	Number of fruits per cluster		34.771**	6.992**	0.268
6	Number of fruits per plant		23,243.391**	5,153.393**	79.966
7	Internodal length (cm)		10.505**	6.209**	0.821
8	Average fruit weight (g)		9,379.176**	2,505.611**	42.301
9	Fruit length (cm)		9.323**	1.137**	0.069
10	Fruit width (cm)		6.663**	1.447**	0.131
11	Fruit shape index		0.238**	0.052**	0.012
12	Plant height (cm)		11,487.656**	7,160.601**	1,646.279
13	100 seed weight (g)		0.017**	0.005**	0.0004
14	Fruit yield per plant (kg)		2.640**	5.654**	0.181
15	Fruit yield per hectare (t/ha)		3,268.173**	7,002.490**	224.121

Table 4.38: Analysis of variance for combining ability in tomato genotypes for quality traits

S. N.	Characters		Mean sum of squares		
			GCA	SCA	Error
		df	7	28	70
1	Number of locules per fruit		2.562**	1.240**	0.085
2	Pericarp thickness (cm)		0.130**	0.105**	0.009
3	Diameter of stalk scar (cm)		0.269**	0.436**	0.012
4	Fruit firmness (kg/cm^2)		7.302**	0.741**	0.109
5	Total soluble solids (%)		0.098**	0.105**	0.018
6	pH of fruit juice		0.052**	0.014**	0.001
7	Titratable acidity (%)		66.961**	13.489**	3.904
8	Ascorbic acid (mg/100g)		2.903**	0.664**	0.042
9	Lycopene (mg/100g)		30.438**	5.710**	0.638
10	Total carotenoids (mg/100g)		92.780**	16.269**	1.161

4.5.2.1. Combining ability effects for yield related traits

In the present investigation, the general combining ability (GCA) effects and specific combining ability (SCA) effects of hybrids for fifteen yield related traits evaluation are presented in Table 4.39 and Table 4.40, respectively. The results obtained are discussed as below:

4.5.2.1.1 Days to 50 per cent flowering

The estimates of GCA and SCA effects for days to 50 per cent flowering are presented in Table 4.39 and Table 4.40, respectively. The GCA effect ranged from -1.717 to 2.817 per cent and out of eight parents, five parents showed significant GCA effect for days to 50 per cent flowering. Among the parents, three parents exhibited significant negative GCA effects which were PBT-2 (-1.717), PCT-1 (-1.617) and PBT-5 (-1.583).

The perusal of data revealed that range of SCA effects for days to 50 per cent flowering was -6.626 to 4.341. Out of 28 crosses, five cross combinations exhibited significant SCA effect for same trait. Desirable significant negative SCA effects was showed in four crosses namely PBT-13 x PBT-10 (-6.626), PBT-5 x PBT-13 (-4.026), PBT-9 x PBT-2 (-3.926) and PCT-1 x PPT-2 (-3.626). Raj *et al*. (2017) and Savale and Patel (2017) also reported significant negative general combining ability and specific combining effects for days to 50 per cent flowering in tomato.

4.5.2.1.2 Days to first fruit set

The estimates of GCA effects for days to first fruit set revealed that the range was -1.983 to 3.217. Among all parent five parents showed significant GCA effect for same trait while, among them three parents *viz*., PBT-5 (-1.983), PCT-1 (-1.949) and PBT-2 (-1.896) exhibited desirable significant negative GCA effect for days to first fruit set.

Data presented in Table 4.40 revealed that SCA effects for days to first fruit set ranged from -6.433 to 4.887. Among all crosses significant SCA effects for same traits was observed in eight cross combinations. Desirable significant negative SCA effects for days to first fruit set were observed in four crosses *i.e*., PBT-13 x PBT-10 (-6.433), PCT-1 x PBT-4 (-4.320), PBT-9 x PBT-2 (-4.287) and PBT-5 x PBT-13 (-3.853). Desirable significant negative GCA and SCA effect for days to first fruit set was also confirmed by Agarwal *et al*. (2017).

4.5.2.1.3 Days to first fruit ripening

The perusal of data revealed that range of GCA effect for days to first fruit ripening was -4.727 to 3.800. Out of all eight parents, seven parents exhibited significant GCA effect for same traits and among them four parents showed desirable significant negative GCA effect for days to first fruit ripening which were PCT-1 (-4.727), PBT-5 (-1.993), PBT-2 (-1.507) and PBT-10 (-1.213).

Data of SCA effect for days to first fruit ripening revealed that range was observed from -6.841 to 6.985. Out of all crosses significant SCA effects for same trait was observed in fifteen crosses and among them six cross combinations showed desirable negative SCA effect. Top five crosses exhibited significant negative SCA effects were PBT-2 x PBT-13 (-6.841), PBT-9 x PBT-5 (-6.168), PBT-9 x PBT-2 (-5.388), PBT-5 x PBT-13 (-3.421) and PBT-13 x PBT-10 (-2.801).

4.5.2.1.4 Number of flowers per cluster

Data presented in Table 4.39 revealed that GCA effects for number of flowers per cluster ranged from -1.573 to 4.427. Among all parents, significant GCA effect was observed for six parents and among them desirable significant positive effect was exhibited by two parents namely PCT-1 (4.427) and PBT-5 (0.973).

The read-through of data for SCA effects revealed that range of SCA for number of flowers per cluster ranged from -2.823 to 8.437. Out of all crosses, fourteen cross combinations exhibited significant SCA effect for same trait whereas, significant positive SCA effects were observes among eight crosses. Top five hybrids showed desirable significant positive SCA effects for number of flowers per cluster were PCT-1 x PBT-5 (8.437), PBT-5 x PBT-4 (4.677), PBT-9 x PBT-4 (4.290), PBT-13 x PBT-10 (3.917) and PBT-13 x PBT-4 (2.430). The results with respect to GCA and SCA effects are similar to the results obtained by Aminu and Mala (2015) and Louis *et al*. (2016).

4.5.2.1.5 Number of fruits per cluster

The estimates of GCA effects for number of fruits per cluster ranged from -0.783 to 2.523. Out of eight parents, seven parents exhibited significant GCA effect for same trait and among them two parents showed desirable significant positive GCA effect for number of fruits per cluster which were PCT-1 (2.523) and PBT-5 (0.370).

Table 4.39: General combining ability effect of parents for different yield related traits in tomato

S. N.	Name of parent	Characters														
		DFF	**DFFS**	**DFFR**	**NFC**	**NFRC**	**NFP**	**IL**	**AFW**	**FL**	**FW**	**FSI**	**PH**	**SW**	**FYP**	**FYH**
1	PCT-1	-1.617*	-1.949**	-4.727**	4.427**	2.523**	68.275**	-0.095	-41.529**	-1.162**	-1.126**	0.004	32.108**	-0.045**	-0.352**	-12.382**
2	PPT-2	2.817**	3.217**	3.287**	-1.093**	-0.323*	-8.099**	-0.535*	16.024**	0.437**	0.194	0.043	13.808	0.009	0.461**	16.221**
3	PBT-9	0.550	0.691	0.413	-1.107**	-0.783**	-12.629**	-0.668*	11.631**	0.141	0.266*	-0.041	-28.152*	0.013*	0.038	1.363
4	PBT-5	-1.583*	-1.983**	-1.993**	0.973**	0.370*	-3.564	-0.715**	2.884	-0.121	0.205	-0.078*	-15.178	-0.007	0.356**	12.537**
5	PBT-2	-1.717*	-1.896**	-1.507**	-1.573**	-0.497**	-14.105**	0.485	2.517	-0.182*	0.043	-0.040	-6.052	0.023**	-0.235	-8.263
6	PBT-13	2.183**	2.277**	3.800**	-0.047	-0.350*	-11.607**	0.738**	3.744	0.076	0.190	-0.030	12.922	0.015*	-0.237	-8.345
7	PBT-10	-0.650	-0.603	-1.213*	-1.300**	-0.670**	-12.573**	0.165	-1.629	0.066	0.305**	-0.058	4.962	0.016**	-0.156	-5.492
8	PBT-4	0.017	0.244	1.940**	-0.280	-0.270	-5.699*	0.625*	6.358**	0.745**	-0.078	0.200**	-14.418	-0.024**	0.124	4.360
	CD 1%	**1.776**	**1.660**	**1.296**	**0.672**	**0.395**	**6.820**	**0.692**	**4.964**	**0.200**	**0.276**	**0.084**	**30.965**	**0.015**	**0.325**	**11.425**
	CD 5%	**1.350**	**1.261**	**0.984**	**0.510**	**0.300**	**5.184**	**0.525**	**3.771**	**0.152**	**0.210**	**0.064**	**23.524**	**0.012**	**0.247**	**8.680**

DFF – Days to 50 per cent flowering, DFFS – Days to first fruit set, DFFR – Days to first fruit ripening, NFC – Number of flowers per cluster, NFRC – Number of fruits per cluster, NFP – Number of fruits per plant, IL – Internodal length, AFW – Average fruit weight, FL – Fruit length, FW – Fruit width, FSI – Fruit shape index, PH – Plant height, SW – 100 seed weight, FYP – Fruit yield per plant and FYH – Fruit yield per hectare.

Table 4.40 Estimation of specific combining ability effects for different yield related traits in F_1's of diallel cross of tomato

		Characters														
S. N.	**Name of crosses**	**DFF**	**DFFS**	**DFFR**	**NFC**	**NFRC**	**NFP**	**IL**	**AFW**	**FL**	**FW**	**FSI**	**PH**	**SW**	**FYP**	**FYH**
1	PCT-1 x PPT-2	-3.626*	-2.627	1.559	-0.763	0.633	-36.573**	0.584	14.502**	0.041	0.028	0.020	-28.567	0.072**	-0.712*	-25.087*
2	PCT-1 x PBT-9	1.974	1.500	3.232*	-2.550**	-0.107	-39.783**	1.117	-26.371**	-0.586**	-0.220	-0.113	50.327	0.008	-1.316**	-46.268**
3	PCT-1 x PBT-5	-1.226	-1.760	-1.361	8.437**	4.340**	-25.055**	1.430*	22.376**	0.292	0.211	-0.006	30.687	-0.002	3.160**	111.214**
4	PCT-1 x PBT-2	3.574	4.287*	3.752**	-1.150	-0.993*	-59.554**	-1.836*	-14.191**	-0.200	-0.198	-0.037	-4.373	0.058**	-0.622	-21.889
5	PCT-1 x PBT-13	2.007	2.713	3.112*	-1.076	-1.607**	-55.193**	-1.556*	-6.818	0.329	0.235	0.013	-5.747	0.076**	-0.891**	-31.377**
6	PCT-1 x PBT-10	1.841	3.460*	3.725**	-2.823**	-2.287**	-69.360**	1.150	-15.644**	-0.008	0.061	-0.042	-9.720	0.032*	-1.082**	-38.021**
7	PCT-1 x PBT-4	-3.493	-4.320*	-1.295	-1.243	-0.487	-42.587**	-0.110	16.236**	0.773**	0.774**	-0.021	45.793	0.025	-0.028	-0.992
8	PPT-2 x PBT-9	0.541	1.333	0.952	-0.896	-0.127	6.724	1.024	23.542**	0.771**	0.440	0.062	2.360	-0.006	1.288**	45.352**
9	PPT-2 x PBT-5	3.007	4.140*	5.359**	-2.643**	-1.213**	-5.081	-0.796	0.689	0.139	0.067	0.019	-50.280	0.004	-0.354	-12.436
10	PPT-2 x PBT-2	1.807	3.053	6.472**	0.504	-0.280	4.353	-1.530*	27.389**	0.450*	0.552	-0.042	6.060	-0.026	1.034**	36.381**
11	PPT-2 x PBT-13	3.241	2.947	1.832	-1.290	-1.027*	-1.919	0.417	13.496**	0.096	-0.191	0.058	9.220	0.002	0.126	4.453
12	PPT-2 x PBT-10	1.074	1.360	2.845*	-0.236	-0.307	7.787	0.057	-9.064	-0.874**	-0.989**	0.043	31.580	-0.029	-0.118	-4.200
13	PPT-2 x PBT-4	0.741	0.047	-2.641*	-1.390*	-0.507	-7.293	-1.270	15.549**	-0.117	-0.170	-0.006	46.560	0.021	-0.215	-7.522
14	PBT-9 x PBT-5	-3.393	-2.867	-6.168**	0.104	-0.887*	-3.658	-1.130	39.016**	0.962**	1.286**	-0.030	15.147	0.000	0.769*	27.072*
15	PBT-9 x PBT-2	-3.926*	-4.287*	-5.388**	1.450*	0.247	4.883	-1.530*	-33.684**	-0.817**	-0.442	-0.095	-113.710**	0.030	-1.063**	-37.400**
16	PBT-9 x PBT-13	0.841	1.273	0.439	-1.076	0.233	4.705	-1.450*	0.356	-0.561**	-0.209	-0.061	58.513	-0.038*	0.006	0.195
17	PBT-9 x PBT-10	4.341*	4.887**	6.985**	1.110	-0.247	2.171	1.190	11.062*	-0.028	-0.381	0.080	-30.327	-0.003	-0.645	-22.715
18	PBT-9 x PBT-4	0.674	0.573	3.365*	4.290**	1.553**	23.943**	-2.736**	-10.591*	-0.487*	-0.278	-0.062	40.253	0.007	1.892**	66.586**
19	PBT-5 x PBT-2	0.541	0.853	1.219	-0.763	-0.707	4.031	-1.283	-29.404**	-0.255	-0.395	0.012	-16.153	0.020	-1.297**	-45.661**
20	PBT-5 x PBT-13	-4.026*	-3.853*	-3.421*	1.577*	0.013	8.693	-0.136	-63.298**	-1.532**	-1.662**	0.026	-8.593	-0.032*	-1.496**	-52.663**
21	PBT-5 x PBT-10	-1.526	-2.040	0.925	-2.370**	-1.467**	-3.235	-1.230	17.009**	0.564**	-0.187	0.157	53.767	-0.033*	0.020	0.727
22	PBT-5 x PBT-4	-2.193	-1.820	-0.361	4.677**	2.267**	38.951**	2.910**	23.022**	-0.079	0.406	-0.132	6.547	-0.003	1.560**	54.896**
23	PBT-2 x PBT-13	-2.226	-2.740	-6.841**	2.057**	2.880**	21.921**	0.597	29.536**	0.408*	0.676*	-0.062	-22.520	-0.002	2.996**	105.431**
24	PBT-2 x PBT-10	0.274	0.273	2.105	1.044	0.467	9.767	1.304	-27.091**	-0.408*	-0.735*	0.055	23.573	-0.003	-0.352	-12.339
25	PBT-2 x PBT-4	-1.393	0.627	-2.115	0.357	-0.200	13.639	1.244	-5.011	0.365	-1.032**	0.427**	47.687	-0.074**	-0.498	-17.521
26	PBT-13 x PBT-10	-6.626**	-6.433**	-2.801*	3.917**	1.320**	19.995**	0.450	69.816**	1.161**	1.328**	-0.021	46.733	0.005	2.250**	79.173**
27	PBT-13 x PBT-4	0.374	0.720	0.645	2.430**	0.987*	1.834	-0.343	8.296	-0.395	0.831**	-0.289**	38.313	0.015	0.707*	24.877*
28	PBT-10 x PBT-4	-1.126	0.000	0.592	-2.050**	-0.893*	-1.54	-1.636*	-29.131**	-0.669**	-0.077	-0.158	11.540	0.044**	-0.544	19.189
	CD 1%	**4.736**	**4.427**	**3.455**	**1.792**	**1.054**	**18.199**	**1.844**	**13.237**	**0.535**	**0.737**	**0.223**	**82.574**	**0.041**	**0.866**	**30.467**
	CD 5%	**3.598**	**3.363**	**2.625**	**1.361**	**0.800**	**13.826**	**1.401**	**10.056**	**0.406**	**0.560**	**0.169**	**62.731**	**0.031**	**0.658**	**23.145**

DFF – Days to 50 per cent flowering, DFFS – Days to first fruit set, DFFR – Days to first fruit ripening, NFC – Number of flowers per cluster, NFRC – Number of fruits per cluster, NFP – Number of fruits per plant, IL – Internodal length, AFW – Average fruit weight, FL – Fruit length, FW – Fruit width, FSI – Fruit shape index, PH – Plant height, SW – 100 seed weight, FYP – Fruit yield per plant and FYH – Fruit yield per hectare.

Data presented in Table 4.40 revealed that SCA effects for number of fruits per cluster ranged from -2.287 to 4.340. Among all crosses significant SCA effects for same traits was observed in fourteen cross combinations while, desirable significant positive SCA effects for number of fruits per cluster were observed in six crosses. Top five cross combinations exhibited desirable significant positive SCA effect for number of fruits per cluster were PCT-1 x PBT-5 (4.340), PBT-2 x PBT-13 (2.880), PBT-5 x PBT-4 (2.267), PBT-9 x PBT-4 (1.553) and PBT-13 x PBT-10 (1.320). These results were also in close confirmation with the observations of Mondal *et al*. (2009), Narasimhamurthy *et al*. (2013), Renuka *et al*. (2015) and Raj *et al*. (2017).

4.5.2.1.6 Number of fruits per plant

The perusal of data revealed that range of GCA effect for number of fruits per plant was -14.105 to 68.275. Among all eight parents, significant GCA effect was observed for seven parents and only one parent *i.e*., PCT-1 (68.275) exhibited desirable significant positive GCA effect for number of fruits per plant.

The estimates of SCA effects for number of fruits per plant ranged from -69.360 to 38.951. Out of twenty eight crosses significant SCA effects for same traits were observed in eleven cross combinations whereas, among them four crosses namely PBT-5 x PBT-4 (38.951), PBT-9 x PBT-4 (23.943), PBT-2 x PBT-13 (21.921) and PBT-13 x PBT-10 (19.995) exhibited desirable significant positive SCA effect for number of fruits per plant. Similar results were observed by Mondal *et al*. (2009), Yadav *et al*. (2013), Cheema *et al*. (2014), Aminu and Mala (2015), Renuka *et al*. (2015), Louis *et al*. (2016), Kumar *et al*. (2016), Agarwal *et al*. (2017) and Savale and Patel (2017), .

4.5.2.1.7 Internodal length (cm)

The read-through of data presented in the Table 4.39 revealed that GCA effect for internodal length ranged from -0.715 to 0.738. Among all parents, five parents showed significant GCA effect for same trait. Desirable significant negative GCA effects was observed among three parents which were PBT-5 (-0.715), PBT-9 (-0.668) and PPT-2 (-0.535).

Data of SCA effects revealed that SCA effects for internodal length ranged from -2.736 to 2.910. Among all crosses significant SCA effects for same traits was observed

in nine cross combinations. Desirable significant negative SCA effects for internodal length were observed in seven crosses and top six hybrids showed significant negative SCA effects for internodal length were PBT-9 x PBT-4 (-2.736), PCT-1 x PBT-2 (-1.836), PBT-10 x PBT-4 (-1.636), PCT-1 x PBT-13 (-1.556), PPT-2 x PBT-2 (-1.530) and PBT-9 x PBT-2 (-1.530).

4.5.2.1.8 Average fruit weight (g)

The estimates of GCA effects for average fruit weight ranged from -41.529 to 16.024. Out of eight parents, four parents exhibited significant GCA effect for same trait and among them three parents showed desirable significant positive GCA effect for average fruit weight which were PPT-2 (16.024), PBT-9 (11.631) and PBT-4 (6.358).

Data presented in Table 4.40 revealed that SCA effects for average fruit weight ranged from -63.298 to 69.816. Among all crosses significant SCA effects for same traits was observed in twenty two cross combinations while, desirable significant positive SCA effects for average fruit weight were observed in thirteen crosses. Top five cross combinations exhibited desirable significant positive SCA effect for average fruit weight were PBT-13 x PBT-10 (69.816), PBT-9 x PBT-5 (39.016), PBT-2 x PBT-13 (29.536), PPT-2 x PBT-2 (27.389) and PPT-2 x PBT-9 (23.542). Similar results have been reported by Mondal *et al*. (2009), Shalaby (2012), Yadav *et al*. (2013), Cheema *et al*. (2014), Renuka *et al*. (2015), Kumar *et al*. (2015), Aisyah *et al*. (2016), Agarwal *et al*. (2017), Raj *et al*. (2017) and Savale and Patel (2017).

4.5.2.1.9 Fruit length (cm)

Data presented in Table 4.39 revealed that GCA effects for fruit length ranged from -1.162 to 0.745. Out of all parents, significant GCA effect was observed for four parents and among them desirable significant positive effect was exhibited by two parents namely PBT-4 (0.745) and PPT-2 (0.437) for fruit length.

The read-through of data for SCA effects revealed that range of SCA for fruit length ranged from -1.532 to 1.161. Out of all crosses, fifteen cross combinations exhibited significant SCA effect for same trait whereas, significant positive SCA effects were observed among seven crosses. Top five hybrids showed desirable significant positive SCA effects for fruit length were PBT-13 x PBT-10 (1.161), PBT-9

x PBT-5 (0.962), PCT-1 x PBT-4 (0.773), PPT-2 x PBT-9 (0.771) and PBT-5 x PBT-10 (0.564). These results are in close agreement with those reported by Mondal *et al*. (2009), Yadav *et al*. (2013), Aisyah *et al*. (2016) and Kumar *et al*. (2016).

4.5.2.1.10 Fruit width (cm)

The read-through of data presented in the Table 4.39 revealed that GCA effect for fruit width ranged from -1.126 to 0.305. Among all parents, three parents showed significant GCA effect for same trait. Desirable significant positive GCA effects was observed among two parents which were PBT-10 (0.305) and PBT-9 (0.266).

The estimates of SCA effects for fruit width ranged from -1.662 to 1.328. Out of twenty eight crosses significant SCA effects for same traits were observed in nine cross combinations whereas, among them five crosses namely PBT-13 x PBT-10 (1.328), PBT-9 x PBT-5 (1.286), PBT-13 x PBT-4 (0.831), PCT-1 x PBT-4 (0.774) and PBT-2 x PBT-13 (0.676) exhibited desirable significant positive SCA effect for fruit width. Mondal *et al*. (2009), Yadav *et al*. (2013), Aisyah *et al*. (2016) and Kumar *et al*. (2016) also reported similar results for fruit width in tomato.

4.5.2.1.11 Fruit shape index

The perusal of data revealed that range of GCA effect for fruit shape index was -0.078 to 0.200. Among all eight parents, significant GCA effect was observed for two parents and only one parent *i.e*., PBT-4 (0.200) exhibited desirable significant positive GCA effect for fruit shape index.

The estimates of SCA effects for fruit shape index ranged from -0.289 to 0.427. Out of twenty eight crosses significant SCA effects for same traits were observed in two cross combinations whereas, among them only one cross namely PBT-2 x PBT-4 (0.427) exhibited desirable significant positive SCA effect for fruit shape index. The results are in parity with those obtained by Raj *et al*. (2017) in tomato.

4.5.2.1.12 Plant height (cm)

The estimates of GCA effects for plant height ranged from -28.152 to 32.108. Out of eight parents, two parents exhibited significant GCA effect for same trait and among them only one parent *i.e*., PCT-1 (32.108) showed desirable significant positive GCA effect for plant height.

The read-through of data for SCA effects revealed that range of SCA for plant height ranged from -113.710 to 58.513. Out of all crosses, only one cross combination exhibited significant SCA effect for same trait and none of the hybrid showed desirable significant positive SCA effect for plant height. Similar results for plant height have been reported by Shalaby (2012), Narasimhamurthy *et al*. (2013), Yadav *et al*. (2013), Aminu and Mala (2015), Renuka *et al*. (2015), Louis *et al*. (2016), Kumar *et al*. (2016), Triveni *et al*. (2017), Raj *et al*. (2017) and Savale and Patel (2017).

4.5.2.1.13 100 seed weight (g)

Data presented in Table 4.39 revealed that GCA effects for 100 seed weight ranged from-0.045 to 0.023. Out of all parents, significant GCA effect was observed for six parents and among them desirable significant positive effect was exhibited by four parents namely PBT-2 (0.023), PBT-10 (0.016), PBT-13 (0.015) and PBT-9 (0.013) for 100 seed weight.

The perusal of data revealed that range of SCA effects for 100 seed weight was -0.074 to 0.076. Out of twenty eight crosses significant SCA effects for same traits were observed in nine cross combinations whereas, among them five crosses namely PCT-1 x PBT-13 (0.076), PCT-1 x PPT-2 (0.072), PCT-1 x PBT-2 (0.058), PBT-10 x PBT-4 (0.044) and PCT-1 x PBT-10 (0.032) exhibited desirable significant positive SCA effect for 100 seed weight.

4.5.2.1.14 Fruit yield per plant (kg)

The read-through of data presented in the Table 4.39 revealed that GCA effect for fruit yield per plant ranged from -0.352 to 0.461. Among all parents, three parents showed significant GCA effect for same trait. Desirable significant positive GCA effects was observed among two parents which were PPT-2 (0.461) and PBT-5 (0.356).

The estimates of SCA effects for fruit yield per plant ranged from -1.496 to 3.160. Out of twenty eight crosses significant SCA effects for same traits were observed in sixteen cross combinations whereas, among them nine crosses exhibited desirable significant positive SCA effect for fruit yield per plant. Top five cross combinations exhibited desirable significant positive SCA effects for fruit yield per plant were PCT-1 x PBT-5 (3.160), PBT-2 x PBT-13 (2.996), PBT-13 x PBT-10 (2.250), PBT-9 x PBT-4 (1.892) and PBT-5 x PBT-4 (1.560). These results are in close

agreement with those reported by Sherpa *et al*. (2005), Shalaby (2012), Narasimhamurthy *et al*. (2013), Yadav *et al*. (2013), Cheema *et al*. (2014), Kumar *et al*. (2015), Renuka *et al*. (2015), Aisyah *et al*. (2016), Basavraj *et al*. (2016), Kumar *et al*. (2016), Raj *et al*. (2017) and Savale and Patel (2017).

4.5.2.1.15 Fruit yield per hectare (t/ha)

The perusal of data revealed that range of GCA effect for fruit yield per hectare was -12.382 to 16.221. Among all eight parents, significant GCA effect was observed for three parents and two parents *i.e*., PPT-2 (16.221) and PBT-5 (12.537) exhibited desirable significant positive GCA effect for fruit yield per hectare.

The read-through of data for SCA effects revealed that range of SCA for fruit yield per hectare ranged from -52.663 to 111.214. Out of all crosses, sixteen cross combinations exhibited significant SCA effect for same trait and among them nine hybrids showed desirable significant positive SCA effect. Top five hybrids exhibited desirable significant positive SCA effects were PCT-1 x PBT-5 (111.214), PBT-2 x PBT-13 (105.431), PBT-13 x PBT-10 (79.173), PBT-9 x PBT-4 (66.586) and PBT-5 x PBT-4 (54.896). Similar results in tomato for fruit yield per hectare have been reported by Yadav *et al*. (2013), Dagade *et al*. (2015), Renuka *et al*. (2015) and Raj *et al*. (2017).

4.5.2.2 Combining ability effects for quality traits

4.5.2.2.1 Number of locules per fruit

The read-through of data presented in the Table 4.41 revealed that GCA effect for number of locules per fruit ranged from -0.333 to 0.467. Among all parents, six parents showed significant positive GCA effect for same trait. Desirable significant positive GCA effects was observed among three parents which were PBT-2 (0.467), PBT-10 (0.333) and PBT-13 (0.200).

The estimates of SCA effects for number of locules per fruit ranged from -0.822 to 1.644 (Table 4.40). Out of twenty eight crosses, significant SCA effects for same trait were observed in eleven cross combinations, whereas among them five crosses namely PBT-2 x PBT-10 (1.644), PBT-9 x PBT-5 (1.144), PBT-2 x PBT-13 (1.111), PCT-1 x PBT-9 (0.844) and PPT-2 x PBT-13 (0.578) exhibited desirable significant positive SCA effect for number of locules per fruit. Joshi *et al*. (2005), Joshi and Kohli

(2006), Mondal *et al*. (2009), Kumar *et al*. (2015), Renuka *et al*. (2015), Aisyah *et al*. (2016), Basavraj *et al*. (2016) and Raj *et al*. (2017) also reported similar results for this trait in tomato.

4.5.2.2.2 Pericarp thickness (cm)

The estimates of GCA effects for pericarp thickness ranged from -0.137 to 0.056. Out of eight parents, three parents exhibited significant GCA effect for same trait and among them only one parent *viz*., PBT-4 (0.056) showed desirable significant positive GCA effect for pericarp thickness.

The perusal of data presented in Table 4.42 revealed that range of SCA effects for pericarp thickness was -0.269 to 0.333. Out of twenty eight crosses, significant SCA effects for same trait was observed in twelve cross combinations whereas, among them eight crosses exhibited desirable significant positive SCA effect. Top six crosses showed desirable significant positive SCA effect for pericarp thickness were PBT-9 x PBT-2 (0.333), PBT-13 x PBT-10 (0.298), PCT-1 x PBT-5 (0.280), PBT-2 x PBT-4 (0.239), PCT-1 x PPT-2 (0.206) and PPT-2 x PBT-4 (2.06). These results are in close agreement with those reported by Joshi *et al*. (2005), Mondal *et al*. (2009), Kumar *et al*. (2015), Renuka *et al*. (2015), Basavraj *et al*. (2016), Agarwal *et al*. (2017), Raj *et al*. (2017) and Savale and Patel (2017).

4.5.2.2.3 Diameter of stalk scar (cm)

The perusal of data revealed that range of GCA effect for diameter of stalk scar was -0.174 to 0.131. Among all eight parents, significant negative GCA effect was observed in three parents for same character. Desirable significant negative GCA effect was exhibited by only by one parent *i.e*., PCT-1 (-0.174) for diameter of stalk scar.

The estimates of SCA effects for diameter of stalk scar ranged from -0.564 to 0.942. Out of twenty eight crosses significant SCA effects for same trait was observed in twenty cross combinations whereas, among them eight crosses exhibited desirable significant negative SCA effect. Top five crosses showed desirable significant negative SCA effect for diameter of stalk scar were PBT-5 x PBT-13 (-0.564), PPT-2 x PBT-13 (-0.317), PBT-10 x PBT-4 (-0.312), PCT-1 x PBT-13 (-0.239) and PBT-9 x PBT-2 (-0.216). Similar results for same trait have been reported by Joshi and Kohli (2006).

4.5.2.2.4 Fruit firmness (kg/cm^2)

Data presented in Table 4.41 revealed that GCA effects for fruit firmness ranged from-0.396 to 0.418. Out of all parents, significant GCA effect was observed for six parents and among them desirable significant positive effect was exhibited by three parents namely PBT-13 (0.418), PBT-4 (0.415) and PBT-5 (0.146) for fruit firmness.

The read-through of data for SCA effects revealed that range of SCA for fruit firmness ranged from -0.842 to 1.089. Out of all crosses, eleven cross combinations exhibited significant SCA effect for same trait and among them seven hybrids showed desirable significant positive SCA effect. Top five hybrids exhibited desirable significant positive SCA effects for fruit firmness were PBT-9 x PBT-5 (1.089), PBT-2 x PBT-13 (0.686), PPT-2 x PBT-13 (0.512), PBT-9 x PBT-2 (0.435) and PBT-9 x PBT-13 (0.387). The results with respect to GCA and SCA effects are similar to the results obtained by Joshi *et al*. (2005), Narasimhamurthy *et al*. (2013), Renuka *et al*. (2015) and Shalaby (2012).

4.5.2.2.5 TSS (%)

The read-through of data presented in the Table 4.41 revealed that GCA effect for TSS ranged from -0.723 to 0.837. Among all parents, five parents showed significant GCA effect for same trait. Desirable significant positive GCA effects was observed among two parents which were PCT-1 (0.837) and PPT-2 (0.447).

The estimates of SCA effects for TSS ranged from -1.286 to 0.550. Out of twenty eight crosses significant SCA effects for same trait were observed in four cross combinations whereas, among them only one cross *i.e*., PCT-1 x PBT-5 (0.550) exhibited desirable significant positive SCA effect for TSS. The findings of Joshi and Kohli (2006), Mondal *et al*. (2009), Narasimhamurthy *et al*. (2013), Yadav *et al*. (2013), Cheema *et al*. (2014), Dagade *et al*. (2015), Kumar *et al*. (2015), Basavraj *et al*. (2016), Agarwal *et al*. (2017), Triveni *et al*. (2017), Raj *et al*. (2017) and Savale and Patel (2017) are in accordance with the results obtained above.

4.5.2.2.6 pH of fruit juice

The perusal of data revealed that range of GCA effect for pH of fruit juice was -0.123 to 0.054. Out of all eight parents, significant GCA effect was observed for single parent and desirable significant negative GCA effect for pH of fruit juice was also showed by single parent which was PCT-1 (-0.123).

Table 4.41: General combining ability effect of parents for different quality traits in tomato

S. N.	Name of parent	Character									
		NLF	**PT**	**DSC**	**FF**	**TSS**	**pH**	**TA**	**AA**	**Lycopene**	**TC**
1	PCT-1	-0.200*	-0.137**	-0.174**	-0.396**	0.837**	-0.123**	0.084**	3.113**	-0.650**	-1.184**
2	PPT-2	-0.333**	0.043	0.011	-0.092	0.447**	-0.035	0.016	1.239*	1.570**	2.805**
3	PBT-9	-0.200*	0.035	-0.058	0.035	-0.330**	0.054	-0.044**	-0.475	-0.672**	-0.977**
4	PBT-5	-0.167	0.041	0.131**	0.146*	-0.383**	0.038	-0.039**	-0.476	0.488*	0.331
5	PBT-2	0.467**	0.016	-0.060	-0.220**	0.030	-0.004	-0.021*	-1.575**	-1.215**	-2.450**
6	PBT-13	0.200*	-0.058*	0.045	0.418**	0.153	0.010	0.024**	-0.754	0.383	0.492
7	PBT-10	0.333**	0.004	0.072*	-0.307**	-0.030	0.019	-0.002	-0.133	1.022**	2.007**
8	PBT-4	-0.100	0.056*	0.032	0.415**	-0.723**	0.041	-0.019*	-0.938	-0.926**	-1.023**
	CD 1%	**0.223**	**0.072**	**0.084**	**0.156**	**0.252**	**0.102**	**0.024**	**1.508**	**0.610**	**0.822**
	CD 5%	**0.169**	**0.055**	**0.064**	**0.119**	**0.191**	**0.078**	**0.018**	**1.146**	**0.463**	**0.625**

NLF – Number of locules per fruit, PT – Pericarp thickness, DSC – Diameter of stalk scar, FF – Fruit firmness, TSS – Total soluble solids, pH – pH of fruit juice, TA – Titratable acidity, AA – Ascorbic acid and TC – Total carotenoids.

Table 4.42: Estimation of specific combining ability effects for different quality traits in F_1's of diallel cross of tomato

S. N.	Name of crosses	Character									
		NLF	PT	DSC	FF	TSS	pH	TA	AA	Lycopene	TC
1	PCT-1 x PPT-2	-0.022	0.206**	0.222*	0.139	-0.046	-0.161	0.166**	-0.565	-0.212	-0.234
2	PCT-1 x PBT-9	0.844**	0.080	0.584**	0.221	0.330	-0.187	0.016	-3.240*	-0.167	-0.725
3	PCT-1 x PBT-5	-0.189	0.280**	0.442**	0.344*	0.550*	-0.028	0.084**	-0.463	0.88	2.347**
4	PCT-1 x PBT-2	-0.489*	-0.134	-0.148	-0.09	0.137	-0.169	-0.087**	-2.087	0.643	1.051
5	PCT-1 x PBT-13	-0.556*	-0.127	-0.239**	-0.785**	-0.420	-0.086	-0.015	-0.019	0.338	-0.815
6	PCT-1 x PBT-10	0.311	0.038	-0.180*	0.363*	0.330	-0.009	0.031	0.027	0.713	1.031
7	PCT-1 x PBT-4	-0.256	0.072	0.227**	-0.049	-1.276**	-0.147	-0.049	-2.891	0.548	-0.373
8	PPT-2 x PBT-9	-0.356	-0.107	-0.194*	-0.129	0.120	-0.132	-0.030	0.744	-2.394**	-4.337**
9	PPT-2 x PBT-5	-0.056	0.040	0.024	-0.593**	-0.493	-0.036	-0.001	1.245	-0.724	-1.492
10	PPT-2 x PBT-2	-0.689**	-0.001	0.468**	0.253	0.127	0.136	0.061*	-0.600	-0.581	-0.185
11	PPT-2 x PBT-13	0.578*	-0.087	-0.317**	0.512**	0.337	-0.114	-0.024	-1.535	0.708	2.063*
12	PPT-2 x PBT-10	0.444	0.184*	0.429**	-0.150	-0.080	-0.017	0.065**	0.391	1.963**	2.876**
13	PPT-2 x PBT-4	-0.122	0.206**	0.056	-0.006	0.280	0.062	-0.002	3.819*	2.217**	3.679**
14	PBT-9 x PBT-5	1.144**	0.021	0.293**	1.089**	0.150	-0.095	-0.005	1.959	1.018	1.730*
15	PBT-9 x PBT-2	-0.822**	0.333**	-0.216*	0.435**	0.170	0.240*	-0.023	0.395	-0.522	0.094
16	PBT-9 x PBT-13	-0.556*	-0.033	-0.114	0.387*	0.180	0.126	-0.021	2.183	-1.617*	-1.141
17	PBT-9 x PBT-10	0.311	-0.248**	-0.115	-0.291	0.364	0.027	0.022	2.506	0.781	1.794*
18	PBT-9 x PBT-4	-0.256	0.166*	0.145	0.243	0.157	0.076	0.048	0.644	1.929**	3.281**
19	PBT-5 x PBT-2	0.144	-0.093	0.228**	-0.842**	0.024	-0.087	0.059*	-0.384	-0.349	-0.154
20	PBT-5 x PBT-13	-0.589*	-0.252**	-0.564**	-0.113	0.300	-0.151	0.088**	0.351	1.603*	2.150*
21	PBT-5 x PBT-10	-0.389	0.052	0.269**	-0.368*	0.250	-0.074	-0.033	2.060	0.688	2.326**
22	PBT-5 x PBT-4	-0.289	-0.026	0.302**	-0.301	-0.723**	0.225*	-0.066**	-0.469**	-0.818	-1.778*
23	PBT-2 x PBT-13	1.111**	0.006	0.007	0.686**	0.220	-0.336**	0.063*	4.006*	0.699	-0.442
24	PBT-2 x PBT-10	1.644**	-0.269**	0.020	0.011	-0.130	-0.195	-0.031	-1.114	-1.263*	-2.197**
25	PBT-2 x PBT-4	0.078	0.239**	-0.194*	0.242	0.230	-0.280**	0.102**	1.354	-1.415*	-2.727**
26	PBT-13 x PBT-10	-0.089	0.298**	0.942**	0.083	-1.286**	0.058	-0.069**	-1.886	-2.197**	-3.782**
27	PBT-13 x PBT-4	0.011	-0.034	0.295**	-0.106	0.274	0.136	-0.079**	-1.245	1.911**	3.728**
28	PBT-10 x PBT-4	0.211	-0.222**	-0.312**	0.005	0.176	-0.103	-0.013	-0.645	-1.488*	-0.417
	CD 1%	**0.593**	**0.193**	**0.223**	**0.417**	**0.672**	**0.273**	**0.064**	**4.021**	**1.626**	**2.193**
	CD 5%	**0.451**	**0.147**	**0.169**	**0.317**	**0.510**	**0.207**	**0.049**	**3.055**	**1.235**	**1.666**

NLF – Number of locules per fruit, PT – Pericarp thickness, DSC – Diameter of stalk scar, FF – Fruit firmness, TSS – Total soluble solids, pH – pH of fruit juice, TA – Titratable acidity, AA – Ascorbic acid and TC – Total carotenoids.

The estimates of SCA effects for pH of fruit juice ranged from -0.336 to 0.240. Out of twenty eight crosses significant SCA effects for same traits were observed in four cross combinations whereas, among them two crosses namely PBT-2 x PBT-13 (-0.336) and PBT-2 x PBT-4 (-0.280) exhibited desirable significant negative SCA effect for pH of fruit juice. These results are in close agreement with those reported by Basavraj *et al*. (2016) and Triveni *et al*. (2017).

4.5.2.2.7 Titratable acidity (%)

Data presented in Table 4.41 revealed that GCA effects for titratable acidity ranged from -0.044 to 0.084. Out of all parents, significant GCA effect was observed for six parents and among them desirable significant positive effect was exhibited by two parents namely PCT-1 (0.084) and PBT-13 (0.024) for titratable acidity.

The estimates of SCA effects for titratable acidity ranged from -0.087 to 0.166. Out of twenty eight crosses significant SCA effects for same traits were observed in twelve cross combinations whereas, among them eight crosses exhibited desirable significant positive SCA effect. Top five hybrids showed desirable significant SCA effect for titratable acidity were PCT-1 x PPT-2 (0.166), PBT-2 x PBT-4 (0.102), PBT-5 x PBT-13 (0.088), PCT-1 x PBT-5 (0.084) and PPT-2 x PBT-10 (0.065). Similar results have been reported by Mondal *et al*. (2009), Cheema *et al*. (2014), Dagade *et al*. (2015), Kumar *et al*. (2015) and Savale and Patel (2017).

.4.5.2.2.8 Ascorbic acid (mg/100g)

The estimates of GCA effects for ascorbic acid ranged from -1.575 to 3.113. Out of eight parents, three parents exhibited significant GCA effect for same trait and among them two parents *viz*., PCT-1 (3.113) and PPT-2 (1.239) showed desirable significant positive GCA effect for ascorbic acid.

The perusal of data revealed that range of SCA effects for ascorbic acid was -3.240 to 4.006. Out of twenty eight crosses significant SCA effects for same trait was observed in four cross combinations whereas, among them two crosses namely PBT-2 x PBT-13 (4.006) and PPT-2 x PBT-4 (3.819) exhibited desirable significant positive SCA effect for ascorbic acid. Similar results have been reported by Joshi and Kohli (2006), Dagade *et al*. (2015), Triveni *et al*. (2017), Raj *et al*. (2017) and Savale and Patel (2017).

4.5.2.2.9 Lycopene (mg/100g)

The read-through of data presented in the Table 4.41 revealed that GCA effect for lycopene ranged from -1.215 to 1.570. Among all parents, seven parents showed significant GCA effect for same trait. Desirable significant positive GCA effects was observed among three parents for lycopene which were PPT-2 (1.570), PBT-10 (1.022) and PBT-5 (0.488).

The estimates of SCA effects for lycopene ranged from -2.394 to 2.217. Out of twenty eight crosses significant SCA effects for same traits were observed in eleven cross combinations while, among them five crosses namely PPT-2 x PBT-4 (2.217), PPT-2 x PBT-10 (1.963), PBT-9 x PBT-4 (1.929), PBT-13 x PBT-4 (1.911) and PBT-5 x PBT-13 (1.603) exhibited desirable significant positive SCA effect for lycopene. These results are in close agreement with those reported by Mondal *et al*. (2009), Narasimhamurthy *et al*. (2013), Cheema *et al*. (2014), Dagade *et al*. (2015), Kumar *et al*. (2015), Basavraj *et al*. (2016), Triveni *et al*. (2017) and Savale and Patel (2017).

4.5.2.2.10 Total carotenoids (mg/100g)

The perusal of data revealed that range of GCA effect for total carotenoids was -2.450 to 2.805. Among all eight parents, significant GCA effect was observed for six parents and two parents *i.e*., PPT-2 (2.805) and PBT-10 (2.007) exhibited desirable significant positive GCA effect for total carotenoids.

The read-through of data presented in Table 4.42 revealed that range of SCA for total carotenoids ranged from -4.337 to 3.728. Out of all crosses, fifteen cross combinations exhibited significant SCA effect for same trait and among them nine hybrids showed desirable significant positive SCA effect. Top five hybrids exhibited desirable significant positive SCA effects for total carotenoids were PBT-13 x PBT-4 (3.728), PPT-2 x PBT-4 (3.679), PBT-9 x PBT-4 (3.281), PPT-2 x PBT-10 (2.876) and PCT-1 x PBT-5 (2.347). The findings of Kumar *et al*. (2015) are in accordance with the results obtained above.

The ranking of genotypes for yield related and quality traits were made as per the general combining ability and specific combining ability of diallel cross (excluding reciprocal) and presented in Table 43 and Table 44. PCT-1 was identified as a best general combiner for maximum number of traits *viz*., earliness related traits, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, plant height,

diameter of stalk scar, TSS, pH of fruit juice, titratable acidity and ascorbic acid followed by PBT-5 (for earliness related traits, number of flowers per cluster, number of fruits per cluster, internodal length, fruit yield per plant, fruit yield per hectare, fruit firmness and lycopene), PPT-2 (for internodal length, average fruit weight, fruit length, fruit yield per plant, fruit yield per hectare, TSS, ascorbic acid, lycopene and total carotenoids), PBT-2 (For earliness related traits, 100 seed weight and number of locules per fruit), PBT-4 (for average fruit weight, fruit length, fruit shape index, pericarp thickness and fruit firmness), PBT-10 (for fruit width, 100 seed weight, number of locules per fruit, lycopene and total carotenoids), PBT-13 (for 100 seed weight, number of locules per fruit, fruit firmness and titratable acidity) and PBT-9 (for internodal length, average fruit weight and fruit width).

On the basis of ranking best specific combiner were PBT-2 x PBT-13 (days to first fruit ripening, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit yield per plant, fruit yield per hectare, number of locules per fruit, fruit firmness, pH of fruit juice and ascorbic acid), PBT-13 x PBT-10 (days to 50 per cent flowering, days to first fruit set, average fruit weight, fruit length, fruit width, fruit yield per plant, fruit yield per hectare and pericarp thickness), PBT-9 x PBT-5 (days to first fruit ripening, average fruit weight, fruit length, fruit width, number of locules per fruit and fruit firmness), PCT-1 x PBT-5 (number of flowers per cluster, number of fruit per cluster, fruit yield per plant, fruit yield per hectare, pericarp thickness and TSS), PBT-9 x PBT-4 (number of flowers per cluster, number of fruits per plant, internodal length, lycopene and total carotenoids), PBT-9 x PBT-2 (days to 50 per cent flowering, days to first fruit set, days to first fruit ripening and pericarp thickness), PBT-5 x PBT-13 (days to 50 per cent flowering, diameter of stalk scar and titratable acidity), PBT-5 x PBT-4 (number of flowers per cluster, number of fruits per cluster and number of fruits per plant), PBT-2 x PBT-4 (fruit shape index, pH of fruit juice and titratable acidity), PPT-2 x PBT-4 (ascorbic acid, lycopene and total carotenoids), PCT-1 x PBT-4 (days to first fruit set and fruit length), PCT-1 x PBT-2 (internodal length and 100 seed weight), PBT-10 x PBT-4 (internodal length and diameter of stalk scar), PBT-13 x PBT-4 (fruit width and total carotenoids), PCT-1 x PPT-2 (100 seed weight and titratable acidity), PPT-2 x PBT-13 (diameter of stalk scar and fruit firmness), PCT-1 x PBT-13 (100 seed weight), PBT-2 x PBT-10 (number of locules per fruit) and PPT-2 x PBT-10 (lycopene).

Table 4.43: Top three tomato genotypes as per GCA and SCA and *per se* performance with respect to each yield related traits

S.N.	Characters	Best general combiners	Best specific combiners
1	**Days to 50% flowering**	PBT-2 PCT-1 PBT-5	PBT-13 x PBT-10 PBT-5 x PBT-13 PBT-9 x PBT-2
2	**Days to first fruit set**	PBT-5 PCT-1 PBT-2	PBT-13 x PBT-10 PCT-1 x PBT-4 PBT-9 x PBT-2
3	**Days to first fruit ripening**	PCT-1 PBT-5 PBT-2	PBT-2 x PBT-13 PBT-9 x PBT-5 PBT-9 x PBT-2
4	**No. of flowers/cluster**	PCT-1 PBT-5	PCT-1 x PBT-5 PBT-5 x PBT-4 PBT-9 x PBT-4
5	**No. of fruits/cluster**	PCT-1 PBT-5	PCT-1 x PBT-5 PBT-2 x PBT-13 PBT-5 x PBT-4
6	**No. of fruits/plant**	PCT-1	PBT-5 x PBT-4 PBT-9 x PBT-4 PBT-2 x PBT-13
7	**Internodal length**	PBT-5 PBT-9 PPT-2	PBT-9 x PBT-4 PCT-1 x PBT-2 PBT-10 x PBT-4
8	**Avg. fruit wt.**	PPT-2 PBT-9 PBT-4	PBT-13 x PBT-10 PBT-9 x PBT-5 PBT-2 x PBT-13
9	**Fruit length**	PBT-4 PPT-2	PBT-13 x PBT-10 PBT-9 x PBT-5 PCT-1 x PBT-4
10	**Fruit width**	PBT-10 PBT-9	PBT-13 x PBT-10 PBT-9 x PBT-5 PBT-13 x PBT-4
11	**Fruit shape index**	PBT-4	PBT-2 x PBT-4
12	**Plant height**	PCT-1	-
13	**100 seed wt.**	PBT-2 PBT-10 PBT-13	PCT-1 x PBT-13 PCT-1 x PPT-2 PCT-1 x PBT-2
14	**Fruit yield/plant**	PPT-2 PBT-5	PCT-1 x PBT-5 PBT-2 x PBT-13 PBT-13 x PBT-10
15	**Fruit yield/ha**	PPT-2 PBT-5	PCT-1 x PBT-5 PBT-2 x PBT-13 PBT-13 x PBT-10

Table 4.44: Top three tomato genotypes as per GCA and SCA and *per se* performance with respect to each quality traits

S.N.	Characters	Best general combiners	Best specific combiners
1	**No. of locules/fruit**	PBT-2 PBT-10 PBT-13	PBT-2 x PBT-10 PBT-9 x PBT-5 PBT-2 x PBT-13
2	**Pericarp thickness**	PBT-4	PBT-9 x PBT-2 PBT-13 x PBT-10 PCT-1 x PBT-5
3	**Diameter of stalk scar**	PCT-1	PBT-5 x PBT-13 PPT-2 x PBT-13 PBT-10 x PBT-4
4	**Fruit firmness**	PBT-13 PBT-4 PBT-5	PBT-9 x PBT-5 PBT-2 x PBT-13 PPT-2 x PBT-13
5	**TSS**	PCT-1 PPT-2	PCT-1 x PBT-5
6	**pH of fruit juice**	PCT-1	PBT-2 x PBT-13 PBT-2 x PBT-4
7	**Titratable acidity**	PCT-1 PBT-13	PCT-1 x PPT-2 PBT-2 x PBT-4 PBT-5 x PBT-13
8	**Ascorbic acid**	PCT-1 PPT-2	PBT-2 x PBT-13 PPT-2 x PBT-4
9	**Lycopene**	PPT-2 PBT-10 PBT-5	PPT-2 x PBT-4 PPT-2 x PBT-10 PBT-9 x PBT-4
10	**Total carotenoids**	PPT-2 PBT-10	PBT-13 x PBT-4 PPT-2 x PBT-4 PBT-9 x PBT-4

4.5.3 Variance components of combining ability

4.5.3.1 Yield related traits

The estimates of variance components of general combining ability (σ^2gca), specific combining ability (σ^2sca), error variance (σ^2error), additive variance σ^2A (D), dominant variance σ^2D (H), GCA/SCA ratio and degree of dominance for yield related traits are shown in Table 4.45. Highest GCA variance was observed for number of fruits per plant (2316.342) followed by plant height (984.138), average fruit weight (933.688) and fruit yield per hectare (304.405). Rest of the characters showed relatively smaller amount of GCA variance.

Maximum variance for SCA was observed for the trait fruit yield per hectare (6778.369) followed by plant height (5514.320), number of fruits per plant (5073.424) and average fruit weight (2463.309). However, rest of the characters showed relatively smaller amount of SCA variance.

The magnitude of specific combining ability variance was higher than the general combining ability variance for all yield related traits. This result indicated predominance of non-additive gene action for all yield related characters.

Highest additive variance was reported in number of fruits per plant (4632.684), plant height (1968.276), average fruit weight (1867.376) and fruit yield per hectare (608.810) while, rest of the characters exhibited relatively smaller amount of additive variance. Maximum dominant variance was found for the traits fruit yield per hectare (6778.369), plant height (5514.320), number of fruits per plant (5073.424) and average fruit weight (2463.309).

It was observed that the magnitude of degree of dominance was more than unity for most of the traits, days to 50 per cent flowering, days to first fruit set, days to first fruit ripening, number of flowers per cluster, number of fruits per plant, internodal length, average fruit weight, fruit width, plant height, 100 seed weight, fruit yield per plant and fruit yield per hectare, which indicates over dominance type of gene action for these traits. For remaining characters *i.e*., number of fruits per cluster, fruit length and fruit shape index degree of dominance was less than unity, thereby indicating partial dominance type of gene actions.

Table 4.45 Estimates of genetic components of variances for various yield related traits of tomato in diallel cross of eight parents

Genetic components	DFF	DFFS	DFFR	NFC	NFRC	NFP	IL	AFW	FL	FW	FSI	PH	SW	FYP	FYH
σ^2 (gca)	8.670	11.426	25.090	11.583	3.450	2316.342	0.968	933.688	0.925	0.653	0.023	984.138	0.002	0.246	304.405
σ2 (sca)	21.571	26.322	53.793	25.636	6.724	5073.424	5.388	2463.309	1.068	1.316	0.040	5514.320	0.005	5.473	6778.369
σ2 error	5.415	4.732	2.889	0.775	0.268	79.966	0.821	42.301	0.069	0.131	0.012	1646.279	0.000	0.181	224.121
σ2 A (D)	17.340	22.852	50.180	23.166	6.900	4632.684	1.936	1867.376	1.850	1.306	0.046	1968.276	0.004	0.492	608.810
σ2 D (H)	21.571	26.322	53.793	25.636	6.724	5073.424	5.388	2463.309	1.068	1.316	0.040	5514.320	0.005	5.473	6778.369
σ2 (gca)/σ2 (sca) ratio	0.402	0.434	0.466	0.452	0.513	0.457	0.180	0.379	0.866	0.496	0.565	0.178	0.361	0.045	0.045
Degree of dominance	1.115	1.073	1.035	1.052	0.987	1.046	1.668	1.149	0.760	1.004	0.943	1.674	1.291	3.335	3.337

DFF – Days to 50 per cent flowering, DFFS – Days to first fruit set, DFFR – Days to first fruit ripening, NFC – Number of flowers per cluster, NFRC – Number of fruits per cluster, NFP – Number of fruits per plant, IL – Internodal length, AFW – Average fruit weight, FL – Fruit length, FW – Fruit width, FSI – Fruit shape index, PH – Plant height, SW – 100 seed weight, FYP – Fruit yield per plant and FYH – Fruit yield per hectare.

4.5.3.2 Quality traits

Variance components of combining ability for quality traits are shown in Table 4.46. Highest GCA variance was observed for total carotenoids (9.126) followed by titratable acidity (6.306) and lycopene (2.980). Rest of the characters showed relatively smaller amount of GCA variance.

Maximum variance for SCA was observed for the trait total carotenoids (15.108), titratable acidity (9.585), lycopene (5.072) and number of locules per fruit (1.155). However, rest of the characters showed relatively smaller amount of SCA variance.

The magnitude of specific combining ability variance was higher than the general combining ability variance for all quality traits except fruit firmness. This result indicated predominance of non-additive gene action for all quality characters except fruit firmness.

Highest additive variance was reported in total carotenoids (18.324), titratable acidity (12.612), lycopene (5.960) and fruit firmness (1.438) while, rest of the characters exhibited relatively smaller amount of additive variance. Maximum dominant variance was found for the traits total carotenoids (15.108) followed by titratable acidity (9.585), lycopene (5.072) and number of locules per fruit (1.155) and rest of the traits showed relatively less dominant variance.

It was observed that the magnitude of degree of dominance was more than unity for most of the traits, number of locules per fruit, pericarp thickness, diameter of stalk scar, TSS, pH of fruit juice and ascorbic acid, which indicates over dominance type of gene action for these traits. For remaining characters *i.e.*, fruit firmness, titratable acidity, lycopene and total carotenoids degree of dominance was less than unity, thereby indicating partial dominance type of gene actions.

Results presented earlier by Dutta *et al*. (2013), Nadeem *et al*. (2013), Shankar *et al*. (2013), Figueiredo *et al*. (2015), Hamada *et al*. (2016) and Sikder *et al*. (2016) also indicated preponderance of non-additive gene action in the expression of various quantitative traits.

Table 4.46 Estimates of genetic components of variances for various quality traits of tomato in diallel cross of eight parents

Genetic components	NLF	PT	DSC	FF	TSS	pH	TA	AA	Lycopene	TC
σ^2 (gca)	0.248	0.012	0.026	0.719	0.008	0.005	6.306	0.286	2.980	9.162
σ2 (sca)	1.155	0.096	0.424	0.632	0.087	0.013	9.585	0.622	5.072	15.108
σ2 error	0.085	0.009	0.012	0.109	0.018	0.001	3.904	0.042	0.638	1.161
σ2 A (D)	0.496	0.024	0.052	1.438	0.016	0.010	12.612	0.572	5.960	18.324
σ2 D (H)	1.155	0.096	0.424	0.632	0.087	0.013	9.585	0.622	5.072	15.108
σ2 (gca)/σ2 (sca) ratio	0.214	0.126	0.061	1.138	0.092	0.392	0.658	0.460	0.588	0.606
Degree of dominance	1.528	2.000	2.883	0.663	2.332	1.140	0.872	1.043	0.923	0.908

NLF – Number of locules per fruit, PT – Pericarp thickness, DSC – Diameter of stalk scar, FF – Fruit firmness, TSS – Total soluble solids, pH – pH of fruit juice, TA – Titratable acidity, AA – Ascorbic acid and TC – Total carotenoids.

Table 4.47 Summary table for gene action in different yield related traits

S. N.	Characters	Gene action
1	Days to 50 per cent flowering	Non additive, over dominance
2	Days to first fruit set	Non additive, over dominance
3	Days to first fruit ripening	Non additive, over dominance
4	Number of flowers per cluster	Non additive, over dominance
5	Number of fruits per cluster	Non additive, partial dominance
6	Number of fruits per plant	Non additive, over dominance
7	Internodal length	Non additive, over dominance
8	Average fruit weight	Non additive, over dominance
9	Fruit length	Non additive, partial dominance
10	Fruit width	Non additive, over dominance
11	Fruit shape index	Non additive, partial dominance
12	Plant height	Non additive, over dominance
13	100 seed weight	Non additive, over dominance
14	Fruit yield per plant	Non additive, partial dominance
15	Fruit yield per hectare	Non additive, partial dominance

Table 4.48 Summary table for gene action in different quality traits

S. N.	Characters	Gene action
1	Number of locules per fruit	Non additive, over dominance
2	Pericarp thickness	Non additive, over dominance
3	Diameter of stalk scar	Non additive, over dominance
4	Fruit firmness	Additive, partial dominance
5	Total soluble solids (TSS)	Non additive, over dominance
6	pH of fruit juice	Non additive, over dominance
7	Titratable acidity	Non additive, partial dominance
8	Ascorbic acid	Non additive, over dominance
9	Lycopene	Non additive, partial dominance
10	Total carotenoids	Non additive, partial dominance

The summary of gene action for different yield related and quality traits are presented in Table 4.47 and 4.48 respectively, it may be concluded among yield related traits, days to 50 per cent flowering, days to first fruit set, days to first fruit ripening, number of flowers per cluster, number of fruits per plant, internodal length, average fruit weight, fruit width, plant height and 100 seed weight were under the control of non additive gene action with over dominance effect and number of fruits per cluster, fruit length, fruit shape index, fruit yield per plant and fruit yield per hectare were non additive with partial dominance effect, hence these characters are suitable for hybrid breeding.

Among quality traits, number of locules per fruit, pericarp thickness, diameter of stalk scar, TSS, pH of fruit juice and ascorbic acid were under the control of non additive gene action with over dominance effect while, titratable acidity, lycopene and total carotenoids were under the non additive with partial dominance effect, hence these characters are also suitable for hybrid breeding. One character *i.e.*, fruit firmness were under the control of additive gene action with partial dominance effect, hence this character could be improved by selection procedures.

4.6 Screening of parents and F_1 hybrids of tomato against late blight (*Phytophthora infestans*)

4.6.1 Symptomatology

During the study, irregularly shaped water soaked lesions observed on the leaves. Under humid conditions, white downy growth of the fungus appeared on the affected areas of the lower surface of leaves. Eventually the leaves shriveled, became necrotic and died. Brown lesions occurred on stems and leaf pedicels. The pathogen also infects tomato fruits and caused circular greasy lesions. The fruits remain firm but spots eventually become leathery, chocolate brown and enlarge to cover the entire fruit (Plate 6).

4.6.2 Late blight incidence (%) under polyhouse condition

All eight parents (PCT-1 as a resistant check) and twenty eight F_1 hybrids were evaluated in three replication. In each replication disease incidence for late blight was recorded for all twelve plants. The first symptom of late blight was observed on 16 December 2016 five days after post-inoculation of suspension (11 December 2016) in three parents and six hybrids. The results of late blight incidence (%) for all parents and

(a)

(b)

(c)

(d)

Plate 6 Various symptoms of late blight in tomato: (a) Leaf, (b) flower truss, (c) stem and (d) fruit

F_1 hybrids presented in Table 4.49. Data revealed significant variable reactions of different parents and F_1 hybrids against late blight incidence in present experiment taken at 15, 30, 45, 60, 75 and 90 days after initiation (DAI) of disease. The details of disease incidence are given below.

4.6.2.1 Late blight incidence at 15 DAI

Mean disease incidence at 15 DAI revealed that the range of disease incidence among all genotypes ranged from 2.78 to 27.78 per cent and general mean was 13.81 per cent. Two parents and fifteen crosses gave less late blight incidence than population mean. Minimum late blight incidence was reported in check, PCT-1 (2.78%) and it was found statistically at par with one parent PPT-2 (8.33%) and seven hybrids namely PCT-1 x PBT-10 (5.56%), PPT-2 x PBT-5 (5.56%), PCT-1 x PBT-5 (8.33%), PCT-1 x PBT-2 (8.33%), PPT-2 x PBT-9 (8.33%), PPT-2 x PBT-4 (8.33%) and PBT-5 x PBT-10 (8.33%).

While, maximum incidence of late blight was observed in PBT-9 (27.78%) and it was statistically at par with five parents PBT-5 (22.22%), PBT-13 (22.22%), PBT-2 (19.44), PBT-4 (19.44%) and PBT-10 (13.89%) and thirteen cross combinations PBT-5 x PBT-13 (22.22%), PBT-5 x PBT-4 (22.22%), PBT-10 x PBT-4 (19.44%), PBT-9 x PBT-5 (19.44%), PBT-9 x PBT-13 (19.44%), PPT-2 x PBT-13 (16.67%), PBT-13 x PBT-4 (16.67%), PCT-1 x PBT-9 (13.89%), PPT-2 x PBT-2 (13.89%), PPT-2 x PBT-10 (13.89%), PBT-9 x PBT-2 (13.89%), PBT-9 x PBT-4 (13.89%) and PBT-2 x PBT-10 (13.89%)

4.6.2.2 Late blight incidence at 30 DAI

Perusal of data revealed that mean late blight incidence at 30 DAI ranged from 13.89 to 41.67 per cent and general mean of incidence was 27.24 per cent. Three parents and fifteen crosses gave less late blight incidence than population mean. Minimum late blight incidence was reported in check parent PCT-1, cross PCT-1 x PBT-5 and PCT-1 x PBT-10 with 13.89 per cent. This was found statistically at par with two parents, PPT-2 (19.44%) and PBT-10 (22.22%) and nine hybrids namely PCT-1 x PBT-2 (16.67%), PPT-2 x PBT-9 (16.67%), PPT-2 x PBT-5 (16.67%), PCT-1 x PPT-2 (19.44%), PPT-2 x PBT-4 (19.44%), PBT-5 x PBT-10 (19.44%), PCT-1 x PBT-9 (22.22%), PBT-9 x PBT-10 (22.22%) and PBT-2 x PBT-10 (22.22%).

Maximum incidence of late blight was observed in three crosses, PBT-9 x PBT-13, PBT-5 x PBT-13 and PBT-5 x PBT-4 with 41.67 per cent incidence. This was found statistically at par with five parents PBT-13 (38.89%), PBT-9 (36.11%), PBT-5 (36.11), PBT-2 (33.33%) and PBT-4 (30.56%) and eight hybrids namely PBT-13 x PBT-4 (38.89%), PPT-2 x PBT-13 (36.11%), PBT-9 x PBT-5 (36.11%), PBT-2 x PBT-13 (33.33%), PBT-9 x PBT-2 (30.56%), PBT-5 x PBT-2 (30.56%), PBT-2 x PBT-4 (30.56%) and PBT-10 x PBT-4 (30.56%). Amongst all the genotypes under study, two crosses namely PCT-1 x PBT-5 and PCT-1 x PBT-10 recorded equal late blight incidence than check cultivar.

4.6.2.3 Late blight incidence at 45 DAI

The read-through data of disease incidence revealed that range for incidence was 16.67 to 55.56 per cent with the general mean 38.50 per cent. Three parents and thirteen crosses gave less late blight incidence than population mean. Minimum late blight incidence was reported in cross PCT-1 x PBT-5 (16.67%) and it was found statistically at par with one parent and five hybrids namely PCT-1 (22.22%), PCT-1 x PBT-2 (22.22%), PCT-1 x PBT-10 (22.22%), PPT-2 x PBT-9 (25.00%), PPT-2 x PBT-5 (25.00%) and PBT-5 x PBT-10 (25.00%).

While, maximum incidence of late blight was observed in one parent and three cross combinations *viz*., PBT-13 (55.56%), PBT-9 x PBT-13 (55.56%), PBT-5 x PBT-13 (55.56%) and PBT-5 x PBT-4 (55.56%). This was statistically at par with three parents PBT-5 (50.00%), PBT-9 (47.22%) and PBT-2 (47.22%) and four hybrids namely PPT-2 x PBT-13 (50.00%), PBT-9 x PBT-5 (50.00%), PBT-13 x PBT-4 (50.00%) and PBT-5 x PBT-2 (47.22%). Amongst all the genotypes under study, one cross PCT-1 x PBT-5 recorded less incidence and two crosses *i.e*., PCT-1 x PBT-2 and PCT-1 x PBT-10 recorded equal late blight incidence than check cultivar.

4.6.2.4 Late blight incidence at 60 DAI

Mean disease incidence at 60 DAI ranged from 19.44 to 69.44 per cent with general mean 46.14 per cent. Three parents and thirteen crosses gave less late blight incidence than population mean. Minimum late blight incidence was reported in cross PCT-1 x PBT-5 (19.44%) and it was found statistically at par with one parent PCT-1 (25.00%) and three hybrids namely PCT-1 x PBT-2 (27.78%), PCT-1 x PBT-10 (27.78%) and PPT-2 x PBT-5 (27.78%).

Table 4.49: Late blight incidence in tomato under polyhouse condition

S. N.	Genotypes	Incidence (%)					
		15 DAI	30 DAI	45 DAI	60 DAI	75 DAI	90 DAI
1	PCT-1	2.78 (5.59)	13.89 (21.65)	22.22 (28.02)	25.00 (29.78)	27.78 (31.74)	27.78 (31.74)
2	PPT-2	8.33 (13.62)	19.44 (26.05)	27.78 (31.74)	38.89 (38.54)	44.44 (41.79)	47.22 (43.38)
3	PBT-9	27.78 (31.74)	36.11 (36.90)	47.22 (43.38)	55.56 (48.18)	61.11 (51.42)	66.67 (54.82)
4	PBT-5	22.22 (28.02)	36.11 (36.90)	50.00 (44.98)	55.56 (48.18)	63.89 (53.22)	72.22 (58.22)
5	PBT-2	19.44 (26.05)	33.33 (35.14)	47.22 (43.38)	58.33 (49.82)	63.89 (53.07)	66.67 (55.19)
6	PBT-13	22.22 (28.02)	38.89 (38.54)	55.56 (48.18)	66.67 (54.82)	75.00 (60.19)	80.56 (63.91)
7	PBT-10	13.89 (21.65)	22.22 (28.02)	33.33 (35.14)	38.89 (38.54)	44.44 (41.79)	47.22 (43.38)
8	PBT-4	19.44 (26.05)	30.56 (33.50)	44.44 (41.79)	52.78 (46.58)	61.11 (51.42)	66.67 (54.82)
9	PCT-1 x PPT-2	11.11 (19.21)	19.44 (25.58)	27.78 (31.74)	30.56 (33.50)	36.11 (36.90)	36.11 (36.90)
10	PCT-1 x PBT-9	13.89 (21.65)	22.22 (28.02)	33.33 (35.14)	38.89 (38.54)	41.67 (40.19)	47.22 (43.38)
11	PCT-1 x PBT-5	8.33 (13.62)	13.89 (21.65)	16.67 (24.09)	19.44 (26.05)	22.22 (28.02)	22.22 (28.02)
12	PCT-1 x PBT-2	8.33 (13.62)	16.67 (23.62)	22.22 (28.02)	27.78 (31.74)	27.78 (31.74)	30.56 (33.50)
13	PCT-1 x PBT-13	11.11 (19.21)	25.00 (29.78)	38.89 (38.54)	47.22 (43.38)	50.00 (44.98)	55.56 (48.18)
14	PCT-1 x PBT-10	5.56 (11.18)	13.89 (21.65)	22.22 (28.02)	27.78 (31.74)	30.56 (33.50)	33.33 (35.14)
15	PCT-1 x PBT-4	11.11 (19.21)	25.00 (29.78)	36.11 (36.90)	44.44 (41.79)	50.00 (44.98)	55.56 (48.23)
16	PPT-2 x PBT-9	8.33 (13.62)	16.67 (23.62)	25.00 (29.78)	30.56 (33.50)	36.11 (36.90)	38.89 (38.54)
17	PPT-2 x PBT-5	5.56 (11.18)	16.67 (23.62)	25.00 (29.78)	27.78 (31.74)	30.56 (33.50)	36.11 (36.90)
18	PPT-2 x PBT-2	13.89 (21.65)	27.78 (31.74)	38.89 (38.54)	47.22 (43.38)	50.00 (44.98)	52.78 (46.63)
19	PPT-2 x PBT-13	16.67 (23.62)	36.11 (36.90)	50.00 (44.98)	61.11 (51.42)	66.67 (54.82)	72.22 (58.22)

20	PPT-2 x PBT-10	13.89 (21.65)	25.00 (29.78)	38.89 (38.54)	44.44 (41.79)	47.22 (43.38)	52.78 (46.58)
21	PPT-2 x PBT-4	8.33 (13.62)	19.44 (25.58)	30.56 (33.50)	36.11 (36.90)	38.89 (38.49)	41.67 (40.10)
22	PBT-9 x PBT-5	19.44 (26.05)	36.11 (36.90)	50.00 (44.98)	58.33 (49.78)	63.89 (53.22)	69.44 (56.47)
23	PBT-9 x PBT-2	13.89 (21.65)	30.56 (33.50)	44.44 (41.79)	50.00 (44.98)	58.33 (49.82)	66.67 (55.19)
24	PBT-9 x PBT-13	19.44 (26.05)	41.67 (40.14)	55.56 (48.18)	63.89 (53.07)	69.44 (56.47)	77.78 (61.94)
25	PBT-9 x PBT-10	11.11 (19.21)	22.22 (28.02)	36.11 (36.90)	44.44 (41.79)	50.00 (44.98)	58.33 (49.82)
26	PBT-9 x PBT-4	13.89 (21.65)	27.78 (31.74)	41.67 (40.14)	50.00 (44.98)	61.11 (51.42)	63.89 (53.22)
27	PBT-5 x PBT-2	11.11 (19.21)	30.56 (33.50)	47.22 (43.38)	55.56 (48.23)	61.11 (51.42)	66.67 (55.19)
28	PBT-5 x PBT-13	22.22 (28.02)	41.67 (40.14)	55.56 (48.18)	69.44 (56.47)	77.78 (61.94)	83.33 (66.35)
29	PBT-5 x PBT-10	8.33 (13.62)	19.44 (25.58)	25.00 (29.78)	30.56 (33.50)	36.11 (36.90)	38.89 (38.54)
30	PBT-5 x PBT-4	22.22 (28.02)	41.67 (40.14)	55.56 (48.18)	63.89 (53.07)	72.22 (58.22)	80.56 (63.91)
31	PBT-2 x PBT-13	11.11 (19.21)	33.33 (35.14)	44.44 (41.74)	50.00 (44.98)	52.78 (46.58)	55.56 (48.23)
32	PBT-2 x PBT-10	13.89 (21.65)	22.22 (28.02)	27.78 (31.74)	38.89 (38.54)	44.44 (41.79)	47.22 (43.38)
33	PBT-2 x PBT-4	11.11 (19.21)	30.56 (33.50)	41.67 (40.19)	50.00 (44.98)	55.56 (48.23)	61.11 (51.42)
34	PBT-13 x PBT-10	11.11 (19.21)	25.00 (29.78)	36.11 (36.79)	47.22 (43.38)	52.78 (46.58)	55.56 (48.23)
35	PBT-13 x PBT-4	16.67 (23.62)	38.89 (38.54)	50.00 (44.98)	61.11 (51.42)	63.89 (53.22)	72.22 (58.22)
36	PBT-10 x PBT-4	19.44 (26.05)	30.56 (33.50)	41.67 (40.14)	52.78 (46.58)	61.11 (51.42)	63.89 (53.22)
	Mean	**13.81 (20.36)**	**27.24 (31.03)**	**38.50 (38.09)**	**46.14 (42.66)**	**51.39 (45.81)**	**55.86 (48.60)**
	± SE(m)	**3.92**	**2.49**	**2.19**	**2.17**	**2.50**	**3.16**
	CD(0.05)	**11.03**	**7.05**	**6.18**	**6.13**	**7.06**	**8.93**

Maximum incidence of late blight was observed in cross PBT-5 x PBT-13 (69.44%) and this was found statistically at par with one parent PBT-13 (66.67%) and four hybrids namely PBT-9 x PBT-13 (63.89%), PBT-5 x PBT-4 (63.89%), PPT-2 x PBT-13 (61.11%) and PBT-13 x PBT-4 (61.11%). Amongst all the genotypes under study, one cross PCT-1 x PBT-5 recorded less incidence and one cross PCT-1 x PBT-2 recorded equal late blight incidence than check cultivar.

4.6.2.5 Late blight incidence at 75 DAI

The read-through data of disease incidence revealed that range for incidence was 22.22 to 77.78 per cent and mean value was recorded 51.39 per cent. Three parents and fifteen crosses gave less late blight incidence than population mean. Minimum late blight incidence was reported in cross PCT-1 x PBT-5 (22.22%) and it was found statistically at par with one parent PCT-1 (27.78%) and three cross combinations namely PCT-1 x PBT-2 (27.78%), PCT-1 x PBT-10 (30.56%) and PPT-2 x PBT-5 (30.56%).

While, maximum incidence of late blight was observed in PBT-5 x PBT-13 (77.78%) and it was statistically at par with one parent PBT-13 (75.00%) and two cross combinations namely PBT-5 x PBT-4 (72.22%) and PBT-9 x PBT-13 (69.44%). Amongst all the genotypes under study, one cross PCT-1 x PBT-5 recorded less incidence and one cross PCT-1 x PBT-2 recorded equal late blight incidence than check cultivar (PCT-1).

4.6.2.6 Late blight incidence at 90 DAI

Perusal of data revealed that mean late blight incidence at 90 DAI ranged from 22.22 to 83.33 per cent with general mean value 55.86 per cent. Three parents and sixteen crosses gave less late blight incidence than population mean. Minimum late blight incidence was reported in cross PCT-1 x PBT-5 (22.22%) and it was found statistically at par with one parent PCT-1 (27.78%) and four hybrids namely PCT-1 x PBT-2 (30.56%), PCT-1 x PBT-10 (33.33%), PCT-1 x PPT-2 (36.11%) and PPT-2 x PBT-5 (36.11%).

Maximum incidence of late blight was observed in cross PBT-5 x PBT-13 (83.33%) and this was found statistically at par with two parents PBT-13 (80.56%) and PBT-5 (72.22%) and four hybrids namely PBT-5 x PBT-4 (80.56%), PBT-9 x PBT-13

(77.78%), PPT-2 x PBT-13 (72.22%) and PBT-13 x PBT-4 (72.22%). Amongst all the genotypes under study, one cross PCT-1 x PBT-5 recorded less incidence of late blight than check cultivar (PCT-1).

In tomato similar findings were also reported by other researchers. Islam *et al.* (2001) assessed fifteen advanced lines of tomato including two checks. The highest late blight disease incidence was found in V-52 and V-215 and the lowest in V-378. Meya *et al.* (2015) observed significant differences in diseases incidence among three tomato varieties: Cal J, Meru and Tanya whereby Cal J and Tanya were susceptible to tomato late blight while, tomato variety Meru was resistant.

4.6.3 Late blight disease severity under polyhouse condition

All eight parents (PCT-1 as a resistant check) and twenty eight F_1 hybrids were evaluated for late blight severity (%) in three replications. In each replication five plants were selected and disease severity for late blight was recorded. The results of late severity (%) for all parents and F_1 hybrids are presented in Table 4.50. Data of disease reactions of different parents and F_1 hybrids against late blight severity in present experiment taken at 10, 20, 30, 40, 50, 60, 70, 80, 90 and 100 days after initiation (DAI) of disease and the details of observations are given below.

4.6.3.1 Late blight severity at 10 DAI

Mean disease severity at 10 DAI revealed that the range of disease severity among all genotypes ranged from 0.00 to 6.67 per cent with an average value 3.07 per cent. Three parents and sixteen crosses gave less late blight severity than population mean. Minimum late blight severity (0.00%) was reported in check parent PCT-1 and six hybrids namely PCT-1 x PPT-2, PCT-1 x PBT-5, PCT-1 x PBT-2, PCT-1 x PBT-13, PCT-1 x PBT-10 and PBT-9 x PBT-2 and this was found statistically at par with two parents and three crosses *i.e.*, PPT-2 (1.33%), PBT-10 (1.33), PPT-2 x PBT-2 (1.33%), PPT-2 x PBT-13 (1.33%) and PBT-13 x PBT-10 (1.33%).

Maximum severity of late blight was observed in PBT-4 (6.67%) and PBT-9 x PBT-5 (6.67%). This was found statistically at par with two parents PBT-2 (5.33%) and PBT-13 (5.33%) and seven hybrids were namely PBT-9 x PBT-13 (5.33%), PBT-5 x PBT-2 (5.33%), PBT-5 x PBT-13 (5.33%), PBT-5 x PBT-4 (5.33%), PBT-2 x PBT-13

(5.33%), PBT-2 x PBT-4 (5.33%) and PBT-13 x PBT-4 (5.33%). Six cross combinations recorded equal severity than check parent.

4.6.3.2 Late blight severity at 20 DAI

Perusal of data revealed that mean late blight severity ranged from 0.00 to 8.00 per cent with a mean severity 4.74 per cent. Three parents and eleven crosses gave less late blight severity than population mean. Minimum late blight severity (0.00%) was reported in check parent PCT-1 and two cross combinations *i.e.*, PCT-1 x PBT-2 and PCT-1 x PBT-10. This was found statistically at par with one parent PPT-2 (1.33%) and three hybrids namely PCT-1 x PBT-5 (1.33%), PCT-1 x PBT-13 (1.33%) and PBT-9 x PBT-2 (1.33%).

Maximum severity of late blight was observed in two parents and two hybrids *viz.*, PBT-5, PBT-4, PBT-5 x PBT-2 and PBT-2 x PBT-13 with 8.00 per cent disease severity and this was found statistically at par with four parents *i.e.*, PBT-9 (6.67%), PBT-2 (6.67%), PBT-13 (5.33%) and PBT-10 (4.00%) and eighteen cross combinations namely PPT-2 x PBT-5 (6.67%), PPT-2 x PBT-10 (6.67%), PBT-9 x PBT-5 (6.67%), PBT-9 x PBT-13 (6.67%), PBT-9 x PBT-10 (6.67%), PBT-5 x PBT-13 (6.67%), PBT-2 x PBT-10 (6.67%), PBT-13 x PBT-4 (6.67%), PCT-1 x PBT-9 (5.33%), PPT-2 x PBT-9 (5.33%), PBT-9 x PBT-4 (5.33%), PBT-5 x PBT-10 (5.33%), PBT-5 x PBT-4 (5.33%), PBT-2 x PBT-4 (5.33%), PBT-10 x PBT-4 (5.33%), PCT-1 x PBT-4 (4.00%), PPT-2 x PBT-2 (4.00%) and PBT-13 x PBT-10 (4.00%). Amongst all the genotypes under study, two crosses PCT-1 x PBT-2 and PCT-1 x PBT-10 recorded equal severities of late blight than check cultivar.

4.6.3.3 Late blight severity at 30 DAI

Mean disease severity at 30 DAI revealed that the range of disease severity among all genotypes ranged from 1.33 to 13.33 per cent with an average mean 6.52 per cent. Three parents and eleven crosses gave less late blight severity than population mean. Minimum late blight severity was reported in check parent PCT-1 (1.33%) and cross PCT-1 x PBT-13 (1.33%) and this was found statistically at par with one parent PPT-2 (2.67%) and two hybrids namely PCT-1 x PBT-5 (2.67%) and PCT-1 x PBT-10 (2.67%).

Table 4.50: Late blight disease severity in tomato under polyhouse condition

S.N.	Genotypes	10 DAI	20 DAI	30 DAI	40 DAI	50 DAI	60 DAI	70 DAI	80 DAI	90 DAI	100 DAI
1	PCT-1	0.00 (0.00)	0.00 (0.00)	1.33 (3.84)	2.67 (7.69)	4.00 (9.32)	5.33 (13.16)	6.67 (14.79)	9.33 (17.70)	9.33 (17.70)	9.33 (17.70)
2	PPT-2	1.33 (3.84)	1.33 (3.84)	2.67 (7.69)	5.33 (13.16)	9.33 (17.70)	13.33 (21.36)	18.67 (25.56)	22.67 (28.40)	22.67 (28.40)	22.67 (28.40)
3	PBT-9	4.00 (9.32)	6.67 (14.79)	10.67 (18.98)	20.00 (26.55)	28.00 (31.94)	36.00 (36.86)	44.00 (41.53)	50.67 (45.36)	54.67 (47.66)	58.67 (49.97)
4	PBT-5	4.00 (9.32)	8.00 (16.42)	13.33 (21.36)	18.67 (25.56)	24.00 (29.18)	32.00 (34.36)	40.00 (39.18)	45.33 (42.29)	52.00 (46.13)	56.00 (48.34)
5	PBT-2	5.33 (13.16)	6.67 (14.79)	6.67 (14.79)	12.00 (20.26)	16.00 (23.57)	24.00 (29.32)	30.67 (33.60)	37.33 (37.64)	38.67 (38.43)	40.00 (39.20)
6	PBT-13	5.33 (13.16)	5.33 (13.16)	8.00 (16.42)	13.33 (21.36)	18.67 (25.56)	26.67 (31.06)	32.00 (34.44)	36.00 (36.84)	40.00 (39.20)	44.00 (41.53)
7	PBT-10	1.33 (3.84)	4.00 (11.53)	4.00 (11.53)	9.33 (17.70)	13.33 (21.36)	17.33 (24.56)	22.67 (28.40)	25.33 (30.19)	29.33 (32.77)	30.67 (33.60)
8	PBT-4	6.67 (14.79)	8.00 (16.42)	10.67 (18.98)	17.33 (24.56)	25.33 (30.19)	33.33 (35.24)	41.33 (39.99)	49.33 (44.60)	53.33 (46.89)	57.33 (49.20)
9	PCT-1 x PPT-2	0.00 (0.00)	2.67 (7.69)	4.00 (11.53)	6.67 (14.79)	10.67 (18.98)	13.33 (21.36)	17.33 (24.56)	18.67 (25.56)	18.67 (25.56)	18.67 (25.56)
10	PCT-1 x PBT-9	2.67 (7.69)	5.33 (13.16)	6.67 (14.79)	9.33 (17.70)	13.33 (21.36)	17.33 (24.56)	22.67 (28.40)	26.67 (31.06)	29.33 (32.77)	33.33 (35.24)
11	PCT-1 x PBT-5	0.00 (0.00)	1.33 (3.84)	2.67 (7.69)	5.33 (13.16)	8.00 (16.42)	8.00 (16.42)	10.67 (18.98)	10.67 (18.98)	10.67 (18.98)	10.67 (18.98)
12	PCT-1 x PBT-2	0.00 (0.00)	0.00 (0.00)	4.00 (11.53)	6.67 (14.79)	9.33 (17.70)	13.33 (21.36)	17.33 (24.56)	18.67 (25.56)	21.33 (27.48)	21.33 (27.48)
13	PCT-1 x PBT-13	0.00 (0.00)	1.33 (3.84)	1.33 (3.84)	5.33 (13.16)	9.33 (17.70)	14.67 (22.47)	16.00 (23.57)	18.67 (25.56)	20.00 (26.48)	20.00 (26.48)
14	PCT-1 x PBT-10	0.00 (0.00)	0.00 (0.00)	2.67 (7.69)	5.33 (13.16)	8.00 (16.42)	10.67 (18.98)	10.67 (18.98)	13.33 (21.36)	13.33 (21.36)	13.33 (21.36)
15	PCT-1 x PBT-4	2.67 (7.69)	4.00 (11.53)	5.33 (13.16)	6.67 (14.79)	8.00 (16.42)	10.67 (18.98)	14.67 (22.47)	18.67 (25.56)	18.67 (25.56)	18.67 (25.56)
16	PPT-2 x PBT-9	4.00 (11.53)	5.33 (13.16)	8.00 (16.42)	10.67 (18.98)	16.00 (23.57)	22.67 (28.40)	26.67 (31.06)	30.67 (33.60)	33.33 (35.22)	36.00 (36.84)
17	PPT-2 x PBT-5	2.67 (7.69)	6.67 (14.79)	6.67 (14.79)	10.67 (18.98)	16.00 (23.57)	20.00 (26.48)	26.67 (31.06)	30.67 (33.60)	32.00 (34.36)	33.33 (35.24)
18	PPT-2 x PBT-2	1.33 (3.84)	4.00 (11.53)	5.33 (13.16)	9.33 (17.70)	13.33 (21.36)	20.00 (26.48)	22.67 (28.40)	26.67 (31.06)	26.67 (31.06)	26.67 (31.06)
19	PPT-2 x PBT-13	1.33 (3.84)	2.67 (7.69)	5.33 (13.16)	12.00 (20.26)	18.67 (25.56)	26.67 (31.06)	30.67 (33.60)	36.00 (36.84)	40.00 (39.20)	44.00 (41.53)
20	PPT-2 x PBT-10	2.67 (7.69)	6.67 (14.79)	6.67 (14.79)	10.67 (18.98)	14.67 (22.47)	18.67 (25.56)	22.67 (28.40)	28.00 (31.94)	29.33 (32.77)	29.33 (32.77)
21	PPT-2 x PBT-4	2.67 (7.69)	2.67 (7.69)	5.33 (13.16)	10.67 (18.98)	16.00 (23.57)	22.67 (28.40)	29.33 (32.77)	33.33 (35.24)	34.67 (36.00)	38.67 (38.43)
22	PBT-9 x PBT-5	6.67 (14.79)	6.67 (14.79)	8.00 (16.42)	13.33 (21.36)	18.67 (25.56)	26.67 (31.06)	34.67 (36.05)	42.67 (40.76)	46.67 (43.06)	50.67 (45.36)
23	PBT-9 x PBT-2	0.00 (0.00)	1.33 (3.84)	4.00 (11.53)	12.00 (20.26)	17.33 (24.56)	24.00 (29.32)	29.33 (32.77)	36.00 (36.86)	38.67 (38.43)	40.00 (39.20)
24	PBT-9 x PBT-13	5.33 (13.16)	6.67 (14.79)	9.33 (17.70)	16.00 (23.57)	22.67 (28.40)	29.33 (32.73)	37.33 (37.62)	42.67 (40.76)	46.67 (43.06)	50.67 (45.36)
25	PBT-9 x PBT-10	2.67 (7.69)	6.67 (14.79)	6.67 (14.79)	12.00 (20.26)	16.00 (23.57)	22.67 (28.40)	25.33 (30.19)	29.33 (32.77)	29.33 (32.77)	29.33 (32.77)
26	PBT-9 x PBT-4	4.00 (9.32)	5.33 (13.16)	9.33 (17.70)	16.00 (23.57)	24.00 (29.27)	32.00 (34.41)	40.00 (39.20)	48.00 (43.83)	52.00 (46.13)	56.00 (48.34)
27	PBT-5 x PBT-2	5.33 (13.16)	8.00 (16.42)	9.33 (17.70)	14.67 (22.47)	20.00 (26.48)	28.00 (31.94)	33.33 (35.24)	38.67 (38.43)	40.00 (39.20)	44.00 (41.53)
28	PBT-5 x PBT-13	5.33 (13.16)	6.67 (14.79)	10.67 (18.98)	14.67 (22.47)	18.67 (25.56)	25.33 (30.19)	30.67 (33.60)	36.00 (36.86)	40.00 (39.20)	42.67 (40.76)
29	PBT-5 x PBT-10	4.00 (9.32)	5.33 (13.16)	5.33 (13.16)	9.33 (17.70)	13.33 (21.36)	17.33 (24.56)	21.33 (27.48)	25.33 (30.19)	25.33 (30.19)	25.33 (30.19)
30	PBT-5 x PBT-4	5.33 (13.16)	5.33 (13.16)	8.00 (16.42)	13.33 (21.36)	18.67 (25.56)	25.33 (30.19)	32.00 (34.41)	38.67 (38.43)	42.67 (40.76)	46.67 (43.07)
31	PBT-2 x PBT-13	5.33 (13.16)	8.00 (16.42)	8.00 (16.42)	12.00 (20.26)	16.00 (23.57)	22.67 (28.40)	26.67 (31.06)	30.67 (33.60)	32.00 (34.44)	32.00 (34.44)
32	PBT-2 x PBT-10	4.00 (9.32)	6.67 (14.79)	8.00 (16.42)	12.00 (20.26)	14.67 (22.47)	21.33 (27.48)	28.00 (31.90)	36.00 (36.86)	38.67 (38.43)	38.67 (38.43)
33	PBT-2 x PBT-4	5.33 (13.16)	5.33 (13.16)	6.67 (14.79)	12.00 (20.26)	17.33 (24.56)	25.33 (30.19)	33.33 (35.20)	38.67 (38.43)	40.00 (39.20)	40.00 (39.20)
34	PBT-13 x PBT-10	1.33 (3.84)	4.00 (11.53)	6.67 (14.79)	10.67 (18.98)	13.33 (21.36)	20.00 (26.48)	24.00 (29.32)	28.00 (31.94)	28.00 (31.94)	28.00 (31.94)
35	PBT-13 x PBT-4	5.33 (13.16)	6.67 (14.79)	6.67 (14.79)	12.00 (20.26)	20.00 (26.48)	28.00 (31.94)	34.67 (36.05)	38.67 (38.43)	41.33 (39.99)	42.67 (40.76)
36	PBT-10 x PBT-4	2.67 (7.69)	5.33 (13.16)	6.67 (14.79)	12.00 (20.26)	17.33 (24.56)	22.67 (28.40)	29.33 (32.77)	34.67 (36.05)	38.67 (38.43)	42.67 (40.76)
Mean		**3.07 (7.69)**	**4.74 (11.19)**	**6.52 (14.04)**	**11.11 (19.02)**	**15.78 (22.97)**	**21.59 (27.28)**	**26.78 (30.75)**	**31.41 (33.69)**	**33.56 (34.97)**	**35.33 (36.02)**
± SE(m)		**1.49**	**2.08**	**1.90**	**1.50**	**1.40**	**1.11**	**1.16**	**1.12**	**1.14**	**1.18**
CD(0.05)		**4.74**	**5.86**	**5.38**	**4.23**	**3.94**	**3.15**	**3.27**	**3.15**	**3.23**	**3.33**

Figures shown in parenthesis are Arc sin transformed value

While, maximum severity of late blight was observed in PBT-5 (13.33%) and it was statistically at par with three parents and nine hybrids namely PBT-9 (10.67%), PBT-4 (10.67%), PBT-13 (8.00%), PBT-5 x PBT-13 (10.67%), PBT-9 x PBT-13 (9.33%), PBT-9 x PBT-4 (9.33%), PBT-5 x PBT-2 (9.33%), PPT-2 x PBT-9 (8.00%), PBT-9 x PBT-5 (8.00%), PBT-5 x PBT-4 (8.00%), PBT-2 x PBT-13 (8.00%) and PBT-2 x PBT-10 (8.00%). Amongst all the genotypes under study one cross PCT-1 x PBT-13 recorded equal severity than check cultivar (PCT-1).

4.6.3.4 Late blight severity at 40 DAI

The read-through data of disease severity revealed that range for severity was 2.67 to 20.00 per cent with average value of 11.11 per cent. Three parents and fourteen crosses gave less late blight severity than population mean. Minimum late blight severity was reported in check parent PCT-1 (2.67%) and none of the parents and hybrids found statistically at par with check parent.

Maximum severity of late blight was observed in PBT-9 (20.00%). This was found statistically at par with two parents PBT-5 (18.67%) and PBT-4 (17.33%) and four hybrids PBT-9 x PBT-13 (16.00%), PBT-9 x PBT-4 (16.00%), PBT-5 x PBT-2 (14.67%) and PBT-5 x PBT-13 (14.67%).

4.6.3.5 Late blight severity at 50 DAI

Perusal of data revealed that mean late blight severity ranged from 4.00 to 28.00 per cent and mean value of disease severity at 50 DAI was 15.78 per cent. Three parents and twelve crosses gave less late blight severity than population mean. Minimum late blight severity was reported in check parent PCT-1 (4.00%) and none of the parents and hybrids were significant at par with the check parent (PCT-1).

Maximum severity of late blight was observed in PBT-9 (28.00%) and this was found statistically at par with two parents *i.e.*, PBT-4 (25.33%) and PBT-5 (24.00%) and two hybrids *i.e.*, PBT-9 x PBT-4 (24.00%) and PBT-9 x PBT-13 (22.67%).

4.6.3.6 Late blight severity at 60 DAI

Mean disease severity at 60 DAI revealed that the range of disease severity among all genotypes ranged from 5.33 to 36.00 per cent with an average value 21.59 per cent. Three parents and thirteen crosses gave less late blight severity than

population mean. Minimum late blight severity was reported in check parent PCT-1 (5.33%) and none of the parents and hybrids found statistically at par with check parent.

In the mean while maximum severity of late blight was observed in PBT-9 (36.00%) and it was statistically at par with two parents and one hybrid namely PBT-4 (33.33%), PBT-5 (32.00%) and PBT-9 x PBT-4 (32.00%).

4.6.3.7 Late blight severity at 70 DAI

The read-through data of disease severity revealed that range for severity at 70 DAI was 6.67 to 44.00 per cent with average severity 26.78 per cent. Three parents and fifteen crosses gave less late blight severity than population mean. Minimum late blight severity was reported in check parent PCT-1 (6.67%) and none of the parents and hybrids found statistically at par with check parent.

Maximum severity of late blight was observed in PBT-9 (44.00%) and this was found statistically at par with two parents PBT-4 (41.33%) and PBT-5 (40.00%) and one hybrid *i.e.*, PBT-9 x PBT-4 (40.00%).

4.6.3.8 Late blight severity at 80 DAI

Mean disease severity at 80 DAI revealed that the range of disease severity among all genotypes ranged from 9.33 to 50.67 per cent with an average value 31.41 per cent. Three parents and fifteen crosses gave less late blight severity than population mean. Minimum late blight severity was reported in check parent PCT-1 (9.33%) and it was found statistically at par with one hybrid namely PCT-1 x PBT-5 (10.67%).

Maximum severity of late blight was observed in PBT-9 (50.67%) and this was found statistically at par with two parents and one hybrid namely PBT-4 (49.33%), PBT-5 (45.33%) and PBT-9 x PBT-4 (48.00%).

4.6.3.9 Late blight severity at 90 DAI

Perusal of data revealed that mean late blight severity ranged from 9.33 to 54.67 per cent with an average value 33.56 per cent. Three parents and fifteen crosses gave less late blight severity than population mean. Minimum late blight severity was reported in check parent PCT-1 (9.33%) and this was found statistically at par with one hybrid *i.e.*, PCT-1 x PBT-5 (10.67%).

While, maximum severity of late blight was observed in PBT-9 (54.67%) and it was found statistically at par with two parents and one hybrid namely PBT-4 (53.33%), PBT-5 (52.00%) and PBT-9 x PBT-4 (52.00%).

4.6.3.10 Late blight severity at 100 DAI

The read-through data of disease severity revealed that range for severity at 100 DAI was 9.33 to 58.67 per cent with mean value 35.33 per cent. Three parents and fourteen crosses gave less late blight severity than population mean. Minimum late blight severity was reported in check parent PCT-1 (9.33%) and it was found statistically at par with one hybrid namely PCT-1 x PBT-5 (10.67%).

Maximum severity of late blight was observed in PBT-9 (58.67%) and this was found statistically at par with two parents and one hybrid namely PBT-4 (57.33%), PBT-5 (56.00%) and PBT-9 x PBT-4 (56.00%).

4.6.4 Total yield per plant (kg)

Data presented in Table 4.51 revealed that total yield per plant ranged from 1.24 to 5.62 kg per plant with an average 2.81 kg per plant. All thirty six genotypes showed significant difference for total yield per plant. Among all the parents and hybrids, highest significant total yield per plant was observed in hybrid PCT-1 x PBT-5 (5.62 kg) while, lowest significant total yield per plant was showed by PBT-13 (1.24 kg) and it was found statistically at par with one parent PBT-4 (1.41 kg) and six hybrids namely PCT-1 x PBT-13 (1.62 kg), PCT-1 x PBT-9 (1.68 kg), PBT-9 x PBT-2 (1.70 kg), PCT-1 x PBT-10 (1.71 kg), PBT-5 x PBT-2 (1.71 kg) and PBT-5 x PBT-13 (1.74 kg).

4.6.5 Marketable fruit yield per plant (kg)

Perusal of data given in Table 4.51 revealed that the mean value for marketable fruit yield per plant ranged from 0.72 to 5.11 kg per plant with an average value 1.93 kg per plant. Three parents and thirteen crosses gave more marketable fruit yield per plant than population mean. Maximum significant marketable fruit yield per plant was reported in cross PCT-1 x PBT-5 (5.11 kg) which was found superior over rest of parents and crosses while, minimum marketable fruit yield per plant was found in PBT-4 (0.72 kg) and it was found at par with PBT-13 (0.86 kg).

Table 4.51: Total yield, marketable yield and % yield loss due to late blight in tomato

S.N.	Genotypes	Total yield (kg)	Marketable fruit yield/plant (kg)	% yield loss
1	PCT-1	3.36	3.20	4.76
2	PPT-2	3.39	2.78	17.99
3	PBT-9	1.93	1.02	47.15
4	PBT-5	2.00	1.03	48.50
5	PBT-2	2.37	1.42	40.08
6	PBT-13	1.24	0.86	30.65
7	PBT-10	2.91	2.02	30.58
8	PBT-4	1.41	0.72	48.94
9	PCT-1 x PPT-2	2.50	2.06	17.60
10	PCT-1 x PBT-9	1.68	1.05	37.50
11	PCT-1 x PBT-5	5.62	5.11	9.07
12	PCT-1 x PBT-2	1.91	1.49	21.99
13	PCT-1 x PBT-13	1.62	1.37	15.43
14	PCT-1 x PBT-10	1.71	1.54	9.94
15	PCT-1 x PBT-4	2.81	2.36	16.01
16	PPT-2 x PBT-9	4.50	2.85	36.67
17	PPT-2 x PBT-5	3.49	2.26	35.24
18	PPT-2 x PBT-2	3.91	2.86	26.85
19	PPT-2 x PBT-13	3.01	1.77	41.20
20	PPT-2 x PBT-10	3.06	2.22	27.45
21	PPT-2 x PBT-4	3.34	2.08	37.72
22	PBT-9 x PBT-5	3.18	1.76	44.65
23	PBT-9 x PBT-2	1.70	1.06	37.65
24	PBT-9 x PBT-13	2.34	1.26	46.15
25	PBT-9 x PBT-10	2.72	2.04	25.00
26	PBT-9 x PBT-4	3.38	1.84	45.56
27	PBT-5 x PBT-2	1.71	1.04	39.18
28	PBT-5 x PBT-13	1.74	0.97	44.25
29	PBT-5 x PBT-10	3.07	2.27	26.06
30	PBT-5 x PBT-4	4.00	2.20	45.00
31	PBT-2 x PBT-13	4.88	3.30	32.38
32	PBT-2 x PBT-10	2.31	1.34	41.99
33	PBT-2 x PBT-4	2.73	1.69	38.10
34	PBT-13 x PBT-10	4.46	3.33	25.34
35	PBT-13 x PBT-4	3.21	1.89	41.12
36	PBT-10 x PBT-4	2.04	1.36	33.33
Mean		**2.81**	**1.93**	**32.42**
± SE(m)		**0.19**	**0.06**	**5.11**
CD(0.05)		**0.53**	**0.18**	**14.42**

4.6.6 Percentage yield loss

The read-through data of percentage yield loss revealed that range was from 4.76 to 48.94 per cent with an average value 32.42 per cent. A significant difference for percentage yield loss was observed for all the genotypes in tomato. Out of thirty six genotypes minimum significant percentage yield loss was observed in parent PCT-1 (4.76%) and it was found statistically at par with five cross combinations namely PCT-1 x PBT-5 (9.07%), PCT-1 x PBT-10 (9.94%), PCT-1 x PBT-13 (15.43%), PCT-1 x PBT-4 (16.01%) and PCT-1 x PPT-2 (17.60%) while, maximum significant percentage yield loss was observed in PBT-4 (48.94%) and it was found statistically at par with three parents *viz*., PBT-5 (48.50%), PBT-9 (47.15%) and PBT-2 (40.08%) and fifteen hybrids namely PBT-9 x PBT-13 (46.15%), PBT-9 x PBT-4 (45.56%), PBT-5 x PBT-4 (45.00%), PBT-9 x PBT-5 (44.65%), PBT-5 x PBT-13 (44.25%), PBT-2 x PBT-10 (41.99%), PPT-2 x PBT-13 (41.20%), PBT-13 x PBT-4 (41.12%), PBT-5 x PBT-2 (39.18%), PBT-2 x PBT-4 (38.10%), PPT-2 x PBT-4 (37.72%), PBT-9 x PBT-2 (37.65%), PCT-1 x PBT-9 (37.50%), PPT-2 x PBT-9 (36.67%) and PPT-2 x PBT-5 (35.24%).

On the basis of late blight severity percentage in F_1 and their parental population, they were categorized into different groups mentioning their susceptible reactions to late blight (Table 4.52). None of the parents and hybrids showed immune reaction against the pathogen. Out of all parents and F_1 hybrids only check parent PCT-1 exhibited highly resistant reaction against late blight while, one parent PPT-2 and six cross combinations namely PCT-1 x PPT-2, PCT-1 x PBT-5, PCT-1 x PBT-2, PCT-1 x PBT-13, PCT-1 x PBT-10 and PCT-1 x PBT-4 showed resistant reaction for same pathogen. Moderately resistance reaction against late blight was showed by fifteen genotypes and among them two were parents *i.e*., PBT-2 and PBT-10 and thirteen were hybrids *viz*., PCT-1 x PBT-9, PPT-2 x PBT-9, PPT-2 x PBT-5, PPT-2 x PBT-2, PPT-2 x PBT-10, PPT-2 x PBT-4, PBT-9 x PBT-2, PBT-9 x PBT-10, PBT-5 x PBT-10, PBT-2 x PBT-13, PBT-2 x PBT-10, PBT-2 x PBT-4 and PBT-13 x PBT-4. Rest of thirteen genotypes exhibited susceptible reaction against late blight disease and among them four were parents *i.e*., PBT-9, PBT-5, PBT-13 and PBT-4 while, nine were hybrids namely PPT-2 x PBT-13, PBT-9 x PBT-5, PBT-9 x PBT-13, PBT-9 x PBT-4, PBT-5 x PBT-2, PBT-5 x PBT-13, PBT-5 x PBT-4, PBT-13 x PBT-4 and PBT-10 x PBT-4. None of the genotypes showed highly susceptible reaction against late blight.

Table 4.52 Grading of F_1 hybrids and their parental population against late blight (*Phytophthora infestans*)

Scale	PDI	Reaction	Number of genotypes	Examples
0	0	Immune	0	-
1	0.01 - 10	Highly resistant	1	PCT-1
2	10.01 - 25	Resistant	7	PPT-2, PCT-1 x PPT-2, PCT-1 x PBT-5, PCT-1 x PBT-2, PCT-1 x PBT-13, PCT-1 x PBT-10 and PCT-1 x PBT-4
3	25.01 - 40	Moderately resistant	15	PBT-2, PBT-10, PCT-1 x PBT-9, PPT-2 x PBT-9, PPT-2 x PBT-5, PPT-2 x PBT-2, PPT-2 x PBT-10, PPT-2 x PBT-4, PBT-9 x PBT-2, PBT-9 x PBT-10, PBT-5 x PBT-10, PBT-2 x PBT-13, PBT-2 x PBT-10, PBT-2 x PBT-4 and PBT-13 x PBT-4
4	40.01 - 60	Susceptible	13	PBT-9, PBT-5, PBT-13, PBT-4, PPT-2 x PBT-13, PBT-9 x PBT-5, PBT-9 x PBT-13, PBT-9 x PBT-4, PBT-5 x PBT-2, PBT-5 x PBT-13, PBT-5 x PBT-4, PBT-13 x PBT-4 and PBT-10 x PBT-4
5	>60.01	Highly susceptible	0	-

On the basis of late blight severity many other researchers also categorized the tomato genotypes against late blight. Baliyan *et al.* (2013) found Heinz 1370 was the highest severely affected tomato variety and FA 593 was the least affected variety by late blight disease. Nowakowska *et al.* (2014) found LA 1033, L 3707, L 3708 displayed the highest resistance for late blight disease. Kumar *et al.* (2015) evaluated fifty-six accessions of tomato and observed that out of 40 hybrids 4 hybrids were observed with high disease resistance to late blight. Meya *et al.* (2015) observed significant differences in severity among three tomato varieties and found Meru was resistant. Akhtar *et al.* (2016) screened 285 tomato genotypes and observed one resistant genotype and 31 moderately resistant genotypes to late blight resistant of the genotypes. Arafa *et al.* (2017) detected highest late blight resistance in six *S. habrochaites* accessions with disease severities ranging from 4.5 to 13.5 per cent. Solankey *et al.* (2017) determined the reaction of 152 tomato genotypes including 4 wild relatives against late blight. None of the test genotypes showed immune reaction.

Moreover, eight genotypes showed high yield potential and lower incidence for late blight. Moreover, wild species showed resistance reaction for late blight. Ray *et al.* (2018) screened one hundred genotypes of tomato during winter season in which eleven genotypes were highly resistant, seventeen genotypes were resistant, nineteen genotypes were moderately resistant, twenty four genotypes were susceptible and twenty nine genotypes were highly susceptible. Fourty eight F_1s were screened along with their parents during rainy season and among them eighteen cross combinations were highly resistant and others were resistant, moderately resistant, susceptible and highly susceptible.

4.7 To estimate the percentage fruits damage due to new invasive pest American pin worm (*Tuta absoluta*) for parents and hybrids.

Succession of damage due to *Tuta absoluta* in tomato crop was studied and five harvesting of tomato fruits were performed for evaluations of the damage and percentage of fruit damage (PFD) was recorded for all parents and their F_1 hybrids. The pin hole symptoms on fruits and different growth stages of *Tuta absoluta* was presented in Plate 7. Data of PFD for every harvesting was presented in Table 4.53 and explained below.

4.7.1 PFD during first harvesting

Perusal of data during first harvesting revealed that mean percentage fruits damage due to *Tuta absoluta* ranged from 9.09 to 71.02 per cent with an average value 30.00 per cent. A significant difference for PFD was observed. Out of all parents and their cross combinations PCT-1 x PBT-2 (9.09%) hybrid showed minimum significant percentage fruits damage while, parent PBT-5 (71.02%) exhibited maximum significant percentage fruits damage.

4.7.2 PFD during second harvesting

Mean percentage fruits damage during second harvesting revealed that the range of PFD among all genotypes ranged from 16.00 to 81.81 per cent and the average of PFD was 47.67 per cent. Significant difference for percentage fruit damage was observed for all the genotypes studied. Among all parents and hybrids, lowest significant PFD was observed in PCT-1 (16.00%) whereas, highest significant percentage fruits damage was observed in PBT-9 (81.81%).

Table 4.53: Percentage fruits damage due to *Tuta absoluta* in tomato under polyhouse

S.N.	Genotypes	% fruits damage					
		First harvesting	Second harvesting	Third harvesting	Fourth harvesting	Fifth harvesting	Mean of harvesting
1	PCT-1	10.34 (18.75)	16.00 (23.57)	22.73 (28.46)	36.84 (37.36)	48.98 (44.40)	**26.43 (30.92)**
2	PPT-2	21.71 (27.58)	33.65 (35.44)	39.66 (39.01)	60.00 (50.76)	87.50 (69.32)	**48.06 (43.87)**
3	PBT-9	56.96 (48.98)	81.81 (64.79)	68.08 (55.59)	100.00 (90.00)	100.00 (90.00)	**82.15 (64.99)**
4	PBT-5	71.02 (57.42)	70.78 (57.28)	71.43 (57.66)	83.33 (65.90)	100.00 (90.00)	**78.89 (62.63)**
5	PBT-2	41.50 (40.09)	50.24 (45.12)	50.00 (44.98)	75.00 (59.99)	80.00 (63.42)	**58.82 (50.06)**
6	PBT-13	19.22 (25.99)	40.90 (39.74)	44.84 (42.02)	60.00 (50.76)	75.00 (59.98)	**46.70 (43.09)**
7	PBT-10	41.28 (39.96)	46.38 (42.91)	62.50 (52.23)	75.00 (59.98)	100.00 (90.00)	**64.28 (53.28)**
8	PBT-4	60.76 (51.19)	63.60 (52.87)	74.70 (59.79)	83.33 (65.89)	100.00 (90.00)	**77.02 (61.34)**
9	PCT-1 x PPT-2	14.29 (22.20)	33.33 (35.25)	50.00 (44.98)	37.50 (37.74)	71.43 (57.67)	**41.18 (39.90)**
10	PCT-1 x PBT-9	20.00 (26.55)	41.67 (40.19)	69.23 (56.30)	83.33 (65.93)	90.00 (71.54)	**61.40 (51.58)**
11	PCT-1 x PBT-5	15.38 (23.08)	25.00 (29.99)	29.41 (32.83)	33.33 (35.25)	42.86 (40.88)	**29.33 (32.78)**
12	PCT-1 x PBT-2	9.09 (17.54)	35.71 (36.68)	58.33 (49.78)	66.67 (54.72)	90.00 (71.73)	**50.85 (45.47)**
13	PCT-1 x PBT-13	12.50 (20.70)	22.22 (28.11)	25.00 (29.99)	37.50 (37.75)	42.86 (40.88)	**27.50 (31.61)**
14	PCT-1 x PBT-10	12.50 (20.70)	33.33 (35.25)	63.64 (52.90)	80.00 (63.43)	77.78 (61.87)	**48.28 (44.00)**
15	PCT-1 x PBT-4	14.29 (22.20)	25.00 (29.99)	44.44 (41.79)	44.44 (41.79)	71.43 (57.67)	**40.00 (39.22)**
16	PPT-2 x PBT-9	33.33 (35.25)	57.14 (49.09)	50.00 (44.98)	87.50 (69.33)	100.00 (90.00)	**66.67 (54.72)**
17	PPT-2 x PBT-5	16.67 (24.09)	42.86 (40.88)	62.50 (52.22)	83.33 (65.90)	83.33 (65.90)	**57.58 (49.34)**
18	PPT-2 x PBT-2	28.57 (32.30)	49.79 (44.86)	69.18 (56.26)	71.43 (57.67)	100.00 (90.00)	**61.67 (51.73)**
19	PPT-2 x PBT-13	32.18 (34.55)	50.00 (44.98)	83.33 (65.89)	85.71 (67.81)	80.00 (63.44)	**65.19 (53.83)**
20	PPT-2 x PBT-10	33.33 (35.25)	38.80 (38.51)	61.49 (51.62)	85.71 (67.77)	100.00 (90.00)	**60.71 (51.17)**
21	PPT-2 x PBT-4	31.71 (34.26)	58.19 (49.70)	83.33 (65.88)	83.33 (65.88)	100.00 (90.00)	**70.27 (56.94)**
22	PBT-9 x PBT-5	63.10 (52.58)	71.43 (57.67)	88.68 (70.31)	85.71 (67.85)	100.00 (90.00)	**80.70 (63.94)**
23	PBT-9 x PBT-2	14.29 (22.20)	32.54 (34.77)	71.43 (57.67)	85.71 (67.79)	100.00 (90.00)	**60.34 (50.95)**
24	PBT-9 x PBT-13	37.38 (37.68)	57.14 (49.09)	58.37 (49.80)	83.33 (65.92)	80.00 (63.43)	**63.18 (52.63)**
25	PBT-9 x PBT-10	16.67 (24.08)	63.82 (53.00)	82.40 (65.18)	83.33 (65.89)	100.00 (90.00)	**67.78 (55.40)**
26	PBT-9 x PBT-4	39.96 (39.19)	64.39 (53.35)	72.73 (58.50)	80.00 (63.41)	100.00 (90.00)	**70.95 (57.38)**
27	PBT-5 x PBT-2	26.77 (31.14)	61.09 (51.39)	84.83 (67.09)	87.50 (69.38)	100.00 (90.00)	**71.61 (57.80)**
28	PBT-5 x PBT-13	25.00 (29.99)	38.53 (38.35)	68.65 (55.93)	81.82 (64.75)	88.89 (70.050)	**57.68 (49.40)**
29	PBT-5 x PBT-10	40.74 (39.65)	52.70 (46.53)	76.22 (60.81)	83.33 (65.94)	100.00 (90.00)	**71.02 (57.42)**
30	PBT-5 x PBT-4	37.43 (37.70)	54.37 (47.49)	53.35 (46.90)	75.00 (59.98)	83.33 (65.90)	**59.67 (50.56)**
31	PBT-2 x PBT-13	22.99 (28.64)	38.17 (38.14)	57.91 (49.54)	88.89 (70.52)	100.00 (90.00)	**61.62 (51.70)**
32	PBT-2 x PBT-10	41.97 (40.36)	49.35 (44.61)	88.31 (70.08)	77.78 (61.85)	100.00 (90.00)	**71.46 (57.70)**
33	PBT-2 x PBT-4	13.76 (21.77)	54.66 (47.66)	62.54 (52.24)	83.33 (65.92)	80.00 (63.42)	**56.04 (48.45)**
34	PBT-13 x PBT-10	33.88 (35.58)	33.64 (35.43)	80.96 (64.16)	85.71 (67.78)	100.00 (90.00)	**65.99 (54.31)**
35	PBT-13 x PBT-4	45.25 (42.26)	72.71 (58.49)	70.34 (56.99)	85.71 (67.84)	100.00 (90.00)	**73.73 (59.15)**
36	PBT-10 x PBT-4	24.32 (29.54)	55.19 (47.96)	55.80 (48.32)	75.00 (59.99)	88.89 (70.54)	**60.31 (50.93)**
Mean		**30.00 (32.53)**	**47.67 (43.59)**	**62.68 (52.74)**	**74.87 (61.01)**	**87.84 (75.62)**	**59.86 (50.84)**
± SE (m)		**0.36**	**0.52**	**0.63**	**0.85**	**0.57**	**0.59**
C.D.		**1.01**	**1.47**	**1.79**	**2.39**	**1.62**	**1.66**

(a)

(b)

(c)

(d)

Plate 7 *Tuta absoluta*: (a) Pin hole symptom in fruit, (b) larvae feeding on leaf, (c) Pupae and (d) Adult moth

4.7.3 PFD during third harvesting

The read-through data of PFD revealed that range during third harvesting was 22.73 to 88.68 per cent with an average value 62.68 per cent. A significant difference for PFD was observed during third harvesting of tomato. Out of thirty six genotypes minimum significant PFD was observed in parent PCT-1 (22.73%) and it was found statistically at par with hybrid PCT-1 x PBT-13 (25.00%) while, maximum significant percentage fruits damage was observed in PBT-9 x PBT-5 (88.68%) and this was found statistically at par with PBT-2 x PBT-10 (88.31%).

4.7.4 PFD during fourth harvesting

Mean percentage fruits damage during fourth harvesting revealed that the range of PFD among all genotypes ranged from 33.33 to 100 per cent and average PFD was 74.87. All thirty six genotypes showed significant difference for PFD. Among all the parents and hybrids, lowest significant percentage fruits damage was observed in hybrid PCT-1 x PBT-5 (33.33%) and it was found statistically at par with PCT-1 (36.84%) while, highest significant percentage fruits damage was showed by PBT-9 (100.00%).

4.7.5 PFD during fifth harvesting

Perusal of data during fifth harvesting revealed that mean percentage fruits damage due to *Tuta absoluta* ranged from 42.86 to 100 per cent with an average of 87.84 per cent. A significant difference for PFD was observed during fifth harvesting of tomato. Out of thirty six genotypes minimum significant PFD was observed in PCT-1 x PBT-5 (42.86%) and PCT-1 x PBT-13 (42.86%) while, maximum significant percentage fruits damage (100.00%) was observed in four parents namely PBT-9, PBT-5, PBT-10 and PBT-4 and fourteen cross combination namely PPT-2 x PBT-9, PPT-2 x PBT-2, PPT-2 x PBT-10, PPT-2 x PBT-4, PBT-9 x PBT-5, PBT-9 x PBT-2, PBT-9 x PBT-10, PBT-9 x PBT-4, PBT-5 x PBT-2, PBT-5 x PBT-10, PBT-2 x PBT-13, PBT-2 x PBT-10, PBT-13 x PBT-10 and PBT-13 x PBT-4.

4.7.6 Mean value of PFD

Mean percentage fruits damage revealed that the range of PFD among all genotypes ranged from 26.43 to 82.15 per cent and average value is 59.86 per cent. A

significant difference for PFD was observed for all genotypes in tomato. Out of thirty six genotypes minimum significant PFD was observed in parent PCT-1 (26.43%) and it was found statistically at par with hybrid PCT-1 x PBT-13 (27.50%) while, maximum significant percentage fruits damage was observed in PBT-9 (82.15%) and this was found statistically at par with PBT-9 x PBT-5 (80.70%).

4.7.7 Total yield per plant (kg)

Data presented in Table 4.54 revealed that total yield per plant ranged from 1.07 to 6.02 kg per plant with an average 3.26 kg per plant. All thirty six genotypes showed significant difference for total yield per plant. Among all the parents and hybrids, highest significant total yield per plant was observed in hybrid PCT-1 x PBT-5 (6.02 kg) while, lowest significant total yield per plant was showed by PBT-13 (1.07 kg).

4.7.8 Marketable fruit yield per plant (kg)

Perusal of data given in Table 4.54 revealed that the mean value for marketable fruit yield per plant ranged from 0.18 to 3.40 kg per plant and the average marketable fruit yield per plant was 1.27 kg. Significant difference for marketable fruit yield per plant was observed for all the genotypes studied. Among all parents and hybrids, highest significant marketable fruit yield per plant was observed in PCT-1 x PBT-5 (3.40 kg) whereas, lowest significant marketable fruit yield per plant was observed in PBT-13 (0.18 kg) and it was found statistically at par with one parent PBT-4 (0.31 kg).

4.4.9 Percentage yield loss

The read-through data of percentage yield loss revealed that range was from 24.19 to 85.24 per cent with an average value 62.34 per cent. A significant difference for percentage yield loss was observed for all the genotypes in tomato. Out of thirty six genotypes minimum significant percentage yield loss was observed in parent PCT-1 (24.19%) while, maximum significant percentage fruits damage was observed in PBT-4 (85.24%) and it was found statistically at par with one parent PBT-13 (83.18%) and two hybrids namely PBT-9 x PBT-2 (77.36%) and PPT-2 x PBT-13 (76.63%).

On the basis of percentage fruits damage in F_1 and their parental population due to American pin worm, they were categorized into different groups mentioning their susceptible reactions (Table 4.55). None of the parents and hybrids showed highly tolerant and tolerant reaction against the insect. Out of all parents and F_1 hybrids one

Table 4.54: Total yield, marketable yield and % yield loss due to *Tuta absoluta* in tomato

S.N.	Genotypes	Total yield (kg)	Marketable fruit yield/plant (kg)	% Yield loss
1	PCT-1	3.39	2.57	24.19
2	PPT-2	3.72	2.15	42.20
3	PBT-9	3.15	0.78	75.24
4	PBT-5	2.93	1.26	57.00
5	PBT-2	2.72	0.88	67.65
6	PBT-13	1.07	0.18	83.18
7	PBT-10	3.20	1.66	48.13
8	PBT-4	2.10	0.31	85.24
9	PCT-1 x PPT-2	2.66	1.50	43.61
10	PCT-1 x PBT-9	1.85	0.87	52.97
11	PCT-1 x PBT-5	6.02	3.40	43.52
12	PCT-1 x PBT-2	2.10	0.73	65.24
13	PCT-1 x PBT-13	1.78	0.55	69.10
14	PCT-1 x PBT-10	1.88	0.75	60.11
15	PCT-1 x PBT-4	3.09	1.01	67.31
16	PPT-2 x PBT-9	4.95	1.71	65.45
17	PPT-2 x PBT-5	3.84	1.77	53.91
18	PPT-2 x PBT-2	4.30	1.49	65.35
19	PPT-2 x PBT-13	3.68	0.86	76.63
20	PPT-2 x PBT-10	3.37	0.94	72.11
21	PPT-2 x PBT-4	3.67	1.37	62.67
22	PBT-9 x PBT-5	4.22	1.46	65.40
23	PBT-9 x PBT-2	2.12	0.48	77.36
24	PBT-9 x PBT-13	2.94	0.83	71.77
25	PBT-9 x PBT-10	2.99	1.19	60.20
26	PBT-9 x PBT-4	5.14	1.32	74.32
27	PBT-5 x PBT-2	2.25	0.87	61.33
28	PBT-5 x PBT-13	1.91	0.51	73.30
29	PBT-5 x PBT-10	3.38	1.74	48.52
30	PBT-5 x PBT-4	4.76	1.63	65.76
31	PBT-2 x PBT-13	5.36	1.93	63.99
32	PBT-2 x PBT-10	2.54	0.75	70.47
33	PBT-2 x PBT-4	3.00	1.31	56.33
34	PBT-13 x PBT-10	4.91	2.43	50.51
35	PBT-13 x PBT-4	3.89	1.26	67.61
36	PBT-10 x PBT-4	2.61	1.13	56.70
Mean		**3.26**	**1.27**	**62.34**
± SE(m)		**0.15**	**0.08**	**3.24**
CD(0.05)		**0.41**	**0.22**	**9.15**

Table 4.55 Grading of F_1 hybrids and their parental population against *Tuta absoluta*

S.N.	% fruit damage	Reaction	No. of genotypes	Examples
1	0-10	Highly tolerant	0	-
2	10.1-25	Resistant	0	-
3	25.1-40	Moderately tolerant	03	PCT-1, PCT-1 x PBT-5 and PCT-1 x PBT-13
4	40.1-60	Moderately susceptible	11	PPT-2, PBT-2, PBT-13, PCT-1 x PPT-2, PCT-1 x PBT-2, PCT-1 x PBT-10, PCT-1 x PBT-4, PPT-2 x PBT-5, PBT-5 x PBT-13, PBT-5 x PBT-4 and PBT-2 x PBT-4
5	60.1-75	Susceptible	18	PBT-10, PCT-1 x PBT-9, PPT-2 x PBT-9, PPT-2 x PBT-2, PPT-2 x PBT-13, PPT-2 x PBT-10, PPT-2 x PBT-4, PBT-9 x PBT-2, PBT-9 x PBT-13, PBT-9 x PBT-10, PBT-9 x PBT-4, PBT-5 x PBT-2, PBT-5 x PBT-10, PBT-2 x PBT-13, PBT-2 x PBT-10, PBT-3 x PBT-10, PBT-13 x PBT-4 and PBT-10 x PBT-4
6	75.1-100	Highly susceptible	04	PBT-9, PBT-5, PBT-4 and PBT-9 x PBT-5

parent PCT-1 and two crosses PCT-1 x PBT-5 and PCT-1 x PBT-13 exhibited moderately tolerant reaction against the insect while, three parents and eight hybrids showed moderately susceptible reaction against *Tuta absoluta* namely PPT-2, PBT-2, PBT-13, PCT-1 x PPT-2, PCT-1 x PBT-2, PCT-1 x PBT-10, PCT-1 x PBT-4, PPT-2 x PBT-5, PBT-5 x PBT-13, PBT-5 x PBT-4 and PBT-2 x PBT-4. Susceptible reaction against the insect was showed by eighteen genotypes and among them one was parents *i.e*., PBT-10 and seventeen were hybrids *viz*., PBT-10, PCT-1 x PBT-9, PPT-2 x PBT-9, PPT-2 x PBT-2, PPT-2 x PBT-13, PPT-2 x PBT-10, PPT-2 x PBT-4, PBT-9 x PBT-2, PBT-9 x PBT-13, PBT-9 x PBT-10, PBT-9 x PBT-4, PBT-5 x PBT-2, PBT-5 x PBT-10, PBT-2 x PBT-13, PBT-2 x PBT-10, PBT-3 x PBT-10, PBT-13 x PBT-4 and PBT-10 x PBT-4. Rest of four genotypes exhibited highly susceptible reaction against the insect and among them three were parents *i.e*., PBT-9, PBT-5 and PBT-4 while, one was hybrid *i.e*., PBT-9 x PBT-5.

Percentage fruits damage for different genotypes of tomato due to *Tuta absoluta* was also reported by many researchers. Oliveira *et al.* (2009) concluded that accessions HGB-674 and HGB1497 appeared to be the most promising among 57 tomato accessions tested and Sobreira *et al.* (2009) evaluated 15 cherry tomato accession and found the accession CCAUFES 40 was the most resistant against *Tuta absoluta*. Oliveira *et al.* (2012) observed strain BPX-367D-238-02 being particularly notable in its resistance. Kalleshwaraswamy *et al.* (2015) observed 1.2 to 12.6 fruits per plant showed pinhole symptoms. Shanmugam *et al.* (2016) first noticed the occurrence of *T. absoluta* in Karimangalam block in the tomato hybrid Sivam. The widely cultivated tomato hybrids Sivam and Sagar were equally susceptible to the *T. absoluta* with 28-53 per cent fruit damage. Ghaderi *et al.* (2017) indicated that Cal JN3 was the most susceptible to infestation and Primo Early and Early Urbana Y were the most resistant to *T. absoluta* among the tomato cultivars tested.

PCT-1 x PBT-5

PBT-9 x PBT-5

PBT-9 x PBT-2

PBT-2 x PBT-13

Plate 8 Promising hybrids for earliness

PCT-1 x PBT-5

PBT-2 x PBT-13

PBT-9 x PBT-4

PBT-5 x PBT-4

Plate 9 Promising hybrids for high yield

PPT-2 x PBT-10

PCT-1 x PPT-2

PBT-9 x PBT-2

PBT-2 x PBT-4

Plate 10 Promising hybrids for fruit quality traits

Summary and Conclusions

Chapter 5 SUMMARY AND CONCLUSION

The present investigation entitled, **"Studies on combining ability, molecular diversity and response to late blight (*Phytophthora infestans* (Mont.) de Bary) in tomato (*Solanum lycopersicum* L.) under polyhouse condition"** was carried out at Vegetable Research Center of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar whereas, PCR based molecular diversity work was carried out in National Agricultural Innovation Project (NAIP) laboratory, Department of Vegetable Science as well as biochemical analysis of fruits was done in Horticulture laboratory, Department of Horticulture, College of Agriculture, Pantnagar. The major objectives of the study were to know the genetic variability, molecular diversity of parents, extent of heterosis, combining ability, gene action, screening for late blight disease and estimation of percentage fruit damage due to *Tuta absoluta* in tomato.

The experimental material for the present study comprised of eight genotypes of tomato (*Solanum lycopersicum* L.). All these genotypes were evaluated under polyhouse conditions for yield related and quality traits as well as for screening against late blight and new invasive pest *Tuta absoluta*. From the eight genotypes, 28 crosses were evolved in a diallel mating design (excluding reciprocals). Thus, the experimental materials finally consisted of 36 treatments (28 F_1s and 8 parents) which were evaluated in a Randomized Block Design (RBD) for combining ability and heterosis studies. The genotypes were studied for fifteen yield related traits as well as ten quality traits *viz*., days to 50 per cent flowering, days to first fruit set, days to first fruit ripening, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, internodal length (cm), average fruit weight (g), fruit length (cm), fruit width (cm), fruit shape index, plant height (cm), 100 seed weight (g), fruit yield per plant (kg), fruit yield per hectare (t/ha), number of locules per fruit, pericarp thickness (cm), diameter of stalk scar (cm), fruit firmness (kg/cm^2), TSS (%), pH of fruit juice, titratable acidity (%), ascorbic acid (mg/100g), lycopene (mg/100g) and total carotenoids (mg/100g). All parents and their hybrids were screened against late blight disease and new invasive pest *Tuta absoluta*. The observations were recorded on five randomly selected plants. The data were subjected to appropriate statistical analysis.

Further, PCR based molecular analysis of eight genotypes of tomato was done using twenty SSR markers. The salient findings of the investigation are summarized as follows:

- The analysis of variance revealed that significant genetic differences were present among the tomato genotypes for all 15 yield related and 10 quality traits studied, which showed the existence of significant amount of variability among the genotypes hence, a greater scope for the improvement of concerned characters through selection.
- Moderate to wide range of mean values among the genotypes for different yield related and quality characters were observed. The magnitudes of PCV estimates were higher than the corresponding GCV estimates for all the characters, indicating the substantial influence of environmental variations on the performance of genotypes. Number of flowers per cluster, number of fruits per cluster, number of fruit per plant, average fruit weight, fruit length, days to first fruit set, days to first fruit ripening and 100 seed weight were less influenced by environmental factors.
- Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except characters related to earliness *viz*., days to 50 per cent flowering, day to first fruit set and days to fruit ripening which indicated that these traits has ample scope for the improvement of concerned traits through selection.
- A total of 20 SSR markers tested out of which 16 were polymorphic and 4 markers had shown monomorphic on agarose gel. Among eight genotypes of tomato total number of 46 bands exhibited by these 16 SSR primers and among them 43 was polymorphic and 3 were monomorphic. The range of amplified products was 100-700bp approximately and number of alleles per locus varied from two (SSR43, SSR47, SSR65, SSR92, SSR110, SSR111, SSR253 and SLM6-12) to six (SLM6-7). Average number of bands per primer was 2.86.
- A range of polymorphism was observed from 50 per cent (SSR47) to 100 per cent (SSR20, SSR43, SSR63, SSR65, SSR92, SSR110, SSR111, SSR248, SSR253, SLM6-5, SLM6-7, SLM6-12 and SLM6-14) with an average of 93.23 per cent.

The PIC value ranged from 0.117 (SSR47) to 0.891 (SLM6-5) with an average 0.596.

- Based on Jaccard's coefficient analysis of SSR primers, it was observed that Jaccard's similarity coefficient varied from 0.52 to 0.94 with an average value of 0.70. PBT-9 and PBT-13 (0.94) were found to be the most similar genotypes among the eight genotypes studied followed by PBT-10 and PBT-13 (0.90). Minimum Jaccard's similarity coefficient was found in PCT-1 with PBT-2 and PBT-5 (0.52).

- The clustering pattern obtained by SSR primer showed that PCT-1 (cherry tomato line) and PBT-4 (potato leaf type) showed deviation from existing cluster was also diverse with respect to their genetic makeup and morphological traits.

- In tomato germplasm analysis of variance due to design of experiment, mean performance and combining ability revealed significant differences among the parents and F_1s for all yield related and quality traits among all the genotypes included in the study.

- In the present study, the extent of heterosis was studied in 28 F_1 hybrids of tomato. For the development of early fruiting genotypes, negative heterosis is desirable for days to 50 per cent flowering, days to first fruit set and days to first fruit ripening while, heterosis is also desirable for inter-nodal length, pH of fruit juice and diameter of stalk scar in negative direction. Most of the crosses manifested highly significant heterosis over mid, better parent and standard parent for all the characters under study.

- For days to 50 per cent flowering, four cross combinations *viz.*, PBT-9 x PBT-5, PBT-5 x PBT-13, PBT-5 x PBT-4 and PBT-13 x PBT-10 showed desirable significant negative heterosis over mid parent, better parent and standard parent while, in case of days to first fruit ripening two hybrids namely PBT-9 x PBT-5 and PBT-9 x PBT-2 exhibited desirable significant negative heterosis in all three cases.

- For number of flowers per cluster PCT-1 x PBT-5 and PBT-5 x PBT-4, for number of fruits per cluster PCT-1 x PBT-5, PBT-5 x PBT-4 and PBT-2 x PBT-13, for number of fruits per plant PBT-5 x PBT-4 and for number of locules per fruit PCT-1 x PBT-9, PCT-1 x PBT-10, PPT-2 x PBT-10, PBT-9 x PBT-5,

PBT-9 x PBT-10, PBT-2 x PBT-13 and PBT-2 x PBT-10 showed desirable significant positive relative heterosis, heterobeltiosis and standard heterosis.

- For internodal length one hybrid PBT-9 x PBT-4 exhibited desirable significant negative heterosis over mid parent, better parent and standard parent and in case of plant height none of the hybrid showed desirable significant positive heterosis in all three cases.

- For average fruit weight desirable significant positive heterosis over mid parent, better parent and over check parent was observed in PPT-2 x PBT-9, PPT-2 x PBT-5, PPT-2 x PBT-2, PPT-2 x PBT-13, PPT-2 x PBT-10, PPT-2 x PBT-4, PBT-9 x PBT-5, PBT-5 x PBT-10, PBT-5 x PBT-4, PBT-13 x PBT-10 and PBT-13 x PBT-4. For fruit length two hybrids PPT-2 x PBT-9 and PBT-13 x PBT-10, for fruit width PBT-9 x PBT-5 and PBT-13 x PBT-10 exhibited desirable significant positive heterosis over mid parent, better parent and over check parent. In case of fruit shape index none of the hybrid showed significant heterosis in all three cases.

- For 100 seed weight hybrid PCT-1 x PPT-2 showed desirable significant positive heterosis over mid parent, better parent and over check parent.

- Desirable significant positive heterosis over mid parent, better parent and over check parent for fruit yield per plant and fruit yield per hectare was observed in crosses namely PCT-1 x PBT-5, PPT-2 x PBT-9, PPT-2 x PBT-2, PBT-9 x PBT-4, PBT-5 x PBT-4, PBT-2 x PBT-13 and PBT-13 x PBT-10.

- PCT-1 x PPT-2, PPT-2 x PBT-4, PBT-9 x PBT-2, PBT-9 x PBT-4 and PBT-2 x PBT-4 crosses exhibited significant positive heterosis in all three cases for pericarp thickness and for fruit firmness two cross combinations *i.e.*, PBT-9 x PBT-5 and PBT-9 x PBT-2 exhibited desirable significant positive relative heterosis, heterobeltiosis and standard heterosis.

- For diameter of stalk scar and TSS none of the cross combination showed desirable significant heterosis over mid parent, better parent and over check parent.

- For pH of fruit juice hybrids PCT-1 x PPT-2, PCT-1 x PBT-9, PCT-1 x PBT-2, PCT-1 x PBT-4, PBT-2 x PBT-13 and PBT-2 x PBT-4, for titratable acidity

crosses PCT-1 x PPT-2, PPT-2 x PBT-2, PPT-2 x PBT-10, PBT-5 x PBT-2 and PBT-2 x PBT-4 showed desirable significant relative heterosis, heterobeltiosis and standard heterosis. In case of lycopene and total carotenoids content one hybrid *i.e*., PPT-2 x PBT-10 showed desirable significant positive heterosis in all three cases.

- PCT-1 was identified as a best general combiner for maximum number of traits *viz*., earliness related traits, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, plant height, diameter of stalk scar, TSS, pH of fruit juice, titratable acidity and ascorbic acid followed by PBT-5 (for earliness related traits, number of flowers per cluster, number of fruits per cluster, internodal length, fruit yield per plant, fruit yield per hectare, fruit firmness and lycopene), PPT-2 (for internodal length, average fruit weight, fruit length, fruit yield per plant, fruit yield per hectare, TSS, ascorbic acid, lycopene and total carotenoids), PBT-2 (For earliness related traits, 100 seed weight and number of locules per fruit), PBT-4 (for average fruit weight, fruit length, fruit shape index, pericarp thickness and fruit firmness), PBT-10 (for fruit width, 100 seed weight, number of locules per fruit, lycopene and total carotenoids), PBT-13 (for 100 seed weight, number of locules per fruit, fruit firmness and titratable acidity) and PBT-9 (for internodal length, average fruit weight and fruit width).

- The best specific combiner were PBT-2 x PBT-13 (days to first fruit ripening, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit yield per plant, fruit yield per hectare, number of locules per fruit, fruit firmness, pH of fruit juice and ascorbic acid), PBT-13 x PBT-10 (days to 50 per cent flowering, days to first fruit set, average fruit weight, fruit length, fruit width, fruit yield per plant, fruit yield per hectare and pericarp thickness), PBT-9 x PBT-5 (days to first fruit ripening, average fruit weight, fruit length, fruit width, number of locules per fruit and fruit firmness), PCT-1 x PBT-5 (number of flowers per cluster, number of fruit per cluster, fruit yield per plant, fruit yield per hectare, pericarp thickness and TSS), PBT-9 x PBT-4 (number of flowers per cluster, number of fruits per plant, internodal length, lycopene and total carotenoids), PBT-9 x PBT-2 (days to 50 per cent flowering, days to first fruit set, days to first fruit ripening and pericarp thickness), PBT-5 x PBT-13 (days to 50 per cent

flowering, diameter of stalk scar and titratable acidity), PBT-5 x PBT-4 (number of flowers per cluster, number of fruits per cluster and number of fruits per plant), PBT-2 x PBT-4 (fruit shape index, pH of fruit juice and titratable acidity), PPT-2 x PBT-4 (ascorbic acid, lycopene and total carotenoids), PCT-1 x PBT-4 (days to first fruit set and fruit length), PCT-1 x PBT-2 (internodal length and 100 seed weight), PBT-10 x PBT-4 (internodal length and diameter of stalk scar), PBT-13 x PBT-4 (fruit width and total carotenoids), PCT-1 x PPT-2 (100 seed weight and titratable acidity), PPT-2 x PBT-13 (diameter of stalk scar and fruit firmness), PCT-1 x PBT-13 (100 seed weight), PBT-2 x PBT-10 (number of locules per fruit) and PPT-2 x PBT-10 (lycopene).

- The estimates of σ^2 gca/σ^2 sca indicated days to 50 per cent flowering, days to first fruit set, days to first fruit ripening, number of flowers per cluster, number of fruits per plant, internodal length, average fruit weight, fruit width, plant height, 100 seed weight, number of locules per fruit, pericarp thickness, diameter of stalk scar, TSS, pH of fruit juice and ascorbic acid were under the control of non additive gene action with over dominance effect while, number of fruits per cluster, fruit length, fruit shape index, fruit yield per plant, fruit yield per hectare, titratable acidity, lycopene and total carotenoids were under the non additive with partial dominance effect.

- For late blight disease resistant reaction out of all parents and F_1 hybrids only check parent *viz*., PCT-1 exhibited highly resistant reaction while, one parent PPT-2 and six cross combinations namely PCT-1 x PPT-2, PCT-1 x PBT-5, PCT-1 x PBT-2, PCT-1 x PBT-13, PCT-1 x PBT-10 and PCT-1 x PBT-4 showed resistant reaction for same pathogen. Moderately resistance reaction against late blight was showed by fifteen genotypes and among them two were parents *i.e*., PBT-2 and PBT-10 and thirteen were hybrids *viz*., PCT-1 x PBT-9, PPT-2 x PBT-9, PPT-2 x PBT-5, PPT-2 x PBT-2, PPT-2 x PBT-10, PPT-2 x PBT-4, PBT-9 x PBT-2, PBT-9 x PBT-10, PBT-5 x PBT-10, PBT-2 x PBT-13, PBT-2 x PBT-10, PBT-2 x PBT-4, PBT-13 x PBT-4.

- For mean data of percentage fruits damage due to *Tuta absoluta* revealed that the range of PFD among all genotypes ranged from 26.43 to 82.15 per cent and average value is 59.86 per cent. Out of eight parents, minimum average PFD was

reported in PCT-1 followed by PBT-13 and PPT-2 while, among 28 hybrids, minimum average PFD was found in PCT-1 x PBT-13, PCT-1 x PBT-5 and PCT-1 x PBT-4.

Conclusion

Thus, based on the findings of present investigation, it can be concluded that sufficient quantum of genetic variability and considerable genetic diversity was generated involving diverse genotypes of tomato, which indicates the existence of considerable scope for the improvement of these genotypes through selection and hybridization. Furthermore, moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except characters related to earliness which indicated that these characters were less influenced by environmental factors thus these traits has ample scope for the improvement of concerned traits through selection.

On the basis of *per se* performance studies, it is concluded that the hybrids, PCT-1 x PBT-5, PBT-9 x PBT-5, PBT-9 x PBT-2 and PBT-2 x PBT-13 were found promising for earliness (Plate 8) while, for fruit yield, PCT-1 x PBT-5, PBT-2 x PBT-13, PBT-9 x PBT-4 and PBT-5 x PBT-4 were found promising hybrids (Plate 9). For most of the quality related traits promising hybrids were PCT-1 x PPT-2, PBT-9 x PBT-2, PBT-2 x PBT-4 and PPT-2 x PBT-10 (Plate 10), hence these crosses could be utilized as commercial hybrids for earliness, high yielding and industrial processing, respectively.

PCT-1 was identified as a best general combiner for maximum number of yield related and quality traits followed by PPT-2 and PBT-5. Thus, these parents could be used for the development of superior varieties suitable for most of the yield related and quality traits. The best specific combiner were PBT-2 x PBT-13 followed by PBT-13 x PBT-10, PBT-9 x PBT-5, PCT-1 x PBT-5 and PBT-9 x PBT-4 for most of the yield related and quality traits studied. Hence, these crosses can be utilized in heterosis breeding for improvement in yield related traits as well as quality related traits for processing industry.

Among all yield related and quality traits most of the characters were under the control of non additive gene action with over or partial dominance effect except fruit firmness, hence these characters are suitable for hybrid breeding.

For late blight disease resistant reaction out of all F_1 hybrids six cross combinations showed resistant and thirteen hybrids showed moderately resistance reaction. Hence, these cross combinations could be utilized for further tomato resistant breeding programmes or directly released as commercial hybrids for late blight resistant after multi-year and multi-location trials.

Among all thirty six genotypes, minimum average percentage fruits damage due to *Tuta absoluta* was found in PCT-1, PCT-1 x PBT-5 and PCT-1 x PBT-13. Using these genotypes reduces the requirement for additional management techniques, such as biological controls, pheromone traps and insecticides. Hence, these crosses can be used in an IPM strategy to control *T. absoluta*. However, further field and laboratory experiments are needed to explore plant–herbivore interactions and basic biochemical studies are needed to undertake the extraction and identification of phytochemicals that reduce the build-up of *T. absoluta* populations on tomato plants.

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Appendices

APPENDIX - Ia

Weakly weather conditions from November 2016 to May 2017 under Polyhouse-1 (Disease screening) at Pantnagar

Date	Temperature (^{o}C)	Relative Humidity (%)
1-5Nov 2016	36.73	45.06
6-12	37.81	41.65
13-19	37.84	42.35
20-26	35.65	49.06
27-3Dec	33.66	48.25
4-10	32.03	52.99
11-17	28.38	67.63
18-24	32.88	61.52
25-31	32.67	58.34
1-7Jan	32.35	44.65
8-14	32.30	53.76
15-21	26.03	74.27
22-28	30.22	61.93
29-4Feb	28.88	45.59
5-11	31.71	41.75
12-18	35.52	31.07
19-25	31.31	59.22
26-04 March	32.34	61.24
05-11	31.39	58.94
12-18	34.28	51.28
19-25	32.64	48.36
26-01 April	34.24	54.54
02-08	33.68	48.32
09-15	35.05	54.33
16-22	34.84	47.84
23-29	35.62	41.33
01-06 May	35.78	44.64

APPENDIX - Ib

Weakly weather conditions from November 2017 to May 2018 under Polyhouse 2 (Evaluation) and Polyhouse 3 (*Tuta absoluta*) at Pantnagar

Date	Polyhouse 2		Polyhouse 3	
	Temperature (^{o}C)		Temperature (^{o}C)	
	Min.	Max.	Min.	Max.
1-4 Nov	10.9	29.2	12.0	30.5
5-11	10.8	27.8	12.0	29.0
12-18	11.6	25.5	12.8	26.7
19-25	11.4	22.1	12.5	23.3
26-02 Dec	10.2	26.2	11.4	27.4
3-9	13.2	26.2	14.3	27.5
10-16	12.8	26.2	14.0	27.5
17-23	10.7	24.9	11.9	26.3
24-30	8.5	25.5	9.7	26.9
31-6 Jan	9.1	20.9	10.2	22.2
7-13	7.2	15.5	8.3	16.8
14-20	5.8	23.1	7.0	24.3
21-27	8.4	23.1	9.5	24.4
28-3 Feb	12.5	22.8	13.5	24.1
4-10	10.9	25.1	12.3	26.5
11-17	10.2	25.2	11.9	26.4
18-24	13.5	28.6	14.5	29.8
25-3Mar	15.9	30.6	17.2	32.1
4-10	14.9	31.9	16.1	33.1
11-17	16.3	33.9	17.3	35.2
18-24	21.1	33.2	20.6	34.4
25-31	22.1	36.3	23.2	37.6
1-7 Apr	21.9	33.1	23.0	34.5
8-14	20.4	28.8	21.5	30.1
15-21	21.5	34.8	22.6	36.2
22-28	23.2	36.4	24.4	37.7
29-5 May	25.8	40.8	26.9	42.3
6-12	23.2	36.7	24.4	38.2
13-19	24.1	41.0	25.2	42.3
20-26	25.3	44.5	26.5	45.8
27-31	28.1	43.6	29.3	44.9

APPENDIX-II

Reagents for Genomic DNA isolation and PCR amplification

I. Reagents for Genomic DNA isolation

Requirements:

Tris base, EDTA-Na2, NaCl, Potassium Acetate, Glacial acetic acid, isoproponol, chloroform, isoamyl alcohol, and Absolute alcohol.

Preparation of solutions:

STOCKS SOLUTIONS:

1. 1M Tris-Cl buffer (pH 8.0), 100 ml

12.114 g Tris-base was dissolved in 80 ml ddw. The pH was adjusted to 8.0 by 6 N HCl. The volume was made upto 100 ml with ddw. Autoclaved and stored at 4ºC.

2. 0.5 M EDTA (pH 8.0), 50 ml

9.3 g EDTA-Na2 was dissolved in 30 ml of ddw (10N NaOH was added to make the pH 8.0). The final vol. was made upto to 50 ml, Autoclaved and stored at 4ºC.

3. 10N NaOH, 50 ml

20 g of NaOH was dissolved in 30 ml of autoclaved ddw. The volume was made upto 50 ml. Stored in a plastic bottle at RT.

4. 5 M NaCl, 50 ml

14.6 g NaCl was dissolved in 30 ml of ddw. The final vol. was made upto 50 ml. Autoclaved and stored at RT.

WORKING SOLUTIONS

1. DNA extraction buffer 25 ml

2% (w/v) CTAB	:	0.5 g
100 mM Tris-Cl	:	2.5 ml (1M stock)
1.4 M NaCl	:	2.0475 g
20 mM EDTA	:	1 ml (0.5 M stock)
0.2 % beta mercaptoethanol	:	50 µl

The final vol. was made upto to 25 ml with ddw.

2. 5 M potassium Acetate (pH 5.4) **50 ml**

24.8 g potassium acetate was dissolved in 30 ml of ddw. The pH was adjusted to 5.4 with glacial acetic acid. The final volume was made upto 50 ml with ddw. Autoclaved and stored at RT.

3. Isopropanol	:	Kept at 0ºC.
4. Chloroform: isoamyl alcohol	:	24:1, 25 ml
5. 70% ethanol	:	10 ml

6. TE Buffer (pH 8.0) 25 ml

10 mM Tris-Cl	:	250 µl (1M stock)
1mM EDTA	:	50 µl (0.5 M stock)

Volume was made up by adding ddw to 25 ml. Autoclaved and stored at RT.

II. PCR Ingredients

(i) Design and Synthesis of the primers

The most essential requirement of PCR is the availability of short oligonucleotides called primers having sequence complementary to either ends of the target DNA segment called tamplate DNA to be synthesized. The primers used in the study are synthesized from Eurofins, Banglore

(ii) *Taq* DNA polymerase

Taq DNA polymerase is a thermostable enzyme that replicates DNA at 72-740C and remains functional even after incubation at 950C. The enzyme has 5'-3' polymerase and 3'-5' exonuclease activity. The concentration of the enzyme was 3units per µl (3U/ µl).

(iii) dNTPs

The dNTPs used in this reaction were obtained from Genei Pvt. Ltd. Banglore as 10mM each (dATP, dGTP, dCTP, dTTP).

(iv) Assay Buffer (10X)

Assay buffer (10X) contained 10 mM Tris-Cl (pH 9.0), 15 mM MgCl2, 50 mM KCl and 0.01% gelatin.

III. Running buffer, Dye and Reagents

Running Buffer

0.5 X TBE buffer

Dye

98% formamide, 10mM EDTA, 0.023mg Bromophenol Blue, 0.023mg Xylene Cynol

Reagents used and preparation

1. Electrophoresis buffer (5X)	**100ml**
Tris base (0.045M)	54 g
Boric acid	27.5g
EDTA (0.001M)	10ml (1M stock)

Components were dissolved in 80ml of de-ionized water. pH was adjusted to 8.0 with 6N. Final volume was made up to 10 ml, autoclaved and stored at 40C. 0.5X was the working solution of TBE buffer.

2. DNA loading dye (Double Dye)	**10ml**
Bromophenol Blue (0.25% w/v)	0.025g
Xylenecynol FF (0.25% w/v)	0.025g
Sucrose (40% w/v)	

The components were dissolved in 8.0ml of sterile de-ionized water. pH was adjusted to 8.0 and finally volume was made 10ml. Aliquots were made and stored at -200C.

3. DNA staining solution and Ethidium Bromide (10000X)

Ethidium Bromide	10ml
Sterile de-ionized water	1ml

Note:

- Working solution for staining gel was made by dissolving 60µl ethidium bromide
- Stock (10mg/ml) in 3000ml of de-ionized water.
- Stock was stored at 40C
- Ethidium bromide being highly carcinogenic was handled wearing gloves

APPENDIX - III

Morphological characteristics of eight tomato genotypes

S. N.	Characters	Genotypes							
		PCT-1	**PPT-2**	**PBT-9**	**PBT-5**	**PBT-2**	**PBT-13**	**PBT-10**	**PBT-4**
1	Plant growth type	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Indeterminate	Semi-determinate
2	Type of leaf blade	Bipinnate	Pinnate	Pinnate	Pinnate	Pinnate	Pinnate	Pinnate	Pinnate (Potato leaf)
3	Diameter of fruit core in cross section	Very small	Medium	Small	Small	Large	Large	Medium	Medium
4	Stigma nature	Exerted	Parallel	Inserted	Parallel	Inserted	Parallel	Parallel	Parallel
5	Fruit shape	Oval	Oval	Oval	Spherical	Spherical	Oval	Spherical	Oval
6	Thickness of pericarp	Thin	Medium	Thick	Very thick	Thick	Thick	Very thick	Thick
7	Fruit colour at maturity	Red	Orange	Red	Red	Orange	Red	Red	Red
8	Flesh colour of fruit at maturity	Red	Red	Red	Red	Orange	Red	Red	Red
9	Time of flowering	Early	Medium	Medium	Medium	Early	Late	Early	Medium
10	Time of maturity	Very early	Medium	Medium	Medium	Medium	Medium	Early	Medium

VITAE

The author, Ankit Panchbhaiya, son of Shri Kishori Lal Panchbhaiya was born on 30th December, 1994 at Vill. Pali, P.O. Ranakot, Pauri Garhwal, Uttarakhand. He passed his High School Examination in 2007 and Intermediate Examination in 2009 from Government Inter College, Srinagar Garhwal, District Pauri Garhwal, Uttarakhand. He obtained his B.Sc. Horticulture degree from G. B. Pant University of Agriculture & Technology, Pantnagar, District Udham Singh Nagar, Uttarakhand in 2013. He obtained his M.Sc. (Ag.) with major in Vegetable Science degree from same university in 2015.

He joined Ph.D. Horticulture (Vegetable Science) Degree Programme with major in Vegetable Science and minor in Genetics and Plant Breeding at Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, in July 2015. He was qualified ASRB net in 2016 with 84 % marks.

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ABSTRACT

Name	: Ankit Panchbhaiya	**Id. No.**	: 38423
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		Department	: Vegetable Science
Major	: Horticulture (Vegetable Science)		
Minor	: Genetics and Plant Breeding		
Thesis Title	: "Studies on combining ability, molecular diversity and response to late blight (*Phytophthora infestans* (Mont.) de Bary) in tomato (*Solanum lycopersicum* L.) under polyhouse condition"		
Advisor	: Dr. Dinesh Kumar Singh		

The present investigation was carried out at Vegetable Research Center of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, with the objectives to assess the genetic variability, molecular diversity, heterosis, combining ability, gene action, screening for late blight disease and estimation of percentage fruits damage due to *Tuta absoluta* in tomato.

The analysis of variance for RBD and combining ability revealed significant genetic differences among 36 tomato genotypes for the fifteen yield related and ten quality traits under study. The magnitudes of PCV estimates were higher than the corresponding GCV estimates for all the characters. Moderate to high GCV together with moderate to high heritability and genetic advance as per cent of mean was reported for majority of the characters under study except characters related to earliness *viz*., days to 50 per cent flowering, day to first fruit set and days to fruit ripening. A total of 20 SSR markers tested out of which 16 were polymorphic and 4 markers had shown monomorphic on agarose gel. Among eight genotypes of tomato total number of 46 bands exhibited by these 16 SSR primers and among them 43 was polymorphic and 3 were monomorphic. The range of amplified products was 100-700bp approximately and number of alleles per locus varied from two to six. Average number of bands per primer was 2.86. A range of polymorphism was observed from 50 per cent to 100 per cent with an average of 93.23 per cent. The PIC value ranged from 0.117 to 0.891 with an average 0.596. Jaccard's similarity coefficient varied from 0.52 to 0.94 with an average value of 0.70. PBT-9 and PBT-13 (0.94) were found to be the most similar genotypes among the eight genotypes studied followed by PBT-10 and PBT-13 (0.90). Minimum Jaccard's similarity coefficient was found in PCT-1 with PBT-2 and PBT-5 (0.52). The clustering pattern obtained by SSR primer showed that PCT-1 (cherry tomato line) and PBT-4 (potato leaf type) showed deviation from existing cluster.

Hybrids, PCT-1 x PBT-5, PBT-9 x PBT-5, PBT-9 x PBT-2 and PBT-2 x PBT-13 were found promising for earliness while, for fruit yield, PCT-1 x PBT-5, PBT-2 x PBT-13, PBT-9 x PBT-4 and PBT-5 x PBT-4 were found promising hybrids. For most of the fruit quality traits promising hybrids were PCT PCT-1 x PPT-2, PBT-9 x PBT-2, PBT-2 x PBT-4 and PPT-2 x PBT-10, hence these crosses could be utilized as commercial hybrids for earliness, high yielding and industrial processing, respectively. PCT-1 was identified as a best general combiner for maximum number of yield related and fruit quality traits followed by PPT-2 and PBT-5. The best specific combiner were PBT-2 x PBT-13 followed by PBT-13 x PBT-10, PBT-9 x PBT-5, PCT-1 x PBT-5 and PBT-9 x PBT-4 for most of the yield related and fruit quality traits studied. Among all yield related and fruit quality traits most of the characters were under the control of non additive gene action with over or partial dominance effect except fruit firmness, hence these characters are suitable for hybrid breeding.

For late blight disease resistant reaction, out of all F_1 hybrids six cross combinations showed resistant and thirteen hybrids showed moderately resistance reaction. Among 28 hybrids, minimum average percentage fruits damage due to *Tuta absoluta* was found in PCT-1, PCT-1 x PBT-5 and PCT-1 x PBT-13.

(Dinesh Kumar Singh)
Advisor

(Ankit Panchbhaiya)
Author

सारांश

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गौण विषय	:	आनुवंशिकी एवं पादप प्रजनन			
शोध ग्रन्थ शीर्षक	:	**पोलीहॉउस के अंतर्गत टमाटर (*सोलेनम लाइकोपरसिकम* एल.) में संयोजन छमता, आण्विक विविधता एवं पछेती झुलसा (*फाइटोफ्थोरा इन्फेस्टांस* (मोंट.) डी बेरी) के प्रतिक्रिया पर अध्ययन।**			
सलाहकार	:	डॉ. दिनेश कुमार सिंह			

वर्तमान अन्वेशण गोविन्द बल्लभ पंत कृषि एवं प्रौद्योगिकी विश्वविद्यालय पंतनगर में अनुवांशिक परिवर्तनशीलता, आण्विक विविधिता, शंकर ओज, संयोजन छमता, जीन क्रिया, पछेती झुलसा बीमारी के लिए जाँच एवं टमाटर में टूटा ऐब्सोलूटा के कारन प्रतिशत फल क्षति की जाँच के उद्देश्य के साथ संपन्न किया गया।

याद्दच्छिकी खण्ड अभिकल्पना (आर. बी. डी.) एवं संयोजन छमता की भिन्नता विश्लेषण से 15 उपज एवं 10 फल गुणवत्ता वाले 36 टमाटर जननद्रव्यों के बीच महत्वपूर्ण अनुवांशिक मतभेदों का अध्ययन किया गया। PCV की अनुमानित मात्रा सभी गुणों के लिए GCV के अनुमानित मात्रा से अधिक पायी गयी। मध्यम से उच्च GCV के साथ मध्यम से उच्च अनुवांशिकी एवं अनुवांशिकी विकास का औसत प्रतिशत टमाटर के अधिकांश गुणों के लिए पाया गया, जिसमे फलों के पकने वाले गुण जैसे 50 प्रतिशत पुष्पीकरण के लिए दिन, प्रथम फलों के लगने के लिए दिन एवं प्रथम फलों के पकने के लिए दिन सम्मिलित नहीं हैं। कुल 20 S.S.R. मार्कर का परिक्षण किया गया जिसमे से 16 बहुरूपी थे एवं 4 मार्करों ने एग्रोस जैल पर एकरूपी दिखया। इस प्रकार टमाटर के 8 जनद्रव्यों में 16 S.S.R. प्राइमरों द्वारा 46 बैंडों की कुल संख्या प्रदर्शित की गयी एवं उसमे से 43 बहुरूपी एवं 3 एकरूपी थे। प्रवर्धित उत्पादों की सीमा लगभग 100 –700 बी.पी. थी एवं प्रति स्थान पर ऐलील की संख्या दो से छह थी। प्रति प्राइमर बैंड की औसत संख्या 2.86 थी। बहुरूपी की सीमा 50 से 100 प्रतिशत देखी गयी जिसका औसत प्रतिशत 93.23 प्रतिशत देखा गया। बहुरूपता संकेतन मात्रा 0.117 से 0.891 देखा गया जिसकी औसत मात्रा 0.596 थी। जैकार्ड समानता गुणांक 0.70 के औसत मूल्य के साथ 0.52 से 0.94 पाया गया। कुल आठ जनद्रव्यों के बीच PBT-9 एवं PBT-13 (0.94) जनद्रव्य समान पाए गए तथा इनके बाद PBT-10 एवं PBT-13 (0.90) भी समान पाए गए। न्यूनतम जैकार्ड समानता गुणांक PCT-1 के साथ PBT-2 एवं PBT-5 (0.52) में पाया गया। S.S.R. प्राइमर द्वारा प्राप्त गुच्छा स्वरुप से पता चला है कि PCT-1 (चेरी टमाटर की लाइन) एवं PBT-4 (आलू के पत्ते समान पत्तियां) ने मौजूदा गुच्छो से विचलन दिखाया है।

जल्दी पकने के लिए शंकर CT-1 x PBT-5, PBT-9 x PBT-5, PBT-9 x PBT-2 एवं PBT-2 x PBT-13 तथा फल उपज के लिए PCT-1 x PBT-5, PBT-2 x PBT-13, PBT-9 x PBT-4 एवं PBT-5 x PBT-4 शंकर उत्कृष्ट आशाजनक पाए गए. फल गुणवत्ता वाले अधिकांश लक्षणों के लिए PCT-1 x PPT-2, PBT-9 x PBT-2, PBT-2 x PBT-4 एवं PPT-2 x PBT-10 शंकर उत्कृष्ट आशाजनक पाए गए इसलिए इन शंकरो को क्रमशः जल्दी पकने के लिए, उच्च उपज के लिए एवं औद्योगिक प्रसंस्करण के लिए वाणिज्यिक शंकरो के रूप में उपयोग किये जा सकते हैं। अधिकतम उपज समन्धित एवं फल गुणवत्ता वाले लक्षणों के लिए क्रमशः PCT-1, PPT-2 एवं PBT-5 को सर्वश्रेष्ठ सामान्य संयोजक के रूप में पहचाना गया। अध्ययन किये गए फल उपज तथा फल गुणवत्ता के अधिकांश लक्षणों के लिए क्रमशः PBT-2 x PBT-13, PBT-13 x PBT-10, PBT-9 x PBT-5, PCT-1 x PBT-5 एवं PBT-9 x PBT-4 उत्कृष्ट विशिष्ट संयोजक पाए गए। सभी उपज सम्बंधित एवं फल गुणवत्ता वाले लक्षणों में से अधिकांश लक्षण फल दृढ़ता को छोड़कर अति या आंशिक प्रभुत्व प्रभाव के साथ गैर–योजक जीन क्रिया के नियंत्रण में थे, इसलिए ये लक्षण शंकर प्रजनन के लिए उपयुक्त हैं।

पछेती झुलसा रोग प्रतिरोधी प्रतिक्रिया के लिए सभी एफ़–1 शंकरो में से छह शंकर संयोजनों ने प्रतिरोध प्रक्रिया तथा तेरह शंकरो ने मध्यम प्रतिरोध प्रक्रिया दिखाई। 28 शंकरो में से टूटा ऐब्सोलूटा के कारन फलो में छतिग्रस्त न्यूनतम औसत प्रतिशत PCT-1, PCT-1 x PBT-5 एवं PCT-1 x PBT-13 में पाया गया।

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