

**Heterosis and combining ability studies for yield and yield
attributing traits in tomato (*Solanum lycopersicum* L.)
under temperate conditions of Kashmir**

Sayed Azrah Indrabi

(2020-1063-D)



Division of Vegetable Science

Faculty of Horticulture

**Sher-e-Kashmir University of Agricultural Sciences and
Technology of Kashmir**

2023

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Submitted to

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Doctor of Philosophy in Vegetable Science

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DEDICATED

TO MY

BELOVED PARENTS

SAYED MOHD AMIN INDRABI

MEHMOODA AKHTER

*Who instilled in me the virtues of perseverance and
commitment and restlessly encouraged me to strive for
excellence.*

Sher-e-Kashmir
University of Agricultural Sciences & Technology of Kashmir
Faculty of Horticulture, Division of Vegetable Science,
Shalimar Campus Srinagar – 190025

Certificate – I

This is to certify that the thesis entitled, “**Heterosis and combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) under temperate conditions of Kashmir**” submitted in partial fulfillment of the requirements for the award of the degree of **Doctor of Philosophy in Vegetable Science**, to the **Faculty of Horticulture, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir** is a record of bonafide research work carried out by **Ms. Sayed Azrah Indrabi (Regd. No. 2020-1063-D)** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

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ABSTRACT

The present investigation entitled, **“Heterosis and combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) under temperate conditions of Kashmir”** was carried out to generate information on various genetic parameters viz., combining ability, nature and magnitude of gene action and heterosis for yield and yield attributing traits along with the average degree of dominance, distribution of dominant and recessive genes in the parents and presence or absence of epistasis in twelve diverse lines of tomato crossed in a diallel fashion. Sixty-six F₁ crosses were evaluated along with the twelve parental lines and one standard check in Randomized complete Block Design (RCBD) at three different locations viz., Vegetable Experimental Farm, SKUAST-Kashmir, Shalimar (E₁), Krishi Vigyan Kendra, Malangpora, Pulwama (E₂) and Krishi Vigyan Kendra, Budgam (E₃) during the Kharif 2022. The observations recorded on various diverse characters were subjected to standard statistical analysis.

The analysis of variance concluded that high level of significant variation was present among the parents for all the traits indicating that the lines selected for the present investigation and the crosses generated from them were diverse for all the traits. The analysis of variance for genetic components of variation concluded that the variances due to SCA (σ^2_s) were higher in magnitude than the corresponding GCA variances (σ^2_g) for all the traits under study. The estimates of additive and dominance variance revealed that the magnitude of dominance variance was higher than the additive variance for all the traits under consideration indicating the prevalence of non-additive gene action. The ratio of additive to dominance variance (σ^2_A / σ^2_D) was found to be less than unity for all the traits.

The general and specific combining ability analysis for quantitative traits concluded that none of the parents and crosses possessed significant and desirable general and specific combining ability for all the traits subsequently. However, different parents were found to reveal desirable combining ability for different traits. The parents exhibiting significant and desirable GCA effects for yield and yield attributing traits were SKAU-T-9801, SKAU-T-0301, SKAU-T-1464 and SKAU-T-9862. Hence, these parents could be selected for use in future crop improvement programme. The crosses exhibiting significant and desirable SCA effects for most of the traits were SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1700 and SKAU-T-9801 × SKAU-T-1429. Hence, these crosses with desirable SCA for maximum traits, could be released after further evaluation.

Average degree of dominance $(\hat{H}_1/D)^{1/2}$ was more than one for all the traits indicating over-dominance. The estimates of $\hat{H}_2/4\hat{H}_1$ were less than 0.25 indicating asymmetrical distribution of genes for the all traits in both individual and pooled data analysis. The KD/KR component estimates were found to be greater than unity for all the traits indicating the excess of dominant genes in parents as compared to the recessive genes. The values of \hat{h}^2/\hat{H}_2 , were found to be positive and less than 0.50 for all traits depicting less proportion of dominance gene groups. Non-significant values of t^2 and deviation of regression coefficient from unity depicted the absence of epistasis in maximum traits. However significant deviation of regression coefficient from 1, 0 and t^2 values depicted presence of epistasis in pericarp thickness.

Heterosis for yield and yield attributing traits revealed that wide range of heterotic patterns were present among the crosses for different traits. The performance of crosses revealed that crosses SKAU-T-1219 × SKAU-T-1429, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1701 and SKAU-T-1009 × SKAU-T-1464 exhibited significant and desirable heterosis over the check for most of the yield and yield attributing traits. However SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-1429 and SKAU-T-1700 × SKAU-T-0922, exhibited significant and desirable SCA and heterosis for most of the traits. The significant heterosis and SCA with respect to yield and yield attributes indicates that some good number of hybrids could be developed in tomato and there exists a great scope for selection of high yielding lines from segregating generations.

Keywords: *Solanum lycopersium*, analysis of variance, combining ability, GCA, SCA, additive variance, dominance variance, heterosis, epistasis.

Signature of Student

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Chapter-1

INTRODUCTION

Tomato (*Solanum lycopersicum* L., $2n = 2x = 24$), a member of solanaceae family, is one of the most important vegetable crop because of its special nutritive value and worldwide cultivation due to its wider adaptability and high yielding potential. Besides, fresh consumption, tomato ranks first among processed vegetables in the world (Dhaliwal *et al.*, 2000). Its cultivation has become widespread over the subsequent centuries and is now one of the world's major food crops (Frusciante *et al.*, 2000). It is considered to be one of the prized vegetable crops globally including India. The current mandate of tomato is depending on the industrial and consumer's needs. There are several species of tomato but the fruits are edible only of two species namely, *Solanum lycopersicum* and *Solanum pimpinellifolium* (Rick *et al.*, 1990). All the species of tomato are native of Western South America. Peru-Ecuador is considered to be the centre of origin of tomato (Rick, 1976). It was introduced by Portuguese in India during colonization era.

Tomato is a warm season crop reasonably resistant to heat, drought and grows under wide range of soil and climatic conditions. It is a herbaceous annual with some species perennial, prostrate and is a sexually propagated plant. It is a day neutral plant and mainly self-pollinated but a certain percentage of cross pollination also occurs. Tomato carves for itself a distinct niche in the realm of the vegetable. Due to its adaptability to a wide range of environment with their characteristic, climatic and cultural conditions, as well as its high nutritive values, tomato remains in the focus of the horticulture industry, as is evidenced by an increase in its cultivation, ever since the mid nineteenth century.

Tomato is the world's second most consumed vegetable after potato (Foolad, 2007) and is grown across all agro-ecological zones. The total world production of tomato is 161.7 million metric tons with a value of ~\$59 billion

(Anonymous, 2019). India ranks second in position in the total world production of tomato after China. In India, tomato occupies an area of 831 thousand hectares with the production of 20300 thousand million tonnes and productivity of 24.42 million tonnes per hectare. The area under tomato cultivation in Jammu and Kashmir is 3.29 thousand hectares with production 79.95 thousand million tonnes and productivity of 24.30 million tonnes per hectare (Anonymous, 2021).

In Kashmir, tomato is grown as a summer crop and the situation for tomato cultivation is not good under Kashmir condition, despite being vegetable of importance, the production is low. Although Kashmir has greater potential to increase the tomato production, despite continuous efforts by scientists and researchers, the production of the crop has remained static from past many years (Katoch, 2015). The low production is often attributed to many limiting factors such as non-availability of high yielding varieties; biotic and abiotic stress tolerant varieties resulting in reduction in yield and quality.

Tomato is identified as protective food not only because of its high nutritional value but also for its high content of antioxidants. It is also an important source of vitamin A, B, C and other nutrient elements. During ripening, there is a 500 fold increase in the level of lycopene in tomato fruit (Bai and Lindhot, 2007). Increased lycopene has an approved nutritional value as an antioxidant that is associated with a low incidence of certain forms of human cancers. Lycopene is especially efficient in neutralizing Reactive Oxygen Species (ROS). The popularity of tomato and its products continues to rise as it is a good source of vitamin A and C in significant amount. The fruit also contains significant amounts of beta-carotene, magnesium, iron, phosphorus, potassium, riboflavin, niacin, sodium and thiamine. The nutritional importance of the tomato indicates that there is a need to formulate breeding programme and to develop cultivars rich in vitamins, nutrients and antioxidants, processing traits with high quality of fruit as well as yield.

Tomato is extensively used in salad as well as for culinary purposes and also used for various processed forms including pastes, sauces, pulps, juices, ketchup and as flavouring ingredients in soups, meat or fish dishes, while the green unripe fruits are used for making pickles and chutney (Gosselin and Trudel, 1984).

Tomato intake reduces LDL cholesterol and triglyceride levels in white blood cells, reducing cardiovascular risk related with type 2 diabetes also decreased risk of breast cancer, neck cancers and strongly protective against neurodegenerative diseases (Freedman *et al.*, 2008). Ascorbic acid may play a key role in delaying the pathogenesis of a variety of degenerative diseases, such as cardiovascular disease, certain cancers, cataracts and it also prevents DNA mutation induced by oxidative stress (Lutsenko *et al.*, 2002).

The replacement of inbred lines by hybrids has remarkably increased yield, while the genetic gain rate has been reduced due to low genetic diversity within cultivated tomatoes. The common approach of selecting parents on the basis of *per se* performance does not necessarily lead to fruitful results (Allard, 1960) whereas choosing parents purely on the basis of their combining ability and nature and extent of gene action for yield and yield attributing traits has been found to be useful tool before going for a hybridization programme.

The adoption of hybrid cultivars greatly boosted tomato production worldwide. As compared to the open-pollinated cultivars, hybrids with higher yields have features that contribute to better agronomic performances (Noonari *et al.*, 2015; Rosa, 2019). These advantages depend on the traits of the parents, which result from heterosis for desirable traits, such as yield potential and fruit quality. Thus, a crucial step to developing superior quality hybrids involves the selection of the best parents (Borem and Miranda, 2005).

Hybrid breeding technique is one of the most important methods used for crop improvement. The information needed to develop proper F₁ hybrid cultivars

via hybrid breeding could be achieved through different methods including diallel analysis, a method to analyse crosses made among (n) lines in all possible combinations. Diallel analysis as suggested by (Griffing, 1956; Hayman, 1954) are sufficient enough to generate basic information on nature of inheritance of traits and to assess the combining ability of parents. The analysis is mainly adopted when dealing with limited number of parental lines and determines genetic parameters such as heterosis, general combining ability, specific combining ability, heritability and nature of gene action. Heterosis demonstrates the superiority of F₁ progenies compared to the average of their parents. It should be noted that despite of the advantages of hybrid cultivars over open pollinated ones, the high price of hybrid seeds developed via hybridization programs makes the use of them more economical for intensive cultivation (Zengin *et al.*, 2015). Information pertaining to different types of gene action, relative magnitude of genetic variance and combining ability estimates are important and vital parameters to mould the genetic makeup of tomato crop. This important information could prove an essential strategy to tomato breeders in the screening of better parental combinations for further enhancement of desired traits.

The combining ability study is a powerful tool to discriminate good as well as poor combiners for choosing appropriate parental material in plant breeding programme. Moreover, information regarding general and specific combining ability enables the plant breeders to evaluate parental material and to decide a suitable breeding procedure for maximum character improvement. Combining ability effects are considerably influenced by environments. For more valid estimation, a study under different environments is likely to bring out the impact of genotype × environment interaction on the estimates and to frame an effective breeding strategy for the crop to enhance the productivity in the target environment.

The knowledge of nature and magnitude of fixable and non-fixable types of gene effects governing the yield and its components is essential in order to

formulate an efficient and a sound breeding programme to achieve the maximum genetic improvement in tomato. Hybrid vigour in tomato was first determined by Hedrick and Booth (1907). The commercial possibilities of F₁ hybrid production in tomato have been reported by Wellington (1912). Tomato is a self-pollinated inbred crop and the high level of heterosis might not be manifested in tomato F₁ hybrids.

Keeping all the facts under consideration, present investigation entitled “Heterosis and combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) under temperate conditions of Kashmir” was proposed with the following objectives.

1. Identification of desirable parents on the basis of *per se* performance and combining ability effect.
2. To estimate general combining ability (GCA) and specific combining ability (SCA) effects of parents and their crosses among tomato genotypes.
3. To study the nature and magnitude of gene action for yield and yield attributing traits.
4. To study the nature and extent of heterosis for different traits in various cross combinations.

Chapter-2

REVIEW OF LITERATURE

Plant breeding deals with the genetic improvement of crop plants so that they become more desirable agronomically and economically. Thus prime objective of plant breeding is to develop superior plants over the existing ones. The ultimate aim of plant breeder is to improve the yield of economic produce, while quality determines the price of produce in market. The yield and quality may get affected by diseases, insects and other environmental stresses. Thus plant breeding should improve the overall characteristics of plants so that they become more desirable and prove to be commercially successful. The basic requirement for the improvement of a crop is the presence of genetic variation in the population. This variation is tapped through a step called selection that involves the identification and isolation of desirable plants from the variable population. The selection of plants from a population is mostly based on their performance i.e., phenotype because the phenotypic variability is observable. The total variation i.e., the phenotypic variation present in a population has both heritable (genotypic) and non-heritable (environmental) components, the relative contribution of which would determine the value of progeny obtained from the selected plant. Variation of phenotypic values is determined by variances attributable to genotypic values and environmental deviations; and genotypic values in turn are composed of additive genetic variance, variance due to dominance deviations and variance arising due to non-allelic deviations.

In self-pollinated species like tomato homozygosity is exploited for the developed of hybrids. For hybridization first we have to select the parents and parents should be chosen on the basis of their genetic value. Among several techniques available for the evaluation of varieties for their genetic architecture, diallel is in common use. Diallel mating design given by Griffing (1956 a, b) helps in identification of superior parents on the basis of their general and specific

combining ability. This technique also provides information on nature and magnitude of genetic components of variance.

It's possible that the impacts of genetics and environment on phenotype aren't necessarily mutually exclusive. The genotype-environment interaction refers to the interaction of genetic and non-genetic factors on development (Comstock and Moll, 1963). Such interactions have significant implications for the breeder in the development of better varieties. Considering all of the above mentioned details, the relevant information in respect of the proposed investigation of tomato has been covered under the following headings:

- 2.1 Variability
- 2.2 Components of genetic variance and combining ability
- 2.3 Heterosis

2.1 Variability

Variability is the foundation stone for initiating vegetable improvement programme. Study of existing variability amongst available germplasm is foremost step in any crop improvement programme. Genetic variability can be described as the level to which heritable material differ within a group of plants. A wider genetic base, assumes priority in plant breeding aimed at developing new varieties for increased crop production. Hence, knowledge of genetic diversity and relatedness in germplasm is needed for the crop improvement programmes, management and evaluation (Staub *et al.*, 1997). The best diverse genotypes having desirable characters with maximum variability could be included in hybridization programme for crop improvement in future. Selection from quantitative characters is less efficient, if it is based on phenotypic expression. Hence it is important to study the extent of genetic and non-genetic variability expressed by individual characters. So, partitioning of overall variability into heritable and non-heritable components by calculating genetic parameters such as

genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is necessary.

The estimates of different genetic parameters and the association of different characters are important for better understanding of the nature and the magnitude of genetic variability present in the breeding material. Yield is a complex character being influenced by various component factors. Knowledge of inter-relationship among these factors is necessary for indirect selection of higher fruit yielding genotypes by giving appropriate emphasis for each of these characters. The components of genetic variability like h^2 and genetic advance (GA) are essential biometric tools for assessing dissimilarity in population for making a selection (Akhter *et al.*, 2021) and evaluating tomato germplasm for improvement through breeding techniques (Eppakayala *et al.*, 2021; Javed *et al.*, 2022) studied the higher PCV and GCV for yield and yield-related traits in tomato hybrids and indicated the role of genetic variability in plant selection.

Kaushik *et al.* (2011) determined the genetic variability in ten genotypes of tomato. The variation was maximum (424 to 825 q/ha) for fruit yield and minimum for fruit width (4.1 to 5.6 cm). The magnitude of genotypic and phenotypic coefficient of variation was higher for number of leaves (21.2 and 22.3), fruit length (19.6 and 19.7 cm) and fruit yield (19.6 and 19.6). High values of heritability coupled with high genetic advance were observed for number of leaves at 60 days after transplanting (99.4 and 64.9) and fruit yield (99.9 and 24.7). A positive association of yield per hectare observed with number of leaves at 60 days after transplanting (0.78) followed by number of leaves at 30 days after transplanting (0.68), fruit length (0.66) and plant height (0.51).

Mohamed *et al.* (2012) studied heritability, genetic advance and genetic advance as percentage over mean and genetic variability among different plant and fruit characters of thirty tomato genotypes and reported significant variation among the genotypes for all characters. Highest genotypic and phenotypic variances (1642.9 and 1779.1) were observed in fruit weight, whereas fruit yield

per plant showed the lowest genotypic and phenotypic variance (0.17 and 0.39). High genotypic variance was observed for most of the characters indicating more contribution of genetic component for the total variation. Genotypic coefficients of variations (GCV) and phenotypic coefficient of variation (PCV) were highest for fruit weight (0.4885 and 0.4905) whereas the lowest ones were for days to 50% flowering (0.0552 and 0.0665). Higher GCV and PVC were recorded for most of the characters indicating higher magnitude of variability for these characters. The highest heritability was recorded on plant height (97%), while the lowest was for fruit yield per plant (43%).

Five genotypes of tomato were evaluated by Osekita *et al.* (2013) to study the interrelationship among various quantitative traits and recorded significant variation among the genotypes. The highest coefficient of variation (66.56%) was observed in average fruit weight.

In a study conducted by Reddy *et al.* (2013) in nineteen tomato genotypes, it was reported that genotypes exhibited a wide range of variability for all the characters studied. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV). High heritability combined with high genetic advance was observed for the characters plant height, number of clusters per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit length, fruit weight, fruit yield per plant, ascorbic acid, acidity, shelf life and TSS.

Ullah *et al.* (2015) studied genetic variability in twenty parental genotypes of tomato for yield and yield attributing traits. Parent TM 371 ranked first with respect to yield followed by TM 390. High genotypic and phenotypic coefficients of variation were recorded for fruits/plant, locule number/fruit and fruit yield/plant. High heritability associated with high genetic advance was observed for fruits/plant (52.30), fruit weight (46.32) and flower/cluster (33.50).

Thirty different tomato genotypes were studied by Hasan *et al.* (2016) for determining genetic variability in yield and yield contributing traits along with quality traits. Yield contributing traits showed higher phenotypic co-efficient of variation as compared to their corresponding genotypic co-efficient of variation indicating considerable environmental influences on them. Individual fruit weight showed high heritability (99.71) with high genetic advance (85.4) followed by fruits/ plant (99.65 and 81.26). High heritability with low genetic advance was observed for number of primary branches (75.87 and 3.67), fruit cluster/plant (99.49 and 6.12), fruit diameter (98.83 and 5.59), total soluble solid (80.51 and 1.85) and ascorbic acid content (90.75 and 9.52).

Rai *et al.* (2016) carried out a study on variability in tomato and observed the phenotypic coefficient of variation was slightly larger than the genotypic coefficient of variation for all the traits investigated. Number of fruits per plant, average fruit weight, fruit yield per plant, locular wall thickness and lycopene content all had high estimates of heritability and genetic gain.

Ashish *et al.* (2017) studied variability and correlation in ten quantitative and three quality traits. Among all the genotypes, DARL-62 showed the highest fruit yield/hectare (232.36 q/ha). Higher phenotypic and genotypic coefficients of variation were observed for average fruit weight, number of fruits/plant and percentage acidity. High heritability coupled with high genetic advance as percent of mean were estimated for average fruit weight, number of fruits/plant, percentage acidity, pericarp thickness and number of locules/fruit. The yield/hectare displayed positive correlation with number of fruits/plant, pericarp thickness, number of locules/fruit, average fruit weight, ascorbic acid content and yield/plant. Path analysis indicated that positive direct effect on fruit yield/ hectare was exerted by yield/ plant, number of flowers /inflorescence, number of locules/ fruit, ascorbic acid content, percentage acidity, fruit diameter, plant height and total soluble solids.

Kumar *et al.* (2017) evaluated thirty five genotypes including one check cultivar. High phenotypic and genotypic coefficients of variation were depicted for the characters like number of fruits per plant (51.80 and 50.00%), fruit yield per plant (52.18 and 51.10%), fruit yield per plot (53.21 and 51.91%), fruit yield per hectare (53.21 and 51.91%) and plant height (36.85 and 36.38%). High heritability coupled with moderate genetic gain was observed for number of fruits per cluster, harvest duration and ascorbic acid content.

Ligade *et al.* (2017) evaluated twenty genotypes of tomato and reported significant variability for all the studied characters. High values of GCV and PCV were observed for characters viz., number of fruits per plant (55.74, 56.21), number of locules per fruit (36.44, 37.15), average fruit weight (35.45, 35.97), fruit yield per plant (31.09, 32.35) and marketable fruit yield per plot (31.10, 32.36). High heritability coupled with high genetic advance were observed for the traits viz., plant height, number of flowers per cluster, number of fruit set per cluster, average fruit weight, number of fruits per plant, fruit yield per plant, fruit yield per plot, fruit shape index, TSS °Brix, ascorbic acid, beta carotene, pericarp thickness and number of locules per fruit.

Thirty-five genotypes of tomato were evaluated for yield and yield attributing characters by Singh *et al.* (2017). High magnitude of phenotypic as well as genotypic co-efficients of variation were observed in fruit yield per plant followed by average fruit weight, number of locules per fruit, number of fruits per plant, plant height and number of primary branches per plant. Days to 50 per cent flowering exhibited low level of variability.

Sureshkumara *et al.* (2017) conducted study on twenty four tomato genotypes for growth, yield and quality attributes. It was observed that D-6-1-9-6-1 and Nandi exhibited least days taken to fifty percent flowering (26.50 days), IIHR-2201 recorded highest number of branches at 45 DAT (5.32), 60 DAT (8.92), number of flowers cluster⁻¹ (6.06), number of fruits cluster⁻¹ (52.32), fruit yield plant⁻¹ (3.06 kg) and fruit yield ha⁻¹ (68.06). Genotype IIHR-2200 recorded

maximum average fruit weight (165.37 g) and number of locules fruit⁻¹ (10). Highest TSS (6.65 °Brix) was recorded in C-13-1-2-1, fruit firmness in Kashi Vishesh (2.97 kg/cm²), titrable acidity in IIHR-2198 (0.57), TSS: Acid ratio in Kashi Amrutha (33.03), ascorbic acid in D-12-1-6-1 (33.16 mg/100 g) pH in A-15-3-2-1 (4.50) and pericarp thickness in IIHR-2199 (5.82 mm).

While studying genetic variability, heritability and genetic advance in tomato Rajolli *et al.* (2017) reported presence of sufficient amount of variability among all the traits. Very little differences were observed between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the characters except fruit firmness (kg/cm²) and TSS (°Brix) indicating that most of the traits were less influenced by environmental factors for their phenotypic expression. High heritability coupled with high genetic advance as per cent mean was observed for plant height, number of branches, number of fruits per plant, average fruit weight, pericarp thickness, number of locules, ascorbic acid and yield per plant.

Kumar *et al.* (2018) conducted study on thirty genotypes of tomato and reported significant variation among genotypes for all the twelve characters. The minimum fruit yield per plant was harvested in (NDT-515) 1.63 kg while maximum fruit yield per plant was recorded in (NDT-517) 2.1 kg. Highest phenotypic coefficient of variation was observed in case of locules per plant followed by average pericarp thickness, plant height, primary branches per plant, diameter of fruit and TSS. The heritability in broad sense ranged from 20.08% for fruit diameter to 97.20% for plant height.

Kerketta and Bahadur (2019) evaluated twenty tomato genotypes for variability, heritability and genetic advance in yield and quality characters. Higher magnitude of GCV and PCV, respectively were recorded in acidity (28.21-42.89) followed by (28.04-40.51) TLCV. All the characters showed high heritability ranging from 95 % to 90%. The traits like fruit weight, locules/fruit and TSS, with

high GCV, PCV, heritability and genetic advance as percentage of mean, indicated that these characters were under additive gene effects.

Reddy *et al.* (2019) estimated genetic variability, heritability and correlation studies on twenty five tomato genotypes for nineteen different characters. On the basis of mean performance highest fruit yield /plant was exhibited by genotypes PKM-1 followed by Arka Rakshak, Pusa Hybrid-4 and Arka Abhay. Highest genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) was observed for plant height followed by fruit weight, number of fruits/plant. High heritability coupled with high genetic advance was observed for plant height, number of primary branches, days to 50% flowering, fruit length and fruit weight.

For all of the characteristics investigated by Saravanan *et al.* (2019), phenotypic variance was high relative to genotypic variance, with the highest levels for yield per plant, average fruit weight and plant height. For yield per plant, number of fruits per plant and number of locules per fruit, high PCV, GCV and genetic advance were observed, showing an additive genetic influence.

Basfore *et al.* (2020) conducted study on genetic variability and heritability using thirty seven genotypes of tomato for different quantitative traits. On the basis of analysis of variance, significant differences were observed among the genotypes for all the characters under study. The high (> 30%) genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for yield per plant (i.e., 57.31% and 58.14%, respectively) followed by fruit weight (i.e., 35.27% and 35.49%, respectively). High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) were present in all the characters depicted the existence of additive gene effect.

Kumar *et al.* (2020) observed highest GCV and PCV for number of fruits per plant. The PCV was larger than the GCV. The highest heritability was observed for number of fruit per plant (99.3%), followed by plant height (98.4%),

days to flowering (97.5%), fruit weight per plant (97.3%), days to maturity (97.1%), fruit length (95.7%), number of locules per fruit (92.6), number of primary branch per plant (92.2%) and number of fruit cluster per plant (89.3%). High heritability estimates along with high genetic advance was reported in number of fruits per plant (145.46) and minimum for days to maturity (41.02).

Rawat *et al.* (2020) carried a study on genetic parameters for yield and attributing traits, recorded high PCV and GCV for number of fruits/plant, followed by average fruit weight (g), fruit yield/hectare (q/ha) and ascorbic acid (mg/100 g). For ascorbic acid (mg/100 g), number of fruits/plant, average fruit weight (g), fruit yield/hectare (q/ha), number of locules/fruit, pericarp thickness (mm) and number of fruits/cluster, the heritability combined with genetic advance as a percentage of mean was high.

Sushma *et al.* (2020) revealed that the phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the traits studied. Number of fruits per plant, average fruit weight, fruit yield per plant, number of primary branches per plant, TSS, beta-carotene content, lycopene content, ascorbic acid content, plant height, fruit length and fruit width all had high heritability and genetic advance as percent of mean.

High PCV and GCV were recorded by Eppakayala *et al.* (2021) in fruit weight, fruit yield per plant, yield per hectare and total soluble solids. For percent fruit set, days to first harvest, days to last harvest and ascorbic acid content, low estimates of GCV and PCV were found. High heritability coupled with high genetic advance was recorded in plant height, days to first flowering, days to 50% flowering, number of flower clusters per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, number of marketable fruits per plant, days to first harvest, days to last harvest, fruit length, fruit width, fruit weight, fruit yield per plant, fruit yield per hectare, total soluble solids, ascorbic acid content, lycopene content and beta-carotene.

Mahebab *et al.* (2021) revealed highest phenotypic and genotypic coefficients of variability for average fruit weight, followed by lycopene content, seed-pulp ratio, fruit firmness, shelf life, number of primary branches per plant, number of locules per fruit and pericarp thickness. Average fruit weight also had the highest heritability and genetic gain. Plant height at 90 DAT, days to 50% blooming, average fruit weight, days to first harvest and days to last fruit harvest all had high heritability and moderate genetic gain, showing a wide range of variance and genetic gain.

Waiba *et al.* (2021) estimated genetic variability among twelve hybrids of tomato in protected conditions. Based on the mean performance, hybrid CLN2126 × CLN1314G was found promising for yield plant⁻¹ (4.37 kg) yield m⁻² area (26.24 kg), TSS (6.53 °B), days to 50% flowering (26.66 days), days to first picking (67.33 days), number of fruits per plant (64.01), inter-nodal length (17.71 cm), number of nodes plant⁻¹ (16.70 nodes) and plant height (316.87 cm). The hybrid combination CLN2126 × CLN1314G is promising for yield contributing traits.

Mishra *et al.* (2022) evaluated the degree of genetic variability, heritability and genetic progress among thirty seven tomato varieties using morphological features. On the basis of mean performance of weight of fruits per plant, genotype superior to check genotype are 7053, 8105, 8202, 8623 and 8730 as compared to the best checks 8716 and 9426. The result showed higher phenotypic coefficients of variation for all characters compared to genotypic coefficients of variation. High phenotypic coefficient of variation recorded by fruit number per plant (38.07) followed by fruit weight per plant (33.49) and days to flowering (28.09) while high genotypic coefficient of variation was identified by fruit number per plant (37.60), followed by fruit weight per plant (32.94) and flowering days (27.52). The number of fruits per plant showed high genetic advance (53.66) followed by maturity days (23.27) and plant height (20.73).

Genetic variability study was conducted in quantitative traits of tomato by Nkansah *et al.* (2022). The individual analysis of variance performed for the data gathered revealed a significant ($P < 0.01$) variability among the cultivars for most of the traits. Variance components estimated on individual location basis indicated a moderate to high genotypic coefficient of variability (GCV), high broad sense heritability as well as high genetic gain for most of the traits.

Rasheed *et al.* (2022) investigated the genetic variability, heritability and genetic advance for yield and yield related traits using eight tomato parents and their fifteen crosses. Significant variation was observed for all studied traits. Higher values of the genotypic coefficient of variability and phenotypic coefficient of variability were recorded for yield per plant (37.62% and 37.79%), as well as the number of fruits per cluster (31.52% and 31.71%), number of flowers per cluster (24.63 and 24.67) and single fruit weight (23.49 and 23.53), which indicated that the selection for these traits would be fruitful. Higher heritability (h^2) estimates were observed for the number of flowers per cluster (0.99%), single fruit weight (g) (0.99%) and yield per plant (0.99%). Single fruit weight (g) exhibited higher values for all components of variability. High genetic advance as a per cent of the mean (GAM) coupled with higher heritability (h^2) was noted for the yield per plant (52.58%) and the number of fruits per cluster (43.91). Among the fifteen hybrids, Nagina \times Continental, Pakit \times Continental and Roma \times BSX-935 were found to be high yielding hybrids.

2.2 Components of genetic variance and combining ability

The genetic variance of any quantitative traits is due to additive variance and non-additive variance and include epistasis (non-allelic interaction) and dominance. It is necessary to partition the observed phenotypic variability into its heritable and non-heritable components with parameters. Exploring natural diversity as a source of novel alleles to improve the productivity, quality and nutritional value of the crop is the base line of any breeding programme (Ferne *et al.* 2006). Exploitation of hybrid vigour and selection of parents on the basis of

combining ability and gene action have been important breeding approaches in crop improvement. The studies of combining ability is essentially useful in connection with testing procedures in which it is desired to study and compare the performance of a line in hybrid combination.

Further, some parents produce superior F_1 's while others do not. Hence, it would be desirable to have information about genetic systems governing the inheritance of traits that need to be improved in order to assess and predict the potential of F_1 generations. Although several approaches for estimating GCA and SCA effects have been proposed in various literatures. Line \times tester mating design (Kempthorne, 1957) and diallel mating design. Diallel analysis is the quickest way to comprehend the genetic nature of polygenic features, as well as determining parent prepotency and is often utilized in this regard. The analysis of a set of F_1 s can yield numerous estimations necessary for studying the genetics of breeding materials.

2.2.1 Diallel analysis

Different biometrical techniques are now available to select parental lines suitable for hybrid seed production. Diallel analysis technique developed and illustrated by Hayman (1957) and Jinks (1956) provides guideline for the assessment of relative breeding potential of the parents and has been extensively used to identify good combiner parents in various crops like tomato (Pratta *et al.*, 2003; Chishti *et al.*, 2008). This technique also provides information on gene action controlling the expression of desired traits. Based on information on combining ability and gene action, the selected lines can be combined either to exploit hybrid vigor by accumulating non-additive gene effects or to evolve cultivars by accumulating additive gene effects.

2.2.2 Griffing's analysis

In this approach, using a suitable statistical model, the component variances due to general and specific combining ability are estimated which, in turn may be translated into genetic components.

In a diallel crossing system 'n' number of homozygous parents of a set are crossed in all possible combinations to produce n^2 number of progenies. Three sets of materials are involved namely, parents, F_1 crosses and reciprocals. Griffing (1956b) provided four methods of diallel depending on the materials involved in the analysis.

Method I: Parents, F_1 's and reciprocals

Method II: Parents and F_1 's only

Method III: F_1 's and reciprocals and

Method IV: F_1 's only

The Griffing (1956 b) method II including parents and their F_1 hybrids provides information about GCA, SCA and heterosis which are very useful parameters in hybrid breeding programme (Singh and Singh, 1984; Christic and Shattuck, 1992).

Griffing has outlined the procedures for combining ability analysis in each type of diallel cross. In addition to these methods, Griffing described models based on the sampling nature of the experimental materials. Out of these models two are important

Model I Fixed effect model: It is a method of diallel analysis which is used with diallel set of crosses made using inbred lines. Here inferences are drawn about individual line or variety

Model II Random effect model: Used when diallel set of crosses made among samples of individuals from random mating population, inferences are drawn about population as whole.

In the present investigation, Method II and Model I have been employed for combining ability analysis for GCA and SCA. GCA estimates the mean performance of a parent relative to all its hybrid combinations and indicates additive genetic effects (Sprague and Tatum, 1942). Additive gene action is the

chief cause of resemblances between relatives and progress by selection is directly proportional to the degree of resemblance between the parent and its progeny. Thus additive gene action is the measure of breeding value of a genotype. SCA measures the specific behaviour of each hybrid relative to their corresponding parents and estimates dominant genetic effects (Sprague and Tatum, 1942). Combining ability analysis plays a role in selection of parents for hybridization and in choice of appropriate breeding procedure. If there is preponderance of additive gene action, reliance should be placed on mass selection and progeny selection in self-pollinated species and synthetic and composite breeding in cross pollinated species. If there is preponderance of non-additive gene action, the breeding objective should be towards development of hybrids for commercial purpose. If both additive and non-additive gene actions are of equal magnitude, population improvement programme should be taken up for the development of superior lines with several desirable genes. In cross pollinated species, recurrent selection for GCA and SCA are effective with additive and non-additive gene effects, respectively and reciprocal recurrent selection utilizes both types of gene effects.

Genetic variances which are the relative measures of gene action are used for working out various genetic parameters e.g., additive genetic variance is required for the estimation of narrow sense heritability and response to selection is directly proportional to narrow sense heritability. The additive and dominance variances are required for the estimation of degree of dominance and various genetic ratios. A GCA/SCA variance ratio gives the importance of additive and dominance/epistatic effects (Bhullar *et al.*, 1979).

2.2.3 Hayman's and Jink's analysis

This approach is based on the estimation of components of variation. It was initially developed by Jinks and Hayman (1953) and later elaborated by them independently using Mather's concept of D, H components of variation. The methods of analysis developed by Jinks and Hayman (1953), Hayman (1954,

1954 b, 1957) and Jinks (1954, 1956) have been widely used for evaluation of the mode of inheritance (Powell, 1988). The additional developments about this technique were described in detail by Mather and Jinks (1971), Aksel and Johnson (1963), Mather and Jinks (1982) and Christic *et al.* (1988). In Hayman's graphical approach, a graph is drawn with the help of variances of array and co-variances between parents and their off-springs. The graph is known as Vr-Wr graph, it gives information about average degree of dominance.

The diallel analysis is based on seven assumptions as given by Hayman (1954): Normal diploid segregation, homozygous parents, no reciprocal differences i.e., lack of maternal effect, absence of epistasis and random mating, no multiple allelism and independent distribution of genes among parents i.e., no linkage.

Six components of variation are estimated *viz.*, D (additive variance), H_1 (dominance variance), H_2 (proportion of positive and negative genes in parents), E (expected environmental component), F (mean of F_r over the array where F_r is the covariance of additive and dominance effect in a single array) and h^2 (dominance effect). From these estimates, some genetic ratios are determined which in case of F_1 generation are average degree of dominance $(H_1/D)^{1/2}$, the ratio of dominant and recessive genes in the parents $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$, the number of gene groups (h^2/H_2) and the proportion of genes with positive and negative effects in the parents ($H_2/4H_1$).

Hannan *et al.* (2007) studied combining ability for yield and yield components in tomato including traits such as plant height at 60 days, number of flowers/cluster, number of fruits/ plant, fruit weight/plant and number of seeds/fruit. Results showed that parents Pusa Ruby, Bari-4 and Dynasagor had good general combining ability effects. For yield, the crosses Deshy \times Ratan, Deshy \times Epoch, Dynasagor \times Ratan, Bari-4 \times Pusa Ruby and Dynamo \times Namdhari had good specific combining ability effects and could produce stable performing rare transgressive segregants.

Solieman (2009) evaluated five commercial tomato cultivars and their ten F₁ hybrids, in a diallel cross system without reciprocals to detect the general and specific combining ability and heritability percentages in broad and narrow senses. The general performances of the F₁ hybrids of some characters reflected the presence of partial to over-dominance, but with different magnitudes. These results showed high estimates of σ^2_s relative to those of σ^2_g . The best general combiner parent was found to be cultivar "Super Marmand" (for the characters plant height, number of branches per plant and total soluble solids), cultivar "Peto-86" (for the characters plant height, days to first flower, number of flowers per cluster, number of fruits per plant and fruit shape index), cultivar "Edkawy" (for the characters fruit weight, fruit diameter, fruit length and fruit locules number) and cultivar "Super Strain-B" (for the character total fruit weight per plant). Also the best hybrid combinations were C x M (for the plant height), S x E (for the four characters number of branches per plant, plant height to the first flower, number of fruits per plant and total fruit weight per plant), C x P (for the characters number of flowers per cluster and fruit shape index), M x E (for fruit weight), S x M (for the fruit length character), P x S (for fruit diameter and number of locules per fruit) and the cross P x M (for total soluble solids).

Rani & Veeraragavathatham (2011) carried out study on combining ability and gene action in F₁ tomato hybrids for yield and processing quality. CLN 2026C × SL120, CLN 2026E × SL 120, LE 812 × SL 120 and CLN 1464A × SL 120 were chosen as the best specific combiners for yield and processing qualities. For all the characters, SCA variance was higher than GCA variance, indicating that non-additive gene action plays a larger role.

Amin *et al.* (2012) studied combining ability effect of ten parental lines of tomato using diallel mating design for different traits including days to first fruit set, days to first picking, plant height, number of primary branches/plant, fruit size, flesh thickness, number of fruits/plant, average fruit weight, fruit yield /plant and number of locules. None of the parents exhibited desirable GCA effects for all

the traits in individual as well as in pooled analysis. However, overall ranking of genotypes revealed that the parents Arka Vikas, KS-227, Roma, DVRT-I and DARL-63 exhibited significant desirable GCA effects for most of the traits.

In a diallel analysis for yield and yield components in tomato, Saleem *et al.* (2013) revealed highly significant differences among tomato genotypes for days to maturity, plant height, number of fruits/plant, fruit weight, fruit length, fruit width and fruit yield/plant. Significant mean squares for general combining ability, specific combining ability and reciprocal combining ability indicated joint role of additive, non-additive and maternal effects for the expression of traits such as days to maturity, fruit length and fruit yield/ plant. The ratio of GCA/SCA variance was less than 1 for days to maturity, plant height, number of fruits/plant, fruit weight, fruit length and fruit yield/plant. Among parents, B 26 and B 27 were found good general combiners for yield and yield related traits. The hybrids *viz.*, B 23 × B 27, B 25 × B 26 and B 24 × B 27 exhibited significant SCA effects.

Combining ability was studied by Souza *et al.* (2012) using a diallel cross excluding reciprocals. IAC-2 was the best parental line for fruit yield per plant with the highest GCA, followed by IAC-4 and IAC-1 lines. Hybrids IAC-1 × IAC-2, IAC-1 × IAC-4 and IAC-2 × IAC-4 showed highest SCA effects.

Aisyah *et al.* (2016) estimated the general combining ability, specific combining ability and heterosis for yield/plant and yield components using diallel cross set of tomato including reciprocals. Significant differences among genotypes were obtained for all the traits. The variances for general combining ability and specific combining ability 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 found to be parent with the best general combining ability for yield/plant, individual fruit weight, fruit length and fruit thickness. The tomato genotype IPB T73 × IPB T3 proved to be the best general combiner for yield and number of fruits/plant. The tomato genotype IPB T3 × IPB T1 proved to exhibit best heterosis for yield/plant and fruit thickness.

Dharva *et al.* (2018) studied combining ability and gene action for yield and yield attributing traits. Twenty one F₁ hybrids were generated through half diallel mating design comprising of seven lines and 'Abhinav' was used as standard check. The analysis of variance for combining ability revealed that variance due to general combining ability and specific combining ability were highly significant for all the characters except days to last picking, plant height and number of locules/fruit. The estimates of GCA effects indicated that parent AVTO-4 was good general combiner for fruit yield and its contributing characters while the hybrids AVTO-2 × AT-4 and AVTO-3 × AVTO-4 had higher *per se* performance and SCA effect for fruit yield and its yield contributing traits.

Kaushik and Dhaliwal (2018) conducted diallel study under the influence of tomato leaf curl virus (TLCV) disease, using the eleven advanced lines of tomato. Firstly, information regarding percent disease index was determined via artificial screening. Later, these lines were crossed in a half diallel mating design to produce fifty five one-way hybrids. These hybrids and parental genotypes were evaluated for morphological and biochemical traits, using the Griffings approach. The significant general combining ability (GCA) and specific combining ability (SCA) values indicate exploitable genetic variation. The broad sense heritability values were larger than narrow sense heritability. Hybrid combinations H23, H42 and H49 were efficient for the multiple traits, including yield.

Sureshkumara *et al.* (2018) studied the combining ability of parents and crosses for fruit yield and quality components in tomato using forty five hybrids involving ten lines in half diallel design. The 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. Five parents viz., C-13-1-2-1, IIHR-2199, D-12-1-6-1, IIHR-2201 and Arka Sourabh were good general combiners for yield per plant as they have shown significant gca effect in positive direction. The crosses, D-12-1-6-1 × D-6-1-9-6-1, Arka Sourabh × C-13-1-2-1, Arka Sourabh × D-6-1-9-6-1 and Arka Sourabh × C-13-1-2-1 are best specific

combiners for average fruit weight, number of fruits per cluster, number of clusters per plant and yield per plant respectively. These are the combinations of parents with positive \times positive gca effects. Among these crosses Arka Sourbah is common parent indicating the presence of additive \times additive type of gene action in the expression of these characters.

Amin *et al.* (2018) evaluated forty five F₁ hybrids produced in a diallel fashion and their ten parents for yield attributing traits. Positive and significant 'F' values for number of primary branches/plant, flesh thickness, number of fruits/plant, average fruit weight and fruit yield/plant indicated positive direction of dominance. Average degree of dominance was more than unity in all the traits indicating over-dominance. Non-significant values of t^2 and deviation of regression coefficient from unity depicted the absence of epistasis for all the traits in all the environments and pooled analysis.

Gautam *et al.* (2018) conducted diallel analysis which revealed highly significant differences among six tomato lines for number of locules/fruit, pericarp thickness, whole fruit firmness, total soluble solids, ascorbic acid and lycopene content. The predictability ratio of GCA/SCA variance was found less than one for number of locules/fruit, pericarp thickness, whole fruit firmness, total soluble solids, ascorbic acid and lycopene content showing preponderance of non-additive gene effects. Among parents, UHFT-9, UHFT-10 and UHFT-55 were found good general combiners whereas hybrids *viz.*, UHFT-9 \times Solan Lalima, UHFT-10 \times Solan Lalima, UHFT-22 \times Solan Lalima and UHFT-55 \times EC-2798 had more and significant SCA effects.

Barragan *et al.* (2019) studied seven elite tomato lines using diallel fashion without reciprocals to produce twenty one F₁'s. Results showed highly significant differences among genotypes, as well as in GCA and SCA effects in all the characteristics, with the exception of days to first fruit harvesting. The results revealed that variance contribution to the yield attributed to the crosses had more non-additive effects (SCA) than additive effects (GCA). The line D4 had the

greatest effect on yield in terms of GCA, as well in average fruit weight, number of fruits/plant and polar diameter followed by D3 and K3. Hybrids K3 × D4, R1 × Y53, D3 × IR13 and F3 × Y53 had the highest level of SCA.

Mishra *et al.* (2020) studied the combining ability of ten parents of tomato and forty five hybrids for fruit yield and quality components developed by half diallel mating. The best general combiners for various traits were BT-507-2-2 for plant height, branches/plant, flowers/cluster, fruits/cluster, yield/plant and yield/plot. Similarly BT-22-4-1 for number of clusters/plant, fruits/plant, diameter of fruit and average fruit weight. Utkal Deepti for days to first flowering, TLCV incidence while BT-317 for days to 50% flowering, acidity content; BT-21 for fruit length; BT-19-1-1-1 for pericarp thickness; BT-1 for number of locules /fruit, total soluble solid content, ascorbic acid content and BT-17-2 for bacterial wilt incidence. Utkal Kumari × BT-22-4-1, BT-19-1-1-1 × BT-3, Utkal Kumari × BT-19-1-1-1, BT-22-4-1 × BT-3 and BT-19-1-1-1 × BT-507-2-2 were found to be best specific combiners for yield/ plant.

Kaveh *et al.* (2020) determined the combining ability of seven inbred lines which were selected from one hundred thirty three tomato lines based on variation in morphological, biological and agronomical traits. F₁ hybrids were evaluated for salinity tolerance during seedling stage using the diallel-cross. Results show that the reciprocal effects and SCA were significant for all traits on probability of 1 %. Analysis of W_r-V_r regression also show that seed germination percentage and seedling emergence percentage and rate under salt stress controlled by over-dominance effects. Best line for resistance to salt stress in juvenility was R205 which has the most GCA for all three traits connected to salt resistance which can be used as parental line for salinity tolerance.

Bhandari *et al.* (2021) evaluated twenty one hybrids of tomato for quality traits viz., total soluble solids, titrable acidity, carotene content and lycopene content. Combined analysis of variance revealed significant effects of locations, genotypes, genotype-location interaction and parents vs hybrids-location

interaction for all the traits. The significance of combining ability effects (general combining ability and specific combining ability) and their interaction with location revealed environmental influences on combining ability effects for all the traits. The higher estimates to lower estimates of heritability and GCA/SCA ratio for quality traits and thereby implied preponderance of non-additive gene action in determination of quality traits studied. Desirable parental lines were identified for different traits like EC 620438 and BS 24-2 for TSS, BS 24-2 and Superbug for titrable acidity, Columbia, EC 620438 and Superbug for carotene content and H 86 and EC 620541 for lycopene content. The hybrid combination EC 620438 × BS 24-2 appeared good specific combiners for TSS, carotene and lycopene content.

The study carried out by Matos *et al.* (2021) for combining ability and heterosis of tomato genotypes included fifteen double-cross hybrids, their genitors and two commercial genotypes as checks using partial diallel crosses. Of the fifteen double-cross hybrids of tomato, two crosses i.e., Aguamiel × Compack and Dominador × Compack, exhibited superiority for the total and commercial fruit yields. The heterosis values were low for most of the crosses, except for Forty × Plutao that represented 107 percent of heterosis for the total fruit yield.

Singh *et al.* (2021) estimated nature and magnitude of gene action involved in inheritance of yield and yield attributing traits in tomato using diallel mating design. Ten diverse parents and their forty five hybrids were evaluated for sixteen different characters. Analysis of variance revealed significant differences for the parents, F_1 's and parents *vs.* F_1 's for all the characters indicating wide variation. Both additive and dominance variance were found important in the inheritance of most of the traits, whereas dominance variance was more prominent than the additive variance.

Soresa *et al.* (2021) estimated the general combining ability and specific combining ability using half diallel cross set of eight tomato lines excluding reciprocals for marketable fruit yield/ plant (kg) and other yield components,

namely number of fruits/plant, individual fruit weight (g), fruit length (cm), fruit diameter (cm) and fruit thickness (cm) and some quality traits such as TSS, pH and pericarp thickness. Significant differences among genotypes were obtained for all the traits except for number of primary branches /plant. The effects of 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 for fruit length and fruit diameter. The genotype P8 was selected as a parent with the best general combining ability for marketable fruit yield/plant, individual fruit weight, fruit density and fruit thickness. The tomato hybrid P5 × P7 followed by P3 × P6 and P3 × P7 proved to be the best specific combiners for marketable fruit yield and number of fruits/plant.

A study conducted by Nayana *et al.* (2021) on combining ability effects for determining superior cross combinations using five parents *viz.*, EC 362941, EC 15127, EC 521061, EC 521069 and VRT 13 with their twenty crosses through full diallel mating design. The results revealed that among the parents, EC 362941 was found good general combiner for pericarp thickness, shelf life, chlorophyll content and firmness. Parent EC 521069 found good general combiner for TSS, beta-carotene content and lower titratable acidity. Parent VRT 13 was considered as best general combiner for lycopene, lower number of locules and total sugars. The highest significant desirable SCA effect was observed by the cross combination EC 362941 × EC 521069 for most of the quality traits. Five quality characters each showed GCA to SCA ratio lesser and more than the unity indicating the predominance of both additive and non-additive gene action in tomato.

Ibirinde *et al.* (2022) conducted study to determine gene actions controlling yield and other quality traits of tomato as well as combining ability among five genotypes and ten F₁'s obtained from a 5 × 5 diallel analysis. Results showed significant differences among the genotypes, for all the measured characters. The ratio of GCA and SCA were < 1 for plant height, number of

cluster per plant, days to 50% flowering (50%FL), individual fruit weight, number of fruits per plant, pericarp thickness, number of lobe, number of seeds per fruit, fruit lycopene, ascorbic acid content and fruit yield thus revealing the preponderance of non-additive gene action. GCA analysis suggested that parents Uc-op and Ibadan-local were the best general combiners while, SCA performance suggested that $FDT_4 \times FDT_2$ was the best specific combiner. Broad sense heritability for number of lobe, number of seeds per fruit, fruit lycopene and ascorbic acid content were above 90%, indicating that they were highly heritable while narrow sense heritability for number of lobes was very high (55% and 83% respectively), Plant height, number of cluster per plant and fruit lycopene were moderate ranging between 20% and 38%.

Gene action studies in tomato for yield and yield attributing traits using diallel analysis was conducted by Farwah *et al.* (2022) for different yield and yield contributing traits using twelve different lines of tomato crossed in diallel fashion (excluding reciprocals). Analysis of variance of the components of genetic variation revealed that the additive variance component (D) and those of dominance components (H_1 and H_2) were found to be significant in all environments and data pooled over environments. Thus both additive and non-additive gene action are involved in the inheritance of characteristics.

The study on combining ability effects for various quantitative traits was determined by Lone *et al.* (2022) using ten diverse lines of cherry tomato crossed in half diallel fashion. Analysis of variance revealed significant differences for all the traits under both environments. The magnitude of SCA variance was higher than the corresponding GCA variance for all the traits under study, indicating the prevalence of non-additive gene action for all the traits except for days to first flowering, days to first fruit set and days to first fruit maturity in E1 and data pooled over environments. Based on GCA effects of parents, lines WIR-5032, EC-520074 and EC-914092 in E1 and lines WIR-3957, WIR-5032 and Sun Cherry in E2 were found to be good general combiners for most of the traits. The

crosses WIR-5032 × WIR-3957, EC-914115 × VRT-02 and EC-520074 × EC-520078 in E1 and EC-520078 × VRT-02, EC-914092 × VRT-02 and EC-165690 × WIR-3957 in E2 were found to be the superior cross combinations on the basis of fruit yield plant⁻¹.

2.3 Heterosis

Heterosis is the superiority of an F₁ over both its parents in terms of yield and some other characters. Generally, heterosis is manifested as an increase in vigour, size, growth rate, yield or some other characteristic. But in some cases the hybrid may be inferior to the weaker parent which is also regarded as heterosis. Often the superiority of F₁ is estimated over the average of two parents or the mid parent which is regarded as average heterosis or simply heterosis. More generally, heterosis is estimated over the superior parent which is referred to as heterobeltiosis. Also heterosis is estimated over the commercial check which is referred to as standard/economic heterosis. Powell (1988) suggested that the term heterosis should be used only when the hybrid is either superior or inferior to both the parents. Later on, the scope of this term was enlarged by scientists to include many other situations as well (Dobzhansky, 1950).

Heterosis manifests in tomato in form of greater vigour, faster growth and development, earliness in maturity, increased productivity and higher levels of resistance to biotic and abiotic stresses. Identification and selection of potential parental lines is required, which can be used in any hybridization programme to produce genetically improved and potentially rewarding germplasm by assembling fixable gene effects in a homozygous line. Exploitation of heterosis is primarily dependent on the screening and selection of available germplasm that could produce better combinations of important agronomic characters.

Sharma and Thakur (2008) crossed ten diverse tomato lines in diallel fashion. The forty five F₁'s along with ten parents were evaluated for different traits and compared to standard hybrid Naveen. On the basis of *per se*

performance and heterosis over better parent, the cross FT-5 × UHF-659 showed the highest positive heterobeltiosis. The cross AI-9 × UHF-612 was identified as early yielding cross. The heterobeltiosis effect for number of fruits/cluster ranged from 34.39 (EC-15998 × FT-5) to 33.0 percent (FT-5 × UHF-612). AI-9 yielded significantly higher than all other parents. The fruit yield among the crosses varied from 764.33 (EC- 174023 × UHF-663) to 1808.23 g (AI 9 × Solan Vajr). Thus high degree of variability and heterosis in positive direction was found among the crosses.

To estimate the level of heterosis for yield and yield components, a study was conducted by Gul *et al.* (2010) in tomato using 8 × 8 diallel set omitting reciprocals. For all of the characteristics investigated, there were highly significant differences across genotypes. Flowers per cluster (53.1 and 37.2%), fruits per cluster (38.9%), fruit length (32.7 and 15.5 %), fruit weight (48.7 and 45.0 %) and yield per plant (34.9 %) showed highly significant positive heterosis over the mid and better parents, respectively. Flowers per cluster (7.4%), fruits per cluster (10.0 and 10.0 %), fruit length (8.9 %), fruit breadth (8.7 and 7.9 %), fruit weight (14.3 and 12.5%) and yield per plant (24%) respectively, showed positive significant heterosis above the mid and better parents.

The research on estimation of heterosis was carried out on tomato by Patel *et al.* (2010). Depending on the nature of the traits, heterosis over superior parent was shown to be significantly high in both positive and negative directions. This clearly indicates that, due to the prevalence of non-additive genetic variances, heterosis breeding would be important for tomato crop genetic development.

Ahmad *et al.* (2011) estimated heterosis of twenty one tomato cross combinations involving seven parents. Analysis of variance indicated highly significant differences for all the characters studied, showed the presence of genetic variability among the materials. Three combinations (P2 × P3, P3 × P4 and P3 × P5) showed significant early flowering, while two P1 × P7 (16.67%) and

P1 × P2 (12.44%) for individual fruit weight. The cross combinations P4 × P7 (62.31%), P2 × P6 (37.44%), P4 × P6 (34.77%), P2 × P7 (33.67%), P3 × P7 (32.09%) and P3 × P4 (29.82%) manifested higher heterosis over better parent for yield per plant.

Baishya *et al.* (2012) carried out heterotic analysis utilizing thirty six hybrids and nine parental lines of tomato. For days to flowering and days to ripening, the majority of the crosses demonstrated desirable negative heterosis over the superior parent. Number of fruits per plant (70.59 %) and fruit weight had the highest heterosis over parent (120%). The best estimation of heterosis for days to flowering, number of fruits per plant and yield per plant were found in EC-4881 × EC-130204, indicating that this cross could be effective for developing hybrids with earliness and high yield.

Chattopadhyay and Paul (2012) examined heterosis in tomato. In terms of the number of locules per fruit, fruit length and other characteristics, there was significant heterosis over the better-parent and the mid parent, on the other hand, was in a negative direction for the majority of the characters. Some parents with a high potential for creating high cross combinations for most of the quality attributes under investigation have been identified. Crosses selected on the basis of *per se* performance appear to be more reliable than crosses selected just on the basis of manifestation of heterosis.

Farzane *et al.* (2012) estimated extent of heterosis, combining ability for yield/ plant (kg) and yield components *viz.*, number of fruits per plant, individual fruit weight (g) and locule number using 10 ×10 diallel cross set of tomato including reciprocals. Significant differences among genotypes were obtained for all traits. The variances for general combining ability and specific combining ability were highly significant indicating the presence of additive as well as non-additive gene effects except the number of fruits/plant and relative magnitude of these variances indicated that additive gene effects were more prominent for all of

the traits. The tomato genotype Mb 3 proved to be the best general combiner for yield and number of fruits/plant.

Singh *et al.* (2012) revealed that for plant height, number of primary branches plant⁻¹, number of secondary branches plant⁻¹, days to 50% flowering, days to maturity, fruit set, fruit length, fruit width, number of locules fruit⁻¹, number of fruits plant⁻¹, fruit weight and fruit yield plant⁻¹, heterosis over better parent (BP) was recorded to the extent of -38.14%, 42.04%, 36.14%, -5.70%, -5.65%, 26.32%, 63.44%, 4.83%, 16.50%, 38.88%, 62.70% and 45.89% respectively. The crosses that showed heterosis for fruit yield plant⁻¹ were not heterotic for all of the traits studied. In most cases, heterosis in yield was accompanied by heterosis in yield components. Arka Ahuti × LO-5973, Arka Vikas × TWC-4, Arka Ahuti × TWC-4, BRH-2 × LO-5973 and CAU-TS-9 × LO-5973 were five potential crosses in tomato.

Patwary *et al.* (2013) observed that for earliness, the majority of the combinations demonstrated heterosis over better parent. For flower production, eight crosses exhibited positive heterosis. The cross P6 × P7 had the highest heterotic effect for fruit set (%), followed by P7 × P8 (60.49 %) and P1 × P7 (40.00 %). Eight crosses yielded more than 15% heterosis over the superior parent in terms of fruits per plant. In case of fruit yield per plant, 24 hybrids had a greater level of heterosis than the better parent, ranging from 13.58 to 282.63 %. P4 × P7 was the cross combination with the most significant positive heterosis. Twelve hybrids showed more than 10% heterosis in fruit flesh thickness.

Agarwal *et al.* (2014) determined heterosis, combining ability and gene action for yield and quality traits in tomato using eight parental lines crossed in 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, for total soluble solids in CLN 2264H and for dry matter content in Best of All. The highest significant heterosis over better and standard parent was recorded for average fruit weight followed by total soluble solids. The range

of heterosis for fruit yield over better parent was 6.63-35.90% 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. Genotypes with positive and moderately high GCA for dry matter were Pith Sel, DARL-1 and Best of All and for TSS were CLN 2264H and DARL-1. Genetic components H1, H2 were highly significant for all the traits exhibiting the importance of both additive and dominant gene effects in these traits.

Twenty-eight tomato hybrids were tested by Chauhan *et al.* (2014) to estimate heterosis for yield and its component traits. For yield and its component traits, the hybrids Pusa Gaurav × Taiwan, Pusa Rohini × Pusa Gaurav and Pusa Rohini × Roma were found to be the most promising. For fruit yield per plant, these hybrids showed heterosis of 48.14 %, 44.47 % and 73.41 % over better parents and 83.43 %, 76.78 % and 74.24 %, respectively, over the check cultivar. The cross combination Pusa Gaurav × Taiwan showed the most significant standard parent heterosis and SCA estimations for yield and its contributing traits.

In a study carried out by Kumar and Paliwal (2016) six diverse tomato cultivars were crossed in a half diallel fashion to obtain fifteen cross combinations. Three cross combinations *viz.*, Arka Meghali × Punjab Chhuhara, Arka Saurabh × Arka Abha and Arka Saurabh × Punjab Chhuhara resulted in significantly positive heterosis over mid parent and better parent for pericarp thickness. For total soluble solids, positive and significant heterosis over mid and better parents were observed in three cross combinations *viz.*, Arka Saurabh × Arka Meghali, Punjab Chhuhara × Best of All and Arka Meghali × Sioux. Best of All × Sioux and Punjab Chhuhara × Sioux showed highest significant positive heterosis over mid parent and better parent for shelf life. Lycopene content in Arka Saurabh × Arka Meghali, Arka Saurabh × Punjab Chhuhara, Arka Saurabh × Best of All and Arka Abha × Best of All showed significantly positive better parent and mid parent heterosis. Arka Saurabh × Arka Meghali was the best cross combination for lycopene content and total soluble solids.

Gautam *et al.* (2018) estimated heterosis in six tomato lines using 6 x 6 diallel design. The crosses as well as parents were evaluated for 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, yield per hectare and plant height, respectively. The crosses showing heterosis for yield per plant were not heterotic for all the characters under study. The heterosis for yield was generally accompanied by heterosis for yield components. 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 F₁ hybrids.

Kattegoudar *et al.* (2018) determined heterosis in eight lines of tomato using 8 x 8 full diallel design. Crosses of tomato were evaluated with parents and checks for various yield and yield attributing characters. The heterosis over commercial check-2 to the extent of 107.08, 59.79, -13.59, 174.70 and 13.58 per cent was recorded for plant height at 60 DAP, number of branches per plant 60 DAT, days to fifty per cent flowering, number of fruits per plant and average fruit weight respectively. The crosses showing heterosis for yield per plant were not heterotic for all the characters. The heterosis for yield was generally accompanied by heterosis for yield components. Promising crosses for yield per plant are Vaibhav x PKM-1, PKM-1 x Anagha and Arka Sourabh x Anagha, for average fruit weight (more than 70 g), Vaibhav x Arka Saurabh and Vaibhav x PKM-1 crosses found promising with high standard heterosis. The yield and yield components indicated the role of both additive and non-additive gene effect in governing these traits.

Rakha and Sabry (2019) determined heterosis, nature of gene action for yield and its components in tomato using half diallel analysis for five parents and ten hybrids. The results indicated that heterosis over high parent gave significant values in most crosses. It was found that 'Red Star' was the best combiner for

plant height, number of branches, fruit length, number of locules and total fruit weight; 'Peto 86' for leaf area index, fruit shape index and number of fruits/plant, 'Super strain B' for TSS and total fruit yield and 'Edkawy' for number of leaves, fruit diameter, number of fruit locules and average fruit weight. The cross P1 × P2 was found to be the best combination for plant height (P1 × P3) for number of branches/ plant (P2 × P5) for number of leaves /plant (P1 × P5) for total fruit yield and number of fruit/plant (P2 × P3) for fruit shape index and leaf area index (P2 × P4) for fruit weight (P2 × P5) for fruit length and number of leaves/ plant (P3 × P4) for fruit diameter (P3 × P5) for number of fruit locules and (P4 × P5) was the best combination for TSS. Additive gene effects appeared to be more important than non-additive gene effect as reflected on plant height, number of leaves/plant, fruit length, fruit diameter, TSS, number of locules, average fruit weight, number of fruit/plant and total fruit weight.

Standard heterosis over one check (DVRT-1) was determined with thirty hybrids of tomato by Sah *et al.* (2020). Most of these hybrids proved to have unique variation for growth and yield traits in tomato. Standard heterosis over check for total yield/plant was recorded 99.76 %. Highest heterosis variation was found to be in number of primary branches/plant, followed by average fruit weight, fruit yield/hectare (q/ha), number of fruits/plant, number of fruits/cluster. The statistically highest significant positive standard heterosis for fruit yield (q/ha) was recorded in hybrid EC-570028 × EC-520061(99.76 %) followed by hybrids EC-552141 × EC520061 (96.57 %) and EC-552141 × Hisar Arun (96.43 %). The hybrid EC620500 × Hisar Arun (-29.82 %) found to have the “statistically highest significant positive standard heterosis” for days to 50 % flowering, followed by hybrids EC538405×EC-520061 (-13.06 %) and EC-538405 × Hisar Arun (-16.26).

Sonagara *et al.* (2020) estimated heterosis using ten diverse lines of tomato and their forty five F₁ hybrids developed through diallel fashion excluding reciprocals. Among forty five hybrids tested, fourteen exhibited significant

positive heterobeltiosis for fruit yield/plant. The best three heterotic hybrids were found to be ATL-17-05 × 2016/TODVAR-3 (202.80%), GAT-5 × 2014/TOLCVRES-1 (178.21%) and GAT-5 × DVRT-2 (132.76%).

Soresa *et al.* (2020) determined the heterosis for yield and yield related components using 8 × 8 half diallel cross in tomato. Analysis of variance showed significant differences between genotypes. The heterosis for yield was generally accompanied by heterosis for yield components. Heterosis for marketable fruit yield per plant ranged from (-63.4%) (P3 × P8) to (33.8%) (P6 × P8) and (-62.5%) (P3 × P8) to (52.6%) (P5 × P7), for mid parent and better parent respectively. Significant heterosis over better and mid-parent was observed for all the traits. Best parent and mid-parent heterosis (MPH) was highest and in desirable direction for number of marketable fruit per plant (29.3%; 29.2%) in crosses (P3 × P6 for both) and pericarp thickness (46.3%; 57.6%) in crosses (P2 × P6 and P4 × P8), number of fruit cluster per plant (32.8%; 35.9%) in cross (P3 × P6 for both), individual fruit weight (36.1%; 41.2%) in cross (P2 × P8, P3 × P5) and fruit diameter (28.4%; 28.3%) in cross (P3 × P5; P2 × P6), fruit length (23.07%; 20.4%) in cross (P2 × P6 for both). Out of twenty eight F₁ crosses, positive and desirable heterosis by ten crosses over better parent and seventeen crosses over mid-parent were observed for total fruit density in tomato. From all the crosses, seven crosses revealed positive from which three crosses are the most important P2 × P7 (31%), P3 × P5 (20%) and P3 × P6 (54%) in better parent heterosis. Similarly for mid-parent heterosis, only ten crosses out of twenty eight revealed positive while the rest eighteen crosses showed the undesirable direction for marketable fruit yield indicating majority of the hybrids exhibited unfavorable heterotic response.

Mishra *et al.* (2021) estimated heterobeltiosis and standard heterosis using ten tomato lines. These lines were crossed in half diallel mating design to produce forty five F₁ hybrids which were evaluated for growth, fruit yield and quality traits. The parental lines, viz., BT-22-4-1, BT-507-2-2 and BT-19-1-1-1 were found most promising for exploiting heterosis. Appreciable amount of heterobeltiosis and standard

heterosis was noticed for majority of the traits studied. The hybrid combinations that out fielded their parents for a maximum number of components for heterobeltiosis and standard heterosis coupled with high *per se* values were BT-19-1-1-1 × BT-22-4-1, BT-22-4-1 × BT-507-2-2 and BT-19-1-1-1 × BT-3.

Liu *et al.* (2021) determined heterosis, heritability and combining ability of eight major agronomic traits in ten tomato parents and forty-five crosses, using TY-301, as a check. The results showed that both additive and non-additive genetic effects are involved in the expression of the traits and the additive genetic effect is dominant in trait inheritance. Although general combining ability (GCA) and specific combining ability (SCA) were not correlated and the strength of heterosis depends on SCA, the sum of the parental GCA values predicts heterosis for some traits with higher predictive accuracy than SCA. The parent 17,969 showed best comprehensive trait performance, especially in yield. High-yielding candidate combination 17,927 × 17,969 and a precocious and good taste candidate combination 17,666 × 17,927 were screened to get better heterotic combinations.

Izzo *et al.* (2021) estimated heterosis and combining ability for yield and other economic traits in six tomato lines in fifteen hybrids resulting from half-diallel mating. Result showed that most of the hybrids were characterized by significant desirable heterosis compared to mid parent and best parent for the traits studied. Heterosis reached 49.03 and 33.4% for single plant yield, -31.2 and -29.27% for the number of days to the beginning of flowering, 89.73 and 61.77% for the number of fruits/cluster, 15.72 and 9.30% for fruit height, 27.29 and 24.18% for fruit diameter, 32.55 and 24.18% for the number of locules/ fruit comparing to mid-parents and best-parent respectively. The hybrids T2 × T6, T2 × T8 and T8 × T16 were significantly superior. The ratio ($\sigma^2\text{GCA}/\sigma^2\text{SCA}$) showed the control of additive gene action in the inheritance of fruit weight, fruit height, fruit diameter and the number of fruits/cluster, while non-additive gene action controlled the inheritance of single plant yield, the number of days to flowering and the number of locules /fruit.

Chapter-3

MATERIALS AND METHODS

The present investigation entitled, “**Heterosis and combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) under temperate conditions of Kashmir**” was conducted during *Kharif* 2021 at three locations *viz.*, Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar; Krishi Vigyan Kendra, Malangpora Pulwama and KVK, Budgam.

3.1 Material used for experiment

The basic experimental material consisted of twelve diverse genotypes of tomato (*Solanum lycopersicum* L.) *viz.*, SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-1424, SKAU-T-1219, SKAU-T-1315, SKAU-T-0301, SKAU-T-1429, SKAU-T-1701, SKAU-T-1009, SKAU-T-9862 and SKAU-T-1464. These lines have been maintained by the Division of Vegetable Science, SKUAST-Kashmir, Shalimar and have been selected for the present study on the basis of genetic variability of various agronomic traits and maturity parameters. The recommended package of practices shall be adopted to raise a healthy crop. Data shall be recorded from five randomly selected plants in each treatment over the replications at all three locations for different characters.

3.2 Location of experimental site

Sixty six F₁ crosses were generated by crossing the above twelve lines in 12 × 12 diallel mating design at Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar during the year 2021. The final experimental materials consisting of twelve parents and sixty six F₁ crosses were evaluated during year 2022 at three locations. The geographical details of three locations are:

I. Vegetable Experimental Field, Division of Vegetable Science, SKUAST-K, Shalimar

The farm is located at the main campus, Shalimar, Srinagar which is 15 km away from Srinagar, city on the foot hills of Mahadev. The altitude of the location is 1685 meters above mean sea level and situated 34°N of latitude and 74.89°E of longitude.

II. Krishi Vigyan Kendra, Malangpora Pulwama

The research station is located at 33.53° N of latitude and 74.58° E of longitude in South Kashmir about 32 km away from Srinagar city. The location is situated at 1600 meter above mean sea level.

III. Krishi Vigyan Kendra, Budgam

The research station is located at 34.06°N latitude and 74.79°E longitude in central Kashmir about 11 km away from Srinagar city. The location is situated at 1610 meters above sea level.

These three locations will be referred to here in after as E₁, E₂ and E₃, respectively.

3.3. Experimental details

At each location the experiment was laid out in Randomized complete block design. The row to row and plant to plant spacing was maintained at 60 x 45 cm. Recommended package of practices were adopted to raise a healthy crop at all the locations. The details of experimental plan are given below:

Crop	:	Tomato (<i>Solanum lycopersicum</i> L.)
Number of lines	:	12
Ist year		Crossing of 12 tomato lines using diallel mating design
2 nd year		Evaluation of crosses along with parents at multi locations (12 parents + 66 crosses + 1 check)

- Locations : Experimental Field, Division of Vegetable Science, SKUAST-K, Shalimar (Ist year)
At three different locations (2nd year), viz.,
Vegetable Experimental Farm, Division of vegetable science, SKUAST-Kashmir, Shalimar,
KVK, Malangpora, Pulwama,
KVK, Budgam
- Number of replications : 03 (Three)
- Experimental design : Diallel excluding reciprocals
(Model I and Method II)
- Spacing : 60 cm × 45 cm

3.4. Observations recorded

The observations were recorded on five randomly selected plants in each replication at all locations. The mean values for various characters of each experimental unit were computed and was used for further statistical analysis. The observations were recorded on the following quantitative and quality characters.

3.4.1. Number of days to first flowering

Days to first flowering were recorded by counting the number of days from the date of transplanting to the date of first flower appearance. The data was recorded in five randomly selected plants and their mean value was calculated.

3.4.2. Number of days to first fruit set

Numbers of days taken from transplanting to the date of first fruit set in the selected plants were recorded and their mean value was worked out.



E₁:Vegetable Experimental Field,
Division of Vegetable Science, SKUAST-
K, (Shalimar,Srinagar)



E₂:Krishi Vigyan Kendra,
Malangpora-Pulwama



E₃:Krishi Vigyan Kendra,
Budgam

Plate 1: Field view after transplanting



E₁:Vegetable Experimental Field, Division of Vegetable Science, SKUAST-K, (Shalimar,Srinagar)



E₂:Krishi Vigyan Kendra, Malangpora-Pulwama

E₃:Krishi Vigyan Kendra, Budgam

Plate 2: Experimental Fields

3.4.3 Number of days to first fruit harvest

The period from the transplanting date to the date of first harvesting was recorded and expressed in terms of number of days. Then the average values of selected plants were calculated.

3.4.4 Number of flowers cluster⁻¹

Number of flowers cluster⁻¹ were counted in five random clusters at flowering stage and their average was calculated.

3.4.5 Number of fruits cluster⁻¹

Number of fruits cluster⁻¹ was counted at the time of first picking from five fruit bunches chosen at random in each of the randomly selected plant and the average was calculated.

3.4.6 Number of pickings

Number of pickings was recorded from first harvest to last harvest in each of the five randomly selected plants and the average was calculated.

3.4.7 Number of fruits plant⁻¹

The total numbers of red ripe fruits were counted at every picking from five randomly selected plants and finally these were added and then average number of fruits per plant was worked out.

3.4.8 Fruit length (cm)

At marketable stage, the fruit length of five randomly selected fruits was measured with the help of vernier calliper from base of calyx to top of fruit and the mean value was calculated and expressed in centimetres.

3.4.9 Fruit diameter (cm)

At marketable stage, the fruit diameter of five randomly selected fruits was measured with the help of vernier calliper at the middle of fruit and the mean value was calculated and expressed in centimetres.

3.4.10 Number of locules fruit⁻¹

Five randomly selected tomato fruits were cut transversely and locules were counted in all the fruits. Later on, average number of locules per fruit was calculated. Number of locules was counted on the same fruits used for flesh thickness.

3.4.11 Pericarp thickness (mm)

Pericarp thickness of five randomly selected fruits was measured with the help of vernier calliper after they were cut transversely into two halves and the average value was calculated and expressed in milli metres.

3.4.12 Number of primary branches plant⁻¹

Number of primary branches per plant was calculated on five randomly selected plants after third picking and the average value was calculated.

3.4.13 Plant height (cm)

The length of the main stem of five randomly selected plants from ground level to the terminal tip was measured with the help of measuring tape in centimetres at the time of last picking.

3.4.14 Average fruit weight (g)

A sample of five fruits from each of the five selected plants was taken and weighed and average fruit weight was worked out.

$$\text{Average Fruit Weight (g)} = \frac{\text{Total fruit weight of 'n' number of fruits}}{\text{Total number of fruits(n)}}$$

3.4.15 Fruit yield plant⁻¹(kg)

The red ripe fruits harvested from the randomly tagged five plants in all pickings of each experimental unit was weighted in kilograms and its average value was calculated to obtain the average fruit yield per plant in kilograms

3.4.16 Fruit yield hectare⁻¹(q)

The fruit yield per hectare was obtained by multiplying the average fruit yield per plant (kg) with the total number of plants per hectare and converting the same to quintals per hectare.

3.4.17 Average number of seeds plant⁻¹

Total number of seeds from randomly selected five red ripe fruits were extracted and counted. Average number of seeds per fruit was worked out.

3.4.18 100 seed weight

After harvesting fruits, the seeds were extracted by fermentation to separate flesh from the seed and the seeds thus obtained were cleaned and dried. One hundred seeds per genotype were counted and weighted in grams on an electronic balance.

3.4.19 Juice to pulp ratio

A composite sample of 500 grams of fruit was taken from the randomly selected plants from each replication and crushed thoroughly in an electrically operated juice extractor. The extract was filtered through dry muslin cloth and the filtrate was collected in the weighed beaker. The weight of juice along with the beaker was recorded and juice content was calculated as:

$$\text{Juice content} = (\text{Juice} + \text{Beaker}) \text{ weight} - \text{Beaker weight}$$

Pulp content was calculated as:

$$\text{Pulp content} = \text{weight of fruit} - \text{weight of juice}$$

Juice to Pulp ratio was calculated as:

$$\text{Juice to Pulp ratio} = \frac{\text{Juice content}}{\text{Pulp content}}$$

3.4.20 TSS (°Brix)

Five randomly selected ripe fruits were crushed and juice was filtered through a muslin cloth, collected in a beaker, shaken well and then TSS was determined with the help of hand refractometer (Digital Abbe Refractometer, Kruss Optroic AOAC, 1980) by squinting a drop of the solution on the prism of refractometer. The percentage of TSS (expressed as °Brix) was obtained from direct reading of instrument.

3.4.21. Titrable acidity (%)

The anhydrous citric acid content was estimated by following the titration procedure given by Ranganna (1986).

Reagents

1. **Sodium hydroxide (0.1N):** Dissolve 4.0 g of sodium hydroxide in 1 litre of distilled water.
2. **Phenolphthalein indicator (1%):** Dissolve 1 g of phenolphthalein powder in 40 ml of 95% alcohol. Make up the volume to 100 ml with absolute alcohol.

Protocol

A known quantity of fruit sample material was macerated in a waring blender to smooth consistency. Fifty grams (50 g) of this fruit pulp was diluted in small amount of distilled water and filtered through muslin cloth. A 10 ml of the sample was taken for estimation from the filtrate and final volume was made up to 100 ml. An aliquot of 30 ml was taken for titration against 0.1 N NaOH (sodium hydroxide) solution using 3-4 drops of 1% phenolphthalein solution as internal indicator. The appearance of light pink colour was marked as the end point and the value of titrate was recorded. The titration was repeated three times for each treatment. Average volume of titrate used was worked out.

Calculation

The anhydrous citric acid content of the sample was calculated according to the following formula:

$$\text{Acidity (\%)} = \frac{\text{Titre value} \times \text{Normality of NaOH} \times \text{volume made up} \times \text{Eq. wt. of acid}}{\text{Aliquot of samples taken} \times \text{volume of samples taken} \times 1000} \times 100$$

Where,

Normality of alkali = 0.1N

Volume made up = 100 ml

Eq. weight of citric acid = 64

Aliquot of sample taken for titration = 30 ml

Volume of sample taken for estimation = 10ml

3.4.22 Lycopene content (mg/100g)

The lycopene content was estimated by the method (Gordon and Diane, 2007); Godwin *et al.* (2015) and Suwanaruang (2016), outlined below:

Reagents

1. HPLC grade Hexane
2. HPLC grade Acetone
3. Absolute ethanol

Protocol

One or two tomato fruits were taken and homogenized with the help of mortar and pestle. The crushed sample was then filtered through muslin cloth. A 100 μ l of the sample was taken for estimation from the filtrate and 8ml of hexane: ethanol: acetone solution (2:1:1) (v/v) was added to it. The samples were capped and vortexed immediately for 1-1.5 hours, then incubated out of bright light. After at-least 10 minutes, 1 ml of distilled water was added to each sample and vortexed

again. Samples were allowed to stand for 10 minutes to allow phases to separate. The upper layer of the solution was pipette out and finally the absorbance of the sample was read at 503 nm by spectrophotometry using the hexane: ethanol: acetone mixture as blank.

Calculation

Lycopene content of the sample was calculated according to the following formula:

$$\text{Lycopene (mg100g}^{-1}\text{)} = \frac{\text{Absorbance} \times 137.4}{10}$$

3.4.23. Ascorbic acid content (mg/100g)

The ascorbic acid content was estimated by following the titration procedure given by Thimmaiah (1999).

Principle

Ascorbic acid reduces the 2, 6-dichlorophenol indo-phenol dye to a colourless leuco-base and itself gets oxidized to dihydroascorbic acid. Though the dye is a blue coloured compound, the end point is the appearance of pink colour for 5-10 seconds. The dye is pink in acid medium. A mixture of meta-phosphoric and acetic acid is used as the titrating medium. The titre of the dye can be determined using working standard ascorbic acid solution.

Reagents

- 1. Metaphosphoric-acetic acid mixture (3%):** Dissolve 15 g of meta-phosphoric acid in a mixture containing 40 ml of glacial acetic acid and 450 ml distilled water. Stable for 10 days.
- 2. Dye solution:** Dissolve 42 mg sodium bicarbonate in 50 ml of distilled water and then, add 50 mg 2, 6-dichlorophenol indo-phenol dye in it. Make up the volume to 200 ml with distilled water.

3. **Stock standard solution (1 mg ml):** Dissolve 100 mg of ascorbic acid in 100 ml of 3% metaphosphoric-acetic acid mixture.
4. **Working Standard solution (0.1 mg ml⁻¹):** Dilute 10 ml of the stock solution to 100 ml with 3% metaphosphoric-acetic acid mixture.

Protocol

Standardization of Dye

5 ml of the working standard solution was pipette out into a 100 ml conical flask. Then, 10 ml of Metaphosphoric-acetic acid mixture was added to it and titrated against dye solution. End point is the appearance of pink color which persists for 5-10 seconds.

Estimation of ascorbic acid

Fruit sample (0.5-5 g) was extracted in 10 ml of Metaphosphoric-acetic acid mixture and final volume was made up to 25 ml with Metaphosphoric-acetic acid mixture. Filter the solution using Whitman filter paper and collect the filtrate. A 5 ml of the sample was taken for titration from the filtrate and 10 ml of the acid mixture was added to it.

Calculation

Ascorbic acid content of the sample was calculated according to the following formula:

$$\text{Ascorbic acid (mg100g}^{-1}\text{)} = \frac{0.5}{V_1} \times \frac{V_2}{15 \text{ ml}} \times \frac{25 \text{ ml}}{\text{Weight of sample taken}} \times 100$$

Where,

V₁ = Volume of dye used in titration of standard (ml)

V₂ = Volume of dye used in titration of sample (ml)

3.4.24. Total carotenoids (mg/100g) (Mahadevan and Sridhar, 1986)

A known weight of sample (1gm) was extracted with acetone and a few drops of sodium sulphate. The extractions were repeated and the extract was totaled in a beaker and to it added 10% KOH. The extract was heated on a water bath for 30 minutes and then transferred to a separating funnel. To this 50ml of petroleum ether was added. The separating funnel was shaken and allowed to stand for at least 10 minutes till the layers got separated. The lower layer was drained and the upper layer of petroleum ether containing pigment was collected in a volumetric flask and the volume was made up to 50 ml with petroleum ether and O.D was recorded as 452 nm against petroleum ether as blank. The total carotenoids were calculated as per the formula:

$$\text{Total carotenoids (mg/100g)} = \frac{\text{O.D} \times 13.9 \times 10^4 \times \text{volume made}}{\text{weight of sample} \times 560 \times 1000}$$

3.5. Statistical and Biometrical procedures

The recorded data was analyzed using following statistical and biometrical procedures to fulfill the objectives of present investigation.

3.5.1 Analysis of variance

Analysis of variance for all the characters in individual environments and pooled over environments was carried out as per the Verma *et al.* (1987).

3.5.2 Analysis for single environment

The analysis for individual environments was done using mathematical model:

$$Y_{ik} = \mu + g_i + r_k + e_{ik}$$

Where,

Y_{ik} = Observation of i th genotype ($p = 1 - i$) in k th replication
($K=1- k$)

μ = general mean,

- g_i = effect of the i^{th} genotype,
 r_k = effect of the k^{th} replication and
 e_{ik} = random error associated with ik^{th} observation.

Based on the model given above the expectations of various mean squares were derived as follows:

ANOVA table for mean squares

Source of variation	d.f.	M.S.	Expected mean squares
Replications	(r-1)	MSR	$\sigma^2e + g \sigma^2r$
Genotypes	(g-1)	MSP	$\sigma^2e + r \sigma^2g$
Error	(g-1)(r-1)	MSE	σ^2e

df: degree of freedom; MS: Mean square

3.5.3. Pooled analysis over environments

The analysis for data pooled over environments was based on the mathematical model:

$$Y_{ijk} = \mu + g_i + l_j + r_{jk} + (G \times l)_{ij} + e_{ijk}$$

Where,

- Y_{ijk} = Mean of i^{th} progeny in k^{th} replicate of j^{th} environment,
 μ = general mean,
 g_i = effect of i^{th} genotype,
 l_j = effect of j^{th} environment,
 r_{jk} = contribution of k^{th} replicate in the j^{th} environment
 $(g \times l)_{ij}$ = interaction, between i^{th} genotype and j^{th} environment and
 e_{ijk} = residual error

Based on the above model, the expectations of various mean squares were derived as follows:

ANOVA table for mean squares

Source of variation	d.f.	M.S.	Expected mean squares
Environments	(l-1)	MSL	$\sigma^2e + rg \sigma^2lg + rg \sigma^2e$
Replications × Environments	(r-1) (l-1)	MSRL	$\sigma^2e + g \sigma^2lr$
Genotype	(g-1)	MSG	$\sigma^2e + r \sigma^2lg + rl \sigma^2g$
Genotypes × Environments	(g-1) (l-1)	MSGE	$\sigma^2e + r \sigma^2lg$
Error	(g-1) (r-1)l	MSE	σ^2e

The combining ability analysis was carried out according to model-1 and method-II of Griffing (1956 a). The combining ability analysis over environments was done following the method given by Singh (1973 a, b, 1979).

3.5.4. Genotypic variance

Genotypic variance was calculated using the method suggested by Al-Jibouri *et al.* (1958).

$$\sigma^2g = \frac{MSG - MSGE}{rl}$$

Where,

- σ^2g = genotypic variance,
- MSG = Mean sum of squares for genotypes
- MSGL = Mean sum of squares for G x E interaction
- r = number of replications and
- l = number of locations (environments)

3.5.5. Phenotypic variance

Phenotypic variance was calculated by the formula devised by Al-Jibouri *et al.* (1958):

$$\sigma^2p = \sigma^2g + \sigma^2gl/l + \sigma^2e/rl$$

Where,

- σ^2p = phenotypic variance,
- σ^2g = genotypic variance,
- σ^2gl = genotypic x environment variance and
- σ^2e = error variance

3.5.6. Combining ability analysis for individual environment

The analysis was carried out for general combining ability (GCA), specific combining ability (SCA) and variance components. The estimates of variance for gca and sca and their effects were computed according to model-1 (fixed effect model) and method-II (parents and crosses, excluding reciprocals) as given by Griffing (1956 b).

The analysis of variance for combining ability was based on the following model :

$$Y_{ijk} = \mu + g_i + g_j + S_{ij} + b_k + e_{ijk}$$

Where,

- Y_{ijk} = phenotype from cross of i^{th} and j^{th} parents in k^{th} block,
- μ = population mean
- g_i = gca of i^{th} parent
- g_j = gca of j^{th} parent,
- S_{ij} = sca effect of $(ixj)^{\text{th}}$ cross,

b_k = effect of k^{th} block

e_{ijk} = error associated with the observation

ANOVA for combining ability

Source of variation	d.f.	Sum of squares	Mean sum of squares	Expected mean of squares
Gca	P-1	SSg	MSg	$\sigma^2e + (P+2) \frac{\sum g^2}{(P-1)}$
Sca	$\frac{P(P-1)}{2}$	SSs	MSs	$\sigma^2e + \frac{\sum \sum S_i^2}{P(P-1)}$
Error	m	SSe	MSe	σ^2

Where,

$$S_g \text{ (SS due to gca)} = \left[\frac{1}{(P+2)} \sum (X_i + X_{ii})^2 - \frac{4}{P} \sum X^2 \right]$$

$$S_s \text{ (SS due to sca)} = \sum \sum X_{ij}^2 - \frac{1}{P+2} \sum (X_i + X_{ii}) + \frac{2X^2}{(P+1)(P+2)}$$

Where,

r = number of blocks

m = error d.f.

P = number of parents

The error mean square (MSe) was obtained after dividing the error mean square (MSe) from RBD Anova by the number of replications.

The significance of mean square due to gca (MSg) and sca (MSs) was tested against error mean square (MSe) by F-test at $p = 0.05$ and $p = 0.01$

3.5.7 Estimates of combining ability effects and their standard errors

The gca effect of parent (I) was calculated as under.

$$g_i = \frac{1}{(P+2)} (X_i + X_{ii}) - \frac{2X_{..}}{P}$$

The sca effect of a cross (i x j) was calculated as under :

$$S_{ij} = X_i - \frac{1}{(P+2)} (X_{i.} + X_{j.} + X_{ij}) - \frac{2X_{..}}{(P+1)(P+2)}$$

where,

X_i = total of array involving i^{th} parent

X_j = total of array involving j^{th} parent,

X_{ii} = parental value of i^{th} parent,

X_{jj} = parental value of j^{th} parent,

X_{ij} = parental value of $(ij)^{\text{th}}$ cross and

$X_{..}$ = total of all $\frac{P(P+1)}{2}$ items of diallel table

The standard errors for test of significance of gca and sca effects were worked out as follows:

$$S.E (g_i) = \left(\frac{P-1}{P(P+2)} MSe \right)^{0.5}$$

$$S.E (g_{ij}) = \left(\frac{P^2 + P + 2}{(P+1)(P+2)} MSe \right)^{0.5}$$

$$S.E (g_i - g_j) = \left(\frac{2 MSe}{(P+2)} \right)^{0.5}$$

$$S.E (S_{ij} - S_{jk}) = \left(\frac{2 P \times MSe}{(P+2)} \right)^{0.5}$$

3.5.8. Estimates of combining ability variances and their standard errors

Variance of effects were computed by following formulae:

$$\text{Var} (g_i) = \frac{(P-1) Mse}{P(P+2)a}$$

$$\text{Var} (S_{ij}) = \frac{(P^2+P+2)MSe}{(P+1) (P+2)a}$$

The standard errors to test different effects were obtained by square root of the above estimates.

3.5.9. Estimation of standard error of components

The standard errors of variance components were computed as per formulae given by Moll *et al.* (1960).

$$\text{Standard error (S.E)} = \sqrt{\frac{2}{C_i^2} \sum_i \frac{M_i^2}{d_i + 2}}$$

Where,

M_i = the i^{th} mean square in the function,

d_i = the d.f associated with i^{th} mean squares and

C_i = the divisor of function of i^{th} mean square

Single environment

$$S.E \text{ of } \sigma^2_g = \sqrt{\frac{1}{(n+2)^2} \left[\frac{2 (MS_{gca})^2}{n-1} + \frac{2(MSe)^2}{1(t-1)(r-1)} \right]}$$

$$S.E \text{ of } \sigma^2_s = \sqrt{\frac{2 (MS_{sca})^2}{n(n-1)} + \frac{2(MSe)^2}{1(t-1)(r-1)}}$$

Over environments

$$\text{S.E of } \sigma^2g = \sqrt{\frac{1}{(n+2)^2L} \left[\frac{2 (MS \text{ gca})^2}{n-1} + \frac{2(MSe)^2}{1(t-1) (r-1)L} \right]}$$

$$\text{S.E of } \sigma^2s = \sqrt{\frac{1}{L} \left[\frac{2 (MS \text{ sca})^2}{n(n-1)} + \frac{2(MSe)^2}{1(t-1)(r-1)L} \right]}$$

3.5.10. Combining ability effects over environments

The combining ability analysis over the environments was carried out as per the procedure carried out by Singh (1973 b) from the data collected from half diallel (Parents and F₁'s). The data was derived from reference population and the environments were random and contrasting. Therefore, both genotypes and locations were fixed and as such method II and model I was adopted for analysis. The analysis was based on the following statistical model:

$$X_{ijk} = \mu + g_i + g_j + S_{ij} + l_k + (gl)_{ik} + (gl)_{jk} + (sl)_{ijk} + \frac{1}{b\sum_{eijk r}}$$

Where,

μ = population mean

g_i = general combining effect of ith parent,

g_j = general combining effect of jth parent,

S_{ij} = specific combining ability effect of the cross between ith and jth parent,

l_k = effect of kth environment,

$(gl)_{ik}$ = interaction effect corresponding to g_i and l_k ,

$(gl)_{jk}$ = interaction effect corresponding to g_j and l_k ,

$(sl)_{ijk}$ = interaction effect corresponding to S_{ij} and l_k and

$e_{ijk r}$ = random error

3.5.11. Computation of sum of squares

The sum of squares corresponding to various sources of variation for combining ability analysis was calculated as per the following formulae:

$$S.S (g) = \frac{\sum_i (x_{i.} + x_{ij})^2}{(P + 2)l} - \frac{4x^2}{(P + 2)l}$$

$$S.S(s) = \sum \sum_{i \leq j} \frac{x_{ij}^2}{1} - \frac{\sum_j (x_{i.} + x_{ij})^2}{(P+2)l} + \frac{2x^2}{(P+1)(P+2)P}$$

$$S.S (l) = \frac{2 \sum x^2 \cdot K}{P (P+1)} - \frac{2 x^2 \dots}{P (P+1)l}$$

$$S.S (gl) = \frac{\sum (x_{i.k} + x_{ijk})^2}{P + 2} - \frac{4 \sum x^2 \cdot k}{P (P+2)}$$

$$\frac{\sum (x_{i.} + x_{ij})^2}{(P+2)l} + \frac{4x^2 \dots}{(P+2)l}$$

$$S.S (sl) = \frac{\sum \sum_{i \leq j} (x_{i.k} + x_{ijk})^2}{P + 2} + \frac{2 \sum x^2 \cdot k}{(P+1)(P+2)} + \frac{\sum x_{ij}^2}{1} + \frac{\sum (x_{i.} + x_{ij})^2}{(P+2)l} - \frac{2x^2}{(P+1)(P+2)l}$$

Where,

$$x_{ij.} = \sum_k x_{ijk},$$

k

$$x_{i.} = \sum_j x_{ijk},$$

$$x_{jik} = \sum_i x_{ijk}$$

$$x_{i.} = \sum_j x_{ij} = \sum_k x_{i.k}$$

i

$$x_{j.} = \sum_j x_{ji} = \sum_k x_{j.k.k.}$$

$$x_{.k} = \sum_{i \leq j} \sum x_{ijk}$$

$$x_{...} = \sum_k x_{.k}$$

3.5.12. Expectation of mean squares

It was calculated as per the procedure proposed by the Singh (1973 a) and the mean squares had the following expectations.

Source	d.f	S.S	M.S	E.M.S
General combining ability (G)	P-1	S.S(g)	Ag	$\frac{\sigma^2 + (P+2)l \sum g_i^2}{P-1}$
Specific combining ability (S)	$\frac{P(P-1)}{2}$	S.S(s)	As	$\frac{\sigma^2 + 2l \sum \sum S_{ij}^2}{P(P-1)^{i \leq j}}$
Environments (L)	l-1	S.S(l)	Al	$\frac{\sigma^2 + \frac{P(P+1)}{2} \sum l_k^2}{2(l-1)^k}$
Interaction (GxL)	(P-1) (l-1)	S.S (gl)	AgL	$\frac{\sigma^2 + \frac{P+2}{2} \sum \sum (g)_{ik}^2}{(P-1) (l-1)^k}$
Interaction (SxL)	$\frac{P(P-1) (l-1)}{2}$	S.S (sl)	Asl	$\frac{\sigma^2 + 2 \sum \sum \sum (Sl)_{ijk}^2}{P(P-1) (l-1)^{k \leq j}}$
Error	1 (t-1) (b-1)	E	Ae	σ^2

Where,

P = Number of parents,

T = Number of treatments,

B = Number of replications

S.S (g)	=	sum of the squares due to gca,
S.S (S)	=	sum of the squares due to sca,
S.S (l)	=	sum of the squares due to environments,
S.S(gl)	=	sum of the squares due to interactions between gca and environments,
S.S (sl)	=	sum of the squares due to interaction between sca and environments,
E	=	sum of the squares due to error

The respective mean sum of squares was obtained by dividing each sum of squares by corresponding degrees of freedom. However, the error mean sum of squares was obtained by dividing error mean square from general analysis with the number of replications. The test of the homogeneity of effects was done by F-test, wherein mean square of a given effect was tested against error mean square at n_1 and n_2 degrees of freedom.

3.5.13 Estimation of GCA and SCA effects

The general combining ability (GCA) effect of the i^{th} parent was calculated as :

$$g_i = 1 / (P+2)l [(X_{i.} + X_{ii.}) - (2/p) X_{...}]$$

The specific combining ability effect (SCA) of ij^{th} cross was calculated as:

$$S_{ij} = 1 / l X_{ij.} - 1 / (P + 2)l [(X_{i.} + X_{ii.} + X_{j.} + X_{jj.})] + 2X_{...} / (P+1) (P+2) l$$

Where,

P = number of parents,

l = number of environments,

$X_{i.}$ = total of arrays of i^{th} parents over environments,

$X_{ii.}$ = mean value of i^{th} parents over environments,

$X_{...}$ = grand total of $P(P+1)/2$ progenies and P parental value over environments,

$X_{ij.}$ = progeny mean value in diallel table (crosses) over environments,

$X_{.j.}$ = total of arrays of j^{th} parents over environments and

$X_{jj.}$ = mean value of j^{th} parents over environments.

3.5.14. Genetic components of variance

Various components of variance were estimated by the following formulae;

$$\sigma_g^2 = \frac{(A_g - A_e)(P-1)}{2Pl}$$

$$\sigma_s^2 = \frac{(A_s - A_e)(P-1)P}{2l}$$

These estimates were translated into genetic components of variance as per the methodology suggested by Griffing (1956 b).

$$2\sigma_g^2 = \sigma_A^2$$

$$\sigma_s^2 = \sigma_D^2$$

3.5.15 Variance of effects and variances of their interactions with environments

$$[\mu] = [1/p^2l] \sigma^2$$

$$[g_i] = [(p-1)/2p^2] \sigma^2$$

$$[g_i - g_j] = [1/pl] \sigma^2 (i \neq j)$$

$$[s_{ii}] = [(p-1)^2/p^2l] \sigma^2$$

$$[s_i] = [(p^2 - 2p + 2)/2p^2l] \sigma^2 (i \neq j)$$

$$[s_{ii} - s_{jj}] = [2(p-2)/pl] \sigma^2 (i \neq j)$$

$$\begin{aligned}
[S_i - S_{ij}] &= [(3p - 2)/2pl] \sigma^2 (i \neq j) \\
[S_{ii} - S_{jk}] &= [(3p - 2)/2pl] \sigma^2 (i \neq j, k ; j \neq k) \\
[S_{ij} - S_{ik}] &= [(p-1)/pl] \sigma^2 (i \neq j, k ; j \neq k) \\
[S_{ij} - S_{km}] &= [(p-2)/pl] \sigma^2 (i \neq j, k, m ; j \neq k, m ; k \neq m) \\
[(gl)_{ik}] &= [(p-1)(1-1)/2p^2 l] \sigma^2 \\
[(gl)_{ik} - (gl)_{jk}] &= [(1-1)/pl] \sigma^2 (i \neq j) \\
[(gl)_{ik} - (gl)_{im}] &= [(p-1)/p^2] \sigma^2 (k \neq m)
\end{aligned}$$

3.5.16 Standard error of effects and their differences

The standard error was calculated by taking the square root of respective variance.

3.5.17 Test of significance

Each gca and sca value was tested against zero for its difference by t-test,

$$t = \frac{g_i - 0}{\text{S.E. of } (g_i)}, \quad t = \frac{S_{ij} - 0}{\text{S.E. of } (S_{ij})}$$

The significance of calculated t-value was tested at error degree of freedom.

3.6. Component analysis

Using Hayman's (1954) least square estimates, the following genetic components of variation in F_1 were calculated:

- i) $D = 4 \sum uv d^2 =$ Components of variation due to additive effect of genes arising from differences between a pair of corresponding homozygotes.

If $u = v = 0.5$ then $D = d^2$

Where,

$u =$ proportion of positive genes in the parents,

v = proportion of negative genes in the parents,

d = additive effect and

u + v = 1

ii) $H_1 = 4\sum uvh^2$ = component of variation due to dominance effect of genes arising from the departure of heterozygotes from the mean of the corresponding pair of homozygotes.

iii) $H_2 = H_1 [1 - (u-v)^2]$ = $16 \sum u^2 v^2 h^2$ = proportion of dominance variance due to positive (u) and negative (v) effects of genes.

iv) $h^2 =$ net dominance effect (algebraic sum over all loci in heterozygous phase in all crosses)

v) E = expected environmental component of variance

vi) F = relative frequency of dominant and recessive alleles in parents

Group of equations based on the following parameters derived from diallel table were constructed to obtain the above components of variance.

$V_0L_0 =$ VP = variance of parental array

$V_r =$ variance of r^{th} array

$V_1L_1 = V_r =$ mean of array variances

$W_r =$ covariance between parents and their off-springs in r^{th} array

$W_0L_0 = W_r =$ mean covariance between the parents and off- springs of all the array

$V_0L_1 = V_m =$ variances of means of arrays

$ML_1 - ML_0 =$ the difference between the means of parents and means of their P^2 progenies

E = expected environmental components of variation (observed from analysis of variance of the design)

Following equations were constructed using above parameters :

$$i) V_0L_0 = V_p = D + E$$

$$\text{ii) } V_1L_1 = V_r = \frac{1}{4} D + \frac{1}{4} H_1 + \frac{1}{4} F + \frac{P+2}{2p} E$$

$$\text{iii) } W_0L_{01} = W_r = \frac{1}{2} D + \frac{1}{4} F + \frac{1}{P} E \text{ and}$$

$$\text{iv) } V_0L_1 = \frac{1}{4} D + \frac{1}{4} H_1 - \frac{1}{4} H_2 - \frac{1}{4} F + \frac{1}{2P} E$$

Where,

$$E = M_e = \frac{\text{Error variance}}{\text{Number of replications} \times \text{number of environments}}$$

The components of genetic variance were estimated as follows:

$$D = V_0L_0 - E$$

$$H_1 = V_0L_0 - 4W_0L_{01} + 4V_1L_1 - (3P-2) \left[\frac{E}{P} \right]$$

$$H_2 = 4V_1L_1 - 4V_0L_1 - 2E$$

$$h^2 = 4(ML_1 - ML_0)^2 - 4(P-1) \left[\frac{E}{P^2} \right]$$

$$F = 2V_0L_0 - 4W_0L_{01} - 2(P-2) \left[\frac{E}{P} \right]$$

$$F_r = 2(V_0L_0 - W_0L_{01} + V_1L_1 - W_r - V_r) - 2(P-2) E/P$$

Where,

P = number of parents

3.6.1 Standard error of genetic components

To test the significance of various components of variance, their standard errors were calculated using the equation $\frac{1}{2} \text{var}(W_r - V_r) = S^2$ and the terms of main diagonal of covariance matrix given by Hayman (1954) as corresponding multipliers.

The standard error of each component of variance was thus computed as follows:

$$\text{S.E of D} = \left(\frac{S^2(P^5 + P^4)}{P^5} \right)^{0.5}$$

$$\text{S.E of H}_1 = \left(\frac{S^2(P^5 + 4L P^4 - 12 P^3 + 4 P^2)}{P^5} \right)^{0.5}$$

$$\text{S.E of H}_2 = \left(\frac{S^2 (36 P^4)}{P^5} \right)^{0.5}$$

$$\text{S.E of h}^2 = \left(\frac{S^2 (16 P^4 + 16 P^2 - 32P + 16)}{P^5} \right)^{0.5}$$

$$\text{S.E of F} = \left(\frac{S^2(4 P^5 + 20P^4 - 16 P^3 + 16P^2)}{P^5} \right)^{0.5}$$

$$\text{S.E of E} = \left(\frac{S^2(P^4)}{P^5} \right)^{0.5}$$

Where,

P = number of parents

3.6.2. Test of significance of genetic components

T-test at P-2 degrees of freedom was used to test the significance of genetic components as follows:

$$t = \frac{\text{Parameter}}{\text{S.E. of parameter}}$$

3.6.3 Proportions of genetic components

Following proportions of variance genetic components were calculated as:

3.6.3.1 Degree of dominance

The degree of dominance was worked out by using estimates of D & H component as suggested by Kempthorne and Curnow (1961). The average degree of dominance was calculated as positive square root of ratio between components of variation due to dominance effects of the genes to component of variation due to additive effects of genes i.e.

$$\text{Degree of dominance (a)} = \left(\frac{H_1}{D} \right)^{0.5}$$

Where,

H = dominance component of variance and

D = additive component of dominance

There is:

- i) No dominance if $a = 0$
- ii) Partial dominance if $a < 1$
- iii) Complete dominance if $a = 1$
- iv) Over dominance if $a > 1$

Its value when less than one indicated that genetic control of the character is largely due to additive gene action though some degree of dominance also exists, whereas, more than one indicates over-dominance. If this ratio equaled zero, no dominance was indicated.

3.6.3.2 Proportions of genes with positive and negative effects in parents

The proportion of positive and negative alleles at loci exhibiting dominance was calculated by formulae:

$$UV = H_2/4H_1.$$

The ratio has maximum value of 0.25 signifying thereby that there is symmetrical distribution of positive and negative alleles. The value less than 0.25 indicate that positive and negative alleles are not in equal proportion in parents.

$$\text{Since } U+V = 1 \text{ and } U-V = (1-4V)^{1/2}$$

The value of U and V could be found out.

3.6.3.3 Ratio of dominant and recessive genes in parents

The prevalence of dominant and recessive genes was calculated by ratio:

$$\frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F} = \frac{KD}{KR}$$

Where positive and negative sign of F indicated dominant and recessive genes respectively. If the ratio was 1, dominant and recessive genes in parents were indicated to be in equal proportion. If it was less than 1, it indicated an excess of recessive genes and if it was more than 1, it indicated an excess of dominant genes.

3.6.3.4 Number of groups of genes which control the character and exhibit dominance

The ratio between h^2 and H_2 i.e. h^2/H_2 provides an approximate measure of group of genes exhibiting dominance

3.6.3.5 Heritability

The heritability in narrow sense was estimated by using the formula proposed by Mather and Jinks (1971):

$$\text{Heritability (n.s)} = \frac{0.5D + 0.5H_1 - 0.5H_2 - 0.5F}{0.5D + 0.5H_1 - 0.25H_2 - 0.5F + E}$$

3.6.3.6. Standard errors for single environment

$$S.E (\sigma^2_m) = \sqrt{\frac{2}{(2r)^2} \left[\frac{(MS_5)^2}{df (MS_5)} + \frac{(MS_1)^2}{2 df (MS_1) + 2} \right]}$$

$$\text{S.E } (\sigma^2_{ml}) = \sqrt{\frac{2}{(2r)^2} \left[\frac{(MS_5)^2}{df (MS_5)} + \frac{(MS_4)^2}{2 df (MS_4) + 2} \right]}$$

$$\text{S.E (D)} = 8 \times [\text{S.E } (\sigma^2_m)]$$

$$\text{S.E (H)} = 8 \times [\text{S.E } (\sigma^2_{ml})]$$

3.6.3.7. Standard errors for pooled estimates

$$\text{S.E } (\sigma^2_m) = \sqrt{\frac{2}{(2r)^2} \left[\frac{(MS_{13})^2}{df (MS_{13})} + \frac{(MS_{12})^2}{2 df (MS_{12}) + 2} \right]}$$

$$\text{S.E } (\sigma^2_{ml}) = \sqrt{\frac{2}{(2r)^2} \left[\frac{(MS_{16})^2}{df (MS_{16})} + \frac{(MS_{15})^2}{2 df (MS_{15}) + 2} \right]}$$

$$\text{S.E } (\sigma^2_{sm}) = \sqrt{\frac{2}{(2r)^2} \left[\frac{(MS_{12})^2}{df (MS_{12})} + \frac{(MS_{11})^2}{2 df (MS_{11}) + 2} \right]}$$

$$\text{S.E } (\sigma^2_{sml}) = \sqrt{\frac{2}{(2rs)^2} \left[\frac{(MS_{15})^2}{df (MS_{15})} + \frac{(MS_{14})^2}{2 df (MS_{14}) + 2} \right]}$$

$$\text{S.E (D)} = 8 \times [\text{SE } (\sigma^2_m)]$$

$$\text{S.E (H)} = 8 \times [\text{S.E } (\sigma^2_{ml})]$$

$$\text{S.E (G}_{2D}) = 8 \times [\text{S.E } (\sigma^2_{sm})]$$

$$\text{S.E (G}_{2H}) = 8 \times [\text{S.E } (\sigma^2_{sml})]$$

3.7 Heterosis

Heterosis (pooled over environments) was estimated in relation to standard check. This was calculated as increase or decrease of F_1 's over standard check, respectively. It was mathematically calculated by the following formula:

$$\text{Heterosis (\%)} \text{ over standard check } (\bar{C}) = \frac{\bar{F}_1 - \bar{C}}{\bar{C}} \times 100$$

Where,

\bar{F}_1 = Mean performance of F_1 hybrid

\bar{C} = Mean value of standard check

Critical Difference (CD) was calculated to test the significance of difference between any two treatments as follows:

$CD = S.E. (d) \times 't'$ value at error degree of freedom at 5 per cent level of significance

Where,

S.E. (d) is the standard error of difference between two treatment means.

$$S.E. (d) = \sqrt{2EMS/r}$$

Where,

EMS is error mean sum of square.

Chapter-4

EXPERIMENTAL FINDINGS

The present investigation entitled, “**Heterosis and combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.)” under temperate conditions of Kashmir**” was initiated at Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar during Kharif 2021 to develop the crosses using twelve diverse genotypes. The crosses were developed by using diallel mating design. The set of sixty six crosses (excluding reciprocals) were evaluated along with the twelve parents in Randomized Complete Block Design with three replications at all the three locations viz., Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar; Krishi Vigyan Kendra Budgam and Krishi Vigyan Kendra Malangpora Pulwama during Kharif 2022 for assessing the magnitude of heterosis, identifying good combiners for various traits and to generate information on other genetic parameters.

The observations were recorded on number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster⁻¹, number of fruits cluster⁻¹, number of pickings, number of fruits plant⁻¹, fruit length (cm), fruit diameter (cm), number of locules fruit⁻¹, pericarp thickness (mm), number of primary branches plant⁻¹, plant height (cm), average fruit weight (g), fruit yield plant⁻¹ (kg), fruit yield hectare⁻¹ (q), average number of seeds fruit⁻¹, 100 seed weight (g), juice to pulp ratio, titrable acidity (%), lycopene content (mg/100g), ascorbic acid content (mg/100g), TSS (°Brix) and total carotenoids (mg/100g)

The relevant results obtained on various aspects are presented under following heads:

- 4.1 Analysis of variance
- 4.2 Analysis of variance for combining ability and genetic components of variance
- 4.3 Estimation of general combining effects of parents
- 4.4 Estimation of specific combining ability of crosses
- 4.5 Estimation of components of genetic variation
- 4.6 Proportion of genetic components of variation
- 4.7 Analysis of quality traits based on mean performance
- 4.8 Estimation of heterosis

4.1 Analysis of variance

Analysis of variance for maturity, yield and yield attributing traits in individual and pooled over environments is presented in Table-1.1 to 1.7. Perusal of the data revealed significant mean squares for the environments in all the characters. Highly significant differences were found among the parents and their crosses for all the traits under consideration in the individual as well as data pooled over environments. Variance due to parents vs crosses was found to be significant for all the traits. The genotype \times environment interaction was significant for all the traits except number of locules fruit⁻¹ and 100 seed weight. Parents \times Environments interaction was significant for all the characters except number of locules fruit⁻¹, pericarp thickness and 100 seed weight. Crosses \times Environments interactions were found significant for days to first fruit harvest, number of fruits cluster⁻¹, number of pickings, number of fruits plant⁻¹, fruit length, fruit diameter, pericarp thickness, number of primary branches plant⁻¹, plant height, average fruit weight, fruit yield plant⁻¹, fruit yield hectare⁻¹, average number of seeds fruit⁻¹ except number of flowers cluster⁻¹, number of loculesfruit⁻¹ and 100 seed weight. Parents \times Crosses \times Environments interaction were found significant for all traits except fruit length, fruit diameter, number of locules fruit⁻¹ and pericarp thickness.

Table 1.1: Analysis of variance for number of days to first flowering and number of days to first fruit set in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Number of days to first flowering				Number of days to first fruit set			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	307.98**	--	--	--	283.45**
Replications	2	51.52**	67.98**	80.32**	--	45.34**	51.16**	56.07**	--
Replications within environments	6	--	--	--	66.61**	--	--	--	50.86**
Genotypes	77	11.03**	11.06	11.02**	32.90**	21.40**	21.42**	21.29**	64.03**
Parents	11	13.02**	12.92**	12.26**	38.12**	27.25**	27.49**	26.97**	81.65**
Crosses	65	10.61**	10.65**	10.76**	31.81**	20.05**	20.02**	20.00**	59.99**
Parents vs Crosses	1	16.48**	16.74**	13.68**	46.81**	45.02**	45.43**	42.49**	132.91**
Genotypes × Environments	154	--	--	--	0.10**	--	--	--	0.14**
Parents × Environments	22	--	--	--	0.15**	--	--	--	0.09**
Crosses × Environments	130	--	--	--	0.12**	--	--	--	0.15**
Parents vs Crosses × Environments	2	--	--	--	0.45**	--	--	--	1.01**
Error	--	--	--	--	--	--	--	--	--
Individual	233	4.14	4.31	4.41	--	7.87	7.93	7.92	--
Pooled	701	--	--	--	5.16	--	--	--	8.69

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.2: Analysis of variance for number of days to first fruit harvest and number of flowers cluster⁻¹ in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Number of days to first fruit harvest				Number of flowers cluster ⁻¹			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	290.10**	--	--	--	18.92**
Replications	2	21.84**	24.19**	34.87**	--	24.75**	23.41**	21.05**	--
Replications within environments	6	--	--	--	26.96**	--	--	--	2.63**
Genotypes	77	49.36**	49.36**	51.68**	150.24**	0.94**	0.94**	0.80**	2.63**
Parents	11	20.27**	20.07**	18.71**	58.87**	0.97**	0.82**	0.72**	2.46**
Crosses	65	53.49**	53.62**	56.36**	163.32**	0.95**	0.97**	0.83**	2.70**
Parents vs Crosses	1	100.75**	94.53**	110.29**	305.26**	0.85**	0.87**	0.90**	2.18**
Genotypes × Environments	154	--	--	--	0.18**	--	--	--	0.08**
Parents × Environments	22	--	--	--	0.29**	--	--	--	0.12**
Crosses × Environments	130	--	--	--	0.17**	--	--	--	0.07
Parents Vs Crosses × Environments	2	--	--	--	0.15**	--	--	--	0.54**
Error	--	--	--	--	--	--	--	--	--
Individual	233	17.00	17.05	17.90	--	0.58	0.56	0.53	--
Pooled	701	--	--	--	18.09	--	--	--	0.61

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.3: Analysis of variance for number of fruits cluster⁻¹, number of pickings and number of fruits plant⁻¹ in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Number of fruits cluster ⁻¹				Number of pickings				Number of fruits plant ⁻¹			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	5.06**	--	--	--	11.55**	--	--	--	296.65**
Replications	2	5.19**	4.79**	4.65**	--	1.39**	1.27**	1.49**	--	14.43**	17.98**	13.13**	--
Replications within environments	6	--	--	--	4.88**	--	--	--	1.38**	--	--	--	15.18**
Genotypes	77	0.74**	0.70**	0.65**	2.07**	9.16**	8.83**	8.70**	26.67**	126.19**	125.73**	127.78**	379.29**
Parents	11	0.35**	0.34**	0.29**	0.96**	16.99**	15.32**	15.16**	47.39**	185.90**	186.08**	191.42**	263.02**
Crosses	65	0.82**	0.77**	0.72**	2.28**	7.97**	7.87**	7.74**	23.57**	117.88**	117.34**	118.87**	353.66**
Parents vs Crosses	1	0.29**	0.25*	0.30**	0.27**	1.28**	1.05**	1.04**	1.31**	19.61**	17.47**	17.12**	24.07**
Genotypes × Environments	154	--	--	--	0.10**	--	--	--	0.96**	--	--	--	1.21**
Parents × Environments	22	--	--	--	0.12**	--	--	--	0.24**	--	--	--	0.18**
Crosses × Environments	130	--	--	--	0.15**	--	--	--	0.31**	--	--	--	0.21**
Parents Vs Crosses × Environments	2	--	--	--	0.17**	--	--	--	0.23**	--	--	--	1.15**
Error	--	--	--	--	--	--	--	--	--	--	--	--	--
Individual	233	0.39	0.37	0.32	--	3.12	3.01	2.98	--	42.66	42.62	43.34	--
Pooled	701	--	--	--	0.38	--	--	--	3.06	--	--	--	43.59

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.4: Analysis of variance for fruit length, fruit diameter and number of locules fruit⁻¹ in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Fruit length (cm)				Fruit diameter (cm)				Number of locules fruit ⁻¹			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	4.96**	--	--	--	3.66**	--	--	--	1.92**
Replications	2	8.87**	8.78**	8.27**	--	6.57**	6.52**	5.83**	--	0.81	0.61	0.57	--
Replications within environments	6	--	--	--	8.64**	--	--	--	6.31**	--	--	--	0.66*
Genotypes	77	1.02**	1.05**	0.98**	3.04**	1.39**	1.37**	1.32**	4.07**	2.00**	1.95**	1.83**	5.75**
Parents	11	0.95**	1.02**	0.93**	2.88**	2.04**	2.00**	1.91**	5.94**	1.94**	1.67**	1.54**	5.05**
Crosses	65	1.01**	1.04**	0.97**	3.01**	1.29**	1.28**	1.23**	3.78**	2.02**	1.99**	1.89**	5.89**
Parents vs Crosses	1	2.11**	2.09**	2.44**	6.63**	0.88*	0.89*	0.87*	1.95*	1.32*	1.79*	1.20*	4.27**
Genotypes × Environments	154	--	--	--	0.09**	--	--	--	0.10**	--	--	--	0.11
Parents × Environments	22	--	--	--	0.12**	--	--	--	0.16**	--	--	--	0.09
Crosses × Environments	130	--	--	--	0.15**	--	--	--	0.24**	--	--	--	0.07
Parents Vs Crosses × Environments	2	--	--	--	0.008	--	--	--	0.05	--	--	--	0.05
Error	--	--	--	--	-	--	--	--	--	--	--	--	--
Individual	233	0.53	0.53	0.51		0.76	0.76	0.73	--	0.80	0.79	0.74	--
Pooled	701	--	--	--	0.54	--	--	--	0.76	--	--	--	0.78

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.5: Analysis of variance for pericarp thickness, number of primary branches plant⁻¹ and plant height in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Pericarp thickness (mm)				Number of primary branches plant ⁻¹				Plant height (cm)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	1.61**	--	--	--	1.71**	--	--	--	292.67**
Replications	2	0.47	0.32	0.32	--	1.78**	1.67**	1.64**	--	159.92**	117.77**	108.11**	--
Replications within environments	6	--	--	--	0.37*	--	--	--	1.69**	--	--	--	128.60**
Genotypes	77	2.23**	2.14**	2.16**	6.52**	0.70**	0.70**	0.70**	2.07**	902.45**	884.27**	877.32**	2662.98**
Parents	11	0.63**	0.64**	0.64**	1.90**	0.70**	0.65**	0.65**	1.97**	690.21**	677.08**	660.68**	2026.78**
Crosses	65	2.52**	2.42**	2.43**	7.35**	0.71**	0.72**	0.71**	2.12**	952.25**	932.88**	927.33**	2811.46**
Parents vs Crosses	1	0.96	0.98	1.24*	3.17**	0.94**	0.96**	0.90**	1.06**	8.16**	8.75**	9.78**	9.94**
Genotypes × Environments	154	--	--	--	0.21**	--	--	--	0.21**	--	--	--	1.53**
Parents × Environments	22	--	--	--	0.09	--	--	--	0.11**	--	--	--	3.59**
Crosses × Environments	130	--	--	--	0.24**	--	--	--	0.12**	--	--	--	6.49**
Parents Vs Crosses × Environments	2	--	--	--	0.03	--	--	--	0.24**	--	--	--	1.87**
Error	--	--	--	--	--	--	--	--	--	--	--	--	--
Individual	233	0.84	0.81	0.83		0.33	0.32	0.34	--	302.16	295.64	293.45	--
Pooled	701	--	--	--	0.83	--	--	--	0.33	--	--	--	297.93

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.6: Analysis of variance for average fruit weight and fruit yield plant⁻¹ in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Average fruit weight (g)				Fruit yield plant ⁻¹ (kg)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	1142.21**	--	--	--	31.33**
Replications	2	25.26	19.06**	18.63**	--	0.03	0.02	0.01	--
Replications within environments	6	--	--	--	0.64	--	--	--	1.05**
Genotypes	77	346.55**	349.04**	349.35**	487.25**	1.02**	0.67**	0.64**	2.12**
Parents	11	418.58**	404.66**	414.77**	538.01**	1.09**	0.98**	0.94**	3.01**
Crosses	65	339.44**	344.53**	343.15**	494.12**	1.41**	0.63**	0.59**	1.93**
Parents vs Crosses	1	26.03**	30.25**	32.49**	57.85**	0.64**	0.52**	0.38**	1.14**
Genotypes × Environments	154	--	--	--	4.12**	--	--	--	0.74**
Parents × Environments	22	--	--	--	9.87**	--	--	--	0.15**
Crosses × Environments	130	--	--	--	2.72**	--	--	--	0.25**
Parents Vs Crosses × Environments	2	--	--	--	2.82**	--	--	--	0.33**
Error	--	--	--	--	--	--	--	--	--
Individual	233	118.54	117.05	117.09	--	0.35	0.22	0.21	--
Pooled	701	--	--	--	276.32	--	--	--	0.55

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.7: Analysis of variance for fruit yield hectare⁻¹, average number of seeds fruits⁻¹ and 100 seed weight in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Fruit yield hectare ⁻¹ (q/ha)				Average number of seeds fruits ⁻¹				100 seed weight (g)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	229695.36**	--	--	--	593.46**	--	--	--	3.00**
Replications	2	2657.26	3940.71	1126.74	--	164.35**	153.09**	149.05**	--	0.20**	0.18**	0.22**	--
Replications within environments	6	--	--	--	2574.90	--	--	--	155.49**	--	--	--	0.54**
Genotypes	77	9999.64**	89731.86**	87309.82**	275945.35**	6528.94**	6510.45**	6480.86**	19518.52**	0.70**	0.68**	0.65**	0.72**
Parents	11	151006.17**	134115.65**	128609.18**	412796.83**	3353.29**	336687**	3342.88**	10061.80**	0.60**	0.57**	0.56**	0.63**
Crosses	65	92792.15**	83560.99**	81622.25**	256854.42**	6907.01**	6887.03**	6850.47**	20642.70**	0.77**	0.75**	0.73**	0.80**
Parents vs Crosses	1	6789.91**	2616.71**	2709.14**	11489.72**	16886.07**	16611.55**	16973.85**	50470.40**	0.30**	0.28**	0.24**	0.31**
Genotypes × Environments	154	--	--	--	543.99**	--	--	--	0.86**	--	--	--	0.20*
Parents × Environments	22	--	--	--	467.08**	--	--	--	0.62**	--	--	--	0.40*
Crosses × Environments	130	--	--	--	560.48**	--	--	--	0.90**	--	--	--	0.30*
Parents Vs Crosses × Environments	2	--	--	--	317.62**	--	--	--	0.53**	--	--	--	0.12**
Error	--	--	--	--	--	--	--	--	--	--	--	--	--
Individual	233	33683.38	30758.74	29401.55	--	2163.28	2156.88	2147.16	--	0.20	0.22	0.18	--
Pooled	701	--	--	--	31847.31	--	--	--	2151.32	--	--	--	0.25

*, ** Significant at 5 and 1 per cent levels, respectively

4.2 Analysis of variance for combining ability and genetic components of variation

The analysis of variance for general combining ability (GCA), specific combining ability (SCA) and their interaction with environments in respect of twelve parents and sixty six F_1 crosses for eighteen quantitative traits presented in Table-2.1 to 2.7, revealed significant differences for all the traits under the environments, in the individual as well as data pooled over environments. Mean squares for GCA and SCA were found to be significant for all the traits studied both in the individual as well as data pooled over the environments. The mean squares due to GCA \times environments and SCA \times environments were found significant for all characters except number of locules fruit⁻¹, pericarp thickness and 100 seed weight for which GCA and SCA effects showed non-significant interaction with environments.

The mean squares due to GCA, SCA, GCA \times environments, SCA \times environments and error were used for the estimation of GCA and SCA variances. Variances due to SCA ($\hat{\sigma}^2_s$) were higher in magnitude than the corresponding GCA variances ($\hat{\sigma}^2_g$) in the individual as well as data pooled over environments for all the traits under study. The estimates of additive genetic variance ($\hat{\sigma}^2_A$) and dominance variance ($\hat{\sigma}^2_D$) revealed that the magnitude of dominance variance was higher in range in the individual as well as data pooled over environments for all the traits under consideration indicating preponderance of non-additive gene action. The ratio of additive genetic variance to dominance variance ($\hat{\sigma}^2_A/\hat{\sigma}^2_D$) was less than unity for all the traits in the individual as well as data pooled over environments.

Table 2.1: Analysis of variance for combining ability and estimates of components of variance for number of days to first flowering, number of days to first fruit set and number of days to first fruit harvest in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Number of days to first flowering				Number of days to first fruit set				Number of days to first fruit harvest			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	102.66**	--	--	--	94.48**	--	--	--	96.70**
GCA	11	2.58**	2.63**	2.75**	7.92**	12.23**	12.46**	12.01**	36.67**	20.54**	20.55**	21.73**	62.76**
SCA	66	3.85**	3.86**	3.83**	11.47**	6.28**	6.25**	6.28**	18.79**	13.77**	15.77**	16.48**	47.97**
GCA x environments	22	--	--	--	0.22**	--	--	--	0.32**	--	--	--	0.13**
SCA × environments	132	--	--	--	0.14**	--	--	--	0.21**	--	--	--	0.33**
Error	154	0.02	0.03	0.04	--	0.20	0.21	0.20	--	0.25	0.27	0.26	
Pooled	462	--	--	--	0.03	--	--	--	0.20	--	--	--	0.26
$\hat{\sigma}^2 g$	-	0.18	0.18	0.19	0.18	0.86	0.87	0.84	0.87	1.45	1.45	1.53	1.49
$\hat{\sigma}^2 s$	-	3.84	3.82	3.79	3.81	6.08	6.04	6.05	6.19	15.52	15.50	16.21	15.90
$\hat{\sigma}^2 A$	-	0.36	0.37	0.39	0.37	1.72	1.75	1.69	1.74	2.90	2.89	3.07	2.97
$\hat{\sigma}^2 D$	-	3.84	3.82	3.71	3.81	6.08	6.04	6.07	6.19	15.52	15.50	16.21	15.90
$\frac{\hat{\sigma}^2 A}{\hat{\sigma}^2 D}$	-	0.09	0.10	0.10	0.10	0.28	0.29	0.28	0.28	0.19	0.19	0.19	0.19

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.2: Analysis of variance for combining ability and estimates of components of variance for number of flowers cluster⁻¹, number of fruits cluster⁻¹ and number of pickings in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Number of flowers cluster ⁻¹				Number of fruits cluster ⁻¹				Number of pickings			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	---	---	6.31**	--	--	--	1.69**	--	--	--	3.85**
GCA	11	0.41**	0.41**	0.37**	1.17**	0.20**	0.18**	0.22**	0.59**	3.78**	3.69**	3.63**	11.10**
SCA	66	0.30**	0.30**	0.25**	0.83**	0.26**	0.24**	0.22**	0.71**	2.93**	2.82**	2.78**	8.52**
GCA x environments	22	--	--	--	0.08**	--	--	--	0.12**	--	--	--	0.14**
SCA × environments	132	--	--	--	0.11**	--	--	--	0.09**	--	--	--	0.10**
Error	154	0.03	0.03	0.04	--	0.05	0.05	0.05		0.04	0.04	0.04	--
Pooled	462	--	--	--	0.03	--	--	--	0.05	--	--	--	0.04
$\hat{\sigma}^2 g$	-	0.03	0.03	0.02	0.03	0.01	0.01	0.01	0.01	0.27	0.26	0.26	0.26
$\hat{\sigma}^2 s$	-	0.27	0.27	0.21	0.26	0.21	0.19	0.17	0.22	2.89	2.78	2.73	2.83
$\hat{\sigma}^2 A$	-	0.05	0.05	0.05	0.05	0.02	0.02	0.02	0.03	0.53	0.52	0.51	0.53
$\hat{\sigma}^2 D$	-	0.27	0.27	0.21	0.26	0.21	0.19	0.17	0.22	2.89	2.78	2.73	2.83
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$	-	0.18	0.18	0.23	0.19	0.10	0.11	0.12	0.14	0.18	0.19	0.19	0.19

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.3: Analysis of variance for combining ability and estimates of components of variance for number of fruits plant⁻¹, fruit length and fruit diameter in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Number of fruits plant ⁻¹				Fruit length (cm)				Fruit diameter (cm)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	98.89**	--	--	--	1.65**	--	--	--	1.22**
GCA	11	54.26**	53.83**	53.92**	161.89**	0.57**	0.66**	0.59**	1.83**	0.75**	0.77**	0.71**	2.23**
SCA	66	40.03**	39.92**	40.71**	120.52**	0.30**	0.30**	0.28**	0.88**	0.41**	0.40**	0.39**	1.21**
GCA x environments	22	--	--	--	2.06**	--	--	--	0.07**	--	--	--	0.05**
SCA × environments	132	--	--	--	3.21**	--	--	--	0.05**	--	--	--	0.04**
Error		0.42	0.46	0.50	--	0.06	0.06	0.06	--	0.13	0.13	0.12	--
Pooled	462	--	--	--	0.46	--	--	--	0.06	--	--	--	0.13
$\hat{\sigma}^2 g$	-	3.84	3.81	3.81	3.84	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.05
$\hat{\sigma}^2 s$	-	39.61	39.46	40.20	40.02	0.24	0.24	0.22	0.27	0.29	0.28	0.27	0.40
$\hat{\sigma}^2 A$	-	7.69	7.62	7.63	7.69	0.07	0.09	0.08	0.08	0.09	0.09	0.08	0.10
$\hat{\sigma}^2 D$	-	39.61	39.46	40.20	40.02	0.24	0.24	0.22	0.27	0.29	0.28	0.27	0.36
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$	-	0.19	0.19	0.18	0.19	0.29	0.37	0.36	0.30	0.31	0.32	0.30	0.28

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.4: Analysis of variance for combining ability and estimates of components of variance for number of locules fruit⁻¹, pericarp thickness and number of primary branches plant⁻¹ in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Number of locules fruit ⁻¹				Pericarp thickness (mm)				Number of primary branches plant ⁻¹			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	0.64**	--	--	--	0.54**	--	--	--	0.57**
SCA	11	0.09**	0.73**	0.66**	2.07**	0.83**	0.78**	0.75**	2.36**	0.14**	0.16**	0.13*	0.43**
SCA	66	0.66**	0.64**	0.60**	1.90**	0.73**	0.70**	0.71**	2.14**	0.25**	0.24**	0.25**	0.74**
GCA x environments	22	--	--	--	0.06	--	--	--	0.04	--	--	--	0.14**
SCA × environments	132	--	--	--	0.05	--	--	--	0.02	--	--	--	0.09**
Error		0.06	0.07	0.06	--	0.05	0.05	0.06	--	0.04	0.04	0.05	--
Pooled	462	--	--	--	0.06	--	--	--	0.053	--	--	--	0.042
$\hat{\sigma}^2 g$	-	0.04	0.05	0.04	0.05	0.05	0.05	0.05	0.05	0.01	0.01	0.01	0.01
$\hat{\sigma}^2 s$	-	0.60	0.57	0.54	0.61	0.68	0.65	0.65	0.70	0.20	0.20	0.20	0.23
$\hat{\sigma}^2 A$	-	0.09	0.09	0.08	0.10	0.11	0.10	0.09	0.11	0.01	0.02	0.01	0.02
$\hat{\sigma}^2 D$	-	0.60	0.57	0.54	0.61	0.68	0.65	0.65	0.69	0.20	0.20	0.20	0.23
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$	-	0.15	0.16	0.15	0.16	0.16	0.15	0.14	0.16	0.05	0.10	0.05	0.10

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.5: Analysis of variance for combining ability and estimates of components of variance for plant height and average fruit weight in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Plant height (cm)				Average fruit weight (g)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	197.56**	--	--	--	116.43**
GCA	11	222.24**	228.08**	232.64**	682.27**	146.81**	143.99**	145.23**	435.70**
SCA	66	313.91**	305.87**	302.41**	921.90**	110.30**	111.74**	111.65**	332.52**
GCA x environments	22	--	--	--	3.35**	--	--	--	2.16**
SCA × environments	132	--	--	--	1.15**	--	--	--	1.59**
Error		1.29	1.21	1.31	--	1.92	0.77	0.75	--
Pooled	462	--	--	--	1.27	--	--	--	1.15
$\hat{\sigma}^2 g$	-	15.78	16.20	16.52	15.78	10.35	10.23	10.32	10.35
$\hat{\sigma}^2 s$	-	312.62	304.66	301.10	312.62	108.38	110.96	110.91	110.46
$\hat{\sigma}^2 A$	-	31.56	32.41	33.05	31.56	20.70	20.46	20.64	20.69
$\hat{\sigma}^2 D$	-	312.62	304.66	301.10	312.62	108.38	110.96	110.91	110.46
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$	-	0.10	0.11	0.11	0.10	0.19	0.18	0.19	0.19

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.6: Analysis of variance for combining ability and estimates of components of variance for fruit yield plant⁻¹ and fruit yield hectare⁻¹ in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Fruit yield plant ⁻¹ (kg)				Fruit yield hectare ⁻¹ (q)			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	17.11**	--	--	--	97557.52**
GCA	11	0.32**	0.24**	0.22**	10.59**	36002.25**	31485.42**	30382.33**	91052.50**
SCA	66	0.25**	0.22**	0.21**	13.24**	32885.26**	29648.16**	28890.09**	76565.12**
GCA x environments	22	--	--	--	18.09**	--	--	--	156.24**
SCA × environments	132	--	--	--	22.22**	--	--	--	185.51**
Error		0.15	0.21	0.20	--	310.73	540.16	271.54	--
Pooled	462	--	--	--	11.92	--	--	--	374.14
$\hat{\sigma}^2 g$	-	0.39	0.02	0.01	0.03	2549.39	2210.38	2150.77	2313.89
$\hat{\sigma}^2 s$	-	1.50	0.23	0.21	0.44	32574.53	29107.99	28618.56	30226.12
$\hat{\sigma}^2 A$	-	0.78	0.03	0.03	0.06	5098.79	4420.75	4301.54	4627.78
$\hat{\sigma}^2 D$	-	1.50	0.22	0.21	0.44	32574.53	29107.99	28618.56	30226.12
$\hat{\sigma}^2 A / \hat{\sigma}^2 D$	-	0.52	0.14	0.14	0.14	0.16	0.15	0.15	0.15

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.7: Analysis of variance for combining ability and estimates of components of variance for average number of seeds plant⁻¹ and 100 seed weight in tomato. (Based on individual and pooled over environments)

Source of variation	d.f	Average number of seeds plant ⁻¹				100 seed weight			
		E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
Environments	2	--	--	--	197.82	--	--	--	0.10**
GCA	11	2226.08**	2203.22**	2205.29**	6633.12**	0.33**	0.28**	0.29**	0.31**
SCA	66	2168.02**	2164.64**	2152.79**	6485.01**	0.42**	0.37**	0.35**	0.48**
GCA x environments	22	--	--	--	0.72**	--	--	--	0.74
SCA × environments	132	--	--	--	0.21**	--	--	--	0.68
Error		2.14	2.04	2.09	--	0.11	0.10	0.12	--
Pooled	462	--	--	--	2.09	--	--	--	0.20
$\hat{\sigma}^2_g$	-	158.85	157.23	157.37	157.88	0.24	0.22	0.23	0.32
$\hat{\sigma}^2_s$	-	2165.88	2162.60	2150.70	2160.97	0.38	0.32	0.22	0.42
$\hat{\sigma}^2_A$	-	317.71	314.45	314.74	315.76	0.35	0.25	0.32	0.28
$\hat{\sigma}^2_D$	-	2165.88	2162.60	2150.70	2160.97	0.62	0.52	0.70	0.84
$\hat{\sigma}^2_A / \hat{\sigma}^2_D$	-	0.15	0.14	0.15	0.15	0.56	0.48	0.45	0.33

*, ** Significant at 5 and 1 per cent levels, respectively

4.3 Estimation of general combining effects of parents

The estimates of general combining ability effects for all the traits under study in the individual and pooled over environments has been presented in table- 3.1 to 3.7. Also the table- 4 shows the maximum trait contribution of the best parents in respect of significant GCA effect.

The scrutiny of results indicated that none of the parents revealed significant and desirable general combining ability for all the traits. The trait wise results are presented as follows:

4.3.1 Number of days to first flowering

Earliness in flowering is a desirable character, hence parents with significant and negative GCA effects were preferred for imparting earliness in their hybrids and their progenies were considered as good general combiners. Among the twelve parents evaluated, estimates of GCA effect showed that seven parents viz., SKAU-T-9801, SKAU-T-1700, SKAU-T-1424, SKAU-T-1219, SKAU-T-0301, SKAU-T-1429 and SKAU-T-1009 manifested significant and negative GCA effects in the individual as well as pooled data over environments and hence these parents are considered as good general combiners for early flowering. Parents SKAU-T-0922, SKAU-T-1315, SKAU-T-1701 and SKAU-T-9862 exhibited positive and significant GCA effects in individual and data pooled over environments, indicating their poor combining ability.

4.3.2 Number of days to first fruit set

Significant negative GCA effects were shown by parents SKAU-T-9801, SKAU-T-1700, SKAU-T-1424, SKAU-T-1219, SKAU-T-0301, SKAU-T-1429 and SKAU-T-1009 for this trait in individual environments and as well as data pooled over environments. SKAU-T-0922, SKAU-T-1315, SKAU-T-1701 and SKAU-T-9862 revealed significant positive GCA effects in individual and data pooled over environments.

4.3.3 Number of days to last fruit harvest

Parents SKAU-T-9801, SKAU-T-1700, SKAU-T-1424, SKAU-T-1219, SKAU-0301, SKAU-T-1429 and SKAU-T-1009 had significant and negative estimates of GCA effect in individual as well as data pooled over environments and hence these parents are considered as good general combiners for early fruit ripening, parents SKAU-T-0922, SKAU-T-1315, SKAU-T-1701 and SKAU-T-9862 had significant positive estimates in individual and in data pooled over environments indicating their poor combining ability.

4.3.4 Number of flowers cluster⁻¹

Positive significant GCA effects for number of flowers cluster⁻¹ were found in parents SKAU-T-9801, SKAU-T-0922, SKAU-T-1424, SKAU-T-1219, SKAU-T-0301, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 in individual environments and in data pooled over environments. SKAU-T-1700, SKAU-T-1315 and SKAU-T-1009 showed significant negative effects in E₁, E₂, E₃ and data pooled over environments.

4.3.5 Number of fruits cluster⁻¹

Positive significant GCA effects for number of fruits cluster⁻¹ is desirable and was found in parents SKAU-T-9801, SKAU-T-0922, SKAU-T-1424, SKAU-T-1219, SKAU-T-0301, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 in individual environments and in data pooled over environments. SKAU-T-1700, SKAU-T-1315 and SKAU-T-1009 showed significant negative effects in individual and data pooled over environments.

4.3.6 Number of pickings

Positive values for the combining ability effects are preferred for number of pickings. Among the twelve parents SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-1219, SKAU-T-0301, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 showed positive and significant effects in both individual and pooled

environments. SKAU-T-1424 showed positive non-significant effects in both individual and pooled analysis. Negative significant effects were found in SKAU-T-1315 and SKAU-T-1009 in both individual and data pooled over environment.

4.3.7 Number of fruits plant⁻¹

For number of fruits plant⁻¹, desirable positive and significant GCA effects were found in SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-0301, SKAU-T-1429, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 in all individual environments and pooled analysis, hence are good combiners and parents SKAU-T-1424, SKAU-T-1219 manifested positive but non-significant GCA in individual and pooled data. Parents SKAU-T-1315 and SKAU-T-1009 manifested significant negative estimates in individual and data pooled over environments indicating poor combining ability of these parents for this trait.

4.3.8 Fruit Length (cm)

Significant positive GCA effects were found in SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-0301, SKAU-T-1429, SKAU-T-1009 and SKAU-T-9862 in individual environments as well as in data pooled over environments. While SKAU-T-1424, SKAU-T-1701 and SKAU-T-1464 manifested positive non-significant GCA effect in individual and pooled data over environments.

4.3.9 Fruit diameter (cm)

Among twelve parents evaluated, SKAU-T-9801, SKAU-T-0922, SKAU-T-0301, SKAU-T-1701, SKAU-T-1009 and SKAU-T-1464 manifested positive significant GCA effects in individual as well as in data pooled over environments. SKAU-T-1700, SKAU-T-1424, SKAU-T-1429 and SKAU-T-9862 positive non-significant in individual and pooled environment.

4.3.10 Number of locules fruit⁻¹

Positive values for the combining ability effects are preferred for number of locules fruit⁻¹. Among twelve parents evaluated, parents SKAU-T-0922,

SKAU-T-1219, SKAU-T-0301, SKAU-T-1429, SKAU-T-9862 and SKAU-T-1464 manifested positive significant GCA effects in individual as well as in data pooled over environments indicating good general combining ability of these parents. SKAU-T-9801 and SKAU-T-1700 showed positive non-significant effects in individual and pooled environment.

4.3.11 Pericarp thickness (mm)

SKAU-T-9801, SKAU-T-1700, SKAU-T-1315, SKAU-T-1429, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 were found to be good combiners with significant positive GCA effects, in individual and data pooled over environments, whereas SKAU-T-1219 showed positive non-significant effect in individual and pooled data. SKAU-T-0922 negative significant effect in individual and pooled environment while SKAU-T-1424 showed significant but negative effects in the data pooled over environments.

4.3.12 Number of primary branches plant⁻¹

Significant positive GCA effects were depicted by SKAU-T-9801, SKAU-T-1219 SKAU-T-1315, SKAU-T-9862 and SKAU-T-1464 in individual and data pooled over environments, whereas SKAU-T-1009 showed positive significant GCA effect in pooled environment. SKAU-T-0922, SKAU-T-0301 and SKAU-T-1701 showed positive non- significant effect in individual and data pooled over environment. SKAU-T-1700 and SKAU-T-1424 manifested negative significant effect in individual and pooled environment and SKAU-T-1429 manifested negative significant effect in pooled environment.

4.3.13 Plant height (cm)

SKAU-T-9801, SKAU-T-0922, SKAU-T-1219, SKAU-T-0301, SKAU-T-1429, SKAU-T-1009, SKAU-T-9862 and SKAU-T-1464 showed positive significant GCA effects (i.e., good combiners) in the individual environments and pooled analysis, SKAU-T-1315 was found to be positive non-significant in both individual and pooled environment. The parents SKAU-T-1700 and SKAU-T-

1701 were found to be poor combiners (with negative significant GCA effects) for plant height in individual environments as well as in pooled data.

4.3.14 Average fruit weight (g)

Positive values of combining ability for average fruit weight is preferred. SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-0301, SKAU-T-1429, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 were found to be good combiners (significant, positive) while as SKAU-T-1424 and SKAU-T-1315 were found to be poor combiners (significant negative) for average fruit weight at all locations as well as in pooled analysis; SKAU-T-1009 showed significant negative effect in E₂, E₃ and pooled environment. SKAU-T-1219 showed non-significant positive effects in the individual environments and data pooled over environments.

4.3.15 Fruit yield plant⁻¹ (kg)

SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-0301, SKAU-T-1429, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 were found to be good combiners with significant positive GCA effect, in individual and data pooled over environments whereas SKAU-T-1219 showed positive non-significant GCA effects in all individual environments as well as in pooled analysis. Negative significant GCA effects were also depicted by SKAU-T-1315 and SKAU-T-1009 in individual and pooled analysis. SKAU-T-1424 showed negative but significant GCA effects in data pooled over environments.

4.3.16 Fruit yield hectare⁻¹ (q)

SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-0301, SKAU-T-1429, SKAU-T-1701, SKAU-T-9862 and SKAU-T-1464 were found to be good combiners with significant positive GCA effects, in individual and data pooled over environments whereas SKAU-T-1315 and SKAU-T-1009 showed significant negative GCA effects in individual environments as well as in pooled analysis.

Whereas SKAU-T-1219 showed non-significant positive effects in the individual environments and data pooled over environments.

4.3.17 Average number of seeds fruits⁻¹

Significant positive GCA effects were depicted by SKAU-T-9801, SKAU-T-0922, SKAU-T-0301, SKAU-T-9862 and SKAU-T-1464 in individual and data pooled over environments, whereas SKAU-T-1424, SKAU-T-1219, SKAU-T-1315, SKAU-T-1429, SKAU-T-1701 and SKAU-T-1009 showed significant negative GCA effects in individual as well as in data pooled over environments, SKAU-T-1700 showed positive but non-significant in the individual environments and data pooled over environments.

4.3.18 100 seed weight (g)

Significant positive GCA effects were depicted by SKAU-T-1700, SKAU-T-1315, SKAU-T-0301, SKAU-T-1701, SKAU-T-1009 and SKAU-T-1464 in individual and data pooled over environments, whereas SKAU-T-9801, SKAU-T-1219, SKAU-T-1429 and SKAU-T-9862 showed significant negative GCA effects in individual as well as in data pooled over environments. Positive but non-significant GCA effects were also depicted by SKAU-T-0922, SKAU-T-1424 in individual as well as in data pooled over environments.

Table 3.1: General combining ability (GCA) effects for number of days to first flowering, number of days to first fruit set and number of days to first fruit harvest in tomato. (Based on individual and pooled over environments)

Parents	Number of days to first flowering				Number of days to first fruit set				Number of days to first fruit harvest			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801	-0.229**	-0.244**	-0.208**	-0.231**	-0.942**	-0.937**	-0.871**	-0.917**	-1.174**	-1.101**	-1.179**	-1.152**
SKAU-T-1700	-0.252**	-0.335**	-0.304**	-0.297**	-0.973**	-1.013**	-0.914**	-0.967**	-1.188**	-1.204**	-1.146**	-1.179**
SKAU-T-0922	0.445**	0.470**	0.408**	0.441**	1.368**	1.430**	1.443**	1.413**	1.040**	1.001**	1.071**	1.037**
SKAU-T-1424	-0.481**	-0.380**	-0.390**	-0.417**	-1.451**	-1.439**	-1.481**	-1.457**	-1.069**	-1.049**	-0.992**	-1.037**
SKAU-T-1219	-0.564**	-0.609**	-0.659**	-0.611**	-0.554**	-0.494**	-0.498**	-0.515**	-1.548**	-1.504**	-1.494**	-1.515**
SKAU-T-1315	0.550**	0.556**	0.615**	0.574**	0.735**	0.711**	0.636**	0.694**	1.204**	1.194**	1.199**	1.199**
SKAU-T-0301	-0.579**	-0.583**	-0.590**	-0.584**	-0.563**	-0.549**	-0.593**	-0.568**	-0.360*	-0.370*	-0.444**	-0.391**
SKAU-T-1429	-0.214**	-0.239**	-0.256**	-0.236**	-0.237*	-0.215*	-0.219*	-0.224**	-2.003**	-2.056**	-2.184**	-2.081**
SKAU-T-1701	0.445**	0.403**	0.396**	0.415**	0.975**	0.977**	1.33**	0.984**	1.109**	1.111**	1.173**	1.131**
SKAU-T-1009	-0.267**	-0.242**	-0.302**	-0.270**	-0.304**	-0.356**	-0.336**	-0.329**	-0.369*	-0.361*	-0.399*	-0.376**
SKAU-T-9862	0.545**	0.272**	0.551**	0.556**	1.375**	1.387**	1.331**	1.364**	1.321**	1.399**	1.425**	1.382**
SKAU-T-1464	0.014	0.053	0.010	0.026	0.137	0.101	0.198	0.179	0.162	0.120	0.187	0.156
SE± (g _i)	0.040	0.049	0.051	0.027	0.116	0.117	0.115	0.066	0.129	0.132	0.131	0.075
SE±(g _i -g _j)	0.059	0.073	0.076	0.040	0.171	0.173	0.170	0.098	0.190	0.196	0.194	0.111

*, ** Significant at 5 and 1 per cent levels, respectively

Table 3.2: General combining ability (GCA) effects for number of flowers cluster⁻¹, number of fruits cluster⁻¹ and number of pickings in tomato. (Based on individual and pooled over environments)

Parents	Number of flowers cluster ⁻¹				Number of fruits cluster ⁻¹				Number of pickings			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801	0.252**	0.209**	0.221**	0.228**	0.117*	0.135*	0.174*	0.142*	1.258**	1.255**	1.262**	1.258**
SKAU-T-1700	-0.155**	-0.167**	-0.140*	-0.121**	-0.129*	-0.133*	-0.116*	-0.119**	0.652**	0.652**	0.646**	0.650**
SKAU-T-0922	0.214**	0.197**	0.221**	0.211**	0.088**	0.282**	0.242**	0.304**	0.626**	0.631**	0.617**	0.624**
SKAU-T-1424	0.224**	0.235**	0.281**	0.247**	0.162*	0.148*	0.190*	0.167**	0.177	0.179	0.162	0.172
SKAU-T-1219	0.193**	0.217**	0.222*	0.224**	0.183**	0.196**	0.182*	0.202**	0.445**	0.457**	0.443**	0.448**
SKAU-T-1315	-0.131*	-0.120**	0.117**	-0.111**	-0.205**	-0.197**	-0.210**	-0.204**	-0.265**	-0.258**	-0.235**	-0.253**
SKAU-T-0301	0.207**	0.225**	0.181**	0.204**	0.115*	0.118*	0.124*	0.189**	0.433**	0.359**	0.346**	0.239**
SKAU-T-1429	-0.050	-0.015	-0.100	-0.055	-0.038	-0.048	-0.035	-0.040	-0.043	-0.043	-0.040	-0.052
SKAU-T-1701	0.200**	0.167**	0.200**	0.189**	0.181*	0.163*	0.177*	0.174**	0.384**	0.348**	0.350**	0.360**
SKAU-T-1009	-0.219**	-0.225**	-0.186**	-0.210**	-0.119*	-0.113*	-0.134*	-0.122*	-0.134*	-0.129*	-0.135*	-0.133**
SKAU-T-9862	0.164**	0.204**	0.176*	0.168**	0.147*	0.167*	0.164*	0.160*	0.217**	0.298**	0.283**	0.299**
SKAU-T-1464	0.114*	0.118*	0.119*	0.117*	0.109*	0.117*	0.097*	0.108*	0.121*	0.112*	0.115*	0.116*
SE± (g_i)	0.043	0.042	0.053	0.026	0.057	0.056	0.057	0.032	0.051	0.051	0.055	0.030
SE±(g_i-g_j)	0.064	0.062	0.078	0.039	0.085	0.083	0.084	0.048	0.075	0.076	0.081	0.044

*, ** Significant at 5 and 1 per cent levels, respectively

**Table 3.3: General combining ability (GCA) effects for number of fruits plant⁻¹, fruit length and fruit diameter in tomato.
(Based on individual and pooled over environments)**

Parents	Number of fruits plant ⁻¹				Fruit length (cm)				Fruit diameter (cm)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801	2.392**	2.349**	2.360**	2.367**	0.528**	0.576**	0.553**	-0.553**	0.552**	0.551**	0.515**	0.539**
SKAU-T-1700	2.301**	2.139**	2.095**	2.178**	0.171*	0.170*	0.175*	0.176**	0.048	0.044	0.056	0.050
SKAU-T-0922	2.365**	2.315**	2.257**	2.312**	0.155*	0.155*	0.137*	0.149**	0.252*	0.272*	0.548*	0.258**
SKAU-T-1424	0.020	0.063	0.066	0.050	0.038	0.033	0.041	0.037	0.045	0.029	0.041	0.038
SKAU-T-1219	0.079	0.056	0.007	0.047	-0.078	-0.071	-0.065	-0.072	-0.031	-0.053	-0.067	-0.050
SKAU-T-1315	-0.530*	-0.594**	-0.598*	-0.574**	-0.119	-0.114	-0.115	-0.116	-0.059	-0.058	-0.082	-0.066
SKAU-T-0301	1.654**	1.606**	1.527**	1.596**	0.198*	0.200*	0.166*	0.118**	0.291*	0.311**	0.309**	0.304**
SKAU-T-1429	3.677**	3.756**	3.852**	3.762**	0.131*	0.148*	0.147*	0.142**	0.088	0.078	0.083	0.083
SKAU-T-1701	2.354**	2.396**	2.443**	2.398**	0.017	0.024	0.035	0.025	0.174*	0.178*	0.161*	0.171*
SKAU-T-1009	-0.649**	-0.670**	-0.743**	-0.688**	0.115*	0.131*	0.133*	0.126**	0.227*	0.233*	0.237*	0.232**
SKAU-T-9862	0.822**	0.937**	0.938**	0.899**	0.118*	0.198*	0.187*	0.191**	0.069	0.056	0.065	0.063
SKAU-T-1464	1.685**	1.651**	1.543**	1.626**	0.079	0.081	0.085	0.082	0.179*	0.175*	0.173*	0.176**
SE± (g _i)	0.166	0.174	0.182	0.100	0.062	0.061	0.062	0.035	0.091	0.091	0.090	0.052
SE±(g _i -g _j)	0.246	0.257	0.268	0.148	0.092	0.090	0.092	0.052	0.135	0.134	0.133	0.077

*, ** Significant at 5 and 1 per cent levels, respectively

Table 3.4: General combining ability (GCA) effects for number of locules fruit⁻¹, pericarp thickness and number of primary branches plant⁻¹ in tomato. (Based on individual and pooled over environments)

Parents	Number of locules fruit ⁻¹				Pericarp thickness (mm)				Number of primary branches plant ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801	0.019	0.018	0.026	0.034	0.439**	0.435**	0.444**	0.439**	0.170**	0.177**	0.178**	0.288**
SKAU-T-1700	0.065	0.044	0.092	0.067	0.247**	0.249**	0.241**	0.246**	-0.135*	-0.172**	-0.150*	-0.152**
SKAU-T-0922	0.215*	0.196*	0.150*	0.187**	-0.251**	-0.244**	-0.223**	-0.239**	0.039	0.021	0.008	0.023
SKAU-T-1424	-0.103	-0.161	-0.123	-0.129**	-0.101*	-0.113*	-0.080*	-0.098*	0.189**	0.191**	0.162*	0.181**
SKAU-T-1219	0.408**	0.415**	0.404**	0.409**	0.035	0.063	0.065	0.054	0.080*	0.104*	0.091*	0.092*
SKAU-T-1315	-0.155*	-0.151*	-0.114	-0.140**	0.375**	0.351**	0.344**	0.357**	0.144*	0.154*	0.167*	0.155*
SKAU-T-0301	0.357**	0.368**	0.360**	0.362**	-0.037	-0.039	-0.054	-0.043	0.018	0.023	0.015	0.019
SKAU-T-1429	0.126*	0.132*	0.103*	0.120*	0.242**	0.246**	0.239**	0.242**	-0.111	-0.112	-0.095	-0.106**
SKAU-T-1701	-0.074	-0.063	-0.050	-0.062	0.223**	0.215**	0.196*	0.212**	0.056	0.066	0.038	0.054
SKAU-T-1009	-0.008	-0.027	-0.035	-0.023	0.097*	0.106*	0.096*	0.100*	0.082	0.104	0.081	0.089*
SKAU-T-9862	0.323**	0.320**	0.346**	0.330**	0.197**	0.170*	0.172*	0.180**	0.142*	0.155*	0.162*	0.176*
SKAU-T-1464	0.202**	0.220**	0.186**	0.203**	0.161*	0.132*	0.137*	0.143**	0.113*	0.115*	0.120*	0.124*
SE± (g_i)	0.065	0.067	0.065	0.037	0.057	0.058	0.062	0.034	0.053	0.051	0.055	0.030
SE±(g_i-g_j)	0.096	0.099	0.096	0.056	0.084	0.086	0.092	0.050	0.078	0.075	0.081	0.045

*, ** Significant at 5 and 1 per cent levels, respectively

Table 3.5: General combining ability (GCA) effects for plant height and average fruit weight in tomato. (Based on individual and pooled over environments)

Parents	Plant height (cm)				Average fruit weight (g)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801	7.597**	7.905**	7.949**	7.817**	6.222**	6.161**	6.151**	6.178**
SKAU-T-1700	-5.356**	-5.498**	-5.728**	-5.527**	2.957**	2.701**	2.804**	2.821**
SKAU-T-0922	1.522**	1.548**	1.646**	1.572**	2.666**	2.635**	2.596**	2.632**
SKAU-T-1424	-0.566	-0.252	0.070	-0.246	-1.200**	-0.854**	-1.082**	-1.079**
SKAU-T-1219	4.413**	4.419**	4.446**	4.426**	0.023	0.132	0.035	0.040
SKAU-T-1315	0.348	0.355	0.413	0.372	-0.255*	-0.175**	-0.146**	-0.159**
SKAU-T-0301	7.670**	7.512**	7.513**	7.565**	5.764**	5.742**	5.875**	5.794**
SKAU-T-1429	1.361**	1.155**	1.066**	1.194**	4.222**	4.196**	4.075**	4.164**
SKAU-T-1701	-0.790*	-1.088**	-1.221**	-1.033**	1.034*	0.965**	1.006**	1.002**
SKAU-T-1009	1.356**	1.460**	1.317**	1.378**	-0.474	-0.942**	-0.863**	-0.760**
SKAU-T-9862	1.006**	0.948**	0.893**	0.979**	2.571**	2.692**	2.689**	2.651**
SKAU-T-1464	1.358**	1.552**	1.541**	1.484**	1.574*	1.608*	1.606*	1.596**
SE± (g)	0.290	0.282	0.292	0.166	0.354	0.225	0.221	0.158
SE±(g_i-g_j)	0.429	0.416	0.432	0.245	0.523	0.333	0.326	0.233

*, ** Significant at 5 and 1 per cent levels, respectively

Table 3.6: General combining ability (GCA) effects for fruit yield plant⁻¹ and fruit yield hectare⁻¹ in tomato. (Based on individual and pooled over environments)

Parents	Fruit yield plant ⁻¹ (kg)				Fruit yield hectare ⁻¹ (q)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801	0.261**	0.254**	0.245**	0.255**	99.042**	94.473**	90.781**	94.765**
SKAU-T-1700	0.172**	0.168**	0.162**	0.174**	71.328**	61.875**	60.047**	64.417**
SKAU-T-0922	0.190**	0.188**	0.178**	0.187**	70.446**	69.106**	65.869**	68.474**
SKAU-T-1424	-0.018	-0.015	-0.013	-0.016**	-8.831	-5.937	-4.943	-6.570
SKAU-T-1219	0.010	0.009	0.005	0.007	3.252	3.058	2.091	2.073
SKAU-T-1315	-0.053**	-0.049**	-0.051**	-0.052**	-19.676**	-18.459*	-18.787**	-18.974**
SKAU-T-0301	0.082**	0.077**	0.083**	0.079**	29.000**	27.925**	30.684**	29.203**
SKAU-T-1429	0.043**	0.042**	0.049**	0.042**	14.009*	17.696*	18.073**	16.593**
SKAU-T-1701	0.151**	0.144**	0.145**	0.145**	55.144**	53.733**	53.619**	54.165**
SKAU-T-1009	-0.059**	-0.058**	-0.57**	-0.058**	-22.145**	-13.523	-21.080**	-18.916**
SKAU-T-9862	0.125**	0.124**	0.117**	0.120**	48.666**	39.564**	43.470**	43.900**
SKAU-T-1464	0.182**	0.188**	0.178**	0.183**	31.865**	33.098**	28.840**	31.267**
SE± (g)	0.012	0.011	0.010	0.023	4.510	5.947	4.217	2.857
SE±(g_i-g_j)	0.018	0.017	0.015	0.005	6.662	8.784	6.228	4.220

*, ** Significant at 5 and 1 per cent levels, respectively

**Table 3.7: General combining ability (GCA) effects for average number of seeds plant⁻¹ and 100 seed weight in tomato.
(Based on individual and pooled over environments)**

Parents	Average number of seeds plant ⁻¹				100 Seed weight			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801	9.350**	9.342**	9.675**	9.456**	-0.12**	-0.13**	-0.12**	-0.15**
SKAU-T-1700	0.419	0.508	0.187	0.371	0.16**	0.17**	0.16**	0.17**
SKAU-T-0922	9.848**	8.769**	9.737**	9.452**	0.10	0.12	0.14	0.16
SKAU-T-1424	-1.683**	-1.269**	-1.296**	-1.416**	0.12	0.11	0.10	0.15
SKAU-T-1219	-9.735**	-9.721**	-9.727**	-9.728**	-0.25**	-0.26**	-0.027**	-0.28**
SKAU-T-1315	-4.554**	-4.626**	-4.439**	-4.540**	0.12**	0.14**	0.16**	0.20**
SKAU-T-0301	16.529**	16.641**	16.349**	16.506**	0.10**	0.12**	0.15**	0.17**
SKAU-T-1429	-2.559**	-2.440**	-2.637**	-2.545**	-0.14**	-0.12**	-0.11**	-0.14**
SKAU-T-1701	-5.416**	-5.247**	-5.139**	-5.267**	0.10**	0.13**	0.14**	0.15**
SKAU-T-1009	-6.290**	-6.369**	-6.203**	-6.287**	0.21**	0.23**	0.25**	0.28**
SKAU-T-9862	1.331**	1.364**	1.394**	1.363**	-0.22**	-0.24**	-0.26**	-0.27**
SKAU-T-1464	5.878**	5.540**	5.765**	5.728**	0.14**	0.15**	0.12**	0.16**
SE± (g)	0.374	0.365	0.370	0.213	0.03	0.02	0.01	0.005
SE±(g_i-g_j)	0.553	0.540	0.546	0.315	0.02	0.01	0.02	0.007

*, ** Significant at 5 and 1 per cent levels, respectively

Table 4: Maximum trait contribution of the parents in respect of significant GCA effects in tomato (*Solanum lycopersicum* L.)

S. No	Parents	Significant traits for GCA
1.	SKAU-T-9801	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), pericarp thickness (mm), number of primary branches plant ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q), average number of seeds fruit ⁻¹ and 100 seed weight (g)
2.	SKAU-T-0301	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), number of loculesfruit ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q), average number of seeds fruit ⁻¹ and 100 seed weight (g)
3.	SKAU-T-1464	Number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruit plant ⁻¹ , fruit length (cm), fruit diameter (cm), pericarp thickness (mm), number of primary branches plant ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q), average number of seeds fruit ⁻¹ and 100 seed weight (g)
4.	SKAU-T-9862	Number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruitsplant ⁻¹ , fruit length (cm), number of loculesfruit ⁻¹ , pericarp thickness (mm), number of primary branches plant ⁻¹ , plant height (cm), average fruit weight (g), fruit yieldplant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and average number of seeds fruit ⁻¹
5.	SKAU-T-0922	Number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm),number of loculesfruit ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and average number of seeds fruit ⁻¹

Contd.....

Table 4: contd...

S. No	Parents	Significant traits for GCA
6.	SKAU-T-1700	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant ⁻¹ , fruit length (cm), pericarp thickness (mm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and 100 seed weight (g)
7.	SKAU-T-1429	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest,, number of locules fruit ⁻¹ , pericarp thickness (mm), fruit length (cm), plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg) and fruit yield hectare ⁻¹ (q)
8.	SKAU-T-1701	Number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , fruit diameter (cm), pericarp thickness (mm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and 100 seed weight (g)
9.	SKAU-T-1219	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, fruit length (cm), Number of locules fruit ⁻¹ and number of primary branches plant ⁻¹
10.	SKAU-T-1009	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, fruit length (cm), fruit diameter (cm), pericarp thickness (mm), plant height (cm) and 100 seed weight (g)
11.	SKAU-T-1424	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ and number of primary branches plant ⁻¹ .
12.	SKAU-T-1315	Pericarp thickness (mm), number of primary branches plant ⁻¹ and 100 seed weight (g)

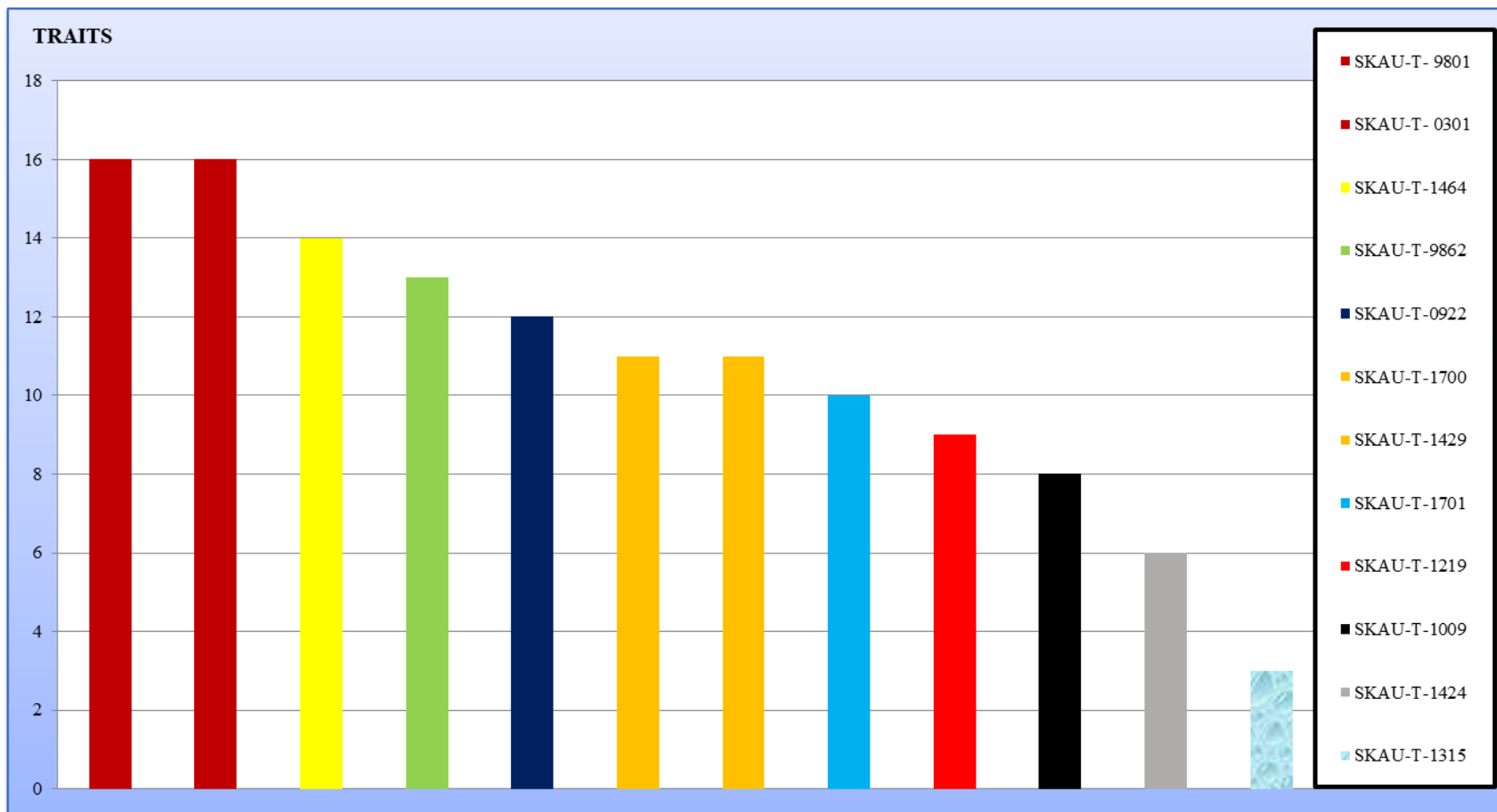


Fig. 1: Best parents in respect of GCA effects for maximum quantitative traits in tomato

4.4 Estimation of specific combining ability of crosses

Table-5.1 to 5.9 presents the specific combining ability (SCA) effects of sixty six crosses (F_1 's) for different traits in the individual environments as well as in data pooled over environments. Also the maximum trait contribution of the best crosses in respect of significant SCA effects is present in table- 6. Perusal of the table indicated that none of the F_1 crosses exhibited significant desirable SCA effects for all the traits in all the environments. However, several cross combinations revealed significant SCA effects for different traits. The results are summarized as follows:

4.4.1 Number of days to first flowering

For this trait, the cross combinations *viz.*, SKAU-T-9801 \times SKAU-T-1700, SKAU-T-9801 \times SKAU-T-1424, SKAU-T-9801 \times SKAU-T-1429, SKAU-T-9801 \times SKAU-T-1009, SKAU-T-9801 \times SKAU-T-9862, SKAU-T-1700 \times SKAU-T-0922, SKAU-T-1700 \times SKAU-T-1424, SKAU-T-1700 \times SKAU-T-0301, SKAU-T-1700 \times SKAU-T-1429, SKAU-T-1700 \times SKAU-T-1701, SKAU-T-1700 \times SKAU-T-1009, SKAU-T-1700 \times SKAU-T-9862, SKAU-T-1700 \times SKAU-T-1464, SKAU-T-0922 \times SKAU-T-1219, SKAU-T-0922 \times SKAU-T-1315, SKAU-T-0922 \times SKAU-T-0301, SKAU-T-0922 \times SKAU-T-1429, SKAU-T-0922 \times SKAU-T-9862, SKAU-T-0922 \times SKAU-T-1464, SKAU-T-1424 \times SKAU-T-1219, SKAU-T-1424 \times SKAU-T-1315, SKAU-T-1424 \times SKAU-T-1009, SKAU-T-1424 \times SKAU-T-9862, SKAU-T-1424 \times SKAU-T-1464, SKAU-T-1219 \times SKAU-T-1315, SKAU-T-1219 \times SKAU-T-1429, SKAU-T-1219 \times SKAU-T-1701, SKAU-T-1219 \times SKAU-T-1009, SKAU-T-1219 \times SKAU-T-9862, SKAU-T-1315 \times SKAU-T-0301, SKAU-T-1315 \times SKAU-T-1009, SKAU-T-0301 \times SKAU-T-1429, SKAU-T-0301 \times SKAU-T-9862, SKAU-T-0301 \times SKAU-T-1464, SKAU-T-1429 \times SKAU-T-1701, SKAU-T-1429 \times SKAU-T-9862, SKAU-T-1429 \times SKAU-T-1464, SKAU-T-1701 \times SKAU-T-9862, SKAU-T-1009 \times SKAU-T-1464 were found to reveal significant negative SCA effect in individual environments as well as data pooled over environments. SKAU-T-9801

× SKAU-T-0922 exhibiting significant negative SCA effects in E₁, E₂ and pooled analysis.

4.4.2 Number of days to first fruit set

Significant negative (desirable) SCA effects were exhibited by crosses *viz.*, SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1009, SKAU-T-9801 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-0301, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-9862, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-1315, SKAU-T-1424 × SKAU-T-1009, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1315 × SKAU-T-0301, SKAU-T-1315 × SKAU-T-1009, SKAU-T-0301 × SKAU-T-9862, SKAU-T-0301 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464 were found to reveal significant negative SCA effects in individual environments as well as data pooled over environments. The cross combination SKAU-T-0301 × SKAU-T-1429 exhibiting significant negative SCA effects in E₁, E₂ and pooled analysis.

4.4.3 Number of days to first fruit harvest

Significant negative (desirable) SCA effects were exhibited by crosses *viz.*, SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-

9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1009, SKAU-T-9801 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-0301, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-9862, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-1315, SKAU-T-1424 × SKAU-T-1009, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1315 × SKAU-T-0301, SKAU-T-1315 × SKAU-T-1009, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-9862, SKAU-T-0301 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464 were found to reveal significant negative SCA effect in individual environments as well as data pooled over environments.

4.4.4 Number of flowers cluster⁻¹

Positive significant SCA effects for number of flowers cluster⁻¹ were found in cross combinations SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1701, SKAU-T-9801 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-0301, SKAU-T-1700 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-0301, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-

1701, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1315 × SKAU-T-1429, SKAU-T-1315 × SKAU-T-1009, SKAU-T-0301 × SKAU-T-1701, SKAU-T-0301 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-9862 and SKAU-T-1701 × SKAU-T-1464 in individual environments and in data pooled over environments. In addition to this, positive significant SCA effects was also revealed by SKAU-T-1424 × SKAU-T-1315, SKAU-T-1424 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1315 and SKAU-T-1219 × SKAU-T-0301 in pooled environments. Significant positive SCA was also depicted by SKAU-T-0301 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464 in E₁, E₂ and pooled analysis.

4.4.5 Number of fruits cluster⁻¹

Positive significant SCA effects for number of fruits cluster⁻¹ was found in cross combination SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-0301, SKAU-T-1700 × SKAU-T-1701, SKAU-T-0922 × SKAU-T-0301, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1315 × SKAU-T-1429, SKAU-T-1315 × SKAU-T-1009, SKAU-T-0301 × SKAU-T-1701, SKAU-T-0301 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 in individual environments and in data pooled over environments. In addition to this, SKAU-T-9801 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1429, SKAU-T-1424 × SKAU-T-1429, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-9862 and SKAU-T-1009 × SKAU-T-1464 depicted positive and significant SCA in pooled environment. Also the cross

SKAU-T-1424 × SKAU-T-1315 showed positive and significant SCA in E₃ and pooled environment.

4.4.6 Number of pickings

For this trait positive significant SCA effects were depicted by SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1701, SKAU-T-9801 × SKAU-T-1009, SKAU-T-9801 × SKAU-T-9862, SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-0301, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-1009, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1429, SKAU-T-1424 × SKAU-T-1701, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1315 × SKAU-T-1009, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-9862 and SKAU-T-1701 × SKAU-T-9862 in individual environments and in data pooled over environments. In addition to this, positive significant SCA effects were also revealed by SKAU-T-9801 × SKAU-T-0922 and SKAU-T-0301 × SKAU-T-1464 in E₁ and pooled analysis. SKAU-T-0922 × SKAU-T-1701 depicted positive and significant SCA effects in E₁, E₂ and pooled environment. Also the cross SKAU-T-0922 × SKAU-T-1464 showed positive and significant SCA effect in pooled environment.

4.4.7 Number of fruits plant⁻¹

The cross combinations exhibiting significant positive SCA effects for number of fruits plant⁻¹ were SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1219, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1701, SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 ×

SKAU-T-1315, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-9862, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-1009, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1315 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-9862 in all individual as well as data pooled over environments. Also the SKAU-T-1219 × SKAU-T-1701 showed significant SCA in E₁ and pooled analysis. Significant SCA in pooled analysis was also depicted by SKAU-T-0301 × SKAU-T-1701 and SKAU-T-0301 × SKAU-T-9862

4.4.8 Fruit length (cm)

For this trait, significant positive SCA effects were depicted by SKAU-T-1700 × SKAU-T-1009, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429 and SKAU-T-1009 × SKAU-T-9862, in all environments and pooled analysis. SKAU-T-9801 × SKAU-T-1700 depicted significant SCA in E₁ and pooled analysis; SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1701, SKAU-T-9801 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1009, SKAU-T-1315 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1701 and SKAU-T-1701 × SKAU-T-1464 in pooled analysis; SKAU-T-9801 × SKAU-T-1219 and SKAU-T-1701 × SKAU-T-1009 in E₃ and pooled analysis.

4.4.9 Fruit diameter (cm)

For this trait, significant positive SCA effects were depicted by SKAU-T-0922 × SKAU-T-1429, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1701 and SKAU-T-1009 × SKAU-T-9862 in all environments and pooled analysis. SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1429, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-1009 and SKAU-T-0301 × SKAU-T-1429 depicted significant SCA in pooled analysis; SKAU-T-1700 × SKAU-T-1009 depicted significant SCA in E₁ and pooled analysis.

4.4.10 Number of locules fruit⁻¹

Significant and positive estimates of SCA are preferred for this trait and were depicted by SKAU-T-9801 × SKAU-T-0301, SKAU-T-9801 × SKAU-T-1009, SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-9862, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-1429, SKAU-T-1315 × SKAU-T-0301, SKAU-T-1315 × SKAU-T-1701, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1009 and SKAU-T-1701 × SKAU-T-9862 in all environments and pooled analysis. SKAU-T-1219 × SKAU-T-1315, SKAU-T-0301 × SKAU-T-1701 and SKAU-T-1429 × SKAU-T-1009 depicted significant SCA in E₁, E₂ and pooled analysis.

4.4.11 Pericarp thickness (mm)

The cross combinations depicting significant positive SCA effects for pericarp thickness were SKAU-T-9801 × SKAU-T-1219, SKAU-T-9801 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-0301, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1315 × SKAU-T-1009, SKAU-T-0301 × SKAU-T-

1464, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009 and SKAU-T-1009 × SKAU-T-9862 in all environments and pooled analysis. SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-1429 and SKAU-T-1701 × SKAU-T-9862, depicted significant SCA in pooled analysis. SKAU-T-1700 × SKAU-T-1701 depicted significant SCA in E₁, E₃ and pooled analysis; SKAU-T-1429 × SKAU-T-1701 in E₁, E₂ and pooled analysis.

4.4.12 Number of primary branches plant⁻¹

The crosses SKAU-T-9801 × SKAU-T-1700, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1701, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701 and SKAU-T-1315 × SKAU-T-0301 showed significant positive SCA effects in individual environments and pooled analysis. The cross combinations exhibiting significant desirable SCA effects were SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-1315, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-1464, SKAU-T-1009 × SKAU-T-9862 and SKAU-T-9862 × SKAU-T-1464 in pooled analysis; SKAU-T-9801 × SKAU-T-1009 in E₂ and pooled analysis and SKAU-T-1315 × SKAU-T-1429 and SKAU-T-1315 × SKAU-T-9862 E₁, E₂ and pooled analysis.

4.4.13 Plant height (cm)

Significant and positive estimates of SCA are preferred for this trait and were depicted by SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1701, SKAU-T-9801 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-9862, SKAU-

T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1701, SKAU-T-1701 × SKAU-T-1009 and SKAU-T-1009 × SKAU-T-9862 in all environments and pooled analysis.

4.4.14 Average fruit weight (g)

The cross combinations depicting significant positive SCA effects for average fruit weight were SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1219, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-9862, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1315 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1701, SKAU-T-0301 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-9862 for individual environments and pooled analysis. Significant positive SCA effects were also found in crosses SKAU-T-1700 × SKAU-T-1424, SKAU-T-1219 × SKAU-T-1315 and SKAU-T-1429 × SKAU-T-9862 in E₂, E₃ and pooled analysis; SKAU-T-0301 × SKAU-T-1464 in E₃ and pooled analysis.

4.4.15 Fruit yield plant⁻¹ (kg)

The cross combinations showing desirable SCA effects for fruit yield plant⁻¹ in all individual environments and pooled analysis were SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1219, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1464, SKAU-

T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-9862, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-9862. Significant positive SCA effects were also found in case of crosses SKAU-T-9801 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1701 and SKAU-T-0301 × SKAU-T-1701 in E₁ and pooled analysis; SKAU-T-0301 × SKAU-T-9862 in E₁, E₂ and pooled analysis.

4.4.16 Fruit yield hectare⁻¹ (q)

The cross combinations showing desirable SCA effects for fruit yield hectare⁻¹ in all individual environments and pooled analysis were SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1219, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-9862, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 ×

SKAU-T-9862. Significant positive SCA effects were also found in case of crosses SKAU-T-0301 × SKAU-T-9862, SKAU-T-0301 × SKAU-T-1701 and SKAU-T-1315 × SKAU-T -1701 in pooled analysis.

4.4.17 Average number of seeds fruit⁻¹

The cross combinations SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-0301, SKAU-T-9801 × SKAU-T-1429, SKAU-T-9801 × SKAU-T-1009, SKAU-T-9801 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-1429, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-0301, SKAU-T-1315 × SKAU-T-1429, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1701, SKAU-T-0301 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1009 × SKAU-T-9862 exhibited significant positive SCA effects in all environments as well as in data pooled over environments.

4.4.18 100 seed weight

The cross combinations SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1219, SKAU-T-9801 × SKAU-T-1701, SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-0922, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1701, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1009, SKAU-T-0922 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1315 × SKAU-T-0301, SKAU-T-1315 × SKAU-T-

1429, SKAU-T-1315 × SKAU-T-9862, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1701, SKAU-T-0301 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464, SKAU-T-1009 × SKAU-T-1464 exhibited significant positive SCA effects in all environments as well as in data pooled over environments. Other cross combinations, SKAU-T-9801 × SKAU-T-1315 and SKAU-T-1009 × SKAU-T-9862 exhibiting desirable SCA effects were in E₁, E₂ and pooled analysis; SKAU-T-9801 × SKAU-T-9862 in E₂ and in pooled analysis; SKAU-T-1700 × SKAU-T-1315 in pooled analysis.

Table 5.1: Specific combining ability (SCA) effects for number of days to first flowering and number of days to first fruit set in tomato. (Based on individual and pooled over environments)

Crosses	Number of days to first flowering				Number of days to first fruit set			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	-1.121**	-1.129**	-1.102**	-1.117**	-1.487**	-1.600**	-1.527**	-1.538**
SKAU-T-9801 × SKAU-T-0922	-0.710**	-0.642**	-0.143	-0.498**	-0.553**	-0.943**	-0.797**	-0.764**
SKAU-T-9801 × SKAU-T-1424	-1.517**	-1.792**	-1.412**	-1.574**	-1.034*	-1.074*	-1.007*	-1.038*
SKAU-T-9801 × SKAU-T-1219	0.433*	0.703**	0.990**	0.709**	2.735**	2.581**	2.910**	2.742**
SKAU-T-9801 × SKAU-T-1315	0.386*	0.272*	0.383*	0.347**	1.780**	1.876**	1.843**	1.833**
SKAU-T-9801 × SKAU-T-0301	2.414**	2.410**	2.188**	2.337**	1.845**	1.602**	1.739**	1.729**
SKAU-T-9801 × SKAU-T-1429	-1.145**	-1.312**	-1.258**	-1.238**	-1.382*	-1.364*	-1.335*	-1.360*
SKAU-T-9801 × SKAU-T-1701	1.057**	0.991**	0.735**	0.928**	1.506**	1.476**	1.479**	1.487**
SKAU-T-9801 × SKAU-T-1009	-1.036**	-1.003**	-0.966**	-1.002**	-1.478*	-1.710**	-1.515*	-1.567*
SKAU-T-9801 × SKAU-T-9862	-1.543**	-1.612**	-1.653**	-1.602**	-4.694**	-4.633**	-4.785**	-4.704**
SKAU-T-9801 × SKAU-T-1464	0.721**	0.708**	0.921**	0.783**	0.615*	0.545*	0.457*	0.539*
SKAU-T-1700 × SKAU-T-0922	-0.462*	-0.219*	-0.265*	-0.315*	-3.655**	-3.633**	-3.488**	-3.592**
SKAU-T-1700 × SKAU-T-1424	-2.169**	-2.369**	-2.567**	-2.368**	-2.336**	-2.131**	-2.364**	-2.277**
SKAU-T-1700 × SKAU-T-1219	0.481*	0.360*	0.369*	0.336**	3.266**	3.057**	2.986**	3.103**
SKAU-T-1700 × SKAU-T-1315	1.200**	1.196**	1.228**	1.208**	1.545**	1.686**	1.686**	1.639**
SKAU-T-1700 × SKAU-T-0301	-1.238**	-1.066**	-1.034**	-1.113**	-1.391*	-1.388*	-1.485**	-1.421**
SKAU-T-1700 × SKAU-T-1429	-0.936**	-0.912**	-1.154**	-1.001**	-0.849*	-0.745*	-0.741*	-0.779*
SKAU-T-1700 × SKAU-T-1701	-2.329**	-2.285**	-2.186**	-2.267**	-1.896**	-2.014**	-1.878**	-1.929**
SKAU-T-1700 × SKAU-T-1009	-3.484**	-3.640**	-3.655**	-3.593**	-4.858**	-4.848**	-4.676**	-4.794**
SKAU-T-1700 × SKAU-T-9862	-6.505**	-6.546**	-6.459**	-6.503**	-4.904**	-4.943**	-4.824**	-4.890**
SKAU-T-1700 × SKAU-T-1464	-2.036**	-1.931**	-1.766**	-1.911**	-2.849**	-2.831**	-2.853**	-2.844**
SKAU-T-0922 × SKAU-T-1424	4.633**	4.727**	4.621**	4.660**	6.656**	6.593**	6.712**	6.654**
SKAU-T-0922 × SKAU-T-1219	-0.817*	-0.812*	-0.810*	0.846*	-2.008**	-2.152**	-2.138**	-2.099**
SKAU-T-0922 × SKAU-T-1315	-2.064**	-2.176**	-2.184**	-2.141**	-2.529**	-2.157**	-2.104**	-2.264**
SKAU-T-0922 × SKAU-T-0301	-0.831**	-0.729**	-0.721**	0.760**	-3.665**	-3.598**	-3.642**	-3.635**
SKAU-T-0922 × SKAU-T-1429	-1.795**	-1.792**	-1.991**	-1.860**	-0.725*	-0.698*	-0.683*	-0.702*

Contd...

Table 5.1: contd....

Crosses	Number of days to first flowering				Number of days to first fruit set			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-1701	-0.007	-0.143	-0.198	-0.016	-0.570	-0.424	-0.535	-0.510
SKAU-T-0922 × SKAU-T-1009	0.252	0.322	0.533	0.369	0.302	0.243	0.167	0.237
SKAU-T-0922 × SKAU-T-9862	-1.293**	-1.292**	-1.453**	-1.346**	-2.830**	-2.867**	-2.834**	-2.844**
SKAU-T-0922 × SKAU-T-1464	-1.562**	-1.640**	-1.746**	-1.649**	-3.158**	-3.012**	-3.171**	-3.114**
SKAU-T-1424 × SKAU-T-1219	-0.976**	-0.928**	-0.921**	-0.945**	-1.289*	-1.350*	-1.314*	-1.318**
SKAU-T-1424 × SKAU-T-1315	-2.172**	-2.226**	-2.319**	-2.239**	-2.277**	-2.288**	-2.180**	-2.248**
SKAU-T-1424 × SKAU-T-0301	1.824**	1.712**	1.785**	1.774**	0.679*	0.895*	1.052*	0.875**
SKAU-T-1424 × SKAU-T-1429	1.331**	0.991**	1.073**	1.132**	1.272*	1.462*	1.792*	1.509*
SKAU-T-1424 × SKAU-T-1701	2.833**	2.993**	3.100**	2.975**	3.916**	4.112**	3.989**	4.005**
SKAU-T-1424 × SKAU-T-1009	-1.255**	-1.395**	-1.469**	-1.373**	-3.146**	-3.055**	-3.176**	-3.125**
SKAU-T-1424 × SKAU-T-9862	-2.400**	-1.242**	-1.122**	-1.588**	-1.217*	-1.164*	-1.176*	-1.186**
SKAU-T-1424 × SKAU-T-1464	-1.669**	-1.757**	-1.715**	-1.714**	-1.261*	-1.390*	-1.553*	-1.402*
SKAU-T-1219 × SKAU-T-1315	-2.555**	-2.131**	-2.050**	-2.245**	-1.541*	-1.500*	-1.764*	-1.602*
SKAU-T-1219 × SKAU-T-0301	0.574*	0.541*	0.554*	0.590*	1.844**	1.774**	1.868**	1.829**
SKAU-T-1219 × SKAU-T-1429	-0.414*	-0.319*	-0.276*	0.336**	-0.730*	-0.793*	-0.691*	-0.805*
SKAU-T-1219 × SKAU-T-1701	-0.884**	-0.745**	-0.731**	-0.787**	-2.948**	-3.200**	-3.195**	-3.114**
SKAU-T-1219 × SKAU-T-1009	-2.372**	-2.466**	-2.900**	-2.579**	-1.056**	-1.233**	-1.108**	1.132**
SKAU-T-1219 × SKAU-T-9862	-1.984**	-2.081**	-2.119**	-2.061**	-2.715**	-2.643**	-2.526**	-2.628**
SKAU-T-1219 × SKAU-T-1464	0.653**	0.762**	0.612*	0.675**	1.164*	1.112	1.301*	1.193**
SKAU-T-1315 × SKAU-T-0301	-1.141**	-1.090**	-1.186**	-1.139**	-0.835*	-1.021*	-0.932*	0.929**
SKAU-T-1315 × SKAU-T-1429	0.766**	0.855**	0.935**	0.952**	0.725*	0.812*	0.676*	-0.737*
SKAU-T-1315 × SKAU-T-1701	-0.002	-0.109	-0.005	-0.037	-0.103	-0.238	-0.095	-0.145
SKAU-T-1315 × SKAU-T-1009	-0.586**	-0.197*	-0.274*	-0.352**	-2.002**	-1.829**	-2.008**	-1.946**
SKAU-T-1315 × SKAU-T-9862	0.469*	0.088*	0.127*	0.144*	1.430*	1.319*	1.374*	1.375**
SKAU-T-1315 × SKAU-T-1464	1.400**	1.174**	1.181**	1.252**	0.758*	0.793*	0.830*	0.794*
SKAU-T-0301 × SKAU-T-1429	-1.838**	-1.507**	-1.660**	-1.668**	-1.127*	-1.319*	-1.047	-1.164**
SKAU-T-0301 × SKAU-T-1701	0.797**	0.696**	0.633*	0.709**	2.561**	2.621**	2.634**	2.605**

Contd...

Table 5.1: contd....

Crosses	Number of days to first flowering				Number of days to first fruit set			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0301 × SKAU-T-1009	1.776**	1.874**	2.031**	1.894**	1.633**	1.688**	1.736**	1.686**
SKAU-T-0301 × SKAU-T-9862	-0.736**	-0.973**	-1.222**	-0.977**	-1.195**	-1.212**	-1.370**	-1.259**
SKAU-T-0301 × SKAU-T-1464	-0.328*	-0.346*	-0.485*	-0.386**	-0.940*	-0.933*	-0.998*	-0.990*
SKAU-T-1429 × SKAU-T-1701	-1.529**	-1.359**	-1.346**	-1.411**	-4.198**	-4.179**	-4.040**	-4.139**
SKAU-T-1429 × SKAU-T-1009	2.886**	2.886**	2.152**	2.640**	3.473**	3.455**	3.362**	3.430**
SKAU-T-1429 × SKAU-T-9862	-0.525*	-0.595*	-0.534*	-0.541*	-2.702**	-2.812**	-2.696**	-2.736**
SKAU-T-1429 × SKAU-T-1464	-2.464**	-2.509**	-2.293**	-2.422**	-2.120**	-2.100**	-2.209**	-2.143**
SKAU-T-1701 × SKAU-T-1009	0.552**	0.522*	0.645*	0.573**	1.339*	1.338*	1.290*	1.322**
SKAU-T-1701 × SKAU-T-9862	-2.960**	-3.159**	-3.008**	-3.042**	-3.644**	-3.714**	-3.823**	-3.727**
SKAU-T-1701 × SKAU-T-1464	-0.762**	-0.307**	-0.334**	-0.468**	-2.532**	-2.493**	-2.595**	-2.540**
SKAU-T-1009 × SKAU-T-9862	0.852**	0.953**	1.323**	1.043**	1.161*	1.052*	1.212*	1.142**
SKAU-T-1009 × SKAU-T-1464	-2.784**	-3.062**	-3.103**	-2.983**	-1.894**	-2.093**	-2.059**	-2.015**
SKAU-T-9862 × SKAU-T-1464	2.071**	2.124**	1.945**	2.047**	1.602**	1.331*	1.374*	1.436**
S.E±(Sij)	0.146	0.182	0.187	0.091	0.422	0.425	0.419	0.223
S.E± (Sij-Sik)	0.214	0.266	0.274	0.146	0.617	0.622	0.614	0.357

*,**Significant at 5 and 1 percent levels, respectively

Table 5.2: Specific combining ability (SCA) effects for number of days to first fruit harvest and number of flowers cluster⁻¹ in tomato. (Based on individual and pooled over environments)

Crosses	Number of days to first fruit harvest				Number of flowers cluster ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	-1.590**	-1.501**	-1.460**	-1.484**	0.439**	0.324**	0.422**	0.395**
SKAU-T-9801 × SKAU-T-0922	-1.505*	-1.704*	-1.756**	-1.655**	0.492*	0.512*	0.449*	0.484**
SKAU-T-9801 × SKAU-T-1424	-3.000**	-2.918**	-3.578**	-3.065**	-0.051	-0.007	-0.010	-0.018
SKAU-T-9801 × SKAU-T-1219	1.550*	1.501*	1.108*	1.386*	-0.134	-0.048	-0.077	-0.086
SKAU-T-9801 × SKAU-T-1315	1.202*	0.863*	0.718*	0.928**	1.438**	1.495**	1.454**	1.462**
SKAU-T-9801 × SKAU-T-0301	1.462*	1.368*	1.525*	1.451**	0.066	0.016	0.057	0.046
SKAU-T-9801 × SKAU-T-1429	-3.095**	-2.947**	-2.635**	-2.892**	0.510*	0.443*	0.329*	0.427**
SKAU-T-9801 × SKAU-T-1701	2.993**	2.987**	2.975**	2.985**	1.193**	1.224**	1.162**	1.193**
SKAU-T-9801 × SKAU-T-1009	-6.367**	-6.297**	-6.218**	-6.294**	0.674**	0.667**	0.677**	0.639**
SKAU-T-9801 × SKAU-T-9862	-1.119*	-0.935*	-0.944*	-0.999**	0.076	0.038	0.035	0.050
SKAU-T-9801 × SKAU-T-1464	2.007**	2.110**	2.260**	2.126**	-0.279	-0.293	-0.284	-0.285*
SKAU-T-1700 × SKAU-T-0922	-1.990**	-1.935**	-1.556*	-1.827**	1.034**	1.079**	1.055**	1.056**
SKAU-T-1700 × SKAU-T-1424	-5.752**	-5.882**	-5.778**	-5.804**	0.590**	0.683**	0.652*	0.642**
SKAU-T-1700 × SKAU-T-1219	2.931**	2.637**	2.441**	2.670**	0.607**	0.562**	0.518*	0.562**
SKAU-T-1700 × SKAU-T-1315	4.579**	4.806**	4.982**	4.789**	-0.289	-0.329	-0.351	-0.0323**
SKAU-T-1700 × SKAU-T-0301	-1.443*	-1.503*	-1.358*	-1.435*	1.527**	1.441**	1.315**	1.427**
SKAU-T-1700 × SKAU-T-1429	-0.814*	-0.978*	-0.801*	-0.864*	-0.170*	-0.167*	-0.106*	-0.146*
SKAU-T-1700 × SKAU-T-1701	-3.760**	-3.844**	-3.825**	-3.810**	0.514*	0.552**	0.499**	0.522**
SKAU-T-1700 × SKAU-T-1009	-2.548**	-2.739**	-2.982**	-2.756**	0.166	0.176	0.152	0.265
SKAU-T-1700 × SKAU-T-9862	-2.071**	-2.166**	-2.344**	-2.194**	-0.984**	-0.953**	-0.870**	-0.935**
SKAU-T-1700 × SKAU-T-1464	-1.912**	-1.787**	-2.073**	-1.924**	0.295**	0.550**	0.545*	0.563**
SKAU-T-0922 × SKAU-T-1424	5.052**	5.113**	5.172**	5.113**	-0.112*	-0.152*	-0.123*	-0.121*
SKAU-T-0922 × SKAU-T-1219	-5.436**	-5.365**	-5.291**	-5.364**	-0.329	-0.403	-0.410	-0.381**
SKAU-T-0922 × SKAU-T-1315	-2.317**	-2.232**	-2.401**	-2.317**	-0.391	-0.493*	-0.479	-0.454**

Contd...

Table 5.2: contd....

Crosses	Number of days to first fruit harvest				Number of flowers cluster ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-0301	-2.719**	-2.601**	-2.659**	-2.660**	0.238*	0.272*	0.210*	0.215*
SKAU-T-0922 × SKAU-T-1429	-2.857**	-2.918**	-2.949**	-2.908**	0.272*	0.231*	0.238*	0.222*
SKAU-T-0922 × SKAU-T-1701	-0.212	-0.251	-0.391	-0.285	0.145	0.254	0.304	0.234
SKAU-T-0922 × SKAU-T-1009	0.452	0.501	0.465	0.473	0.703**	0.655**	0.743**	0.700**
SKAU-T-0922 × SKAU-T-9862	- 2.233**	-2.129**	-2.106**	-2.156**	0.114	0.216	0.235	0.188
SKAU-T-0922 × SKAU-T-1464	-5.407**	-5.459**	-5.456**	-5.441**	0.626**	0.652**	0.683**	0.653**
SKAU-T-1424 × SKAU-T-1219	-7.240**	-7.218**	-7.403**	-7.287**	0.128	0.141	0.170	0.161
SKAU-T-1424 × SKAU-T-1315	-5.979**	-5.913**	-6.156**	-6.016**	0.333	0.402	0.328	0.354**
SKAU-T-1424 × SKAU-T-0301	1.052*	1.184*	1.320*	1.186**	0.339*	0.410*	0.370*	0.373**
SKAU-T-1424 × SKAU-T-1429	2.962**	3.037**	2.927**	2.975**	0.348	0.269	0.189	0.269*
SKAU-T-1424 × SKAU-T-1701	3.683**	3.737**	3.703**	3.708**	0.365*	0.317*	0.255*	-0.312*
SKAU-T-1424 × SKAU-T-1009	-4.510**	-4.513**	-4.623**	-4.549**	0.221	0.240	0.197	0.219
SKAU-T-1424 × SKAU-T-9862	-3.705**	-3.682**	-3.718**	-3.701**	0.329*	0.355*	0.391*	0.325*
SKAU-T-1424 × SKAU-T-1464	-4.236**	-4.273**	-4.244**	-4.251**	0.283	0.214	0.157	0.218
SKAU-T-1219 × SKAU-T-1315	-0.862*	-0.828*	-0.937*	-0.876*	0.383	0.347	0.295	0.342**
SKAU-T-1219 × SKAU-T-0301	0.702*	0.737*	0.806*	0.748*	0.011	0.069	0.097	0.059
SKAU-T-1219 × SKAU-T-1429	-13.455**	-13.378**	-14.421**	-13.751**	0.468	0.509	0.578	0.519
SKAU-T-1219 × SKAU-T-1701	-3.00**	-2.978**	-3.044**	-3.007**	-0.582**	-0.572**	-0.555*	-0.570**
SKAU-T-1219 × SKAU-T-1009	-0.974*	-0.972*	-0.863*	-0.936**	0.029	0.015	0.036	0.027
SKAU-T-1219 × SKAU-T-9862	-1.912**	-1.466*	-1.197*	-1.525**	0.446*	0.410*	0.476*	0.507*
SKAU-T-1219 × SKAU-T-1464	3.081**	3.213**	3.108**	3.134**	0.234*	0.174*	0.177*	0.195*
SKAU-T-1315 × SKAU-T-0301	-1.050*	-1.161*	-1.021*	-1.011**	-0.517*	-0.555**	-0.505	-0.526**
SKAU-T-1315 × SKAU-T-1429	2.526**	2.591**	2.787**	2.635**	1.060**	1.148**	1.058**	1.089**
SKAU-T-1315 × SKAU-T-1701	-0.019	-0.075	-0.004	-0.033	-0.077	-0.062	0.009	-0.043
SKAU-T-1315 × SKAU-T-1009	-10.112**	-10.325**	-10.397**	-10.278**	0.942**	0.962**	0.961**	0.955**

Contd...

Table 5.2: contd....

Crosses	Number of days to first fruit harvest				Number of flowers cluster ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-1315 × SKAU-T-9862	2.069**	2.137**	2.110**	2.105**	-0.041	-0.034	0.040	-0.012
SKAU-T-1315 × SKAU-T-1464	5.662**	5.315**	5.282**	5.420**	-0.762**	-0.765**	-0.812**	-0.780**
SKAU-T-0301 × SKAU-T-1429	-5.810**	-5.944**	-5.937**	-5.897**	-0.032	-0.027	-0.111	-0.018
SKAU-T-0301 × SKAU-T-1701	2.045**	2.122**	2.172**	2.113**	0.618**	0.659**	0.645**	0.674**
SKAU-T-0301 × SKAU-T-1009	1.919**	1.939**	1.879**	1.913**	0.162	0.084	0.036	0.094
SKAU-T-0301 × SKAU-T-9862	-1.633**	-1.701**	-1.720**	-1.685**	0.721**	0.721**	0.576*	0.673**
SKAU-T-0301 × SKAU-T-1464	-1.707**	-2.054**	-2.009**	-1.923**	0.566**	0.523*	0.457	0.515**
SKAU-T-1429 × SKAU-T-1701	-1.312*	-1.425*	-1.121*	-1.286**	0.042	-0.034	0.092	0.034
SKAU-T-1429 × SKAU-T-1009	5.495**	5.558**	5.753**	5.602**	0.061	0.123	0.211	0.132
SKAU-T-1429 × SKAU-T-9862	-2.290**	-2.313**	-2.440**	-2.348**	1.045**	1.028**	1.423**	1.832**
SKAU-T-1429 × SKAU-T-1464	-2.802**	-2.932**	-2.732**	-2.822**	-0.010	-0.103	-0.029	-0.047
SKAU-T-1701 × SKAU-T-1009	0.650*	0.675*	0.737*	0.687*	-0.322	-0.358	-0.455	-0.378**
SKAU-T-1701 × SKAU-T-9862	-4.502**	-4.547**	-4.863**	-4.637**	0.005	0.014	0.123	0.044
SKAU-T-1701 × SKAU-T-1464	-3.243**	-3.168**	-3.559**	-3.323**	1.040**	0.983**	0.938**	0.987**
SKAU-T-1009 × SKAU-T-9862	5.171**	5.003**	4.944**	5.039**	-0.486*	-0.496*	-0.491	-0.491**
SKAU-T-1009 × SKAU-T-1464	-1.364*	-1.282*	-1.282**	-1.309**	0.526*	0.573**	0.457	0.519**
SKAU-T-9862 × SKAU-T-1464	0.779*	0.710*	0.956*	0.815*	-0.858**	-0.855**	-0.565*	-0.759**
S.E±(Sij)	0.468	0.482	0.477	0.251	0.158	0.153	0.192	0.089
S.E±(Sij-Sik)	0.685	0.705	0.698	0.402	0.231	0.224	0.281	0.142

*,**Significant at 5 and 1 percent levels, respectively

Table 5.3: Specific combining ability (SCA) effects for number of fruits cluster⁻¹ and number of pickings in tomato. (Based on individual and pooled over environments)

Crosses	Number of fruits cluster ⁻¹				Number of pickings			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	0.664*	0.661*	0.446*	0.590**	-0.374*	-0.349*	-0.355*	-0.359*
SKAU-T-9801 × SKAU-T-0922	0.514*	0.480*	0.308*	0.434**	0.552*	0.440*	0.406*	0.466**
SKAU-T-9801 × SKAU-T-1424	-0.194	-0.220	-0.273	-0.229	-0.346	-0.284	-0.315	-0.315*
SKAU-T-9801 × SKAU-T-1219	-0.655*	-0.601*	-0.568*	-0.608**	-0.134	-0.087	-0.020	-0.080
SKAU-T-9801 × SKAU-T-1315	0.706*	0.692*	0.694*	0.697**	-1.124**	-1.106**	-1.141**	-1.124**
SKAU-T-9801 × SKAU-T-0301	0.284	0.220	0.092	0.199	-3.255**	-3.189**	-3.089**	-3.178**
SKAU-T-9801 × SKAU-T-1429	0.470*	0.324*	0.218*	0.347*	1.854**	1.747**	1.730**	1.777**
SKAU-T-9801 × SKAU-T-1701	0.783**	0.725**	0.827**	0.778**	1.795**	1.751**	1.740**	1.762**
SKAU-T-9801 × SKAU-T-1009	0.521	0.508	0.484	0.504**	1.378**	1.366**	1.359**	1.368**
SKAU-T-9801 × SKAU-T-9862	0.179	0.239	0.213	0.211	0.928**	1.001**	1.040**	0.990**
SKAU-T-9801 × SKAU-T-1464	-0.641*	-0.623*	-0.580*	-0.615**	1.990**	1.925**	1.809**	1.908**
SKAU-T-1700 × SKAU-T-0922	0.725**	0.711**	0.696*	0.711**	0.976**	0.966**	0.899**	0.947**
SKAU-T-1700 × SKAU-T-1424	0.648*	0.656*	0.651*	0.685*	-0.989**	-1.091**	-1.122**	-1.067**
SKAU-T-1700 × SKAU-T-1219	0.510*	0.570*	0.580*	0.587*	-0.910**	-0.927**	-0.760**	-0.866**
SKAU-T-1700 × SKAU-T-1315	-0.782**	-0.644*	-0.685*	-0.703**	0.966**	0.921**	0.918**	0.935**
SKAU-T-1700 × SKAU-T-0301	0.728**	0.744**	0.730**	0.734**	-3.065**	-2.929**	-2.863**	-2.952**
SKAU-T-1700 × SKAU-T-1429	-0.858**	-0.889**	-0.697*	-0.815**	0.211	0.273	0.256	0.247
SKAU-T-1700 × SKAU-T-1701	0.739*	0.711*	0.751*	0.767*	1.418**	1.411**	1.433**	1.421**
SKAU-T-1700 × SKAU-T-1009	0.266	0.206	0.306	0.259	3.068**	3.059**	3.052**	3.060**
SKAU-T-1700 × SKAU-T-9862	-0.267*	-0.275*	-0.192*	-0.245*	-1.082**	-1.039**	-1.067**	-1.063**
SKAU-T-1700 × SKAU-T-1464	0.537	0.508	0.508	0.518**	0.053	0.058	0.068	0.071
SKAU-T-0922 × SKAU-T-1424	-0.898**	-0.770**	-0.689*	-0.786**	-0.596*	-0.537*	-0.560*	-0.564**
SKAU-T-0922 × SKAU-T-1219	-0.227	-0.151	-0.185	-0.188	-0.051	0.028	0.035	0.004

Contd....

Table 5.3: contd....

Crosses	Number of fruits cluster ⁻¹				Number of pickings			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-1315	0.068	0.008	-0.089	-0.004	-0.674**	-0.625*	-0.553*	-0.617**
SKAU-T-0922 × SKAU-T-0301	0.645*	0.630*	0.758**	0.677**	0.939**	0.908**	0.867**	0.905**
SKAU-T-0922 × SKAU-T-1429	0.492	0.530	0.499	0.507**	0.529*	0.572*	0.448*	0.517**
SKAU-T-0922 × SKAU-T-1701	0.355	0.358	0.323	0.346	0.611*	0.499*	0.395	0.502**
SKAU-T-0922 × SKAU-T-1009	0.651*	0.642*	0.666*	0.653**	0.495*	0.513*	0.514	0.507**
SKAU-T-0922 × SKAU-T-9862	0.549	0.511	0.570	0.543	-1.789**	-1.784**	-1.839**	-1.804**
SKAU-T-0922 × SKAU-T-1464	0.587*	0.527*	0.523*	0.573*	0.473	0.473	0.497	0.481**
SKAU-T-1424 × SKAU-T-1219	0.199	0.182	0.268	0.216	-1.648**	-1.596**	-1.586**	-1.610**
SKAU-T-1424 × SKAU-T-1315	0.505	0.525	0.570*	0.534**	-0.139	-0.149	-0.041	-0.109
SKAU-T-1424 × SKAU-T-0301	0.371	0.363	0.344	0.359*	2.203**	2.432**	2.455**	2.463**
SKAU-T-1424 × SKAU-T-1429	0.485	0.496	0.484	0.489**	1.693**	1.696**	1.703**	1.698**
SKAU-T-1424 × SKAU-T-1701	0.571*	0.575*	0.563*	0.570**	1.253**	1.225**	1.194**	1.224**
SKAU-T-1424 × SKAU-T-1009	0.491	0.542	0.413	0.482	0.064	0.123	0.092	0.093
SKAU-T-1424 × SKAU-T-9862	0.509	0.477	0.523	0.503**	4.747**	4.759**	4.740**	4.748**
SKAU-T-1424 × SKAU-T-1464	0.286	0.273	0.177	0.246	3.609**	3.516**	3.575**	3.567**
SKAU-T-1219 × SKAU-T-1315	0.133	0.127	0.168	0.173*	2.773**	2.649**	2.454**	2.625**
SKAU-T-1219 × SKAU-T-0301	0.375	0.382	0.315	0.358*	1.942**	1.999**	1.873**	1.938**
SKAU-T-1219 × SKAU-T-1429	0.277	0.318	0.311	0.302	-2.082**	-2.065**	-2.108**	-2.085**
SKAU-T-1219 × SKAU-T-1701	-0.558*	-0.539	-0.532	-0.543**	0.759**	0.773**	0.735**	0.756**
SKAU-T-1219 × SKAU-T-1009	0.214	0.111	0.125	0.150	-0.258	-0.213	-0.213	-0.228
SKAU-T-1219 × SKAU-T-9862	0.647*	0.630*	0.561*	0.612**	1.041**	1.010**	1.032**	1.028**
SKAU-T-1219 × SKAU-T-1464	0.318	0.380	0.361	0.353*	-3.746**	-3.687**	-3.663**	-3.698**
SKAU-T-1315 × SKAU-T-0301	-0.563*	-0.592*	-0.623*	-0.592**	-1.115**	-0.987**	-1.015**	-1.039**

Contd....

Table 5.3: contd....

Crosses	Number of fruits cluster ⁻¹				Number of pickings			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-1315 × SKAU-T-1429	0.752**	0.708**	0.684*	0.715**	0.128	0.116	0.071	0.105
SKAU-T-1315 × SKAU-T-1701	-0.063	-0.013	0.063	-0.004	0.202	0.121	0.180	0.168
SKAU-T-1315 × SKAU-T-1009	0.642*	0.670*	0.553*	0.622**	0.682**	0.799**	0.801**	0.706**
SKAU-T-1315 × SKAU-T-9862	-0.725**	-0.711**	-0.644*	-0.693**	-0.565*	-0.563*	-0.286*	-0.571**
SKAU-T-1315 × SKAU-T-1464	-0.186	-0.227	-0.277	-0.230	-0.136	-0.039	0.049	-0.042
SKAU-T-0301 × SKAU-T-1429	-1.072**	-0.037**	-0.868**	-0.992**	3.430**	3.566**	3.556**	3.518**
SKAU-T-0301 × SKAU-T-1701	0.520*	0.525*	0.589*	0.545**	0.671**	0.537**	0.833**	0.747**
SKAU-T-0301 × SKAU-T-1009	0.318	0.292	0.234	0.281	-1.112**	-1.015**	-1.015**	-1.048**
SKAU-T-0301 × SKAU-T-9862	0.485	0.477	0.437	0.466**	-0.329	-0.246	-0.201	-0.259
SKAU-T-0301 × SKAU-T-1464	0.577*	0.573*	0.597*	0.549*	0.499*	0.478	0.435	0.471**
SKAU-T-1429 × SKAU-T-1701	0.328	0.308	0.251	0.296	2.147**	2.173**	2.185**	2.168**
SKAU-T-1429 × SKAU-T-1009	0.133	0.125	0.008	0.089	-1.636**	-1.646**	-1.663**	-1.648**
SKAU-T-1429 × SKAU-T-9862	0.367*	0.389*	0.489*	0.415**	0.753**	0.744**	0.782**	0.759**
SKAU-T-1429 × SKAU-T-1464	0.037	0.027	-0.023	0.014	-0.091	-0.153	-0.179	-0.141
SKAU-T-1701 × SKAU-T-1009	-0.382	-0.363	-0.380	-0.375*	-0.262	-0.241	-0.220	-0.241
SKAU-T-1701 × SKAU-T-9862	0.185	0.223	0.189	0.199	0.721**	0.661**	0.628*	0.670**
SKAU-T-1701 × SKAU-T-1464	0.377*	0.361*	0.411*	0.383*	-0.051	-0.082	-0.103	-0.079
SKAU-T-1009 × SKAU-T-9862	-0.877**	-0.861**	-0.620*	-0.786**	0.004	-0.091	-0.020	-0.036
SKAU-T-1009 × SKAU-T-1464	0.461	0.456	0.413	0.443**	-1.167**	-1.134**	-1.151**	-1.151**
SKAU-T-9862 × SKAU-T-1464	-0.339*	-0.225*	-0.285*	-0.283*	-1.217**	-1.232**	-1.203**	-1.217**
S.E±(Sij)	0.209	0.205	0.207	0.109	0.185	0.187	0.199	0.101
S.E± (Sij-Sik)	0.306	0.300	0.304	0.175	0.271	0.273	0.291	0.161

*,**Significant at 5 and 1 percent levels, respectively

Table 5.4: Specific combining ability (SCA) effects for number of fruits plant⁻¹ and fruit length in tomato. (Based on individual and pooled over environments)

Crosses	Number of fruits plant ⁻¹				Fruit length (cm)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	6.433**	6.231**	6.188**	6.284**	0.645*	0.558	0.519	0.574**
SKAU-T-9801 × SKAU-T-0922	6.436**	6.622**	6.692**	6.583**	0.335	0.362	0.333	0.342*
SKAU-T-9801 × SKAU-T-1424	-5.586**	-5.559**	-5.884**	-5.66**	-0.505	-0.549	-0.555	-0.537**
SKAU-T-9801 × SKAU-T-1219	8.488**	8.615**	8.676**	8.593**	0.535	0.589	0.602*	0.575**
SKAU-T-9801 × SKAU-T-1315	-5.703**	-5.702**	-5.553**	-5.652**	-0.358	-0.368	-0.415	-0.380*
SKAU-T-9801 × SKAU-T-0301	-11.545**	-11.723**	-11.691**	-11.653**	-0.675*	-0.649*	-0.596	-0.640**
SKAU-T-9801 × SKAU-T-1429	6.857**	6.981**	6.031**	6.623**	0.125	0.070	0.090	0.095
SKAU-T-9801 × SKAU-T-1701	7.155**	6.800**	7.026**	6.994**	0.406	0.360	0.335	0.367*
SKAU-T-9801 × SKAU-T-1009	-2.283**	-2.374**	-2.626**	-2.428**	-0.258	-0.214	-0.162	-0.211
SKAU-T-9801 × SKAU-T-9862	-8.455**	-8.100**	-7.955**	-8.170**	0.468	0.486	0.516	0.490**
SKAU-T-9801 × SKAU-T-1464	6.386**	6.222**	6.159**	6.255**	-0.689*	-0.697*	-0.648*	-0.678**
SKAU-T-1700 × SKAU-T-0922	4.576**	4.867**	5.038**	4.827**	-0.005	0.060	0.162	0.072
SKAU-T-1700 × SKAU-T-1424	5.855**	6.353**	6.228**	6.179**	-0.213	-0.152	-0.160	-0.175
SKAU-T-1700 × SKAU-T-1219	-9.005**	-8.473**	-8.479**	-8.652**	-0.272	-0.314	-0.369	-0.318
SKAU-T-1700 × SKAU-T-1315	6.538**	5.977**	6.192**	6.236**	-1.098**	-1.104**	-0.919**	-1.041**
SKAU-T-1700 × SKAU-T-0301	-14.372**	-14.212**	-14.046**	-14.210**	-0.182	-0.218	-0.234	-0.211
SKAU-T-1700 × SKAU-T-1429	-8.769**	-8.407**	-8.358**	-8.511**	0.518	0.534	0.485	0.513**
SKAU-T-1700 × SKAU-T-1701	-7.772**	-7.454**	-7.196**	-7.474**	-0.101	-0.042	-0.169	-0.104
SKAU-T-1700 × SKAU-T-1009	5.557**	5.419**	5.338**	5.438**	0.668*	0.717*	0.633*	0.673**
SKAU-T-1700 × SKAU-T-9862	2.452**	2.246**	2.290**	2.329**	-0.339	-0.383	-0.455	-0.392*
SKAU-T-1700 × SKAU-T-1464	-5.074**	-5.233**	-6.062**	-5.456**	-0.296	-0.299	-0.386	-0.327
SKAU-T-0922 × SKAU-T-1424	2.824**	3.443**	3.633**	3.300**	-0.455	-0.380	-0.346	-0.394*
SKAU-T-0922 × SKAU-T-1219	-3.269**	-3.583**	-3.641**	-3.498**	0.418	0.391	0.412	0.407*
SKAU-T-0922 × SKAU-T-1315	-6.526**	-6.533**	-7.269**	-6.776**	-0.208	-0.199	-0.272	-0.226

Contd....

Table 5.4: contd...

Crosses	Number of fruits plant ⁻¹				Fruit length (cm)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-0301	-2.431**	-2.512**	-2.492**	-2.479**	-0.458	-0.480	-0.519	-0.486**
SKAU-T-0922 × SKAU-T-1429	-4.567**	-5.150**	-5.253**	-4.990**	0.109	0.105	0.100	0.105
SKAU-T-0922 × SKAU-T-1701	-1.803*	-1.831*	-1.991*	-1.975**	-0.344	-0.371	-0.322	-0.345*
SKAU-T-0922 × SKAU-T-1009	2.926**	3.043**	3.276**	3.082**	0.459	0.455	0.381	0.432**
SKAU-T-0922 × SKAU-T-9862	-5.045**	-5.031**	-5.038**	-5.038**	-0.015	-0.045	-0.074	-0.045
SKAU-T-0922 × SKAU-T-1464	5.595**	5.458**	5.976**	5.676**	-0.405	-0.428	-0.405	-0.413*
SKAU-T-1424 × SKAU-T-1219	-1.824*	-2.464**	-2.350**	-2.213**	-0.222	-0.254	-0.210	-0.229
SKAU-T-1424 × SKAU-T-1315	-1.986*	-1.719*	-1.821*	-1.842**	0.085	0.022	0.107	0.071
SKAU-T-1424 × SKAU-T-0301	-2.224**	-2.302**	-2.384**	-2.303**	-0.265	-0.292	-0.308	-0.288
SKAU-T-1424 × SKAU-T-1429	-4.355**	-4.931**	-5.029**	-4.771**	-0.732*	-0.740*	-0.755*	-0.742**
SKAU-T-1424 × SKAU-T-1701	-8.091**	-8.178**	-8.100**	-8.123**	0.083	0.051	-0.010	0.041
SKAU-T-1424 × SKAU-T-1009	2.871**	3.029**	3.366**	3.089**	-0.515	-0.457	-0.474	-0.482**
SKAU-T-1424 × SKAU-T-9862	3.333**	3.455**	3.619**	3.469**	1.478**	1.443**	1.471**	1.464**
SKAU-T-1424 × SKAU-T-1464	10.974**	11.243**	10.900**	11.039**	0.787**	0.827**	0.773*	0.796**
SKAU-T-1219 × SKAU-T-1315	3.793**	4.027**	4.081**	3.967**	-0.008	-0.007	0.031	0.005
SKAU-T-1219 × SKAU-T-0301	7.816**	7.672**	7.276**	7.588**	0.209	0.212	0.150	0.190
SKAU-T-1219 × SKAU-T-1429	-7.514**	-7.357**	-7.269**	-7.380**	-0.158	-0.202	-0.165	-0.175
SKAU-T-1219 × SKAU-T-1701	1.650*	1.629	1.626	1.635**	-0.710*	-0.645*	-0.619*	-0.658**
SKAU-T-1219 × SKAU-T-1009	4.688**	4.897**	4.774**	4.787**	-0.175	-0.185	-0.217	-0.192
SKAU-T-1219 × SKAU-T-9862	-1.426	-1.871*	-1.722	-1.673**	-0.215	-0.252	-0.205	-0.224
SKAU-T-1219 × SKAU-T-1464	-9.053**	-8.516**	-8.974**	-8.848**	-0.172	-0.168	-0.236	-0.192
SKAU-T-1315 × SKAU-T-0301	-1.674*	-1.478	-1.653	-1.602**	0.283	0.289	0.266	0.279
SKAU-T-1315 × SKAU-T-1429	-1.938*	-1.873*	-1.965*	-1.925**	-0.117	-0.092	-0.181	-0.130
SKAU-T-1315 × SKAU-T-1701	5.293**	5.012**	5.064**	5.123**	0.464	0.498	0.431	0.464**
SKAU-T-1315 × SKAU-T-1009	-2.155**	-2.186**	-2.197*	-2.179**	-0.201	-0.242	-0.234	-0.226

Contd....

Table 5.4: contd...

Crosses	Number of fruits plant ⁻¹				Fruit length (cm)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-1315 × SKAU-T-9862	-0.250	-0.546	-0.583	-0.459	-0.575	-0.576	-0.622*	-0.591**
SKAU-T-1315 × SKAU-T-1464	4.976**	4.966**	4.869**	4.937**	0.402	0.441	0.447	0.430*
SKAU-T-0301 × SKAU-T-1429	5.219**	5.238**	5.297**	5.252**	1.133**	1.160**	1.138**	1.143**
SKAU-T-0301 × SKAU-T-1701	5.450	5.276	5.174	5.300**	0.147	0.151	0.116	0.138
SKAU-T-0301 × SKAU-T-1009	-4.422**	-4.335**	-4.208**	-4.321**	-0.617*	-0.623*	-0.581	-0.607**
SKAU-T-0301 × SKAU-T-9862	2.093	2.109	2.522	2.241**	-0.258	-0.257	-0.236	-0.250
SKAU-T-0301 × SKAU-T-1464	7.547**	7.212**	7.126**	7.295**	0.218	0.227	0.233	0.226
SKAU-T-1429 × SKAU-T-1701	6.852**	6.729**	6.481**	6.687**	0.547	0.536	0.502	0.528**
SKAU-T-1429 × SKAU-T-1009	3.486**	3.431**	3.653**	3.523**	-0.217	-0.238	-0.229	-0.228
SKAU-T-1429 × SKAU-T-9862	3.576**	3.796**	3.600**	3.657**	-1.425**	-1.371**	-1.284**	-1.360**
SKAU-T-1429 × SKAU-T-1464	4.616**	4.584**	6.547**	5.249**	-0.782**	-0.721*	-0.615*	-0.706**
SKAU-T-1701 × SKAU-T-1009	7.245**	7.655**	7.909**	7.603**	0.564	0.586	0.683*	0.611**
SKAU-T-1701 × SKAU-T-9862	4.874**	4.781**	4.762**	4.805**	-0.177	-0.147	-0.138	-0.154
SKAU-T-1701 × SKAU-T-1464	3.681**	4.169**	4.109**	3.986**	0.533	0.503	0.497	0.511**
SKAU-T-1009 × SKAU-T-9862	3.302**	3.322**	3.395**	3.340**	0.859**	0.846**	0.797**	0.834**
SKAU-T-1009 × SKAU-T-1464	-5.157**	-5.357**	-5.558**	-5.357**	-0.565	-0.604*	-0.634*	-0.601**
SKAU-T-9862 × SKAU-T-1464	-9.762**	-9.864**	-9.905**	-9.844**	-0.172	-0.171	-0.122	-0.155
S.E±(Sij)	0.606	0.633	0.662	0.335	0.226	0.223	0.226	0.119
S.E± (Sij-Sik)	0.886	0.926	0.968	0.535	0.331	0.326	0.331	0.190

*,**Significant at 5 and 1 percent levels, respectively

Table 5.5: Specific combining ability (SCA) effects for fruit diameter and number of locules ⁻¹ in tomato. (Based on individual and pooled over environments)

Crosses	Fruit diameter (cm)				Number of locules fruit ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	0.553	0.526	0.491	0.523*	-0.880**	-0.862**	-0.794**	-0.845**
SKAU-T-9801 × SKAU-T-0922	0.586	0.609	0.596	0.597*	-0.263	-0.277	-0.304	-0.281
SKAU-T-9801 × SKAU-T-1424	0.746	0.733	0.722	0.734**	0.191	0.254	0.237	0.228
SKAU-T-9801 × SKAU-T-1219	-0.335	-0.376	-0.385	-0.365	-0.037	-0.024	-0.049	-0.037
SKAU-T-9801 × SKAU-T-1315	-0.640	-0.672	-0.671	-0.661**	-0.290	-0.288	-0.339	-0.306
SKAU-T-9801 × SKAU-T-0301	0.244	0.193	0.172	0.203	1.632**	1.626**	1.587**	1.615**
SKAU-T-9801 × SKAU-T-1429	0.513	0.526	0.498	0.512*	-0.337	-0.372	-0.356	-0.355
SKAU-T-9801 × SKAU-T-1701	-0.006	-0.007	-0.014	-0.009	-0.337	-0.343	-0.337	-0.339
SKAU-T-9801 × SKAU-T-1009	0.275	0.305	0.344	0.308	1.029**	1.021**	1.049**	1.033**
SKAU-T-9801 × SKAU-T-9862	-0.864	-0.807	-0.721	-0.797**	0.165	0.207	0.168	0.180
SKAU-T-9801 × SKAU-T-1464	0.355	0.328	0.308	0.331	0.720**	0.707**	0.727**	0.718**
SKAU-T-1700 × SKAU-T-0922	0.053	0.081	0.191	0.108	0.253	0.252	0.163	0.223
SKAU-T-1700 × SKAU-T-1424	-0.754	-0.729	-0.716	-0.733**	0.575*	0.650**	0.537*	0.587**
SKAU-T-1700 × SKAU-T-1219	0.098	0.128	0.110	0.112	0.679**	0.604**	0.684**	0.656**
SKAU-T-1700 × SKAU-T-1315	0.294	0.266	0.258	0.273	2.527**	2.507**	2.527**	2.520**
SKAU-T-1700 × SKAU-T-0301	-0.423	-0.436	-0.433	-0.431	-0.318	-0.346	-0.347	-0.337
SKAU-T-1700 × SKAU-T-1429	-0.287	-0.236	-0.240	-0.254	-0.521*	-0.543**	-0.523*	-0.529**
SKAU-T-1700 × SKAU-T-1701	-0.706	-0.736	-0.752	-0.731**	-0.354	-0.381	-0.404*	-0.380*
SKAU-T-1700 × SKAU-T-1009	0.908*	0.876	0.805	0.863**	-0.087	-0.050	0.015	-0.041
SKAU-T-1700 × SKAU-T-9862	0.136	0.164	0.075	0.125	-0.985**	-0.998**	-0.999**	-0.994**
SKAU-T-1700 × SKAU-T-1464	-0.311	-0.300	-0.364	-0.325	-0.563*	-0.431	-0.406	-0.467**
SKAU-T-0922 × SKAU-T-1424	-1.187**	-1.145**	-0.978*	-1.104**	-0.609**	-0.531*	-0.506*	-0.549**
SKAU-T-0922 × SKAU-T-1219	-0.835	-0.855	-0.885*	-0.858**	-0.104	-0.077	0.008	-0.057
SKAU-T-0922 × SKAU-T-1315	0.027	0.016	-0.037	0.002	-0.490**	-0.508*	-0.416	-0.471**

Contd....

Table 5.5: contd....

Crosses	Fruit diameter (cm)				Number of locules fruit ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-0301	-1.323**	-1.319**	-1.328**	-1.323**	-0.401	-0.427	-0.523*	-0.450*
SKAU-T-0922 × SKAU-T-1429	1.346**	1.314**	1.298**	1.319**	-0.404	-0.424	-0.499*	-0.442*
SKAU-T-0922 × SKAU-T-1701	-0.006	0.014	0.053	0.020	-0.237	-0.262	-0.147	-0.215
SKAU-T-0922 × SKAU-T-1009	0.208	0.193	0.177	0.192	-0.504*	-0.565*	-0.627**	-0.565**
SKAU-T-0922 × SKAU-T-9862	0.370	0.381	0.346	0.366	2.365**	2.321**	2.192**	2.293**
SKAU-T-0922 × SKAU-T-1464	-0.345	-0.350	-0.359	-0.351	1.253**	1.221**	1.151**	1.208**
SKAU-T-1424 × SKAU-T-1219	0.191	0.169	0.175	0.178	0.051	-0.046	-0.151	-0.049
SKAU-T-1424 × SKAU-T-1315	-0.447	-0.393	-0.445	-0.428	-0.735**	-0.677**	-0.508*	-0.640**
SKAU-T-1424 × SKAU-T-0301	-0.330	-0.229	-0.168	-0.242	-1.313**	-1.196**	-1.116**	-1.208**
SKAU-T-1424 × SKAU-T-1429	-0.461	-0.462	-0.442	-0.455	0.918**	1.073**	1.142**	1.044**
SKAU-T-1424 × SKAU-T-1701	-0.214	-0.195	-0.221	-0.210	-0.549*	-0.465	-0.406	-0.473**
SKAU-T-1424 × SKAU-T-1009	-0.333	-0.317	-0.397	-0.349	-0.582*	-0.467*	-0.420	-0.490**
SKAU-T-1424 × SKAU-T-9862	1.863**	1.838**	1.839**	1.846**	-0.213	-0.115	-0.035	-0.121
SKAU-T-1424 × SKAU-T-1464	0.848	0.840	0.801	0.830**	-0.292	-0.215	-0.308	-0.272
SKAU-T-1219 × SKAU-T-1315	0.705	0.697	0.682	0.695**	0.503**	0.245*	0.439	0.496**
SKAU-T-1219 × SKAU-T-0301	-0.145	-0.138	-0.142	-0.142	-0.742**	-0.741**	-0.801**	-0.761**
SKAU-T-1219 × SKAU-T-1429	-0.275	-0.305	-0.283	-0.288	-0.144	-0.138	-0.144	-0.142
SKAU-T-1219 × SKAU-T-1701	0.172	0.195	0.139	0.169	-0.178	-0.143	-0.025	-0.115
SKAU-T-1219 × SKAU-T-1009	0.620	0.640	0.663	0.641**	0.256	0.288	0.227	0.257
SKAU-T-1219 × SKAU-T-9862	0.082	0.062	0.032	0.058	-0.309	-0.260	-0.254	-0.274
SKAU-T-1219 × SKAU-T-1464	-0.299	-0.269	-0.240	-0.269	0.113	0.040	-0.061	0.031
SKAU-T-1315 × SKAU-T-0301	0.151	0.166	0.239	0.185	0.772**	0.728**	0.642**	0.714**
SKAU-T-1315 × SKAU-T-1429	-0.014	0.000	-0.002	-0.005	-0.697**	-0.703**	-0.735**	-0.711**
SKAU-T-1315 × SKAU-T-1701	-0.233	-0.234	-0.214	-0.227	0.770**	0.759**	0.684**	0.738**
SKAU-T-1315 × SKAU-T-1009	-0.052	-0.022	-0.023	-0.032	-0.197	-0.177	-0.230	-0.201

Contd....

Table 5.5: contd....

Crosses	Fruit diameter (cm)				Number of locules fruit ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-1315 × SKAU-T-9862	-0.023	0.000	0.046	0.008	-0.428	-0.524*	-0.611**	-0.521**
SKAU-T-1315 × SKAU-T-1464	-0.304	-0.298	-0.359	-0.320	-0.773**	-0.758**	-0.618**	-0.716**
SKAU-T-0301 × SKAU-T-1429	0.836	0.831	0.808	0.825**	0.925**	0.945**	0.925**	0.932**
SKAU-T-0301 × SKAU-T-1701	0.451	0.431	0.396	0.426	0.458*	0.473*	0.411	0.447*
SKAU-T-0301 × SKAU-T-1009	-0.568	-0.591	-0.647	-0.602*	0.591**	0.571**	0.563*	0.575**
SKAU-T-0301 × SKAU-T-9862	-0.073	-0.103	-0.045	-0.073	-0.373	-0.377	-0.418*	-0.389*
SKAU-T-0301 × SKAU-T-1464	0.046	0.066	0.184	0.099	-0.618**	-0.677**	-0.658**	-0.651**
SKAU-T-1429 × SKAU-T-1701	1.453**	1.497**	1.522**	1.491**	0.056	0.009	-0.032	0.011
SKAU-T-1429 × SKAU-T-1009	-0.299	-0.291	-0.287	-0.292	0.489**	0.473**	0.453	0.472**
SKAU-T-1429 × SKAU-T-9862	-0.404	-0.436	-0.385	-0.408	0.058	0.059	0.173	0.097
SKAU-T-1429 × SKAU-T-1464	-0.285	-0.300	-0.290	-0.292	-0.987**	-1.008**	-1.101**	-1.032**
SKAU-T-1701 × SKAU-T-1009	0.482	0.409	0.401	0.431	0.222	0.235	0.239	0.232
SKAU-T-1701 × SKAU-T-9862	-0.290	-0.269	-0.297	-0.285	1.825**	1.788**	1.692**	1.768**
SKAU-T-1701 × SKAU-T-1464	-0.304	-0.300	-0.302	-0.302	-0.787**	-0.812**	-0.782**	-0.794**
SKAU-T-1009 × SKAU-T-9862	1.025*	0.976*	0.960*	0.987**	0.291	0.252	0.211	0.251
SKAU-T-1009 × SKAU-T-1464	-0.523	-0.555	-0.511	-0.530*	-0.154	-0.115	0.003	-0.088
SKAU-T-9862 × SKAU-T-1464	-0.328	-0.267	-0.242	-0.279	0.215	0.171	0.156	0.181
S.E±(Sij)	0.333	0.332	0.328	0.175	0.236	0.245	0.236	0.126
S.E±(Sij-Sik)	0.487	0.485	0.479	0.279	0.345	0.358	0.346	0.202

*,**Significant at 5 and 1 percent levels, respectively

Table 5.6: Specific combining ability (SCA) effects for pericarp thickness and number of primary branches plant⁻¹ in tomato. (Based on individual and pooled over environments)

Crosses	Pericarp thickness				Number of primary branches plant ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	-1.016**	-0.975**	-0.973**	-0.988**	0.527*	0.506*	0.440	0.491**
SKAU-T-9801 × SKAU-T-0922	-0.886**	-0.882**	-0.842**	-0.970**	0.287	0.246	0.216	0.250
SKAU-T-9801 × SKAU-T-1424	-0.502	-0.446	-0.485	-0.478**	0.282	0.258	0.352	0.297*
SKAU-T-9801 × SKAU-T-1219	1.562**	1.511**	1.470**	1.514**	-0.154	-0.071	-0.167	-0.131
SKAU-T-9801 × SKAU-T-1315	-0.395	-0.375	-0.387	-0.386*	-0.518*	-0.487	-0.477	-0.494**
SKAU-T-9801 × SKAU-T-0301	-0.300	-0.320	-0.311	-0.310	-0.225	-0.223	-0.124	-0.191
SKAU-T-9801 × SKAU-T-1429	0.255	0.295	0.396	0.315	0.437	0.446	0.452	0.445**
SKAU-T-9801 × SKAU-T-1701	0.074	0.059	0.139	0.091	0.137	0.134	0.052	0.108
SKAU-T-9801 × SKAU-T-1009	0.700**	0.768**	0.772*	0.780**	0.477	0.529*	0.476	0.494**
SKAU-T-9801 × SKAU-T-9862	-0.833**	-0.829**	-0.904**	-0.855**	-0.299	-0.361	-0.308	-0.323*
SKAU-T-9801 × SKAU-T-1464	0.436	0.442	0.365	0.414**	0.339	0.368	0.390	0.366*
SKAU-T-1700 × SKAU-T-0922	0.829**	0.802**	0.739*	0.790**	-0.175	-0.175	-0.127	-0.159
SKAU-T-1700 × SKAU-T-1424	0.112	0.104	0.063	0.093	-0.180	-0.197	-0.291	-0.223
SKAU-T-1700 × SKAU-T-1219	0.143	0.161	0.118	0.141	-0.016	0.008	0.057	0.016
SKAU-T-1700 × SKAU-T-1315	0.886**	0.842**	0.894**	0.874**	-0.280	-0.309	-0.386	-0.325*
SKAU-T-1700 × SKAU-T-0301	0.581*	0.630*	0.703*	0.638**	-0.187	-0.211	-0.267	-0.222
SKAU-T-1700 × SKAU-T-1429	0.469	0.445	0.444	0.543**	-0.025	-0.042	0.042	-0.008
SKAU-T-1700 × SKAU-T-1701	0.588*	0.542	0.620*	0.583**	-0.259	-0.387	-0.291	-0.312*
SKAU-T-1700 × SKAU-T-1009	1.414**	1.385**	1.387**	1.395**	0.749**	0.708**	0.799**	0.752**
SKAU-T-1700 × SKAU-T-9862	-0.652*	-0.613*	-0.590	-0.618**	-0.128	-0.049	-0.117	-0.098
SKAU-T-1700 × SKAU-T-1464	-0.083	-0.075	-0.087	-0.082	0.577*	0.513*	0.614*	0.568**
SKAU-T-0922 × SKAU-T-1424	-0.457	-0.503	-0.440	-0.467**	-0.154	-0.156	-0.215	-0.175
SKAU-T-0922 × SKAU-T-1219	0.341	0.287	0.249	0.292	1.077**	1.082**	0.999**	1.053**
SKAU-T-0922 × SKAU-T-1315	0.284	0.368	0.425	0.359*	-0.921**	-0.835**	-0.943**	-0.900**

Contd...

Table 5.6: contd....

Crosses	Pericarp thickness				Number of primary branches plant ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-0301	-0.255	-0.277	-0.332	-0.288	0.139	0.196	0.242	0.192
SKAU-T-0922 × SKAU-T-1429	0.500	0.437	0.475	0.471**	-0.399	-0.501*	-0.515	-0.472**
SKAU-T-0922 × SKAU-T-1701	-0.214	-0.198	-0.316	-0.243	1.001**	0.987**	0.985**	0.991**
SKAU-T-0922 × SKAU-T-1009	-0.255	-0.222	-0.182	-0.220	-0.692**	-0.618*	-0.591*	-0.634**
SKAU-T-0922 × SKAU-T-9862	0.112	0.147	0.275	0.178	-0.535*	-0.575*	-0.474	-0.528**
SKAU-T-0922 × SKAU-T-1464	-0.519	-0.482	-0.456	-0.486**	-0.797**	-0.713**	-0.743**	-0.751**
SKAU-T-1424 × SKAU-T-1219	-0.243	-0.210	-0.194	-0.216	0.006	-0.006	0.235	0.078
SKAU-T-1424 × SKAU-T-1315	0.267	0.271	0.182	0.240	0.375	0.377	0.426	0.392**
SKAU-T-1424 × SKAU-T-0301	0.195	0.192	0.158	0.182	-0.132	-0.159	-0.222	-0.171
SKAU-T-1424 × SKAU-T-1429	-0.216	-0.094	-0.035	-0.115	-0.037	-0.090	-0.079	-0.069
SKAU-T-1424 × SKAU-T-1701	-0.597*	-0.629*	-0.659*	-0.628**	0.263	0.232	0.254	0.250
SKAU-T-1424 × SKAU-T-1009	-1.605**	-1.620**	-1.659**	-1.628**	-0.630*	-0.673**	-0.655*	-0.653**
SKAU-T-1424 × SKAU-T-9862	1.729**	1.649**	1.699**	1.692**	0.560*	0.603*	0.595*	0.586**
SKAU-T-1424 × SKAU-T-1464	1.131**	1.154**	1.201**	1.162**	-0.568*	-0.568*	-0.574*	-0.570**
SKAU-T-1219 × SKAU-T-1315	-0.769**	-0.839**	-0.797**	-0.801**	-0.428	-0.385	-0.460	-0.424**
SKAU-T-1219 × SKAU-T-0301	0.860**	0.816**	0.779*	0.818**	-0.168	-0.254	-0.274	-0.232
SKAU-T-1219 × SKAU-T-1429	-0.152	-0.203	-0.147	-0.167	0.827**	0.815**	0.802**	0.815**
SKAU-T-1219 × SKAU-T-1701	-0.533	-0.505	-0.504	-0.514**	0.594*	0.603*	0.602*	0.600**
SKAU-T-1219 × SKAU-T-1009	-0.707*	-0.696*	-0.637*	-0.680**	0.301	0.232	0.226	0.253
SKAU-T-1219 × SKAU-T-9862	-0.207	-0.194	-0.147	-0.182	-0.175**	-0.792**	-0.824**	-0.797**
SKAU-T-1219 × SKAU-T-1464	-0.338	-0.355	-0.311	-0.335*	-0.337	-0.363	-0.360	-0.354*
SKAU-T-1315 × SKAU-T-0301	-0.064	-0.070	-0.078	-0.071	1.101**	1.096**	1.216**	1.138**
SKAU-T-1315 × SKAU-T-1429	-0.943**	-0.755**	-0.937**	-0.878**	0.596*	0.565*	0.526	0.562**
SKAU-T-1315 × SKAU-T-1701	-0.990**	-0.958**	-0.928**	-0.959**	-0.637*	-0.613*	-0.608*	-0.619**
SKAU-T-1315 × SKAU-T-1009	0.869**	0.852**	0.906**	0.876**	-0.263	-0.285	-0.217	-0.255

Contd...

Table 5.6: contd....

Crosses	Pericarp thickness				Number of primary branches plant ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-1315 × SKAU-T-9862	0.069	0.054	0.096	0.073	0.527*	0.525*	0.533	0.528**
SKAU-T-1315 × SKAU-T-1464	-0.962**	-1.008**	-0.935**	-0.968**	0.099	0.087	-0.003	0.061
SKAU-T-0301 × SKAU-T-1429	-0.181	-0.201	-0.194	0.192	-0.611*	-0.571*	-0.445*	0.579**
SKAU-T-0301 × SKAU-T-1701	-0.228	-0.170	-0.218	-0.205	-0.144	-0.116	-0.189	-0.150
SKAU-T-0301 × SKAU-T-1009	-1.636**	-1.594**	-1.585**	-1.605**	-0.271	-0.287	-0.232	-0.263
SKAU-T-0301 × SKAU-T-9862	-0.92	-0.88	-0.128	-0.105	0.020	0.022	0.252	0.084
SKAU-T-0301 × SKAU-T-1464	0.767**	0.680*	0.675*	0.708**	-0.175	-0.216	-0.251	-0.223**
SKAU-T-1429 × SKAU-T-1701	0.660*	0.645*	0.589	0.617**	0.118	0.120	0.088	0.141**
SKAU-T-1429 × SKAU-T-1009	-0.814**	-0.846**	-0.844**	-0.871**	0.258	0.382	0.378	0.346**
SKAU-T-1429 × SKAU-T-9862	-1.181**	-1.177**	-1.187**	-1.154**	-0.251	-0.275	-0.239	-0.254**
SKAU-T-1429 × SKAU-T-1464	2.788**	2.461**	2.749**	2.786**	-0.413	-0.380	-0.141	-0.294**
SKAU-T-1701 × SKAU-T-1009	0.905**	0.885**	0.965**	0.893**	0.225	0.270	0.278	0.246**
SKAU-T-1701 × SKAU-T-9862	0.405	0.487	0.456	0.443**	-0.185	-0.221	-0.239	-0.254**
SKAU-T-1701 × SKAU-T-1464	-0.159	-0.175	-0.209	-0.183**	0.053	0.108	0.092	0.106*
SKAU-T-1009 × SKAU-T-9862	1.464**	1.464**	1.456**	1.488**	0.422	0.475	0.385	0.451**
SKAU-T-1009 × SKAU-T-1464	-0.300	-0.232	-0.309	-0.271**	-0.440	-0.463	-0.517	-0.490**
SKAU-T-9862 × SKAU-T-1464	-0.500	-0.529	-0.451	-0.488**	0.151	0.279	0.233	0.244**
S.E±(Sij)	0.208	0.211	0.227	0.114	0.192	0.186	0.201	0.102
S.E± (Sij-Sik)	0.304	0.309	0.332	0.182	0.281	0.271	0.294	0.163

*,**Significant at 5 and 1 percent levels, respectively

Table 5.7: Specific combining ability (SCA) effects for plant height and average fruit weight in tomato. (Based on individual and pooled over environments)

Crosses	Plant height(cm)				Average fruit weight (g)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	-7.066**	-6.926**	-7.066**	-7.019**	11.140**	10.606**	10.982**	10.909**
SKAU-T-9801 × SKAU-T-0922	-16.212**	-16.404**	-16.740**	-16.452**	8.750**	8.561**	8.925**	8.745**
SKAU-T-9801 × SKAU-T-1424	19.834**	19.696**	20.203**	19.911**	-2.083	-2.018	-2.563*	-2.221**
SKAU-T-9801 × SKAU-T-1219	-11.202**	-11.576**	-11.206**	-11.328**	14.493**	14.230**	14.956**	14.560**
SKAU-T-9801 × SKAU-T-1315	-5.238**	-5.078**	-5.673**	-5.330**	-8.362**	-8.296**	-8.832**	-8.597**
SKAU-T-9801 × SKAU-T-0301	-7.726**	-8.035**	-8.006**	-7.923**	-1.014	-1.246	-1.487	-1.249
SKAU-T-9801 × SKAU-T-1429	-1.928	-2.035	-2.494	-2.153**	13.838**	13.992**	13.997**	13.942**
SKAU-T-9801 × SKAU-T-1701	24.600**	24.131**	23.927**	24.220**	-6.783**	-7.106**	-6.706**	-6.865**
SKAU-T-9801 × SKAU-T-1009	-7.978**	-8.350**	-7.811**	-8.040**	-7.576**	-7.196**	-6.915**	-7.229**
SKAU-T-9801 × SKAU-T-9862	8.417**	8.624**	8.789**	8.610**	-1.588	-1.496	-1.586	-1.451
SKAU-T-9801 × SKAU-T-1464	-1.447	-1.476	-1.768	-1.564	6.857**	6.970**	7.194**	7.007**
SKAU-T-1700 × SKAU-T-0922	36.114**	35.788**	35.339**	35.747**	2.329	2.201	1.829	2.120
SKAU-T-1700 × SKAU-T-1424	-19.440**	-19.712**	-19.885**	-19.679**	2.638	2.354*	2.682*	2.558**
SKAU-T-1700 × SKAU-T-1219	-12.409**	-12.650**	-12.761**	-12.607**	-3.881*	-4.268**	-4.035**	-4.061**
SKAU-T-1700 × SKAU-T-1315	3.088*	2.981*	3.306*	3.125**	4.460**	5.142**	5.047**	4.883**
SKAU-T-1700 × SKAU-T-0301	-14.133**	-13.843**	-13.461**	-13.812**	-13.026**	-13.342**	-13.741**	-13.370**
SKAU-T-1700 × SKAU-T-1429	-6.136**	-5.976**	-5.882**	-5.998**	-1.240	-1.537	-1.458	-1.412
SKAU-T-1700 × SKAU-T-1701	-9.440**	-9.609**	-10.094**	-9.715**	4.571**	4.599**	4.873**	4.681**
SKAU-T-1700 × SKAU-T-1009	55.148**	54.810**	54.634**	54.864**	8.912**	9.075**	9.363**	9.117**
SKAU-T-1700 × SKAU-T-9862	-17.057**	-16.650**	-16.399**	-16.702**	4.600**	4.842**	4.511**	4.651**
SKAU-T-1700 × SKAU-T-1464	-0.588	-0.816	-0.890	-0.765	-3.712*	-3.408**	-3.040**	-3.387**
SKAU-T-0922 × SKAU-T-1424	-18.452**	-18.057**	-18.092**	-18.200**	8.829**	8.820**	7.790**	8.479**
SKAU-T-0922 × SKAU-T-1219	30.779**	30.972**	30.465**	30.739**	-6.029**	-6.065**	-5.891**	-5.995**
SKAU-T-0922 × SKAU-T-1315	-9.357**	-9.097**	-8.801**	-9.085**	-13.817**	-14.025**	-14.113**	-13.985**

Contd....

Table 5.7: contd...

Crosses	Plant height(cm)				Average fruit weight (g)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-0301	-14.212**	-13.354**	-13.368**	-13.645**	-18.736**	-18.708**	-18.368**	-18.604**
SKAU-T-0922 × SKAU-T-1429	13.253**	11.879**	12.044**	12.392**	-3.583*	-2.870**	-2.918**	-3.124**
SKAU-T-0922 × SKAU-T-1701	-11.452**	-11.688**	-11.701**	-11.614**	-1.129	-1.232	-1.347	-1.236
SKAU-T-0922 × SKAU-T-1009	9.303**	9.965**	9.294**	9.520**	7.136**	6.408**	6.371**	6.638**
SKAU-T-0922 × SKAU-T-9862	8.631**	8.272**	8.627**	8.510**	-12.276**	-12.858**	-13.482**	-12.872**
SKAU-T-0922 × SKAU-T-1464	-8.200**	-8.495**	-8.397**	-8.364**	4.469**	4.975**	5.013**	4.819**
SKAU-T-1424 × SKAU-T-1219	0.391	0.905	0.975	0.757	-9.195**	-9.511**	-8.813**	-9.173**
SKAU-T-1424 × SKAU-T-1315	-1.578	-1.931	-1.692	-1.734*	-4.983**	-4.837**	-4.768**	-4.896**
SKAU-T-1424 × SKAU-T-0301	-13.000**	-13.088**	-13.359**	-13.149**	-20.936**	-20.887**	-20.989**	-20.937**
SKAU-T-1424 × SKAU-T-1429	-1.236	-1.421	-1.547	-1.401	-10.983**	-11.082**	-11.139**	-11.068**
SKAU-T-1424 × SKAU-T-1701	-8.974**	-8.888**	-8.892**	-8.918**	-2.195*	-1.820*	-2.392*	-2.169*
SKAU-T-1424 × SKAU-T-1009	-17.952**	-17.569**	-17.697**	-17.739**	-3.764*	-3.137**	-3.118**	-3.340**
SKAU-T-1424 × SKAU-T-9862	14.443**	42.005**	41.937**	42.128**	17.257**	17.463**	16.563**	17.095**
SKAU-T-1424 × SKAU-T-1464	-4.021**	-4.628**	-4.187**	-4.279**	10.502**	9.930**	10.225**	10.219**
SKAU-T-1219 × SKAU-T-1315	3.253*	3.931**	4.299**	3.827**	2.893	3.177**	3.418**	3.163**
SKAU-T-1219 × SKAU-T-0301	52.464**	50.774**	50.999**	51.412**	4.174**	3.861**	3.963**	3.999**
SKAU-T-1219 × SKAU-T-1429	5.695**	5.741**	5.710**	5.716**	-12.207**	-12.068**	-11.987**	-12.087**
SKAU-T-1219 × SKAU-T-1701	0.757	1.241	0.665	0.888	10.205*	10.132*	10.189*	10.039*
SKAU-T-1219 × SKAU-T-1009	0.845	0.893	0.327	0.529	20.079**	20.644**	20.535**	20.419**
SKAU-T-1219 × SKAU-T-9862	-16.426**	-16.766**	-16.673**	-16.622**	-13.667**	-13.226**	-13.651**	-13.624**
SKAU-T-1219 × SKAU-T-1464	-20.590**	-20.200**	-20.463**	-20.418**	-14.655**	-14.056**	-14.389**	-14.367**
SKAU-T-1315 × SKAU-T-0301	1.229	1.538	1.599	1.455	-2.219	-2.335*	-1.775	-2.210**
SKAU-T-1315 × SKAU-T-1429	-1.574	-1.962	-1.890	-1.808*	-0.062	-0.194	-0.208	-0.155
SKAU-T-1315 × SKAU-T-1701	0.688	0.905	1.265	0.953	4.983**	5.292**	5.477**	5.251**
SKAU-T-1315 × SKAU-T-1009	-24.590**	-24.642**	-24.673**	-24.635**	-10.910**	-10.515**	-10.087**	-10.504**

Contd....

Table 5.7: contd...

Crosses	Plant height(cm)				Average fruit weight (g)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-1315 × SKAU-T-9862	-16.628**	-16.369**	-16.373**	-16.457**	-8.755**	-8.782**	-8.406**	-8.647**
SKAU-T-1315 × SKAU-T-1464	7.741**	7.998**	8.303**	8.014**	28.124**	28.451**	27.990**	28.188**
SKAU-T-0301 × SKAU-T-1429	17.638**	17.115**	16.810**	17.188**	10.219**	10.556**	10.937**	10.571**
SKAU-T-0301 × SKAU-T-1701	19.467**	18.115**	17.532**	18.371**	19.164**	18.825**	19.168**	19.053**
SKAU-T-0301 × SKAU-T-1009	-15.112**	-14.366**	-14.273**	-14.584**	-3.605*	-3.901**	-3.925**	-3.810**
SKAU-T-0301 × SKAU-T-9862	-11.616**	-11.192**	-11.106**	-11.323**	9.560**	9.101**	8.906**	9.049**
SKAU-T-0301 × SKAU-T-1464	-7.347**	-6.692**	-7.097**	-7.020**	2.205	2.168	2.401*	2.280**
SKAU-T-1429 × SKAU-T-1701	-1.102	-1.019	-1.456	-1.187**	14.383**	14.330**	14.618**	14.449**
SKAU-T-1429 × SKAU-T-1009	-13.281**	-13.633**	-13.461**	-13.458**	5.610**	11.661**	11.458**	11.723**
SKAU-T-1429 × SKAU-T-9862	0.681	0.774	1.006	0.835**	2.921	3.606**	4.123**	3.761**
SKAU-T-1429 × SKAU-T-1464	0.250	0.374	0.582	0.404	9.424**	7.873**	8.051**	8.458**
SKAU-T-1701 × SKAU-T-1009	5.814**	5.667**	5.894**	5.804**	10.269**	11.575**	10.273**	10.968**
SKAU-T-1701 × SKAU-T-9862	-2.257	-2.259	-2.540	-2.370**	0.224	0.375	0.687	0.251
SKAU-T-1701 × SKAU-T-1464	-10.888**	-10.426**	-9.997**	-10.434**	14.364**	14.258**	14.484**	14.385**
SKAU-T-1009 × SKAU-T-9862	30.631**	30.260**	29.222**	30.058**	6.831**	7.851**	7.844**	9.746**
SKAU-T-1009 × SKAU-T-1464	-12.033**	-12.007**	-11.968**	-12.006**	-10.657**	-10.382**	-10.527**	-10.556**
SKAU-T-9862 × SKAU-T-1464	-0.005	-0.033	0.332	0.087	-6.502**	-6.382**	-6.213**	-6.506**
S.E±(Sij)	1.057	1.026	1.065	0.554	1.289	0.820	0.805	0.526
S.E±(Sij-Sik)	1.546	1.500	1.558	0.886	1.886	1.200	1.177	0.842

*,**Significant at 5 and 1 percent levels, respectively

Table 5.8: Specific combining ability (SCA) effects for fruit yield plant⁻¹ and fruit yield hectare⁻¹ in tomato. (Based on individual and pooled over environments)

Crosses	Fruit yield plant ⁻¹				Fruit yield hectare ⁻¹ (q)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	0.186**	0.135*	0.161**	0.147**	57.483**	49.578	59.773**	55.611**
SKAU-T-9801 × SKAU-T-0922	0.532**	0.522**	0.520**	0.526**	202.659**	193.804**	192.429**	196.297**
SKAU-T-9801 × SKAU-T-1424	0.275**	-0.295**	-0.316**	-0.307**	-113.128**	-108.923**	-117.007**	-113.019**
SKAU-T-9801 × SKAU-T-1219	0.906**	0.797**	0.798**	0.803**	305.650**	295.656**	295.422**	298.909**
SKAU-T-9801 × SKAU-T-1315	-0.476**	-0.401**	-0.388**	-0.397**	-131.669**	-148.257**	-143.905**	-147.944**
SKAU-T-9801 × SKAU-T-0301	-0.607**	-0.583**	-0.579**	-0.582**	-217.625**	-215.628**	-214.363**	-215.872**
SKAU-T-9801 × SKAU-T-1429	0.800**	0.708**	0.642**	0.689**	266.499**	260.031**	237.751**	254.760**
SKAU-T-9801 × SKAU-T-1701	0.062**	0.051	0.072	0.062**	25.779	19.113	26.733	23.875
SKAU-T-9801 × SKAU-T-1009	-0.151**	-0.125*	-0.056	-0.105**	-47.960*	-54.430	-20.622	-41.004**
SKAU-T-9801 × SKAU-T-9862	-0.551**	-0.418**	-0.417**	-0.423**	-168.157**	-148.254**	-154.306**	-156.906**
SKAU-T-9801 × SKAU-T-1464	0.431**	0.432**	0.419**	0.437**	166.696**	160.212**	155.037**	160.648**
SKAU-T-1700 × SKAU-T-0922	0.168**	0.173**	0.189**	0.174**	60.682**	64.616*	69.994**	65.097**
SKAU-T-1700 × SKAU-T-1424	0.355**	0.376**	0.367**	0.370**	138.723**	139.663**	135.869**	138.085**
SKAU-T-1700 × SKAU-T-1219	-0.402**	-0.332**	-0.330**	-0.349**	-140.026**	-122.419**	-122.066**	-128.171**
SKAU-T-1700 × SKAU-T-1315	0.486**	0.483**	0.484**	0.477**	186.608**	179.344**	179.340**	181.764**
SKAU-T-1700 × SKAU-T-0301	-0.975**	-0.962**	-0.939**	-0.965**	-371.945**	-355.929**	-347.908**	-358.594**
SKAU-T-1700 × SKAU-T-1429	-0.521**	-0.424**	-0.409**	-0.424**	-164.364**	-159.277**	-151.344**	-158.329**
SKAU-T-1700 × SKAU-T-1701	-0.312**	-0.272**	-0.248**	-0.270**	-108.799**	-100.198**	-91.998**	-100.328**
SKAU-T-1700 × SKAU-T-1009	0.611**	0.559**	0.554**	0.576**	223.643**	199.095**	205.090**	209.276**
SKAU-T-1700 × SKAU-T-9862	0.301**	0.270**	0.259**	0.271**	100.983**	106.508**	96.096**	101.196**
SKAU-T-1700 × SKAU-T-1464	-0.232**	-0.191**	-0.242**	-0.206**	-69.107**	-70.210*	-89.614**	-76.310**
SKAU-T-0922 × SKAU-T-1424	0.435**	0.433**	0.388**	0.407**	153.188**	160.825**	143.624**	152.546**
SKAU-T-0922 × SKAU-T-1219	-0.394**	-0.358**	-0.245**	-0.353**	-129.268**	-132.120**	-127.891**	-129.760**
SKAU-T-0922 × SKAU-T-1315	-0.775**	-0.643**	-0.648**	-0.650**	-242.140**	-237.760**	-240.058**	-239.986**
SKAU-T-0922 × SKAU-T-0301	-0.506**	-0.455**	-0.432**	-0.451**	-173.533	-168.097**	-158.899**	-167.177**

Contd....

Table 5.8: contd....

Crosses	Fruit yield plant ⁻¹				Fruit yield hectare ⁻¹ (q)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-1429	-0.230**	-0.331**	-0.328**	-0.334**	-127.679**	-124.535**	-121.362**	-124.525**
SKAU-T-0922 × SKAU-T-1701	-0.065*	-0.074*	-0.077*	-0.074**	-25.193	-27.176	-28.683	-27.017*
SKAU-T-0922 × SKAU-T-1009	0.464**	0.333**	0.328**	0.346**	144.278**	115.323**	121.492**	127.031**
SKAU-T-0922 × SKAU-T-9862	-0.725**	-0.606**	-0.600**	-0.605**	-263.569**	-218.010**	-222.065**	-234.548**
SKAU-T-0922 × SKAU-T-1464	0.384**	0.403**	0.419**	0.401**	151.525**	149.715**	155.181**	152.141**
SKAU-T-1424 × SKAU-T-1219	-0.213**	-0.385**	-0.354**	-0.370**	-136.408**	-142.260**	-131.149**	-136.606**
SKAU-T-1424 × SKAU-T-1315	-0.089*	-0.074	-0.067	-0.067**	-24.593	-26.917	-24.803	-25.438
SKAU-T-1424 × SKAU-T-0301	-0.790**	-0.649**	-0.577**	-0.635**	-248.580**	-239.967**	-213.778**	-234.108**
SKAU-T-1424 × SKAU-T-1429	-0.650**	-0.535**	-0.527**	-0.531**	-196.552**	-200.105**	-194.994**	-197.217**
SKAU-T-1424 × SKAU-T-1701	-0.431**	-0.345**	-0.330**	-0.341**	-126.162**	-127.446**	-122.068**	-125.226**
SKAU-T-1424 × SKAU-T-1009	0.051	0.012	0.016	0.012	0.102	3.460	5.883	0.842
SKAU-T-1424 × SKAU-T-9862	0.705**	0.693**	0.655**	0.684**	256.448**	263.207**	242.570**	254.075**
SKAU-T-1424 × SKAU-T-1464	0.947**	0.816**	0.800**	0.837**	320.925**	302.535**	296.356**	306.606**
SKAU-T-1219 × SKAU-T-1315	0.296**	0.282**	0.280**	0.280**	100.364**	104.832**	103.682**	102.959**
SKAU-T-1219 × SKAU-T-0301	0.604**	0.507**	0.476**	0.509**	201.071**	188.074**	176.434**	188.527**
SKAU-T-1219 × SKAU-T-1429	-0.776**	-0.626**	-0.600**	-0.627**	-243.198**	-233.793**	-222.069**	-233.020**
SKAU-T-1219 × SKAU-T-1701	0.080**	0.054	0.054	0.060**	24.722*	20.349*	19.997*	21.689*
SKAU-T-1219 × SKAU-T-1009	0.302**	0.222**	0.206**	0.226**	94.193**	73.965*	76.342**	81.500**
SKAU-T-1219 × SKAU-T-9862	-0.480**	-0.484**	-0.462**	-0.475**	-185.264**	-172.948**	-170.922**	-176.378**
SKAU-T-1219 × SKAU-T-1464	-0.702**	-0.665**	-0.663**	-0.685**	-268.931**	-245.963**	-245.526**	-253.473**
SKAU-T-1315 × SKAU-T-0301	-0.042	-0.022	-0.053	-0.032	-9.338	-7.692	-19.686	-12.234
SKAU-T-1315 × SKAU-T-1429	-0.091*	-0.081	-0.086	-0.081**	-31.380	-32.030	-31.773	-31.728*
SKAU-T-1315 × SKAU-T-1701	0.092*	0.079	0.071	0.086**	36.536	29.522	26.343	30.801*
SKAU-T-1315 × SKAU-T-1009	-0.232**	-0.200**	-0.183**	-0.195**	-77.943**	-82.295**	-67.922**	-76.053**
SKAU-T-1315 × SKAU-T-9862	-0.260**	-0.233**	-0.208**	-0.229**	-98.136**	-79.828**	-76.919**	-84.961**
SKAU-T-1315 × SKAU-T-1464	0.405**	0.356**	0.331**	0.354**	136.714**	132.344**	122.224**	130.537**

Contd....

Table 5.8: contd....

Crosses	Fruit yield plant ⁻¹				Fruit yield hectare ⁻¹ (q)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0301 × SKAU-T-1429	0.741**	0.627**	0.631**	0.631**	235.987**	230.227**	233.573**	233.262**
SKAU-T-0301 × SKAU-T-1701	0.082*	0.057	0.051	0.061**	26.130	21.409	18.84	28.129**
SKAU-T-0301 × SKAU-T-1009	-0.172**	-0.156**	-0.160**	-0.156**	-58.719**	-65.715*	-59.367**	-61.267**
SKAU-T-0301 × SKAU-T-9862	0.085*	0.095*	0.052	0.086**	38.371	41.692	19.290	34.181**
SKAU-T-0301 × SKAU-T-1464	0.432**	0.408**	0.397**	0.413**	160.874**	151.387**	147.156**	154.015**
SKAU-T-1429 × SKAU-T-1701	0.785**	0.788**	0.758**	0.792**	305.321**	289.661**	280.839**	292.860**
SKAU-T-1429 × SKAU-T-1009	-0.521**	-0.478**	-0.470**	-0.485**	-186.938**	-120.069*	-173.917**	-179.075**
SKAU-T-1429 × SKAU-T-9862	0.295**	0.283**	0.286**	0.287**	103.978**	124.757**	105.970**	107.054**
SKAU-T-1429 × SKAU-T-1464	0.492**	0.445**	0.537**	0.484**	188.212**	162.856**	196.800**	179.555**
SKAU-T-1701 × SKAU-T-1009	0.732**	0.712**	0.657**	0.681**	252.585**	255.446**	243.446**	252.237**
SKAU-T-1701 × SKAU-T-9862	0.243**	0.222**	0.226**	0.221**	81.775**	88.779**	83.836**	82.806**
SKAU-T-1701 × SKAU-T-1464	0.254**	0.232**	0.232**	0.243**	98.439**	85.472**	85.824**	89.217**
SKAU-T-1009 × SKAU-T-9862	0.372**	0.383**	0.278**	0.376**	137.666**	139.926**	140.187**	140.502**
SKAU-T-1009 × SKAU-T-1464	-0.494**	-0.468**	-0.470**	-0.470**	-176.864**	-181.236**	-173.920**	-173.821**
SKAU-T-9862 × SKAU-T-1464	-0.653**	-0.617**	-0.601**	-0.618**	-241.505**	-221.979**	-222.420**	-226.792**
S.E±(Sij)	0.071	0.041	0.041	1.697	16.424	21.655	15.352	9.510
S.E± (Sij-Sik)	0.068	0.059	0.061	2.716	24.022	31.672	22.456	15.218

*,**Significant at 5 and 1 percent levels, respectively

Table 5.9: Specific combining ability (SCA) effects for average number of seeds fruit⁻¹ and 100 seed weight in tomato. (Based on individual and pooled over environments)

Crosses	Average number of seeds fruit ⁻¹				100 seed weight			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-9801 × SKAU-T-1700	55.069**	55.323**	56.430**	55.607**	-0.058**	-0.062**	-0.056**	-0.059**
SKAU-T-9801 × SKAU-T-0922	-17.226**	-15.839**	-17.487**	-17.184**	-0.051**	-0.048**	-0.047**	-0.048**
SKAU-T-9801 × SKAU-T-1424	-51.362**	-51.268**	-50.953**	-51.194**	0.076**	0.076**	0.077**	0.076**
SKAU-T-9801 × SKAU-T-1219	-46.310**	-45.882**	-45.622**	-45.938**	0.017**	0.018**	0.015**	0.017**
SKAU-T-9801 × SKAU-T-1315	6.510**	6.856**	5.756**	6.374**	0.018*	0.010*	0.016	0.018**
SKAU-T-9801 × SKAU-T-0301	49.126**	48.823**	48.601**	48.850**	-0.034**	-0.030**	-0.031**	-0.032**
SKAU-T-9801 × SKAU-T-1429	34.681**	35.170**	35.287**	35.040**	-0.052**	-0.054**	-0.056**	-0.058**
SKAU-T-9801 × SKAU-T-1701	-62.162**	-62.256**	-62.277**	-62.232**	0.024**	0.027**	0.025**	0.026**
SKAU-T-9801 × SKAU-T-1009	10.179**	9.699**	9.687**	9.855**	-0.054**	-0.055**	-0.050**	-0.053**
SKAU-T-9801 × SKAU-T-9862	30.752**	30.727**	30.778**	30.752**	0.065	0.069*	0.064	0.066**
SKAU-T-9801 × SKAU-T-1464	1.667	1.770	2.216	1.884	0.041**	0.045**	0.044**	0.043**
SKAU-T-1700 × SKAU-T-0922	-14.162**	-13.589**	-15.049**	-14.267**	0.107**	0.108**	0.105**	0.107**
SKAU-T-1700 × SKAU-T-1424	-30.331**	-29.585**	-29.615**	-29.844**	-0.010**	-0.011	-0.012*	-0.018**
SKAU-T-1700 × SKAU-T-1219	15.755**	15.701**	15.049**	15.502**	-0.015**	-0.016**	-0.018**	-0.020**
SKAU-T-1700 × SKAU-T-1315	50.407**	50.073**	49.394**	49.958**	0.026	0.025	0.028	0.036**
SKAU-T-1700 × SKAU-T-0301	-50.743**	-51.127**	-50.760**	-50.877**	-0.072	-0.076	-0.075	-0.084
SKAU-T-1700 × SKAU-T-1429	16.612**	16.387**	16.892**	16.630**	0.082**	0.079**	0.080**	0.084**
SKAU-T-1700 × SKAU-T-1701	-19.731**	-20.106**	-20.172**	-20.003**	0.025**	0.028**	0.029**	0.030**
SKAU-T-1700 × SKAU-T-1009	2.043	1.815	1.425	1.761	-0.031	0.035	0.030	0.048
SKAU-T-1700 × SKAU-T-9862	5.850**	6.044**	6.816**	6.237**	-0.080**	-0.082**	-0.078**	-0.084**
SKAU-T-1700 × SKAU-T-1464	5.431**	5.387**	6.321**	5.713**	-0.072**	-0.074**	-0.069**	-0.076**
SKAU-T-0922 × SKAU-T-1424	14.940**	13.187**	14.368**	14.265**	-0.027**	-0.028**	-0.029**	-0.030**
SKAU-T-0922 × SKAU-T-1219	107.160**	107.039**	107.366**	107.188**	0.022**	0.021**	0.024**	0.026**
SKAU-T-0922 × SKAU-T-1315	38.612**	37.911**	37.978**	38.167**	-0.043	-0.045	-0.044	-0.054

Contd....

Table 5.9: contd....

Crosses	Average number of seeds fruit ¹				100 seed weight			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-0922 × SKAU-T-0301	-9.905**	-10.156**	-10.177**	-10.079**	-0.011**	-0.012**	-0.015**	-0.013**
SKAU-T-0922 × SKAU-T-1429	6.150**	5.892**	6.909**	6.317**	-0.024**	-0.025**	-0.021**	-0.023**
SKAU-T-0922 × SKAU-T-1701	-8.126**	-9.235**	-9.022**	-8.794**	-0.016**	-0.017**	-0.019**	-0.021**
SKAU-T-0922 × SKAU-T-1009	-64.319**	-64.013**	-63.325**	-63.886**	0.027**	0.029**	0.030**	0.032**
SKAU-T-0922 × SKAU-T-9862	-12.212**	-12.551**	-12.024**	-12.266**	0.042**	0.040**	0.047**	0.049**
SKAU-T-0922 × SKAU-T-1464	21.936**	23.758**	22.871**	22.855**	-0.092**	-0.091**	-0.093**	-0.095**
SKAU-T-1424 × SKAU-T-1219	43.124**	43.844**	43.899**	43.622**	0.022	0.031	0.034	0.036
SKAU-T-1424 × SKAU-T-1315	-38.057**	-37.918**	-38.089**	-38.021**	-0.017**	-0.016**	-0.018**	-0.020**
SKAU-T-1424 × SKAU-T-0301	-73.474**	-73.251**	-72.744**	-73.156**	-0.017**	-0.018**	-0.014**	-0.026**
SKAU-T-1424 × SKAU-T-1429	7.348**	7.230**	7.075**	7.218**	-0.012**	-0.013**	-0.015**	-0.017**
SKAU-T-1424 × SKAU-T-1701	-6.929**	-6.663**	-6.922**	-6.838**	-0.018**	-0.019**	-0.021**	-0.025**
SKAU-T-1424 × SKAU-T-1009	-7.821**	-7.875**	-8.191**	-7.963**	-0.041**	-0.042**	-0.044**	-0.046**
SKAU-T-1424 × SKAU-T-9862	136.586**	136.554**	136.132**	136.424**	0.010**	0.012*	0.013**	0.015**
SKAU-T-1424 × SKAU-T-1464	43.700**	43.596**	44.104**	43.800**	0.051	0.054	0.055	0.056
SKAU-T-1219 × SKAU-T-1315	-63.905**	-64.166**	-64.091	-64.054**	0.024**	0.025**	0.027**	0.028**
SKAU-T-1219 × SKAU-T-0301	-13.588**	-13.532**	-13.780**	-13.633**	0.029**	0.032**	0.031**	0.035**
SKAU-T-1219 × SKAU-T-1429	-13.800	-14.251**	-14.360**	-14.137**	0.022**	0.021**	0.024**	0.027**
SKAU-T-1219 × SKAU-T-1701	18.624**	18.556**	18.575**	18.585**	-0.026	-0.035	-0.037	-0.046**
SKAU-T-1219 × SKAU-T-1009	-17.102**	-17.089**	-16.760**	-16.984**	0.011**	0.014**	0.012**	0.017**
SKAU-T-1219 × SKAU-T-9862	-37.762**	-37.694**	-37.137**	-37.531**	0.031**	0.034**	0.029**	0.036**
SKAU-T-1219 × SKAU-T-1464	-13.681**	-13.585**	-13.932**	-13.732**	-0.015**	-0.016**	-0.017**	-0.026**
SKAU-T-1315 × SKAU-T-0301	40.464**	40.573**	40.499**	40.512**	0.030**	0.035**	0.036**	0.038**
SKAU-T-1315 × SKAU-T-1429	25.219**	25.620**	25.651**	25.497**	0.012**	0.014**	0.016*	0.020**
SKAU-T-1315 × SKAU-T-1701	-26.024**	-26.906**	-24.579**	-25.836**	-0.019**	-0.022**	-0.018**	-0.025**
SKAU-T-1315 × SKAU-T-1009	-34.117**	-34.985**	-32.282**	-33.794**	-0.029**	-0.032**	-0.027**	-0.032**

Contd....

Table 5.9: contd....

Crosses	Average number of seeds fruit ⁻¹				100 seed weight			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
SKAU-T-1315 × SKAU-T-9862	-8.910**	-8.389**	-9.258**	-8.852**	0.024**	0.025**	0.023**	0.034**
SKAU-T-1315 × SKAU-T-1464	110.238**	110.187**	109.180**	109.868**	-0.014**	-0.015**	-0.017**	-0.025**
SKAU-T-0301 × SKAU-T-1429	-23.664**	-23.780**	-23.837**	-23.760**	0.015**	0.018**	0.022*	0.024**
SKAU-T-0301 × SKAU-T-1701	127.426**	127.361**	127.399**	127.395**	0.029**	0.033**	0.030**	0.035**
SKAU-T-0301 × SKAU-T-1009	0.933	1.549	1.530	1.337	0.045**	0.043**	0.045**	0.048**
SKAU-T-0301 × SKAU-T-9862	-46.560**	-46.856**	-46.846**	-46.738**	-0.031**	-0.034**	-0.028**	-0.037**
SKAU-T-0301 × SKAU-T-1464	44.755**	44.387**	44.025**	44.405**	-0.049**	-0.050**	-0.053**	-0.055**
SKAU-T-1429 × SKAU-T-1701	-28.486**	-27.525**	-27.649**	-27.867**	0.026**	0.028**	0.030**	0.035**
SKAU-T-1429 × SKAU-T-1009	42.455**	41.430**	41.016**	41.612**	-0.074**	-0.076**	-0.077**	-0.079**
SKAU-T-1429 × SKAU-T-9862	-46.738**	-46.275**	-46.460**	-46.579**	-0.043**	-0.045**	-0.048**	-0.053**
SKAU-T-1429 × SKAU-T-1464	-2.824	-3.666*	-3.889*	-3.436**	0.052**	0.055**	0.061**	0.066**
SKAU-T-1701 × SKAU-T-1009	-4.288**	-4.530*	-5.149**	-4.667**	0.030**	0.029**	0.031**	0.035**
SKAU-T-1701 × SKAU-T-9862	4.319*	4.365*	4.109*	4.243**	0.016**	0.018**	0.020**	0.026**
SKAU-T-1701 × SKAU-T-1464	-30.500**	-30.225**	-30.620**	-30.448**	0.092**	0.091**	0.089**	0.095**
SKAU-T-1009 × SKAU-T-9862	91.260**	91.353**	90.906**	91.188**	0.016**	0.018**	0.024	0.032**
SKAU-T-1009 × SKAU-T-1464	-29.060**	-27.937**	-28.222**	-28.403**	0.165**	0.166**	0.163**	0.168**
SKAU-T-9862 × SKAU-T-1464	-16.386**	-17.342**	-17.265**	-17.026**	-0.079	-0.080	-0.082**	-0.085**
S.E±(Sij)	1.363	1.330	1.346	0.710	0.003	0.003	0.003	0.002
S.E± (Sij-Sik)	1.993	1.946	1.969	1.137	0.004	0.004	0.005	0.003

*,**Significant at 5 and 1 percent levels, respectively

Table 6: Maximum trait contribution of the best crosses in respect of significant SCA effects in tomato (*Solanum lycopersicum* L.)

S. No.	CROSSES	Significant Traits for SCA
1.	SKAU-T-1424 × SKAU-T-9862	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), pericarp thickness (mm), number of primary branches plant ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q), average number of seeds fruit ⁻¹ and 100 seed weight (g)
2.	SKAU-T-1219 × SKAU-T-1315	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, fruit diameter (cm), number of locules fruit ⁻¹ , pericarp thickness (mm), plant height (cm), number of fruits plant ⁻¹ , average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and 100 seed weight (g)
3.	SKAU-T-9801 × SKAU-T-1700	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , fruit length (cm), fruit diameter (cm), number of primary branches plant ⁻¹ , number of fruits plant ⁻¹ , average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and average number of seeds fruit ⁻¹ .
4.	SKAU-T-9801 × SKAU-T-1429	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , fruit diameter (cm), number of primary branches plant ⁻¹ , average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and average number of seeds fruit ⁻¹

Contd....

Table 6: contd....

S. No.	CROSSES	Significant Traits for SCA
5.	SKAU-T-1700 × SKAU-T-0922	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , pericarp thickness (mm), plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and 100 seed weight (g)
6.	SKAU-T-1700 × SKAU-T-1009	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), pericarp thickness (mm), number of primary branches plant ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg) and fruit yield hectare ⁻¹ (q)
7.	SKAU-T-0301 × SKAU-T-1429	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), number of locules fruit ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and 100 seed weight (g)
8.	SKAU-T-1429 × SKAU-T-1701	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), pericarp thickness (mm), number of primary branches plant ⁻¹ , average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and 100 seed weight (g)
10.	SKAU-T-1424 × SKAU-T-1464	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), pericarp thickness (mm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and average number of seeds fruit ⁻¹

Contd....

Table 6: contd....

S. No.	CROSSES	Significant Traits for SCA
11.	SKAU-T-0301 × SKAU-T-1464	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , pericarp thickness (mm), average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and average number of seeds fruit ⁻¹
12.	SKAU-T-1701 × SKAU-T-1464	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of fruits plant ⁻¹ , fruit length (cm), number of primary branches plant ⁻¹ , average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and 100 seed weight (g)
13.	SKAU-T-0922 × SKAU-T-1464	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q) and average number of seeds fruit ⁻¹
14.	SKAU-T-1429 × SKAU-T-9862	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of fruits plant ⁻¹ , plant height (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg) and fruit yield hectare ⁻¹ (q)
15.	SKAU-T-1701 × SKAU-T-9862	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of locules fruit ⁻¹ , number of fruits plant ⁻¹ , pericarp thickness (mm), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q), average number of seeds fruit ⁻¹ and 100 seed weight (g)

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Table 6: contd....

S. No.	CROSSES	Significant Traits for SCA
16.	SKAU-T-1009 × SKAU-T-9862	Fruit length (cm), fruit diameter (cm), pericarp thickness (mm), number of primary branches plant ⁻¹ , plant height (cm), number of fruits plant ⁻¹ , average fruit weight (g), fruit yield plant ⁻¹ (kg), fruit yield hectare ⁻¹ (q), average number of seeds fruit ⁻¹ and 100 seed weight (g)
17.	SKAU-T-9801 × SKAU-T-0922	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant ⁻¹ , fruit length (cm), fruit diameter (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg) and fruit yield hectare ⁻¹ (q).
18.	SKAU-T-9801 × SKAU-T-1009	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, number of locules fruit ⁻¹ , pericarp thickness (mm), number of primary branches plant ⁻¹ and average number of seeds fruit ⁻¹
19.	SKAU-T-1700 × SKAU-T-1424	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of fruits plant ⁻¹ , fruit length (cm), average fruit weight (g), fruit yield plant ⁻¹ (kg) and fruit yield hectare ⁻¹ (q).
20.	SKAU-T-0922 × SKAU-T-1429	Number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster ⁻¹ , number of fruits cluster ⁻¹ , number of pickings, fruit diameter (cm), pericarp thickness (mm), plant height (cm) and average number of seeds fruit ⁻¹

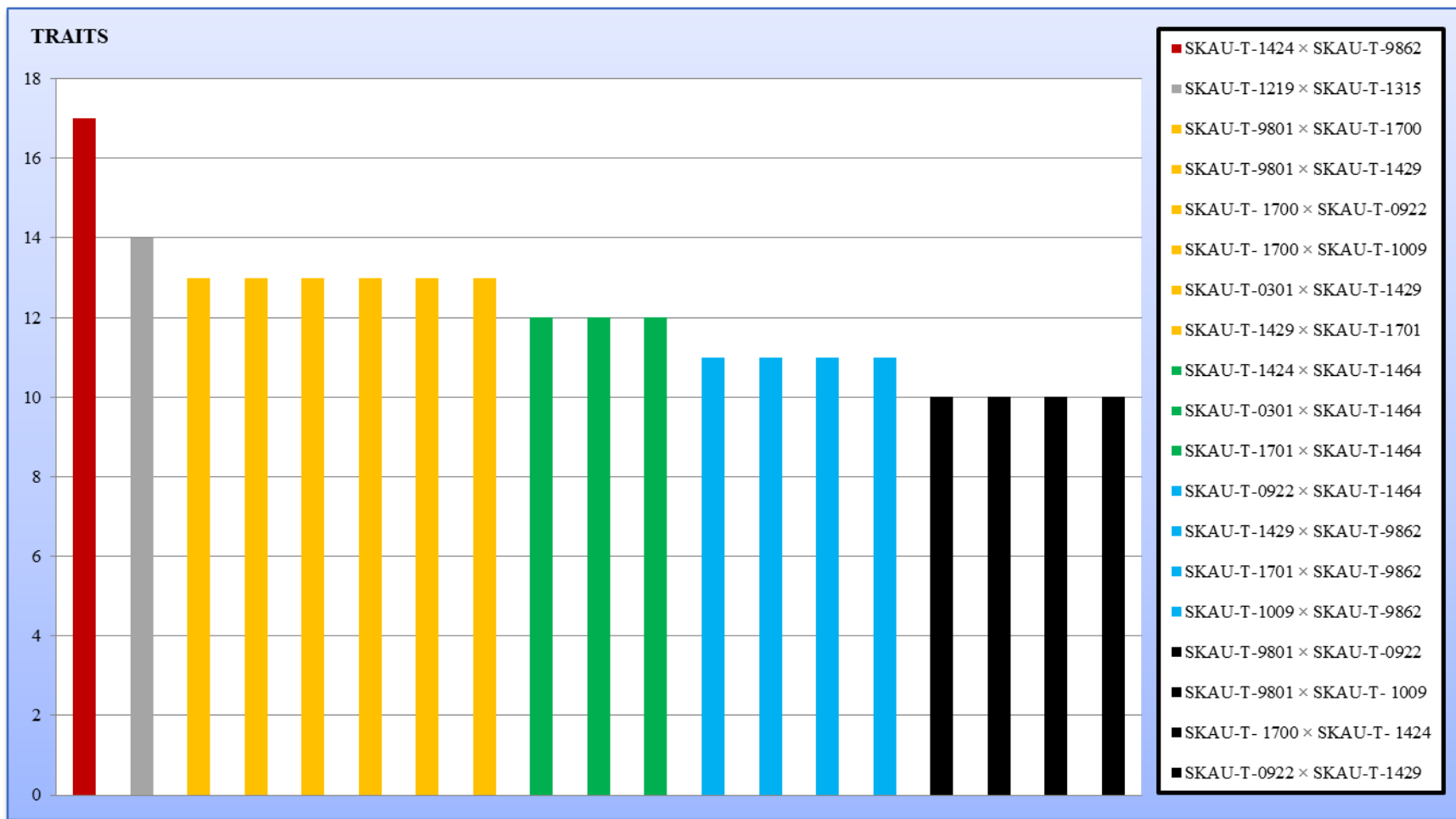


Fig. 2: Best crosses in respect of SCA effects for maximum quantitative traits in tomato

Table 7: Best parents and crosses identified with respect to maximum significant GCA and SCA for maturity, yield and yield attributing traits in tomato (*Solanum lycopersicum* L.)

Traits	Parents with significant GCA	Crosses with significant SCA
Number of days to first flowering	SKAU-T-1219 (-0.611) SKAU-T -0301 (-0.584) SKAU-T -1424 (-0.417) SKAU-T -1700 (0.297) SKAU-T-1009 (-0.270)	SKAU-T-1700 × SKAU-T-9862 (-6.503) SKAU-T-1700 × SKAU-T-1009 (-3.593) SKAU-T -1701 × SKAU-T-9862 (-3.042) SKAU-T-1009 × SKAU-T-1464 (-2.983) SKAU-T-1219 × SKAU-T-1009 (-2.579) SKAU-T-1429 × SKAU-T-1464 (-2.422)
Number of days to first fruit set	SKAU-T-1424 (-1.457) SKAU-T-1700 (-0.967) SKAU-T-9801 (-0.917) SKAU-T-0301 (-0.568) SKAU-T-1219 (-0.515)	SKAU-T-1700 × SKAU-T-9862 (-4.890) SKAU-T-1700 × SKAU-T-1009 (-4.794) SKAU-T-9801 × SKAU-T-9862 (-4.704) SKAU-T-1429 × SKAU-T-1701 (-4.139) SKAU-T -1701 × SKAU-T-9862 (-3.727) SKAU-T-1700 × SKAU-T-0922 (-3.592)
Number of days to first fruit harvest	SKAU-T-1429 (-2.081) SKAU-T-1219 (-1.515) SKAU-T-1700 (1.179) SKAU-T-9801 (-1.152) SKAU-T-1424 (-1.391)	SKAU-T-1219 × SKAU-T-1429 (-13.751) SKAU-T-1315 × SKAU-T-1009 (-10.278) SKAU-T-1424 × SKAU-T-1219 (-7.287) SKAU-T-9801 × SKAU-T-1009 (-6.294) SKAU-T-1424 × SKAU-T-1315 (-6.016) SKAU-T- 0301 × SKAU-T-1429 (-5.897)
Number of flowers cluster ⁻¹	SKAU-T-1424 (0.247) SKAU-T-9801(0.228) SKAU-T-1219 (0.224) SKAU-T-0922 (0.211) SKAU-T-0301(0.204)	SKAU-T-1429 × SKAU-T-9862 (1.823) SKAU-T -9801 × SKAU-T-1315 (1.462) SKAU-T -1700 × SKAU-T-0301 (1.427) SKAU-T -9801× SKAU-T-1701 (1.193) SKAU-T -1315 × SKAU-T-1429 (1.089) SKAU-T-1701 × SKAU-T-1464 (0.987) SKAU-T-1315 × SKAU-T-1009 (0.955) SKAU-T-1429 × SKAU-T-9862 (0.832)
Number of fruits cluster ⁻¹	SKAU-T-0922 (0.304) SKAU-T-1219 (0.202) SKAU-T-0301(0.189) SKAU-T-1701 (0.174) SKAU-T-1424 (0.167) SKAU-T-1464 (0.108)	SKAU-T -9801 × SKAU-T-1701 (0.778) SKAU-T -1700 × SKAU-T-1701 (0.767) SKAU-T -1700 × SKAU-T-0301 (0.734) SKAU-T -1315 × SKAU-T-1429 (0.715) SKAU-T -1700 × SKAU-T-0922 (0.711) SKAU-T -9801 × SKAU-T-1315 (0.697)
Number of pickings	SKAU-T-9801(1.258) SKAU-T-1700 (0.650) SKAU-T-0922 (0.624) SKAU-T-1701 (0.560) SKAU-T-1219 (0.448)	SKAU-T-1424 × SKAU-T-9862 (4.748) SKAU-T-1424 × SKAU-T-1464 (3.567) SKAU-T-0301 × SKAU-T-1429 (3.518) SKAU-T-1700 × SKAU-T-1009 (3.060) SKAU-T-1219 × SKAU-T-1315 (2.625)
Number of fruits plant ⁻¹	SKAU-T-1429 (3.762) SKAU-T-1701 (2.398) SKAU-T-9801 (2.367) SKAU-T-0922 (2.312) SKAU-T-1700 (2.178)	SKAU-T-1424 × SKAU-T-1464 (11.039) SKAU-T-9801 × SKAU-T-1219 (8.593) SKAU-T-1701 × SKAU-T-1009 (7.603) SKAU-T-1219 × SKAU-T-0301 (7.588) SKAU-T-0301 × SKAU-T-1464 (7.295)
Fruit length (cm)	SKAU-T-9801 (0.553) SKAU-T-9862 (0.191) SKAU-T-1700 (0.176) SKAU-T-0922 (0.149) SKAU-T-1429 (0.142) SKAU-T-1009 (0.126)	SKAU-T-1424 × SKAU-T-9862 (1.464) SKAU-T-0301 × SKAU-T-1429 (1.143) SKAU-T-1009 × SKAU-T-9862 (0.834) SKAU-T-1424 × SKAU-T-1464 (0.796) SKAU-T-1700 × SKAU-T-1009 (0.673)

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Table 7: contd....

Traits	Parents with significant GCA	Crosses with significant SCA
Fruit diameter (cm)	SKAU-T-9801 (0.539) SKAU-T-0301 (0.304) SKAU-T-0922 (0.258) SKAU-T-1009 (0.232) SKAU-T-1464 (0.176) SKAU-T-1701 (0.171)	SKAU-T-1424 × SKAU-T-9862 (1.846) SKAU-T-1429 × SKAU-T-1701 (1.491) SKAU-T-0922 × SKAU-T-1429 (1.319) SKAU-T-1009 × SKAU-T-9862 (0.987) SKAU-T-1700 × SKAU-T-1009 (0.863)
Number of locules fruit ⁻¹	SKAU-T-1219 (0.409) SKAU-T-0301 (0.362) SKAU-T-9862 (0.330) SKAU-T-1464 (0.203) SKAU-T-0922 (0.187) SKAU-T-1429 (0.120)	SKAU-T-1700 × SKAU-T-1315 (2.520) SKAU-T-0922 × SKAU-T-9862 (2.293) SKAU-T-1701 × SKAU-T-9862 (1.768) SKAU-T-9801 × SKAU-T-0301 (1.615) SKAU-T-0922 × SKAU-T-1464 (1.208)
Pericarp thickness (mm)	SKAU-T-9801(0.439) SKAU-T-1315 (0.357) SKAU-T-1700 (0.246) SKAU-T-1429 (0.242) SKAU-T-1701 (0.212) SKAU-T-9862 (0.180)	SKAU-T-1429 × SKAU-T-1464 (2.78) SKAU-T-1424 × SKAU-T-9862 (1.692) SKAU-T-9801 × SKAU-T-1219 (1.514) SKAU-T-1009 × SKAU-T-9862 (1.488) SKAU-T-1700 × SKAU-T-1009 (1.395)
Number of primary branches plant ⁻¹	SKAU-T-9801 (0.288) SKAU-T-9862 (0.176) SKAU-T-1315 (0.155) SKAU-T-1464 (0.124) SKAU-T-1219 (0.092)	SKAU-T-1315 × SKAU-T-0301 (1.138) SKAU-T-0922 × SKAU-T-1219 (1.053) SKAU-T-0922 × SKAU-T-1701 (0.991) SKAU-T-1219 × SKAU-T-1429 (0.815) SKAU-T-1700 × SKAU-T-1009 (0.752)
Plant height (cm)	SKAU-T-9801 (7.817) SKAU-T-0301 (7.565) SKAU-T-1219 (4.426) SKAU-T-0922 (1.572) SKAU-T-1464 (1.484) SKAU-T-1009 (1.378)	SKAU-T-1700 × SKAU-T-1009 (54.864) SKAU-T-1219 × SKAU-T-0301 (51.412) SKAU-T-1424 × SKAU-T-9862 (42.128) SKAU-T-1700 × SKAU-T-0922 (35.747) SKAU-T-0922 × SKAU-T-1219 (30.739)
Average fruit weight (g)	SKAU-T-9801 (6.178) SKAU-T-0301 (5.794) SKAU-T-1429 (4.164) SKAU-T-1700 (2.821) SKAU-T-9862 (2.651) SKAU-T-0922 (2.632)	SKAU-T-1315 × SKAU-T-1464 (28.188) SKAU-T-1219 × SKAU-T-1009 (20.419) SKAU-T-0301 × SKAU-T-1701 (19.053) SKAU-T-1424 × SKAU-T-9862 (17.095) SKAU-T-9801 × SKAU-T-1219 (14.560)
Fruit yield plant ⁻¹ (kg)	SKAU-T-9801 (0.255) SKAU-T-0922 (0.187) SKAU-T-1464 (0.183) SKAU-T-1700 (0.174) SKAU-T-1701 (0.145) SKAU-T-9862 (0.120)	SKAU-T-1424 × SKAU-T-1464 (0.837) SKAU-T-9801 × SKAU-T-1219 (0.803) SKAU-T-1429 × SKAU-T-1701 (0.792) SKAU-T-9801 × SKAU-T-1429 (0.689) SKAU-T-1424 × SKAU-T-9862 (0.684)
Fruit yield hectare ⁻¹ (q)	SKAU-T-9801 (94.765) SKAU-T-0922 (68.474) SKAU-T-1700 (64.417) SKAU-T-1701 (54.165) SKAU-T-9862 (43.900)	SKAU-T-1424 × SKAU-T-1464 (306.606) SKAU-T-9801 × SKAU-T-1219 (298.909) SKAU-T-1429 × SKAU-T-1701 (292.860) SKAU-T-9801 × SKAU-T-1429 (254.760) SKAU-T-1424 × SKAU-T-9862 (254.075)

Contd...

Table 7: contd....

Traits	Parents with significant GCA	Crosses with significant SCA
Average number of seeds fruit ⁻¹	SKAU-T-0301(16.506) SKAU-T-9801(9.456) SKAU-T-0922 (9.452) SKAU-T-1464 (5.728) SKAU-T-9862 (1.394)	SKAU-T-1424 × SKAU-T-9862 (136.424) SKAU-T-0301 × SKAU-T-1701 (127.395) SKAU-T-1315 × SKAU-T-1464 (109.868) SKAU-T-0922 × SKAU-T-1219 (107.188) SKAU-T-1009 × SKAU-T-9862 (91.188)
100 seed weight (g)	SKAU-T-1009 (0.280) SKAU-T-1315 (0.200) SKAU-T-1700 (0.170) SKAU-T-0301 (0.170) SKAU-T-1464 (0.160)	SKAU-T-1009 × SKAU-T-1464 (0.168) SKAU-T-1700 × SKAU-T-0922 (0.107) SKAU-T-1701 × SKAU-T-1464 (0.095) SKAU-T-1700 × SKAU-T-1429 (0.084) SKAU-T-9801 × SKAU-T-1424 (0.076)

4.5 Estimation of Components of genetic variation

The estimates of components of genetic variance and their corresponding standard errors for the traits under in E₁, E₂, E₃ and pooled analysis have been presented from Table-8.1 to 8.9. The results are presented as follows:

4.5.1 Number of days to first flowering

The estimates of components of genetic variation indicated that the additive (\hat{D}) as well as dominance (\hat{H}_1 and \hat{H}_2) components were significant in the individual and data pooled over environments revealing the importance of both additive and dominance components for this trait. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. The estimates of net dominance effect over all loci in a heterozygote (\hat{h}^2) were positive but non-significant indicated absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance for this traits. The \hat{F} values were significant in all individual environments as well as in pooled analysis depicting higher frequency of dominant alleles. The environmental component of variance (\hat{E}) was positive but non-significant in both individual and pooled environments indicating that the environment plays less role in the expression of this trait.

4.5.2 Number of days to first fruit set

Additive (\hat{D}) as well as dominance components (\hat{H}_1 and \hat{H}_2) were found significant in all environments and in pooled analysis for this trait. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. Positive and significant estimates of (\hat{h}^2) in E₁, E₂, E₃ and pooled analysis indicated presence of significantly high dominance effect in heterozygote over all loci and presence

of directional dominance for this trait but positive direction of dominance. The (\hat{F}) values were significant in all individual environments as well as in pooled analysis depicting higher frequency of dominant alleles. The environmental component of variance (\hat{E}) was positive but non- significant in both individual and pooled environments indicating that the environment plays less role in the expression of this trait.

4.5.3 Number of days to first fruit harvest

Additive (\hat{D}) as well as dominance components (\hat{H}_1 and \hat{H}_2) were found significant in all environments and in pooled analysis for this trait. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. Positive and non-significant estimates of (\hat{h}^2) in E₁, E₂, E₃ and pooled analysis indicated absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The (\hat{F}) values were significant in all individual environments as well as in pooled analysis depicting higher frequency of dominant alleles. The environmental component of variance (\hat{E}) was positive but non-significant in both individual and pooled environments indicating that the environment plays less role in the expression of this trait.

4.5.4 Number of flowers cluster⁻¹

The significant values of additive (\hat{D}) in pooled data and dominance (\hat{H}_1 and \hat{H}_2) components in all environments suggested the equal importance of both additive and dominance components for the expression of this trait with preponderance of dominance component over additive component. Estimates of (\hat{h}^2) was positive but non-significant in all environments indicating absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The (\hat{F}) values were positive but non- significant

indicating that the direction of dominant and recessive alleles was equally distributed in the parents in all environments and also in pooled analysis. The environmental component of variance (\hat{E}) was significant in E₁, E₂ and E₃ environments and non-significant in pooled environment depicted that environment plays some role in expression of this trait in individual environments.

4.5.5 Number of fruits cluster⁻¹

The significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components suggested the equal importance of both additive and dominance components for the expression of this trait with preponderance of dominance component over additive component. Estimate of (\hat{h}^2) was positive but non-significant in all environments indicated absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The (\hat{F}) values were positive but non-significant indicating that the direction of dominant and recessive alleles was equally distributed in the parents in all environments and also in pooled analysis. The environmental component of variance (\hat{E}) was positive but non-significant in both individual and pooled environments indicating that the environment plays less role in the expression of this trait.

4.5.6 Number of pickings

The significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components suggested the equal importance of both additive and dominance components for the expression of this trait with preponderance of dominance component over additive component. Estimate of (\hat{h}^2) was non-significant in all environments indicated absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance for this traits. The positive and significant value of (\hat{F}) suggested higher frequency of dominant

alleles. The environmental component of variance (\hat{E}) was non-significant indicating that the environment plays less role in the expression of this trait.

4.5.7 Number of fruits plant⁻¹

The significant estimates of additive component (\hat{D}) and dominance components (\hat{H}_1 and \hat{H}_2) suggested equal importance of additive and dominance components for this trait expression. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. The (\hat{h}^2) values were positive and significant indicated presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance for this trait but positive direction of dominance. The positive and significant values of (\hat{F}) indicated more frequency of dominant alleles. Estimates of environmental component of variance (\hat{E}) were non-significant in individual and pooled data indicating that the environment plays less role in the expression of this trait.

4.5.8 Fruit length (cm)

The significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components suggested the equal importance of both additive and dominance components for the expression of this trait with preponderance of dominance component over additive component. Estimate of (\hat{h}^2) was significant in all environments indicated presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance for this trait but positive direction of dominance. The (\hat{F}) values were positive but non-significant indicating that the direction of dominant and recessive alleles was equally distributed in the parents in all environments and also in pooled analysis. The environmental component of variance (\hat{E}) was significant in E₁, E₂, E₃ and pooled

data depicted that environment plays some role in expression of this trait in individual environments.

4.5.9 Fruit diameter (cm)

Significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components indicated the equal importance of additive and dominance components with preponderance of dominance component over additive component. The (\hat{h}^2) values were positive but non-significant suggesting absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The (\hat{F}) values were positive and significant in pooled environment suggested higher frequency of dominant alleles. Estimates of environmental component of variance (\hat{E}) were non-significant in individual and pooled data indicating that the environment plays less role in the expression of this trait.

4.5.10 Number of locules fruit⁻¹

Significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components indicated the equal importance of additive and dominance components with preponderance of dominance component over additive component. The (\hat{h}^2) values were positive but non-significant suggesting absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The (\hat{F}) values were positive but non-significant indicating that the direction of dominant and recessive alleles was equally distributed in the parents in all environments and also in pooled analysis. Estimates of environmental component of variance (\hat{E}) were non-significant in individual and pooled data indicating that the environment plays less role in the expression of this trait.

4.5.11 Pericarp thickness (mm)

Non-significant values of additive (\hat{D}) and significant values of dominance (\hat{H}_1 and \hat{H}_2) components indicated the more importance of dominance component for this trait. The (\hat{h}^2) values were positive but non-significant suggesting absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The (\hat{F}) values were positive but non-significant indicating that the direction of dominant and recessive alleles was equally distributed in the parents in all environments and also in pooled analysis. The environmental component of variance (\hat{E}) was non-significant in both individual and pooled environments indicating that the environment plays less role in the expression of this trait.

4.5.12 Number of primary branches plant⁻¹

The estimates of additive (\hat{D}) as well as dominance (\hat{H}_1 and \hat{H}_2) components over all environments revealed the significant importance of both components with preponderance of dominance component in individual and pooled analysis. Moreover, higher magnitude of dominance component as compared to their corresponding additive component indicated the greater role of dominance component. Non-significant and positive value of (\hat{h}^2) indicated absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The positive and non-significant value of (\hat{F}) indicating that the direction of dominant and recessive alleles was equally distributed in the parents in all environments and also in pooled analysis. Estimates of environmental component of variance (\hat{E}) were non-significant in individual and pooled data indicating that the environment plays less role in the expression of this trait.

4.5.13 Plant height (cm)

The significant estimates of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components in the individual and pooled analysis revealed the equal importance of both additive and dominance components in the inheritance of this trait. Moreover, higher magnitude of dominance component as compared to their corresponding additive component indicated the greater role of dominance component. The estimates of (\hat{h}^2) were positive and non-significant depicting absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The values of (\hat{F}) is positive but non-significant indicating that the direction of dominant and recessive alleles was equally distributed in the parents in all environments and also in pooled analysis. The environmental component of variance (\hat{E}) was non-significant in individual and pooled data indicating that the environment plays less role in the expression of this trait.

4.5.14 Average fruit weight (g)

The estimates of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components were all significant indicating the equal importance of both these components in the inheritance of this trait. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. The (\hat{h}^2) values were positive and significant for all environments and pooled analysis indicated presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance for this trait but positive direction of dominance. The (\hat{F}) values were positive and significant suggesting more frequency of dominant alleles. The environmental component of variance (\hat{E}) was non-significant in individual and pooled data indicating environment plays less role in the expression of this trait.

4.5.15 Fruit yield plant⁻¹ (kg)

For this trait, the additive components (\hat{D}) and the dominance components (\hat{H}_1 and \hat{H}_2) were found to be significant, thereby suggesting equal importance of additive and dominance components. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. The (\hat{h}^2) values were positive and significant indicated presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance for this trait but positive direction of dominance. The (\hat{F}) values were positive and significant suggesting more frequency of dominant alleles. Estimates of environmental component of variance (\hat{E}) were non-significant in individual and pooled data indicating environment plays less role in the expression of this trait.

4.5.16 Fruit yield hectare⁻¹ (q)

The additive (\hat{D}) and dominance components (\hat{H}_1 and \hat{H}_2) were found to be significant, thereby suggesting equal importance of additive and dominance components for this trait. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. The (\hat{h}^2) values were positive and significant indicated presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance for this trait but positive direction of dominance. The (\hat{F}) values were positive and significant suggesting more frequency of dominant alleles. Estimates of environmental component of variance (\hat{E}) were non-significant in individual and pooled data indicating environment plays less role in the expression of this trait.

4.5.17 Average number of seeds fruit⁻¹

Significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components indicated the equal importance of additive and dominance components. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. The (\hat{h}^2) values were positive and significant indicated presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance for this trait but positive direction of dominance. The values of (\hat{F}) being positive but non-significant in E₁, E₂, E₃ and pooled analysis depicting the equal proportion of frequency of dominant and recessive alleles in the parental genotypes. The environmental component of variance (\hat{E}) was non-significant in individual and pooled data indicating environment plays less role in the expression of this trait.

4.5.18 100 seed weight

Positive and significant values of additive (\hat{D}) and dominance (\hat{H}_1 and \hat{H}_2) components indicated the more importance of dominance component than additive. The magnitude of dominance component was found to be higher than corresponding additive component indicating the greater role of dominance component. The (\hat{h}^2) estimates were positive and non-significant depicting absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance. The values of (\hat{F}) being positive but non-significant in E₁, E₂, E₃ and pooled analysis indicated the equal proportion of frequency of dominant and recessive alleles in the parental genotypes. The environmental component of variance (\hat{E}) was non-significant in individual and pooled data indicating environment plays less role in the expression of this trait.

Table 8.1: Estimates of components of genetic variation for number of days to first flowering and number of days to first fruit set in in tomato. (Based on individual and pooled over environments)

Components	Number of days to first flowering				Number of days to first fruit set			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	4.09* ±1.31	3.98* ±1.37	3.70* ±1.38	3.75* ±1.37	8.69* ±1.89	8.74* ±1.88	8.55* ±1.79	8.71* ±1.84
\hat{H}_1	17.21* ±2.62	16.93* ±2.73	16.60* ±2.75	16.37* ±2.74	26.79* ±3.78	26.57* ±3.77	26.65* ±3.57	36.67* ±3.68
\hat{H}_2	13.76* ±2.18	13.61* ±2.27	13.41* ±2.29	13.17* ±2.28	22.65* ±3.15	22.47* ±3.14	22.56* ±2.97	22.54* ±3.06
\hat{h}^2	1.74 ±1.46	1.75 ±1.52	1.39 ±1.53	1.57 ±1.52	4.84* ±2.10	4.88* ±2.09	4.55* ±1.99	4.78* ±2.05
\hat{F}	6.92* ±2.97	6.68* ±3.09	6.21* ±3.12	6.33* ±3.11	9.69* ±4.29	9.65* ±4.28	9.58* ±4.05	9.72* ±4.17
\hat{E}	0.24 ±0.36	0.33 ±0.38	0.38 ±0.38	0.46 ±0.38	0.39 ±0.52	0.42 ±0.52	0.44 ±0.49	0.40 ±0.51

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.2: Estimates of components of genetic variation for number of days to first fruit harvest and number of flowers cluster⁻¹ in tomato. (Based on individual and pooled over environments)

Components	Number of days to first fruit harvest				Number of flowers cluster ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	6.41* ±6.95	6.32* ±6.86	5.83* ±7.54	6.11* ±7.12	0.19* ±0.12	0.15* ±0.12	0.11* ±0.10	0.24* ±0.11
\hat{H}_1	66.35* ±13.91	66.29* ±13.73	68.65* ±15.09	66.82* ±14.25	0.91* ±0.24	0.92* ±0.24	0.72* ±0.20	1.11* ±0.22
\hat{H}_2	59.40* ±11.57	59.41* ±11.42	62.10* ±12.55	60.09* ±11.85	0.88* ±0.20	0.89* ±0.20	0.70* ±0.17	1.00* ±0.18
\hat{h}^2	11.01 ±7.74	10.32 ±7.64	12.04 ±8.39	11.13 ±7.93	0.04 ±0.13	0.04 ±0.13	0.04 ±0.11	0.01 ±0.12
\hat{F}	6.66* ±15.76	6.50* ±15.55	5.26* ±17.09	6.03* ±16.15	0.13 ±0.27	0.08 ±0.27	0.05 ±0.23	0.24 ±0.25
\hat{E}	0.34 ±1.92	0.37 ±1.90	0.41 ±2.09	0.42 ±1.97	0.13* ±0.03	0.13* ±0.03	0.13* ±0.03	0.03 ±0.03

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.3: Estimates of components of genetic variation for number of fruits cluster⁻¹ and number of pickings in tomato. (Based on individual and pooled over environments)

Components	Number of fruits cluster ⁻¹				Number of pickings			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	0.42* ±0.06	0.35* ±0.06	0.33* ±0.05	0.44* ±0.06	5.62* ±0.97	5.06* ±0.95	5.00* ±0.95	5.23* ±0.95
\hat{H}_1	0.89* ±0.13	0.84* ±0.12	0.74* ±0.10	0.97* ±0.11	144.09* ±1.94	13.34* ±1.90	13.16* ±1.91	13.60* ±1.91
\hat{H}_2	0.85* ±0.11	0.80* ±0.10	0.70* ±0.09	0.89* ±0.09	10.64* ±1.61	10.32* ±1.58	10.13* ±1.59	10.42* ±1.59
\hat{h}^2	0.01 ±0.07	0.01 ±0.07	0.02 ±0.06	0.00 ±0.06	0.03 ±1.08	0.02 ±1.06	0.02 ±1.06	0.05 ±1.06
\hat{F}	0.04 ±0.15	0.05 ±0.14	0.01 ±0.12	0.13 ±0.13	8.26* ±2.20	7.28* ±2.25	7.23* ±2.16	7.61* ±2.16
\hat{E}	0.07 ±0.02	0.05 ±0.02	0.04 ±0.01	0.08 ±0.01	0.04 ±0.27	0.04 ±0.26	0.05 ±0.26	0.02 ±0.26

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.4: Estimates of components of genetic variation for Number of fruits plant⁻¹ and fruit length in tomato. (Based on individual and pooled over environments)

Components	Number of fruits plant ⁻¹				Fruit length (cm)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	61.49* ±14.28	61.49* ±13.62	63.25* ±13.66	62.04* ±13.83	0.22 ±0.12	0.24* ±0.11	0.21* ±0.10	0.30* ±0.11
\hat{H}_1	188.17* ±28.57	187.84* ±27.25	192.40* ±27.34	189.28* ±27.67	1.03* ±0.24	1.03* ±0.23	0.96* 0.21	1.24* ±0.22
\hat{H}_2	147.27* ±23.76	146.67* ±22.67	149.17* ±22.74	147.56* ±23.01	0.94* ±0.20	0.93* ±0.19	0.87* ±0.17	1.08* ±0.18
\hat{h}^2	0.91* ±15.89	0.66* ±15.15	0.61* ±15.20	0.78* ±15.39	0.20* ±0.13	0.20* ±0.13	0.24* ±0.12	0.30* ±0.12
\hat{F}	88.81* ±32.36	89.20* ±30.87	92.99* ±30.97	90.28* ±31.34	0.17 ±0.27	0.17 ±0.26	0.15 ±0.24	0.29 ±0.25
\hat{E}	0.48 ±3.96	0.53 ±3.78	0.55 ±3.79	0.44 ±3.83	0.09* ±0.03	0.09* ±0.03	0.09* ±0.03	0.10* ±0.03

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.5: Estimates of components of genetic variation for fruit diameter and number of locules fruit⁻¹ in tomato. (Based on individual and pooled over environments)

Components	Fruit diameter (cm)				Number of locules fruit ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	0.53* ±0.18	0.51* ±0.17	0.49* ±0.16	0.65* ±0.17	0.58* ±0.25	0.48* ±0.23	0.45* ±0.20	0.55* ±0.22
\hat{H}_1	1.59* ±0.36	1.53* ±0.35	1.49* ±0.33	1.94* ±0.34	2.96* ±0.50	2.74* ±0.45	2.59* ±0.39	2.94* ±0.45
\hat{H}_2	1.20* ±0.30	1.17* ±0.29	1.13* ±0.27	1.45* ±0.28	2.30* ±0.42	2.22* ±0.38	2.11* ±0.33	2.35* ±0.37
\hat{h}^2	0.02 ±0.20	0.03 ±0.19	0.03 ±0.18	0.07 ±0.19	0.12 ±0.28	0.17 ±0.25	0.11 ±0.23	0.16 ±0.25
\hat{F}	0.74 ±0.41	0.69 ±0.39	0.67 ±0.37	0.93* ±0.39	1.02 ±0.57	0.78 ±0.51	0.72 ±0.45	0.91 ±0.51
\hat{E}	0.16 ±0.05	0.15 ±0.04	0.15 ±0.04	0.17 ±0.05	0.07 ±0.07	0.07 ±0.06	0.07 ±0.05	0.004 ±0.06

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.6: Estimates of components of genetic variation for pericarp thickness and number of primary branches plant⁻¹ in tomato. (Based on individual and pooled over environments)

Components	Pericarp thickness				Number of primary branches plant ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	0.16 ±0.28	0.16 ±0.27	0.15 ±0.28	0.21 ±0.28	0.18 ±0.11	0.17 ±0.10	0.16 ±0.09	0.22* ±0.09
\hat{H}_1	3.21* ±0.56	3.09* ±0.55	3.12* ±0.55	3.28* ±0.57	1.05* ±0.21	1.02* ±0.19	1.01* ±0.18	1.16* ±0.20
\hat{H}_2	2.62* ±0.46	2.52* ±0.46	2.54* ±0.46	2.67* ±0.47	0.81* ±0.18	0.81* ±0.16	0.82* ±0.15	0.90* ±0.16
\hat{h}^2	0.09 ±0.31	0.09 ±0.30	0.12 ±0.31	0.11 ±0.31	0.01 ±0.12	0.01 ±0.11	0.01 ±0.10	0.003 ±0.11
\hat{F}	0.42 ±0.63	0.42 ±0.62	0.43 ±0.63	0.50 ±0.64	0.38 ±0.24	0.33 ±0.22	0.32 ±0.21	0.43 ±0.22
\hat{E}	0.05 ±0.08	0.05 ±0.08	0.06 ±0.08	0.07 ±0.08	0.05 ±0.03	0.05 ±0.03	0.05 ±0.02	0.04 ±0.03

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.7: Estimates of components of genetic variation for plant height and average fruit weight in tomato. (Based on individual and pooled over environments)

Components	Plant height (cm)				Average fruit weight (g)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	428.12* ±163.64	433.99* ±160.38	418.47* ±156.95	424.65* ±160.34	137.53* ±29.10	134.04* ±28.60	137.44* ±28.82	135.20* ±28.51
\hat{H}_1	1434.04* ±327.37	1396.64* ±320.84	1373.56* ±313.98	1403.86* ±320.77	495.09* ±58.21	500.94* ±57.22	502.11* ±57.66	505.77* ±57.04
\hat{H}_2	1178.16* ±272.32	1148.84* ±266.88	1138.35* ±261.17	1156.63* ±266.83	413.18* ±48.42	422.31* ±47.60	421.43* ±47.96	425.31* ±47.45
\hat{h}^2	0.58 ±182.07	0.10 ±178.44	0.54 ±174.62	0.48 ±178.40	3.16* ±32.37	3.08* ±31.83	3.33* ±32.07	3.68* ±31.72
\hat{F}	411.79 ±370.89	398.06 ±363.49	379.49 ±355.71	398.45 ±363.41	182.15* ±65.94	175.96* 64.83	181.26* ±65.32	178.09* ±64.62
\hat{E}	1.95 ±45.39	1.70 ±44.48	1.75 ±43.53	0.90 ±44.47	2.00 ±8.06	0.85 ±7.93	0.82 ±7.99	0.51 ±7.91

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.8: Estimates of components of genetic variation for fruit yield plant⁻¹ and fruit yield hectare⁻¹ in tomato. (Based on individual and pooled over environments)

Components	Fruit yield plant ⁻¹ (kg)				Fruit yield hectare ⁻¹ (q)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	0.37* ±0.06	0.32* ±0.05	0.31* ±0.05	0.33* ±0.48	50017.29* ±7390.98	44155.14* ±6471.17	42596.86* ±6318.94	44906.56** ±6638.83
\hat{H}_1	0.98* ±0.10	1.00* ±0.09	0.96* ±0.09	1.00* ±0.10	150167.60* ±14785.73	135329.80* ±12945.80	132079.10* ±12641.25	138847.30* ±13281.21
\hat{H}_2	0.80* ±0.08	0.83* ±0.08	0.79* ±0.08	0.83* ±0.08	123005.60* ±12299.18	110140.30* ±10768.68	108062.80* ±10515.35	114088.90* ±11047.69
\hat{h}^2	0.003* ±0.06	0.002* ±0.05	0.001* ±0.05	0.001* ±0.05	352.99* ±8223.34	120.65* ±7200.03	215.55* ±7030.66	259.86* ±7386.58
\hat{F}	0.48* ±0.12	0.45* ±0.10	0.44* ±0.10	0.46* ±0.11	69702.63* ±16751.01	62728.10* ±14666.52	60212.78* ±14321.50	62928.87* ±15046.52
\hat{E}	0.004 ±0.03	0.002 ±0.01	0.002 ±0.01	0.002 ±0.01	318.10 ±2049.86	550.07 ±1794.78	272.87 ±1752.56	346.60 ±1841.28

*, ** Significant at 5 and 1 per cent levels, respectively

Table 8.9: Estimates of components of genetic variation for average number of seeds fruit⁻¹ and 100 seed weight in tomato. (Based on individual and pooled over environments)

Components	Average number of seeds fruit ⁻¹				100 seed weight			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	1114.95* ±639.60	1119.62* ±640.34	1111.60* ±629.50	1117.48* ±636.53	0.02 ±0.01	0.04 ±0.02	0.06 ±0.03	0.08 ±0.04
\hat{H}_1	9177.62* ±1279.53	9168.87* ±1281.02	9108.41* ±1259.33	9156.84* ±1273.40	0.01* ±0.03	0.03* ±0.03	0.04* ±0.04	0.06* ±0.04
\hat{H}_2	8242.14* ±1064.32	8230.73* ±1065.59	8183.75* ±1047.55	8222.55* ±1059.25	0.01* ±0.02	0.09* ±0.02	0.08* ±0.04	0.10* ±0.03
\hat{h}^2	1862.34* ±711.63	1832.09* ±712.46	1872.06* ±700.40	1856.13* ±708.22	0.03 ±0.02	0.04 ±0.02	0.04 ±0.03	0.06 ±0.04
\hat{F}	1361.19 ±1449.61	1376.52 ±1451.30	1354.91 ±1426.72	1367.55 ±1442.65	0.03 ±0.03	0.03 ±0.02	0.05 ±0.03	0.06 ±0.03
\hat{E}	2.81 ±177.39	2.67 ±177.60	2.70 ±174.59	0.94 ±176.54	0.002 ±0.004	0.004 ±0.004	0.005 ±0.003	0.006 ±0.004

*, ** Significant at 5 and 1 per cent levels, respectively

4.6 Proportion of genetic components of variation

Table 9.1 to 9.9 represents the proportion of genetic components of variation along with the estimates of average degree of dominance and heritability in narrow sense. The results are presented as follows:

4.6.1 Number of days to first flowering

Average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ was greater than unity in individual and pooled analysis indicating over dominance in the expression of the trait. $\frac{\hat{H}_2}{4\hat{H}_1}$ giving the measure of proportion of genes with positive and negative effects, was less than 0.25 revealing asymmetrical distribution of genes for this trait in parents. The proportion of dominant and recessive alleles $\frac{KD}{KR}$ was more than unity in all environments and in pooled analysis suggesting the excess of dominant alleles in the parents. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting less proportion of dominant gene groups. Estimates of heritability (n.s) were 10, 8, 8 and 10 percent in E₁, E₂, E₃ and pooled analysis respectively.

Non-allelic interaction was present for this trait that was depicted by significant deviation of regression coefficient from unity but was not confirmed by non-significant deviation of regression coefficient from zero and t^2 values in E₁, E₂ and E₃ as well as in pooled analysis.

4.6.2 Number of days to first fruit set

The values of average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ being greater than unity indicated over dominance in the trait expression. The estimate of $\frac{\hat{H}_2}{4\hat{H}_1}$ was less

than 0.25 in individual and pooled analysis revealing asymmetrical distribution of genes in the parents. The value of $\frac{KD}{KR}$ being greater than unity, revealed excess of dominant genes or gene groups as compared to recessive ones in parents in all the environments and pooled analysis. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting less proportion of dominance gene groups. The estimates of heritability (n.s) were 21 percent in E₁ and E₂ ; 20 per cent in E₃ and pooled data.

Non-allelic interaction was present for this trait that was depicted by significant deviation of regression coefficient from unity but was not confirmed by deviation of regression coefficient from zero and t² values in E₁, E₂ and E₃ as well as in pooled analysis.

4.6.3 `Number of days to first fruit harvest

The average degree of dominance $[\frac{\hat{H}_1}{D}]^{1/2}$ was more than unity in all environments and in pooled analysis thereby indicating over dominance. The asymmetrical distribution of genes in the parents was confirmed as the ratio $\frac{\hat{H}_2}{4\hat{H}_1}$ was less than 0.25. The value of $\frac{KD}{KR}$ was found to be more than unity depicting the presence of more dominant genes than recessive genes for this trait. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting less proportion of dominance gene groups. The estimates of heritability (n.s) found to be 18 percent in E₁, E₂, E₃ and pooled analysis.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.4 Number of flowers cluster⁻¹

Over dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ greater than unity, asymmetrical distribution of genes ($\frac{\hat{H}_2}{4\hat{H}_1}$ lesser than 0.25 and excess of dominant genes $\frac{KD}{KR}$ greater than unity) were detected for this trait in all environments and in pooled analysis. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. Heritability (n.s) estimates for E₁, E₂, E₃ and pooled data were 10, 11, 11, 15 per cent respectively.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.5 Number of fruits cluster⁻¹

Over dominance ($[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ greater than unity), asymmetrical distribution of genes ($\frac{\hat{H}_2}{4\hat{H}_1}$ lesser than 0.25) and excess of dominant genes ($\frac{KD}{KR}$ greater than unity) were detected for this trait in all environments and in pooled analysis. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. Heritability (n.s) estimates for E₁, E₂, E₃ and pooled data were 8, 8, 11 and 12 per cent respectively.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.6 Number of pickings

Over dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ greater than unity, asymmetrical distribution of genes $\frac{\hat{H}_2}{4\hat{H}_1}$ lesser than 0.25 and excess of dominant genes $\frac{KD}{KR}$ greater than unity were detected for this trait in all environments and in pooled analysis. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. Heritability (n.s) estimates for E₁, E₂, E₃ and pooled data were found to be 13 percent.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.7 Number of fruits plant⁻¹

Over dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ greater than unity, asymmetrical distribution of genes $\frac{\hat{H}_2}{4\hat{H}_1}$ lesser than 0.25 and excess of dominant genes $\frac{KD}{KR}$ greater than unity were detected for this trait in all environments and in pooled analysis. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominant gene groups. Heritability (n.s) estimates for E₁, E₂, E₃ and pooled data were 15, 14, 15 and 15 per cent respectively.

Presence of non-allelic interaction for this trait was depicted by significant deviation of regression coefficient from unity along with values of t² but was not confirmed by deviation of regression coefficient from zero in E₁, E₂, E₃ and pooled analysis.

4.6.8 Fruit length (cm)

Average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ was found to be greater than unity in all environments indicating the presence of over dominance. The ratio $\frac{\hat{H}_2}{4\hat{H}_1}$ was less than 0.25 suggesting asymmetrical distribution of genes in parents. Greater than unity value of $\frac{KD}{KR}$ ratio indicated the presence of more dominant genes than recessive ones in this trait. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. The estimates of heritability (n.s) were 18, 21, 20 and 24 for E₁, E₂, E₃ and pooled data respectively.

Presence of non-allelic interaction for this trait was depicted by significant deviation of regression coefficient from unity along with values of t^2 but was not confirmed by deviation of regression coefficient from zero in E₁, E₂, E₃ and pooled analysis.

4.6.9 Fruit diameter (cm)

Over dominance was revealed by greater than unity values of average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$. Less than 0.25 values of $\frac{\hat{H}_2}{4\hat{H}_1}$ in all environments in pooled analysis suggested asymmetrical distribution of genes in the parents. More than unity values of $\frac{KD}{KR}$ ratio indicated excess of dominant alleles as compared to recessive ones. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominant gene groups. The estimates of heritability (n.s) were 17, 18, 17 and 22 per cent in E₁, E₂, E₃ and pooled analysis.

The significant deviation of regression coefficient from unity revealed the presence of non-allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.10 Number of locules fruit⁻¹

Average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ was found to be greater than unity in all environments indicating the presence of over dominance. The ratio $\frac{\hat{H}_2}{4\hat{H}_1}$ was less than 0.25 suggesting asymmetrical distribution of genes in parents. Greater than unity value of $\frac{KD}{KR}$ ratio indicated the presence of more dominant genes than recessive ones in this trait. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups and the estimates of heritability (n.s) were 14, 15, 14 and 16 for E₁, E₂, E₃ and pooled data respectively.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.11 Pericarp thickness

Over dominance was revealed by greater than unity values of average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$. Less than 0.25 values of $\frac{\hat{H}_2}{4\hat{H}_1}$ in all environments in pooled analysis suggested asymmetrical distribution of genes in the parents. More than unity values of $\frac{KD}{KR}$ ratio indicated excess of dominant alleles as compared to recessive ones. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of

dominance gene groups. The estimates of heritability (n.s) were 19, 18, 17 and 19 per cent in E₁, E₂, E₃ and pooled analysis.

Non-allelic interaction for this trait was indicated by significant deviation of regression coefficient from unity and significant deviation of regression coefficient from zero in E₁, E₂, E₃ and pooled analysis that was further confirmed by significant values of t^2 .

4.6.12 Number of primary branches plant⁻¹

Over dominance was revealed by greater than unity values of average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$. Asymmetrical distribution of genes $\frac{\hat{H}_2}{4\hat{H}_1}$ lesser than 0.25 and excess of dominant genes $\frac{KD}{KR}$ greater than unity were detected for this trait in all environments and in pooled analysis. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. Heritability (n.s) estimates for E₁, E₂, E₃ and pooled data were 7, 9, 6 and 9 per cent respectively.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t^2 values.

4.6.13 Plant height (cm)

The average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ was greater than unity depicting over dominance. The $\frac{\hat{H}_2}{4\hat{H}_1}$ estimates being less than 0.25 indicated asymmetrical distribution of genes in the parents. $\frac{KD}{KR}$ estimates were greater than unity revealing excess of dominant genes as compared to recessive genes. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis,

depicting very less proportion of dominance gene groups. The narrow sense heritability estimates were 11 per cent for E₁, E₂, E₃ and pooled analysis.

The significant deviation of regression coefficient from unity along with significant values of t^2 indicated presence of non-allelic interaction in E₁, E₂, E₃ and pooled analysis, which was not confirmed by deviation of regression coefficient from zero.

4.6.14 Average fruit weight (g)

The value of $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ ratio was greater than unity indicating the presence of over dominance in individual and in pooled data. The value of $\frac{\hat{H}_2}{4\hat{H}_1}$ ratio was less than 0.25, indicating asymmetrical distribution of genes in the parents. $\frac{KD}{KR}$ ratio was more than unity suggesting preponderance of dominant alleles as compared to recessive ones. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. The heritability (n.s) estimates were 15, 15, 14 and 15 per cent in E₁, E₂, E₃ and pooled analysis respectively.

Presence of non-allelic interaction for this trait was confirmed by significant deviation of regression coefficient from unity but non-significant deviation of regression coefficient from zero and t^2 values in E₁, E₂, E₃ and pooled analysis depicted absence of epistasis.

4.6.15 Fruit yield plant⁻¹ (kg)

Average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ was found to be greater than unity in all environments indicating the presence of over dominance. $\frac{\hat{H}_2}{4\hat{H}_1}$ value was less than 0.25 indicating asymmetrical distribution of genes in the parents. $\frac{KD}{KR}$ ratio was

more than unity indicated more prevalence of dominant genes than recessive ones. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. The heritability (n.s) estimates for E₁, E₂, E₃ and pooled analysis were 9, 11, 10 and 11 per cent respectively.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.16 Fruit yield hectare⁻¹ (q)

Average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ was found to be greater than unity in all environments indicating the presence of over dominance. $\frac{\hat{H}_2}{4\hat{H}_1}$ value was less than 0.25 indicating asymmetrical distribution of genes in the parents. $\frac{KD}{KR}$ ratio was more than unity indicated more prevalence of dominant genes than recessive ones. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. The heritability (n.s) estimates for E₁, E₂, E₃ and pooled analysis were 11, 10, 10 and 10 per cent respectively.

The significant deviation of regression coefficient from unity revealed the presence of non- allelic interaction in E₁, E₂, E₃ and pooled analysis which was not confirmed by deviation of regression coefficient from zero and t² values.

4.6.17 Average number of seeds fruit⁻¹

Average degree of dominance $[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$ was found to be greater than unity in all environments indicating the presence of over dominance. $\frac{\hat{H}_2}{4\hat{H}_1}$ values were

found to be less than 0.25 in all the environments and pooled analysis indicating asymmetrical distribution of genes in the parents. $\frac{KD}{KR}$ values were more than unity in magnitude in all the environments and pooled analysis revealing greater role of dominance genes. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. Heritability (ns) values were 14, 13, 14 and 14 per cent in E₁, E₂, E₃ and pooled analysis respectively.

The presence of non-allelic interaction was confirmed by significant deviation of regression coefficient from unity along with the significant values of t^2 but was not confirmed by deviation of regression coefficient from zero in individual environments and pooled analysis.

4.6.18 100 Seed Weight

Over dominance was revealed by greater than unity values of average degree of dominance ratio $\frac{\hat{H}_1}{\hat{D}}$. Less than 0.25 values of $\frac{\hat{H}_2}{4\hat{H}_1}$ in all environments in pooled analysis suggested asymmetrical distribution of genes in the parents. More than unity values of $\frac{KD}{KR}$ ratio indicated excess of dominant alleles as compared to recessive ones. The values of $\frac{\hat{h}^2}{\hat{H}_2}$ were found to be positive and less than 0.50 in both individual and pooled data analysis, depicting very less proportion of dominance gene groups. The estimates of heritability (n.s) were 20, 20, 21 and 20 per cent in E₁, E₂, E₃ and pooled analysis.

The presence of non-allelic interaction was confirmed by significant deviation of regression coefficient from unity along with the significant values of t^2 but was not confirmed by deviation of regression coefficient from zero in individual environments and pooled analysis.

Table 9.1: Proportion of genetic components of variation for number of days to first flowering and number of days to first fruit set in tomato. (Based on individual and pooled environment)

Proportion	Number of days to first flowering				Number of days to first fruit set			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	2.05	2.06	2.12	2.09	1.76	1.74	1.76	1.75
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.20	0.20	0.20	0.20	0.21	0.21	0.21	0.21
$\frac{KD}{KR}$	2.40	2.37	2.31	2.35	1.93	1.93	1.93	1.94
$\frac{\hat{h}^2}{\hat{H}_2}$	0.13	0.13	0.10	0.12	0.21	0.22	0.20	0.21
Heritability (n.s)	0.10	0.08	0.08	0.10	0.21	0.21	0.20	0.20
B	0.22 ±0.12	0.21 ±0.13	0.22 ±0.13	0.21 ±0.13	0.50 ±0.18	0.51 ±0.18	0.54 ±0.18	0.52 ±0.18
b-0/SE(b)	-1.78	-1.65	-1.66	-1.53	-2.76	-2.87	-3.07	-2.94
b-1/S.E(b)	6.19*	6.16*	6.03*	5.89*	2.76*	2.74*	2.59*	2.68*
t ²	9.98	9.56	9.12	8.27	1.36	1.39	1.23	1.33

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.2: Proportion of genetic components of variation for number of days to first fruit harvest and number of flowers cluster⁻¹ in tomato. (Based on individual and pooled environment)

Proportion	Number of days to first fruit harvest				Number of flowers cluster ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$\frac{\hat{H}_1}{[\frac{\hat{H}_1}{\hat{D}}]^{1/2}}$	3.22	3.24	3.43	3.31	2.19	2.50	2.57	2.16
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.22	0.22	0.23	0.22	0.24	0.24	0.24	0.23
$\frac{KD}{KR}$	1.39	1.38	1.30	1.35	1.39	1.25	1.19	1.61
$\frac{\hat{h}^2}{\hat{H}_2}$	0.18	0.17	0.19	0.18	0.09	0.10	0.08	0.10
Heritability (n.s)	0.18	0.18	0.18	0.18	0.10	0.11	0.11	0.15
B	0.08 ±0.12	0.08 ±0.12	0.08 ±0.10	0.08 ±0.11	0.15 ±0.27	0.17 ±0.24	0.14 ±0.21	0.13 ±0.24
b-0/SE(b)	-0.69	-0.70	-0.73	-0.69	-0.55	-0.68	-0.66	-0.51
b-1/S.E(b)	7.66*	7.68*	8.78*	8.02*	3.11*	3.43*	4.07*	3.56*
t ²	12.56	12.69	17.68	14.10	0.58	0.81	1.60	0.60

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.3: Proportion of genetic components of variation for number of fruits cluster⁻¹ and number of pickings in tomato. (Based on individual and pooled environment)

Proportion	Number of fruits cluster ⁻¹				Number of pickings			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	4.53	4.26	5.13	3.10	1.58	1.62	1.62	1.61
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.24	0.24	0.24	0.23	0.19	0.19	0.19	0.19
$\frac{KD}{KR}$	1.20	1.27	1.08	1.52	2.73	2.59	2.61	2.64
$\frac{\hat{h}^2}{\hat{H}_2}$	0.10	0.11	0.10	0.12	0.20	0.18	0.17	0.21
Heritability (n.s)	0.08	0.08	0.11	0.12	0.13	0.13	0.13	0.13
B	-0.06 ±0.28	-0.05 ±0.27	-0.01 ±0.24	0.01 ±0.28	0.39 ±0.25	0.31 ±0.25	0.27 ±0.25	0.33 ±0.25
b-0/SE(b)	0.20	0.17	0.14	0.22	-1.53	-1.22	-1.07	-1.29
b-1/S.E(b)	3.76*	3.81*	4.20*	3.58*	2.41*	2.72*	2.83*	2.66*
t ²	0.14	0.19	0.17	0.17	0.26	0.26	0.27	0.25

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.4: Proportion of genetic components of variation for number of fruits plant⁻¹ and fruit length in tomato. (Based on individual and pooled environment)

Proportion	Number of fruits plant ⁻¹				Fruit length (cm)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	1.75	1.75	1.74	1.75	2.15	2.06	2.11	2.02
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.20	0.19	0.19	0.19	0.23	0.23	0.23	0.22
$\frac{KD}{KR}$	2.41	2.42	2.46	2.43	1.43	1.41	1.38	1.62
$\frac{\hat{h}^2}{\hat{H}_2}$	0.10	0.15	0.16	0.17	0.22	0.22	0.27	0.22
Heritability (n.s)	0.15	0.14	0.15	0.15	0.18	0.21	0.20	0.24
B	0.18 ±0.21	0.20 ±0.21	0.17 ±0.21	0.19 ±0.21	-0.05 ±0.18	0.02 ±0.19	0.04 ±0.19	-0.01 ±0.18
b-0/SE(b)	-0.86	-0.97	-0.80	-0.90	0.28	-0.10	-0.24	0.06
b-1/S.E(b)	4.00*	3.80*	3.95*	3.89*	5.79*	5.11*	5.12*	5.48*
t ²	2.75*	2.54*	2.57*	2.61*	3.40*	2.70*	3.04*	3.21*

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.5: Proportion of genetic components of variation for fruit diameter and number of locules fruit⁻¹ in tomato. (Based on individual and pooled environment)

Proportion	Fruit diameter (cm)				Number of locules fruit ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	1.74	1.73	1.75	1.72	2.26	2.38	2.41	2.31
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.19	0.19	0.19	0.19	0.19	0.20	0.20	0.20
$\frac{KD}{KR}$	2.34	2.27	2.29	2.40	2.28	2.03	2.00	2.12
$\frac{\hat{h}^2}{\hat{H}_2}$	0.12	0.12	0.13	0.15	0.15	0.18	0.15	0.17
Heritability (n.s)	0.17	0.18	0.17	0.22	0.14	0.15	0.14	0.16
B	0.01 ±0.33	0.05 ±0.33	0.06 ±0.34	0.06 ±0.33	-0.13 ±0.19	-0.05 ±0.16	0.02 ±0.17	-0.04 ±0.17
b-0/SE(b)	-0.03	-0.16	-0.17	-0.17	0.67	0.31	-0.14	0.26
b-1/S.E(b)	2.97*	2.85*	2.80*	2.84*	5.95*	6.48*	5.78*	6.17*
t ²	0.03	0.02	0.04	0.03	3.71	5.16	4.47	4.42

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.6: Proportion of genetic components of variation for pericarp thickness and number of primary branches plant⁻¹ in tomato. (Based on individual and pooled environment)

Proportion	Pericarp thickness				Number of primary branches plant ⁻¹			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	4.49	4.39	4.50	3.97	2.41	2.46	2.49	2.28
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.20	0.20	0.20	0.20	0.19	0.20	0.20	0.19
$\frac{KD}{KR}$	1.84	1.86	1.91	1.86	2.52	2.33	2.31	2.46
$\frac{\hat{h}^2}{\hat{H}_2}$	0.13	0.14	0.15	0.14	0.12	0.12	0.11	0.15
Heritability (n.s)	0.19	0.18	0.17	0.19	0.07	0.09	0.06	0.09
B	-0.05 ±0.13	-0.07 ±0.13	-0.06 ±0.14	-0.06 ±0.13	-0.26 ±0.23	-0.22 ±0.27	-0.12 ±0.27	-0.21 ±0.26
b-0/SE(b)	0.35*	0.51*	0.42*	0.46*	1.11	0.83	0.43	0.81
b-1/S.E(b)	8.03*	8.01*	7.74*	8.04*	5.36*	4.55*	4.14*	4.61*
t ²	10.10*	9.40*	8.82*	9.74*	0.64	0.18	0.23	0.25

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.7: Proportion of genetic components of variation for plant height and average fruit weight in tomato. (Based on individual and pooled environment)

Proportion	Plant height (cm)				Average fruit weight (g)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	2.51	2.50	2.51	2.50	1.90	1.93	1.91	1.93
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.20	0.21	0.21	0.21	0.21	0.21	0.21	0.21
$\frac{KD}{KR}$	2.12	2.10	2.06	2.10	2.07	2.03	2.05	2.03
$\frac{\hat{h}^2}{\hat{H}_2}$	0.18	0.20	0.19	0.22	0.25	0.26	0.28	0.30
Heritability (n.s)	0.11	0.11	0.11	0.11	0.15	0.15	0.14	0.15
B	-0.22 ±0.16	-0.22 ±0.16	-0.21 ±0.17	-0.22 ±0.16	0.37 ±0.34	0.40 ±0.32	0.41 ±0.34	0.42 ±0.32
b-0/SE(b)	1.37	1.36	1.24	1.33	-1.09	-1.26	-1.22	-1.33
b-1/S.E(b)	7.53*	7.43*	7.20*	7.38*	1.88*	1.88*	1.75*	1.80*
t ²	4.46*	4.23*	4.06*	4.23*	0.16	0.07	0.20	0.09

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.8: Proportion of genetic components of variation for fruit yield plant⁻¹ and fruit yield hectare⁻¹ in tomato. (Based on individual and pooled environment)

Proportion	Fruit yield plant ⁻¹				Fruit yield hectare ⁻¹ (q)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	1.26	1.76	1.76	1.75	1.73	1.75	1.76	1.76
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.33	0.21	0.20	0.20	0.20	0.20	0.20	0.20
$\frac{KD}{KR}$	2.21	2.31	2.34	2.32	2.34	2.37	2.34	2.32
$\frac{\hat{h}^2}{\hat{H}_2}$	0.24	0.27	0.28	0.30	0.15	0.18	0.22	0.28
Heritability (n.s)	0.09	0.11	0.10	0.11	0.11	0.10	0.10	0.10
B	0.30 ±0.45	0.26 ±0.34	0.17 ±0.34	0.21 ±0.34	0.23 ±0.38	0.35 ±0.35	0.17 ±0.34	0.21 ±0.35
b-0/SE(b)	-0.60	-0.76	-0.51	-0.63	-0.59	-0.99	-0.51	-0.60
b-1/S.E(b)	2.31*	2.16*	2.45*	2.29*	2.03*	1.83*	2.45*	2.27*
t ²	0.15	0.12	0.06	0.11	0.44	0.29	0.06	0.14

*, ** Significant at 5 and 1 per cent levels, respectively

Table 9.9: Proportion of genetic components of variation for average number of seeds fruit⁻¹ and 100 seed weight in tomato. (Based on individual and pooled environment)

Proportion	Average number of seeds fruit ⁻¹				100 seed weight			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]^{1/2}$	2.87	2.86	2.86	2.81	2.32	2.33	2.36	2.35
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.22	0.22	0.22	0.22	0.20	0.20	0.20	0.20
$\frac{KD}{KR}$	1.54	1.55	1.54	1.54	2.02	1.97	1.98	1.98
$\frac{\hat{h}^2}{\hat{H}_2}$	0.23	0.22	0.23	0.23	0.14	0.14	0.15	0.14
Heritability (n.s)	0.14	0.13	0.14	0.14	0.20	0.20	0.21	0.20
B	0.21 ±0.16	0.21 ±0.16	0.22 ±0.16	0.21 ±0.16	-0.11 ±0.10	-0.10 ±0.10	-0.11 ±0.10	-0.11 ±0.10
b-0/SE(b)	-1.27	-1.28	-1.34	-1.30	1.22	1.06	1.20	1.16
b-1/S.E(b)	4.87*	4.84*	4.81*	4.84*	11.96*	11.47*	12.21*	11.90*
t ²	4.51*	4.45*	4.49*	4.48*	23.38*	21.79*	24.86*	23.42*

*, ** Significant at 5 and 1 per cent levels, respectively

4.7 Analysis of quality traits based on mean performance

The best parents and crosses of tomato identified on the basis of their mean performance is given in Table 10. TSS is the important parameter that determines processing quality of tomato. Maximum mean value for TSS (°Brix) was found in parent SKAU-T-1315 (7.0) followed SKAU-T-1009 (5.2) and in crosses SKAU-T-1700 × SKAU-T-1219 (7.1) followed by SKAU-T-1315 × SKAU-T-0301 (6). Titrable acidity (%) was found to be maximum in parent SKAU-T-1429 (0.82) followed SKAU-T-0301 (0.72) and in crosses SKAU-T-1429 × SKAU-T-9862 (1.25) followed by SKAU-T-1429 × SKAU-T-1009 (1.21). Lycopene content (mg/100g) was found to be maximum in SKAU-T-1429 (5.69) followed by SKAU-T-9801 (5.42) and in crosses SKAU-T-1429 × SKAU-T-1701 (5.78) followed by SKAU-T-1429 × SKAU-T-1009 (5.67). Juice to pulp ratio was found to be maximum in parent SKAU-T-9801 (3.13) followed by SKAU-T-1701 (3.05) and in crosses SKAU-T-1701 × SKAU-T-1009 (3.15) followed by SKAU-T-1701 × SKAU-T-9862 (3.08). Ascorbic acid content (mg/100g) was found to be maximum in SKAU-T-1429 (47.7) followed by SKAU-T-1464 (47.5) and in crosses SKAU-T-1429 × SKAU-T-9862 (49.5) followed by SKAU-T-1429 × SKAU-T-1009 (46.8). Total carotenoid (mg/100g) was found to be maximum in SKAU-T-1429 (3.95) followed by SKAU-T-9801 (3.85) and in crosses SKAU-T-1429 × SKAU-T-1464 (5.95) followed by SKAU-T-1429 × SKAU-T-9862 (4.85).

Table 10: Desirable parents and crosses of tomato (*Solanum lycopersicum* L.) for various quality traits based on their mean values.

Quality Traits	Best Parents
TSS (° Brix)	SKAU-T-1315 (7.0), SKAU-T-1009 (5.2), SKAU-T-1429 (4.7), SKAU-T-1219 (4.4) and SKAU-T-1701 (4.4)
Titration acidity (%)	SKAU-T-1429 (0.82), SKAU-T-0301 (0.72), SKAU-T-1464 (0.43), SKAU-T-1700 (0.38) and SKAU-T-1219 (0.33)
Lycopene content (mg/100g)	SKAU-T-1429 (5.69), SKAU-T-9801 (5.42), SKAU-T-0301 (4.75), SKAU-T-1700 (4.72) and SKAU-T-1424 (4.37)
Ascorbic acid content (mg/100g)	SKAU-T-1429 (47.7), SKAU-T-1464 (47.5), SKAU-T-1701 (33.3), SKAU-T-0301 (31.5) and SKAU-T-1219 (30.9)
Juice to pulp ratio	SKAU-T-9801 (3.13), SKAU-T-1701 (3.05), SKAU-T-9862 (2.80), SKAU-T-1424 (2.30) and SKAU-T-1429 (2.14)
Total Carotenoids (mg/100g)	SKAU-T-1429 (3.95), SKAU-T-8901 (3.85), SKAU-T-0922 (3.71), SKAU-T-1701 (3.54) and SKAU-T-1219 (3.40)
Quality Traits	Best crosses
TSS (° Brix)	SKAU-T-1700 × SKAU-T-1219 (7.1), SKAU-T-1315 × SKAU-T-0301 (6), SKAU-T-0301 × SKAU-T-1009 (5.3), SKAU-T-1009 × SKAU-T-9862 (5.3) and SKAU-T-9801 × SKAU-T-9862 (5.2)
Titration acidity (%)	SKAU-T-1429 × SKAU-T-9862 (1.25), SKAU-T-1429 × SKAU-T-1009 (1.21), SKAU-T-1429 × SKAU-T-1464 (1.06), SKAU-T-0301 × SKAU-T-9862 (1.02) and SKAU-T-1429 × SKAU-T-1701 (0.96)
Lycopene content (mg/100g)	SKAU-T-1429 × SKAU-T-1701 (5.78), SKAU-T-1429 × SKAU-T-1009 (5.67), SKAU-T-0922 × SKAU-T-1464 (5.48), SKAU-T-1700 × SKAU-T-1429 (5.34) and SKAU-T-9801 × SKAU-T-1424 (5.23)
Ascorbic acid content (mg/100g)	SKAU-T-1429 × SKAU-T-9862 (49.5), SKAU-T-1429 × SKAU-T-1009 (46.8), SKAU-T-0922 × SKAU-T-1429 (38.8), SKAU-T-1429 × SKAU-T-1701 (38.7) and SKAU-T-9801 × SKAU-T-1701 (38.6)
Juice to pulp ratio	SKAU-T-1701 × SKAU-T-1009 (3.15), SKAU-T-1701 × SKAU-T-9862 (3.08), SKAU-T-9801 × SKAU-T-1219 (3.01), SKAU-T-1701 × SKAU-T-1464 (2.85) and SKAU-T-1424 × SKAU-T-1009 (2.80)

4.8 Estimation of heterosis

Heterosis was estimated over economic check using pooled data over environments for all sixty six cross combinations and expressed as per cent as given in Table-11. The detailed results are as under:

4.8.1 Fruit length (cm)

The standard heterosis ranged from -27.0 to 52.3 per cent in SKAU-T-1700 × SKAU-T-1429 and SKAU-T-1219 × SKAU-T-1429 respectively. Significant positive heterosis over standard parent was observed in SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-1315, SKAU-T-1424 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464, SKAU-T-1009 × SKAU-T-9862, SKAU-T-1009 × SKAU-T-1464 and SKAU-T-9862 × SKAU-T-1464. Three best cross combinations based on standard parent heterosis were SKAU-T-1219 × SKAU-T-1429 (52.3), SKAU-T-1429 × SKAU-T-9862 (47.7) and SKAU-T-1219 × SKAU-T-1701 (30.6).

4.8.2 Fruit diameter (cm)

The standard heterosis ranged from -48.1 to 33.3 per cent in SKAU-T-9801 × SKAU-T-1700 and SKAU-T-1219 × SKAU-T-1429 respectively. Significant positive heterosis over standard parent was observed in SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-

1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464. Three best cross combinations based on standard parent heterosis were SKAU-T-1219 × SKAU-T-1429 (33.3), SKAU-T-1009 × SKAU-T-1464 (32.6) and SKAU-T-1429 × SKAU-T-9862 (21.7).

4.8.3 Number of fruits plant⁻¹

The standard heterosis was in the range of -58.6 to 30.3 per cent in SKAU-T-9801 × SKAU-T-1429 and SKAU-T-1700 × SKAU-T-1424 respectively. Significant positive heterosis over standard parent was observed in SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1009 × SKAU-T-9862 and SKAU-T-1009 × SKAU-T-1464. Three best superior cross combinations based on standard heterosis were SKAU-T-1700 × SKAU-T-1424 (30.3), SKAU-T-1219 × SKAU-T-1701 (25.7) and SKAU-T-1009 × SKAU-T-9862 (25.3).

4.8.4 Average fruit weight (g)

The standard heterosis was in the range of -37.6 to 53.5 per cent in SKAU-T-1424 × SKAU-T-1464 and SKAU-T-1429 × SKAU-T-1701 respectively. Significant positive heterosis over standard parent was observed in SKAU-T-9801 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-0301, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-1464, SKAU-

T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464. Superior cross combinations based on standard parent heterosis were SKAU-T-1429 × SKAU-T-1701 (53.5), SKAU-T-1429 × SKAU-T-1464 (46.0) and SKAU-T-1315 × SKAU-T-1701 (37.4).

4.8.5 Fruit yield plant⁻¹ (kg)

The extent of heterosis over standard parent was in the range of-63.40 to 44.76 per cent in SKAU-T-9801 × SKAU-T-1700 and SKAU-T-1219 × SKAU-T-1429 respectively. Significant positive heterosis over standard parent was observed in SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464. Based on standard parent heterosis best cross combinations were SKAU-T-1219 × SKAU-T-1429, SKAU-T-1429 × SKAU-T-9862 and SKAU-T-1219 × SKAU-T-1701 exhibiting the heterosis of 44.76, 44.29 and 43.36 per cent respectively.

4.8.6 Fruit yield hectare⁻¹ (q)

The extent of heterosis over standard parent was in the range of -63.23 to 46.85 per cent in SKAU-T-9801×SKAU-T-1700 and SKAU-T-1219 × SKAU-T-1429 respectively. Significant positive heterosis over standard parent was observed in SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922× SKAU-T-1424, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464. Based on standard parent heterosis best cross combinations were SKAU-T-1219 × SKAU-T-1429, SKAU-T-1429 × SKAU-T-9862 and SKAU-T-1219 × SKAU-T-1701 exhibiting the heterosis of 46.85, 44.29 and 43.35 per cent respectively.

Table-11: Estimation of heterosis (%) over economic check for fruit length, fruit diameter, number of fruits plant⁻¹, average fruit weight, fruit yield plant⁻¹ and fruit yield hectare⁻¹ in Tomato (Based on individual and pooled analysis)

Crosses	Fruit length (cm)	Fruit diameter (cm)	Number of fruits plant ⁻¹	Average fruit weight (g)	Fruit yield plant ⁻¹ (kg)	Fruit yield hectare ⁻¹ (q)
SKAU-T-9801 × SKAU-T-1700	-22.5**	-48.1	-43.2**	-35.4**	-63.40**	-63.23**
SKAU-T-9801 × SKAU-T-0922	5.4	-7.8	14.3*	-33.4**	-24.24**	-24.40**
SKAU-T-9801 × SKAU-T-1424	6.3	-10.1*	15.9**	7.2	23.78**	23.78**
SKAU-T-9801 × SKAU-T-1219	-22.5**	-2.3	-32.9**	-23.5**	-48.72**	-48.64**
SKAU-T-9801 × SKAU-T-1315	6.3	-29.5**	14.9*	13.9*	30.54**	30.53**
SKAU-T-9801 × SKAU-T-0301	-19.8**	-36.4**	-35.5**	-34.8	-57.58**	-57.58**
SKAU-T-9801 × SKAU-T-1429	-18.9**	-8.5*	-58.6**	-6.9	-61.31**	-61.31**
SKAU-T-9801 × SKAU-T-1701	-0.9	-5.4	21.9**	3.7	24.94**	24.94**
SKAU-T-9801 × SKAU-T-1009	4.5	-16.3**	1.2	-32.9**	-31.93**	-31.78**
SKAU-T-9801 × SKAU-T-9862	-9.0	-7.0	-8.2*	-33.2**	-37.53**	-37.37**
SKAU-T-9801 × SKAU-T-1464	11.7*	-39.5**	-38.5**	-14.1*	-47.32**	-47.40**
SKAU-T-1700 × SKAU-T-0922	-23.4**	-8.5*	1.6	-3.2	-1.40	-1.63
SKAU-T-1700 × SKAU-T-1424	11.7*	1.6	30.3**	2.4	33.33**	33.33**
SKAU-T-1700 × SKAU-T-1219	11.7*	-9.3*	25.2**	3.3	29.14**	29.14**
SKAU-T-1700 × SKAU-T-1315	-1.8	-23.3**	22.1**	5.3	28.67**	28.67**
SKAU-T-1700 × SKAU-T-0301	-5.4	-3.9	-27.7**	10.7*	-20.05**	-19.81**
SKAU-T-1700 × SKAU-T-1429	-27.0**	-0.8	20.2**	12.0*	34.50**	34.50**

Contd....

Table 11: contd...

Crosses	Fruit length (cm)	Fruit diameter (cm)	Number of fruits plant ⁻¹	Average fruit weight (g)	Fruit yield plant ⁻¹ (kg)	Fruit yield hectare ⁻¹ (q)
SKAU-T-1700 × SKAU-T-1701	4.5	-8.5*	-51.9**	-13.5*	-58.04**	-58.20**
SKAU-T-1700 × SKAU-T-1009	22.5**	-9.3*	-14.7*	-9.4*	-22.84**	-22.77**
SKAU-T-1700 × SKAU-T-9862	1.8	-18.6**	-31.9	9.9*	-25.17**	-25.18**
SKAU-T-1700 × SKAU-T-1464	26.1**	20.2**	17.2**	19.8**	40.09**	40.09**
SKAU-T-0922 × SKAU-T-1424	-0.9	-3.9	12.0**	17.5**	31.24**	29.84**
SKAU-T-0922 × SKAU-T-1219	-1.8	-9.3*	-22.5**	8.1*	-16.32**	-18.84**
SKAU-T-0922 × SKAU-T-1315	22.5**	-7.0	3.1	35.1**	39.39**	39.39**
SKAU-T-0922 × SKAU-T-0301	0.0	-40.3**	13.0*	17.2**	32.17**	32.17**
SKAU-T-0922 × SKAU-T-1429	21.6**	-34.1**	-10.0*	-10.6*	-19.35**	-19.35**
SKAU-T-0922 × SKAU-T-1701	2.7	-14.7*	-22.9**	-27.6**	-44.29**	-44.13**
SKAU-T-0922 × SKAU-T-1009	3.6	-37.2**	4.6	-24.9**	-21.21**	-21.29**
SKAU-T-0922 × SKAU-T-9862	18.9**	19.4**	-2.6	-13.4*	-15.62**	-15.62**
SKAU-T-0922 × SKAU-T-1464	3.6	-8.5	-12.6*	2.3	-10.49*	-10.57*
SKAU-T-1424 × SKAU-T-1219	27.0**	-2.3	9.7*	14.0*	24.94**	24.94**
SKAU-T-1424 × SKAU-T-1315	16.2**	-6.2	-12.2*	-19.5**	-29.14**	-31.24**
SKAU-T-1424 × SKAU-T-0301	3.6	-17.1**	15.2**	10.6*	27.04**	27.04**
SKAU-T-1424 × SKAU-T-1429	12.6*	-9.3*	-15.5**	3.3	-12.59*	-12.59*
SKAU-T-1424 × SKAU-T-1701	-1.8	-4.7	-13.3**	-24.9**	-34.73**	-34.81**
SKAU-T-1424 × SKAU-T-1009	5.4	-19.4**	-1.7	-16.5**	-17.72**	-17.79**

Contd....

Table 11: contd...

Crosses	Fruit length (cm)	Fruit diameter (cm)	Number of fruits plant ⁻¹	Average fruit weight (g)	Fruit yield plant ⁻¹ (kg)	Fruit yield hectare ⁻¹ (q)
SKAU-T-1424 × SKAU-T-9862	4.5	-5.4	-18.9**	-37.5**	-48.25**	-48.10**
SKAU-T-1424 × SKAU-T-1464	-9.0	-16.3**	-9.3*	-37.6**	-43.59**	-43.51**
SKAU-T-1219 × SKAU-T-1315	8.1	-8.5*	-41.3**	-3.5	-43.36**	-43.28**
SKAU-T-1219 × SKAU-T-0301	-2.7	-10.1*	2.1	-14.4*	-12.59*	-12.82*
SKAU-T-1219 × SKAU-T-1429	52.3**	33.3**	8.7*	33.3**	44.76**	46.85**
SKAU-T-1219 × SKAU-T-1701	30.6**	15.5**	25.7**	14.2*	43.36**	43.35**
SKAU-T-1219 × SKAU-T-1009	16.2**	-8.5*	19.8**	6.0	27.04**	26.96**
SKAU-T-1219 × SKAU-T-9862	2.7	6.2	5.5	2.6	8.16*	8.08*
SKAU-T-1219 × SKAU-T-1464	16.2**	-3.9	14.1*	16.7**	33.33**	33.33**
SKAU-T-1315 × SKAU-T-0301	5.4	-13.2*	-18.0**	-37.4**	-48.72**	-48.64**
SKAU-T-1315 × SKAU-T-1429	-10.8*	0.0	-8.5*	-5.8	-13.75*	-13.91*
SKAU-T-1315 × SKAU-T-1701	3.6	11.6*	-24.3**	37.4**	3.96	4.04
SKAU-T-1315 × SKAU-T-1009	5.4	-8.5*	-8.6*	-26.5**	-32.63**	-32.79**
SKAU-T-1315 × SKAU-T-9862	2.7	-10.9*	-41.1**	-34.7**	-61.54**	-61.54**
SKAU-T-1315 × SKAU-T-1464	19.8**	-3.9	-8.1*	9.9*	0.23	0.93
SKAU-T-0301 × SKAU-T-1429	18.0**	3.1	-18.8**	12.6*	-8.62*	-8.55*
SKAU-T-0301 × SKAU-T-1701	5.4	-6.2	-1.8	-13.1*	-14.69*	-14.61*
SKAU-T-0301 × SKAU-T-1009	18.0**	-10.1*	1.0	-17.0*	-16.08**	-16.16**
SKAU-T-0301 × SKAU-T-9862	0.9	-3.1	-3.1	-27.5**	-29.60**	-29.68**

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Table 11: contd...

Crosses	Fruit length (cm)	Fruit diameter (cm)	Number of fruits plant ⁻¹	Average fruit weight (g)	Fruit yield plant ⁻¹ (kg)	Fruit yield hectare ⁻¹ (q)
SKAU-T-0301 × SKAU-T-1464	-6.3	-9.3*	-3.5	-16.5**	-19.58**	-19.50**
SKAU-T-1429 × SKAU-T-1701	18.9**	-12.4*	-30.1**	53.5**	6.99	6.99
SKAU-T-1429 × SKAU-T-1009	25.2**	20.2**	15.1**	23.6**	41.96**	41.96**
SKAU-T-1429 × SKAU-T-9862	47.7**	21.7**	18.8**	21.7**	44.29**	44.29**
SKAU-T-1429 × SKAU-T-1464	18.0**	14.0*	-37.4**	46.0**	-8.62*	-8.70*
SKAU-T-1701 × SKAU-T-1009	0.0	-8.5*	-28.3**	14.8*	-17.72**	-17.79**
SKAU-T-1701 × SKAU-T-9862	11.7*	-2.3	-16.0**	33.1**	11.66*	11.89*
SKAU-T-1701 × SKAU-T-1464	21.6**	5.4	7.5	11.9*	20.28**	20.36**
SKAU-T-1009 × SKAU-T-9862	27.9**	-27.9**	25.3**	-33.1**	-16.55*	-16.32*
SKAU-T-1009 × SKAU-T-1464	26.1**	32.6**	20.9**	15.7**	39.86**	39.86**
SKAU-T-9862 × SKAU-T-1464	9.0*	-6.2	-7.6	-38.3**	-43.36**	-43.12**



SKAU-T-9801



SKAU-T-0922



SKAU-T-1464



SKAU-T-0301



SKAU-T-9862

Plate 3: Best Five Parents



SKAU-T – 1429 × SKAU-T -1009



SKAU-T – 1429 × SKAU-T - 9862



SKAU-T – 1219 × SKAU-T -1701



SKAU-T – 1700 × SKAU-T -1464



SKAU-T-1700 × SKAU-T -1424

Plate 4: Best Cross Combinations

Chapter-5

DISCUSSION

The present investigation entitled “**Heterosis and combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) under temperate conditions of Kashmir**” was conducted to generate information on nature and magnitude of gene effects involved in the inheritance of various maturity, yield and yield related traits; combining ability effects and nature and magnitude of heterosis. Sixty six F₁ crosses generated from ten diverse lines crossed in diallel fashion were evaluated along with the parents at three locations. Observations were recorded on various maturity, yield and yield related traits. The results of the experiment and their relevance for future breeding programmes may be discussed as follows:

5.1 Analysis of variance

Analysis of variance (Table-1.1 to 1.7) revealed significant mean squares for the environment in all the characters. Highly significant differences were observed among the parents and their crosses for all the traits in all the environments as well as in pooled analysis, indicating that the parents as well as the crosses generated from them were diverse for all the traits. Variance due to parents vs crosses were found to be significant for all the traits indicating the significant contribution of hybrids for specific combining ability which is important for exploitation of heterosis.

The genotype x environment interaction was significant for all the traits except number of locules fruit⁻¹ and 100 seed weight. Parents × Environments interaction was significant for all the characters except number of locules fruit⁻¹, pericarp thickness and 100 seed weight. Crosses × Environments interactions were found significant for first fruit harvest, number of fruits cluster⁻¹, number of pickings, number of fruits plant⁻¹, fruit length, fruit diameter, pericarp thickness, number of primary branches plant⁻¹, plant height, average fruit weight, fruit yield

plant⁻¹, fruit yield hectare⁻¹, average number of seeds fruit⁻¹ except number of flowers cluster⁻¹, number of locules fruit⁻¹ and 100 seed weight. Again parents × Crosses × Environments interaction were found significant for all traits except fruit length, fruit diameter, number of locules fruit⁻¹ and pericarp thickness. These results indicated significant variation in the behaviour of parents and crosses and their interaction under different environments. These interactions arise due to differences in the sensitivities of genotypes to the different environmental conditions.

Similar findings with respect to analysis of variance were also reported Singh *et al.* (2018), Saravanan *et al.* (2019), Venkadeswaran *et al.* (2018), Chaudhari *et al.* (2019), Kannaujia, *et al.* (2019), Basfore *et al.* (2020), Tsagaye *et al.* (2020), Limbani *et al.* (2020), Kumar *et al.* (2020), Maurya *et al.* (2020), Rawat *et al.* (2020), Kumari *et al.* (2020), Eppakayala *et al.* (2021), Bhandari *et al.* (2021), Waiba *et al.* (2021), Nkansah *et al.* (2022), Mishra *et al.* (2022), Rasheed *et al.* (2022).

5.2 Analysis of variance for combining ability

The analysis of variance for general combining ability (GCA), specific combining ability (SCA) and their interaction with environments (Table-2.1 to 2.7) in respect of twelve parents and sixty six F₁ crosses for eighteen diverse traits depicts that the mean squares due to environments were significant for all traits under consideration revealing that the environments chosen for the present investigation were diverse. Mean squares for general and specific combining ability were also significant for all traits under study in the individual and pooled analysis which indicates importance of both additive and non-additive gene action in the inheritance of these traits. The mean squares due to GCA × environments and SCA × environments were found significant for number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster⁻¹, number of fruits cluster⁻¹, number of pickings, number of fruits plant⁻¹, fruit length (cm), fruit diameter (cm), number of primary

branches plant⁻¹, plant height (cm), average fruit weight (g), fruit yield plant⁻¹ (kg), fruit yield hectare⁻¹ (q), average number of seeds fruit⁻¹ except number of locules fruit⁻¹, pericarp thickness and 100 seed weight for which GCA and SCA effects showed non-significant interaction with environments.

Variances due to SCA ($\hat{\sigma}^2s$) were higher than the corresponding GCA variances ($\hat{\sigma}^2g$) for all the traits under consideration in all individual environments as well as in pooled analysis. The magnitude of dominance variance was higher in range in all cases indicating the preponderance of non-additive gene action which was further confirmed by the ratio of additive genetic variance to dominance variance ($\hat{\sigma}^2A / \hat{\sigma}^2D$) being less than unity for all the traits. This means that non-additive gene action played a major role in the inheritance of all traits as compared to additive gene action in both the environment and pooled analysis. So, all traits under study were controlled by both additive and non-additive gene action with preponderance of latter in both environments and pooled analysis.

Similar findings with respect to analysis of variance for combining ability and genetic variation were also reported by Solieman (2009), Rani & Veeraragavathatha (2011), Farzane *et al.* (2012), Saleem *et al.* (2013), Aisyah *et al.* (2016), Gautam *et al.* (2018), Barragan *et al.* (2019), Veena *et al.* (2019), Bhandari *et al.* (2021), Liu *et al.* (2021), Singh *et al.* (2021), Lone *et al.* (2022), Izzo *et al.* (2022).

5.3 Combining ability analysis

Combining ability of a line indicates its potentiality in cross combination with other lines. Combining ability analysis helps in selection of parents for hybridization and also in selecting a proper breeding procedure. General combining ability (GCA) measures the average performance of a parent in various hybrid combinations while as specific combining ability (SCA) refers to those instances in which the performance of a hybrid is relatively better or worse than

would be expected on the basis of average performance of the parents involved. A relatively large GCA/SCA variance ratio suggests the importance of additive gene effects and a low ratio implies the presence of dominant and /or epistatic gene effects (Griffing, 1956 a; Bhullar *et al.*, 1979). If additive \times additive effects are present, the GCA component will also contain some of those effects in addition to additive effects. When SCA is small relative to the GCA, performance of a single cross progeny can be predicted on the basis of the GCA of the parents.

Combining ability analysis was performed in the present investigation by crossing twelve genetically diverse genotypes of tomato in diallel fashion and information was generated by following Griffing's (1956) Model I and Method II and Hayman's component analysis. The diallel technique stated by Griffing (1956b) was helpful in estimating the combining ability of genotypes and assessing the nature and extent of gene action. Griffing's analysis for combining ability requires no genetic presumptions (Wright, 1985) and has been manifested to fetch reliable information on the combining ability potential of parents. The pre-eminent parental combiners once identified can be either hybridized with the intent of selecting promising genotypes within the segregating generation or crossed to recognize the optimal hybrid combinations and at the same time, to elucidate the nature and magnitude of different types of generation. The choice of Griffing's method depends on the researcher's preference and on the characteristic of the crop and trait under evaluation.

Several studies (Matzinger *et al.*, 1959; Hayes and Paroda, 1974) have revealed that GCA and SCA interact significantly with the environment. It was then concluded that in order to attain reliable estimates for GCA effects, the analysis should be conducted in more than one environment and where SCA \times environment interaction occurs, selection of parents and crosses should be matched to the selection site.

5.3.1 General combining ability effects

The GCA effects represent the additive nature of the gene action. A high general combiner parent is characterized by its better breeding value when crossed with number of other parents. Depending upon the character concerned, the nature (direction/sign) and magnitude (size) of GCA are both considered. Besides *per se* (mean) performance of the parent is also considered in union with GCA since the former offers reliability to GCA as a guide to selection of the parent. Further the GCA variance ($\hat{\sigma}^2 g$) of parent and SCA variance ($\hat{\sigma}^2 s$) of cross play significant role in choice of parents.

In the present investigation the general combining ability effects of the parental lines were estimated to know their genetic worth for use in the production of hybrids. The GCA estimates of parents and close examination of the results pooled over environments revealed that none of parent showed significant GCA effects in the desired direction corollary for all the traits under study. However, different parents were found to reveal desirable general combining ability for different traits. Hence, the parents with desirable GCA for maximum traits could be selected for use in future breeding programmes *i.e.*, mass and progeny selection and the multiple crosses and segregating population obtained thereof, could be used for identifying and selecting the segregants which are expected to recombine most of the favorable alleles distributed among the parents.

Perusal of results (Table-3.1 to 3.7) indicated that none of the parents revealed significant and desirable general combining ability for all the traits simultaneously. However, different parents were found to reveal desirable general combining ability for different traits (Table 12). The parents exhibiting significant desirable GCA effects in all environments as well as in pooled analysis included SKAU-T-1219, SKAU-T-0301, SKAU-T-1424, SKAU-T-1700 and SKAU-T-1009 for number of days to first flowering; SKAU-T-1424, SKAU-T-1700, SKAU-T-9801, SKAU-T-0301 and SKAU-T-1219 for number of days to first

fruit set; SKAU-T-1429, SKAU-T-1219, SKAU-T-1700, SKAU-T-9801 and SKAU-T-1424 for number of days to first fruit harvest; SKAU-T-1424, SKAU-T-9801, SKAU-T-1219, SKAU-T-0922 and SKAU-T-0301 for number of flowers cluster⁻¹; SKAU-T-0922, SKAU-T-1219, SKAU-T-0301, SKAU-T-1701, SKAU-T-1424 and SKAU-T-1464 for number of fruits cluster⁻¹; SKAU-T-9801, SKAU-T-1700, SKAU-T-0922, SKAU-T-1701 and SKAU-T-1219 for number of pickings. For number of fruits plant⁻¹ significant desirable GCA was found in SKAU-T-1429, SKAU-T-1701, SKAU-T-9801, SKAU-T-0922 and SKAU-T-1700. For fruit length SKAU-T-9801, SKAU-T-9862, SKAU-T-1700 and SKAU-T-0922 showed positive and significant GCA effects. Also for fruit diameter significant positive GCA was observed in SKAU-T-9801, SKAU-T-0301, SKAU-T-0922 and SKAU-T-1009. For number of locules fruit⁻¹, SKAU-T-1219, SKAU-T-0301, SKAU-T-9862 and SKAU-T-1464 manifested positive significant GCA effects; For pericarp thickness SKAU-T-9801, SKAU-T-1315, SKAU-T-1700 and SKAU-T-1429 were found to be good combiners. For number of primary branches plant⁻¹ significant positive GCA effects were depicted by SKAU-T-9801, SKAU-T-9862, SKAU-T-1315 and SKAU-T-1464. For plant height SKAU-T-9801, SKAU-T-0301, SKAU-T-1219 and SKAU-T-0922 were found to be good combiners; SKAU-T-9801, SKAU-T-0301, SKAU-T-1429 and SKAU-T-1700 depicted significant GCA effects for average fruit weight. For fruit yield plant⁻¹ SKAU-T-9801, SKAU-T-0922, SKAU-T-1464 and SKAU-T-1700 were found to be good combiners with significant positive GCA effect. Also for fruit yield hectare⁻¹ SKAU-T-9801, SKAU-T-0922, SKAU-T-1700 and SKAU-T-1701 were found to be good combiners. For average number of seeds fruit⁻¹ significant positive GCA effects were depicted by SKAU-T-0301, SKAU-T-9801, SKAU-T-0922 and SKAU-T-1464. Significant positive GCA effects were depicted by SKAU-T-1009, SKAU-T-1315, SKAU-T-1700 and SKAU-T-0301 for 100 seed weight.

A close relationship between parents *per se* performance and their general combining ability is important in the choice of parents for crossing programme. In most of the cases, high general combining ability for the traits was associated with their high to average *per se* performance (Table-12) and poor general combining ability was associated with low *per se* performance. Table 12 depicts ranking of genotypes on the basis of desirable GCA effects and *per se* for different traits in tomato. Persual of table 12 depicted that parents SKAU-T-9801, SKAU-T-0301, SKAU-T-1464, SKAU-T-9862 and SKAU-T-0922 revealed desirable GCA effects for most of the traits including yield and yield attributing traits. None of the parents exhibited superior general combining ability for all traits simultaneously. But also in some cases the best general combiners based on GCA and best parents based on *per se* performance were different for the trait, suggesting that inter allelic interaction was important for these characters. Similar results have been reported by Rai (1992) and Premalakshme *et al.* (2006). In case of self-pollinated species, like tomato, mass selection and progeny selection should be followed. Nandadevi and Salimath (2003) suggested that the genotypes which showed significant gca effect in desirable direction for various characters could be used in multiple crosses and segregating population obtained thereof, could be used for identifying and selecting segregants which are expected to recombine most of the favourable alleles distributed among the parents. Similar findings with respect to GCA effects were also reported by Hannan *et al.* (2007), Amin *et al.* (2012), Kumar *et al.* (2015), Bhattarai *et al.* (2016), Jose *et al.* (2016), Jadav *et al.* (2017), Barragan *et al.* (2019), Dharva *et al.* (2018), Sureshkumara *et al.* (2018), Gautam *et al.* (2018), Bhandari *et al.* (2021), Mishra *et al.* (2020), Soresa *et al.* (2021), Nayana *et al.* (2021).

5.3.2 Specific combining ability

Specific combining ability measures the performance of a specific cross/hybrid with respect to its parents and estimates the dominant genetic effects (Sprague and Tatum, 1942). The result revealed that the specific combining

ability was predominantly due to dominant effects and epistatic interactions of genes. In such cases, where there is preponderance of non-additive gene action, breeding strategy should be aimed at the development of hybrids.

Perusal of the findings on SCA effects indicated that none of the crosses possessed significant and desirable specific combining ability for all the traits at the same time. However, different crosses were found to reveal desirable specific combining ability for different traits. Hence, the crosses with desirable SCA for maximum traits, could be selected for use in future breeding programmes i.e., hybrid development. The results indicated that crosses having significantly high SCA effects involved high, average and low general combiners as parents. The specific combining ability of sixty six crosses for different traits as given in Table-5.1 to 5.9 revealed that none of the F_1 crosses exhibited significant desirable specific combining ability effects for all the traits. However, different crosses exhibited significant desirable SCA effects for different traits (Table 13).

The crosses exhibiting significant desirable SCA effects in all environments as well as in pooled analysis were SKAU-T-1700 \times SKAU-T-9862, SKAU-T-1700 \times SKAU-T-1009, SKAU-T-1701 \times SKAU-T-9862 and SKAU-T-1009 \times SKAU-T-1464 for number of days to first flowering; SKAU-T-1700 \times SKAU-T-9862, SKAU-T-1700 \times SKAU-T-1009, SKAU-T-9801 \times SKAU-T-9862 and SKAU-T-1429 \times SKAU-T-1701 for number of days to first fruit set; SKAU-T-1219 \times SKAU-T-1429, SKAU-T-1315 \times SKAU-T-1009, SKAU-T-1424 \times SKAU-T-1219 and SKAU-T-9801 \times SKAU-T-1009. For number of flowers and fruits cluster⁻¹ significant SCA effects were depicted by crosses SKAU-T-1429 \times SKAU-T-9862, SKAU-T-9801 \times SKAU-T-1315, SKAU-T-1700 \times SKAU-T-0301, SKAU-T-9801 \times SKAU-T-1701 and SKAU-T-9801 \times SKAU-T-1701, SKAU-T-1700 \times SKAU-T-1701, SKAU-T-1700 \times SKAU-T-0301, SKAU-T-1315 \times SKAU-T-1429 respectively. For number of pickings SKAU-T-1424 \times SKAU-T-9862, SKAU-T-1424 \times SKAU-T-1464, SKAU-T-0301 \times SKAU-T-1429 and SKAU-T-1700 \times SKAU-T-1009 were found to be

good combiners. For number of fruits plant⁻¹ maximum significant SCA effects were depicted by SKAU-T-1424 × SKAU-T-1464, SKAU-T-9801 × SKAU-T-1219, SKAU-T-1701 × SKAU-T-1009 and SKAU-T-1219 × SKAU-T-0301; SKAU-T-1424 × SKAU-T-9862, SKAU-T-0301 × SKAU-T-1429, SKAU-T-1009 × SKAU-T-9862 and SKAU-T-1424 × SKAU-T-1464 showed significant SCA effects for fruit length. Also for fruit diameter SKAU-T-1424 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1701, SKAU-T-0922 × SKAU-T-1429 and SKAU-T-1009 × SKAU-T-9862 were found to be good combiners. For number of locules fruit⁻¹ significant positive SCA were depicted by crosses SKAU-T-1700 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-9862 and SKAU-T-9801 × SKAU-T-0301; SKAU-T-1429 × SKAU-T-1464, SKAU-T-1424 × SKAU-T-9862, SKAU-T-9801 × SKAU-T-1219 and SKAU-T-1009 × SKAU-T-9862 for pericarp thickness. Significant SCA for number of primary branches plant⁻¹ were showed by crosses SKAU-T-1315 × SKAU-T-0301, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1701 and SKAU-T-1219 × SKAU-T-1429. For plant height SKAU-T-1700 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-9862 and SKAU-T-1700 × SKAU-T-0922 depicted significant SCA effects. Crosses SKAU-T-1315 × SKAU-T-1464, SKAU-T-1219 × SKAU-T-1009, SKAU-T-0301 × SKAU-T-1701 and SKAU-T-1424 × SKAU-T-9862 depicted significant SCA effects for average fruit weight. For fruit yield plant⁻¹ SKAU-T-1424 × SKAU-T-1464, SKAU-T-9801 × SKAU-T-1219, SKAU-T-1429 × SKAU-T-1701 and SKAU-T-9801 × SKAU-T-1429 depicted significant SCA effects. Also for fruit yield hectare⁻¹ significant SCA were depicted by crosses SKAU-T-1424 × SKAU-T-9862, SKAU-T-0301 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1464 and SKAU-T-0922 × SKAU-T-1219. For average number of seeds fruit⁻¹ SKAU-T-1424 × SKAU-T-9862, SKAU-T-0301 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1464 and SKAU-T-0922 × SKAU-T-1219 showed significant SCA effects. Also for 100 seed weight significant SCA effects were depicted by

SKAU-T-1009 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-0922, SKAU-T - 1701 × SKAU-T-1464 and SKAU-T-1700 × SKAU-T-1429.

The good general combining parents used for hybridization do not always produced high SCA effects. Similarly the poor general combining parent do not always produced low SCA effects. Thus desirable specific cross combinations resulted out of crosses between the parents with high × high, high × low, low × high, low × low, high × average, average × low or low × average general combining ability. Similar findings with respect to SCA effects were also reported by Rani & Veeraragavathatham (2011), Kumar *et al.* (2013), Agarwal *et al.* (2014), Panchal (2015), Sankhla (2015), Saleem *et al.* (2013), Dharva *et al.* (2018), Sureshkumara *et al.* (2018), Gautam *et al.* (2018), Veena *et al.* (2019), Vekariya *et al.* (2019), Mishra *et al.* (2020), Liu *et al.* (2021), Lone *et al.* (2022).

The overall ranking of genotypes based on their general combining ability, specific combining ability and *per se* performance of the parents and crosses revealed that the SKAU-T-9801, SKAU-T-0301, SKAU-T-1464, SKAU-9862 and SKAU-T-0922 genotypes are good general combiners for most of the traits and these could be used for the development of improved varieties in tomato. Table 13 gives the ranking of crosses on the basis of desirable SCA effects in various traits in tomato. The perusal of table depicts that the cross combinations SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1315, SKAU-T - 9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-0922 recorded desirable SCA effects for most economic traits. Dass *et al* (1997) concluded that good cross combination is not always result of result of high × high general combiners. Labna *et al* (1978) suggested that manifestation of high SCA effects in some cross combination results in the concentration of more favorable genes and their interaction by the parents that usually are high or average general combiners. The superiority of crosses involving high × high, high × average and average × average combiners as parents might have possibly resulted from the concentration and interaction of favorable alleles contributed by

parents. The crosses could be exploited for isolation of pure lines through pedigree method of breeding involving progeny testing, since that non-additive component is predominant. The superiority of crosses involving high \times low or average \times low combiners as parents could be explained on the basis of interaction between positive alleles from good/average combiners and negative alleles from the poor combiners as parents (Dubey, 1975). The high yield of such crosses would be non-fixable and thus could be exploited for heterosis breeding. The superior cross combination involving low \times low general combiners could result from over dominance and epistasis (Rehman *et al.*, 1981). The crosses between good and poor general combiners resulting in significant SCA effects could be used to throw superior transgressive segregants when the additive gene effects of the parents and the complimentary epistatic effects in crosses act in the same direction to maximize the desirable plant attributes (Andrus, 1963).

Table 12: Best parents identified on the basis of GCA and *per se* performance for different traits in tomato (*Solanum lycopersicum* L.) (based on individual and pooled analysis)

S. No.	Trait	Parent GCA		Parent <i>per se</i> performance	
1.	Number of days to first flowering	SKAU-T-1219	-0.611	SKAU-T-1701	30.4
		SKAU-T-0301	-0.584	SKAU-T-1700	31.4
		SKAU-T-1424	-0.417	SKAU-T-1219	31.6
		SKAU-T-1700	-0.297	SKAU-T-1315	33.6
		SKAU-T-1009	-0.270	SKAU-T-9801	34.3
2.	Number of days to first fruit set	SKAU-T-1424	-1.457	SKAU-T-1700	42.3
		SKAU-T-1700	-0.967	SKAU-T-1701	42.6
		SKAU-T-9801	-0.917	SKAU-T-1315	43.1
		SKAU-T-0301	-0.568	SKAU-T-1219	43.5
		SKAU-T-1219	-0.515	SKAU-T-1424	44.5
3.	Number of days to first fruit harvest	SKAU-T-1429	-2.081	SKAU-T-8901	76.6
		SKAU-T-1219	-1.515	SKAU-T-1219	77.5
		SKAU-T-1700	-1.179	SKAU-T-1315	77.6
		SKAU-T-9801	-1.152	SKAU-T-1424	80.5
		SKAU-T-1424	-1.037	SKAU-T-1009	80.5
4.	Number of flowers cluster ⁻¹	SKAU-T-1424	0.247	SKAU-T-9801	6.8
		SKAU-T-9801	0.228	SKAU-T-1315	6.6
		SKAU-T-1219	0.224	SKAU-T-1009	6.5
		SKAU-T-0922	0.211	SKAU-T-1701	6.1
		SKAU-T-0301	0.204	SKAU-T-1219	5.9

Contd...

Table 12: contd....

S. No.	Trait	Parent GCA		Parent per se performance	
4.	Number of fruits cluster ⁻¹	SKAU-T-0922	0.304	SKAU-T-1701	3.9
		SKAU-T-1219	0.202	SKAU-T-1464	3.8
		SKAU-T-0301	0.189	SKAU-T-1009	3.7
		SKAU-T-1701	0.174	SKAU-T-1700	3.5
		SKAU-T-1424	0.167	SKAU-T-1219	3.5
		SKAU-T-1464	0.108		
5.	Number of pickings	SKAU-T-9801	1.258	SKAU-T-1219	8.4
		SKAU-T-1700	0.650	SKAU-T-1009	8.1
		SKAU-T-0922	0.624	SKAU-T-1464	8.1
		SKAU-T-1701	0.560	SKAU-T-1700	7.9
		SKAU-T-1219	0.448	SKAU-T-0301	7.8
6.	Number of fruits plant ⁻¹	SKAU-T-1429	3.762	SKAU-T-9801	36.3
		SKAU-T-1701	2.398	SKAU-T-1700	34.7
		SKAU-T-8901	2.367	SKAU-T-1009	43.2
		SKAU-T-0922	2.312	SKAU-T-1424	32.5
		SKAU-T-1700	2.178	SKAU-T-1429	31.5
7.	Fruit length (cm)	SKAU-T-9801	0.553	SKAU-T-1429	5.2
		SKAU-T-9862	0.191	SKAU-T-1424	4.7
		SKAU-T-1700	0.176	SKAU-T-1464	4.7
		SKAU-T-0922	0.149	SKAU-T-1315	4.6
		SKAU-T-1429	0.142	SKAU-T-1009	4.6
		SKAU-T-1009	0.126		

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Table 12: contd....

S. No.	Trait	Parent GCA		Parent per se performance	
8.	Fruit diameter (cm)	SKAU-T-9801	0.539	SKAU-T-1429	5.2
		SKAU-T-0301	0.304	SKAU-T-1464	5.1
		SKAU-T-0922	0.258	SKAU-T-1424	4.8
		SKAU-T-1009	0.232	SKAU-T-1315	4.1
		SKAU-T-1464	0.176	SKAU-T-1700	3.9
		SKAU-T-1701	0.171		
9.	Number of locules fruit ⁻¹	SKAU-T-1219	0.409	SKAU-T-1219	5.2
		SKAU-T-0301	0.362	SKAU-T-1464	4.5
		SKAU-T-9862	0.330	SKAU-T-9862	3.8
		SKAU-T-1464	0.203	SKAU-T-8901	3.7
		SKAU-T-0922	0.187	SKAU-T-1429	3.7
		SKAU-T-1429	0.120		
11.	Pericarp thickness (mm)	SKAU-T-9801	0.439	SKAU-T-1700	7.4
		SKAU-T-1315	0.357	SKAU-T-1429	5.9
		SKAU-T-1700	0.246	SKAU-T-1424	5.4
		SKAU-T-1429	0.242	SKAU-T-1219	5
		SKAU-T-1701	0.212	SKAU-T-0922	4.6
		SKAU-T-9862	0.180		
12	Number of primary branches plant ⁻¹	SKAU-T-9801	0.288	SKAU-T-1464	3.6
		SKAU-T-9862	0.176	SKAU-T-1429	3.5
		SKAU-T-1315	0.155	SKAU-T-1424	3.4
		SKAU-T-1464	0.124	SKAU-T-1315	3.2
		SKAU-T-1219	0.092	SKAU-T-1009	3.2

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Table 12: contd....

S. No.	Trait	Parent GCA		Parent per se performance	
13.	Plant height (cm)	SKAU-T-9801	7.817	SKAU-T-1464	115.2
		SKAU-T-0301	7.565	SKAU-T-1429	114.5
		SKAU-T-1219	4.426	SKAU-T-1424	90.2
		SKAU-T-0922	1.572	SKAU-T-1700	84.7
		SKAU-T-1464	1.484	SKAU-T-9862	84.6
		SKAU-T-1009	1.378		
14.	Average fruit weight (g)	SKAU-T-9801	6.178	SKAU-T-1429	55.6
		SKAU-T-0301	5.794	SKAU-T-1424	55.5
		SKAU-T-1429	4.164	SKAU-T-1009	51.6
		SKAU-T-1700	2.821	SKAU-T-1700	49.9
		SKAU-T-9862	2.651	SKAU-T-9801	48.6
		SKAU-T-0922	2.632		
15.	Fruit yield plant ⁻¹ (kg)	SKAU-T-9801	0.255	SKAU-T-1424	1.79
		SKAU-T-0922	0.187	SKAU-T-9801	1.76
		SKAU-T-1464	0.183	SKAU-T-1009	1.76
		SKAU-T-1700	0.174	SKAU-T-1700	1.75
		SKAU-T-1701	0.145	SKAU-T-1429	1.75
		SKAU-T-9862	0.120		
16.	Fruit yield hectare ⁻¹ (q)	SKAU-T-9801	94.765	SKAU-T-1424	662.96
		SKAU-T-0922	68.474	SKAU-T-1009	653.08
		SKAU-T-1700	64.417	SKAU-T-9801	651.85
		SKAU-T-1701	54.165	SKAU-T-1700	649.38
		SKAU-T-9862	43.900	SKAU-T-1429	648.14

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Table 12: contd....

S. No.	Trait	Parent GCA		Parent per se performance	
17.	Average number of seeds plant ⁻¹	SKAU-T-0301	16.506	SKAU-T-1429	211.1
		SKAU-T-9801	9.456	SKAU-T-0922	135.2
		SKAU-T-0922	9.452	SKAU-T-1219	125.2
		SKAU-T-1464	5.728	SKAU-T-0301	119.9
		SKAU-T-9862	1.394	SKAU-T-1700	115.8
18.	100 Seed weight	SKAU-T-1009	0.280	SKAU-T-1701	0.449
		SKAU-T-1315	0.200	SKAU-T-1315	0.362
		SKAU-T-1700	0.170	SKAU-T-1700	0.303
		SKAU-T-0301	0.170	SKAU-T-1424	0.274
		SKAU-T-1464	0.160	SKAU-T-1464	0.259

Table 13: Best specific cross combinations for different traits on the basis of SCA effect and GCA of parents involved in tomato (*Solanum lycopersicum* L.) (based on individual and pooled analysis)

S. No.	Traits	SCA effect		GCA effect of parents
1.	Number of days to first flowering	SKAU-T-1700 × SKAU-T-9862	-6.503	H × L
		SKAU-T-1700 × SKAU-T-1009	-3.593	H × H
		SKAU-T-1701 × SKAU-T-9862	-3.042	L × L
		SKAU-T-1009 × SKAU-T-1464	-2.983	H × L
		SKAU-T-1219 × SKAU-T-1009	-2.579	H × H
		SKAU-T-1429 × SKAU-T-1464	-2.422	H × L
2.	Number of days to first fruit set	SKAU-T-1700 × SKAU-T-9862	-4.890	H × L
		SKAU-T-1700 × SKAU-T-1009	-4.794	H × H
		SKAU-T-9801 × SKAU-T-9862	-4.704	L × L
		SKAU-T-1429 × SKAU-T-1701	-4.139	H × L
		SKAU-T-1701 × SKAU-T-9862	-3.727	L × L
		SKAU-T-1700 × SKAU-T-0922	-3.592	H × L
3.	Number of days to first fruit harvest	SKAU-T-1219 × SKAU-T-1429	-13.751	H × H
		SKAU-T-1315 × SKAU-T-1009	-10.278	L × H
		SKAU-T-1424 × SKAU-T-1219	-7.287	H × H
		SKAU-T-9801 × SKAU-T-1009	-6.294	L × H
		SKAU-T-1424 × SKAU-T-1315	-6.016	H × L
		SKAU-T-0301 × SKAU-T-1429	-5.897	H × H
4.	Number of flowers cluster ⁻¹	SKAU-T-1429 × SKAU-T-9862	1.823	L × H
		SKAU-T-9801 × SKAU-T-1315	1.462	H × L
		SKAU-T-1700 × SKAU-T-0301	1.427	L × H
		SKAU-T-9801 × SKAU-T-1701	1.193	H × H
		SKAU-T-1315 × SKAU-T-1429	1.089	L × L
		SKAU-T-1701 × SKAU-T-1464	0.987	H × A
		SKAU-T-1315 × SKAU-T-1009	0.955	L × L
		SKAU-T-1429 × SKAU-T-9862	0.832	L × H
5.	Number of fruits cluster ⁻¹	SKAU-T-9801 × SKAU-T-1701	0.778	A × H
		SKAU-T-1700 × SKAU-T-1701	0.767	L × H
		SKAU-T-1700 × SKAU-T-0301	0.734	L × H
		SKAU-T-1315 × SKAU-T-1429	0.715	L × L
		SKAU-T-1700 × SKAU-T-0922	0.711	L × H
		SKAU-T-9801 × SKAU-T-1315	0.697	A × L
6.	Number of pickings	SKAU-T-1424 × SKAU-T-9862	4.748	L × H
		SKAU-T-1424 × SKAU-T-1464	3.567	L × A
		SKAU-T-0301 × SKAU-T-1429	3.518	H × L
		SKAU-T-1700 × SKAU-T-1009	3.060	H × L
		SKAU-T-1219 × SKAU-T-1315	2.625	H × L

Contd....

Table 13: contd....

S. No.	Traits	SCA effect		GCA effect of parents
7.	Number of fruits plant ⁻¹	SKAU-T-1424 × SKAU-T-1464	11.039	L × H
		SKAU-T-9801 × SKAU-T-1219	8.593	H × L
		SKAU-T-1701 × SKAU-T-1009	7.603	H × L
		SKAU-T-1219 × SKAU-T-0301	7.588	L × H
		SKAU-T-0301 × SKAU-T-1464	7.295	H × H
8.	Fruit length (cm)	SKAU-T-1424 × SKAU-T-9862	1.464	L × H
		SKAU-T-0301 × SKAU-T-1429	1.143	H × H
		SKAU-T-1009 × SKAU-T-9862	0.834	H × H
		SKAU-T-1424 × SKAU-T-1464	0.796	L × L
		SKAU-T-1700 × SKAU-T-1009	0.673	H × H
9.	Fruit diameter (cm)	SKAU-T-1424 × SKAU-T-9862	1.846	L × L
		SKAU-T-1429 × SKAU-T-1701	1.491	L × A
		SKAU-T-0922 × SKAU-T-1429	1.319	H × L
		SKAU-T-1009 × SKAU-T-9862	0.987	H × L
		SKAU-T-1700 × SKAU-T-1009	0.863	L × H
10.	Number of locules fruit ⁻¹	SKAU-T-1700 × SKAU-T-1315	2.520	L × L
		SKAU-T-0922 × SKAU-T-9862	2.293	H × H
		SKAU-T-1701 × SKAU-T-9862	1.768	L × H
		SKAU-T-9801 × SKAU-T-0301	1.615	L × H
		SKAU-T-0922 × SKAU-T-1464	1.208	H × H
11.	Pericarp thickness (mm)	SKAU-T-1429 × SKAU-T-1464	2.78	H × H
		SKAU-T-1424 × SKAU-T-9862	1.692	L × H
		SKAU-T-9801 × SKAU-T-1219	1.514	H × L
		SKAU-T-1009 × SKAU-T-9862	1.488	A × H
		SKAU-T-1700 × SKAU-T-1009	1.395	H × A
12.	Number of primary branches plant ⁻¹	SKAU-T-1315 × SKAU-T-0301	1.138	A × L
		SKAU-T-0922 × SKAU-T-1219	1.053	L × A
		SKAU-T-0922 × SKAU-T-1701	0.991	L × L
		SKAU-T-1219 × SKAU-T-1429	0.815	A × L
		SKAU-T-1700 × SKAU-T-1009	0.752	L × H
13.	Plant height (cm)	SKAU-T-1700 × SKAU-T-1009	54.864	L × H
		SKAU-T-1219 × SKAU-T-0301	51.412	H × L
		SKAU-T-1424 × SKAU-T-9862	42.128	L × H
		SKAU-T-1700 × SKAU-T-0922	35.747	L × H
		SKAU-T-0922 × SKAU-T-1219	30.739	H × H
14.	Average fruit weight (g)	SKAU-T-1315 × SKAU-T-1464	28.188	L × H
		SKAU-T-1219 × SKAU-T-1009	20.419	L × L
		SKAU-T-0301 × SKAU-T-1701	19.053	H × H
		SKAU-T-1424 × SKAU-T-9862	17.095	L × H
		SKAU-T-9801 × SKAU-T-1219	14.560	H × L

Contd....

Table 13: contd....

S. No.	Traits	SCA effect		GCA effect of parents
15.	Fruit yield plant ⁻¹ (kg)	SKAU-T-1424 × SKAU-T-1464	0.837	L × H
		SKAU-T-9801 × SKAU-T-1219	0.803	H × L
		SKAU-T-1429 × SKAU-T-1701	0.792	H × H
		SKAU-T-9801 × SKAU-T-1429	0.689	H × H
		SKAU-T-1424 × SKAU-T-9862	0.684	L × H
16.	Fruit yield hactare ⁻¹ (q)	SKAU-T-1424 × SKAU-T-1464	306.606	L × H
		SKAU-T-9801 × SKAU-T-1219	298.909	H × L
		SKAU-T-1429 × SKAU-T-1701	292.860	H × H
		SKAU-T-9801 × SKAU-T-1429	254.760	H × H
		SKAU-T-1424 × SKAU-T-9862	254.075	L × H
17.	Average number of seeds plant ⁻¹	SKAU-T-1424 × SKAU-T-9862	136.424	L × H
		SKAU-T-0301 × SKAU-T-1701	127.395	H × L
		SKAU-T-1315 × SKAU-T-1464	109.868	L × H
		SKAU-T-0922 × SKAU-T-1219	107.188	H × L
		SKAU-T-1009 × SKAU-T-9862	91.188	L × H
18.	100 Seed weight	SKAU-T-1009 × SKAU-T-1464	0.168	H × H
		SKAU-T-1700 × SKAU-T-0922	0.107	H × L
		SKAU-T-1701 × SKAU-T-1464	0.095	H × H
		SKAU-T-1700 × SKAU-T-1429	0.084	H × L
		SKAU-T-9801 × SKAU-T-1424	0.076	L × L

5.4 Gene action for quantitative traits using dialled analysis

Gene action is the behavior or mode of expression of genes in a genetic population. It is measured in terms of genetic variances, combining ability and effects. Diallel design is most common design used for studying gene action. The genetic analysis in the present investigation was done as per the Hayman's approach Model II. As, the Hayman's approach is based on some assumptions, so it is important for the conformity of the data to those assumptions before interpreting the results. Hayman's approach has been criticized by many investigators because of the assumptions underlying the diallel analysis (Kempthorne, 1957, Baker 1978). Among the assumptions uncorrelated gene distribution, absence of epistasis and multiple allelism are impossible to satisfy in practice.

Some investigations (Allard, 1956; Crumpacker and Allard, 1962 and Aksel and Johnson, 1963) found that partial invalidity of assumptions did not create a significant source of bias in the genetic analysis of their respective data. Sangha and Labana (1982) observed that Hayman's method provides detailed description of the relative genetic properties of the inbred lines while, the Griffing's approach stresses statistical concepts of GCA and SCA at the loss of some genetic information. This contention was severely criticized by Arunachalam (1976) saying that there was no such thing in the definition of additive and dominance effects which was genetic and these terms arose from the statistical approaches of Hayman's and Griffing (1956) led Arunachalam (1976) and Baker (1978) to conclude that Griffing's approach for diallel analysis has a more general utility, especially for the plant breeders.

Genetic variances are used for working out various genetic parameters. Six components of variance are worked out i.e., additive variance (D), dominance variance (H), proportion of positive and negative genes in parents (H_2), expected environmental component (E) (F) mean of Fr over the array (Fr= Co-variance of additive and dominant effect in a single array) dominance effect (h^2). These

estimates were used to generate some genetic ratios i.e., average degree of dominance $(H_1/D)^{1/2}$, ratio of dominant and recessive genes in the parents (KD/KR) $[(4DH_1)^{1/2} + F]/[(4DH_1)^{1/2} - F]$, the number of gene groups (h^2/H_2) and the proportion of positive and negative genes $(H_2/4H_1)$, regression coefficient (b), (b-1) (b-0) and t^2 values. Perusal of data pooled over environments (Table-8.1-8.9) indicated that additive genetic variance component (\hat{D}) was significant for all the traits under study except pericarp thickness and 100 seed weight. Measures of dominance components (\hat{H}_1 and \hat{H}_2) were also significant for all the traits. These results indicated the involvement of both additive and dominance components in the inheritance of these traits. However, the magnitude of dominance components, in general, was higher than the corresponding additive component. This suggests the greater role of dominance component in the inheritance of these traits.

The net dominance effect (\hat{h}^2) was significant and positive for number of days to first fruit set, number of fruits plant⁻¹, fruit length, average fruit weight, fruit yield plant⁻¹, fruit yield hectare⁻¹ and average number of seeds fruit⁻¹ suggesting presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance for these traits. For rest of the traits \hat{h}^2 was non-significant and positive suggesting absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance.

\hat{F} values were found to be positive and significant for, number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant⁻¹, fruit diameter, average fruit weight, fruit yield plant⁻¹, fruit yield hectare⁻¹ depicting higher frequency of dominant alleles in the parents with respect to these traits. For rest of traits \hat{F} values were found to be positive and non-significant depicted the equal proportion of frequency of dominant and recessive alleles in the parental genotypes. For

maximum of the traits (E) values i.e., environmental component were found to be non-significant depicted environment plays less role in the expression of traits.

Average degree of dominance (\hat{H}_1/\hat{D})^{0.5} (Table 9.1 to 9.9) was greater than unity in all the characters indicating over dominance in the expression of these traits. This dominance was due to high heterozygosity in F₁ indicating that parents selected were diverse and from different source population. However, the discrepancy in the degree of dominance estimated from genetic components resulted mostly from G × E interaction or from sampling error, which subsequently had an influence on the estimation of dominance components. Further while discussing the limitations of component analysis Mather and Jinks (1971) suggested that due to unequal gene distribution (if u=v=0.5, H₂ / 4H₁ is not equal to 0.25), H₁ gets more inflated than H₂ and result is over estimation of degree of dominance secondly the component D gets also deflated in presence of additive x dominance (j type) of epistasis (Pooni *et al*, 1980). The estimate of $\hat{H}_2 / 4\hat{H}_1$ was less than 0.25 in all the traits revealing asymmetrical distribution of genes in the parents with respect to these traits. While if the values were equal to 0.25 that means symmetrical distribution of genes in the parents. The value of KD/KR i.e., ratio of dominant and recessive genes was greater than unity in all the traits indicating excess of dominant alleles as compared to recessive. The estimates of \hat{h}^2 / \hat{H}_2 were less than 0.50 for all the traits depicted the less proportion of dominant gene groups. Such genetic variation among parents would help in identification of parents carrying genes with positive effects for traits of interest in improvement programme.

The heritability (narrow sense) estimates were found to be low less than 40 for all the traits including number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster⁻¹, number of fruits cluster⁻¹, number of pickings, number of fruits plant⁻¹, fruit length, fruit diameter, number of locules fruit⁻¹, pericarp thickness, number of

primary branches plant⁻¹, plant height, average fruit weight, fruit yield plant⁻¹, fruit yield hectare⁻¹, average number of seeds fruit⁻¹ and 100 seed weight. Similar results with heritability were observed by Bhandari *et al.* (2021) and Ibirinde *et al.* (2022) for various traits. The moderate estimate of heritability in narrow sense indicates the presence of medium degree of non-additive gene action and low narrow sense heritability estimates for most traits indicated that in the present set of materials, the genes were showing non-additive gene action and isolation of high yielding inbreds would not be feasible unless the non-allelic interactions and / or linkage are not dissipated through a selection procedure, which can slow down the rate of homozygosity in the segregating generation. Diallel selective mating design proposed by Jenson (1970) would be appropriate for the present set of material to increase chances of good recombination often fixation of alleles.

The significant values of b-1, t² depicted the presence of epistasis in number of fruits plant⁻¹, fruit length, plant height, average number of seeds fruit⁻¹ and 100 seed weight which was not confirmed the deviation of regression coefficient from zero. Also significant deviation of regression coefficient from unity indicated the presence of epistasis which was not confirmed by non-significant deviation of regression coefficient from zero and non-significant values of t² in number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster⁻¹, number of fruits cluster⁻¹, number of pickings, fruit diameter, number of locules fruit⁻¹, average fruit weight, fruit yield plant⁻¹ and fruit yield hectare⁻¹. Also the significant deviation of regression coefficient from unity, zero and t² values confirmed the presence of epistasis in pericarp thickness.

The results related to above study are in accordance with the findings of Shankar *et al.* (2014), Reddy *et al.* (2016), Triveni *et al.* (2017), Amin *et al.* (2018), Dharva *et al.* (2018), Kumar *et al.* (2018), Rajkumar *et al.* (2018), Veena *et al.* (2019), Vekariya *et al.* (2019), Bindal *et al.* (2019), Singh *et al.* (2021), Gaurani *et al.* (2020), Farwah *et al.* (2022).

5.5 Quality analysis

Signification variation was present in the mean values of the different parents and their crosses (Table-10). Maximum mean value for TSS (°Brix) was found in parent SKAU-T-1315 (7.0) followed SKAU-T-1009 (5.2) and in crosses SKAU-T-1700 × SKAU-T-1219 (6.1) followed by SKAU-T-1315 × SKAU-T-0301 (6). These findings are in support to the findings of Dufera (2013), Jyothi *et al.* (2012), Raju *et al.* (2014). Titrable acidity (%) was found to be maximum in parent SKAU-T-1429 (0.82) followed SKAU-T-0301 (0.72) and in crosses SKAU-T-1429 × SKAU-T-9862 (1.25) followed by SKAU-T-1429 × SKAU-T-1009 (1.21). Lycopene content (mg/100g) was found to be maximum in SKAU-T-1429 (5.69) followed by SKAU-T-9801 (5.42) and in crosses SKAU-T-1429 × SKAU-T-1701 (5.78) followed by SKAU-T-1429 × SKAU-T-1009 (5.67). Juice to pulp ratio was found to be maximum in parent SKAU-T-9801 (3.13) followed by SKAU-T-1701 (3.05) and in crosses SKAU-T-1701 × SKAU-T-1009 (3.15) followed by SKAU-T-1701 × SKAU-T-9862 (3.08). Ascorbic acid content (mg/100g) was found to be maximum in SKAU-T-1429 (47.7) followed by SKAU-T-1464 (47.5) and in crosses SKAU-T-1429 × SKAU-T-9862 (49.5) followed by SKAU-T-1429 × SKAU-T-1009 (46.8). These results are in accordance with the findings of Zahedi *et al.* (2012), Gosavi *et al.* (2010), Cheema *et al.* (2013), Reddy *et al.* (2013). Total Carotenoids (mg/100g) was found to be maximum in SKAU-T-1429 (3.95) followed by SKAU-T-9801 (3.85) and in crosses SKAU-T-1429 × SKAU-T-1464 (5.95) followed by SKAU-T-1429 × SKAU-T-9862 (4.85). Since no genotype could be identified to have superior performance for all the growth, yield and quality characters, Similar pattern of results for quality parameters have also been reported by Ramya *et al.* (2016), Renuka *et al.* (2017), Spaldon and Hussain (2017), Jatav *et al.* (2017), Najeema *et al.* (2018), Venkadeswaran *et al.* (2018), Prakash *et al.* (2019).

5.6 Heterosis

In addition to cross pollinated species, the phenomenon of heterosis has also been commercially exploited in self-pollinated species wherever it was technically feasible because of manifestation of heterosis for different traits. Tomato being a highly self-pollinated species, the scope for exploitation of hybrid vigour depends on the direction and magnitude of heterosis and ease with which hybrid seeds can be produced. Commercial exploitation of hybrid vigour in tomato has received greater importance on account of several advantages of hybrids over pure line varieties with resistance/tolerance to biotic and abiotic stresses. Identification of high yielding and stable varieties and the development of F₁ hybrids will help the farmers to adopt variety/hybrid for successful commercial cultivation of tomato. Heterosis in tomato was first observed by Hedrick and Booth (1907) for higher yield and more number of fruits. The reproductive biology and production of appreciable quantity of seeds per fruit provide plentiful opportunity for manifestation of heterosis in tomato

In the present study, the heterosis was computed over standard parent (economic check) for various yield and yield attributing traits in the pooled data is presented in table-11. The results revealed the wide range of heterotic patterns for different traits. Significant and desirable heterosis over standard parent was observed in SKAU-T-9801 × SKAU-T-1464, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1009, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-1429, SKAU-T-0922 × SKAU-T-9862, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-1315, SKAU-T-1424 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1315, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-0301 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-

1464, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464, SKAU-T-1009 × SKAU-T-9862, SKAU-T-1009 × SKAU-T-1464 and SKAU-T-9862 × SKAU-T-1464 for fruit length; SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464 for fruit diameter. The cross combinations SKAU-T-9801 × SKAU-T-0922, SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1009 × SKAU-T-9862 and SKAU-T-1009 × SKAU-T-1464 showed significant heterosis for number of fruits plant⁻¹; SKAU-T-9801 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-0301, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-9862, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1219, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1701, SKAU-T-1315 × SKAU-T-1464, SKAU-T-0301 × SKAU-T-1429, SKAU-T-1429 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1429 × SKAU-T-1464, SKAU-T-1701 × SKAU-T-1009, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464 for average fruit weight.

The cross combinations SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464 significant heterosis for fruit yield plant⁻¹; SKAU-T-9801 × SKAU-T-1424, SKAU-T-9801 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1701, SKAU-T-1700 × SKAU-T-1424, SKAU-T-1700 × SKAU-T-1219, SKAU-T-1700 × SKAU-T-1315, SKAU-T-1700 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-1464, SKAU-T-0922 × SKAU-T-1424, SKAU-T-0922 × SKAU-T-1315, SKAU-T-0922 × SKAU-T-0301, SKAU-T-1424 × SKAU-T-1219, SKAU-T-1424 × SKAU-T-0301, SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1219 × SKAU-T-1009, SKAU-T-1219 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1464, SKAU-T-1429 × SKAU-T-1009, SKAU-T-1429 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-9862, SKAU-T-1701 × SKAU-T-1464 and SKAU-T-1009 × SKAU-T-1464 for fruit yield hectare⁻¹. The heterosis over standard parent ranged from -27.0 to 52.3 per cent in fruit length; -48.1 to 33.3 per cent in fruit diameter; -58.6 to 30.3 per cent in number of fruits plant⁻¹; -37.6 to 53.5 per cent in average fruit weight; 63.40 to 44.76 per cent in fruit yield plant⁻¹; -63.23 to 46.85 per cent in fruit yield hectare⁻¹.

Significant and desirable heterosis of variable magnitude for various yield and yield attributing traits has been reported by several workers Agarwal *et al.* (2014), Chauhan *et al.* (2014), Paliwal (2016), Kumar *et al.* (2016), Kattagoudar *et al.* (2018), Rakha and Sabry (2019), Soresa *et al.* (2020), Sah *et al.* (2020),

Mishra *et al.* (2021), Izzo *et al.* (2021). The overall genetic analysis suggested high role of dominant genetic variation that could be cause for expression of heterosis. The results obtained from the present study suggest that judicious selection of parents having desirable yield and yield attributing traits is necessary to exploit heterosis in tomato. In order to make hybrid production more feasible, the use of male sterile lines could help to overcome the problems associated with conventional hand emasculatation and pollination practices.

Chapter-6

SUMMARY AND CONCLUSION

The present investigation entitled, “**Heterosis and combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) under temperate conditions of Kashmir**” was undertaken at three locations viz. E₁: Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar; E₂: Krishi Vigyan Kendra, Malangpora Pulwama and E₃: Krishi Vigyan Kendra, Budgam, during the *Kharif* season, 2021-22 to elicit information on the general combining ability effects of parents, specific combining ability effects of crosses, nature and magnitude of gene action involved in the inheritance of various traits and heterosis for fruit yield along with the average degree of dominance, distribution of dominant and recessive genes in the parents and presence or absence of epistasis in twelve diverse lines of tomato crossed in a diallel fashion.

The experimental material for the present investigation consisted of twelve diverse lines of tomato and standard check (Shalimar Tomato Hybrid 2). Sixty-six F₁ crosses were then generated from these twelve diverse lines through 12 × 12 diallel mating design during the *Kharif* season, 2021 as per the Method II and Model I of Griffing (1956 a, b). These twelve parents and sixty six F₁ crosses along with the check were then evaluated in Randomized Block Design during the *kharif* season, 2022 at three locations.

The observations were recorded on eighteen diverse quantitative and six quality traits viz., number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster⁻¹, number of fruits cluster⁻¹, number of pickings, number of fruits plant⁻¹, fruit length (cm), fruit diameter (cm), number of locules fruit⁻¹, pericarp thickness (mm), number of primary branches plant⁻¹, plant height (cm), average fruit weight (g), fruit yield plant⁻¹ (kg), fruit yield hectare⁻¹ (q), average number of seeds fruit⁻¹, 100-seed

weight (g), juice to pulp ratio, titrable acidity (%), lycopene content (mg/100g), ascorbic acid content (mg/100g), TSS (°Brix) and total carotenoids (mg/100g).

The data thus generated in the individual as well as in pooled environments, was then subjected to standard statistical procedures. The results thus obtained are summarized as under:

Analysis of variance revealed highly significant differences among parents and crosses for all traits in all environments as well as in pooled analysis indicating that the material used for the present study was diverse. Variance due to parents vs crosses were found to be significant for all the traits. The genotype \times environment interaction was significant for all the traits except number of locules fruit⁻¹ and 100 seed weight. Parents \times Environments interaction was significant for all the characters except number of locules fruit⁻¹, pericarp thickness and 100 seed weight. Crosses \times Environments interactions were found significant for maximum traits except number of flowers cluster⁻¹, number of locules fruit⁻¹ and 100 seed weight. Parents \times Crosses \times Environments interaction were found significant for all traits except fruit length, fruit diameter, number of locules fruit⁻¹ and pericarp thickness indicating that parents and crosses behaved differently under different environments with respect to these traits.

Analysis of variance for combining ability revealed that mean squares for general and specific combining ability were significant for all the traits in all the environments as well as in data pooled over environments. The estimates of components due to $\hat{\sigma}^2_g$ and $\hat{\sigma}^2_s$ revealed that under present situation, the magnitude of $\hat{\sigma}^2_s$ was greater than that of corresponding $\hat{\sigma}^2_g$ for all the traits indicating the greater role of non-additive gene effects. The magnitude of dominance variance was found to be higher than the corresponding additive variance for all the traits again indicating the importance of non-additive gene action. The ratio of additive genetic variance to dominance variance was also less

than unity for all traits under study in the individual as well as data pooled over environments.

The general combining ability analysis for quantitative traits concluded that none of the parents possessed significant and desirable general combining ability for all the traits concomitantly. However, different parents were found to reveal desirable general combining ability for different traits. The parents exhibiting significant and desirable GCA effects for most of the traits were SKAU-T-9801, SKAU-T-0301, SKAU-T-1464, SKAU-T-9862 and SKAU-T-0922 in individual and data pooled over environments. Hence, these parents could be selected for use in future crop improvement programmes and direct selection for higher values of yield plant⁻¹ can be made in the advanced generations of their heterotic crosses.

The specific combining ability analysis for quantitative traits concluded that none of the crosses possessed significant and desirable specific combining ability for all the traits concomitantly. However, different crosses were found to reveal desirable specific combining ability for different traits. The crosses exhibiting significant and desirable SCA effects for most of the traits were SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-1429, SKAU-T-1700 × SKAU-T-0922 in individual and data pooled over environments. Hence, these crosses with desirable SCA for maximum traits could be selected for use in future breeding programmes.

The additive components (\hat{D}) and those of dominance components (\hat{H}_1 and \hat{H}_2) were found to be significant for maximum traits in all environments and data pooled over environments. This shows the involvement of both additive and dominance components in the inheritance of these traits. The net dominance effect (\hat{h}^2) was significant and positive for number of days to first fruit set, number of fruits plant⁻¹, fruit length, average fruit weight, fruit yield

plant⁻¹, fruit yield hectare⁻¹ and average number of seeds fruit⁻¹. For rest of the traits \hat{h}^2 was non-significant and positive suggesting absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance.

\hat{F} values were found to be positive and significant for, number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of pickings, number of fruits plant⁻¹, fruit diameter, average fruit weight, fruit yield plant⁻¹, fruit yield hectare⁻¹ depicting higher frequency of dominant alleles in the parents with respect to these traits. For rest of traits \hat{F} values were found to be positive and non-significant depicted the equal proportion of frequency of dominant and recessive alleles in the parental genotypes. For maximum traits (E) values i.e., environmental component were found to be non-significant depicted environment plays less role in the expression of traits.

Average degree of dominance $(\hat{H}_1/\hat{D})^{0.5}$ was greater than unity in all the characters indicating over dominance in the expression of these traits. The estimate of $\hat{H}_2/4\hat{H}_1$ was less than 0.25 in all the traits revealing asymmetrical distribution of genes in the parents with respect to these traits. The value of KD/KR was greater than unity in all the traits indicating excess of dominant alleles as compared to recessive. The estimates of \hat{h}^2/\hat{H}_2 were less than 0.50 for all the traits depicted the less proportion of dominant gene groups. The narrow sense heritability estimates were low for maximum traits under study indicating high degree of non-additive gene action.

The significant values of b-1, t^2 depicted the presence of epistasis in number of fruits plant⁻¹, fruit length, plant height, average number of seeds fruit⁻¹ and 100 seed weight which was not confirmed by the deviation of regression coefficient from zero. Also significant deviation of regression coefficient from unity indicated the presence of epistasis which was not confirmed by non-

significant deviation of regression coefficient from zero and non-significant values of t^2 in number of days to first flowering, number of days to first fruit set, number of days to first fruit harvest, number of flowers cluster⁻¹, number of fruits cluster⁻¹, number of pickings, fruit diameter, number of locules fruit⁻¹, average fruit weight, fruit yield plant⁻¹ and fruit yield hectare⁻¹. Also the significant deviation of regression coefficient from unity, zero and t^2 values confirmed the presence of epistasis in pericarp thickness.

Heterosis for yield attributing traits revealed that wide range of heterotic patterns was present among the crosses for different traits. The performance of crosses revealed that crosses SKAU-T-1219 × SKAU-T-1429, SKAU-T-1219 × SKAU-T-1701, SKAU-T-1429 × SKAU-T-1009 and SKAU-T-1700 × SKAU-T-1464 exhibited significant and desirable heterosis over check (Shalimar Tomato Hybrid-2), in individual and data pooled over environments for most of traits. However SKAU-T-1424 × SKAU-T-9862, SKAU-T-1219 × SKAU-T-1315, SKAU-T-9801 × SKAU-T-1700, SKAU-T-9801 × SKAU-T-1429 and SKAU-T-1700 × SKAU-T-0922, exhibited significant and desirable SCA and heterosis for most of the traits. Hence, these crosses could be released after further evaluation.

Based on all the findings of present study, following broad conclusions can be drawn: -

- The analysis of variance concluded that high level of significant variation was present among the parents which indicated that the parental lines selected for the research programme were diverse for all the traits.
- The estimates of additive variance and dominance variance revealed that the magnitude of dominance variance was higher than the additive variance indicating the prevalence of non-additive gene action.

- Significant interaction of GCA and SCA with environment suggests that selection of parents and crosses should be matched with the environment. The greater magnitude of non-additive genetic variance indicates that the situation is favorable for heterosis breeding programme.
- The parental lines with desirable GCA effects for yield attributing and maturity traits, could be crossed with each other to constitute a base population from which subsequent selections can be made.
- The parents involved in the crosses with desirable SCA and heterosis for most of the traits can be used for hybrid development. But before such programme, these parental lines and crosses need to be evaluated vigorously. Further evaluation is also needed over multiple environments to generate information on stability in order to reduce the influence of $G \times E$ interaction.

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APPENDICES

Mean performance of different genotypes (parents with their crosses) for growth, yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) (Data pooled over environments)

PARENT S	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-9801	34.3	48.8	76.6	6.8	3.1	7.2	36.3	3.0	3.6	3.7	3.5	2.6	82.7	48.6	1.76	651.85	77.1	0.169
SKAU-T-1700	31.4	42.3	80.6	5.7	3.5	7.9	34.7	3.5	3.9	2.5	7.4	2.6	84.7	49.9	1.75	649.38	115.8	0.303
SKAU-T-0922	35.9	51.5	85.8	5.1	3.3	4.3	16.1	3.4	3.9	2.6	4.6	2.5	78.9	31.1	0.50	186.42	135.2	0.174
SKAU-T-1424	34.4	44.5	80.5	5.1	2.8	7.5	32.5	4.7	4.8	3.3	5.4	3.4	90.2	55.5	1.79	662.96	111.3	0.274
SKAU-T-1219	31.6	43.5	77.5	5.9	3.5	8.4	31.3	4.1	3.8	5.2	5.0	2.8	79.6	48.3	1.51	558.02	125.2	0.252
SKAU-T-1315	33.6	43.1	77.6	6.6	2.9	7.7	27.9	4.6	4.1	2.5	4.4	3.2	74.0	30.3	0.84	311.02	89.4	0.362
SKAU-T-0301	34.3	45.4	82.3	5.6	3.3	7.8	22.0	4.3	3.6	2.4	4.3	3.1	81.6	36.2	0.79	293.82	119.9	0.241
SKAU-T-1429	35.0	47.4	86.5	5.3	2.6	7.8	31.5	5.2	5.2	3.7	5.9	3.5	114.5	55.6	1.75	648.14	211.1	0.258
SKAU-T-1701	30.4	42.6	81.5	6.1	3.9	6.8	20.3	3.6	3.9	3.2	4.2	2.6	74.9	34.4	0.70	258.84	87.1	0.449
SKAU-T-1009	35.2	46.4	80.5	6.5	3.7	8.1	34.2	4.6	3.1	2.6	4.4	3.2	68.7	51.6	1.76	653.08	74.9	0.249
SKAU-T-9862	36.3	47.4	82.0	5.2	3.3	6.8	17.4	4.1	3.8	3.8	4.1	3.2	84.6	41.9	0.73	270.37	103.4	0.161
SKAU-T-1464	35.4	46.9	80.6	5.0	3.8	8.1	22.2	4.7	5.1	4.5	3.4	3.6	115.2	35.7	0.79	293.82	48.3	0.259

CROSSES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-9801 × SKAU-T-1700	32.5	41.8	81.5	6.5	2.9	4.0	16.9	2.9	2.2	2.4	3.7	2.4	71.9	31.0	0.52	194.77	102.7	0.257
SKAU-T-9801 × SKAU-T-0922	34.5	43.6	77.8	5.6	3.8	7.1	34.1	3.9	4.0	2.3	3.0	3.3	63.6	32.0	1.08	400.41	174.1	0.194
SKAU-T-9801 × SKAU-T-1424	33.6	44.6	77.9	6.8	3.9	7.9	34.5	3.9	3.9	2.7	2.6	3.3	61.4	51.4	1.77	655.55	110.4	0.187
SKAU-T-9801 × SKAU-T-1219	31.7	42.5	76.5	6.1	3.3	6.5	20.0	2.9	4.2	3.3	3.2	3.2	95.9	36.7	0.73	272.01	65.5	0.313
SKAU-T-9801 × SKAU-T-1315	33.8	46.2	77.4	5.8	2.8	7.2	34.2	3.9	3.0	2.7	5.4	3.0	69.3	54.7	1.87	691.35	62.4	0.224
SKAU-T-9801 × SKAU-T-0301	34.6	46.5	78.8	7.5	3.8	5.5	19.2	3.0	2.7	2.7	3.0	2.7	71.3	31.3	0.61	224.68	119.9	0.246
SKAU-T-9801 × SKAU-T-1429	35.4	45.6	79.6	6.4	3.1	4.1	12.3	3.0	3.9	5.2	3.4	2.8	75.9	44.7	0.55	204.93	203.4	0.213
SKAU-T-9801 × SKAU-T-1701	32.6	43.4	73.5	5.6	3.0	8.6	36.3	3.7	4.1	2.9	4.3	3.4	72.9	49.8	1.79	661.72	150.6	0.169

CROSS ES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-9801 × SKAU-T-1009	35.0	46.5	82.6	5.7	3.9	8.3	30.2	3.9	3.6	2.7	4.1	3.2	99.4	32.2	0.97	361.31	50.6	0.272
SKAU-T-9801 × SKAU-T-9862	34.4	44.5	72.6	5.2	3.8	8.1	27.4	3.4	4.0	4.2	4.6	3.6	69.6	32.1	0.89	331.68	128.9	0.206
SKAU-T-9801 ES × SKAU-T-1464	32.5	40.6	78.9	6.3	3.2	7.7	18.3	4.1	2.6	3.6	3.1	2.7	83.9	41.2	0.75	278.60	147.5	0.220
SKAU-T-1700 × SKAU-T-0922	34.5	43.2	80.8	5.7	2.8	8.8	30.3	2.8	3.9	4.1	4.4	3.4	76.1	46.5	1.41	520.98	114.3	0.293
SKAU-T-1700 × SKAU-T-1424	31.4	43.1	79.9	6.0	3.1	9.2	38.8	4.1	4.4	2.8	3.1	2.5	69.2	49.1	1.91	706.17	110.1	0.287
SKAU-T-1700 × SKAU-T-1219	33.5	41.7	77.7	5.9	4.1	10.3	37.3	4.1	3.9	3.1	5.0	2.7	115.8	49.6	1.85	683.95	123.1	0.371
SKAU-T-1700 × SKAU-T-1315	30.5	40.2	73.7	6.4	3.2	7.6	36.4	3.6	3.3	3.5	4.5	2.4	58.6	50.6	1.84	681.48	96.6	0.257
SKAU-T-1700 × SKAU-T-0301	33.1	46.5	79.6	6.1	3.3	8.3	21.5	3.5	4.1	3.4	4.6	2.9	70.3	53.1	1.14	424.69	133.7	0.220
SKAU-T-1700 × SKAU-T-1429	35.1	46.3	84.5	5.4	2.4	9.4	35.8	2.7	4.3	5.5	5.0	2.6	82.0	53.8	1.92	712.34	173.3	0.273

CROSSES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-1700 × SKAU-T-1701	32.6	42.5	78.5	4.5	3.4	6.2	14.3	3.9	3.9	3.1	5.1	2.6	72.2	41.5	0.60	221.39	113.5	0.269
SKAU-T-1700 × SKAU-T-1009	34.1	44.5	75.5	5.6	2.5	8.9	25.4	4.5	3.9	2.7	5.2	2.7	71.3	43.5	1.10	409.05	142.0	0.330
SKAU-T-1700 × SKAU-T-9862	31.5	43.0	75.8	6.1	3.0	9.9	20.3	3.8	3.5	2.6	5.3	2.6	67.8	52.7	1.07	396.29	102.6	0.301
SKAU-T-1700 × SKAU-T-1464	29.5	39.1	81.6	5.8	3.5	11.7	34.9	4.7	5.2	3.0	5.9	3.7	134.7	57.5	2.00	741.97	123.4	0.287
SKAU-T-0922 × SKAU-T-1424	40.4	50.1	77.7	5.0	3.1	7.6	33.4	3.7	4.1	2.4	4.0	2.7	60.8	56.4	1.88	687.65	132.8	0.162
SKAU-T-0922 × SKAU-T-1219	35.3	46.5	76.7	6.2	3.9	8.7	23.1	3.6	3.9	2.8	4.5	3.4	79.2	51.9	1.20	429.87	127.9	0.206
SKAU-T-0922 × SKAU-T-1315	35.1	51.2	80.5	6.3	3.1	10.1	30.7	4.5	4.0	2.4	4.0	3.6	77.4	64.9	1.99	738.26	115.3	0.261
SKAU-T-0922 × SKAU-T-0301	38.3	51.5	86.8	6.1	2.9	8.1	33.7	3.7	2.6	2.3	3.4	2.6	67.2	56.3	1.89	699.99	149.9	0.221
SKAU-T-0922 × SKAU-T-1429	33.3	43.7	84.5	5.5	3.4	9.2	26.8	4.5	2.8	2.5	4.3	4.2	120.8	42.9	1.15	427.15	234.5	0.242

CROSS ES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-0922 × SKAU-T-1701	32.5	44.7	79.6	5.6	3.3	7.8	23.0	3.8	3.7	2.4	4.0	2.3	76.8	34.7	0.80	295.88	170.6	0.246
SKAU-T-0922 × SKAU-T-1009	34.3	42.6	77.6	6.3	4.2	8.2	31.2	3.8	2.7	2.9	3.6	3.2	79.5	36.1	1.13	416.87	163.4	0.245
SKAU-T-0922 × SKAU-T-9862	32.3	45.4	81.5	6.0	4.0	8.2	29.0	4.4	5.1	2.6	4.7	2.4	96.8	41.6	1.21	446.91	140.8	0.211
SKAU-T-0922 × SKAU-T-1464	34.5	46.8	82.1	6.1	3.0	8.9	26.0	3.8	3.9	2.7	4.0	4.1	72.9	49.1	1.28	473.66	122.9	0.241
SKAU-T-1424 × SKAU-T-1219	35.2	46.5	81.5	5.2	2.8	9.1	32.7	4.7	4.2	2.4	3.8	2.5	96.5	54.7	1.79	661.72	66.9	0.297
SKAU-T-1424 × SKAU-T-1315	33.3	50.5	84.2	6.4	4.1	6.8	26.2	4.3	4.0	5.6	4.4	2.5	93.1	38.6	1.01	364.19	123.4	0.270
SKAU-T-1424 × SKAU-T-0301	32.5	42.9	75.4	6.6	3.8	9.2	34.3	3.8	3.6	4.4	3.6	2.3	78.8	53.1	1.82	672.83	154.1	0.169
SKAU-T-1424 × SKAU-T-1429	32.5	42.3	81.5	5.8	3.9	8.3	25.2	4.2	3.9	3.9	4.1	2.8	94.6	49.6	1.25	462.96	105.6	0.276
SKAU-T-1424 × SKAU-T-1701	33.5	41.6	86.5	5.7	3.9	6.9	25.8	3.6	4.1	2.6	3.9	3.0	89.0	36.0	0.93	345.26	160.0	0.221

CROSS ES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-1424 × SKAU-T-1009	31.5	41.9	75.9	6.3	2.8	7.6	29.3	3.9	3.5	2.3	4.0	3.4	82.4	40.1	1.18	435.39	83.6	0.234
SKAU-T-1424 × SKAU-T-9862	34.4	42.5	81.5	5.8	3.9	5.9	24.2	3.9	4.1	2.2	4.3	2.6	78.2	30.0	0.74	274.89	89.5	0.242
SKAU-T-1424 × SKAU-T-1464	34.5	42.7	81.7	5.6	4.1	6.3	27.0	3.4	3.6	4.2	4.2	2.6	81.2	29.9	0.81	299.17	130.8	0.222
SKAU-T-1219 × SKAU-T-1315	36.6	48.4	85.5	5.4	3.9	6.5	17.5	4.0	3.9	2.5	3.7	3.1	73.9	46.3	0.81	300.41	114.0	0.239
SKAU-T-1219 × SKAU-T-0301	31.6	40.3	76.5	5.9	3.0	8.0	30.4	3.6	3.9	2.5	2.6	2.3	67.4	41.1	1.25	461.72	111.9	0.227
SKAU-T-1219 × SKAU-T-1429	32.2	43.6	85.8	5.9	4.1	12.7	32.4	5.6	5.7	3.3	6.0	3.4	124.9	64.0	2.07	777.77	261.2	0.238
SKAU-T-1219 × SKAU-T-1701	31.5	43.6	76.6	6.0	3.4	11.6	37.5	4.8	5.0	3.0	5.4	2.2	81.0	54.8	2.05	759.25	164.2	0.262
SKAU-T-1219 × SKAU-T-1009	35.4	45.4	75.9	5.4	3.5	11.1	35.7	4.3	3.9	2.3	4.4	2.7	76.3	50.9	1.82	672.42	118.7	0.130
SKAU-T-1219 × SKAU-T-9862	31.3	44.5	78.4	6.0	3.4	10.9	31.4	3.8	4.6	3.1	3.1	2.8	92.6	49.3	1.55	572.42	49.2	0.247

CROSS ES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-1219×SKAU-T-1464	32.5	42.5	78.5	5.9	3.8	10.9	34.0	4.3	4.1	2.4	5.1	2.8	147.4	56.0	1.91	706.17	140.7	0.259
SKAU-T-1315 × SKAU-T-0301	33.5	44.6	62.3	6.2	3.2	6.4	24.4	3.9	3.7	2.7	4.3	3.8	93.0	30.0	0.73	272.01	101.1	0.228
SKAU-T-1315 × SKAU-T-1429	32.6	42.3	76.3	4.9	2.7	9.1	27.3	3.3	4.3	2.6	4.0	3.7	88.3	45.2	1.23	455.96	131.2	0.223
SKAU-T-1315 × SKAU-T-1701	30.2	45.5	79.4	5.4	3.6	8.2	22.6	3.8	4.8	3.0	3.7	3.4	90.5	65.9	1.49	551.02	94.6	0.251
SKAU-T-1315 × SKAU-T-1009	31.5	43.1	78.0	5.8	4.2	7.4	27.2	3.9	3.9	2.8	4.3	2.3	70.8	35.3	0.96	355.96	78.9	0.228
SKAU-T-131 × SKAU-T-9862	32.4	45.3	81.4	5.4	3.9	4.9	17.6	3.8	3.8	3.0	4.1	2.7	69.5	31.3	0.55	203.70	98.3	0.217
SKAU-T-1315×SKAU-T-1464	37.2	45.8	85.3	5.9	3.3	7.8	27.4	4.4	4.1	2.4	4.3	3.4	105.6	52.7	1.43	534.56	68.6	0.240
SKAU-T-0301×SKAU-T-1429	32.5	46.5	79.4	5.5	2.5	7.2	24.2	4.4	4.4	4.1	3.7	4.3	93.4	54.1	1.31	484.36	200.1	0.293
SKAU-T-0301×SKAU-T-1701	34.7	44.6	81.4	4.7	3.9	7.9	29.3	3.9	4.0	2.4	3.2	3.6	81.1	41.7	1.22	452.26	145.9	0.246
SKAU-T-0301 × SKAU-T-1009	34.6	46.4	81.9	5.6	3.0	7.8	30.1	4.4	3.9	3.7	3.1	2.6	84.3	39.8	1.20	444.03	91.9	0.240

CROSS ES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-0301 × SKAU-T-9862	33.6	47.5	70.9	6.6	3.7	7.0	28.9	3.7	4.2	2.8	4.8	3.0	61.1	34.8	1.01	372.42	82.9	0.241
SKAU-T-0301 × SKAU-T-1464	34.9	48.3	84.3	6.0	2.5	7.2	28.8	3.5	3.9	2.8	4.1	3.6	66.9	40.1	1.15	426.33	112.8	0.252
SKAU-T-1429 × SKAU-T-1701	35.5	44.5	86.4	5.0	3.1	7.8	20.8	4.4	3.8	2.5	3.0	3.2	90.5	73.7	1.53	566.66	227.1	0.249
SKAU-T-1429 × SKAU-T-1009	30.5	45.6	79.8	6.6	3.4	11.5	34.3	4.6	5.2	3.6	4.3	3.4	92.4	59.3	2.03	751.85	178.5	0.263
SKAU-T-1429 × SKAU-T-9862	31.5	43.5	71.3	6.0	2.4	11.9	35.4	5.5	5.2	4.6	4.2	2.3	107.6	58.4	2.06	764.19	137.7	0.257
SKAU-T-1429 × SKAU-T-1464	34.2	48.4	82.5	6.3	2.6	9.0	18.7	4.4	4.9	3.9	4.2	2.9	108.9	70.1	1.31	483.53	286.2	0.298
SKAU-T-1701 × SKAU-T-1009	34.7	46.5	81.6	5.7	3.3	7.3	21.4	3.7	3.9	4.1	2.7	2.8	78.4	55.1	1.18	435.39	159.1	0.321
SKAU-T-1701 × SKAU-T-9862	33.3	46.5	82.3	6.9	3.9	8.1	25.0	4.1	4.2	3.5	4.3	3.1	79.3	63.9	1.60	592.59	116.0	0.205
SKAU-T-1701 × SKAU-T-1464	33.4	44.6	77.5	6.5	3.3	9.0	32.0	4.5	4.5	3.1	5.0	2.8	86.1	53.7	1.72	637.44	202.7	0.222

CROSS ES	Number of days to first flowering	Number of days to first fruit set	Number of days to first fruit harvest	Number of flowers cluster ⁻¹	Number of fruits cluster ⁻¹	Number of pickings	Number of fruits plant ⁻¹	Fruit length (cm)	Fruit diameter (cm)	Number of locules fruit ⁻¹	Pericarp thickness	Number of primary branches plant ⁻¹	Plant height (cm)	Average fruit weight (g)	Fruit yield plant ⁻¹	Fruit yield hectare ⁻¹ (q)	Average number of seeds fruit ⁻¹	100 Seed Weight
SKAU-T-1009 × SKAU-T-9862	35.5	45.6	80.5	6.0	3.8	7.5	37.3	4.7	3.1	3.7	4.1	2.5	76.4	32.1	1.19	443.21	114.2	0.218
SKAU-T-1009 × SKAU-T-1464	32.8	41.5	77.4	5.6	3.5	10.0	36.0	4.7	5.7	3.2	5.3	3.1	80.6	55.5	2.00	740.74	91.9	0.268
SKAU-T-9862 × SKAU-T-1464	36.1	48.1	83.5	5.7	3.5	6.3	27.5	4.0	4.0	3.7	3.7	3.3	70.8	29.6	0.81	301.23	160.3	0.176
Mean	33.63	44.90	79.66	5.87	3.39	8.11	27.97	4.01	4.02	3.16	4.22	3.00	84.04	46.25	1.31	485.45	127.55	0.24
C.V	0.67	0.24	0.20	1.59	1.92	0.79	0.77	1.25	1.17	2.18	1.19	2.14	0.49	0.66	1.79	1.90	0.41	0.93
S.Em±	0.13	0.06	0.09	0.05	0.03	0.03	0.12	0.02	0.02	0.03	0.02	0.03	0.24	0.17	0.01	5.32	0.30	0.01
C.D at 5%	0.36	0.17	0.26	0.15	0.10	0.10	0.35	0.08	0.07	0.11	0.08	0.10	0.67	0.49	0.03	14.89	0.86	0.02

Mean performance of tomato (*Solanum lycopersicum L.*) genotypes (parents with their crosses) for different quality traits (individual and pooled date)

PARENTS	TSS(°Brix)	Ascorbic acid (mg/100gm)	Juice to pulp ratio	Lycopene content (mg/100gm)	Titration Acidity(% citric acid)	Carotenoid content (mg/100gm)
SKAU-T 9801	4.1	30.2	3.13	5.42	0.28	3.85
SKAU-T-1700	3.2	23.5	1.48	4.72	0.38	2.89
SKAU-T-0922	3.5	26.1	1.05	3.25	0.21	3.71
SKAU-T-1424	3.4	28.7	2.30	4.37	0.26	3.21
SKAU-T-1219	4.4	30.9	1.32	4.32	0.33	3.40
SKAU-T-1315	7.0	20.1	1.21	3.85	0.23	2.69
SKAU-T-0301	4.2	31.5	1.89	4.75	0.72	2.85
SKAU-T-1429	4.7	47.7	2.14	5.69	0.82	3.95
SKAU-T-1701	4.4	33.3	3.05	2.95	0.16	3.54
SKAU-T-1009	5.2	22.8	1.13	3.23	0.25	2.83
SKAU-T-9862	4.3	18.9	2.80	2.79	0.32	2.10
SKAU-T-1464	3.9	37.5	1.85	3.87	0.43	2.66
CROSSES						
SKAU-T-9801 × SKAU-T-1700	3.5	34.2	2.41	4.78	0.32	4.05
SKAU-T-9801 × SKAU-T-0922	4.1	32.7	2.35	4.52	0.25	4.20
SKAU-T-9801 × SKAU-T-1424	3.3	35.4	1.85	5.23	0.3	4.35
SKAU-T-9801 × SKAU-T-1219	4.0	31.8	3.01	4.15	0.34	3.95
SKAU-T-9801 × SKAU-T-1315	4.1	37.2	2.48	4.32	0.24	4.12
SKAU-T-9801 × SKAU-T-0301	4.0	30.9	1.98	4.05	0.29	4.00
SKAU-T-9801 × SKAU-T-1429	5.1	33.2	1.78	5.12	0.36	3.92

CROSSES	TSS(°Brix)	Ascorbic acid (mg/100gm)	Juice to pulp ratio	Lycopene content (mg/100gm)	Titration Acidity(% citric acid)	Carotenoid content (mg/100gm)
SKAU-T-9801 × SKAU-T-1701	4.4	38.6	2.32	3.98	0.4	4.45
SKAU-T-9801 × SKAU-T-1009	5.1	30.4	2.62	4.68	0.42	4.62
SKAU-T-9801 × SKAU-T-9862	5.2	31.4	1.92	4.92	0.31	3.78
SKAU-T-9801 × SKAU-T-1464	3.6	36.2	2.46	5.02	0.26	3.89
SKAU-T-1700 × SKAU-T-0922	5.1	30.8	1.23	4.32	0.43	3.32
SKAU-T-1700 × SKAU-T-1424	4.2	33.8	1.52	5.20	0.45	3.44
SKAU-T-1700 × SKAU-T-1219	6.1	35.4	1.62	4.62	0.39	3.48
SKAU-T-1700 × SKAU-T-1315	3.2	32.6	1.48	4.82	0.36	3.30
SKAU-T-1700 × SKAU-T-0301	4.4	30.2	1.41	3.78	0.47	3.50
SKAU-T-1700 × SKAU-T-1429	5.1	31.4	1.36	5.34	0.37	3.62
SKAU-T-1700 × SKAU-T-1701	5.2	28.7	1.68	4.15	0.41	3.42
SKAU-T-1700 × SKAU-T-1009	4.1	29.4	1.72	4.68	0.36	3.38
SKAU-T-1700 × SKAU-T-9862	3.3	27.5	1.38	3.78	0.34	2.80
SKAU-T-1700 × SKAU-T-1464	4.2	32.8	1.46	4.10	0.32	3.08
SKAU-T-0922 × SKAU-T-1424	5.2	35.8	1.15	3.92	0.28	3.92
SKAU-T-0922 × SKAU-T-1219	4.3	32.1	1.23	3.62	0.32	4.21
SKAU-T-0922 × SKAU-T-1315	4.4	30.4	1.28	4.38	0.34	4.48
SKAU-T-0922 × SKAU-T-0301	3.5	36.4	1.31	3.78	0.36	4.52
SKAU-T-0922 × SKAU-T-1429	4.1	38.8	1.11	4.92	0.25	4.65

CROSSES	TSS(°Brix)	Ascorbic acid (mg/100gm)	Juice to pulp ratio	Lycopene content (mg/100gm)	Titration Acidity(% citric acid)	Carotenoid content (mg/100gm)
SKAU-T-0922 × SKAU-T-1701	3.4	27.4	1.18	4.28	0.26	4.72
SKAU-T-0922 × SKAU-T-1009	3.5	28.9	1.29	4.52	0.29	4.75
SKAU-T-0922 × SKAU-T-9862	4.2	30.9	1.34	3.42	0.30	4.62
SKAU-T-0922 × SKAU-T-1464	4.2	31.2	1.36	5.48	0.37	4.34
SKAU-T-1424 × SKAU-T-1219	3.4	37.2	2.42	4.72	0.30	3.52
SKAU-T-1424 × SKAU-T-1315	4.3	33.2	2.12	3.32	0.32	3.48
SKAU-T-1424 × SKAU-T-0301	4.1	35.2	2.24	3.72	0.28	3.57
SKAU-T-1424 × SKAU-T-1429	4.4	31.4	2.31	4.78	0.42	3.50
SKAU-T-1424 × SKAU-T-1701	4.1	28.5	2.45	3.68	0.45	3.62
SKAU-T-1424 × SKAU-T-1009	3.5	30.8	2.80	3.42	0.36	3.72
SKAU-T-1424 × SKAU-T-9862	4.3	29.5	1.85	3.15	0.29	3.28
SKAU-T-1424 × SKAU-T-1464	5.1	32.5	1.68	4.19	0.31	3.45
SKAU-T-1219 × SKAU-T-1315	4.6	28.9	1.38	4.52	0.38	3.80
SKAU-T-1219 × SKAU-T-0301	3.7	27.4	1.42	3.62	0.42	4.21
SKAU-T-1219 × SKAU-T-1429	4.2	35.7	1.24	3.92	0.44	4.24
SKAU-T-1219 × SKAU-T-1701	5.1	33.5	1.52	2.94	0.46	4.28
SKAU-T-1219 × SKAU-T-1009	4.2	28.4	1.18	3.32	0.52	4.29
SKAU-T-1219 × SKAU-T-9862	4.2	30.4	1.15	3.81	0.55	4.32
SKAU-T-1219 × SKAU-T-1464	4.5	31.4	1.36	3.42	0.35	4.15

CROSSES	TSS(°Brix)	Ascorbic acid (mg/100gm)	Juice to pulp ratio	Lycopene content (mg/100gm)	Titration Acidity(% citric acid)	Carotenoid content (mg/100gm)
SKAU-T-1315 × SKAU-T-0301	6.0	28.7	1.28	3.95	0.34	3.41
SKAU-T-1315 × SKAU-T-1429	4.1	23.2	1.32	2.75	0.25	3.21
SKAU-T-1315 × SKAU-T-1701	4.0	30.8	1.18	2.45	0.27	3.15
SKAU-T-1315 × SKAU-T-1009	4.2	21.8	1.22	3.54	0.29	2.94
SKAU-T-131 × SKAU-T-9862	3.4	25.4	1.35	2.68	0.32	2.78
SKAU-T-1315 × SKAU-T-1464	5.0	34.5	1.37	3.82	0.38	3.48
SKAU-T-0301 × SKAU-T-1429	4.1	32.5	1.62	4.48	0.82	3.95
SKAU-T-0301 × SKAU-T-1701	4.2	30.4	1.78	4.21	0.78	3.85
SKAU-T-0301 × SKAU-T-1009	5.3	31.2	1.82	3.92	0.94	3.92
SKAU-T-0301 × SKAU-T-9862	4.2	28.7	1.96	3.72	1.02	4.20
SKAU-T-0301 × SKAU-T-1464	4.4	29.5	1.75	3.64	0.86	4.26
SKAU-T-1429 × SKAU-T-1701	4.3	38.7	1.86	5.78	0.96	4.20
SKAU-T-1429 × SKAU-T-1009	3.6	46.8	2.18	5.67	1.21	4.25
SKAU-T-1429 × SKAU-T-9862	4.3	49.5	2.28	4.92	1.25	4.85
SKAU-T-1429 × SKAU-T-1464	4.5	36.3	2.32	4.78	1.06	5.95
SKAU-T-1701 × SKAU-T-1009	4.3	34.8	3.15	2.98	0.21	4.20
SKAU-T-1701 × SKAU-T-9862	3.4	32.5	3.08	3.12	0.24	4.12
SKAU-T-1701 × SKAU-T-1464	4.2	31.2	2.85	2.42	0.28	3.82
SKAU-T-1009 × SKAU-T-9862	5.3	34.7	1.17	3.52	0.42	3.42

CROSSES	TSS(°Brix)	Ascorbic acid (mg/100gm)	Juice to pulp ratio	Lycopene content (mg/100gm)	Titration Acidity(% citric acid)	Carotenoid content (mg/100gm)
SKAU-T-1009 × SKAU-T-1464	3.8	38.4	1.21	3.12	0.54	3.74
SKAU-T-9862 × SKAU-T-1464	4.4	25.8	2.62	2.82	0.45	2.92
Mean	4.3	31.88	1.81	4.08	0.43	3.78
SD	0.70	5.29	0.59	0.81	0.23	0.63
CV	0.16	0.16	0.33	0.20	0.55	0.16

Metrological data of Shalimar for the year 2022

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-01-22	6.5	-4	0	92	59	0
2	6.5	-0.6	2.4	97	71	0
3	6	2	0	88	73	0
4	2.5	-0.5	5.2	93	83	0
5	2	0	14.8	93	93	0
6	5.5	-0.5	18.8	97	97	0
7	4	1.4	5.8	90	91	0
8	3.5	-0.5	20.5	93	93	0
9	2	-0.7	31	87	90	0
10	4	-0.5	0	93	85	0
11	5.5	-2	0	93	79	2.3
12	5.5	-4	0	92	70	4.2
13	5	-4	0	92	94	0
14	6.5	-3.6	0	92	76	5.6
15	6	-5.5	0	96	79	3.1
16	7.5	-2	0	83	71	2.3
17	4	-1	0	93	84	0
18	5.5	1.5	0	94	84	0
19	3.5	2	0	94	81	0
20	8	1.5	4.8	94	72	0
21	8.5	1.9	0	88	67	0
22	4.5	1.5	1.2	88	91	0
23	4.5	0	4.6	93	82	0
24	8.6	-0.5	6	84	62	0
25	9.5	1	1.2	91	67	2
26	8.5	-0.5	20.4	93	72	0
27	8.5	-2	2	93	67	4.7
28	8.5	-5	0	82	70	7.8
29	11	-1.5	0	78	46	5.8
30	10.5	-3	0	90	52	6.6
31	10	-2.5	0	93	67	4.5

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-02-22	10.5	1	1.2	91	52	2.7
2	6	-2.5	0	83	85	6.2
3	3.5	-0.5	7	90	85	0
4	10	0	11.8	94	45	0
5	11	-3.5	0	83	39	7.7
6	5.5	0.5	0	85	89	0
7	7.5	1.8	1.4	85	87	0
8	11	-0.5	1.6	85	54	6.6
9	11.5	-1	0	85	52	6.8
10	11.5	-1	0	83	52	7.9
11	11.5	-4	0	85	50	8
12	12.5	-4	0	96	54	6.3
13	13.5	-3	0	89	61	6.9
14	11	-1	0	85	52	0
15	13.5	-1	0	79	50	5.1
16	15	-1	0	85	42	6.9
17	14	-2	0	83	37	5.9
17	11	-1	0	83	54	1.8
18	15	-2.5	0	83	37	5.4
20	14	-2	0	89	29	7.7
21	15.5	-3	0	86	28	7.5
22	4.5	2	0	77	84	0
23	3	-0.5	77.2	90	84	0
24	6	-0.5	40	91	94	0
25	5	0.5	0	97	94	0
26	9	0	7.4	85	62	3.4
27	11	1	4	85	54	6.9
28	9.5	-2	0	84	64	0

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-03-22	7	3	0	86	74	0
2	11	3.5	1.4	86	66	0
3	9	3	0	87	83	0
4	11.5	4	11.4	92	72	0
5	14.5	2	0	87	58	5.7
6	16	4.5	0	83	61	2
7	9.5	6.5	0	87	80	0
8	14.5	4.5	10.8	87	58	3.2
9	17	4.5	0	83	52	5.5
10	18.5	3.5	0	85	51	5.5
11	21	3	0	87	30	7.8
12	20	3	0	87	46	5.4
13	22.5	3.5	0	75	32	7.7
14	23.5	5	0	77	43	7.6
15	23	9	1	73	46	8.8
16	24.5	6.5	0	74	42	9.2
17	25	6	0	64	26	9.2
18	26.5	6	0	69	33	7.6
19	18	10.5	4.8	69	49	3.4
20	19.5	6.5	6.4	89	48	2.2
21	22	5	0	77	40	8.9
22	23.5	5	0	78	38	9.3
23	25	5	0	72	31	6.8
24	18.5	7.5	6.2	81	48	7.6
25	22	4.5	0	78	27	9.4
26	23.5	3	0	58	21	8.6
27	25	4.5	0	88	26	8.8
28	27	6.5	0	78	20	9
29	27	5.5	0	79	25	9.6
30	26.5	5.5	0	64	21	9.5
31	25.5	5.5	0	69	21	9.8

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-04-22	25.5	4.5	0	61	23	8.8
2	26.5	6	0	74	25	8.5
3	24.5	7.5	0	69	42	8.9
4	25	6	0	75	32	9.5
5	25.5	6	0	69	34	9.4
6	27	6.5	0	63	28	10.2
7	28	6.5	0	64	25	10.3
8	28	6.6	0	63	28	7.6
9	22	7	0	57	52	3.5
10	26.5	6.5	0	78	41	9.7
11	28	7	0	62	45	7.5
12	25.5	8	0	63	61	1.4
13	19.5	11.5	3.4	80	73	0
14	19	6	1	78	69	3.2
15	22	5	0	69	39	9.1
16	24	6.5	0	71	47	7.3
17	27	6	0	63	46	8.3
18	28	7.5	0	71	30	6.7
19	21.5	8	0	80	58	3.8
20	21.5	8	1.4	75	73	0
21	11.5	9	12.4	81	95	0
22	16	8	9.6	89	62	1.3
23	19	8	0.2	79	57	7.7
24	23	5	0	67	19	7
25	22.5	10	0	80	46	4.6
26	23.6	6.5	3.6	65	36	11.1
27	27.5	7.5	0	80	40	10.8
28	27.5	9.5	0	72	43	5.2
29	22.5	10.5	6.2	80	53	5.5
30	25.5	9	0	81	61	6.2

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-05-22	29	10	0	71	24	11.4
2	25.5	11	0	73	42	5.6
3	21	12.5	0	69	58	2
4	16	10	7.2	85	90	0
5	22	9.5	7.2	84	46	7.3
6	24	9.5	0	90	80	7.3
7	26	7.5	16.4	63	45	10.7
8	28.5	10	0	81	37	2.9
9	29.5	10.5	0	73	51	8.9
10	28.5	10	0	73	36	10.9
11	30	11.6	0	73	29	11.1
12	28.5	11	0	66	36	8.3
13	29.5	11	0	59	29	10.8
14	30.5	10	0	58	34	10.7
15	28	10.5	0	76	45	5
16	25.5	14	0	65	68	2.7
17	27	9.5	0	62	45	7.3
18	26.5	9	0	65	45	9.7
19	28.5	10.5	0	76	44	4.8
20	18	10.5	0	80	90	6
21	21	10	11.6	89	59	5.4
22	25.5	8	0	90	59	7.6
23	21.5	10.5	5	63	56	3.1
24	23.5	9.5	5	68	46	10.8
25	26.6	9.5	0	73	47	10.8
26	28.5	12	0	67	46	9
27	28.5	11	1.6	66	44	5.2
28	22	12.5	11	81	47	0
29	25.5	11.5	0	77	47	4.8
30	25	13	0	63	41	5.3
31	25	11.5	0.8	59	49	4.9

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-06-22	24	13.5	0	65	53	4.5
2	25.5	9.5	0	68	49	6.4
3	27.5	10.2	0	65	40	9.5
4	29.5	10	0	64	32	8.9
5	31	11.5	0	66	41	10.1
6	31	11	0	56	22	9.7
7	31	12.5	0	53	31	4
8	30	12.5	0	53	36	7.1
9	30	13.5	0	53	61	6.3
10	26.5	13.4	4	58	40	7.8
11	25	13	9	73	52	8.4
12	27	14	0	82	43	4.1
13	28.5	14	0	62	42	10.2
14	31.5	13.5	0	78	28	8.5
15	32	13.5	0	60	35	5.9
16	31	15.5	0	59	30	1.7
17	26	13	0	70	51	0
18	19.5	14	0	73	96	0
19	18.4	12.5	17.6	94	80	0
20	17.5	12	1.4	90	80	0
21	15	12	4	90	94	0
22	16	10.5	78.6	78	90	0
23	22	11.5	3	94	75	2.8
24	27	12.5	0	78	54	10
25	30	12.5	0	82	40	8.9
26	31.5	15	0	75	45	8.4
27	32.5	16.5	0	72	42	9.3
28	33	17	0	70	44	9.5
29	34	20	0	79	41	7.8
30	34.5	20	0	76	47	5.7

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-07-22	33	21.6	0	76	49	8
2	33	21	0	70	52	9.4
3	33	21	0	66	56	8.1
4	33.5	21.5	0	70	50	9.2
5	26.5	19.8	8.2	86	74	0
6	29.5	19.5	0	83	64	2.9
7	31.5	19	0.6	83	54	6.6
8	32.2	20.5	0	84	56	7
9	29	17.5	53.2	91	63	0
10	29.5	17	0	83	56	3.3
11	26	19	14.6	83	72	3.7
12	27	17.5	0	91	58	1.4
13	25	17.5	0	91	76	0
14	21	16.5	24.6	90	86	2.3
15	26	16	4	91	64	4.6
16	22.5	17	1.4	91	79	1.5
17	25	17	2	91	69	5.4
18	32.5	18	0	82	42	11.7
19	33.5	19	0	71	46	9.3
20	32.5	20.5	0	72	76	6
21	28	18	3	83	70	0
22	31	19.5	0	91	48	5.4
23	27.5	19.5	0	79	57	1.5
24	31	19	1	89	53	1.8
25	27.5	18.5	10.8	75	64	7.1
26	30.6	18	3.6	91	48	8.3
27	31	20.5	0	83	69	4.1
28	25	18	30.4	91	76	0
29	24	19	17	91	69	0
30	29	18.5	0	88	57	5.6
31	29	19	3.4	82	55	8.6

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-08-22	23.5	16	19.2	90	84	0
2	28.5	16.5	0	91	57	8.9
3	29	16	0	80	82	5.9
4	30	16.5	0	76	58	7.2
5	30	18	0	83	46	1.9
6	29.5	18.5	0	89	46	3.7
7	32.5	17.5	0	91	46	9.7
8	29	18	6.2	95	56	6.1
9	31.5	19	0	83	65	8.1
10	33.5	18.5	0	76	54	9.4
11	25	20.5	0	83	80	0
12	28	18	0	88	63	4.3
13	32.5	17	0	76	49	7.6
14	33.5	18	0	84	46	10.3
15	23	20	8.2	91	76	0
16	27.5	18.5	35.8	91	62	2.5
17	26	19.5	0	91	69	1
18	30	18.5	1.6	86	60	9.9
19	32.5	17	0	76	49	0
20	33	18	0	62	54	7.8
21	29	15	3.6	83	69	7.2
22	30	16.5	0	82	52	4
23	30	17.4	0	82	62	3.3
24	26	16.5	1.2	82	62	1.3
25	23	17.5	6	91	91	0
26	25.5	18	0	91	76	0
27	29	17.5	0.2	91	57	5
28	29	16	0	83	76	5.4
29	28	14.5	0	82	63	6.8
30	30	15	0	75	53	8.9
31	30.5	15.5	0	73	43	9.8

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-09-22	32	15	0	83	38	10.5
2	31.5	15	0	71	39	10.2
3	32.5	16.5	0	76	41	8.2
4	30	16.5	0	91	41	6.5
5	23	15.5	1.4	78	75	0
6	29.5	15	5.6	82	48	9.7
7	31	14	0	75	44	9.8
8	32	14.5	0	68	38	9.9
9	32	16	0	76	36	9.7
10	30	16	0	80	50	7.6
11	23	14.5	6.2	91	83	0
12	27.5	13.5	1.2	91	42	8
13	29.5	12	0	71	34	9.5
14	30	12	0	67	64	7.6
15	30	11.5	0	74	34	9.6
16	30	12	0	70	58	7.6
17	25	14	0	76	50	9.2
18	29	11	4.8	64	39	9.4
19	29.5	10	0	73	42	9.3
20	28.5	10	0	81	68	6.1
21	28.5	14	0	90	43	8.8
22	29	11	0	70	42	9.2
23	29.5	12	0	66	37	8.5
24	28	14	0	74	62	4.9
25	21	14.5	0	90	74	0
26	26.5	14	0.8	85	42	7.3
27	28.5	9.5	0	82	32	7.1
28	29	10.5	0	81	39	8.8
29	27	11.5	0	91	42	8.7
30	28.5	9	0	95	36	8.9

Date	Temperature		Rain (mm)	RH1	RH2	SSH
	Max.	Min.				
01-10-22	27	9.5	0	91	38	7.4
2	25	9.5	0	80	47	8.3
3	26.5	7.5	0	86	53	7.5
4	27.5	8.5	0	93	26	8.4
5	27	7	0	93	33	7.7
6	27	6.5	0	78	38	6.8
7	26	7	0	73	49	8.4
8	26.5	6.6	0	85	52	8.3
9	26.6	7	0	80	59	8.1
10	25.5	10.5	0	72	47	5.7
11	24.5	8.5	0	42	58	6
12	22.5	8.5	0	81	52	7.5
13	24	5.5	0	82	36	7.6
14	23.5	4.5	0	85	35	7.4
15	25	4	0	92	41	8.2
16	26	4.5	0	88	44	7.9
17	25.5	5	0	95	41	8.2
18	22.5	6	0	93	61	4.2
19	19	3.5	0	95	55	5.2
20	8	4	19	92	89	0
21	14.5	5	21	95	46	4.3
22	13	3	0	92	69	7.2
23	20	2.5	0	92	61	7.1
24	21	2.5	0	87	87	7.4
25	21.5	2.5	0	89	71	6.2
26	21.5	2.5	0	94	63	5.4
27	21.5	2	0	92	68	6.4
28	21.2	2	0	92	72	6.3
29	22.5	1.5	0	87	57	6.9
30	21.5	1.5	0	92	62	6.5
31	17.5	2.5	0	87	52	0.9

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CERTIFICATE

Certified that all the corrections/amendments as suggested by External Examiner **Dr. Kouser Parveen Wani**, Retired Professor Division of Vegetable Science SKUAST-Kashmir during Viva-Voce examination held on **04-12-2023** have been incorporated in the manuscript entitled “**Heterosis and Combining ability studies for yield and yield attributing traits in tomato (*Solanum lycopersicum* L.) under temperate conditions of Kashmir**” submitted by **Ms. Sayed Azrah Indrabi (Regd. No. 2020-1063-D)**.

(Dr. Syed Faheema Mushtaq)

Chairperson

Advisory Committee