

Genetic divergence studies in Tomato (*Solanum lycopersicum* L.)

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(2017-H-194-M)



**Division of Vegetable Science
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Sher-e-Kashmir
University of Agricultural Sciences & Technology of Kashmir
Faculty of Horticulture, Division of Vegetable Science

Certificate – I

This is to certify that the thesis entitled “**Genetic divergence studies in Tomato (*Solanum lycopersicum* L.)**” submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science in Horticulture (Vegetable Science)**, to the Faculty of Horticulture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, is a record of bonafide research work carried out by **Mr. B. Srinivasulu (Regd. No. 2017-H-194-M)** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

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ABSTRACT

The investigation entitled “Genetic divergence studies in Tomato (*Solanum lycopersicum* L.)” was carried out at Vegetable Experimental Field SKUAST-K, Shalimar Srinagar during *Kharief*-2018 in which twenty seven genotypes of tomato (*Solanum lycopersicum* L.) were evaluated to estimate the genetic variability, heritability, genetic advance, correlation coefficients, path analysis and genetic diversity for twenty two growth, yield and quality characters. The experiment was laid in a randomized block design with three replications and observations were recorded on various traits *viz.*, plant height (cm), plant spread (cm), number of primary branches plant⁻¹, days to first flowering, days to 50% flowering, days to fruit set, days to red ripen fruit stage, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of locules fruit⁻¹, pericarp thickness (cm), 1000 seed weight (g), seed weight fruit⁻¹ (mg), number of fruits plant⁻¹, fruit yield plot⁻¹ (kg), fruit yield (q/ha), total soluble solids (%), ascorbic acid (mg/100g), lycopene content (mg/100g), titrable acidity (%), juice to pulp ratio. Analysis of variance revealed significant differences among genotypes for all the traits studied. The highest phenotypic and genotypic coefficients of variability were observed for Number of primary branches plant⁻¹ followed by number of fruits plant⁻¹, lycopene content, fruit yield (q/ha), fruit yield plot⁻¹, titrable acidity, seed weight fruit⁻¹, fruit length, fruit diameter. In general the

phenotypic coefficients of variation are slightly higher than genotypic coefficients of variation in general for most of the yield contributing characters which indicates the minor role of environment in expression of these traits. High heritability (bs) was demonstrated by all the traits with maximum genetic advance (percent of mean) for number of primary branches plant⁻¹ followed by number of fruits plant⁻¹, ascorbic acid (mg/100g), fruit yield (q/ha), fruit yield plot⁻¹ (kg), number of locules fruit⁻¹, titrable acidity (%), juice to pulp ratio, seed weight fruit⁻¹ (mg), fruit length (cm), fruit diameter (cm), plant spread (cm), pericarp thickness (cm), plant height (cm), total soluble solids (%), days to first flowering, lycopene content (mg/100g), 1000 seed weight (g), average fruit weight (g). Correlation coefficients revealed that the fruit yield (q/ha) showed positive and significant correlation with fruit yield plot⁻¹ (kg), number of fruits plant⁻¹, days to first flowering, average fruit weight (g), number of primary branches plant⁻¹, days to 50% flowering, 1000 seed weight (mg). Path coefficient analysis revealed fruit yield (q/ha) was result of direct effect of number of fruits plant⁻¹, fruit yield plot⁻¹ (kg), average fruit weight (g). Analysis for divergence, using D² statistics revealed highly significant differences for traits indicating diversity among the genotypes, grouping the 27 genotypes into 8 clusters. Cluster I had maximum number of genotypes (9) followed by cluster II (8), cluster III (4), cluster V (2), while as clusters IV, VI, VII, VIII were monogenotypic. Maximum inter-cluster distance was observed in cluster IV and cluster VI (7021.27) followed by cluster II and VI (5628.93) whereas the maximum intra-cluster distance was observed in cluster III (770.46) and cluster I (721.11). Highest contribution to divergence came from lycopene content (mg/100g), fruit yield (q/ha) and ascorbic acid content (mg/100g) and days to red ripen fruit stage. The crosses between the genotypes of cluster VI with IV and Cluster VI with II are likely to exhibit high heterosis and could produce recombinants with desired traits in segregating generations. The genotypes selected on the basis of *per se* performance of fruit yield, yield contributing and quality traits can be used in tomato improvement programme as elite germplasm lines or may be recommended as such for commercial cultivation after testing them over years and locations.

Key words: Variability, Heritability, Genetic advance, Correlation, Path analysis, Divergence, *Solanum lycopersicum* L.

Signature of Student

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Chapter 1

INTRODUCTION

India occupies the prime position in the vegetable production and is second largest producer of vegetables in the world crops and it is universally accepted that these are cheaper sources of proteins, vitamins, carbohydrates and minerals. The nutritional security of a country can be achieved only when enough vegetables are consumed. The area and production of vegetables in India has been increasing year after year during the past green revolution period and the country is leading towards another revolution in the form of “golden revolution”. Tomato is the world’s largest vegetable crop after potato and sweet potato. The major tomato producing states in the country are Andhra Pradesh, Madhya Pradesh, Karnataka, Gujarat, West Bengal, Maharashtra, Uttar Pradesh, Chattisgarh, Haryana, Tamilnadu and Telangana. These states contribute about 91% of the total production of the country.

The tomato production in the country during the year 2017-18 (NHB) was estimated to be about 6.6% higher as compared to past five years. During the year 2016-17 the area under tomato cultivation in India was 808.54 thousand hectares with an annual production of 19696.92 thousand million tonnes. The productivity is 24.4 metric tonnes per hectare. In Jammu and Kashmir state the area under tomato cultivation is 3.58 thousand hectares with an annual production of 88.09 thousand metric tonnes. (Horticulture Statistics Division, Department of Agriculture, 2016-17).

Tomato (*Solanum lycopersicum* L.) is an important member of Solanaceae family having chromosome number of $2n=2x=24$. The probable ancestor of tomato is *Solanum lycopersicum* var. *cerasiforme* Bailey. It is originated in wild form in the Peru Equador region of Andes (South America) and it is grown in almost every corner of the world (Robertson and Labate, 2007). It is typically day

neutral plant and is mainly self-pollinated, but a certain percentage of cross pollination also occurs (Depra *et al.*, 2014).

Tomato is universally treated as “Protective food” (Thamburaj and Singh, 2013). It is a very good source of income to small and marginal farmers and has a great nutritional value. Tomato is a rich source of minerals, vitamins and organic acids. It is a reservoir of diverse antioxidant like ascorbic acid, vitamin C, carotenoides, flavonoides and phenolic acids. Ascorbic acid content in tomato is 31 mg/100 g. Red colour of tomato is due to the presence of pigment ‘lycopene’ and it is 20-50 mg/100 g in edible portion. The total sugar content is 2.5% in ripe fruit and the total amino acid is 100-350 mg/100 g of fruit weight. A survey made by M.A. Stens indicated that among the main fruits and vegetables, tomato ranks 16th as the source of both vitamins A and C (Thamburaj and Singh, 2013). It contains moderate amounts of lutein that reduce risk of lung cancer (Sies, 1991). It is very versatile vegetable for culinary purpose. Tomatoes are used directly as raw vegetables in sandwiches, salad etc. Several processed items like paste, puree, syrup, juice, ketchup, drinks, whole peeled tomato, etc. are prepared on a large scale. Tomato is a very good appetizer and its soup is said to be a good remedy for patients suffering from constipation. Tomato fruits have undoubtedly assumed the status of a functional food considering the overwhelming epidemiological evidence for its reducing risk of certain types of cancers (Nguyen and Schwartz, 1999).

Under the agro-climatic conditions of Kashmir, the main season for the cultivation of tomato is spring-summer.

India is the source of diversity in genotypes of tomato. Identification of superior genotypes among the existing germplasm becomes extremely important for future breeding programme and also for promoting production per unit area. The development of effective improvement programme depends upon the existence of genetic variability and knowledge of genotypic and phenotypic correlation of yield and yield attributing components. Genetic variability is the

measure of tendency of individual genotypes in a population to vary from each other. In plant breeding genetic diversity plays a very important role as it helps in selecting the suitable parents in hybridization programme resulting in superior hybrids and recombinants (Rathi *et al.*, 2011). D^2 statistic proposed by Mahalanobis (1928) has been generally used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in breeding programme.

Genetic variability in the existing germplasm gives an idea about the selection of suitable genotypes for conducting the breeding programme. Variability depends on genetic factors, environmental factors (edaphic and climatic factors) and bioactive factors caused by physiological factors etc (Galton, 1889) observed that part of continuous variation is due Heritability. It helps in proportionating the total variation into heritable and environmental effects. The correlation coefficient measures the mutual relationship between the two or more variables (yield and quality) gives an idea about the various associations existing between the yield and yield components. The study of path coefficient analysis gives the magnitude of contribution made by different plant characters towards yield there by imparting the confidence in selection of important yield attributes.

Therefore, the present study was carried out to find out suitable selection criteria for higher fruit yield through study of genetic variability, heritability, genetic advance and relationship between yield and its components in tomato. The main objectives of the present study were as under:

1. To study nature and extent of genetic variability in tomato genotypes for various growth, yield and quality characters.
2. To work out the correlation and path analysis for yield and its component characters in tomato.

Chapter 2

REVIEW OF LITERATURE

Differentiation of elite genotypes, based on reliable traits will not only help in preserving identity but also reflect genetic variation valuable in analyzing genetic diversity, monitoring and promoting efficient conservation of genetic resources and effective utilization of germplasm. The success of any breeding programme depends on the quantum of genetic variability available for exploitation. The information on the type of variation in the available genetic material and the factors exclusively affecting those traits has significant importance for the possible improvement of a crop. Parameters like genetic variability, heritability and genetic gain have direct or indirect influence on the fate of the breeding programme of crop. To make selection of the genotypes more efficient, knowledge of association of character is very much important. Several investigators have screened tomato genotypes from different resources, which exhibited immense range of variation in morphological and physiological traits that govern the performance. The literature related to the present investigation has been collected and is reviewed under the following headings.

- 2.1 Genetic variability
- 2.2 Heritability and Genetic advance
- 2.3 Correlation coefficient studies
- 2.4 Path coefficient analysis
- 2.5 Genetic divergence

2.1 Genetic variability

Genetic variability denotes the portion of phenotypic variance which is caused by variation in the genetic constitution of individual population. Genetic variability in the existing germplasm gives an idea about the selection of suitable genotypes for conducting the breeding programme.

Golani *et al.* (2007) evaluated 20 genotypes of tomato, elucidated high heritability with high GCV and genetic gain for average fruit weight, number of locules per fruit and fruit yield which could be improved by simple selection. They observed that fruit yield per hectare ranged from 190.49 to 442.90 with all over mean of 307.81.

Shashikanth (2008) reported that significant variability (GCV & PCV) was seen among 30 tomato genotypes evaluated for 19 quantitative traits. The mean fruit yield per plant noticed was 1.26 kg with a mean range of 0.67 to 2.33 kg.

Sivaprasad (2008) indicated that hybrid sasya-54 had highest yield with Average fruit weight, Number of fruits per plant and Number of fruiting clusters per plant. The maximum plant height was recorded in J.K. Desi followed by Shivaji, and the highest pericarp thickness and Number of primary branches observed in Shivaji.

Kaushik *et al.* (2011) evaluated ten genotypes and concluded that the variation was maximum for fruit yield and minimum for fruit width. The magnitude of genotypic and phenotypic coefficient of variation was higher for number of leaves, fruit length and fruit yield.

Patel *et al.* (2013) observed that highest GCV was observed for fruit yield per plant and PCV for fruit yield per plant and number of locules per fruit, while lowest GCV was noticed for days to first harvest, days to 50% flowering and pericarp thickness, they also found high PCV for days to first harvest and days to 50% flowering.

Shankar *et al.* (2013) observed that high estimates of PCV and GCV were obtained for plant height, number of fruits per cluster, average fruit weight, yield per plant, ascorbic acid and lycopene indicating a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement.

Shusnay Chernet *et al.* (2013) evaluated 36 genotypes in 6x6 simple lattice design with two replications, to estimate the extent of genetic variability and association among the characters. Highest genotypic and phenotypic coefficient of variation was observed for number of matured fruits per plant and fruit set percentage.

Rajasekhar *et al.* (2013) were studied various genetic parameters to elucidate the genetic variability, heritability and genetic advance. The genotypes exhibited high range of phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) for all the characters studied.

Osekita *et al.* (2014) observed that the PCV and GCV showed wide differences in number of fruits per plant and number of locules per plant.

Henerah (2015) concluded that analysis of variance has significant difference among genotypes for all the studied characters.

2.2 Heritability and Genetic advance

The term heritability in a broad sense was defined as the ratio of genotypic variance to the total phenotypic variance (Lush, 1949; Jhonson *et al.*, 1955)

Heritability estimate provides the information regarding the amount of transmissible genetic variation to total variation and determines genetic improvement and response to selection.

The expected genetic advance defined as the differences between the mean of progeny of selected individuals and the base population. The estimate of genetic advance in percentage of mean provides more reliable information regarding the effectiveness of selection in improving a trait. Thus the estimates of heritability and genetic advance are of great significance to the plant breeders for developing suitable selection strategy.

Singh *et al.* (2002) found that the heritability was high for all characters except days from fruit setting to red ripe stage. The highest genetic advance was

predicted for average fruit weight. Total yield was significantly and positively correlated with marketable yield and average fruit weight.

Joshi and Singh (2003) observed that the wide range of variation was observed among the characteristics. Plant height gave the highest heritability (78.82%), while the number of fruits per plant gave the highest phenotypic and genotypic coefficient of variation (61.21 & 44.05, respectively) and genetic advance as percentage of mean (65.24).

Joshi *et al.* (2004) observed that heritability estimate in narrow sense was observed low for yield per plant suggested that direct selection for higher yield may be ineffective as the trait was largely governed by dominant genes.

Kumar *et al.* (2004) found that number of primary branches per plant, plant height, and number of fruits per plant, fruit yield per plant, average fruit weight, total soluble solids, acidity and pericarp thickness showed that mean squares due to genotype were highly significant. The genotypic and phenotypic coefficient of variations (96.50%) along with high genetic advance (108.91%) indicated that it was less affected by the environment. The average fruit weight showed high heritability that ranged from 89.10 to 96.50 percent.

Mehta *et al.* (2008) conducted an experiment on fourteen genotypes of diverse origin of tomato and reported fruit yield per hectare, plant height, number of clusters per plant, number of locules per fruit, TSS, number of branches per plant and weight of fruit per plant showed high heritability in percent coupled with high genetic advance (as percentage of mean).

Ghosh *et al.* (2010) studied the F₂ segregating generations of exotic tomato hybrids to measure variability, character association and path coefficient analysis. High heritability associated with high genetic advance were observed for fruit clusters per plant (105.11), fruits per plant, branches per plant, fruits per cluster, individual fruit weight and fruit yield per plant.

Kaushik *et al.* (2011) reported that high values of heritability coupled with high genetic advance were observed for number of leaves at 60 days after transplanting and fruit yield.

Dar *et al.* (2011) observed that high heritability for the characters Beta-carotene, ascorbic acid and lycopene content in tomato inferring easy selection and improvement of these characters in breeding lines.

Mohammad *et al.* (2012) reported that the highest heritability was recorded on plant height, while the lowest was for fruit yield per plant. High heritability (broad sense) estimates were observed for all the tested characters indicating that these characters are controlled by additive gene action which is very useful in selection.

Manna *et al.* (2012) reported that high and moderate to high heritability coupled with moderate to high genetic gain in number of locules per fruit, fruit weight, fruit length, number of fruits per plant, pericarp thickness, vitamin-C (mg/100g) and total acid (%) indicated the pre dominance of additive gene action and therefore, these are more reliable for effective selection.

Ahirwar *et al.* (2013) observed that genetic advance at 5% was high for plant height after 120 DAT, number of fruits per plant, ascorbic acid and fruit yield per plant, which is noticed for all the traits except days to flower initiation and days to first harvest.

Patel *et al.* (2013) observed high heritability with genetic advance as percent of mean for the traits fruit yield per plant and average fruit weight which could be improved by simple selection.

Saleem *et al.* (2013) observed that fruit width, fruit length, plant height, fruit weight, fruit yield per plant and number of fruits per plant and high heritability in tomato.

Reddy *et al.* (2013) found that high heritability combined with 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 and TSS in tomato.

Shusnay Chernet *et al.* (2013) evaluated 36 genotypes in 6×6 simple lattice design with two replications, to estimate the extent of genetic variability and association among the characters. Highest heritability estimate was recorded for number of matured fruits per plant and least for number of primary branches.

Meitei *et al.* (2014) reported that high heritability with moderate to low genetic advance was observed for days to 50% flowering and fruiting, first and second picking, plant height and fruit diameter in tomato.

Paul *et al.* (2014) observed that all the characters of tomato which were in investigation were highly heritable in broad sense.

Amarjeet *et al.* (2016) evaluated 56 genotypes of tomato in RCBD design with 3 replications for the estimation of genetic variability, heritability and genetic gain. High estimates of heritability and genetic gain were recorded for number of fruits per plant, average fruit weight, fruit yield per plant, locular wall thickness and lycopene content.

2.3 Correlation coefficient

The correlation coefficient measures the mutual relationship between the two or more variables (yield and quality) gives an idea about the various associations existing between the yield and yield components.

Hyder *et al.* (2007) observed that fruit weight had significant positive correlation with number of leaves, number of flowers, number of fruits and total number of leaves at flowering.

Hidayatullah *et al.* (2008) reported days to first harvest showed negative correlation with number of pickings that could be exploited for developing determinate cultivars, whereas, number of pickings had positive correlation with fruit weight per plant and 1000 seed weight. However, number of fruits per plant

showed positive association with fruit weight per plant and number of seeds per plant.

Mehta *et al.* (2008) conducted an experiment on 14 genotypes of diverse origin of tomato for estimation of correlation co-efficient analysis and observed that fruit yield was positively associated with days to 50% flowering and days to 50% fruiting.

Islam *et al.* (2010) observed that yield per plant was found highly significant and positively correlated with flowers per plant, fruits per plant, fruit length, fruit diameter and individual fruit weight which indicated that yield could be increased by improving the traits.

Rana and Singh (2010) conducted experiment on 33 genotypes of tomato to study the correlation between characters and found that, number of primary branches, leaf area and number of fruits per plant were positively associated with fruit yield per plant.

Tiwari and Upodhyay (2011) conducted an experiment on nineteen genotypes along with two checks of tomato and reported that significant positive correlation, therefore fruit weight as an important character which may be included in selection criterion for improvement in fruit yield per plant.

Paul *et al.* (2014) revealed that germination percentage, fruits per bunch, harvest index were significantly correlated with yield per plant.

Nowsoo *et al.* (2014) reported that fruits per plant of tomato is positively and significantly correlated to plant height, number of branches per plant and leaf length.

Wali *et al.* (2014) found that correlation of parameters as affected by application of mulch indicated significant and positive correlation of fruit yield with plant height, number of leaves, leaf area, leaf area index, days to 1st flowering, number of fruits and weight of fruits but significantly negatively correlated with number of branches and days to 50% flowering. Days to 1st

flowering had significant positive correlation with days to 50% flowering, number of fruits and weight of fruits both as affected by cultivar and mulch.

Rashwan (2015) reported that the correlation coefficient in M₃ populations showed highly significant positive among total yield fruits per plant character and each of number of clusters per plant, number of flowers per plant, number of fruits per plant, weight of fruit, marketable yield per plant in tomato. Results of the study confirm that the total yield components such as fruit weight, number of fruits per plant, number of clusters per plant and number of flowers per plant.

2.4 Path coefficient analysis

According to Wright (1921) path coefficient analysis is a standard regression coefficient which permits the separation of correlation coefficient into measures of direct and indirect effect. The study of Path coefficient analysis gives the magnitude of contribution made by different plant characters towards yield there by imparting the confidence in selection of important yield attributes.

Kumar *et al.* (2003) reported that the number of fruits per plant had maximum positive direct effect on fruit yield per plant followed by average fruit weight.

Veershetty (2004) observed that maximum direct positive effect on fruit yield per plant was exhibited by number of fruits per plant followed by number of fruits per cluster.

Mayavel *et al.* (2005b) concluded that number of branches per plant had the highest positive direct effect on fruit yield. Whereas, plant height, number of fruits per cluster, number of fruits per plant and number of locules per fruit had negative direct effects on fruit yield.

Golani *et al.* (2007) reported that plant height manifested significant and negative relationship with fruit yield and its direct effect was negative but its indirect *via* fruit girth was high and positive in tomato.

Prashant *et al.* (2007) conducted experiment on 67 genotypes of tomato reported that early yield and average fruit weight had high direct positive effects on total yield.

Shivaprasad (2008) observed that number of fruits per plant and average fruit weight had high direct and indirect effect on yield per plant in all the populations.

Ghosh *et al.* (2010) studied the F_2 segregating generations of exotic tomato hybrids to measure variability, character association and path coefficient analysis. Fruits per plant showed the highest positive direct effect on fruit yield per plant followed by individual fruits per plant.

Atugwu *et al.* (2012) conducted an experiment on six advanced generations (F_7 - F_{12}) of tomato hybrids for path analysis and result revealed that highest positive direct effect of number of flowers per plant on fruit yield. The high negative indirect effect exhibited by number of flowers per plant on fruit yield. The high negative indirect effect exhibited by number of flowers per plant at the F_7 , F_{10} and F_{12} generations were counteracted by the high positive indirect effect via number of flowers per truss at F_7 , number of truss at F_{10} and number of fruits at F_{12} .

Tasisa *et al.* (2012) conducted an experiment on twenty three tomato genotypes and reported that positive and direct effects were exerted by days to flowering, fruit clusters per plant and plant height on yield per plant and, suggesting their importance in yield improvement and that these traits would be considered in selection programme.

Meitei *et al.* (2014) revealed that the positive direct for fruit diameter, single fruit weight, fruits and fruit cluster plant on yield plant and selection based on these characters would be more reliable for yield improvement in tomato.

Paul *et al.* (2014) resulted that the percent (%), height of first leaf appearance, days to first flowering, and harvest index, exhibited direct effect on grain yield.

Rasheed *et al.* (2017) evaluated eight parents and 15 F₁ of tomato to study the path analysis. Analysis revealed that plant height, number of branches per plant, number of clusters per plant, number of flowers per cluster, single fruit weight and fruit setting percentage per cluster were directly contributing to yield improvement.

2.5 Genetic divergence

The multivariate analysis using Mahalanobis D² statistics is a valuable tool to quantify the degree of divergence at genetic level. India is the source of diversity in genotypes of tomato. Identification of superior genotypes among the existing germplasm becomes extremely important for future breeding programme. In plant breeding genetic diversity plays a very important role as it helps in selecting the suitable parents in hybridization programme resulting in superior hybrids and recombinants (Rathi *et al.*, 2011). D² statistic proposed by Mahalanobis (1928) has been generally used as an efficient tool in the quantitative estimation of genetic diversity for a rational choice of potential parent in breeding programme.

Veershetty (2004) grouped 32 tomato genotypes into 10 clusters based on D² analysis, revealed that number of fruits per cluster, plant height, number of branches, pericarp thickness, average fruit weight and TSS content of fruit were reported as chief contribution towards divergence.

Mahesh *et al.* (2006) grouped 30 tomato genotypes into nine clusters based on D² analysis. The cluster mean indicated that days to 50% flowering, plant height, number of branches per plant, number of cluster per plant, number of fruits per cluster and fruit yield per plant were reported as chief contributors towards divergence.

Sharma *et al.* (2006) studied genetic divergence by grouping 60 genotypes of tomato into 10 clusters using D^2 analysis, which revealed that maximum divergence within a cluster was exhibited by the cluster VII, closely followed by cluster III and cluster V, whereas, cluster VIII and II were the most divergent from each other followed by cluster VII and VIII.

Narolia *et al.* (2010) observed wide range of genetic diversity among tomato genotypes which provides a tremendous scope for genetic improvement of economic traits in tomato varieties.

Rajasekhar *et al.* (2013) conducted a study by using 19 exotic collections of tomato by using Mahalanobis D^2 statistics, which were revealed that quantitative characters which are pertaining to the growth, yield, earliness, yield and quality. Fruit weight, plant height, number of fruits per plant contributed to 92.40% to the total divergence. Five clusters formed, among these clusters, cluster II topped with maximum number of genotypes.

Shusnay Chernet *et al.* (2014) evaluated 36 genotypes, which were grouped into six clusters by using Mahalanobis D^2 cluster analysis to study the genetic diversity among them. Genetic distance between any pair of clusters showed very high significant difference. The maximum and minimum distances were recorded in clusters IV and V and clusters II and III. The study conformed presence of adequate genetic diversity between any pair of clusters which could be exploited through hybridization.

Henareh *et al.* (2015) observed that tomato genotypes showed genetic diversity in all the studied characters. Cluster analysis classified genotypes in six groups, so that genotypes with different vegetative and generative characters were located separate groups.

Ullah *et al.* (2015) evaluated twenty genotypes of tomato for their genetic divergence using Mahalanobis D^2 statistics. Genotypes were grouped into five clusters, based on D^2 values of eleven yield related characters. The mean intra and

inter cluster distance (D) revealed that cluster I had highest intra cluster distance (0.979), while the inter cluster distance was maximum between cluster III and I (13.546) followed by III and V (11.218). The characters like plant height, fruit weight, fruits per plant contributed maximum to genetic divergence.

Lekshmi *et al.* (2016) evaluated forty tomato genotypes in RCBD design with three replications. Genetic divergence analysis was carried out using Mahalanobis D^2 Statistics and 40 genotypes are grouped into 8 clusters. The highest intra cluster distance was notified in cluster II followed by I. Highest inter cluster distance is observed between clusters VII and VIII. Lycopene content and truss per plant had maximum contribution towards total divergence followed by fruit length, fruit weight and yield per plant.

Pushpam Patel *et al.* (2017) evaluated 24 genotypes of tomato, which were grouped into five clusters using Tocher method. The genotypes in cluster IV and II followed by III and II and cluster V and II, due to maximum inter cluster distance between them, exhibited high degree of genetic diversity. Cluster IV has high desirable quantitative characters. Maximum contribution towards divergence was obtained by lycopene content, average fruit weight and ascorbic acid, all together they have contributed 67%.

Chapter 3

MATERIALS AND METHODS

The present investigation entitled “Genetic divergence studies in Tomato (*Solanum lycopersicum* L.)” was undertaken at vegetable Experimental Farm of Division of Vegetable Science, SKUAST-Kashmir, Shalimar during summer 2018. The site is situated 34° N of latitude and 74.89° E of longitude. The climate is temperate characterized by mild summers. June and July are the hottest months while January and February are the coldest. The maximum rainfall is received during March to April.

3.1 Experimental material and design

Twenty seven diverse genotypes of tomato were evaluated for various yield and yield attributing traits at the Experimental farm of the Division of Vegetable Science, SKUAST-K Shalimar Srinagar. The genotypes were grown in a Randomized Complete Block Design (RCBD) with three replications. The details of genotypes along with their source are given in the Table-1. The experimental field consisted of 27 treatments in each replication, such that there were 81 treatments (genotypes) in total. The spacing followed for the row to row and plant to plant distance is 60 × 35 cm. The experimental field was well prepared and standard cultural, manural and plant protection practices were followed to ensure a healthy crop.

3.2 Characters Studied and Observational Procedures

For the sake of recording the data, five plants in each plot were selected randomly i.e. five plants for one genotype in each replication and they were tagged and numbered. These tagged plants were used for recording observations for the following characters.

Table 1: Genotypes of tomato (*Solanum lycopersicum* L.)

S.No.	Genotype/variety	Source
1.	Kashi Hemanth	IIVR (Varanasi)
2.	Kashi Amrit	IIVR (Varanasi)
3.	Kashi Sharad	IIVR (Varanasi)
4.	Kashi Vishesh	IIVR (Varanasi)
5.	Kashi Chayan	IIVR (Varanasi)
6.	Kashi Aman	IIVR (Varanasi)
7.	Kashi Anupam	IIVR (Varanasi)
8.	TOLCV-16	IIVR (Varanasi)
9.	TOLCV-28	IIVR (Varanasi)
10.	TOLCV-32	IIVR (Varanasi)
11.	VRT-01	IIVR (Varanasi)
12.	VRT-19	IIVR (Varanasi)
13.	VRT-13	IIVR (Varanasi)
14.	Sel-7	IIVR (Varanasi)
15.	Jawahar-99	IIVR (Varanasi)
16.	2016/TOVDVAR-12	AICRP, IIVR (Varanasi)
17.	2016/TODVAR-11	AICRP, IIVR (Varanasi)
18.	2016/TODVAR-1	AICRP, IIVR (Varanasi)
19.	2016/TODVAR-3	AICRP, IIVR (Varanasi)
20.	2016/TODVAR-10	AICRP, IIVR (Varanasi)
21.	2016/TODVAR-5	AICRP, IIVR (Varanasi)
22.	2016/TODVAR-2	AICRP, IIVR (Varanasi)
23.	2015/TODHYB-4	AICRP, IIVR (Varanasi)
24.	2015/TODBYB-1	AICRP, IIVR (Varanasi)
25.	Roma	SKUAST-K, Shalimar
26.	Shalimar Hybrid Tomato-1	SKUAST-K, Shalimar
27.	Marglobe	SKUAST-K, Shalimar



Plate 1: Experimental field at an early stage



Plate 2: Staking operation in the field



Plate 3: Best performed genotypes regarding yield and quality traits

3.2.1 Growth and yield characters

3.2.1.1 Plant height (cm)

The height of the plant was measured with the help of meter scale at harvesting time. The measurement of the plant height of all five plants in each replication was taken in order to assess the optimum length of plants in different replications. The measurement was recorded (in centimeter) in terms of vertical distance from ground level to tip of the plant.

3.2.1.2 Plant spread (cm)

The spread of the plant was measured with the help of meter scale at harvesting time. The measurement of the plant spread of all five plants in each replication was taken in order to assess the optimum spread of plants in different replications. The measurement taken from north-south and east-west direction at final picking.

3.2.1.3 Number of primary branches plant⁻¹

The number of primary branches was recorded at the peak fruiting stage and average was calculated.

3.2.1.4 Days to 1st flowering

The total number of days from the date of transplanting to days of first anthesis was recorded and average was calculated.

3.2.1.5 Days to 50% flowering

The total number of days from the date of transplanting to the days of plants showing 50% flowering.

3.2.1.6 Days to fruit set

It is the total number of days counted from the date of transplanting to fruit bud differentiation stage i.e. pea stage of fruits.

3.2.1.7 Days to red ripen fruit stage

It is total number of days counted from the date of transplanting to fruit marketable maturity.

3.2.1.8 Fruit length (cm)

Five randomly selected fruits were measured for their length at maximum edible maturity with the help of slide calliper and recorded in centimeter.

3.2.1.9 Fruit diameter (cm)

Five randomly selected fruits were measured for their diameter at maximum edible maturity with the help of slide calliper and recorded in centimeter.

3.2.1.10 Average fruit weight (g)

Five marketable fruits were weighed and the average fruit weight was worked out and expressed in grams (g).

3.2.1.11 Number of locules fruit⁻¹

Five representative and fully ripen fruits were taken from each treatment. The fruit were halved transversely and locule numbers were counted from the five fruits. The average was worked out.

3.2.1.12 Pericarp thickness (cm)

Five fully ripen fruits were taken from each treatment. The fruits were halved transversely and pericarp thickness can be calculated with the help of slide calliper. The average was calculated.

3.2.1.13 1000 seed weight (g)

1000 well-developed seeds were collected from the bulk of five selected plants and weight was recorded with the help of electronic balance and expressed in gram (g).

3.2.1.14 Seed weight fruit⁻¹ (mg)

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

3.2.1.15 Number of fruits plant⁻¹

The number of ripen fruits obtained at each picking from the total plants were counted and average was calculated.

3.2.1.16 Fruit yield plot⁻¹ (kg)

It was worked out by adding yield of all harvests of individual plot and was expressed in kilograms (kg).

3.2.1.17 Fruit yield (q/ha)

Total yield per plot was worked out by adding yield of all harvests and was expressed in kilogram (kg) per plot and converted in per hectare yield (q/ha).

3.2.2 Quality characters

3.2.2.1 Total soluble solids (%)

The total soluble solids (TSS) contents of the fruits were measured with the help of hand refractometer. Tomato juice was collected from red ripen fruits. A drop of juice was placed over the prism of digital refractometer and was noted in percent.

3.2.2.2 Titrable acidity (%)

Acid content of the extracted juice was determined by titrating 5 ml of juice against N/10 NaOH using Phenolphthalein as an indicator. Acidity was expressed in term of anhydrous citric acid (A.O.A.C.1960) per 100 ml of tomato juice.

3.2.2.3 Ascorbic acid content (mg/100g)

Ascorbic acid content was determined by 2,6-dichlorophenol indophenol titration method (A.O.A.C.1960) and expressed in mg/100g of fruits.

3.2.2.4 Lycopene content (mg/100g)

Total lycopene content of tomato was determined by the method of Lee (2000) with some modifications. With the help of mortar and pestle 5g of tomato pulp was crushed in acetone, till it became colourless. Then the extracted solution was poured into a separating funnel. Then added, petroleum ether and small amount of sodium sulphate and shaken rigorously for mixing well. Then the separating funnel was kept undisturbed to separate the lycopene pigment from the acetone to petroleum ether layer. After that, coloured solution was separated in a 500 ml volumetric flask and the volume will be adjusted with petroleum ether. Finally, the sample absorbance was measured at 503 nm in a spectrophotometer, using the petroleum as blank. The results were expressed as 100 g⁻¹FW (fresh weight) basis.

$$\text{Lycopene content (mg/100g)} = \frac{3.1206 \times \text{vol. made up} \times \text{dilution}}{\text{Weight of sample}} \times 100$$

3.2.2.5 Juice to pulp ratio

A composite sample of 500g 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 :

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

Juice to pulp ratio was calculated as:

$$\text{Juice to pulp ratio} = \text{juice content/pulp content}$$

3.3 Statistical analysis

The experimental data was compiled by taking the mean value of the 27 genotypes of tomato for yield and its components traits from all the three replications. Then it was subjected to the following statistical analyses:

- Analysis of variance for design of experiment,
- Genetic variability, heritability in broad sense (h^2_{bs}) and genetic advance (GA) in per cent of mean,
- Correlation coefficient,
- Path coefficient analysis, and
- Genetics divergence (D^2) analysis

3.3.1 Analysis of variance

Analysis of variance for all characters was carried out for testing variation among the genotypes. The characteristic of this design is that every unit of experimental plot has an equal chance of getting any treatment.

The analysis of variance table was set up as under:

Source of variation	d.f.	S.S	M.S.S	F(cal)
Replication	r-1	SSr	MSR= SSr/r-1	MSR/MSE
Treatments	t-1	SSt	MST=SSt/t-1	MST/MSE
Error	(r-1) (t-1)	SSe	MSE=SSe/(r-1) (t-1)	
Total	rt-1			

Where,

R = Number of replications

T	=	Number of treatments
SS	=	Sum of squares
MSS	=	Mean sum of squares
SSr	=	Sum of squares due to replication
MSR	=	Mean sum of squares due to replication
SSe	=	Sum of squares due to intra-block error
MSE	=	Mean sum of squares due to intra-block error
SSt	=	Sum of squares due to treatments
MST	=	Mean sum of squares due to treatments

The significance of varietal differences was tested by F-test comparing calculated F-value at 5 and 1 per cent level of significance at treatment (t-1) and error (t-1) (r-1) degrees of freedom. If the F-value was found to be significant, comparison was further extended to compare each treatment mean with every other treatment utilizing critical difference (C.D.), which was calculated by the following formula:

$$\text{Critical difference (C.D.)} = \frac{\text{Standard error of difference SE (d)} \times t(0.05) \text{ at error d.f.}}{(2\text{MSe/r})^{1/2} \times t(0.05) \text{ at error d.f.}}$$

Where,

MSe	=	Error mean square
r	=	Number of replications

3.3.1.1 Genotypic variance

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

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

Where,

- $\hat{\sigma}^2_g$ = Genotypic variance,
MSG = Mean sum of squares due to genotypes,
MSE = Mean sum of squares due to error, and
R = Number of replications

3.3.1.2 Phenotypic variance

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

$$\hat{\sigma}^2_p = \hat{\sigma}^2_g + \hat{\sigma}^2_e$$

Where,

- $\hat{\sigma}^2_p$ = Phenotypic variance
 $\hat{\sigma}^2_g$ = Genotypic variance, and
 $\hat{\sigma}^2_e$ = Error variance

3.3.1.3 Phenotypic and genotypic co-efficient of variation

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

$$PCV = \frac{\sqrt{\hat{\sigma}^2_p}}{\bar{X}} \times 100$$

Where,

- $\hat{\sigma}^2_p$ = Phenotypic variance, and
 $\bar{X}$ = Grand mean of the trait studied

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

Where,

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

$\bar{X}$ = Grand mean of the trait studied

3.3.2 Estimation of heritability, genetic advance and expected genetic gain

3.3.2.1 Heritability (broad sense)

It was estimated as per the procedure presented by Johnson *et al.* (1955) and Hanson *et al.* (1956).

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

Where,

h^2 = Estimate of heritability in broad sense,

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

$\sigma^2 p$ = Phenotypic variance

3.3.2.2 Genetic advance

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

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

Where,

GA = Genetic advance of the trait,

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

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

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

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

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

$$\text{Genetic gain} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

G.A. = Genetic advance of the trait, and

$\bar{X}$ = Mean of the trait

3.3.3 Estimation of genotypic and phenotypic co-variances and correlation coefficients

Covariance analysis followed the same pattern as the variance analysis.

The genotypic and phenotypic co-variances between two characters were obtained in the same fashion as corresponding variances. Estimates of genotypic and phenotypic variances and covariances were substituted in the following formula suggested by Panse and Sukatme (1985) to calculate correlation co-efficient between all possible pairs of characters.

3.3.3.1 Genotypic correlation co-efficient

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

3.3.3.2 Phenotypic correlation coefficient

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

Where,

$r_{xy} (g), r_{xy} (p)$ = Genotypic and phenotypic correlation coefficients, respectively, between a pair of characters x and y

$\hat{\sigma}_{xy}^2 (g), \hat{\sigma}_{xy}^2 (p)$ = Genotypic and phenotypic co-variances, respectively, for a pair of characters x and y

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

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

3.3.3.3 Test of significance

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

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

Where,

R = Correlation coefficient and

N = number of observations

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

3.3.4 Path-coefficient analysis

Path-coefficient analysis was carried out according to Dewey and Lu (1959). Fruit yield was assumed to be dependent variable (effect) which was influenced by all the sixteen quantitative characters in tomato under both drought and control conditions. The independent variables (causes), indirectly effects on yield through other characters. The variation in yield unexplained by the twenty one characters was presumed to be contributed by a residual factor (X) which is uncorrelated with other factors. Path-coefficients were estimated by solving the following simultaneous equation indicating the basic relationship between correlation and path-coefficient.

The equations used are as follows:

$$r_{iy} = P_{iy} + \sum_{i=1}^9 r_{iy} p_{jy} \text{ for } i=1,2\ldots 9,$$

$$r_{iy} = \sum_{i=1}^9 r_{iy} p_{jy} \text{ for, } r_{ii} = 1$$

The above equations can be written in the form of matrix.

$$[A]_{9 \times 1} = [B]_{9 \times 1} [C]_{9 \times 1}$$

Where,

A is column vector of correlations r_{iy}

B is the correlation matrix of r_{ij}

C is the column vector of direct effects, P_{iy}

Residual factor was calculated as follows:

$$P_{xy} = \sqrt{1 - R^2}$$

The r_{ij} 's i.e., r_{1-2} to r_{9-10} denotes correlation between all possible combinations of independent characters P_{1y} to P_{13y} denote direct effect of various characters on character y.

r_{iy} = Correlation coefficient between i^{th} and y character.

P_{iy} = Direct effect of i^{th} character on Y.

3.3.5 Estimation of genetic divergence (D^2)

The genetic divergence of twenty seven genotypes of tomato was marked using Mahalanobis (1928) D^2 statistics. The twenty two characters in tomato were included for these analyses which had the smaller average D^2 value from the first two. Similar the fourth was chosen to have the smallest average D^2 from the first three and so on. The D^2 values did not fit within with the former group and was, therefore, taken as another cluster. The genetic divergence was computed using the procedure as described by Rao (1952) and Singh and Chaudhary (1985). The details of analysis are described under the following heads:

- 1) Transformation of correlated variables,
- 2) Computation of D^2 values,
- 3) Relative contribution of individual characters towards total divergence, and
- 4) Group constellation

3.3.5.1 Transformation of correlated variables

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

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

$$\begin{array}{cccc} \lambda_{11} & \lambda_{12} & \dots & \lambda_{1p} \\ \lambda_{21} & \lambda_{22} & \dots & \lambda_{2p} \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ & \lambda_{p1} \lambda_{p2} & \dots & \lambda_{pp} \end{array}$$

and consider the extended matrix

$$\begin{array}{cccc} \lambda_{11} & \lambda_{12} & \dots & \lambda_{1p \times 1} \\ \lambda_{21} & \lambda_{22} & \dots & \lambda_{2p \times 2} \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ \bullet & \bullet & \dots & \bullet \\ & \lambda_{p1} \lambda_{p2} & \dots & \lambda_{pp \times p} \end{array}$$

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

$$1 \quad \frac{\lambda_{12}}{\lambda_{11}} \quad \dots \quad \frac{\lambda_{1p}}{\lambda_{11}} \quad \frac{x_1}{\lambda_{11}}$$

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

$$\left(\begin{array}{cccc} \lambda_{22'} & \dots & \dots & \lambda_{2p'} \\ \cdot & & & \cdot \\ \cdot & & & \cdot \\ \cdot & & & \cdot \\ \cdot & & & \cdot \\ \lambda_{p2'} & \dots & \dots & \lambda_{pp'} \end{array} \right) \left(\begin{array}{c} X_{2'} \\ \cdot \\ \cdot \\ \cdot \\ \cdot \\ X_{p'} \end{array} \right)$$

Where,

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

$$x_i = - \frac{\lambda_{i1}}{\lambda_{11}} X_1$$

$$\begin{aligned} \text{Now, } V_{(xi)} &= V_{(xi)} - \frac{2\lambda_{i1}}{\lambda_{11}} \text{Cov.}(x_i x_1) + \frac{2\lambda_{i1}}{\lambda_{11}} V(X_1) \\ &= \lambda_{ii} - \frac{\lambda_{i1}^2}{\lambda_{11}} X_{1i} \end{aligned}$$

$$\text{Now, } V_{(xi')} = + \frac{\lambda_{i1}}{\lambda_{11}} V(x_1)$$

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

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

$$\begin{aligned} \text{also, cov.}(x_1 x'_i) &= \text{cov.}(x_1 x_i) - \frac{\lambda_{i1}}{\lambda_{11}} v(x_i) \\ &= \lambda_{1i} - \lambda_{i1} = 0 \end{aligned}$$

So the new variables are uncorrelated.

Considering the second pivotal row

$$\frac{\lambda_{23}}{\lambda_{22'}} \quad \frac{\lambda_{2p'}}{\lambda_{22'}} \quad \frac{x_{2'}}{22'}$$

the further reduced matrix is

$$\left| \begin{array}{cc} \lambda_{33}'' & \dots \dots \dots \lambda_{3p}'' \\ \vdots & \vdots \\ \lambda_{p3}'' & \lambda_{pp}'' \end{array} \right| \quad \left| \begin{array}{c} \lambda_{x3}'' \\ \vdots \\ x_p'' \end{array} \right|$$

resulting into variables

$x_1' \times 2' \times 3'' \dots \dots \dots$ with variance

$x_{11}' \times \lambda_{22}' \lambda_{33}'' \dots \dots \dots$

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

3.3.5.2 Computation of D^2 values

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

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

Where,

P = number of characters studied, and

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

3.3.5.3 Relative contribution of individual characters towards total divergences

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

3.3.5.4 Group constellation

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

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

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

In all combinations each character was ranked on the basis of $d_i = y_{ij} - y_{ik}$ values. Rank 1 was given to the highest mean difference and rank p to the lowest mean difference, where p is the total number of characters. In this manner contribution of each character to the total divergence was computed.

Tocher method for grouping of varieties into various clusters was adopted. This method is detailed in a simplified way by Rao (1952) and Singh and Chaudhary (1985).

All the above computations were carried out using the software Windostat at Bio-informatics Laboratory of the Division of Genetics and Plant Breeding, SKUAST-Kashmir, Shalimar.

Chapter – 4

EXPERIMENTAL FINDINGS

The present investigation entitled “Genetic divergence studies in Tomato (*Solanum lycopersicum* L.)” was carried out with twenty seven genotypes of tomato at SKUAST-Kashmir, Shalimar campus during *Kharief* 2018. The Data recorded on twenty two characters was subjected to various statistical analysis. The results obtained, are presented in the following sub heads:

- 4.1 Analysis of variance
- 4.2 Mean performance of genotypes
- 4.3 Coefficient of variability, heritability and genetic advance in per cent of mean
- 4.4 Correlation coefficient studies
- 4.5 Path coefficient analysis
- 4.6 Estimation of genetic divergence
- 4.7 Per cent contribution of the traits.

4.1 Analysis of variance

The data recorded on seventeen quantitative & five qualitative characters were subjected to analysis of variance to test the significance of difference among the genotypes. Analysis of variance presented in Table-1, showed that the mean square due to genotypes were highly significant for all the characters. Mean sum of squares due to genotypes for all the characters were found to be highly significant (Table-2).

Table 2: Analysis of variance for twenty two characters in tomato (*Solanum lycopersicum* L.)

S. No.	Character	Mean sum of squares		
		Replication	Treatment	Error
	d.f	2	26	52
1.	Plant height (cm)	0.8492	342.5798**	2.3381
2.	Plant spread (cm)	5.9393	552.5597**	8.3681
3.	No. of primary branches plant ⁻¹	0.8981	7.9230**	0.3212
4.	Days to first flowering	0.2949	28.8820**	0.2001
5.	Days to fruit set	0.0538	14.5454**	0.1353
6.	Days to 50% flowering	0.3144	19.1047**	0.1227
7.	Days to red ripen fruit stage	0.3482	76.3705**	0.2416
8.	Fruit length (cm)	0.0127	3.5471**	0.0677
9.	Fruit diameter (cm)	0.1593	3.4443**	0.0609
10.	Average fruit weight (g)	0.3456	128.1661**	2.4226
11.	No. of locules fruit ⁻¹	8.0171	2.4190**	0.0854
12.	Pericarp thickness (cm)	0.0028	0.0202**	0.0007
13.	1000-seed weight (g)	0.0237	0.6623**	0.0480
14.	Seed weight per fruit (mg)	0.1225	0.4230**	0.0206
15.	No. of fruits plant ⁻¹	0.5925	444.8461**	4.7079
16.	Fruit yield per plot (kg)	0.0064	20.0112**	0.1162
17.	Fruit yield (q/ha)	4.8625	10466.3775**	11.7693
18.	Total soluble solids (%)	0.0509	1.3094**	0.0270
19.	Lycopene content (mg/100g)	0.0075	29.8218**	0.0400
20.	Ascorbic acid content (mg/100g)	0.0208	35.6402**	0.0365
21.	Titrate acidity (%)	0.0001	0.0140**	0.0003
22.	Juice to pulp ratio	0.0004	0.0387**	0.0003

** significant at 1%, * significant at 5%

The genetic variability estimates including mean, range, genotypic variance (GV), phenotypic variance (PV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (bs) and genetic advance as percent of mean were estimated for each character. Similarly, the variability components like genotypic mean, range, genotypic variance (GV), phenotypic variance (PV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (bs) and genetic advance as a per cent of mean (Table-4) were estimated for each quality character. A comparative performance of all the genotypes under study has been described as follows;

4.2 Mean performance of genotypes

Mean performance of genotypes in respect of twenty two characters have been presented in Table 3 and the same is described character wise in the ensuing paragraphs.

4.2.1 Plant height (cm)

The plant height ranged from 47.66 cm (VRT-01) to 90.90 cm (Kashi Amrit) comprising mean value was 72.95 cm. The genotypes VRT-19 (87.13 cm), Selection-07 (81.76 cm), Kashi Chayan (78.93 cm) TOLCV-16 (75.90 cm), Kashi Aman (74.96 cm), Kashi Anupam (74.40 cm), had significantly higher plant height as compared to general mean. The genotypes namely VRT-01 (47.66 cm), TOLCV-32 (58.33 cm), 2015/TODHYB-1 (59.86 cm), 2016/TODVAR-11 (64.26 cm) had significantly lower plant height as compared to the general mean.

4.2.2 Plant spread (cm)

The plant spread ranged from 49.66 cm (VRT-01) to 102.66 cm (Kashi Amrit) with the mean value of 81.22 cm. The genotypes TOLCV-16 (96.50 cm), Kashi Sharad (88.83 cm), Kashi Hemanth (88.16 cm), Kashi Chayan (87.56 cm), 2016/TODVAR-3 (87.06 cm), are having significantly higher plant spread as compared to general mean, whereas, VRT-01 (49.66 cm), TOLCV-32 (67.40 cm),

2015/TODHYB-1 (69.00 cm), 2016/TODVAR-12 (76.23 cm) are having significantly lower plant spread as compared to general mean.

4.2.3 Number of primary branches plant⁻¹

The number of primary branches in different genotypes ranged from 1.83 (2016/TODVAR-2) to 7.50 (Shalimar Hybrid Tomato-1) with average value was 4.94. The genotypes TOLCV-28, Kashi Aman and Kashi Sharad (6.50), Selection-7, TOLCV-16, Kashi Amrit and Kashi Vishesh (5.50), showed significantly higher number of primary branches plant⁻¹ as compared to general mean whereas Kashi Anupam (3.50), Kashi Chayan (2.83), 2015/TODHYB-2 (2.50), 2016/TODVAR-10 (2.50) are showing significantly lower number of primary branches plant⁻¹.

4.2.4 Days to first flowering

Always earliness in flowering is considered to be a favorable factor with respect to yield and also to avoid different biotic and abiotic stresses during the crop period. The data ranged from 18.23 days (Jawahar-99) to 27.93 days (2015/TODHYB-1) comprising the mean value was 22.23 days. The genotypes viz., Jawahar-99 (18.23), VRT-13 (18.83), Kashi Hemanth (19.60), Kashi Anupam (20.50), TOLCV-28 (21.60) took significantly less number of days for the first flowering whereas 2015/TODHYB-4 (27.46), 2016/TODVAR-2 (27.00), 2016/TODVAR-5 (25.50), 2016/TODVAR-3 (24.83), 2016/TODVAR-10 (24.50), genotypes took more number of days for first flowering as compared to general mean.

4.2.5 Days to fruit set

Days to fruit set ranged from 26.86 days (VRT-13) to 35.26 days (2016/TODVAR-12) with the mean value of 31.11. The genotypes namely Jawahar-99 (28.20), VRT-01 (29.80), Sel.07 (30.23), VRT-19 (30.56) were significantly earlier in number of days in order or merit as compared to general mean, whereas the genotypes namely, 2015/TODHYB-1 (33.80),

2016/TODVAR-10 (33.73), 2016/TODVAR-1 (33.53), 2015/TODHYB-4 (33.40), 2016/TODVAR-2 (33.46), 2016/TODVAR-3 (33.20) took significantly more number of days for fruit set.

4.2.6 Days to 50% flowering

The analysed data for this trait revealed that days to 50% flowering ranged from 46.40 days (Shalimar Hybrid Tomato-1) to 55.00 days (2016/TODVAR-10) with the mean value of 48.80. The genotypes Kashi Hemanth, VRT-13 and 2015/TODHYB-1 (46.60), Kashi Anupam and VRT-01 (46.40) were significantly earlier in number of days in order or merit as compared to general mean, whereas the genotypes, 2016/TODVAR-1 (54.33), Kashi Sharad (50.60), 2016/TODVAR-10 (50.20), 2015/TODHYB-4(49.20) took significantly more number of days for 50% flowering.

4.2.7 Days to red ripen fruit stage

The analysed data for these traits revealed that days to red ripen fruit stage ranged from 63.50 days (Jawahar-99) to 84.36 days (2015/TODVAR-1) with the mean value of 72.98. The genotypes viz., Kashi Vishesh (64.13), VRT-13 (64.26), TOLCV-16 (67.46), Kashi Hemanth and Kashi Anupam (71.40) were significantly earlier in number of days in order or merit as compared to general mean, whereas the genotypes, VRT-19 (74.06), Kashi Sharad (74.80), 2015/TODHYB-4 (75.53), 2016/TODVAR-12 (78.13), 2016/TODVAR-3 (83.73), took significantly more number of days to red ripen fruit stage.

4.2.8 Fruit length (cm)

The maximum (8.50) and minimum (3.60) length of fruit was recorded in Roma and Kashi Amrit, respectively with overall mean value 4.93 cm. Five genotypes, 2016/TODVAR-3 (6.36 cm), 2015/TODHYB-1 (5.63 cm), Kashi Anupam (5.46), Kashi Vishesh (5.36), Kashi Hemanth (5.23 cm), had significantly higher fruit length. Whereas the genotypes, 2016/TODVAR-5 (4.73 cm), Kashi Chayan (4.70 cm), VRT-01 (4.43 cm), VRT-19 (4.23 cm), TOLCV-16

(3.70 cm), TOLCV-28 (3.60 cm), are having significantly lower fruit length than general mean.

4.2.9 Fruit diameter (cm)

The variation for diameter of the fruit ranged from 3.53 cm (TOLCV-16, TOLCV-28) to 8.40 cm (Roma) comprising the mean value of 4.94 cm. The genotypes namely, Kashi Vishesh (5.10 cm), Kashi Anupam (5.43 cm), 2016/TODVAR-10 (5.43 cm), 2015/TODHYB-1 (5.66 cm), 2016/TODVAR-11 (6.40 cm) had significantly higher fruit diameter whereas the genotypes, 2016/TODVAR-5 (4.80 cm), Sel. 07 (4.70 cm), Jawahar-99 (3.80 cm), Kashi Amrit (3.60 cm), were showing significantly lower fruit length than the general mean.

4.2.10 Average fruit weight (g)

The range of average fruit weight varies from 50.33 g (Jawahar-99) to 72.66 g (2016/TODVAR-3) with the average mean value of 61.01 g. The highest fruit weight as compared to general mean was observed in the genotypes, 2016/TODVAR-11 (72.00 g), 2015/TODHYB-1 (69.33 g), 2016/TODVAR-5 (67.66 g), Kashi Hemanth (64.66 g), Kashi Anupam (63.33 g), The lowest fruit weight as compared to the general mean was observed in Kashi Chayan (59.00 g), TOLCV-32, Kashi Sharad (58.00 g), 2015/TODHYB-4 (55.00 g), Kashi Amrit, VRT-01 (54.33 g) genotypes respectively.

4.2.11 Number of locules fruit⁻¹

The maximum number of locule fruit⁻¹ was recorded for the genotype Kashi Anupam (5.70) which was significantly higher as compared to the general mean (3.71). Minimum number of locules fruit⁻¹ was observed in the genotype Roma.

4.2.12 Pericarp thickness (cm)

The variation for the pericarp thickness is ranged from 0.36 cm

(2016/TODVAR-5) to 0.72 cm (2016/TODVAR-11) with the general mean of 0.51 cm. The genotypes namely, 2015/TODHYB-4 (0.65 cm), 2016/TODVAR-1 (0.62 cm), Kashi Amrit (0.57 cm), Kashi Vishesh (0.55cm), TOLCV-32 (0.54 cm), were showing significantly higher pericarp thickness as compared to general mean, whereas the genotypes viz., Kashi Hemanth (0.41 cm), TOLCV-16, 2016/TODVAR-10 (0.44 cm), Jawahar-99 (0.45 cm), 2015/TODHYB-1(0.47 cm), were showed significantly lower pericarp thickness.

4.2.13 1000-seed weight (g)

From the Table it is obvious that, the range of 1000 seed weight varies between 2.43 g (Kashi Chayan) to 3.76 g (Kashi Anupam). The general mean was obtained as 3.00 g. The genotypes namely TOLCV-28 (3.63 g), Kashi Vishesh (3.66 g), 2016/TODVAR-13 (3.13 g), Sel.07 (3.30 g) are showing significantly higher value as compared to general mean. Kashi Aman, Kashi Amrit (2.70 g), TOLCV-32 (2.66 g), 2016/TODVAR-5, 2016/TODVAR-10, 2016/TODVAR-1 (2.60 g) genotypes were showing significantly lower value.

4.2.14 Seed weight fruit⁻¹ (mg)

The variation for the seed weight fruit⁻¹ is ranged from 1.10 mg (Roma) to 2.33 mg (Kashi Vishesh) with the mean value of 1.56 mg. Higher seed weight per fruit is observed in the genotypes, TOLCV-16 (2.23 mg), 2015/TODHYB-1 (2.23 mg), Kashi Anupam (2.13 mg), TOLCV-28 (1.70 mg), as compared to general mean, whereas lower seed weight fruit⁻¹ was recorded in Kashi Aman (1.20 mg), Kashi Amrit (1.23 mg), 2016/TODVAR-2 (1.30 mg), VRT-13 (1.50 mg), genotypes respectively.

4.2.15 Number of fruits plant⁻¹

From the Table, data indicated that genotype Sel.7 had maximum number of fruits (65.33) followed by Kashi Sharad (56.33). The lowest value for this trait was recorded for the genotype 2016/TODVAR-12 (13.66). The general mean was 41.33 for this trait. The genotypes TOLCV-32, VRT-01 (55.00), 2015/TODHYB-

4 (42.33), 2016/TODVAR-10 (51.66) were showing significantly more number of fruits plant⁻¹ as compared to general mean. The genotypes viz., Kashi Amrit (37.33), Kashi Vishesh (38.66), Kashi Chayan (36.66), Jawahar-99 (40.33), 2016/TODVAR-2 (25.00), 2016/TODVAR-11 (15.00) had less number of fruits plant⁻¹.

4.2.16 Fruit yield plot⁻¹ (kg)

From the data recorded, it was found that fruit yield per plot varied from 5.36 kg (2016/TODVAR-12) to 16.13 kg (Kashi Sharad) with the general mean of 9.63 kg. The genotypes namely, Sel.7 (14.90 kg), TOLCV-28 (12.90 kg), VRT-01 (12.90 kg), 2016/TODVAR-10 (12.90 kg) were showing significantly higher fruit yield plot⁻¹ as compared to the general mean. 2015/TODHYB-1, 2016/TODVAR-1 (9.23 kg), Kashi Aman (8.80 kg), Kashi Hemanth (8.16 kg), Kashi Chayan (7.56 kg), 2016/TODVAR-11 (5.66 kg) genotypes were showing significantly lower fruit yield plot⁻¹.

4.2.17 Fruit yield (q/ha)

Fruit yield (q/hectare) ranged from 124.66 q (2016/TODVAR-12) to 362.66 q (Kashi Sharad) with the general mean of 211.86 q. The genotypes namely, Sel.7 (326.23 q), 2016/TODVAR-10 (294.00 q), TOLCV-28 (292.93 q), VRT-01 (290.70 q), were showing significantly higher fruit yield as compared to the general mean, whereas, Kashi Aman (195.13 q), 2015/TODHYB-1 (194.33 q), Jawahar-99 (192.13 q), Kashi Hemanth (186.86 q), Kashi Chayan (156.13 q), 2016/TODVAR-11 (133.66 q) genotypes were showing significantly lower fruit yield per hectare.

4.2.18 Total soluble solids (%)

Total soluble solid (%) ranged from 3.20 % (2016/TODVAR-2) to 6.23 % (2015/TODHYB-4) with the mean value of 4.46%. Top ranking genotypes as compared to mean are, Kashi Aman (4.93 %), Jawahar-99 (4.86 %), Kashi Vishesh (4.80%), Sel.7 (4.73 %), whereas the genotypes, 2016/TODVAR-10

(3.93 %), Kashi Hemanth (3.90 %), VRT-01, 2015/TODHYB-1 (3.80 %), were showing significantly lower value.

4.2.19 Lycopene content (mg/100g)

The lycopene content ranged from 6.80 mg/100 g (2016/TODVAR-12) to 18.50 mg/100 g (Kashi Aman) with the general mean of 12.13 mg/100 g. The genotypes, 2015/TODHYB-1 (16.80 mg/100 g), VRT-19 (15.06 mg/100g), TOLCV-28 (14.56 mg/100 g), VRT-13 (14.36 mg/100 g), Kashi Anupam (13.60 mg/100 g), were showing significantly highest lycopene content as compared to general mean, whereas the genotypes viz., 2016/TODVAR-5 (10.63 mg/100 g), Kashi Hemanth (10.23 mg/100 g), Kashi Amrit (9.36 mg/100 g), Kashi Chayan, Jawahar-99 (8.70 mg/100 g), 2016/TODVAR-3 (7.90 mg/100 g) had lowest lycopene content as compared to general mean.

4.2.20 Ascorbic acid content (mg/100g)

The ascorbic acid content ranges from 18.73 mg/100 g (Marglobe) to 29.30 mg/100 g (Kashi Chayan) with the mean value of 22.91 mg/100 g. The genotypes Kashi Hemanth (26.26 mg/100g), 2016/TODVAR-1 (25.63 mg/100 g), Jawahar-99 (24.86 mg/100 g), Sel.7 (24.73 mg/100 g), TOLCCV-16 (23.93 mg/100 g), were showing significantly highest ascorbic acid as compared to general mean. The genotypes viz., Kashi Aman (19.30 mg/100g), 2015/TODHYB-4 (19.30 mg/100 g), VRT-01(19.53 mg/100 g), Kashi Anupam (22.60 mg/100 g), 2016/TODVAR-12 (22.80 mg/100 g) had lowest ascorbic acid content.

4.2.21 Titrable acidity (%)

The highest and lowest titrable acidity was observed in Marglobe (0.46 %) and Kashi Amrit (0.16 %). The general mean for this trait was 0.28 %. The genotypes namely, 2015/TODHYB-4 (0.37 %), Kashi Hemanth (0.35 %), TOLCV-28 (0.32 %), 2016/TODVAR-11 (0.32 %), Jawahar-99 (0.31 %), were showing significantly highest titrable acidity as compared to general mean, whereas the genotypes viz., VRT-13, Kashi Anupam (0.17 %), VRT-19, 2016/TODVAR-3

Table 3: Mean performance of the various genotypes for the different traits in tomato (*Solanum lycopersicum* L.)

S. No.	Genotypes	Plant height (cm)	Plant spread (cm)	No. of primary branches plant ⁻¹	Days to first flowering	Days to 50 % flowering	Days to fruit set	Days to red ripen fruit stage	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	No. of locules fruit ⁻¹
1.	Kashi Hemanth	69.00	88.16	4.50	19.60	31.26	46.60	71.40	5.23	5.20	6.66	3.73
2.	Kashi Aman	74.96	78.80	6.50	20.86	30.40	47.66	70.30	4.60	4.70	61.33	4.70
3.	Kashi Amrit	90.90	102.63	5.50	22.40	31.80	48.86	72.60	3.60	3.60	54.33	4.73
4.	Kashi Vishesh	58.60	62.66	5.50	20.86	27.80	47.90	64.13	5.36	5.10	64.00	3.73
5.	Kashi Anupam	74.40	75.00	3.50	20.50	29.66	46.40	71.40	5.46	5.43	63.33	5.70
6.	Kashi Chayan	78.93	87.56	2.83	20.06	29.66	46.73	75.66	4.70	4.56	59.00	2.73
7.	Kashi Sharad	69.00	88.83	6.50	20.53	29.60	50.60	74.80	4.46	4.46	58.00	2.73
8.	VRT-01	47.66	49.66	6.50	18.90	29.80	46.40	72.46	4.43	4.43	54.33	3.73
9.	VRT-13	88.66	82.00	4.50	18.83	26.86	46.60	64.26	4.23	4.30	52.33	3.70
10.	VRT-01	47.66	49.66	6.50	18.90	29.80	46.40	72.46	4.43	4.43	54.33	3.73
11.	Tolcv-16	75.90	96.50	5.50	20.60	29.86	49.53	67.46	3.70	3.53	54.00	3.96
12.	Tolcv-28	71.50	79.16	6.50	21.60	30.66	49.06	72.70	3.60	3.53	55.33	3.70
13.	Tolcv-32	58.33	67.40	5.50	20.60	29.60	48.20	72.13	4.33	4.36	58.00	3.73
14.	Sel-7	81.76	90.66	5.50	19.00	30.23	54.80	71.70	4.66	4.70	57.66	2.73
15.	Jawahar-99	80.06	101.00	6.83	18.23	28.20	48.00	63.50	3.70	3.80	50.33	3.73
16.	2016/TODVAR-1	83.40	85.80	1.83	24.50	33.53	54.33	84.36	5.56	5.60	67.66	2.76
17.	2016/TODVAR-2	57.33	87.00	2.83	27.00	33.46	49.73	73.96	5.46	5.50	66.00	2.70
18.	2016/TODVAR-3	70.60	87.06	3.83	24.83	33.20	55.00	83.73	6.36	6.26	72.66	3.76
19.	2016/TODVAR-5	75.00	77.40	3.83	25.50	34.00	49.26	77.73	4.73	4.80	67.66	5.63
20.	2016/TODVAR-10	75.56	58.00	2.50	24.50	33.73	50.20	76.13	5.30	5.43	64.00	4.16
21.	2016/TODVAR-11	64.26	83.66	3.50	26.50	33.33	46.60	74.13	6.30	6.40	72.00	2.70
22.	2016/TODVAR-12	67.83	76.23	4.83	27.50	35.26	46.53	78.13	6.20	6.23	69.00	4.10
23.	2015/TODHYB-1	59.86	69.00	6.83	27.93	33.80	46.60	74.26	5.63	5.66	69.33	3.70
24.	2015/TODHYB-4	83.50	80.00	2.50	27.46	33.40	49.20	75.53	4.56	4.56	55.00	3.76
25.	Shalimar Hybrid Tomato-1	70.03	59.66	7.50	18.60	30.20	46.40	66.36	3.60	3.80	51.66	3.73
26.	Roma	85.50	83.50	6.50	20.66	28.40	48.83	74.40	8.50	8.40	66.33	1.73
27.	Marglobe	70.16	92.86	6.83	22.13	31.80	50.33	73.26	4.76	4.80	63.00	3.40
	Mean	72.95	81.22	4.94	22.23	31.11	48.80	72.98	4.93	4.94	61.01	3.71
	CV	2.09	3.56	11.46	2.01	1.18	0.71	0.67	5.26	4.99	2.55	7.87
	C.D. 5%	2.50	4.73	0.92	0.73	0.60	0.57	0.80	0.42	0.40	2.55	0.47
	C.D. 1%	3.33	6.31	1.23	0.97	0.80	0.76	1.07	0.56	0.53	3.39	0.63

Contd...

Table 3 contd...

S. No.	Genotypes	Pericarp thickness (cm)	1000 seed weight (g)	Seed weight fruit ⁻¹ (mg)	No. of fruits plant ⁻¹	Fruit yield plot ⁻¹ (kg)	Fruit yield (q/ha)	Total soluble solids (%)	Lycopene content (mg/100g)	Ascorbic acid (mg/100g)	Titration Acidity (%)	Juice to pulp ratio
1.	Kashi Hemanth	0.41	2.73	1.40	42.00	8.16	186.86	3.90	10.23	26.26	0.35	0.50
2.	Kashi Aman	0.57	2.70	1.20	41.66	8.80	195.13	4.93	18.50	19.30	0.32	0.64
3.	Kashi Amrit	0.46	2.70	1.23	37.33	8.93	194.86	5.53	9.36	20.10	0.16	0.44
4.	Kashi Vishesh	0.55	3.66	2.33	38.66	8.50	192.46	4.80	13.30	20.60	0.26	0.66
5.	Kashi Anupam	0.41	3.76	2.13	44.33	9.36	200.13	3.86	13.60	22.60	0.17	0.62
6.	Kashi Chayan	0.46	2.43	1.13	36.66	7.56	156.13	5.20	8.70	29.30	0.25	0.47
7.	Kashi Sharad	0.43	2.63	1.43	56.33	16.13	362.66	4.20	11.26	28.80	0.32	0.48
8.	VRT-01	0.54	3.43	1.30	55.00	12.90	290.70	3.80	15.43	19.53	0.23	0.41
9.	VRT-13	0.45	3.40	1.50	46.00	8.70	196.60	4.96	14.36	21.33	0.17	0.37
10.	VRT-01	0.54	3.43	1.30	55.00	12.90	290.70	3.80	15.43	19.53	0.23	0.41
11.	Tolcv-16	0.47	3.73	2.23	51.66	8.83	198.00	4.70	10.90	23.93	0.22	0.47
12.	Tolcv-28	0.54	3.63	1.73	55.00	12.90	292.93	4.36	14.56	25.13	0.32	0.45
13.	Tolcv-32	0.54	2.66	1.76	41.33	9.46	205.50	4.40	8.23	21.36	0.37	0.59
14.	Sel-7	0.53	3.30	1.50	65.33	14.90	326.23	4.73	11.23	24.73	0.25	0.32
15.	Jawahar-99	0.45	2.53	1.23	40.33	9.30	192.13	4.86	8.70	24.86	0.31	0.37
16.	2016/TODVAR-1	0.62	2.60	1.76	43.00	9.23	195.00	4.10	8.33	25.63	0.32	0.51
17.	2016/TODVAR-2	0.47	3.13	1.30	25.00	7.16	153.33	3.20	16.96	21.63	0.36	0.56
18.	2016/TODVAR-3	0.55	2.50	1.23	42.33	8.43	188.00	4.03	7.90	20.30	0.25	0.65
19.	2016/TODVAR-5	0.36	2.60	1.40	18.00	6.60	145.00	4.06	10.63	24.90	0.33	0.71
20.	2016/TODVAR-10	0.44	2.60	1.66	51.66	12.90	294.00	3.93	10.33	23.93	0.32	0.39
21.	2016/TODVAR-11	0.72	2.70	1.33	15.00	5.66	133.66	3.90	9.56	25.10	0.32	0.46
22.	2016/TODVAR-12	0.57	2.70	1.23	13.66	5.36	124.66	3.76	6.80	20.80	0.26	0.56
23.	2015/TODHYB-1	0.47	3.46	2.23	34.33	9.23	194.33	3.80	16.89	20.73	0.23	0.64
24.	2015/TODHYB-4	0.65	3.33	2.20	42.33	9.06	190.00	6.23	16.43	19.30	0.37	0.53
25.	Shalimar Hybrid Tomato-1	0.53	3.66	1.40	43.66	12.43	289.20	4.83	8.36	21.70	0.26	0.56
26.	Roma	0.63	2.53	1.10	46.66	10.80	207.63	4.93	16.33	19.66	0.28	0.27
27.	Marglobe	0.52	2.53	1.80	41.66	9.80	214.33	4.23	15.73	18.73	0.46	0.42
	Mean	0.51	3.00	1.56	41.33	9.63	211.86	4.46	12.13	22.91	0.28	0.50
	CV	5.33	7.29	9.17	5.24	3.53	1.61	3.68	1.57	0.87	6.66	3.65
	C.D. 5%	0.04	0.35	0.23	3.55	0.55	5.62	0.26	0.31	0.32	0.03	0.02
	C.D. 1%	0.06	0.47	0.31	4.73	0.74	7.48	0.35	0.41	0.43	0.04	0.03

(0.25%), 2015/TODHYB-1 (0.43%) were showing significantly lowest titrable acidity.

4.2.22 Juice to pulp ratio

The highest and lowest values for the trait juice to pulp ratio was recorded as 2016/TODVAR-5 (0.71) and Roma (0.27). The general mean for this trait was 0.50. The genotypes viz., Kashi Vishesh (0.66), 2016/TODVAR-3 (0.65), 2015/TODHYB-1 (0.64), TOLCV-32 (0.59), 2016/TODVAR-12 (0.56) were significantly highest values for the trait as compared to general mean. The genotypes, TOLCV-16 (0.47), 2016/TODVAR-11 (0.46), Kashi Amrit (0.44), VRT-01 (0.41), Kashi Chayan (0.37), were showing significantly lowest value.

4.3 Coefficient of variability, heritability and genetic advance in per cent of mean

4.3.1 Coefficient of variability

The coefficient of genotypic and phenotypic variability is helpful to measure the extent of variability present in particular trait. This also provides a helpful measure to compare the variability present among various quantitative traits.

The estimates of coefficient of variances revealed that magnitude of phenotypic coefficient of variation for all the traits were higher in magnitude than the genotypic coefficient of variation (Table-4). The estimates of genotypic as well as phenotypic coefficient of variability were observed higher for number of primary branches plant⁻¹ (32.19 %) followed by number of fruits plant⁻¹ (29.30 %) ascorbic acid content (28.32 %) fruit yield (q/ha) (27.86 %), fruit yield plot⁻¹ (26.71 %), number of locules fruit⁻¹ (23.75 %), titrable acidity (23.38 %), seed weight fruit⁻¹ (23.37 %), Juice to pulp ratio (22.62 %), fruit length (21.80 %), fruit diameter (21.48 %) whereas plant spread (16.58 %), pericarp thickness (15.58 %), 1000 seed weight (15.06 %), total soluble solids (14.65 %), plant height (14.59 %), days to first flowering (13.90 %) average fruit weight (10.01 %) were

Table 4: Estimates of mean, range, phenotypic variance, genotypic variance, phenotypic and genotypic coefficients of variation, heritability (bs) and genetic advance (as percent of mean) for different characters in Tomato (*Solanum lycopersicum* L.)

S. No.	Characters	Mean	Range	Genotypic coefficient of variation (GCV)	Phenotypic coefficient of variation (PCV)	Genotypic variance (gv) (σ_g^2)	Phenotypic variance (pv) (σ_p^2)	Heritability (bs)%	Genetic advance (as percent of mean)
1	Plant height (cm)	72.95	47.66-90.90	14.59	14.74	113.41	115.75	98.00	29.76
2	Plant spread (cm)	81.22	49.66-102.66	16.58	16.96	181.39	189.76	95.60	33.39
3	No. of primary branches plant ⁻¹	4.94	1.83-7.50	32.19	34.17	2.53	2.85	88.70	62.47
4	Days to first flowering	22.24	18.23-27.93	13.90	14.04	9.56	9.76	97.90	28.34
5	Days to fruit set	31.11	26.86-35.26	7.04	7.14	4.80	4.93	97.30	14.30
6	Days to 50% flowering	48.80	46.40-55.00	5.15	5.20	6.32	6.45	98.10	10.51
7	Days to red ripen fruit stage	72.98	63.50-84.36	6.90	6.93	25.37	25.61	99.10	14.15
8	Fruit length (cm)	4.93	3.60-8.50	21.80	22.43	1.16	1.22	94.50	43.66
9	Fruit diameter (cm)	4.94	3.53-8.40	21.48	22.05	1.12	1.18	94.90	43.10
10	Average fruit weight (g)	61.01	50.33-72.66	10.61	10.91	41.91	44.33	94.50	21.25
11	Number of locules fruit ⁻¹	3.71	1.73-5.70	23.75	25.02	0.77	0.86	90.10	46.43
12	Pericarp thickness (cm)	0.51	0.36-0.72	15.58	16.46	0.006	0.007	89.50	30.36
13	1000 Seed weight (g)	3.00	2.43-3.76	15.06	16.74	0.20	0.25	81.00	27.93
14	Seed weight fruit ⁻¹ (mg)	1.56	1.10-2.33	23.37	25.11	0.13	0.15	86.60	44.82
15	Number of fruits plant ⁻¹	41.33	13.66-65.33	29.30	29.77	146.71	151.42	96.90	59.42
16	Fruit yield plot ⁻¹ (kg)	9.64	5.36-16.13	26.71	26.94	6.63	6.74	98.30	54.55
17	Fruit yield (q/ha)	211.86	124.66-362.66	27.86	27.91	3484.86	3496.63	99.70	57.30
18	Total soluble solids (%)	4.46	3.20-6.23	14.65	15.11	0.42	0.45	94.10	29.28
19	Lycopene content (mg/100g)	12.13	6.80-18.50	28.38	28.43	11.86	11.90	99.70	58.38
20	Ascorbic acid content (mg/100g)	22.91	18.73-29.30	13.75	13.77	9.92	9.96	99.60	28.27
21	Titrate acidity (%)	0.28	0.16-0.46	23.38	24.31	0.005	0.005	92.50	46.33
22	Juice to pulp ratio	0.50	0.27-0.71	22.62	22.91	0.013	0.013	97.50	46.00

moderate coefficient of variability while days to fruit set (7.04 %), days to red ripen fruit stage (6.90 %) and days to 50 % flowering were the lowest coefficients of variation.

4.3.2 Heritability in broad sense

Estimates of heritability in broad sense (h^2_{bs}) for twenty two characters in tomato genotypes are shown in Table-4. The estimates of heritability in broad sense (h^2_{bs}) ranged from 81.00 per cent (1000 seed weight) to 99.70 per cent (fruit yield (q/ha), lycopene content). Highest estimates of heritability (> 70.00%) were observed for all the characters.

4.3.3 Genetic advance as per cent of mean

Highest estimates of genetic advance as per cent of mean was recorded for number of primary branches per plant (62.47) followed by number of fruits plant⁻¹ (59.42), lycopene content (58.38), fruit yield (q/ha) (57.30), fruit yield plot⁻¹ (54.55), number of locules fruit (46.43), titrable acidity (46.33), juice to pulp ratio (46.00), seed weight fruit⁻¹ (44.82), fruit length (43.66), fruit diameter (43.10), plant spread (33.39), pericarp thickness (30.36), plant height (29.76), total soluble solids (29.28), days to first flowering (28.34), ascorbic acid (28.27), 1000 seed weight (27.93), average fruit weight (21.25), while days to fruit set (14.30), days to red ripen fruit stage (14.5), days to 50% flowering (10.5) showed moderate genetic advance in per cent of mean.

4.4 Correlation coefficient studies

In order to find out the degree and direction of relationship of the yield contributing characters with yield and inter relationship between themselves, correlation (phenotypic and genotypic) coefficient analysis was carried out for all traits under investigation. Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield.

Correlation analysis showed phenotypic and genotypic correlation for most of the character pairs were in same direction and genotypic estimates were higher than the phenotypic one, indicating inherent association between the characters. The test of significance was carried out for phenotypic correlation but the appropriate test of significance for genotypic correlation is not available. The correlation coefficient analyses were presented in Table 5 and 6, respectively.

Plant spread showed positive and significant correlation with plant height (0.5960), days to fruit set showed positive and significant correlation with days to first flowering (0.8624), days to 50% flowering showed positive and significant correlation with plant spread (0.2825), days to fruit set (0.2358) and plant height (0.2269), Days to red ripen fruit stage showed positive and significant correlation with days to fruit set (0.7204), days to first flowering (0.6102) and days to 50% flowering (0.5052), fruit length showed positive and significant correlation with days to red ripen fruit stage (0.4473), days to first flowering (0.3933), days to fruit set (0.2482), fruit diameter showed positive and significant correlation with fruit length (0.9889), days to red ripen fruit stage 0.4557), days to first flowering (0.4090), days to fruit set (0.2802), average fruit weight showed positive and significant correlation with fruit diameter (0.7644), fruit length (0.576), days to first flowering (0.6488), days to red ripen fruit stage (0.6204), days to fruit set (0.5960), days to 50% flowering (0.2119), pericarp thickness showed positive and significant correlation with fruit diameter (0.3739), fruit length (0.3629), days to first flowering (0.2472), days to red ripen fruit stage (0.2097), average fruit weight (0.2079), 1000 seed weight showed positive and significant correlation with number of locules per fruit (0.2140), seed weight fruit⁻¹ showed positive and significant correlation with 1000 seed weight (0.5422), number of locules fruit⁻¹ (0.2022), number of fruits plant⁻¹ showed positive and significant correlation with days to 50% flowering (0.3324), 1000 seed weight (0.2815), number of primary branches plant⁻¹ (0.2716), fruit yield plot⁻¹ showed positive and significant association with number of fruits plant⁻¹ (0.8420), days to first flowering (0.4630),

Table 5: Estimates of genotypic (above diagonal) correlation coefficients among different characters in tomato (*Solanum lycopersicum* L.)

[illegible]

Table 6: Estimates of phenotypic (above diagonal) correlation coefficients among different characters in tomato (*Solanum lycopersicum* L.)

Characters	Plant height (cm)	Plant spread (cm)	Number of primary branches plant ⁻¹	Days to first flowering	Days to fruit Set	Days to 50% flowering	Days to red ripen fruit stage	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	Number of locules fruit ⁻¹	Pericarp Thickness (cm)	1000 seed weight (g)	Seed weight fruit ⁻¹ (mg)	Number of fruits plant ⁻¹	Fruit yield plot ⁻¹ (kg)	Fruit yield (q/ha)
Plant height (cm)	1.00	0.5960	-0.1997	-0.1628	-0.1398	0.2269*	0.0286	-0.0973	-0.0908	-0.2760*	0.0781	-0.0477	-0.1303	-0.1304	0.2000	0.0072	-0.0422
Plant spread (cm)		1.00	-0.0645	-0.0676	-0.0346	0.2825*	0.0468	-0.1220	-0.1330	-0.1024	-0.0989	-0.0730	-0.2606*	-0.2076	-0.0095	-0.1894	-0.2320*
No. of primary branches plant ⁻¹			1.00	-0.4607	-0.4282	-0.2163	-0.5040	-0.2427*	-0.2342*	-0.3429	-0.0560	-0.0351	0.1847	-0.0624	0.2716*	0.3928	0.3950
Days to first flowering				1.00	0.8624	0.1455	0.6102	0.3933	0.4090	0.6488	0.0254	0.2472*	-0.1718	0.1484	-0.6214	0.4630	-0.4611
Days to fruit set					1.00	0.2358	0.7204	0.2482*	0.2802*	0.5960	0.1196	0.1399	-0.2632*	-0.0049	-0.5267	-0.3375	-0.3101
Days to 50% flowering						1.00	0.5052	0.1140	0.1123	0.2119	-0.2668	0.1216	-0.2476*	0.0033	0.3324	0.3065	0.2761*
Days to red ripen Fruit stage							1.00	0.4473	0.4557	0.6204	-0.1024	0.2097	-0.4522	-0.1655	-0.2132	-0.1243	-0.1440
Fruit length (cm)								1.00	0.9889	0.7576	-0.3670	0.3629	-0.3154	-0.1448	-0.3095	-0.2559*	-0.3187
Fruit diameter (cm)									1.00	0.7644	-0.3680	0.3739	-0.3324	-0.1671	-0.3285	-0.2513*	-0.3118
Average fruit weight (g)										1.00	-0.1092	0.2079	-0.3465	-0.0326	-0.5327	-0.4312	-0.4384
No. of locules fruit ⁻¹											1.00	-0.4261	0.2140	0.2022	-0.1356	-0.2169	-0.1633
Pericarp thickness (cm)												1.00	-0.0280	0.0019	-0.1001	-0.1143	-0.1264
1000 seed weight (g)													1.00	0.5422**	0.2815*	0.1848	0.2213*
Seed weight fruit ⁻¹ (mg)														1.00	0.1751	0.0526	0.0547
Number of fruits plant ⁻¹															1.00	0.8420	0.8167
Fruit yield plot ⁻¹ (kg)																1.00	0.9851
Fruit yield (q/ha)																	1.00

Level of significance $p < 0.05 = *$

number of primary branches plant⁻¹ (0.3928), days to 50% flowering, fruit yield (q/ha) showed positive and significant association with fruit yield plot⁻¹ (0.9851), number of fruits plant⁻¹ (0.8167), days to first flowering (0.4611), average fruit weight (0.4384), number of primary branches plant⁻¹ (0.3950), days to 50% flowering (0.2761), 1000 seed weight (0.2213).

While positive and non-significant correlation was observed in days to 50% flowering with days to fruit set (0.1455), days to red ripen fruit stage with plant spread (0.0468), plant height (0.0286), fruit length with days to 50% flowering (0.1140), fruit diameter with days to 50% flowering (0.1123), number of locules fruit⁻¹ with days to fruit set (0.1196), plant height (0.0781), days to first flowering (0.0254), pericarp thickness with days to 50% flowering (0.1216), days to fruit set (0.1309), 1000 seed weight with number of primary branches plant⁻¹ (0.1847), seed weight fruit⁻¹ with days to 50% flowering (0.0033), pericarp thickness (0.0019), number of fruits plant⁻¹ with seed weight fruit⁻¹ (0.1751), fruit yield plot⁻¹ with 1000 seed weight fruit⁻¹ (0.1848), seed weight fruit⁻¹ (0.0526), plant height (0.0072), fruit yield (q/ha) with seed weight fruit⁻¹ (0.0547).

Whereas negative and significant correlation was observed in days to first flowering with number of primary branches plant⁻¹ (-0.4607), days to fruit set with number of primary branches plant⁻¹ (-0.4282), days to 50% flowering with number of primary branches plant⁻¹ (-0.2163), days to red ripen fruit stage with number of primary branches plant⁻¹ (-0.5040), fruit length with number of primary branches plant⁻¹ (-0.2427), fruit diameter with number of primary branches plant⁻¹ (-0.2342), average fruit weight with number of primary branches plant⁻¹ (-0.3429), plant height (-0.2760), number of locules fruit⁻¹ with fruit diameter (-0.3680), fruit length (-0.3670), days to 50% flowering (-0.2668), pericarp thickness with number of locules fruit⁻¹ (-0.4261), 1000 seed weight with days to red ripen fruit stage (-0.4522), fruit diameter (-0.3324), fruit length (-0.3154), seed weight fruit⁻¹ with plant spread (-0.2606), number of fruits plant⁻¹ with days to first flowering (-0.6214), days to fruit set (-0.5267), average fruit weight (-0.5327), fruit length

(-0.3095), fruit diameter (-0.3285), fruit yield plot⁻¹ with average fruit weight (-0.4312), days to fruit set (-0.3375), fruit length (-0.2559), fruit diameter (-0.2513), number of locules fruit⁻¹ (-0.2169), fruit yield hectare⁻¹ with fruit diameter (-0.3118), fruit length (-0.3187), days to fruit set (-0.3101).

The negative and non-significant correlation was observed in number of primary branches plant⁻¹ with plant height (-0.1997), plant spread (-0.0645), days to fruit set with plant height (-0.398), plant spread (-0.0676), fruit length with plant spread (-0.1220), plant height (-0.0973), fruit diameter with plant spread (-0.1330), fruit length (-0.0908), average fruit weight with plant spread (-0.1024), number of locules fruit⁻¹ with average fruit weight (-0.1092), days to red ripen fruit stage (-0.1024), plant spread (-0.0989), number of primary branches plant⁻¹ (-0.0560), pericarp thickness with plant height (-0.0477), plant spread (-0.0730), number of primary branches plant⁻¹ (-0.0351), 1000 seed weight with days to first flowering (-0.1718), plant height (-0.1303), seed weight fruit⁻¹ with days to red ripen fruit stage (-0.1655), fruit diameter (-0.161671), fruit length (-0.1448), plant height (-0.1303), number of primary branches plant⁻¹ (-0.0624), number of fruits plant⁻¹ with number of locules fruit⁻¹ (-0.1356), pericarp thickness (-0.1001), plant spread (-0.0095), fruit yield plot⁻¹ with plant spread (-0.1894), days to red ripen fruit stage (-0.1243), pericarp thickness (-0.1143), fruit yield (q/ha) with number of locules fruit⁻¹ (-0.1633), days to red ripen fruit stage (-0.1440), pericarp thickness (-0.1264), plant height (-0.0422).

4.4.1 Phenotypic path coefficient analysis

Phenotypic path coefficient analysis was estimated (Table-7) to resolve the direct and indirect effects of different characters on fruit yield (q/ha).

Plant height had negligible positive direct effect (0.0267) on fruit yield (q/ha) and it also showing negligible positive indirect effects via fruit diameter (0.0287). Plant spread is showing negligible negative direct effect (-0.0622) on fruit yield (q/ha) and moderate negative indirect effect via fruit yield plot⁻¹

Table 7: Phenotypic path coefficient analysis of sixteen characters on fruit yield of tomato (*Solanum lycopersicum* L.)

Characters	Plant height (cm)	Plant spread (cm)	No. of primary branches plant ⁻¹	Days to first flowering	Days to fruit Set	Days to 50% flowering	Days to red ripen fruit stage	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	Number of locules fruit ⁻¹	Pericarp Thickness (cm)	1000 seed weight (g)	Seed weight fruit ⁻¹ (mg)	Number of fruits plant ⁻¹	Fruit yield plot ⁻¹ (kg)
Plant height (cm)	0.0267	0.0162	-0.0055	-0.0044	-0.0038	-0.0042	0.0019	-0.0026	-0.0025	-0.0078	0.0023	-0.0011	-0.0042	-0.0039	0.0054	0.0002
Plant spread (cm)	-0.0378	-0.0622	0.0045	0.0041	0.0027	-0.0076	-0.0003	0.0075	0.0082	0.0074	0.0062	0.0051	0.0177	0.0136	0.0006	0.0122
No. of primary branches plant ⁻¹	0.0048	0.0017	-0.0232	0.0110	0.0104	0.0043	0.0110	0.0057	0.0057	0.0081	0.0009	0.0012	-0.0044	0.0015	-0.0068	-0.0096
Days to first flowering	0.0086	0.0034	0.0247	-0.0520	-0.0456	-0.0045	-0.0287	-0.0211	-0.0220	-0.0349	-0.0011	-0.0136	0.0093	-0.0085	0.0329	0.0244
Days to fruit set	-0.0074	-0.0023	-0.0236	0.0461	0.0524	0.0091	0.0344	0.0135	0.0151	0.0324	0.0067	0.0075	-0.0147	-0.0004	-0.0279	-0.0180
Days to 50% flowering	-0.0072	0.0056	-0.0086	0.0040	0.0080	0.0461	0.0019	0.0107	0.0111	0.0159	-0.0085	0.0091	-0.0091	-0.0072	-0.0131	-0.0132
Days to red ripen Fruit stage	-0.0036	-0.0002	0.0239	-0.0278	-0.0331	-0.0020	-0.0505	-0.0158	-0.0168	-0.0213	0.0064	-0.0083	0.0189	0.0035	0.0121	0.0034
Fruit length (cm)	-0.0132	-0.0160	-0.0329	0.0543	0.0343	0.0309	0.0419	0.1334	0.1329	0.1054	-0.0525	0.0515	-0.0446	-0.0202	-0.0420	-0.0352
Fruit diameter (cm)	0.0287	0.0407	0.0753	-0.1297	-0.0884	-0.0742	-0.1023	-0.3056	-0.3068	-0.2437	0.1183	-0.1197	0.1091	0.0562	0.1024	0.0793
Average fruit weight (g)	-0.0405	-0.0165	-0.0487	0.0933	0.0859	0.0480	0.0586	0.1098	0.1104	0.1390	-0.0124	0.0305	-0.0487	-0.0013	-0.0745	-0.0588
Number of locules fruit ⁻¹	0.0025	-0.0006	-0.0003	0.0001	0.0008	-0.0012	-0.0008	-0.0025	-0.0025	-0.0006	0.0065	-0.0030	0.0016	0.0014	-0.0009	-0.0015
Pericarp thickness (cm)	-0.0013	-0.0024	-0.0015	0.0077	0.0042	0.0058	0.0049	0.0114	0.0115	0.0065	-0.0135	0.0294	-0.0010	-0.0003	-0.0031	-0.0034
1000 seed weight (g)	-0.0067	-0.0119	0.0079	-0.0075	-0.0117	-0.0083	-0.0157	-0.0140	-0.0149	-0.0147	0.0102	-0.0014	0.0419	0.0253	0.0131	0.0086
Seed weight fruit ⁻¹ (mg)	0.0067	0.0101	0.0030	-0.0075	0.0004	0.0072	0.0032	0.0070	0.0085	0.0004	-0.0101	0.0004	-0.0277	-0.0462	-0.0086	-0.0024
Number of fruits plant ⁻¹	-0.0108	0.0005	-0.0155	0.0338	0.0284	0.0152	0.0128	0.0168	0.0178	0.0286	0.0078	0.0057	-0.0167	-0.0099	-0.0534	-0.0452
Fruit yield plot ⁻¹ (kg)	0.0073	-0.2054	0.4322	-0.4910	-0.3590	-0.2999	-0.0702	-0.2762	-0.2704	-0.4431	-0.2378	-0.1220	0.2142	0.0547	0.8856	1.0468
Fruit yield (q/ha)	-0.0453	-0.2392	0.4116	-0.4655	-0.3139	-0.2353	-0.0979	-0.3223	-0.3147	-0.4222	-0.1705	-0.1288	0.2416	0.0583	0.8219	0.9875

Residual effect = 0.0826

Table 8: Genotypic path coefficient analysis of sixteen characters on fruit yield of tomato (*Solanum lycopersicum* L.)

Characters	Plant height (cm)	Plant spread (cm)	Number of primary branches plant ⁻¹	Days to first flowering	Days to fruit Set	Days to 50% flowering	Days to red ripen fruit stage	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	Number of locules fruit ⁻¹	Pericarp Thickness (cm)	1000 seed weight (g)	Seed weight Fruit ⁻¹ (mg)	No. of fruits plant ⁻¹	Fruit yield Plot ⁻¹ (kg)
Plant height (cm)	0.1063	0.0653	-0.0223	-0.0177	-0.0150	0.0536	0.0084	-0.0106	-0.0101	-0.0315	0.0094	-0.0043	-0.0187	-0.0162	0.0217	0.0007
Plant spread (cm)	-0.0831	-0.1354	0.0103	0.0089	0.0065	0.0464	-0.0004	0.0161	0.0179	0.0160	0.0135	0.0116	0.0404	0.0304	0.0014	0.0270
Number of primary branches plant ⁻¹	-0.0106	-0.0038	0.0504	-0.0243	-0.0233	0.0315	-0.0316	-0.0125	-0.0127	-0.0189	-0.0016	-0.0030	0.0097	-0.0033	0.0152	0.0214
Days to first flowering	0.0282	0.0111	0.0817	-0.1694	-0.1501	0.0534	-0.1271	-0.0701	-0.0728	-0.1156	-0.0032	-0.0456	0.0310	-0.0290	0.1085	0.0800
Days to fruit set	0.0308	0.0105	0.1007	-0.1934	-0.2182	0.1036	-0.1925	-0.0571	-0.0638	-0.1370	-0.0290	-0.0313	0.0631	0.0022	0.1169	0.0754
Days to 50% flowering	0.0599	-0.0407	0.0742	-0.0375	-0.0564	0.1187	-0.0118	-0.0869	-0.0940	-0.1310	0.0706	-0.0690	0.0703	0.0568	0.1028	0.1061
Days to red ripen Fruit stage	0.0228	0.0009	-0.1815	0.2169	0.2550	-0.0288	0.2890	0.1191	0.1291	0.1719	-0.0547	0.0684	-0.1512	-0.0134	-0.0982	-0.0302
Fruit length (cm)	-0.1975	-0.2352	-0.4902	0.8172	0.5171	-1.4448	0.8133	1.9746	1.9744	1.5981	-0.8033	0.7877	-0.6810	-0.3057	-0.6278	-0.5292
Fruit diameter (cm)	0.2546	0.3556	0.6752	-1.1543	-0.7857	2.1273	-1.2000	-2.6871	-2.6874	-2.1796	1.0637	-1.0747	0.9907	0.5150	0.9054	0.7038
Average fruit weight (g)	-0.2445	-0.0973	-0.3097	0.5631	0.5181	-0.9108	0.4908	0.6680	0.6694	0.8253	-0.0746	0.1820	-0.3070	-0.0087	-0.4487	-0.3545
No. of locules fruit ⁻¹	-0.0108	-0.0123	0.0040	-0.0023	-0.0163	-0.0730	0.0232	0.0500	0.0486	0.0111	-0.1228	0.0583	-0.0321	-0.0280	0.0190	0.0287
Pericarp thickness (cm)	-0.0036	-0.0078	-0.0054	0.0244	0.0130	-0.0526	0.0214	0.0361	0.0362	0.0200	-0.0430	0.0905	-0.0032	-0.0014	-0.0100	-0.0107
1000 seed weight (g)	-0.0530	-0.0900	0.0579	-0.552	-0.0873	0.1789	-0.1579	-0.1041	-0.1113	-0.1123	0.0789	-0.0106	0.3019	0.1920	0.1000	0.0652
Seed weight fruit ⁻¹ (mg)	0.0562	0.0829	0.0242	-0.0631	0.0037	-0.1764	0.0171	0.0571	0.0707	0.0039	-0.0842	0.0058	-0.2345	-0.3688	-0.0710	-0.0192
Number of fruits plant ⁻¹	-0.0070	0.0004	-0.0104	0.0220	0.0184	-0.0297	0.0117	0.0109	0.0116	0.0187	0.0053	0.0038	-0.0114	-0.0066	-0.0344	-0.0291
Fruit yield plot ⁻¹ (kg)	0.0058	-0.1704	0.3617	-0.4029	-0.2950	0.7624	-0.0891	-0.2287	-0.2235	-0.3665	-0.1995	-0.1006	0.1844	0.0444	0.7237	0.8533
Fruit yield (q/ha)	-0.0455	-0.2417	0.4207	-0.4676	-0.3156	0.7597	-0.1355	-0.3254	-0.3176	-0.4274	-0.1745	-0.1308	0.2523	0.0597	0.8245	0.9888

Residual effect = 0.119

(-0.2054). Number of primary branches plant⁻¹ had negligible direct effect (-0.0232) on fruit yield (q/ha) and high positive indirect effect via fruit yield plot⁻¹ (0.4322). Days to first flowering had showed negligible negative direct effect (-0.0520) on fruit yield (q/ha). It also exhibited high negative indirect effects via fruit yield plot⁻¹ (-0.4910) followed by low negative effects via fruit diameter (-0.1297). Days to fruit set had showed negligible positive direct effect (0.0524) on fruit yield (q/ha) and it also exhibited high negative indirect effect via fruit yield plot⁻¹ (-0.3590). Fruit length had showed low positive direct effect (0.1334) on fruit yield (q/ha) followed by average fruit weight (0.1098). It also exhibited moderate negative indirect effect via fruit yield plot⁻¹ (-0.2762). Fruit yield plot⁻¹ had showed very high positive direct effect (1.0468) on fruit yield (q/ha).

4.4.2 Genotypic path coefficient analysis

Genotypic path coefficient analysis was estimated (Table-8) to resolve the direct and indirect effects of different characters on fruit yield (q/ha).

Plant height had showed low positive direct effect (0.1063) on fruit yield (q/ha) Whereas fruit diameter had showed moderate positive indirect effect via fruit diameter (0.2546). It also exhibited moderate indirect negative effects of average fruit weight (-0.2445) on fruit yield (q/ha) followed by low negative effects via fruit length (-0.1975). Plant spread had showed low negative direct effect (-0.1354) on fruit yield (q/ha) whereas fruit length (-0.2532) had showed moderate negative indirect effect on fruit yield (q/ha). Number of primary branches plant⁻¹ had showed negligible positive direct effect (0.0504) on fruit yield (q/ha), whereas fruit length had showed high negative indirect effect (-0.4902) on fruit yield (q/ha) followed by average fruit weight (-0.3097). It also exhibited high positive indirect effect via fruit diameter (0.6752) followed by fruit yield plot⁻¹ (0.3617).

Days to first flowering had showed low negative direct effect (-0.1694) on fruit yield (q/ha). It also exhibited high positive indirect effects via fruit length (0.8172) on fruit yield (q/ha) followed by average fruit weight (0.5631) and moderate effects via days to red ripen fruit stage (0.2169). Days to fruit set had showed moderate negative direct effect (-0.2182) on fruit yield (q/ha) followed by high negative indirect effects via fruit diameter (-0.7857) and moderate negative indirect effects by fruit yield plot⁻¹ (-0.2950). It also exhibited high positive indirect effects via average fruit weight (0.5181) followed by fruit length (0.5171). Days to 50% flowering had showed moderate positive direct effect (0.1187) on fruit yield (q/ha). It also exhibited very high positive indirect effect via fruit diameter (2.1273) whereas high positive indirect effect via fruit yield plot⁻¹ (0.7624) on fruit yield (q/ha). Days to red ripen fruit stage had showed high positive direct effect (0.2890) and very high negative indirect effect via fruit diameter (-1.2000) on fruit yield (q/ha). It also exhibited high positive indirect effects via fruit length (0.8133) followed by average fruit weight (0.4908) on fruit yield (q/ha).

Fruit length is showing very high positive direct effect (1.9746) on fruit yield (q/ha). It also exhibited very high negative indirect effects via fruit diameter (-2.6871) and high positive indirect effects via average fruit weight (0.6680) on fruit yield (q/ha). Fruit diameter had showed very high negative indirect effect (-2.6874) on fruit yield (q/ha) whereas moderate negative indirect effect via fruit yield plot⁻¹ (-0.2235). It also exhibited very high positive indirect effects via fruit length (1.9744) followed by high positive effects by average fruit weight (0.6694) on fruit yield (q/ha). Average fruit weight is showing high positive direct effect (0.8253) followed by very high positive indirect effect via fruit length (1.5981) on fruit yield (q/ha). It also exhibited very high negative indirect effects via fruit diameter (-2.1796) followed by moderate negative indirect effects via fruit yield plot⁻¹ (-0.3665). Number of locules fruit⁻¹ had showed low negative direct effect (-0.1228) on fruit yield (q/ha) followed by low negative indirect effect via fruit yield plot⁻¹ (-0.1995). It also exhibited very high positive indirect effect via fruit

diameter (1.0637). Pericarp thickness is showing negligible positive direct effect (0.0905) followed by low positive indirect effects via average fruit weight (0.1820). It also exhibited very high negative indirect effect via fruit diameter (-1.0747). 1000 seed weight had showed high positive direct effect (0.3019) on fruit yield (q/ha) followed by low positive indirect effects via fruit yield plot⁻¹ (0.1844) and also high positive indirect effects via fruit diameter (0.9907) on fruit yield (q/ha). Seed weight fruit⁻¹ is showing high negative direct effect (-0.3688) on fruit yield (q/ha) whereas high positive indirect effects via fruit diameter (0.5150) on fruit yield (q/ha).

Number of fruits plant⁻¹ had showed negligible negative direct effect (-0.0344) on fruit yield (q/ha) whereas high negative indirect effects via fruit length (-0.6278) followed by average fruit weight (-0.4487) on fruit yield (q/ha). It also exhibited high positive indirect effect via fruit diameter (0.9054) followed by fruit yield plot⁻¹ (0.7237). Fruit yield plot⁻¹ had shown high positive direct effect (0.8533) on fruit yield (q/ha) followed by indirect effect via fruit diameter (0.7038). It also exhibited high negative indirect effects via fruit length (-0.5292) followed by average fruit weight (-0.3545) on fruit yield (q/ha).

4.5 Estimation of genetic divergence (D^2)

The studies of genetic divergence among the 27 genotypes of tomato were carried out by using Mahalanobis D^2 statistics. All the genotypes were grouped into different clusters on the basis of genetic distance among the genotypes. The distribution pattern of genotypes, cluster mean for different clusters, intra and inter cluster divergence (D^2) value and contribution percentage of various traits towards genetic divergence were presented in the table 8, 9, 10, 11 respectively.

27 genotypes were grouped into 8 different non-overlapping clusters (Table-9). Cluster I had highest number of genotypes (9) followed by cluster II (8), III (4), V (2) and the clusters IV (1), VI (1), VII (1) and VIII (1) were having only one genotype in each respectively.

Table 9: Distribution of tomato genotypes in different clusters

Cluster No.	No. of genotypes	Genotypes
I	9	Kashi Hemanth, TOLCV-16, Jawahar-99, Kashi Chayan, 2016/TODVAR-5, 2016/TODVAR-11, TOLCV-32, Kashi Amrit, Kashi Anupam
II	8	2015/TODHYB-1, 2016/TODVAR-2, Marglobe, 2015/TODHYB-4, Kashi Aman, Roma, VRT-13, Kashi Vishesh
III	4	TOLCV-28, 2016/TODVAR-10, Sel.7, Shalimar Hybrid Tomato-1
IV	1	2016/TODVAR-12
V	2	2016/TODVAR-3, 2016/TODVAR-1
VI	1	Kashi Sharad
VII	1	VRT-19
VIII	1	VRT-01

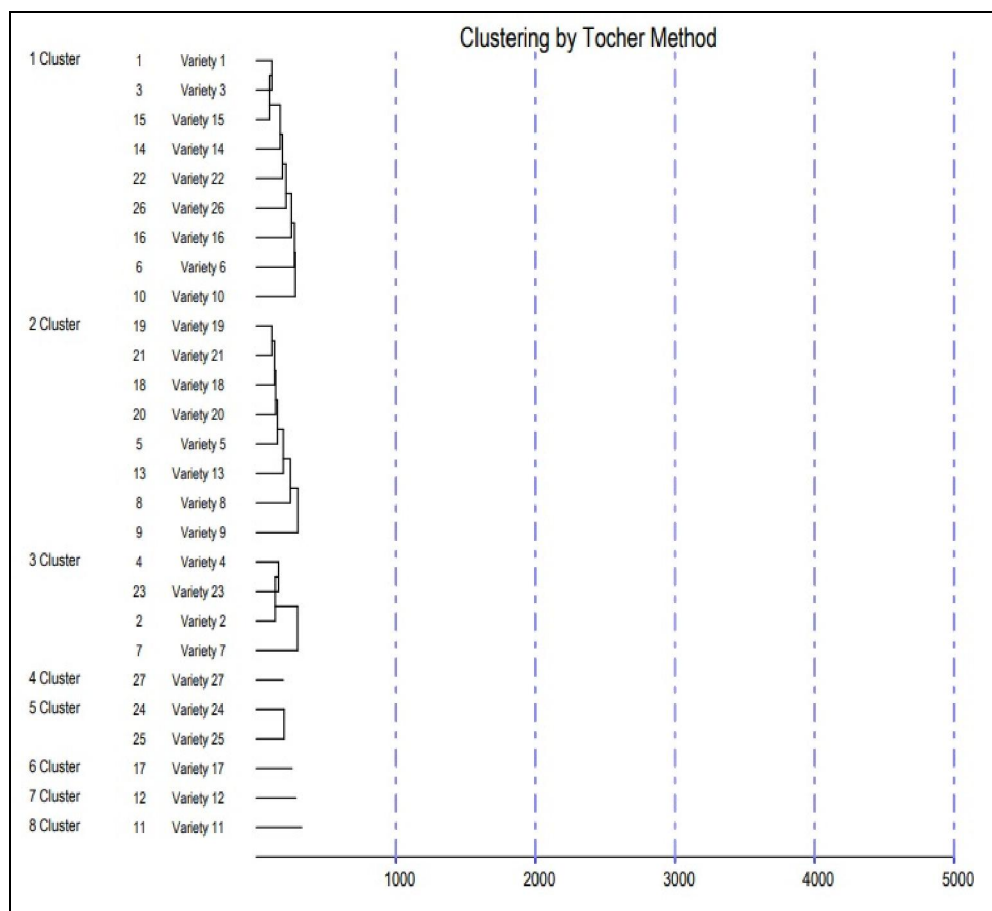


Fig. 3: Clustering by Tocher method (Dendrogram)

1 =Kashi Hemanth, 2 =Sel-07, 3 =TOLCV-16, 4 =TOLCV=28, 5 =Kashi Aman, 6 =Kashi amrit, 7 =Shalimar Hybrid Tomato-1, 8 =VRT-13, 9 =Kashi Vishesh, 10 =Kashi Anumpam, 11 =VRT-01, 12 =VRT-19, 13 =Roma, 14 =Kashi Chayan, 15 =Jawahar-99, 16 =TOLCV-32, 17 =Kashi Sharad, 18 =Marglobe, 19 =2015/TODHYB-1, 20 = 2015/TODBHYB-4, 21 =2016/TODVAR-2, 21 =2016/TODVAR-5, 23 =2016/TODVAR-10, 24 =2016/TODVAR-3, 25 =2016/TODVAR-1, 26 =2016/TODVAR-11, 27 =2016/TODVAR-12

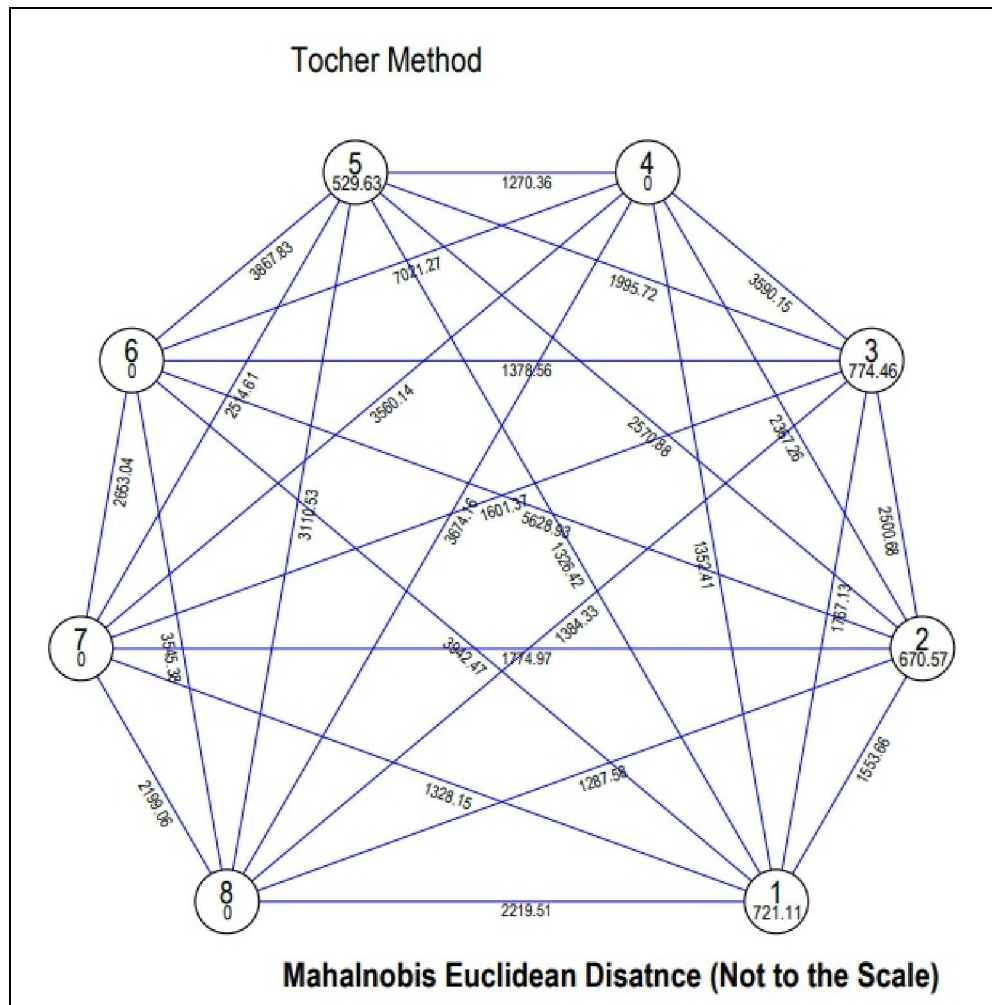


Fig. 4: Mahalanobis Euclidean Distance

The estimates of intra and inter-cluster distances represented by D^2 values are given in Table-10. Minimum intra-cluster distance was found for 0.00 (cluster IV) followed by cluster VI, VII, VIII and maximum was recorded for 770.46 (cluster III). The maximum inter cluster distance was observed between cluster IV and cluster VI (7021.27), which suggested that members of these two clusters are genetically very diverse to each other. The inter cluster distance between cluster II to VI (5628.23), cluster I to cluster VI (3942.27), cluster V to cluster VI (3867.83), cluster IV to cluster VIII (3674.16), cluster VI to cluster VIII (3545.38), cluster VI to VIII (3110.53), cluster VI to cluster VII (2653.04), cluster II to cluster IV (2570.88), cluster II to cluster III (2500.68) and cluster I to cluster VIII (2219.51) were very high.

The minimum inter cluster D^2 values were recorded in case of cluster I to cluster V (1326.42). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other.

The intra-cluster means for twenty two characters in tomato are given in Table-11. A perusal of data showed that cluster means for different traits had considerable differences between the clusters. Cluster VII showed maximum mean values for the characters plant height (87.33), plant spread (102.67), number of locules fruit⁻¹ (4.73) and minimum mean values for fruit length (4.23), fruit diameter (4.27). Cluster IV showed maximum cluster mean values for days to first flowering (27.50), days to fruit set (35.27), fruit length (6.20), fruit diameter (6.23) and minimum cluster mean values for seed weight fruit⁻¹ (1.23), number of fruits plant⁻¹ (13.67), fruit yield plot⁻¹ (5.37), fruit yield (q/ha) (124.67). Cluster V showed maximum mean values for days to 50% flowering (54.67), days to red ripen fruit stage (84.05), average fruit weight (70.17), pericarp thickness (0.59) and minimum mean values for number of primary branches plant⁻¹ (2.83), 1000 seed weight (1.50). Cluster VI showed maximum cluster mean values for number

of primary branches plant⁻¹ (6.5), number of fruits plant⁻¹ (56.33), fruit yield plot⁻¹ (16.33), fruit yield (q/ha) (362.67) and minimum mean values for days to fruit set (29.60), number of locules fruit⁻¹ (2.73), pericarp thickness (0.43). Cluster VIII showed maximum cluster mean values for number of primary branches plant⁻¹ (6.50), 1000 seed weight (3.43) and minimum mean values for plant height (47.67), plant spread (49.67), days to first flowering (18.90), days to 50% flowering (46.40). Cluster I showed minimum cluster value for fruit yield plot⁻¹ (8.21). Cluster II showed maximum cluster mean value for seed weight fruit⁻¹ (1.71) and minimum mean value for days to red ripen fruit stage (71.27). Cluster III did not showed maximum and minimum cluster mean values for any character.

4.6 Per cent contribution of the traits

The contribution percentages of traits under studied towards total divergence are tabulated in Table 12. The highest contribution in the manifestation of genetic divergence was exhibited by lycopene content (31.34) followed by fruit yield (q/ha) (27.92), ascorbic acid content (26.5), days to red ripen fruit stage (6.84), juice to pulp ratio (2.58), days to 50% flowering (1.99), whereas, days to fruit set (0.85), plant height, fruit length, total soluble solids (0.57%), days to first flowering, pericarp thickness (0.28) had minimum contribution (0.36) towards total divergence. The contribution of remaining trait in manifestation of genetic divergence was zero.

Table 10: Average intra cluster (Diagonal) and inter cluster (Above Diagonal) distance values in tomato (*Solanum lycopersicum* L.)

[illegible]

Table 11: Clusters means for various quantitative characters in tomato (*Solanum lycopersicum* L.) genotypes

Clusters	Plant height (cm)	Plant spread (cm)	No. of primary branches plant ⁻¹	Days to 1st flowering	Days to fruit set	Days to 50% flowering	Days to red ripen fruit stage	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	Number of locules fruit ⁻¹	Pericarp thickness (cm)	1000 seed weight (g)	Seed weight fruit ⁻¹ (mg)	Number of fruits plant ⁻¹	Fruit yield plot ⁻¹ (kg)	Fruit yield (q/ha)	TSS (%)	Lycopene content (mg/100g)	Ascorbic acid (mg/100g)	Titrable acidity (%)	Juice to pulp ratio
I	74.09	86.59	4.61	21.56	30.82	47.80	71.78	4.64	4.63	60.37	4.07	0.48	2.87	1.54	36.30	8.21	179.14	4.49	9.99	24.27	0.28	0.52
II	72.33	79.48	5.25	23.22	30.74	48.36	71.27	5.39	5.38	62.17	3.43	0.54	3.10	1.71	39.54	9.01	192.60	4.64	16.05	20.10	0.31	0.51
III	74.72	71.88	5.50	20.93	31.21	50.12	71.73	4.29	4.37	57.17	3.58	0.51	3.30	1.58	53.92	13.28	300.59	4.47	11.13	23.88	0.29	0.43
IV	67.83	76.23	4.83	27.50	35.27	46.53	78.13	6.20	6.23	69.00	4.10	0.57	2.70	1.23	13.67	5.37	124.67	3.77	6.80	20.80	0.27	0.56
V	77.00	86.45	2.83	24.67	33.37	54.67	84.05	5.97	5.93	70.17	3.27	0.59	2.55	1.50	42.67	8.83	191.50	4.07	8.12	22.97	0.29	0.58
VI	69.00	88.83	6.50	20.53	29.60	50.60	74.80	4.47	4.47	58.00	2.73	0.43	2.63	1.43	56.33	16.13	362.67	4.20	11.27	28.80	0.32	0.49
VII	87.13	102.67	4.50	20.73	30.57	47.40	74.07	4.23	4.27	56.33	4.73	0.53	3.40	1.50	47.00	9.10	203.77	5.13	15.07	28.83	0.25	0.38
VIII	47.67	49.67	6.50	18.90	29.80	46.40	72.47	4.43	4.43	54.33	3.73	0.54	3.43	1.30	55.00	12.90	290.70	3.80	15.43	19.53	0.23	0.42

Table 12: Percent contribution in twenty two characters towards total divergence in tomato

S. No.	Characters	Percent contribution
1.	Plant height (cm)	0.57
2.	Plant spread (cm)	0.00
3.	Number of primary branches plant ⁻¹	0.00
4.	Days to first flowering	0.28
5.	Days to fruit set	0.85
6.	Days to 50% flowering	1.99
7.	Days to red ripen fruit stage	6.84
8.	Fruit length (cm)	0.57
9.	Fruit diameter (cm)	0.00
10.	Average fruit weight (g)	0.00
11.	Number of locules fruit ⁻¹	0.00
12.	Pericarp thickness (cm)	0.28
13.	1000 Seed weight (g)	0.00
14.	Seed weight fruit ⁻¹ (mg)	0.00
15.	Number of fruits plant ⁻¹	0.00
16.	Fruit yield plot ⁻¹ (kg)	0.00
17.	Fruit yield (q/ha)	27.92
18.	Total soluble solids (%)	0.57
19.	Lycopene content (mg/100g)	31.34
20.	Ascorbic acid content (mg/100g)	26.5
21.	Titration acidity (%)	0.00
22.	Juice to pulp ratio	2.28
Total		100%

Table 13: Top ranking genotypes in respect of yield and quality traits in tomato based on *per se* performance

S. No.	Characters	Best genotypes
1.	Average fruit weight (g)	2016/TODVAR-3, 2016/TODVAR-11, 2015/TODHYB-1, Kashi Vishesh, Kashi Anupam, Roma, Kashi Hemanth
2.	Number of fruits plant ⁻¹	Sel-7, Kashi Sharad, VRT-01, TOLCV-16, TOLCV-28, 2016/TODVAR-10, 2016/TODVAR-1, Roma, VRT-19
3.	Fruit yield (q/ha)	Kashi Sharad, Sel-7, 2016/TODVAR-10, Shalimar Hybrid Tomato-1, VRT-01, TOLCV-28.
4.	Lycopene content (mg/100g)	2016/TODVAR-2, Kashi Amrit, 2015/TODHYB-1, Roma, Marglobe.
5.	Ascorbic acid content (mg/100g)	Kashi Chayan, VRT-19, Kashi Sharad, Kashi Hemanth, Sel-07.
6.	Titration acidity (%)	Marglobe, 2016/TODVAR-2, TOLCV-32, Kashi Hemanth, Kashi Chayan.

Chapter-5

DISCUSSION

Tomato (*Solanum lycopersicum* L.) is an important commercial vegetable belonging to the family solanaceae, genus Solanum. It is a large genus with many species of annual of *Solanum lycopersicum* L. is widely cultivated, and is rich in medicinal and nutritive value. Further tomato is grown in large scale in *khareif* season. The situation is unlikely to improve further unless distinctly high yielding varieties devoid of excessive vegetative growth are developed, however there is much scope to evolve high productive varieties to suit different agro-climatic conditions of the country. Good amount of genetic diversity exist in the land races/strains of tomato in the centers of diversity. Thus, existing genetic variability offers great scope for the systematic improvement of tomato. The reports and information with respect to systematic exploitation of variability in different crops of world are available even in pre Mendellian period which is attributed to cause significant increase in the yield and quality of the crops.

The prime objective of most of the vegetable breeding programmes is to make an improvement in yield, but yield is a complex character and a combined result of a number of component traits. Since yield is controlled polygenically and influenced greatly by the environmental fluctuations. Therefore, the selection of superior genotype based on yield alone would not be effective. One has to put attention on the component characters, which contribute yield in positive direction. In such a situation the available variability in the gene pool provides opportunity for selecting superior genotypes, which can be obtained through screening and evaluation. The knowledge of association between the characters helps vegetable breeders in deciding the selection criteria. The identification of donor parents for important characters, assessment of genetic variation and diversity in the available genotypes and the information about characters association are required for diversity as successful breeding programmes.

The present study involved to study nature and extent of genetic variability present in 27 genotypes of tomato with three checks namely, Shalimar Hybrid-1, Roma, Marglobe. The experiment was conducted in Randomized Block Design with three replications at SKUAST-K, Shalimar campus during *Khareif* 2018. The observations recorded on plant height (cm), plant spread (cm), number of primary branches plant⁻¹, days to first flowering, days to fruit set, days to 50% flowering, days to red ripen fruit stage, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of locules fruit⁻¹, pericarp thickness (cm), 1000 seed weight (g), seed weight fruit⁻¹ (mg), number of fruits plant⁻¹, fruit yield plot⁻¹ (kg), fruit yield (q/ha), total soluble solids(%), lycopene content (mg/100g), ascorbic acid content (mg/100g), titrable acidity (%), juice to pulp ratio.

The assessment of existing variability in the materials was done by computing coefficient of variability of genotypic and phenotypic level (Burton and Devan, 1953). The heritability in broad sense (Johnson *et al.*, 1955) was calculated to understand the transmissibility of the traits. The nature and magnitude of association among different characters was studied by using phenotypic and genotypic correlation (Dewey and Lu, 1959). Path analysis gives a cause and effect relationship. It critically breaks up different direct and indirect effects which finally make up correlation coefficient.

In the recent years, the cognizance of genetic diversity and evolutionary history of crop plants yielded major advances in crop improvement. Measure of genetic divergence reveals the difference in gene frequencies. Mahalanobis's generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating population by considering a set of parameter together. In addition to estimation of variability, cognizance of the genetic diversity of the germplasm is necessary for effective choice of parents in hybridization. The salient features of the result are discussed under the followed sub-heads.

5.1 Analysis of variance

The result obtained in the present investigation indicated that the genotypes evaluated differed significantly for all the twenty two traits. Thus, suggested existence of sufficient variability in the germplasm studied. The average value of the genotypes for different characters and their range indicated that the materials used for estimating genetic and statistical information were suitable for the study.

5.2 Mean performance

The mean performance of 27 genotypes for twenty two characters are given in Table-3. The plant height ranged from 47.66 cm (VRT-01) to 90.90 cm (Kashi Amrit) comprising mean value was 72.95 cm. The genotypes VRT-19 (87.13 cm), Selection-07 (81.76 cm), Kashi Chayan (78.93 cm) TOLCV-16 (75.90 cm), Kashi Aman (74.96 cm), Kashi Anupam (74.40 cm), had significantly higher plant height as compared to general mean. The genotypes namely, VRT-01 (47.66 cm), TOLCV-32 (58.33 cm), 2015/TODHYB-1 (59.86 cm), 2016/TODVAR-11 (64.26 cm) had significantly lower plant height. The plant spread ranged from 49.66 cm (VRT-01) to 102.66 cm (Kashi Amrit) with the mean value of 81.22 cm. The genotypes TOLCV-16 (96.50 cm), Kashi Sharad (88.83 cm), Kashi Hemanth (88.16 cm), Kashi Chayan (87.56 cm), 2016/TODVAR-3 (87.06 cm), are having significantly higher plant spread as compared to general mean, whereas, VRT-01 (49.66 cm), TOLCV-32 (67.40 cm), 2015/TODHYB-1 (69.00 cm), 2016/TODVAR-12 (76.23 cm) are having significantly lower plant spread. The number of primary branches plant⁻¹ in different genotypes ranged from 1.83 (2016/TODVAR-2) to 7.50 (Shalimar Hybrid Tomato-1) with average value was 4.94. The genotype viz., TOLCV-28, Kashi Aman and Kashi Sharad (6.50), Sel-7, TOLCV-16, Kashi Amrit and Kashi Vishesh (5.50), showed significantly higher number of primary branches plant⁻¹ as compared to general mean, whereas, Kashi Anupam (3.50), Kashi Chayan (2.83),

2015/TODHYB-2 (2.50), 2016/TODVAR-10 (2.50) are showing significantly lower number of primary branches plant⁻¹.

Always earliness in flowering is considered to be a favorable factor with respect to yield and also to avoid different biotic and abiotic stresses during the crop period. The data ranged from 18.23 days (Jawahar-99) to 27.93 days (2015/TODHYB-1) comprising the mean value was 22.23 days. The genotypes viz., Jawahar-99 (18.23), VRT-13 (18.83), Kashi Hemanth (19.60), Kashi Anupam (20.50), TOLCV-28 (21.60) took significantly less number of days for the first flowering, whereas, 2015/TODHYB-4 (27.46), 2016/TODVAR-2 (27.00), 2016/TODVAR-5 (25.50), 2016/TODVAR-3 (24.83), 2016/TODVAR-10 (24.50), genotypes took more number of days for first flowering as compared to general mean. Days to fruit set ranged from 26.86 days (VRT-13) to 35.26 days (2016/TODVAR-12) with the mean value of 31.11. The genotypes namely Jawahar-99 (28.20), VRT-01 (29.80), Sel.07 (30.23), VRT-19 (30.56) were significantly earlier in number of days in order or merit as compared to general mean, whereas the genotypes namely, 2015/TODHYB-1 (33.80), 2016/TODVAR-10 (33.73), 2016/TODVAR-1 (33.53), 2015/TODHYB-4 (33.40), 2016/TODVAR-2 (33.46), 2016/TODVAR-3 (33.20), took significantly more number of days for fruit set.

The analysed data for this trait revealed that days to 50% flowering ranged from 46.40 days (Shalimar hybrid-1) to 55.00 days (2016/TODVAR-10) with the mean value of 48.80. The genotypes Kashi Hemanth, VRT-13 and 2015/TODHYB-1 (46.60), Kashi Anupam and VRT-01 (46.40) were significantly earlier in number of days in order or merit as compared to general mean, whereas the genotypes, 2016/TODVAR-1 (54.33), Kashi Sharad (50.60), 2016/TODVAR-10 (50.20), 2015/TODHYB-4 (49.20) took significantly more number of days for 50% flowering. Days to red ripen fruit stage ranged from 63.50 days (Jawahar-99) to 84.36 days (2015/TODVAR-1) with the mean value of 72.98. The genotypes viz., Kashi Vishesh (64.13), VRT-13 (64.26), TOLCV-16 (67.46), Kashi Hemanth

and Kashi Anupam (71.40) were significantly earlier in number of days in order or merit as compared to general mean, whereas the genotypes, VRT-19 (74.06), Kashi Sharad (74.80), 2015/TODHYB-4 (75.53), 2016/TODVAR-12 (78.13), 2016/TODVAR-3 (83.73), took significantly more number of days to red ripen fruit stage.

This suggested that the genotypes which were showing early and late in flowering, fruiting and maturity stages are selected based on the objective of programme and could be exploited in suitable breeding programme.

The maximum (8.50) and minimum (3.60) length of fruit was recorded in Roma and Kashi Amrit, respectively with overall mean value 4.93 cm. Five genotypes, 2016/TODVAR-3 (6.36 cm), 2015/TODHYB-1 (5.63 cm), Kashi Anupam (5.46), Kashi Vishesh (5.36), Kashi Hemanth (5.23 cm), had significantly higher fruit length. The variation for diameter of the fruit ranged from 3.53 cm (TOLCV-16, TOLCV-28) to 8.40 cm (Roma) comprising the mean value of 4.94 cm. The genotypes namely, Kashi Vishesh (5.10 cm), Kashi Anupam (5.43 cm), 2016/TODVAR-10 (5.43 cm), 2015/TODHYB-1 (5.66 cm), 2016/TODVAR-11 (6.40 cm) had significantly higher fruit diameter.

On above basis promising genotypes for the fruit length and diameter are, 2016/TODVAR-3, 2015/TODHYB-1, Kashi Anupam, Kashi Vishesh, Kashi Hemanth.

The range of average fruit weight varies from 50.33 g (Jawahar-99 to 72.66 g (2016/TODVAR-3) with the average mean value of 61.01 g. The highest fruit weight as compared to general mean was observed in the genotypes, 2016/TODVAR-11 (72.00 g), 2015/TODHYB-1 (69.33 g), 2016/TODVAR-5 (67.66 g), Kashi Hemanth (64.66 g), Kashi Anupam (63.33 g).

The maximum number of locules fruit⁻¹ was recorded for the genotype Kashi Anupam (5.70) which was significantly higher as compared to the general

mean (3.71). Minimum number of locules per fruit was observed in the genotype Roma.

The variation for the pericarp thickness is ranged from 0.36 cm (2016/TODVAR-5) to 0.72 cm (2016/TODVAR-11) with the general mean of 0.51 cm. The genotypes namely, 2015/TODHYB-4 (0.65 cm), 2016/TODVAR-1 (0.62 cm), Kashi Amrit (0.57 cm), Kashi Vishesh (0.55cm), TOLCV-32 (0.54 cm), were showing significantly higher pericarp thickness.

From the Table it is obvious that, the range of 1000 seed weight varies between 2.43 g (Kashi Chayan) to 3.76 g (Kashi Anupam). The general mean was obtained as 3.00g. The genotypes namely TOLCV-28 (3.63 g), Kashi Vishesh (3.66g), 2016/TODVAR-13 (3.13 g), Sel.07 (3.30 g) are showing significantly higher value. The variation for the seed weight fruit⁻¹ is ranged from 1.10 mg (Roma) to 2.33 mg (Kashi Vishesh) with the mean value of 1.56 mg. Higher seed weight fruit⁻¹ is observed in the genotypes, TOLCV-16 (2.23 mg), 2015/TODHYB-1 (2.23 mg), Kashi Anupam (2.13 mg), TOLCV-28 (1.70 mg), as compared to general mean.

From the Table, data indicated that genotype Sel-7 had maximum number of fruits (65.33) followed by Kashi Sharad (56.33). The lowest value for this trait was recorded for the genotype 2016/TODVAR-12 (13.66). The general mean was 41.33 for this trait. The genotypes TOLCV-32, VRT-01 (55.00), 2015/TODHYB-4 (42.33), 2016/TODVAR-10 (51.66) were showing significantly more number of fruits plant⁻¹ as compared to general mean.

From the data recorded, it was found that fruit yield plot⁻¹ varied from 5.36 kg (2016/TODVAR-12) to 16.13 kg (Kashi Sharad) with the general mean of 9.63 kg. The genotypes namely, Sel.7 (14.90 kg), TOLCV-28 (12.90 kg), VRT-01 (12.90 kg), 2016/TODVAR-10 (12.90 kg) were showing significantly higher fruit yield plot⁻¹ as compared to the general mean. 2015/TODHYB-1, 2016/TODVAR-1 (9.23 kg), Kashi Aman (8.80 kg), Kashi Hemanth (8.16 kg), Kashi Chayan (7.5

kg), 2016/TODVAR-11 (5.66 kg) genotypes were showing significantly lower fruit yield plant⁻¹.

Fruit yield (q/ha) ranged from 124.66 q (2016/TODVAR-12) to 362.66 q (Kashi Sharad) with the general mean of 211.86 q. The genotypes namely, Sel.7 (326.23 q), 2016/TODVAR-10 (294.00 q), TOLCV-28 (292.93 q), VRT-01 (290.70 q), were showing significantly higher fruit yield as compared to the general mean, whereas, Kashi Aman (195.13 q), 2015/TODHYB-1 (194.33 q), Jawahar-99 (192.13 q), Kashi Hemanth (186.86 q), Kashi Chayan (156.13 q), 2016/TODVAR-11 (133.66 q) genotypes were showing significantly lower fruit yield (q/ha).

Total soluble solids (%) ranged from 3.20% (2016/TODVAR-2) to 6.23% (2015/TODHYB-4) with the mean value of 4.46%. Top ranking genotypes as compared to mean are, Kashi Aman (4.93%), Jawahar-99 (4.86%), Kashi Vishesh (4.80%), Sel.7 (4.73%).

The lycopene content ranged from 6.80 mg/100g (2016/TODVAR-12) to 18.50 mg/100g (Kashi Aman) with the general mean of 12.13 mg/100g. The genotypes, 2015/TODHYB-1 (16.80 mg/100g), VRT-19 (15.06 mg/100g), TOLCV-28 (14.56 mg/100g), VRT-13 (14.36 mg/100g), Kashi Anupam (13.60 mg/100g), were showing significantly highest lycopene content as compared to general mean.

The ascorbic acid content ranges from 18.73 mg/100g (Marglobe) to 29.30 mg/100g (Kashi Chayan) with the mean value of 22.91 mg/100g. The genotypes Kashi Hemanth (26.26 mg/100g), 2016/TODVAR-1 (25.63 mg/100g), Jawahar-99 (24.86 mg/100g), Sel.7 (24.73 mg/100g), TOLCCV-16 (23.93 mg/100g), were showing significantly highest ascorbic acid as compared to general mean.

The highest and lowest titrable acidity was observed in Marglobe (0.46%) and Kashi Amrit (0.16%). The general mean for this trait was 0.28%. The genotypes namely, 2015/TODHYB-4 (0.37%), Kashi Hemanth (0.35%), TOLCV-

28 (0.32%), 2016/TODVAR-11 (0.32%), Jawahar-99 (0.31%), were showing significantly highest titrable acidity as compared to general mean.

The highest and lowest values for the trait juice to pulp ratio was recorded as 2016/TODVAR-5 (0.71) and Roma (0.27). The general mean for this trait was 0.50. The genotypes viz., Kashi Vishesh (0.66), 2016/TODVAR-3 (0.65), 2015/TODHYB-1 (0.64), TOLCV-32 (0.59), 2016/TODVAR-12 (0.56) were showing significantly highest values.

A critical review of mean, performance of genotypes suggested the presence of wide range of genetic variation, among the genotypes. Pradeep Kumar *et al.* (2001), Gonzalez-Cebrino *et al.* (2011), Singh *et al.* (2010), George *et al.* (2004), Kaur *et al.* (2002) and Toor *et al.* (2006), presence of ample amount of genetic variability in present investigation are in agreement of earlier work done in tomato.

5.3 Coefficient of variability, heritability and genetic advance

Coefficient of variability is the relative measure of dispersion. The phenotypic coefficient of variability is the product of genotypic and environmental of interaction (error variation).

The genetic variability present in the genotypes provided the raw material for any plant breeding programme on which selection acts to evolve superior genotypes. Coefficient of variability is the measure of dispersion. The phenotypic coefficient of variability is the product of genotypes and environmental of interaction (error variation). The genetic variability present in the genotypes provides, the raw material for any plant breeding programme on which selection acts to evolve superior genotypes. Thus, higher the amount of variation present for character in the breeding material greater, is the scope for its improvement through selection.

The phenotypic and genotypic coefficient of variations were estimated to assess the existing variability are present in Table-4. In general the phenotypic

coefficient of variability was higher than genotypic coefficient of variability which indicated that environment influenced considerably in expression of these traits.

The higher magnitude of coefficient of variation at estimates of genotypic as well as phenotypic coefficient of variability were observed higher for number of primary branches plant⁻¹ (32.19%) followed by number of fruits plant⁻¹ (29.30%) lycopene content (28.32%) fruit yield (q/ha) (27.86%), fruit yield plot⁻¹ (26.71%), number of locules fruit⁻¹ (23.75%), titrable acidity (23.38%), seed weight fruit⁻¹ (23.37%), Juice to pulp ratio (22.62%), Fruit length (21.80%), fruit diameter (21.48%) whereas plant spread (16.58%), pericarp thickness (15.58%), 1000 seed weight (15.06%), total soluble solids (14.65%), plant height (14.59%), days to first flowering (13.90%) average fruit weight (10.01) were showed moderate coefficient of variability while days to fruit set (7.04%), days to red ripen fruit stage (6.90%) and days to 50% flowering were showing the lowest coefficients of variation. Results obtained in present investigations are in agreement with the finding of Neeraj Singh *et al.* (2015), Dar *et al.* (2011), Dar and Sharma (2011), Shankar *et al.* (2013).

Heritability estimate which provides the assessment of transmissible genetic variability to total variability happens to the most important basic factor in determining the genetic improvement and response to selection.

However, the degree of improvement attained through selection is not only depending on heritability but also on the amount of genetic variation present in the breeding material and extent of selection pressure applied by the breeder. The parameter genetic advance in per cent of mean (GA) is more reliable index for understanding the effectiveness of selection to improve the traits because its estimate is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus heritability and genetic advance in per cent of mean in combination provides clear picture regarding the effectiveness of selection for improving the plant characters.

The high magnitude of heritability in broad sense was observed for all the traits. The finding obtained in present study indicates good response of selection for these characters. Estimates of heritability in broad sense (h^2_{bs}) for twenty characters in tomato genotypes are shown in Table-4. The estimates of heritability in broad sense (h^2_{bs}) ranged from 81.00 per cent (1000 seed weight) to 99.70 per cent (fruit yield (q/ha), lycopene content). Highest estimates of heritability (>70.00%) were observed for all the characters. Results obtained in present investigation are in agreement with the finding of Neeraj Singh *et al.* (2015), Singh *et al.* (2002), Mohammed *et al.* (2012).

Highest estimates of genetic advance as per cent of mean was recorded for number of primary branches plant⁻¹ followed by number of fruits plant⁻¹, lycopene content, fruit yield (q/ha), fruit yield plot⁻¹, number of locules fruit⁻¹, titrable acidity, juice to pulp ratio, seed weight fruit⁻¹, fruit length, fruit diameter, plant spread, pericarp thickness, plant height, total soluble solids, days to first flowering, ascorbic acid content, 1000 seed weight, average fruit weight, while days to fruit set, days to red ripen fruit stage, days to 50% flowering showed moderate genetic advance in per cent of mean. Results obtained in present investigation are in agreement with the finding of Neeraj Singh *et al.* (2015), Prasanth *et al.* (2007), Mehta and Asati (2008) and, Mohamed *et al.* (2012), Ahirwar *et al.* (2013).

5.4 Correlation and Path coefficient analysis

There is ample evidence to show that direct selection for fruit yield is not sufficiently effective, as yield is polygenically controlled and associated with number of related traits. Therefore indirect selection is desirable for improvement of yield. A knowledge of association between yield and its component traits and inter relationship among themselves may provide information fruitful for planning an effective and successful breeding program.

In present study the phenotypic and genotypic correlation coefficients

were worked out in respect of seventeen quantitative characters in all possible combinations (Table 5 and 6). In general, it was found that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic values. High genotypic correlation coefficients suggested that there was inherent relationship between the traits under study and environment had not played much role in reducing their actual association. The statistics which measures the relationship between two or more variable is known as correlation coefficient.

Basically yield is the main character with which all other characters are positively or negatively correlated. Fruit yield (q/ha) showed positive and significant association with fruit yield plot⁻¹, number of fruits plant⁻¹, days to first flowering, average fruit weight, number of primary branches plant⁻¹, days to 50% flowering, 1000 seed weight, however positive and non-significant correlation with seed weight fruit⁻¹. Similar results in tomato were obtained by Singh *et al.* (2006), Prashanth *et al.* (2008), Meitei *et al.* (2014), Rana *et al.* (2014) and Nowsu *et al.* (2014).

Days to 50% flowering had shown positive and significant correlation with fruit yield (q/ha) comprising there low positive direct effect as well as very high positive indirect effect via fruit diameter. Number of primary branches plant⁻¹ is showing significant and positive correlation with fruit yield (q/ha) comprising there negligible positive direct effect. This result in close conformity with the findings of Singh *et al.* (1976) and Mehta and Asati (2008), Tasisa *et al.* (2012) in tomato. Average fruit weight had shown significant and positive correlation with fruit yield (q/ha) due to very high positive direct effect. This is an agreement with the findings of Mohanty (2003), Prashanth *et al.* (2007), Kapte and Jansirani (2014), Meena and Bahadur (2015). 1000 seed weight is showing significant and positive correlation with fruit yield (q/ha) due to high positive direct effect. Similar findings are obtained by Hidayatullah *et al.* (2008). Fruit yield plot⁻¹ had showed positive and significant correlation with fruit yield (q/ha) due to

corresponding high positive direct effect as well as very high positive indirect effect via fruit diameter.

Suggesting that these above mentioned traits may be treated as prime traits during the course of selection to enhance the yield of tomato.

5.5 Genetic divergence studies

Assessment of divergence in the germplasm is essential to know the spectrum of diversity so that improvement in fruit yield can be normally attained through involvement of the genetically diverse parents in breeding programs. Mahalanobis D^2 statistics, a powerful tool has been used to quantify the genetic divergence between the genotypes and to identify diverse parents for crossing. This also helps to relate clustering pattern with the geographical origin. This technique has been employed widely to resolve divergence at inter varietal, species and sub species levels in classifying problems in crop plants.

In the present investigation, 27 genotypes were grouped into eight clusters based on their D^2 values, Cluster I (9) had highest number of genotypes followed by cluster II (8), III (4), V (2) and the clusters IV (1), VI (1), VII (1) and VIII (1) were having only one genotype in each respectively. Similar studies based on D^2 statistic were also performed by, Arun Kumar *et al.* (2016), Nalla *et al.* (2014) and Lekshmi and Celine (2016).

The data of the cluster means for different characters (table 10) indicated the wide difference between cluster means. Cluster VII showed maximum mean values for the characters plant height, plant spread, number of locules fruit⁻¹ and minimum mean values for fruit length, fruit diameter. Cluster IV showed maximum cluster mean values for days to first flowering, days to fruit set, fruit length, fruit diameter and minimum cluster mean values for seed weight fruit⁻¹, number of fruits plant⁻¹, fruit yield plot⁻¹, fruit yield (q/ha). Cluster V showed maximum mean values for days to 50% flowering, days to red ripen fruit stage, average fruit weight, pericarp thickness and minimum mean values for number of

primary branches plant⁻¹, 1000 seed weight. Cluster VI showed maximum cluster mean values for number of primary branches plant⁻¹, number of fruits plant⁻¹, fruit yield plot⁻¹, fruit yield (q/ha) and minimum mean values for days to fruit set, number of locules fruit⁻¹, pericarp thickness. Cluster VIII showed maximum cluster mean values for number of primary branches plant⁻¹, 1000 seed weight and minimum mean values for plant height, plant spread, days to first flowering, days to 50% flowering. Cluster I showed minimum cluster value for fruit yield plot⁻¹. Cluster II showed maximum cluster mean value for seed weight fruit⁻¹ and minimum mean value for days to red ripen fruit stage. Cluster III did not showed maximum and minimum cluster mean values for any character. Therefore, the clusters which were showing maximum cluster mean values may be chosen for transferring the traits having high mean values through hybridization programme. Selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by Rai *et al.* (1998), Joshi and Kohli (2003), Sharma *et al.* (2006), Arun kumar *et al.* (2016), Nalla *et al.* (2014) and Lekshmi and Celine (2016).

Inter and intra cluster distance (D) were computed for eight clusters and presented in table 9. The maximum inter cluster distance was observed between cluster IV and cluster VI, which suggested that members of these two clusters are genetically very diverse to each other. The minimum inter cluster D² values were recorded in case of cluster I to cluster V. Minimum intra-cluster distance was found for 0.00 (cluster IV) followed by cluster VI, VII, VIII and maximum was recorded for cluster III. The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. The genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varieties. These results of genetic diversity study were in agreement with that of

Mahesh *et al.* (2006), Prashanth *et al.* (2007), Reddy *et al.* (2013), Nalla *et al.* (2014), Lekshmi and Celine (2016), Arun Kumar *et al.* (2016).

Contribution of different plant character for genetic divergence is important for the purpose of further selection and choice of parents for hybridization. The highest contribution in the manifestation of genetic divergence was exhibited by lycopene content followed by fruit yield (q/ha), ascorbic acid content, days to red ripen fruit stage, juice to pulp ratio, days to 50% flowering, whereas, days to fruit set, plant height, fruit length, total soluble solids, days to first flowering, pericarp thickness had minimum contribution towards total divergence. The contribution of remaining trait in manifestation of genetic divergence was zero. These result are in similar with the findings of Lekshmi and Celine (2016) in tomato

Chapter-6

SUMMARY AND CONCLUSION

The present investigation entitled “Genetic divergence studies in Tomato (*Solanum lycopersicum* L.)”.

The experiment was conducted in randomized block design with three replications in *Khareif* season 25th May, 2018 at the Experimental fields of the Division of Vegetable science SKUAST-Kashmir, Shalimar Srinagar during the *Khareif* Summer season 2018. Observations recorded on twenty two characters i.e., plant height (cm), plant spread (cm), number of primary branches plant⁻¹, days to first flowering, days to 50% flowering, days to fruit set, days to red ripen fruit stage, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of locules fruit⁻¹, pericarp thickness (cm), 1000 seed weight (g), seed weight fruit⁻¹ (mg), number of fruits plant⁻¹, fruit yield plot⁻¹ (kg), fruit yield (q/ha), total soluble solids (%), ascorbic acid (mg/100g), lycopene content (mg/100g), titrable acidity (%), juice to pulp ratio were studied for various statistical and biometrical parameters.

The results obtained on different aspects are summarized here are:

- Analysis of variance in the present investigation indicated that the genotypes evaluated differed significantly among all the treatment for all the twenty two traits. The genotypes namely, Kashi Sharad, Sel-7, VRT-01, Shalimar Hybrid-1, 2016/TODVAR-10 and TOLCV-28 produced highest fruit yield per plot. These genotypes also exhibited average mean performance for number of fruits per plant, fruit yield per hectare. The genotypes Jawahar-99, Shalimar Hybrid-1, Roma, VRT-13, Kashi Hemanth, Kashi Anupam, TOLCV-28 were earlier in performance for the traits days to first flowering, days to fruit set, days to 50% flowering, days to red ripen fruit stage. The genotypes Roma, 2016/TODVAR-3, 2016/TODVAR-11, 2016/TODVAR-1, 2015/TODHYB-1, Kashi Vishesh,

Kashi Hemanth were exhibited best performance for fruit length, fruit diameter, average fruit weight.

- In quality characters, highest TSS content was exhibited by Kashi Aman, Roma, Jawahar-99, Shalimar Hybrid Tomato-1, Kashi Vishesh and sel-7, whereas highest lycopene content was recorded in 2015/TODHYB-1, Roma, VRT-19, Marglobe and TOLCV-28. Highest ascorbic acid was recorded in Kashi Chayan, Kashi Hemanth, 2016/TODVAR-1, Jawahar-99 and Sel-7. Highest titrable acidity recorded in Marglobe followed by 2015/TODHYB-4, Kashi Hemanth, TOLCV-28 and Jawahar-99. Maximum Juice to pulp ratio was recorded in 2016/TODVAR-5 followed by Kashi Vishesh, 2016/TODVAR-3, 2015/TODHYB-1 and TOLCV-32. The genotypes namely Kashi Vishesh, Kashi chayan, Roma, Sel-7 were performed best for the quality characters.

Based on the present findings the following broad conclusions could be drawn :

1. Significant genetic variability was present for all the traits contributing towards yield as well as quality indicating that the present set of material should enable their use in future tomato improvement programmes.
2. The higher magnitude of coefficient of variation at phenotypic as well as genotypic levels were observed for all genotypes in number of primary branches plant⁻¹ followed by number of fruits plant⁻¹, lycopene content, fruit yield q/ha), fruit yield plot⁻¹, number of locules fruit⁻¹, titrable acidity, seed weight fruit⁻¹, Juice to pulp ratio, fruit length, fruit diameter whereas plant spread, pericarp thickness, 1000 seed weight, total soluble solids, plant height, days to first flowering and average fruit weight were moderate coefficient of variability while days to fruit set, days to red ripen fruit stage and days to 50% flowering were the lowest coefficients of variation.
3. The presence of high heritability in broad sense along with high genetic

advance in percent of mean were observed for number of fruits plant⁻¹, fruit yield (q/ha), fruit yield plot⁻¹ (kg), ascorbic acid content (mg/100g), juice to pulp ratio and number of primary branches plant⁻¹, whereas high heritability in broad sense were observed for fruit yield (q/ha), ascorbic acid content (mg/100g), lycopene content (mg/100g), days to first flowering, juice to pulp ratio, number of primary branches plant⁻¹, fruit yield plot⁻¹ (kg). In case of high genetic advance as percent of mean were observed for number of primary branches plant⁻¹ followed by number of fruits plant⁻¹, lycopene content (mg/100g), fruit yield (q/ha), fruit yield plot⁻¹ (kg), number of locules fruit⁻¹, titrable acidity (%), juice to pulp ratio, seed weight per fruit (mg), fruit length (cm), fruit diameter (cm), plant spread (cm), pericarp thickness (cm), plant height (cm), total soluble solids (%), days to first flowering, ascorbic acid content (mg/100g), 1000 seed weight (g), average fruit weight (g).

4. The phenotypic correlation coefficients between different characters were generally similar in magnitude and nature to the corresponding genotypic correlation coefficient. Fruit yield (q/ha) showed positive and significant association with fruit yield plot⁻¹, number of fruit plant⁻¹, days to first flowering, average fruit weight, number of primary branches plant⁻¹, days to 50% flowering, 1000 seed weight.
5. Maximum direct contribution towards yield came from fruit length, average fruit weight and fruit yield plot⁻¹ and these traits might be considered as high yield symbols of tomato and might be used as selection traits in breeding of high yielding tomato genotypes.
6. The 27 genotypes of tomato germplasm were grouped into 8 clusters. The different clusters showed intra-cluster group means for twenty two characters. Therefore, crosses between members of clusters having high cluster means for important characters coupled with high inter cluster distances between them, are likely to be more useful. Maximum cluster

mean for fruit yield (q/ha) was observed in cluster VI followed by cluster III. The maximum direct effect for fruit yield (q/ha) indicated more emphasis should be given on these characters in selection programme.

7. Major cluster in divergence analysis contained genotypes of heterogeneous origin, thereby, indicating no parallelism between genetic and geographic diversity. Therefore, crosses between members of clusters separated by high inter cluster distance are likely to produce desirable segregates. The very high inter cluster value was observed between the cluster IV and cluster VI, which suggested that members of these two clusters are genetically very diverse to each other. The inter cluster distance between cluster II to VI, cluster I to cluster VI, cluster V to cluster VI, cluster IV to cluster VIII, cluster VI to cluster VIII, cluster VI to VIII, cluster VI to cluster VII, cluster II to cluster IV, cluster II to cluster III and cluster I to cluster VIII were very high.
8. Maximum percent contribution was observed for lycopene content followed by fruit yield (q/ha), ascorbic acid content, titrable acidity, days to red ripen fruit stage, juice to pulp ratio, days to 50% flowering.
9. *Per se* performance of tomato genotypes/varieties for yield hectare⁻¹ revealed that Kashi Sharad, Sel-7, 2016/TODVAR-10, Shalimar Hybrid Tomato-1, VRT-01, TOLCV-28 were the best, hence these genotypes/varieties can be used as such in promotion of tomato production programme as elite germplasm lines/varieties or may be recommended for commercial cultivation after testing them over years and locations.

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CERTIFICATE

Certified that all the corrections/amendments as suggested by External Examiner Dr. Rajesh Kumar Singh, Associate Professor, BAU, UP during Viva-Voce examination held on 17-07-2019 have been incorporated in the manuscript entitled “**Genetic divergence studies in Tomato (*Solanum lycopersicum* L.)**” submitted by **Mr. B. Srinivasulu (Regd. No. 2017-H-194-M)**.

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