GENETIC DIVERSITY OF YIELD AND QUALITY TRAITS IN TOMATO (*Solanum lycopersicum* L.)

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(S*olanum lycopersicum* L.)

BY

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CERTIFICATE

This is to certify that thesis entitled, "Genetic diversity analysis of yield and quality traits in tomato (Solanum lycopersicum L.)" submitted to the faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by Muhammad Muktader Rashid Bhuiyan, Registration No.: 11-04391 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or source of information, as has been availed of during the course of this investigation has been duly been acknowledged by him.

Dated: June, 2017
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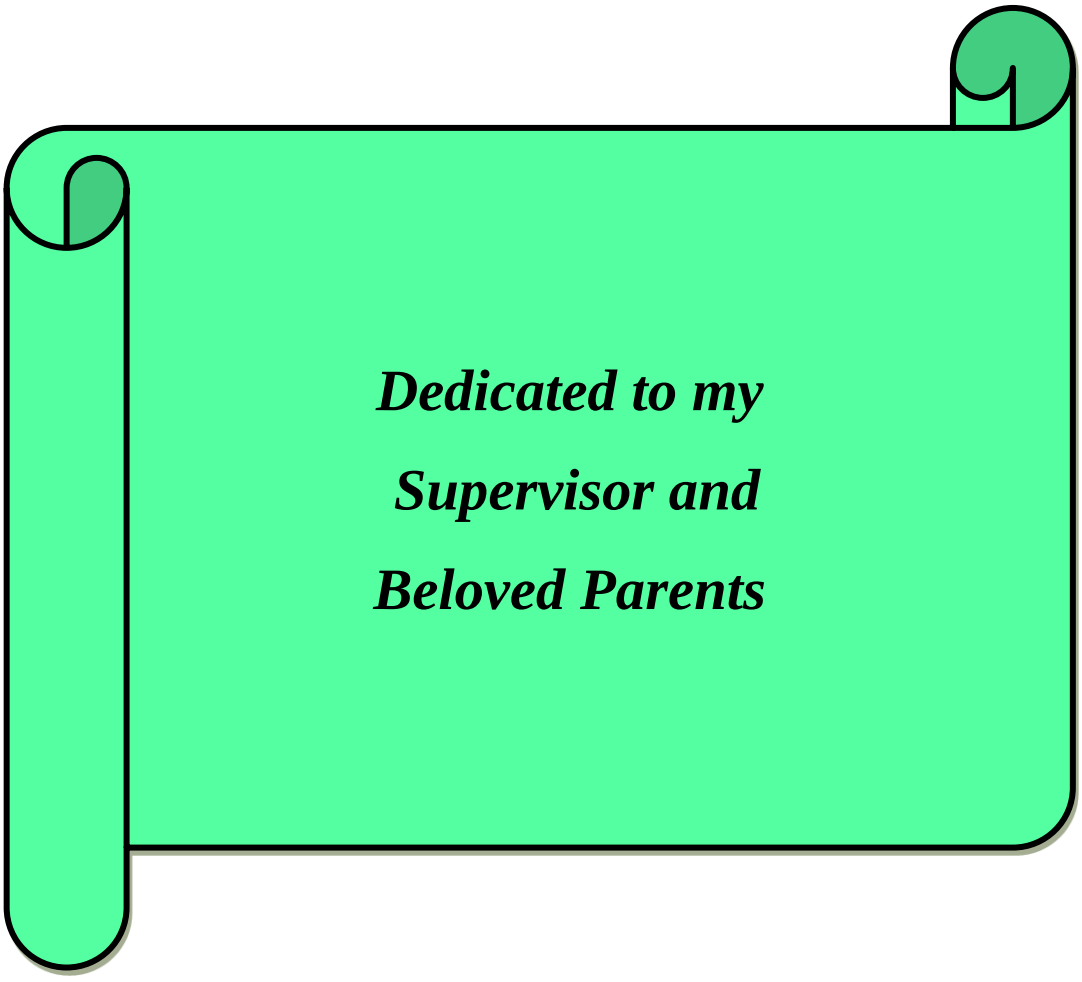
(Prof. Dr. Naheed Zeba)
Supervisor


Dedicated to my
Supervisor and
Beloved Parents

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Some commonly used abbreviations

Full word	Abbreviations	Full word	Abbreviations
Agricultural	*Agril.*	Horticulture	*Hort.*
Agriculture	*Agric.*	Horticulture	*Hort.*
And others	*et al.*	International	*Intl.*
Applied	*App.*	Journal	*J.*
Agronomy	*Agron.*	Kilogram	Kg
Applied	*Appl.*	Number	No.
Bangladesh Agricultural Research Council	BARC	Percentage	%
Bangladesh Agricultural Research Institute	BARI	Physiology	*Physiol.*
Bangladesh Bureau of Statistics	BBS	Research and Resource	*Res.*
Biology	*Biol.*	Review	*Rev.*
Breeding	*Breed.*	Science	*Sci.*
Botany	*Bot.*	Serial	Sl.
Centimeter	Cm	Society	*Soc.*
Environment	*Environ.*	Tropical	*Tropi.*
Etcetera	etc.	Technology	*Technol.*
Food and Agricultural Organization	FAO	That is	i.e.
Genetics	*Genet.*	Ton	T
Gram	G	Universal	*Univ.*
Hectare	ha.	Videlicet (namely)	viz.

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GENETIC DIVERSITY ANALYSIS OF YIELD AND QUALITY TRAITS IN TOMATO (*Solanum lycopersicum* L.)

By

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ABSTRACT

An experiment was conducted with 19 genotypes of tomato (*Solanum lycopersicum* L.) at experiment field of Sher-e-Bangla Agricultural University, Dhaka-1207 in completely randomized design (CRD) to study the genetic diversity, variability, correlation and path coefficient analysis using yield and quality traits during November 2016 to May 2017. Analysis of variance for agromorphogenic and quality traits showed significant differences among the genotypes. GCV and PCV were close to each other for all the characters except no. flower per cluster in case of yield and pH content in qualitative traits indicating the minor environmental influence on the expression of these characters. High heritability associated with high genetic advance in percent of mean was observed in no. of fruit per cluster, fruit per plant, fruit weight for yield and lycopene content at 502 nm, vitamin C content and dry matter content % pointed out that selection for these characters would be effective. The significant positive correlation with fruit yield per plant was found in no. of fruit per cluster, fruit per plant and lycopene content at 472 nm, brix %, vitamin C in qualitative traits pointed that selection on the basis of these traits would improve yield ultimately. Path coefficient analysis evidenced that no. of fruit per cluster, fruit weight; fruit per plant had the positive direct effect on yield per plant. In qualitative analysis brix %, lycopene content at 472 nm, vitamin C content had the positive direct effect on dry matter content %. Therefore, importance has to be given for these characters in further breeding program to improve tomato yield and nutritional value. Multivariate analysis based on eleven characters in yield and eight characters in qualitative traits of nineteen tomato genotypes was divided into four distant clusters in both cases. The maximum contribution of agromorphogenic traits towards diversity was observed by days to first flowering, plant height, days to maturity, no. of cluster per plant and no. of flower per cluster. Maximum contribution found in qualitative traits from brix %, vitamin C, pH, lycopene content at 472 nm and 502 nm. As a result, these traits could be emphasized during selection of parents for hybridization. The highest inter cluster distance was observed between cluster III and IV and for qualitative traits cluster IV and cluster I showed maximum distance. The maximum intra cluster distance was found in cluster IV in both traits. Considering group distance and other agro-morphogenic and qualitative performance, genotypes G_2 (SL-006), G_4 (SL-008), G_8 (Sl-013), and G_{18} (BARI Tomato 11) found potential for future hybridization program in response of increase tomato yield.

CHAPTER I

INTRODUCTION

All tomato species are diploid (2n = 2x = 24) and have the same chromosome number. Tomato (*Solanum lycopersicum* L.) belongs to family Solanaceae. It is one of the most important vegetables in the world because of its wider adaptability, high yielding potential and suitability for variety of uses in fresh as well as processed food industries (Meena and Bahadur, 2015). The cultivated tomato is the second most important vegetable crop in the world in terms of consumption per capita and is the most popular garden vegetable. In the U.S. diet, tomato ranks first among all fruits and vegetables as a source of vitamins and minerals (Rick and Chetelat, 1995). Tomato contribute significantly to the dietary intake of vitamins A and C as well as essential minerals and nutrients.

Tomato is adaptable to wide range of soil and climate in Bangladesh (Ahamed, 1995). It ranks fourth in respect of production and third in respect of area (BBS, 2014). Although a tropical plant, it is widely cultivated in tropical, sub-tropical and temperate climates and thus it ranks third in terms of world vegetable production (FAO, 2016). Worldwide, a total of 4.79 million hectares of tomato harvested in 2016 with a total production of 177.05 million Metric tons (http://www.faostat.fao.org.). Major production countries include China, U.S.A., India, Turkey, Egypt, Italy and Iran.

Tomato has great demand in Bangladesh throughout the year but it is available and cheaper during the winter season. In Bangladesh, it is cultivated as winter vegetable occupied an area of 27342.105 ha and total production was 368.121 thousand metric tons (BBS, 2016). The average tomato yield in Bangladesh is very low compared to other countries like India (16.67 t ha-1), Japan (55.82 t ha-1), USA (66.22 t ha-1), China (31.39 t ha-1), Egypt (34.00 t ha-1) and Turkey (41.77 t ha-1) (FAO, 2016).

It is a rich source of lycopene, an antioxidant that reduces the risk of prostate cancer (Hassan *et al*., 1999). It contains a number of nutritive elements almost

double compared to fruit apple (Bhuiyan, 2014). Food value of tomato is greatly dependent on its chemical composition such as dry matter, titratable acidity, total sugar, total soluble solids, ascorbic acid etc. Studies in USA indicate that flavour and taste of tomato associated to free sugars, organic acids and sugar acid ratios (Kasrawi *et al*., 1990).

Malnutrition in Bangladesh remains a severe problem, especially for women and children. Poverty and food insecurity limits one's ability to live on a diet that provides all the nutrients necessary for healthy living, leading to malnutrition. Therefore, there is an urgent need to develop highly nutritious, health benefit vegetables of which tomato is one of them to reduce malnutrition.

Since tomato seed production is a highly specialized activity, therefore growers cannot produce their own seed and forced to purchase seed of unknown sources and quality. Consistent efforts for developing hybrids as well as open pollinated varieties in vegetable crops, especially tomato, have yet to be made. Hence there exists a large scope for vegetable breeding in general and for tomato in particular, especially through hybridization programs.

Tomato is an excellent model crop for basic and applied research. This is due to many reasons, including ease of culture, short life cycle, high self-fertility and homozygosity. It has also great reproductive potential, ease of use for controlled pollination and hybridization. The availability of a wide array of mutants and genetic stocks (Miller and Tanksley, 1990), diploid with a rather small genome (0.86 pg, 950 kb) (Amaral *et al*., 1997), and amenability to asexual propagation like as protoplast, cell and tissue cultures and whole plant regeneration (McCormick, *et al*., 1986).

Parameters of genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment expression of the characters and the extent to which improvement is possible after selection (Robinson *et al*., 1949). Crop improvement depends

upon the level of genetic variability and extent to which the desirable character are heritable. High heritability alone is not enough to make efficient selection in segregating generation, unless the information is accompanied for substantial amount of genetic advance (Johnson *et al.*, 1995).

A breeder's first objective is to increase yield, which need the knowledge of association between yield and its contributing traits. According to Burton (1952), the extent of variability in a species is essential for improving any character in breeding.

Information regarding genetic diversity and genetic relationships among different genotypes is very valuable in crop improvement. Analysis of genetic diversity of agro-morphogenic and nutritional traits is useful in selecting diverse parental combinations, reliable classification of accessions, and for exact identification of variety. Breeding and domestication has resulted in reduction of tomato genetic diversity. Therefore, it is important to know the genetic relationship between the tomato species.

Considering the above facts, the present study was therefore undertaken

- To estimate genetic variation among the tomato genotypes based on their agromorphogenic and nutritional traits
- To know the nature of association of traits, direct and indirect relation between yield contributing characters.
- To provide farmers with better and superior genotype of tomatoes

CHAPTER II

REVIEW OF LITERATURE

The high degree of genetic uniformity in tomato cultivars is not only strongly influenced by domestication away from the center of origin, but also above all by the considerable genetic improvement, which, culminated in the achievement of uniformity, separated from the truth that only a limited number of genotypes were used for breeding.

The requirements for the preservation of wild species, local varieties and traditional genotypes in gene banks is apparent, which have become a vital frame of gene maintenance (Gepts, 2006). However, the accessions in gene banks should be characterized and evaluated in order to determine the magnitude of genetic diversity, which would allow the identification of redundant accessions and genotypes of interest in breeding programmes (Balestre *et al.*, 2008; Terzopoulos and Bebeli, 2008).

Tomato is a well-studied crop species for breeding, genetics, and genomics in plants. Various resources are accessible now fan or its research, which can lead an uprising in the evaluation of tomato biology (Barone *et al*., 2008). Many studies have been done using different genes to examine its genetic diversity (Carelli *et al*., 2006, Asamizu and Azure, 2009, Martinez *et al*., 2006).

2.1 Tomato

The tomato (*Solanum lycopersicum* L.), is an autogamous species with a narrow genetic base. Tomato typically 1-3 m tall, with a weakly woody stem that usually scrambles over other plants. The nomenclature, origin, distribution, nutritional and medicinal values of tomato are reviewed in this section.

2.1.1 Nomenclature, origin and distribution of tomato

The tomato (*Solanum lycopersicum* L.), is an autogamous species with a narrow genetic base. The introduction of the species in Europe, from Mexico, was pivotal in the reduction of genetic variability since in the European habitat

tomatoes were generally cultivated in protected environments. This protected the wild forms, then allogamous, from the action of wind and insect pollinators, culminating in the maintenance of a germplasm adapted to autogamy only (Foolad, 2007).

According to “International Plant Name Index” and “Slow Food ® Upstate”, in 1753, Linnaeus placed the tomato in the genus *Solanum* as *Solanum lycopersicum* and in 1768; Philip Miller moved it to its own genus, naming it *Lycopersicon esculentum*. This name came into wide use but was in violating of the plant naming rules. Genetic evidence has now shown that Linnaeus was correct to put the tomato in the genus *Solanum*, making *Solanum lycopersicum* the correct name (Natural History Museum; Peralta and Spoonar, 2001). However, both names will probably be found in the literature for some time.

Tomato translates to *"wolf peach”* because it was round and luscious and wolf because it was erroneously considered poisonous (Fillipone, 2014). The English word “tomato” comes from the Spanish word, *tomate*, which in turn comes from the Nahuatl (Aztec language) word *tomatotl*, meaning “the swelling fruit”. It first appeared in print in 1595. A member of the deadly nightshade family, tomatoes were erroneously thought to be poisonous (although the leaves *are* poisonous) by Europeans who were suspicious of their bright, shiny fruit. Native versions were small, like cherry tomatoes, and most likely yellow rather than red (Filippone, 2014).

The tomato is native to western South America and Central America (Filippone, 2014). Tomato is a tropical plant and grown in almost every corner of the world from tropics to within a few degrees of the Arctic Circle. Mexico has been considered the most likely center of domestication of tomato. Italy and Spain are thought about secondary centers of diversification (Gentilcore, 2010; Smith, 1994). The cultivated tomato originated in the Peru-Ecuador-Bolivia area of the South American (Vavilov, 1951). Major tomato producing countries are Spain, Brazil, Iran, Mexico, Greece, Russia, China, USA, India, Turkey, Egypt and

Italy. It is believed that the tomato was introduced in the subcontinent during the British regime. It is adapted to a wide range of climates. In tomato (*Solanum lycopersicum* L.), one cultivated species and 12 wild relatives have been reported (Peralta *et al*., 2006). Genetic variation in modern cultivars or hybrids is limited (Chen *et al*., 2009). It is estimated that cultivated tomato genome contains less than 5% of the genetic variation of the wild relatives (Miller and Tanksley, 1990). It has been suggested by Yi *et al*. (2008) that domestication and inbreeding dramatically reduced the genetic variation.

2.1.2 Nutritional and medicinal value of tomato

Tomato is most popular as salad in the raw state and is made into soups, juice, ketchup, pickles, sauces, conserves, puree, paste, powder and other products. (Naz and Zafrullah, 2013). It is highly nutritious and rich source of health building substances particularly vitamins and minerals. Vitamin C, total soluble solids (TSS) and acid contents are commonly considered as fruit quality determining properties in tomato. Vitamin C is a principal nutrient of tomato fruit. More than 7% of total vitamin-C of vegetable origin comes from tomato in Bangladesh. It contains 94 g water, 0.5 g minerals, 0.8 g fiber, 0.9 g protein, 0.2 g fat and 3.6 g carbohydrate. It also contains other elements like 48 mg calcium, 0.4 mg iron, 356 mg carotene, 0.12 mg vitamin B1, 0.06 mg vitamin B2 and 27 mg vitamin C in each 100 g edible ripen tomato (BARI, 2010). Vitamins are highly significant from the nutritional point of view. Soluble solids include mainly the sugars such as glucose, fructose and sucrose. In tomato fruit, organic acid with sugars make a major contribution to the taste of the fruit. Flavor can be related to differences in the sugars and acids contents of the fruits.

The tomato's medicinal properties had already been endorsed in Continental Europe in the 16th Century and their consumption was believed to benefit the heart among other things, as it contains lycopene, one of the most powerful natural antioxidants which, especially when cooked, have been found to help prevent prostate, lung, stomach, pancreatic, colorectal, esophageal, oral, breast and cervical cancers. Lycopene’s, bioflavonoid closely related to beta carotene,

are potent antioxidants present in tomatoes and seem to be responsible for these natural cancer-fighting properties. (Anonymous, 2016**)**. Lycopene is responsible for the characteristic deep red color of ripe tomato fruits and tomato products (Hannan *et al*., 2007).

2.2 Variability

The fundamental key to achieving the genetic improvement of a crop through a proper breeding programme is to judge the amount and nature of variation of plant characters in the breeding population. It helps the breeder for improving the selection efficiency. For this reason, many researchers studied the variation of various characters in tomato. Some of those are presented here.

The success of any crop improvement programme depends on the presence of genetic variability and the extent to which the desired trait is heritable. Genetic diversity can be estimate using both morphological and molecular markers. The presence of genetic variability in the breeding material has been emphasized by previous researchers (Naz *et al*., 2013; Reddy *et al*., 2013; Singh, 2009; Shuaib *et al*., 2007).

Some of the previous research reports are discussed here. A field experiment was carried out to study the genetic variation among twenty-five tomato accessions that helped in the reliable varietal selection programme for breeding. All tomato accessions were analyzed by two parameters e.g. morphological and molecular parameters. This study revealed that height of the plant, fruit color and fruit size show variability (Naz *et al*., 2013).

Alternatively, by using nineteen exotic collections of tomato, Reddy *et al*. (2013) revealed considerable genetic variability for all the eighteen quantitative characters, which was pertaining to the growth, earliness, yield and quality. Fruit weight, plant height, and a number of fruits per plant contributed to the total variation.

Alam *et al*. (2012) also suggested that Multivariate and biochemical analysis of genetic affinity among the tomato varieties are necessary before setting any program for their improvement. They collected many tomato accessions to judge the BARI released varieties and the other commercially available varieties based on their genomic information.

Shashikanth *et al.* (2010) carried out a field experiment to study the genetic variation among 30 tomato germplasm lines and observed that the range of variation and mean values were high for plant height, days to 50% flowering and average fruit weight. He also observed that high genotypic variance was for most of the characters indicating a high contribution of the genetic component for the total variation.

Morphological trait measurements can provide a simple technique of quantifying genetic variation and simultaneously assessing genotype performance under relevant growing environments (Shuaib *et al*., 2007). Data recorded by Kumari *et al*. (2007) for days to flowering, days to maturity, number of fruits per branch, plant height etc. and found that there were highly significant differences for all the characters among parents except early yield, total yield and days to flowering.

Mahesh *et al.* (2006) carried out an experiment to study genetic variability in 30 genotypes of tomato revealed significant difference for all the characters under study and observed a wide range of variation for plant height, number of branches per plant, fruit weight, fruit length, fruit diameter, fruits per plant, fruit yield per plant, vitamin C content and total soluble solids.

Singh *et al.* (2005) conducted a field experiment on 15-advance generation breeding lines of tomato, to study the variation for total soluble solids (TSS), pericarp thickness, fruit firmness, pH, lycopene content and dry matter content and observed significant differences among the genotypes under normal conditions, whereas differences were not significant under high-temperature

conditions. The population means were higher during November than February planting for all the characters except acid content and TSS.

2.2.1 Days to first flowering

Farzaneh *et al.* (2013) showed earliness in a number of days to first flowering while studying combining ability from a 9x9 diallel cross. Whereas Monamodi *et al.* (2013) had not found any significant differences in days to first flowering among tomato genotypes. Matin *et al.* (2001) reported significant differences among the 26 tomato genotypes for days to first flowering ranging between 49.67 and 68.33 days. He also reported that the phenotypic variance was comparatively higher than the genotypic variance indicating high degrees of environmental effect for days to first flowering.

Kumari *et al.* (2007) recorded data for total soluble solids, dry matter content, Vitamin C, lycopene, pH, days to flowering, days to maturity, individual fruit weight, fruit length, fruit diameter, total number of fruits per plant, plant height, early yield and total yield and found that there were highly significant differences for all the characters among parents except pH, early yield, total yield, and days to flowering.

Singh *et al*. (1993) conducted an experiment on heterosis breeding in tomato. Eight cultivars with diverse values for quantitative characters were crossed in a diallel set. Data on yield and nine component traits were recorded for the 28 F1 hybrids and parents. Hybrids Punjab Chhuhara × 84-8, HS102 × Pusa Ruby, HS102 × 84-8 and Pusa Ruby × 84-10 showed significant negative heterosis for days to first flowering over the better parent, indicating their potential for producing an early crop. Hybrid Punjab Chhuhara × 84-8 showed the highest heterosis for fruit yield plant-1 (1200 g).

Biswas and Mallik (1989) observed that a minimum of 66 days was necessary for first flowering for cv. *Selection-7* and a maximum of 83 days for cv. *Mtuatham* in an experiment with 18 promising cultivars of tomato considering local cultivar Patharkutchi as control at Mymensingh reported significant

variation for days to first flowering in six cultivars of tomato. The phenotypic variance was comparatively higher than the genotypic variance indicating high degrees of environmental effect for days to first flowering (Aditya, 1995 and Matin, 2001).

Godekar *et al.* (1992) reported that pre-flowering periods of the varieties ranged from 56 to 76 days.

2.2.2 Plant height

Naz *et al*. (2013) used 25-tomato germplasm to characterize morphologically by comparing the height of the plant, leaf length, shape and arrangement, fruit shape and size. This study revealed that height of plant shows the highest variability. Kumari *et al*. (2007) observed the highest genotypic coefficient of variation for plant height.

Hannan *et al*. (2007) conducted an experiment, to estimate heterosis and character association in 45 single cross hybrids, obtained from 10 parental lines of tomato for yield and yield component traits. The characters studied were plant height, days to first flowering, number of flowers cluster^{-1}, number of fruits plant^{-1}, fruit weight plant^{-1} and days to first fruit ripening. They obtained significant differences among genotypes for all the traits and found positive high significant heterosis over the mid-parent, better parent and standard parent heterosis, respectively. They concluded that five hybrids positively correlated with fruit plant^{-1}, number of fruit cluster^{-1} and plant height.

Joshi *et al.* (2004) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and noticed that plant height gave the highest heritability (78.82%). Ravindra *et al.* (2003) observed significant genotype x environment interaction for plant height.

Shravan *et al*. (2004) and Aditya (1995) reported significant variation in plant height. Parthasarathy and Aswath (2002) conducted a study with 23 genotypes of tomato and observed a considerable variability among genotypes for 8

morphological characters. Plant height, fruit number, fruit size were contributed higher variability among them.

Singh *et al*. (2002) carried out a field experiment with 92 tomato genotypes to study genetic variability and reported that the analysis of variance revealed highly significant genetic variation for plant height, number of days to first fruit set, number of fruit clusters per plant, number of fruits per plant, fruit weight per plant and fruit yield. The traits characterized by adequate variability may be considered in a hybridization program for yield improvement in tomato.

Matin *et al*. (2001) also reported that phenotypic variance was relatively higher than genotypic variance for plant height. They again observed that genotypic coefficient of variation was lowering than the phenotypic coefficient of variation indicating the influence of environment for expression of this character.

Ghosh *et al*. (1995) and Nandpuri *et al.* (1974) reported a high degree of variation for plant height while Ahmed (1987) observed a narrow range of variations. Sonone *et al*. (1986) and Prasad (1977) also reported high phenotypic and genotypic coefficient of variation for plant height in tomato.

2.2.3 Days of maturity

Saleem *et al*. (2013) carried out an experiment using twenty-five F_1 hybrids generated from 5×5 diallel crosses and found moderate heritability for days to maturity indicated the favorable influence of environment rather than genotypes consequently, selection of superior genotypes to develop early maturing genotypes would not be rewarding in early generations. Prashanth (2003) evaluated 67 genotypes of tomato and found the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for days to maturity.

kumar *et al.* (2001) conducted an experiment to quantify genetic variation in tomato for yield and resistance to Bacterial Wilt based on the idea that proper and systematic evaluation of genetic resources as essential to understand and

estimate the genetic variability, heritability, and genetic advance. Data were recorded on plant height, days to maturity, number of fruits plant^{-1}, pericarp thickness, locule number, total soluble solids, average fruit weight, number of fruit plant^{-1} and plant yield. They observed highly significant differences among the genotypes for all the traits as well as the high genotypic coefficient of variation for all the characters. Higher heritability estimates and high genetic advance for all the characters indicated the lesser influence of environment and higher role of additive gene action, respectively, so they suggested selection for rewarding improvement of these traits.

2.2.4 Number of cluster per plant

Dufera (2013) conducted an experiment using twenty-one tomato germplasm. Higher genotypic and phenotypic coefficients variation values recorded by the character fruit clusters plant^{-1}, indicating the presence of variability among the genotypes and the scope to improve these characters through selection**.**

Singh *et al.* (2006) observed a considerable range of genetic variability for yield and yield components in the materials under study and maximum genotypic coefficient of variation found for a number of clusters per plant.

2.2.5 Number of fruits per cluster

Samadia *et al.* (2006) evaluated 14 cultivars of tomato and reported almost similar estimates of PCV and GCV for this character. In contrast, Arun *et al.* (2003) evaluated 37 genotypes of tomato and observed the PCV was higher than GCV for Number of fruits cluster^{-1}. Aradhana et al. (2003) also observed a similar result.

Singh *et al.* (1997) derived information on genetic variability, heritability and yield correlations from data on 14 agronomic and yield-related traits in 23 genotypes of tomato. They came to an end based on heritability and genetic advance values, effective selection may be made for fruit weight and a number of fruits plant^{-1} as fruit yield showed strong positive correlation with the number

of fruits plant^{-1} and number of fruits cluster^{-1}. They recommended that a number of fruits plant^{-1} and number of fruits cluster^{-1} are the most important character for consideration in a selection programme for improvement of yield.

Pujari *et al*. (1994) studied the results from an 8 × 8 half-diallel cross in tomato, which indicated high heterosis for yield plant^{-1}, fruits plant^{-1}, fruits cluster^{-1} and earliness. Punjab Chhuhara × Roma was the top ranking hybrid, which produced 6.4 fruits cluster^{-1}.

2.2.6 Number fruits per plant

Thakur (2009) evaluated seventeen diverse genotypes of tomato for their performance and interaction with changing environments through the characters like fruit yield, number of fruits plant^{-1}. The analysis of variance indicated highly significant differences between the genotypes and environments for all the characters studied. According to Buckseth *et al.* (2012) high GCV obtained for average fruit weight, yield per plant, pericarp thickness, and a number of seeds per fruit.

Saeed *et al*. (2007) observed the variation among the accessions. The coefficient of variation was greater in traits such as a number of fruits per plant followed by a number of flowers per plant and yield per plant.

Joshi *et al.* (2003) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and observed the number of fruits per plant, which provide the highest phenotypic and genotypic coefficient of variation. Mohanty *et al.* (2003) observed that the number of fruits per plant had positive direct effects on the yield and negative indirect effects on average fruit weight.

Brar *et al*. (2000) estimated the phenotypic and genotypic coefficient of variation and observed high variability in the characters of a number of fruits per plant of 186 genotypes of tomatoes. Islam *et al.* (1996) reported a wide range of genotypic variation for a number of fruits per plant. Singh *et al*. (1997) studied variability for yield related characters in 23 genotypes of tomato and reported

that phenotypic variation was quite large but genotypic variation was low. The phenotypic and genotypic coefficient of variation indicated that selection may be made for a number of fruits per plant.

Das *et al*. (1998) and Sahu and Mishra (1995) reported a wide range of genotypic variation for a number of fruits per plant. They also reported high genotypic variation for a number of fruits per plant. Singh *et al*. (1997) studied variability for yield related characters in 23 genotypes of tomato and reported that phenotypic variation was quite large but genotypic variation was low. The phenotypic and genotypic coefficients of variation indicated that selection may be made for members of fruits per plant. Islam *et al.* (1996) recorded highest genetic variability for a number of fruits per plant in 26 diverse genotypes of tomato.

Reddy and Reddy (1992) evaluated 139 tomato genotypes and estimated phenotypic and genotypic variances, phenotypic and genotypic co-coefficients of variation. Considerable variation was observed for a number of fruits per plant (4.0—296.5). Islam and Khan (1991) and Sharma and Rastogi *et al.* (1993) reported significant variations in a number of fruits per plant.

Sidhu and Singh (1989) and Bhutani *et al.* (1989) suggested that maximum genetic improvement would be possible by genetic variability for a number of fruits. Prasad and Prasad (1977), Dudi *et al*. (1983) and Sonone *et al.* (1986) estimated the high genotypic and phenotypic coefficients of variation for fruits per plant.

2.2.7 Fruit weight

A study was conducted by Farzaneh *et al.* (2013) and found significant variation due to general combining ability (GCA) as well as specific combining ability (SCA) indicated the importance of additive and non-additive types of gene action in inheritance of all characters except number of fruits per plants.

Kumar *et al.* (2004) and Shravan *et al.* (2004) studied genetic variability with 30 tomato genotypes in Utter Pradesh of India and reported significant difference for average fruit weight among the genotypes.

Mohanty *et al.* (2003) carried out in a field experiment to study genetic variability of 18 tomato cultivars and observed that the average fruit weight had positive direct effects on the yield and negative indirect effects on a number of fruits per plant.

Singh *et al.* (2002) carried out a field experiment to study genetic variability of fifteen heat tolerant tomato and showed that phenotypic (PCV) and genetic (GCV) coefficients of variation were high for average fruit weight. Matin (2001) reported similar results for average fruit weight in an experiment with 26 tomato genotypes.

Brar *et al*. (1998) reported that varietal differences were significant among 20 cultivars of tomato for average fruit weight ranged between 24.1g and 76.6g. Padmini and Vadivel (1997) performed an experiment to study genetic variability of six F2 crosses and their parental cultivars and reported that progeny of cross In Memory 5.30 p. m. X PKM-1 produced the highest mean values for the individual. They also reported that small difference was observed between genotypic and phenotypic variance for individual fruit weight.

Sahu and Mishra (1995) reported that fruit weight had a high genotypic coefficient of variation in 16 lines of tomato. Considerable variation was observed for average individual fruit weight. Reddy and Reddy (1992) estimated phenotypic and genotypic variances, phenotypic and genotypic coefficient of variation for individual fruit weight.

Aditya (1995) reported that analysis of variances showed highly significant mean squares due to variety for average fruit weight among the 44 varieties of tomato. Genotypic variance associated with a genotypic coefficient of variation was

smaller than a phenotypic variance and phenotypic coefficient of variation respectively.

Ahmed (1995) reported that a wide range of variation was observed for individual & unit weight among 4 genotypes of tomato. He also reported that genotypic coefficient of variation was very high for individual fruit weight in four tomato varieties namely EC32099, HS102, HS107, and Columbia respectively. Sonone *et al*. (1986) reported that genotypic and phenotypic variances were high for individual fruit weight in the study of genetic variability with 13 genetically diverse tomato lines.

Arora *et al*. (1982) reported that a wide range of variation was observed in fruit weight of four genotypes of tomato. He also reported that genotypic coefficient of variation was very high for individual fruit weight in four tomato varieties. Kumar and Tewari (1999) also obtained similar results in their experiments with tomato.

2.2.8 Fruit length

Kumari *et al.* (2007) recorded data for fruit length and found that there were highly significant differences for this character among parents. Singh *et al*. (2002) reported the high phenotypic coefficient of variation for this character.

Chowdhury *et al*. (2002) conducted a study on the analysis of combining ability for yield, yield components and quality characters in tomato (*Lycopersicon esculentum* Mill.), on plant material comprising 12 parental lines and their F1 hybrids (direct crosses). They recorded data on days to flowering, number of flowers per cluster, number of fruits per cluster, number of marketable fruits per plant, fruit length, fruit width, and fruit weight, fruit yield per plant, pericarp thickness, and fruit firmness at red stage, total soluble solids, and pH of juice. Analysis of variance revealed highly significant differences among genotypes, parents, and hybrids, as well as highly significant mean squares due to GCA and SCA for all the characters.

Agong *et al*. (1997) conducted research on the genotypic variation of 35 Kenyan tomatoes (*Lycopersicon esculentum* Mill.) germplasm, to examine the variation in tomato germplasm based on the morphological, agronomic and biochemical traits with an ultimate view of identifying potential accessions to improve tomato production. They found a large and significant variation in quantitative traits between the accessions largely attributable to the genotypic variability within and between the individual tomato groups and suggested that genetic improvement of tomato should not only depend on the introduction but also on the gradual development of more closely adapted accessions suited to local conditions. They also suggested that fruit number plant^{-1} and fruit index (length/width) can be used to create a better understanding of diversity in the tomato for yield and crop improvement.

2.2.9 Fruit diameter

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

Kumari *et al.* (2007) recorded data for fruit width and found that there were highly significant differences among parents. Anupam *et al.* (2002) evaluated 30 genotypes of tomato and found similar results for this character. Singh *et al.* (2002) reported that phenotypic coefficient of variation was greatest for this character.

2.2.10 Yield per plant

Singh *et al*. (2009) assessed 48 genotypes for their genetic divergence using Mahalar statistics. They observed that clustering pattern indicated no difference between the geographical distribution of genotypes and genetic divergence. They concluded that characters like a number of fruits plant^{-1}, average fruit weight, plant height and fruit yield contributed the maximum to genetic divergence.

Singh *et al.* (2006) observed a considerable range of genetic variability for yield, yield components and biochemical characters in the materials under study and maximum genotypic coefficient of variation was recorded for a number of leaves per plant, followed by a number of clusters per plant.

Matin *et al.* (2001) reported significant differences in yield per plant among the genotypes tested. He also reported that phenotypic variance was little higher than genotypic variance indicating a slight environmental influence on this trait. Sachan *et al*. (2001) performed an experiment with certain tomato genotypes and he also reported significant differences among the genotypes for yield per plant.

Kumar and Tewari (1999) reported the higher genotypic coefficient of variation for average yield per plant among thirty-two tomato genotypes. Brar *et al*. (1998) reported high degrees of variation for average yield per plant among the 186 genotypes tested. Reddy and Reddy (1990) observed considerable variations in yield per plant in 139 tomato varieties.

Pujari *et al.* (1995) and Ghosh *et al*. (1995) observed the highest variation in yield per plant. Aditya *et al.* (1995) observed highly significant differences for average yield per plant among 44 genotypes of tomato. She also reported that phenotypic variance and phenotypic coefficient of variation were higher than a genotypic variance and genotypic coefficient of variation respectively. Sonone *et al*. (1986) and Dudi *et al*. (1983) reported that genotypic and phenotypic variances were high for average yield per plant.

2.3 Heritability and genetic advance

Selection of plants with phenotypic characteristics is the most important task for all plant-breeding practices. The effectiveness of selection for yield depends upon heritability. A character with high heritability gives a better response to selection. Heritability and genetic advance are the most important parameters to judge the breeding potentiality of a population for future development through selection. Many researchers have studied heritability and the genetic advance of

yield and many yield contributing characters of tomato. The literature very relevant to the present study are reviewed below:

According to Saleem *et al.* (2013) a study of the quantitative genetics of yield and some yield-related traits. The highest estimates of genotypic and phenotypic coefficients of variability (GCV and PCV) were recorded for a number of fruits per plant while fruit width was the most heritable trait. Buckseth *et al*. (2012) found high heritability with the high genetic advance for a number of fruits per plant, average fruit weight, yield per plant and pericarp thickness indicating that most likely the heritability is due to additive gene effects and selection may be effective.

Narolia (2012) studied thirteen quantitative characters in 55 genotypes of tomato. High heritability coupled with high genetic advance as percent of the mean was observed for all the characters except days to 50% flowering indicating the presence of additive gene action in the expression of these characters.

Shashikanth *et al.* (2011) observed the range of variation and mean values were high for plant height, days to 50% flowering and average fruit weight. He also observed high genotypic variance for most of the characters indicating a high contribution of the genetic component for the total variation.

Ponnusviamy *et al.* (2010) evaluated 12 varieties of tomato to estimate heritability and reported that high heritability coupled with high genetic advance as a percentage of the mean for average fruit weight, indicating the control of such character by the additive gene. He also recorded that high heritability coupled with low genetic advance as a percentage of mean for rest of the characters except pericarp thickness, indicating most of the characters were governed by non-additive genetic components.

Pandit *et al.* (2010) evaluated 12 varieties of tomato to estimate heritability and reported that high heritability coupled with high genetic advance as a percentage of the mean for average fruit weight, indicating the control of such character by

the additive gene. He also recorded that high heritability coupled with low genetic advance as a percentage of mean for rest of the characters except pericarp thickness, indicating most of the characters were governed by non-additive genetic components.

Nardar *et al.* (2007) evaluated 20 tomato genotypes and observed high heritability with a high genotypic coefficient of variation and genetic gain for fruit weight and fruit yield, which could be improved by simple selection. Padda *et al*. (2007) observed that broad sense heritability was highest for a number of fruits per plant (96.56%), followed by a number of flowers per plant (93.45%), reflecting the effectiveness of selection in the present germplasm of tomato improvement.

Kumari *et al.* (2007) reported that the estimates of heritability were high for all the characteristics and the genetic advance was high for plant height, moderate for a total number of fruit-bearing branches, weight per fruit and days to maturity, while the remaining characteristics had low values of genetic advance. Golani *et al.* (2007) evaluated 20 tomato genotypes and observed high heritability with a high genotypic coefficient of variation and genetic gain for 10-fruit weight, number of locules per fruit and fruit yield, which could be improved by simple selection. Saeed *et al.* (2007) observed that broad sense heritability was highest for a number of fruits per plant (96.56%), followed by a number of flowers per plant (93.45%), reflecting the effectiveness of selection in the present germplasm of tomato improvement.

Singh *et al.* (2006) estimated heritability for nineteen genotypes of tomato and observed high heritability for ascorbic acid content, the average weight of fruits, number of leaves per plant, number of locules per fruit, number of fruits per plant, leaf area and dry matter content. High estimates of heritability with high genetic advance was recorded in case of a number of leaves per plant, the average weight of fruits, number of fruits per plant and plant height, whereas high

heritability with low genetic advance was recorded for a number of locules per fruit, dry matter content, pericarp thickness and yield per plant.

Mahesh *et al.* (2006) estimated heritability and expected a genetic advance in 30 genotypes of tomato and observed that fruit weight, fruits per plant and plant height exhibited very high heritability values along with high genetic gain. It indicated the importance of considerable additive gene effects and therefore greater emphasis should be given to these characters while selecting the better genotypes in tomato.

Joshi *et al.* (2004) observed moderate heritability and moderate genetic gain for a number of fruits per cluster, fruit length, fruit breadth, stem end scar size, number of locules per fruit, whole fruit firmness, ascorbic acid content and plant height indicating additive gene effects. Low heritability and the low genetic gain were observed for pericarp thickness. Moderate heritability and low genetic gain for harvest duration suggest the presence of dominance and epistatic effects. High heritability combined with high genetic gain was observed for shelf life indicating additive gene action.

Shravan *et al*. (2004) estimated heritability and genetic advance in 30 tomato genotypes for the characters like number of primary branches per plant, plant height, number of fruits per plant, fruit yield per plant and average fruit weight. The average fruit weight showed high heritability that ranged from 89.10% to 96.50%. The rest of the characters showed moderate heritability and low genetic advance. Moderate heritability associated with the moderate genetic advance for plant height of 37 tomato genotypes of tomato were reported by Arun *et al.* (2004). Mohanty (2003) observed that high heritability with a high genotypic coefficient of variation was for fruit weight, plant height, number of fruits and number of branches per plant.

Nessa *et al*. (2000) reported high heritability for number fruits per plant, plant height and moderate heritability for yield per plant. Vikram and Kohli (1998)

reported high heritability and genetic advance for mean fruit weight, which suggested that improvement for this character should be straight forward.

2.4 Correlation and path coefficient analysis

2.4.1 Correlation between the characters

Correlation between the characters is an estimate to evaluate the inter-relationships between the characters, which will help the breeders to choose selection techniques. In most cases, the correlation between yield and yield contributing characters was studied because yield is one of the main targets of most of the breeders. The yield contributing characters are also interrelated among themselves. Therefore, an association of characteristics with yield and among its components is important for planning effective selective breeding programme for maximization of yield. Such correlation studies may vary due to agro-climatological variations from year to year. If any component of yield has higher heritability than yield itself and there is a positive correlation between these, then there may be some possibility to increase the total yield by selecting that component. However, negative correlation coefficient among yield components was observed indicating selection for any component might not bring improvement for yield. Many authors have studied the correlation between yield and yield contributing characters of tomato. Some relevant recent literature is reviewed in this section.

Forty-nine genotypes of tomato (*Solanum lycopersicum* L.) were evaluated for various quantitative and quality traits by Kumar *et al.* (2013).The character association analysis indicated that total numbers of fruits/plant were significantly and positively correlated with gross yield (g/plant), marketable yield (g/plant), number of marketable fruits/plant and plant height (cm). Mahapatra *et al.* (2013) found fruit yield had a positive and significant correlation with plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, and average fruit weight. It was observed that with an increase in plant height, there was a corresponding

increase in a number of primary branches per plant, days to 50% flowering and number of flower clusters per plant.

According to Monamodi *et al*. (2013), there was a strong positive significant correlation between numbers of branches per plant with fruit number per plant. This was because the more the branch number in a plant, such plant will produce more fruits in a plant. The experiment carried out by Buckseth *et al*. (2012) consisting of 40 genotypes of tomato to study the correlation among different quantitative and qualitative traits in tomato genotypes. The study revealed highly significant differences among the genotypes for all the characters studied.

Rani *et al*. (2010) revealed that fruit weight was positively and significantly associated with yield per plant, while a number of fruits per plant were associated negatively. According to Ara *et al*. (2009), there was a strong positive significant correlation between numbers of trusses per plant with fruit number per plant. This was because the more the truss number in a plant, such plant will produce more fruits resulting in more fruit weight. This is supported by the observed strong positive association between fruit number per plant and fruit weight per plant. Wright (2007) performed correlation analysis and observed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant. Golani *et al*. (2007) observed that fruit weight had a significant and positive correlation with fruit length at both levels.

Correlation analysis performed by Wagh *et al*. (2007) showed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant along with fruit quality characters such as lycopene, beta-carotene, ascorbic acid and titratable acidity. Kumar *et al.* (2006) performed correlation coefficient analysis of 30 tomato genotypes and observed that number of fruits per plant had a significant and positive correlation with fruit yield per plant. Megha *et al*. (2006) studied correlation in exotic tomato cultivars to determine the correlation of 26 tomato cultivars for a number of flowers per cluster, number of fruits per cluster, weight per fruit, yield per plant and total

yield. They observed that improvement in yield could be managed by selection for a number of flowers per cluster, flower clusters at first picking, number of fruits per cluster and weight per fruit. Manivannan *et al*. (2005) carried out correlation coefficient analysis in cherry and observed that fruit yield was significantly and positively correlated with the number of leaves and fruit weight. Similarly, inter-relationships was studied in 92 tomato genotypes. The highly significant positive correlation was observed between the number of fruits per plant and yield and between plant height and number of fruits per plant while negative correlation was noticed between the number of primary branches per plant and number of fruits per plant (Singh *et al*., 2005).

Joshi *et al*. (2004) performed a correlation analysis of 37 tomato genotypes and showed that yield per plant was positively and significantly correlated with average fruit weight, fruit length, plant height and harvest duration. The average fruit weight was positively correlated with fruit length, fruit breadth. However, fruit weight was negatively correlated with the number of fruits per plant, number of fruits per cluster and ascorbic acid content. Correlation coefficient analysis of 30 tomato genotypes was performed and observed that a number of fruits per plant had a significant and positive correlation with fruit yield per plant Kumar *et al*. (2004).

Arun *et al.* (2003) observed that in case of tomato yield per plant was positively and significantly correlated with average fruit weight and plant height. Mohanty (2003) studied correlation coefficient analysis of 18 tomato cultivars and reported that yield was significantly and positively correlated with number of fruits per plant and number of day to harvest, and significantly but negatively correlated with plant height, number of branches per plant and average fruit weight and the number of fruits per plant was inversely related to average fruit weight. He also reported that most early cultivars were small-fruited and low yielders.

Harer *et al*. (2002) studied the correlation of thirty-seven tomato genotypes and showed that the number of fruits per cluster and number of fruits per plant was significantly and positively correlated with fruit yield per plant, whereas the number of primary branches per plant, fruit weight had a negative association with fruit yield. Nesgea *et al*. (2002) studied correlation coefficient analysis in 13 tomato genotypes and revealed that plant height, number of branches per plant, plant spread, fresh plant weight, number of fruiting clusters, number of days to 50% flowering, number of fruits per cluster and number of fruits per plant should be considered for the enhancement of the yield of tomato. Susic (2002) showed that a significant negative correlation was between mean fruit mass and a number of fruits per plant and a significant positive correlation were found between fruit length and fruit width. Tiwari *et al*. (2002) observed that the highest positive and significant association was between the yield and length of fruit. At the genotypic level, the highest positive association was observed between the yield and length of fruit.

Dhaliwal *et al*. (2002) studied genetic parameters and correlations concerning fruit weight, yield plant^{-1}. The correlation studies indicated that it would be possible to develop firm fruited-high yielding true breeding lines. Dhankar *et al*. (2001) reported the average fruit weight under normal condition showed the highest positive effect on yield, therefore selection for average fruit weight, a number of fruits per plant and number of fruits per cluster are important for improvement of fruit yield.

2.4.2 Path coefficient analysis between yield and yield contributing characters

The study of correlation does not provide an exact picture of the relative importance of the direct and indirect influence of each of the component character towards the desired character. Therefore, this can be overcome by following path coefficient analysis technique by further partitioning the correlation coefficient into direct and indirect effects. Path coefficient is a standard tool, which measures the direct influence of one character upon another

and permits the separation of correlation coefficient into components of direct and indirect effects. Path coefficient between yield and yield contributing characters provides an exact picture of the relative importance of direct and indirect influences of each other component characters on fruit yield. It also provides valuable additional information for improving fruit yield via selection for its yield components. Recent publications involving path coefficient analysis between yield and components of yield relevant to the present study are reviewed in this section:

Meena and Bahadur (2015) studied the character association for tomato germplasm under open field condition. They evaluated nineteen indeterminate tomato germplasm to estimate the nature and magnitude of associations of different characters with fruit yield and among themselves. In order to obtain a clear picture of the interrelationship between fruit yield per plant and its components, direct and indirect effects were measured using path coefficient analysis. The character showed the high direct effect on yield per plant indicated that direct selection for these traits might be effective and there is a possibility of improving yield per plant through selection based on no. of flowers per plant, fruits per plant and fruit weight. Low residual effect indicates that the characters used explained almost all variability towards yield.

Monamodi *et al.* (2013) used six determinate tomatoes. Results obtained suggest that fruit number and single fruit weight are relevant components to use as selection criteria for improving tomato yield. Path coefficient analysis results showed that marketable fruit number and single fruit weight were directly related to yield.

Rani *et al*. (2010) conducted a field experiment to study path coefficient for yield components and quality traits in 23 hybrids of tomato and exhibited that fruit weight had the highest positive direct effect on yield per plant, while, fruit weight was also having a high positive indirect effect on yield per plant. Golani *et al.* (2007) performed path analysis and confirmed that the 10-fruit weight had the

highest positive direct effect. Dhankhar and Dhankhar (2006) reported that a number of fruits per plant had the maximum positive direct effect. Manivannan *et. al*. (2005) carried out path coefficient analysis in cherry tomato and showed that fruit weight had the highest direct effect on fruit yield.

Singh and Cheema (2006) have revealed that positive direct effect of a number of fruits per plant on yield. It was also reported by Kumar *et al*. (2004). Its positive indirect effects through average fruit weight mainly contributed towards its strong association with yield.

Singh *et al*. (2005) performed path analysis between yield and yield contributing characters of 92 tomato genotypes and reported that number of fruits per plant exerted the high positive direct effect on yield followed by average weight per fruit, number of primary branches per plant, plant height, days to 50% flowering, number of fruits per cluster and days to first fruit harvest.

Kumar *et al*. (2004) performed path analysis of thirty diverse tomato genotypes and indicated that fruit number per plant had the highest positive direct effect on yield per plant followed by average fruit weight. Mohanty (2003) conducted a field experiment to study path coefficient analysis of eighteen tomato cultivars and observed that the number of fruits per plant and average fruit weight had positive direct effects on the yield and negative indirect effects on each other.

Bodunde *et al.* (2002) carried out a field experiment on path coefficient analysis and observed that plant height and fruit diameter directly affected yield in tomato. Harer *et al*. (2002) carried out a field experiment to study path analysis of thirty-seven tomato genotypes and reported that a number of fruits per cluster, average fruit weight and a number of fruits per plant had direct maximum effects on fruit yield. Padma *et al.* (2002) performed path analysis and revealed that a number of branches, fruit weight, fruit length and a number of fruits per plant exhibited a positive effect on yield per plant at the genotypic and phenotypic levels. Verma and Sarnaik (2000) conducted a field experiment to perform path analysis of yield components in thirty tomato genotypes and observed that a total

number of fruits per plant, the average weight of fruit and number of branches per plant exhibited positive as well as high direct effects.

2.5 Genetic divergence

In crop improvement programme, genetic divergence has been considered as an important parameter to identity most diverse parents for obtaining highly heterotic F_1 generation through selection. Many scientists have studied genetic divergence of tomato on the basis of Mahalanobis' D^2-statistics based on multivariate analysis. Among the most relevant recent publications are reviewed below:

Those characters may be given high emphases which have more contribution in divergence during selection the lines for hybridization programme to generate large variability and will provide immense scope for the improvement of yield through selection. An experiment was carried out by Nalla *et al*. (2014) and data were recorded on fifteen characters and found that fruit yield per plant, total soluble solids, and equatorial diameter contributed high divergence. Other characters like a number of flower clusters per plant and days to 50% flowering contributed very little to divergence.

According to Reddy (2013), the percent contribution of eighteen characters for genetic divergence showed that fruit weight contributed maximum towards genetic divergence followed by plant height and number of fruits per plant. Xiong et al. (2012) did a study using twenty-six morphological trait to investigate genetic diversity in 67 tomato varieties. Cluster analysis indicated that tomato varieties could be grouped into three clusters at morphological levels.

Shashikanth *et al*. (2010) carried out a field experiment to study genetic divergence of 30 tomato genotypes and grouped into 10 clusters. He found that there was no parallelism between genetic diversity and geographical divergence in tomato and suggested that high diversity among the genotypes belonging to cluster VII and X can be selected in hybridization programmes to obtain good

segregants. Large morphological variations have been observed and molecular markers in wild species have revealed great genetic diversity (Zhu et al., 2004).

Landraces and local varieties contain much more genetic diversity than modern cultivars or hybrids (Terzopoulos *et al.,* 2009). Therefore, they are among the most important sources of genetic variation for breeders. Clustering pattern indicated no difference between the geographical distribution of genotypes and genetic divergence observed by Singh *et al*. (2009). They assessed 48 genotypes for their genetic divergence using Mahalar statistics. They concluded that characters like a number of fruits plant^{-1}, average fruit weight, plant height and fruit yield contributed the maximum to genetic divergence.

Vidal (2009) grouped 32 tomato genotypes into 10 clusters based on D^2 analysis number of fruits per cluster, plant height, a number of branches, pericarp thickness, average fruit weight and TSS content of fruit were reported as a chief contribution towards divergence. Arun *et al.* (2003) studied the nature and magnitude of genetic divergence in 73 tomato genotypes of a different origin for quantitative characters and they grouped genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes. The mean fruit yield/plant and average fruit weight were the highest in cluster 5 and 3 respectively. The plant height was maximum in cluster 15 and lowest in cluster 9 and cluster 6 consist of the highest number of fruits/cluster. Markovic *et al*. (2002) studied genetic divergence of 25 cultivars of tomato originating from the area of the former Yugoslavia and recorded the presence of a high degree of genetic divergence in different genotypes consisting of 5 clusters.

Mohanty and Prusti (2001) carried out a study on genetic diversity. They grouped the genotypes into 5 clusters including two solitary groups and reported that genetic diversity was not associated with geographic distribution. The maximum intercluster distance was observed between the clusters V and I. The distance between clusters I and II, III and IV, IV and V was moderate. They also reported that a number of fruits per plant and average fruit weight contributed

predominantly towards the total divergence. Sharma and Verma (2001) studied genetic divergence of 18 genotypes of tomato and grouped them into 5 clusters irrespective of geographic divergence indicating no parallelism between genetic diversity and geographical divergence. Fruit yield was one of the three characters, which played an important role in divergence between the populations.

2.6 Nutritional analysis

In the present world, tomatoes are the most popular vegetable crop. It has an important source of antioxidants such as lycopene, vitamin C, phenolics and total soluble solids (% of brix) in the human diet and has been linked with decreased risk of heart diseases, diabetes, prostate and various forms of cancer. Lycopene, a precursor of beta-carotene with well-known antioxidant activity and powerful health properties. Current research for new anticancer drugs focuses more on the natural compounds such as physicochemical constituent from the regular human diet. Because of the lack of severe side effects yet efficiently can act on a wide range of receptors or molecular targets involved in carcinogenesis and cardiovascular diseases. *In vivo*, *in vitro* and clinical studies conducted in recent years have revealed an inverse association between the dietary intakes of lycopene with the risk of prostate cancer (PCa). L-Ascorbic acid (AsA), which is an essential nutrient component for human health and plant metabolism that plays key roles in diverse biological processes such as cell cycle, cell expansion, stress resistance, hormone synthesis, and signaling. Many scientists have studied quality character as well as anti-carcinogenic properties of tomato on human and many animals. Among them, most relevant recent publications are reviewed below:

2.6.1 Lycopene

Lycopene (LYC) is the red pigment and a major carotenoid in tomatoes. Lycopene's antioxidant capacity is roughly twice that of β-carotene. Numerous epidemiological and intervention studies have demonstrated that dietary intake

of LYC-rich foods results in decreased incidence of certain cancers, including the prostate, lung, mouth, and colon cancer, coronary heart diseases, cataracts and possibly macular degeneration. Although the tomato is the richest source of lycopene among all fruits and vegetables, its concentration in the fruit of commercial cultivars is rather low, on average ranging from 30 to 60 μg lycopene/g fresh tomato tissue. Using different traditional breeding techniques, Dr. Kinkade recently (2013) has developed tomato breeding lines having fruit lycopene content from 100 – 200 μg lycopene/g fresh fruit tissue. Lycopene is an important intermediate in the biosynthesis of many carotenoids, including beta-carotene, responsible for yellow, orange or red pigmentation, photosynthesis, and photo-protection. Like all carotenoids, lycopene is a polyunsaturated hydrocarbon (an unsubstituted alkene). Some of the previous reports on Lycopene experiment are discussed here (Datta *et al*., 2013; Cucu and Loco, 2011; Dong *et al*., 2010; Alda *et al*., 2009; Moigrădean *et al*., 2007;).

According to Datta, *e. al*. (2013), lycopene may lower the incidence of prostate cancer. This study aimed to evaluate the tolerance and acceptance of three different amounts (4, 8, or 12 oz) of tomato juice and their effect on serum lycopene during radiotherapy in 20 men with localized prostate cancer. A significant positive correlation between serum lycopene, weight, and body mass index, and a negative correlation between serum lycopene and prior nutritional supplement use was detected. Panthee (2013) uses 44 vintage tomato varieties and evaluated them. Pearson's correlation analysis indicated that estimated lycopene content was negatively correlated with the other physicochemical traits whereas vitamin C, TSS, and TTA were positively correlated with each other.

Dufera (2013) was conducted an experiment using twenty-one tomato germplasm. Higher genotypic and phenotypic coefficients variation values were recorded for lycopene content. Mendelova *et al*. (2013) conducted an experiment to analyze the content of total carotenoids and lycopene in 8 varieties of tomato and to monitor dynamic changes after their different treatments (heating, drying). The experiment included following tomato varieties: Bambino F1, Darina F1,

Diana F1, Denar, Milica F1, Orange F1 Paulina F1, Sejk F1. They found that processing of tomato fruits into juices and dried slices positively affected the presence of carotenoids and lycopene. Zhu *et. al.* (2013) studied that lycopene, with its acyclic structure and a large array of conjugated double bonds, carries many distinct biological and physicochemical properties. Lycopene is among the most efficient singlet oxygen quenchers of the natural carotenoids without pro-vitamin 'A' activity. It acts as a natural antioxidant in human serum and other tissues to protect the oxidative damage of lipids, proteins, and DNA.

Elumalai *et al.* (2013) conducted an experiment in human. Oxidative stress is recognized as one of the major contributors to the increased risk of cancer and lycopene is a potent antioxidant has been found to inhibit proliferation of several types of human cancer cells, including endometrial, prostate, breast, upper aerodigestive tract, and lung. Lycopene has tumor suppressor activity.

The lycopene content in fifteen varieties and three brands of tomato paste, three brands of ketchup and three brands of tomato hot sauce were determined by spectrophotometry and HPLC methods ranged from < 0.05 to 5.82 mg/100 g, and from 0.01 to 4.90 mg/100 g respectively (Bradbury *et al*., 2012). Dong *et al*. (2010) showed that the lycopene content is very significantly positively correlated with single inflorescence flower numbers, single inflorescence fruit numbers and soluble solids content, but significantly negatively correlated with pedicel length and single fruit weight. He also reported that the lycopene content is significantly positively correlated with fruit shape index, but significantly negatively correlated with fruit firmness, flesh thickness, longitudinal diameter of fruit.

Wright (2007) performed correlation analysis and observed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant along with fruit quality characters such as lycopene, beta-carotene, ascorbic acid and titratable acidity. Kumari *et al*. (2007) recorded data for total soluble solids, dry matter content, reducing sugars, titratable

acidity, ascorbic acid, lycopene and found there were insignificant differences for acidity, early yield, total yield, and days to flowering.

Singh *et al*. (2005) conducted a field experiment on 15 advance generation breeding lines of tomato, to study the variation for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene content and dry matter content. They observed significant differences among the genotypes under normal conditions, whereas differences were not significant under high-temperature conditions. The population means were higher during November than February planting for all the characters except acid content and TSS.

Davis *et.al* (2003) evaluated 13 tomatoes (four different cultivars) and 38 tomato products. They used absorbance method (PAM) and had linear correlation coefficients with lycopene content determined by hexane extraction/spectrophotometry of R2=0.97 for fresh tomato, and 0.88 for tomato products. The fruits of 11 recent hybrids of processing tomato, grown under optimal conditions, were assessed for color using Colorgard System 05 and for lycopene content examined by Siviero *et al*. (2000). Fresh DM regularly showed more mg lycopene/100 g than processed material.

Jones *et al*. (1983) studied inheritance and characterization of anthocyanin fruit (Aft) in tomato, to estimate the genetic potential for increased levels of this important class of phytonutrients in tomato fruit. They concluded that fruit of accession LA 1996 contained predominantly petunidin, followed by malvidin and delphinidin, while the levels of lycopene, β-carotene, phytoene, and phytofluene were similar to those of normal tomatoes and lower than those found in high-pigmented tomatoes.

2.6.2 Vitamin-C

Tomatoes are excellent sources of vitamin C, with some varieties containing concentrations comparable to those found in oranges. Although all tomatoes contribute to our vitamin C intake, there are different amounts of vitamin C in different genotypes. For example, raw green tomatoes contain 23.4 milligrams,

orange tomatoes contain 16 milligrams and yellow tomatoes contain 9 milligrams per 100 grams, which is slightly more than half of a large, 3-inch tomato. Sun-dried tomatoes are much richer in vitamin C, containing 39.2 milligrams per 100 grams. Crushed, canned tomatoes and tomato juice contain smaller amounts, respectively contributing 9.2 and 18.3 milligrams of vitamin C to our daily intake (Lee and Media, 2014).

Borguini *et al.* (2013) were analyzed tomatoes regarding ascorbic acid (Vit. C), lycopene content and antioxidant activity. Organic tomatoes presented higher content of ascorbic acid and total phenolics (641.39 and 4466.66 mg/100 g EAG on dry wt. basis) than did the conventional tomatoes (510.16 and 3477.50 mg/100 g EAG on dry wt. basis, respectively). There was no difference in lycopene concentrations between the organic and conventional.

Schwarz *et.al.* (2013) evaluated ten tomato hybrids (Supra, Granadero, AP-529, AP-533, Katia, Laura, Fascinio, Tinto, Red Spring and Venus) for their quality, viz. soluble solids, ascorbic acid, lycopene and reducing sugars. The best performing hybrid for traits and for both segments was Granadero, but this hybrid showed low genotypic stability. So Venus and Tinto, despite lower yields, could be recommended because they presented good quality and stability.

Five tomato cultivars: four large-fruit (Rumba, Juhas, Kmicic, Gigant) and one cherry cultivar (Koralik) were selected for study by Hallmann *et al.* (2007). The organic tomato fruits contained more dry matter, total and reducing sugars, vitamin C, total flavones, and beta-carotene, but less lycopene in comparison to conventionally grown tomatoes. The study was done by Schulzova *et al.* (2007) to investigate the effects of tomato cultivation systems on the content of both health promoting and of toxic components represented by carotenoids (lycopene, beta-carotene), vitamin C and glycoalkaloids (alpha-tomatine, dehydroemetine). The levels of biologically active compounds were shown to be strongly affected by the degree of fruit maturity.

A study was conducted by Ramirez (2005) to test whether tomato fruits from a genotype with elevated levels of natural antioxidants produce seeds with a functionally greater total antioxidant capacity. The tomato genotype 'T4099', which produces elevated levels of lycopene and ascorbic acid, and the recurrent parent 'Flora-Dade' were grown in the field and greenhouse under standard agronomic practices. Harer *et al.* (2002) grew 37 tomato genotypes in a field experiment. Correlation studies showed that genotypic correlation was higher than the phenotypic correlation for all characters examined. Among them, the ascorbic acid content had negative direct effects and association with fruit yield.

2.6.3 Total soluble solids (Brix %)

Brix percentage is the sugar content of an aqueous solution. One percent Brix is 1 gram of sucrose in 100 grams of solution and represents the strength of the solution as a percentage by mass. If the solution contains dissolved solids other than pure sucrose, then the Brix % only approximates the dissolved solid content. Various reports are available on the variation of Brix % for different genotypes of tomato. Nalla *et al*. (2014) done a field experiment using 27 tomato genotypes and reported fruit yield per plant (20.51), total soluble solids (17.38), and equatorial diameter (15.38) contributed high for divergence. For total fruit number, total soluble solids content, fruit firmness, length, and pH, in a general way and for the majority of the genotypes, there were no statistical differences between the averages of the F_1 and F_2 generations found by Hernandez (2013). There was a significant ($p<0.01$) difference among genotypes and environments for all quality traits, Genotype x Environment interaction was significant ($p<0.01$) for all quality traits except for TSS found by Panthee *et al.* (2013). Narolia *et al.* (2012) found high estimates of the genotypic coefficient of variation, heritability and genetic advance for acidity, total soluble solids, ascorbic acid content, and shelf life.

A study by Silva *et al*. (2012) evaluated the components of production and total soluble solids (Brix) of tomato cultivar Carolina. The fruits were harvested when

they began the color change from green to red; on the occasion were evaluated the content of soluble solids, number, weight, length, and diameter.

Seven tomato lines studied by Chen (2009) and found general heritability for vitamin C and total soluble solid content was high. Lines belonging to L. *esculentum* var. *cerasiforme* were better breeding materials in terms of vitamin C, organic acid, and total soluble solid content.

Krishna *et al.* (2005) found highest fruit yield (27.79 t/ha), total soluble solid content (6.11%), acidity (0.93%) and lycopene content (7.64 mg/100 g of juice). Cheema *et al.* (2003) studies on combining ability for 10 important characters and significant general (GCA) and specific combining ability (SCA) variances were observed for different characters except for total soluble solids indicating the importance of both additive and non-additive gene effects in the expression of these characters. Four commercial brands of tomato juices and ketchup were studied. Results showed that Brix is higher in ketchup (25-33 degrees Brix) than in tomato juices (4.8-5.5 degrees Brix). Pearson correlations showed statistically significant ($P<0.05$) correlations between Brix and HMF, lycopene, dry matter (negative correlation) and juice (negative); HMF and lycopene and dry matter (negative correlation); lycopene and dry matter (negative), pulp and juice; dry matter and pulp (negative) and juice; and pulp and juice (negative correlation).

Harer *et al*. (2002) were grown 37 tomato genotypes in a field experiment and correlation studies showed that genotypic correlation was higher than the phenotypic correlation for all characters examined. Among them, the total soluble solid content had positive but low direct effects and positive association with fruit yield. Dhaliwal *et al*. (2002) conducted an experiment with twelve parents and their 66 F_1 hybrids to study the genetics of traits that are important for processing and bulk handling of tomatoes viz. TSS%, pericarp thickness, and a number of locules. The analysis of variance for combining ability exhibited the significance of both general combining ability and specific combining ability effects for all characters studied.

The chemical constituents are concerned in the quality of tomato fruit in respect to color, texture, flavor, nutritive value. In general, high sugar contents, redness of color, and firm texture are associated with the prominence of rich flavor. Biochemical changes as influenced by growth, maturation, and environment of tomato fruit are discussed.

2.2.3 Moisture content

Accumulation of water accounts for more than 90% of the total weight of ripe tomato fruit; only 5-8% of the fruit weight is due to dry matter (Davies and Hobson, 1981; Ho *et al*., 1981).Therefore, factors affecting water accumulation may determine both the size and the quality of tomato fruit. Fruit grown at high salinity accumulated less water but not less dry matter than fruit grown at low salinity.

2.2.4 Dry matter content

Root restriction significantly decreased the dry weights of root, stem and leaves (about 30%) and fruit (about 20%). Although root restriction has been reported to reduce dry matter production, it has been shown that this reduction was not a result of nutrient deficiency (Peterson and Krizek, 1992; Ruff *et al*.,1987; Carmi and Heuer, 1981).

However, Bar-Tal *et al*. (1995) reported that root restriction reduced both dry matter production and K concentration in plant organs, indicating a possible K deficiency effect of restricting the roots. The increasing K and Ca concentrations in the solution did not significantly affect the dry weight of any plant organ and there was no significant interaction between root restriction and solution composition on any organ dry weight. The reduction in DM production following root restriction could not be compensated by elevating CCa above 3 mmol (+)· L–1 or increasing CK above 2.5 mmol·L–1.These results indicate that the reduction in plant growth under conditions of root restriction was not caused by nutrient deficiency, but it was probably related to hormone synthesis and metabolism in the root system (Jackson,1993; Carmi and Heuer, 1981; Richards and Rowe, 1977).

2.2.5 pH

Acid concentration and pH are important quality and processing characteristics of tomatoes. Several studies have revealed that a proper sugar/acid ratio is paramount to good tomato flavor (Stevens, 1972; Simandle *et al*., 1966 Dennison, 1955). Both [H+] and potential aciditycontribute to tartness (Harvey, 1920).The pH is important to process ability, as it should be lower than 4.4 to avoid problems with thermo phylic organisms (Rice and Pederson, 1954). Higher pH values necessitate longer processing times, increasing the difficulty of obtaining a high quality product. Total acidity and pH in a tomato should be closely related, but sometimes the relationship between these two factors is not good. Anderson (1957) found that pH and acidity are not always inversely related, and that in some varieties both values are relatively high. Lower and Thamburaj (1998) also found poor correlation between pH and acidity in certain tomato lines and their progeny. Stevens (1972) found wide variation in the $[H^+]$/titratable acidity (TA) ratio among 55 divergent accessions and obtain edevidence indicating that variation in phosphorus concentration of the fruits is an important factor in the poor relationship between pH and acidity. It should be possible to explain the relationship between TA and pH using model systems, as the TA is equal to the sum of TAs contributed by the buffers in the fruit. These buffers also establish the pH.

CHAPTER III

MATERIALS AND METHODS

This chapter illustrates information concerning methodology that was used in the execution of the experiment. The experiments were then divided into two parts viz. Experiment 1: Evaluation of tomato genotypes based agro-morphological traits and Experiment 2: Evaluation of tomato genotypes based on nutritional analysis. The different steps of the experiments are stated here chronologically in section 3.1 and in 3.2 respectively.

3.1 Experiment 1: Evaluation of tomato genotypes based agromorphogenic traits

It comprises a brief description of locations of experimental site, planting materials, climate and soil, seedbed preparation, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data collection procedure, statistical procedure etc., which are presented as follows:

3.1.1 Experimental site

The experiment was accomplished in the experimental field, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from November 2016 to April 2017. Location of the site is 23°74' N latitude and 90°35' E longitude with an elevation of 8 meters from sea level (Anon., 2004) in Agro-ecological zone of "Madhupur Tract" (AEZ-28) (Anon.1988). The experimental site is shown in the map of AEZ of Bangladesh in (Appendix I).

3.1.2 Planting materials

A total of nineteen genotypes of tomato originated from different places of Bangladesh were used in this experiment. The materials were collected from the research supervisor, Department of Genetics and Plant Breeding, SAU and Plant Genetic Resource Centre (PGRC) at Bangladesh Agricultural Research

Table1. Name and origin of nineteen tomato genotypes used in the present study

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Origin
1	G1	SL-006	GEPB, SAU
2	G2	SL-007	GEPB, SAU
3	G3	SL-008	GEPB, SAU
4	G4	SL-009	GEPB, SAU
5	G5	SL-010	GEPB, SAU
6	G6	SL-011	GEPB, SAU
7	G7	SL-012	GEPB, SAU
8	G8	SL-013	GEPB, SAU
9	G9	SL-014	GEPB, SAU
10	G10	SL-015	GEPB, SAU
11	G11	SL-016	GEPB, SAU
12	G12	SL-017	GEPB, SAU
13	G13	SL-018	GEPB, SAU
14	G14	BARI Hybrid 4	PGRC, BARI
15	G15	BARI Hybrid 5	PGRC, BARI
16	G16	BARI Tomato-2	HRC, BARI
17	G17	BARI Tomato-3	HRC, BARI
18	G18	BARI Tomato-11	HRC, BARI
19	G19	BARI Tomato-15	HRC, BARI

GEPB= Genetics and Plant Breeding Department, SAU= Sher-e-Bangla Agricultural University, PGRC= Plant Genetic Research Centre, HRC= Horticulture Research Centre BARI=Bangladesh Agricultural Research Institute

Institute (BARI), Gazipur. The name and origin of these genotypes are presented in Table 1.

3.1.3 Soil and climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agroecological region of "Madhupur Tract" (AEZ No. 28). The soil was clay loam in texture and olive gray with common fine to

medium distinct dark yellowish brown mottles. The pH was 5.47 to 5.63 and organic carbon content is 0.82% (Appendix II). The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.1.4 Seedbed preparation and raising of seedling

The sowing was carried out on October 18, 2016 in the seedbed. Before sowing, seeds were treated with Bavistin for 5 minutes. Seedlings of all genotypes were raised in seedbeds in the Sher-e-Bangla Agricultural University, Dhaka-1207 farm unit. Seeds were sown in rows spaced at 10 cm apart, beds were watered regularly. Seedlings were raised using regular nursery practices. Recommended cultural practices were taken up before and after sowing the seeds. When the seedlings become 25 days old, those were transplanted in the main field.

3.1.5 Design and layout of the experiment

The experiment was laid out and evaluated under field condition during Rabi 2016- 17 in Randomized Complete Block Design (RCBD).

Genotype	:	19
Replications	:	3
Spacing	:	40 cm × 60 cm
Plot size	:	14× 19 m
Date of transplanting	:	16th November 2016

3.1.6 Land preparation

The experimental plots were ploughed and brought into a fine tilth and raised the nursery bed, applied the recommended dose of fertilizers and farmyard manure (FYM). Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on November 12, 2016. The land preparation is displayed in Plate 1 and Plate 2.

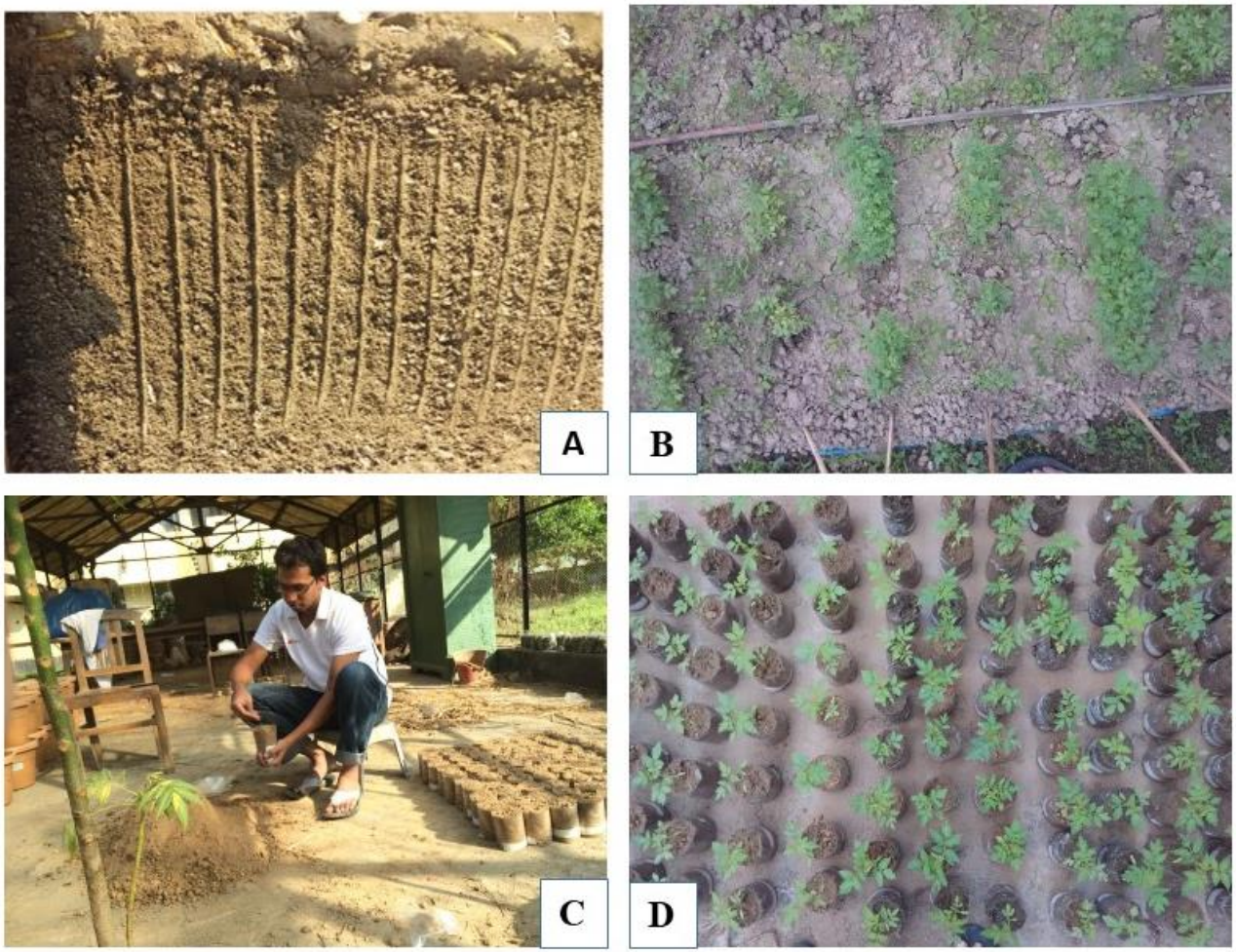


Plate 1. Different stages related to raising of seedling in the experiment-

A. Seedbed preparation, B. Raising of seedling,

C. Poly bag preparation, D. Raising of seedling in polybag

Plate 2. Different stages related to experiment in the field -A. Land preparation, B. Bed preparation in the field,

C. Transferring of seedling, D. seedling in field.

3.1.7 Transplanting of seedlings

The seedlings were raised in the seedbed in the usual way and 25 days old seedlings were transplanted in the main field on November 16, 2016. The transplanted seedlings were watered regularly to make a firm relation with roots and soil to stand along.

3.1.8 Manure and fertilizers application

Total cow dung and Triple Super Phosphate (TSP) were applied in the field during final land preparation. Half Urea and half Muriate of Potash (MOP) were applied in the plot after three weeks of transplanting. Remaining Urea and Muriate of Potash (MOP) were applied after five weeks of transplanting. Doses of manure and fertilizers used in the study are presented in (Table 2).

Table 2. Doses of manures and fertilizers used in the study

Sl. No.	Fertilizers/ Manures	Dose	
		Applied in the plot	Quantity/ha
1.	Urea	10.5 kg	550 kg
2.	TSP	08 kg	450 kg
3.	MOP	4.5 kg	250 kg
4.	Cow dung	200 kg	10 ton

3.1.9 Intercultural operations

When the seedlings were well established, first weeding was done uniformly in all the plots. Second weeding was done after 20 days of the first one. Mechanical support was provided to the growing plants by bamboo sticks to keep them erect. During early stages of growth, pruning was done by removing some of the lateral branches to allow and plants to get more sunlight and to reduce the self-shading and incidence of increased insect infestation. Thinning and gap filling, staking, pesticide application, irrigation and after-care were also done as per requirement.

3.1.10 Harvesting and processing:

All of the tomato varieties used in this experiment was indeterminate types. So, harvesting continued for about one and half month because fruits of different lines matured progressively at different dates and over a long time. The fruits per entry were allowed to ripe and then seeds were collected and stored at 4^{o}C for future use. Harvesting was started from February 2, 2017 and completed by April 6, 2017. Raising of seedlings, an experimental field in growing condition of plants, growth stage of a single tomato plant, flowering and fruiting stages of the tomato plant and different tomato genotypes fruit is displayed in Plate 3 and Plate 4.

3.1.11 Data recording

Five plants in each entry were selected randomly and were tagged. These tagged plants were used for recording observations for the following characters.

3.1.11.1 Plant height (cm)

The plant height was measured from ground level to tip of the plant expressed in centimeters (cm) and mean was computed.

3.1.11.2 Days to first flowering

The number of days was counted from the date of sowing to days to first flowering.

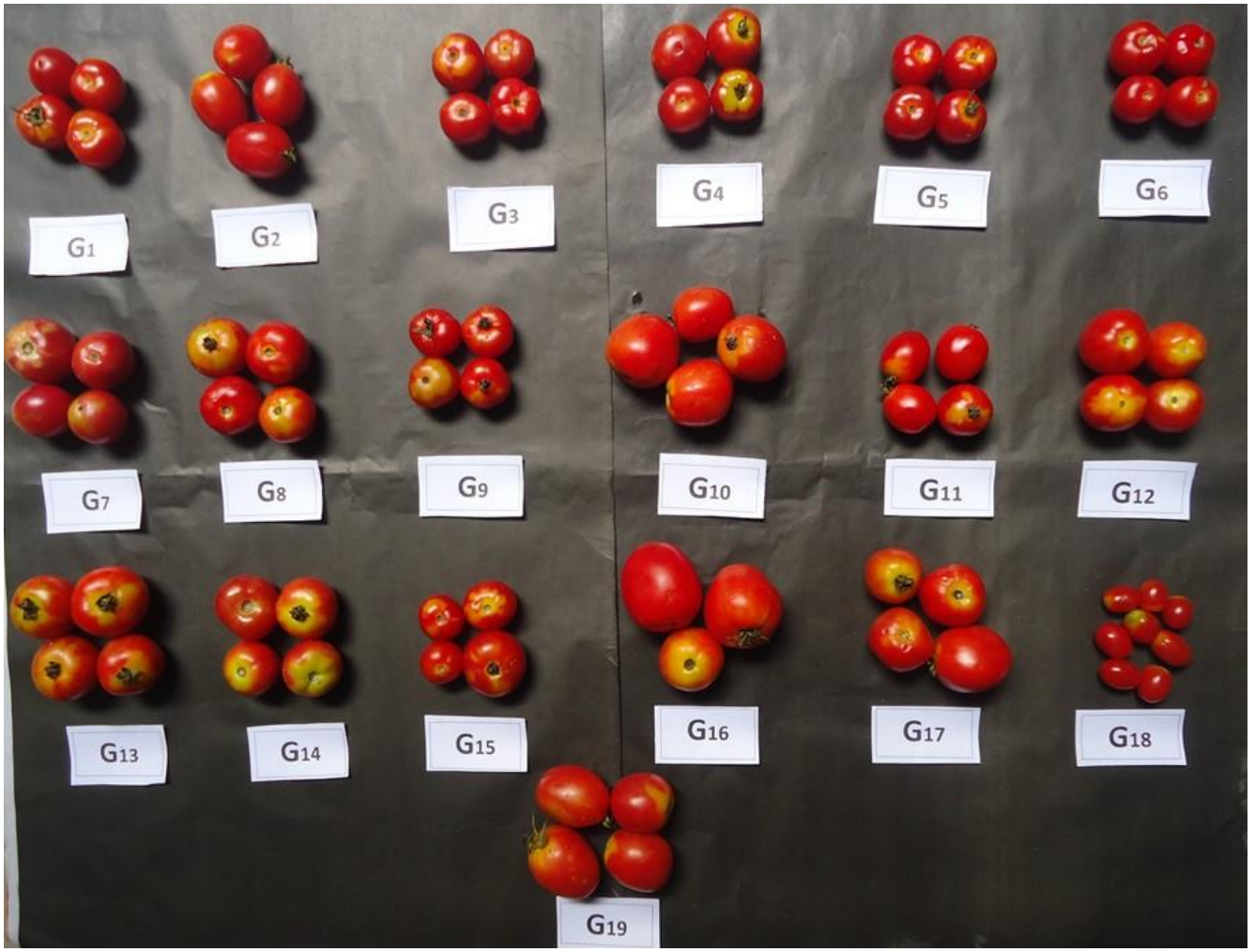
3.1.11.3 Days to maturity

The number of days was counted from the date of sowing to first harvesting.

3.1.11.4 Number of cluster per plant

The number of clusters per plant was recorded at the time of harvesting

Plate 3: Different stages of tomato plant in the experimental field. A. A tomato plant, B. Flowering of tomato plant in the experimental field. C. Fruiting stage of tomato plant. D. Ripening stage of tomato.


G1
G2
G3
G4
G5
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G11
G12
G13
G14
G15
G16
G17
G18
G19

Plate 4. Showing phenotypic variation in fruits among different genotypes of tomato (G1-G19)

3.1.11.5 Number of flower per clusters

The number of flower per plant was recorded at the time of flowering.

3.1.11.6 Number of fruits per cluster

Three clusters in each plant were taken at random and the number of fruits in each cluster was counted. Then the average number of fruits per cluster was calculated.

3.1.11.7 Number of fruits per plant

The total number of marketable fruits harvested from the five plants was counted and the average number of fruits per plant was calculated.

3.1.11.8 Fruit weight (g)

The total number of marketable fruits was weighed and the fruit weight was worked out and expressed in grams (g).

3.1.11.9 Fruit length (mm)

It was measured from stalk end to blossom end by using vernier caliper.

3.1.11.10 Fruit Diameter (mm)

It was measured from fruit breadth at a highest bulged portion of the fruit by using vernier caliper.

3.1.11.11 Fruit yield per plant (g)

The weight of fruits from each picking was recorded from the five labeled plants of each experimental plot. Total yield per plant was worked out by adding yield of all harvests and was expressed in kilogram (kg) per plant.

3.1.12 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-

C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and coefficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2016 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.1.12.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

Genotypic variance, $\sigma^2_g = \frac{GMS - EMS}{r}$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance, $\sigma^2_{ph} = \sigma^2_g + EMS$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

Environmental variance ($\sigma^2 e$) = EMS

Where,

EMS = Mean Square Error

3.1.12.2 Estimation of genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficient of variation was calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation, GCV % = $\frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation, PCV = $\frac{\sqrt{\sigma^2 ph}}{\bar{x}} \times 100$

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.1.12.3 Estimation of heritability

Broad-sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

Heritability, $h^2_b\% = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.1.12.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, GA = K. h^2. σ_p

Or Genetic advance, GA = K. $\frac{\sigma^2_g}{\sigma^2_{ph}} . \sigma_{ph}$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.1.12.5 Estimation of genetic advance mean's percentage

Genetic advance as a percentage of the mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance}}{\text{Population mean } (\bar{X})} \times 100$$

3.1.12.6 Estimation of simple correlation coefficient:

Simple correlation coefficients (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{\left[\left\{\sum x2 - \frac{(\sum x)2}{N}\right\}\left\{\sum y2 - \frac{(\sum y)2}{N}\right\}\right]}}$$

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.1.12.7 Estimation of genotypic and phenotypic correlation coefficient

For calculating the genotypic and phenotypic correlation coefficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component

were derived in the same way as for the corresponding variance components. The covariance components were used to compute the genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation, } r_{gxy} = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{py})}}$$

Where,

σ_{pxy} = Phenotypic covariance between the trait x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.1.12.8 Estimation of path coefficient

It was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects on yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3….and 12 on yield y, a set of simultaneous equations (twelve equations in this example) is required to be formulated as shown below:

$$r_{1.y} = P_{1.y} + r_{1.2}\,P_{2.y} + r_{1.3}\,P_{3.y} + r_{1.4}\,P_{4.y} + r_{1.5}\,P_{5.y} + r_{1.6}\,P_{6.y} + r_{1.7}\,P_{7.y} + r_{1.8}\,P_{8.y} + r_{1.9}\,P_{9.y} + r_{1.1}P_{10.y} + r_{1.11}\,P_{11.y} + r_{1.12}\,P_{12.y}$$

$$r_{2.y} = r_{1.2}\,P_{1.y} + P_{2.y} + r_{2.3}\,P_{3.y} + r_{2.4}\,P_{4.y} + r_{2.5}\,P_{5.y} + r_{2.6}\,P_{6.y} + r_{2.7}\,P_{7.y} + r_{2.8}\,P_{8.y} + r_{2.9}\,P_{9.y} + r_{2.10}P_{10.y} + r_{2.11}\,P_{11.y} + r_{2.12}\,P_{12.y}$$

$$r_{3.y} = r_{1.3}\,P_{1.y} + r_{2.3}\,P_{2.y} + P_{3.y} + r_{3.4}\,P_{4.y} + r_{3.5}\,P_{5.y} + r_{3.6}\,P_{6.y} + r_{3.7}\,P_{7.y} + r_{3.8}\,P_{8.y} + r_{3.9}\,P_{9.y} + r_{3.10}P_{10.y} + r_{3.11}\,P_{11.y} + r_{3.12}\,P_{12.y}$$

$$r_{4.y} = r_{1.4}\,P_{1.y} + r_{2.4}\,P_{2.y} + r_{3.4}\,P_{3.y} + P_{4.y} + r4_{1.5}\,P_{5.y} + r_{4.6}\,P_{6.y} + r_{4.7}\,P_{7.y} + r_{4.8}\,P_{8.y} + r_{4.9}\,P_{9.y} + r_{4.10}P_{10.y} + r_{4.11}\,P_{11.y} + r_{4.12}\,P_{12.y}$$

$$r_{5.y} = r_{1.5}\,P_{1.y} + r_{2.5}\,P_{2.y} + r_{3.5}\,P_{3.y} + r_{4.5}\,P_{4.y} + P_{5.y} + r_{5.6}\,P_{6.y} + r_{5.7}\,P_{7.y} + r_{5.8}\,P_{8.y} + r_{5.9}\,P_{9.y} + r_{5.10}P_{10.y} + r_{5.11}\,P_{11.y} + r_{5.12}\,P_{12.y}$$

$$r_{6.y} = r_{1.6}\,P_{1.y} + r_{2.6}\,P_{2.y} + r_{3.6}\,P_{3.y} + r_{4.6}\,P_{4.y} + r_{5.6}\,P_{5.y} + P_{6.y} + r_{6.7}\,P_{7.y} + r_{6.8}\,P_{8.y} + r_{6.9}\,P_{9.y} + r_{6.10}P_{10.y} + r_{6.11}\,P_{11.y} + r_{6.12}\,P_{12.y}$$

$$r_{7.y} = r_{1.7}\,P1.y + r_{2.7}\,P_{2.y} + r_{3.7}\,P_{3.y} + r_{4.7}\,P_{4.y} + r_{5.7}\,P_{5.y} + r_{6.7}\,P_{6.y} + P_{7.y} + r_{7.8}\,P_{8.y} + r_{7.9}\,P_{9.y} + r_{7.10}P_{10.y} + r_{7.11}\,P_{11.y} + r_{7.12}\,P_{12.y}$$

$$r_{8.y} = r_{1.8}\,P_{1.y} + r_{2.8}\,P_{2.y} + r_{3.8}\,P_{3.y} + r_{4.8}\,P_{4.y} + r_{5.8}\,P_{5.y} + r_{6.8}\,P_{6.y} + r_{7.8}\,P_{7.y} + P_{8.y} + r_{8.9}\,P_{9.y} + r_{8.10}P_{10.y} + r_{8.11}\,P_{11.y} + r_{8.12}\,P_{12.y} +$$

$$r_{9.y} = r_{1.9}\,P_{1.y} + r_{2.9}\,P_{2.y} + r_{3.9}\,P_{3.y} + r_{4.9}\,P_{4.y} + r_{5.9}\,P_{5.y} + r_{6.9}\,P_{6.y} + r_{7.9}\,P_{7.y} + r_{8.9}\,P_{8.y} + P_{9.y} + r_{9.10}P_{10.y} + r_{9.11}\,P_{11.y} + r_{9.12}\,P_{12.y} +$$

$$r_{10.y} = r_{1.10}\,P_{1.y} + r_{2.10}\,P_{2.y} + r_{3.10}\,P_{3.y} + r_{4.10}\,P_{4.y} + r_{5.10}\,P_{5.y} + r_{6.10}\,P_{6.y} + r_{7.10}\,P_{7.y} + r_{8.10+}\,P_{8.y} + r_{9.10}\,P_{9.y} + P_{10.y} + r_{10.11}\,P_{11.y} + r_{10.12}\,P_{12.y}$$

$$r_{11.y} = r_{1.11}\,P_{1.y} + r_{2.11}\,P_{2.y} + r_{3.11}\,P_{3.y} + r_{4.11}\,P_{4.y} + r_{5.11}\,P_{5.y} + r_{6.11}\,P_{6.y} + r_{7.11}\,P_{7.y} + r_{8.11}\,P_{8.y} + r_{9.11}\,P_{9.y} + r_{10.11}\,P_{10.y} + P_{11.y} + r_{11.12}\,P_{12.y} + r_{11.13}\,P_{13.y}$$

$$r_{12.y} = r_{1.12}\,P_{1.y} + r_{2.12}\,P_{2.y} + r_{3.12}\,P_{3.y} + r_{4.12}\,P_{4.y} + r_{5.12}\,P_{5.y} + r_{6.12}\,P_{6.y} + r_{7.12}\,P_{7.y} + r_{8.12}\,P_{8.y} + r_{9.12}\,P_{9.y} + r_{10.12}\,P_{10.y} + r_{11.12}\,P_{11.y} + P_{12.y}$$

$$r_{13.y} = r_{1.12}\,P_{1.y} + r_{2.12}\,P_{2.y} + r_{3.12}\,P_{3.y} + r_{4.12}\,P_{4.y} + r_{5.12}\,P_{5.y} + r_{6.12}\,P_{6.y} + r_{7.12}\,P_{7.y} + r_{8.12}+ P_{8.y} + r_{9.12}\,P_{9.y} + r_{10.12}\,P_{10.y} + r_{11.12}\,P_{11.y} + P_{12.y}$$

$$r_{14.y} = r_{1.12}\,P_{1.y} + r_{2.12}\,P_{2.y} + r_{3.12}\,P_{3.y} + r_{4.12}\,P_{4.y} + r_{5.12}\,P_{5.y} + r_{6.12}\,P_{6.y} + r_{7.12}\,P_{7.y} + r_{8.12}+ P_{8.y} + r_{9.12}\,P_{9.y} + r_{10.12}\,P_{10.y} + r_{11.12}\,P_{11.y} + P_{12.y}$$

$$r_{15.y} = r_{1.12}\,P_{1.y} + r_{2.12}\,P_{2.y} + r_{3.12}\,P_{3.y} + r_{4.12}\,P_{4.y} + r_{5.12}\,P_{5.y} + r_{6.12}\,P_{6.y} + r_{7.12}\,P_{7.y} + r_{8.12}+ P_{8.y} + r_{9.12}\,P_{9.y} + r_{10.12}\,P_{10.y} + r_{11.12}\,P_{11.y} + P_{12.y}$$

Where,

r_{1y} = Genotypic correlation coefficients between y and I th character (y = Fruit yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,….12)

1 = Days to first flowering

2 = Plant Height

3 = Days to maturity

4 = Number of cluster per plant

5 = Number of flower per plant

6 = Number of fruit per cluster

7 = Number of fruits per plant

8 = Fruit weight (gm)

9= Fruit length (mm)

10 = Fruit diameter (mm)

11 = Fruit yield per plant (gm)

Total correlation, say between 1 and y i. e., r_{1y} is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2}\, P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3}\, P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4}\, P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5}\, P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6}\, P_{6.y}$ = indirect effect of 1 via 6 on y

$r_{1.7}\, P_{7.y}$ = indirect effect of 1 via 7 on y

$r_{1.8}\, P_{8.y}$ = indirect effect of 1 via 8 on y

$r_{1.9}\, P_{9.y}$ = indirect effect of 1 via 9 on y

$r_{1.10}\, P_{10.y}$ = indirect effect of 1 via 10 on y

$r_{1.11}\, P_{11.y}$ = indirect effect of 1 via 11 on y

$r_{1.12}\, P_{12.y}$ = indirect effect of 1 via 12 on y

$r_{1.13}\, P_{12.y}$ = indirect effect of 1 via 13 on y

$r_{1.14}\, P_{12.y}$ = indirect effect of 1 via 14 on y

$r_{1.15}\, P_{12.y}$ = indirect effect of 1 via 15 on y

Where,

$P_{1.y,}$ $P_{2.y,}$ $P_{3.y.}$ …… $P_{15.y}$ = Path coefficient of the independent variables 1, 2, 3,….,15 on the dependent variable y, respectively.

$r_{1.y,}$ $r_{2.y,}$ $r_{3.y,}$ …., $r_{15.y}$ = Correlation coefficient of 1, 2, 3,…., 15 with y, respectively.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula (Singh and Chaudhary, 1985) given below

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} +……..+ r_{15.y}P_{15.y})$

Where,

$P^2_{RY} = R^2$

and hence residual effect, $R = (P^2_{RY})^{1/2}$

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y.

3.1.12.9 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are an efficient method of evaluating genetic diversity. These are as follows:

3.1.12.10 Principal component analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from

the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. The

contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.1.12.11 Principal coordinate analysis (PCO)

The principal Coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimension of p it gives the minimum distance between each pair of the n points using similarity matrix (Digby *et al.*, 1989).

3.1.12.12 Cluster analysis (CA)

Cluster analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In Genstat, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.1.12.13 Canonical vector analysis (CVA)

Canonical vector analysis (CVA) finds a linear combination of original variabilities that maximize the ratio of between-group to within-group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing the ratio of among groups to the within-group variations. The canonical vector is based upon the roots and vectors of WB, where W is the pooled within-groups covariance matrix and B is the among groups covariance matrix.

3.1.12.14 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 ----to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

3.1.12.15 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

D_i^2 = the sum of distances between all possible combinations (n) of genotypes included in a cluster.

n = Number of all possible combinations between the populations in cluster.

3.1.12.16 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

Average inter-cluster distance= $\frac{\sum D_{ij}^2}{n_i \times n_j}$

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in cluster i and j.

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.1.13 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by a largest statistical distance (D^2) express the maximum divergence among the genotypes included in these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

1. Choice of the cluster from which genotypes are selected for use as a parent (s)
2. Selection of particular genotype(s) from the selected cluster(s)
3. The relative contribution of the characters to the total divergence
4. Other important characters of the genotypes performance

3.2 Experiment 2: Evaluation of tomato genotypes based on nutritional traits

It comprises a brief description of nutritional traits. The nutritional traits included lycopene content, vitamin C content, pH, moisture %, dry matter %, SPAD % and brix percentage, data collection procedure, statistical procedure etc., which are presented as follows:

3.2.1 Determination of brix percentage

Brix percentages were measured by a portable refractometer (ERMA, Tokyo, Japan). The single fruit was blend and juice was collected to measure brix percentage. Mean was calculated for each genotype. Brix percentage of fruits was measured at room temperature.

3.2.2 Determination of vitamin-C

Vitamin-C was measured by Oxidation Reduction Titration Method (Tee *et al*., 1988). The single fruit was a blend and tomato extract was filtrated by Whatman No.1 filter paper. It was then mixed with 3% metaphosphoric acid solution. The titration was conducted in presence of glacial acetic acid and metaphosphoric acid to inhibit aerobic oxidation with dye solution (2, 6-dichlorophenolindophenol). The solution was titrated with dye. The observations mean will give, the amount of dye required to oxidize definite amount of L-ascorbic acid solution of unknown concentration, using L-ascorbic acid as a known sample. Different types of activities for estimation of vitamin C are shown in Plate 5.

Plate 5: Different types of activities for estimation of vitamin C. A. Measuring the weight of tomato, B. Extraction of tomato juice, C. Titration for estimate vitamin C in tomato, D. Estimation of vitamin C.

3.2.3 Determination of lycopene content

Absorption determination for lycopene content was estimated following the method of Alda *et al*. (2009) by using T60 UV-Visible Spectrophotometer. Lycopene in the tomato was extracted using hexane:ethanol: acetone (2:1:1) (v/v) mixture. One gram of each sample was homogenized with 25 ml of hexane:ethanol: acetone, which was then placed on the orbital shaker for 30 min., adding 10 ml distilled water and was continued agitation for another two min. The solution was then left to separate into distinct polar and non- polar layers (Plate 6). The absorbance was measured at 472 nm and 502 nm, using hexane as a blank. The lycopene concentration was calculated using its specific extinction coefficient (E 1%, 1cm) of 3450 in hexane at 472 nm and 3150 at 502 nm. The lycopene concentration was expressed as a mg/100g product.

All determination was repeated for three times.

$$\text{At } \lambda = 472\text{nm: lycopene content (mg/100g)} = \frac{E}{3.45} \cdot \frac{20}{m}$$

$$\text{At } \lambda = 502\text{ nm: lycopene content (mg /100g)} \quad \frac{E}{3.15} \cdot \frac{20}{m}$$

Where,

m = the weight of the product (g)

E = extinction coefficient

3.2.4 Determination of pH of the flesh

A sample of 5gm each of the fresh mesocarp was homogenous in 5 ml of boil distill water and deionize water (pH 7) and the pH of the homogenate was measured with a pH meter.

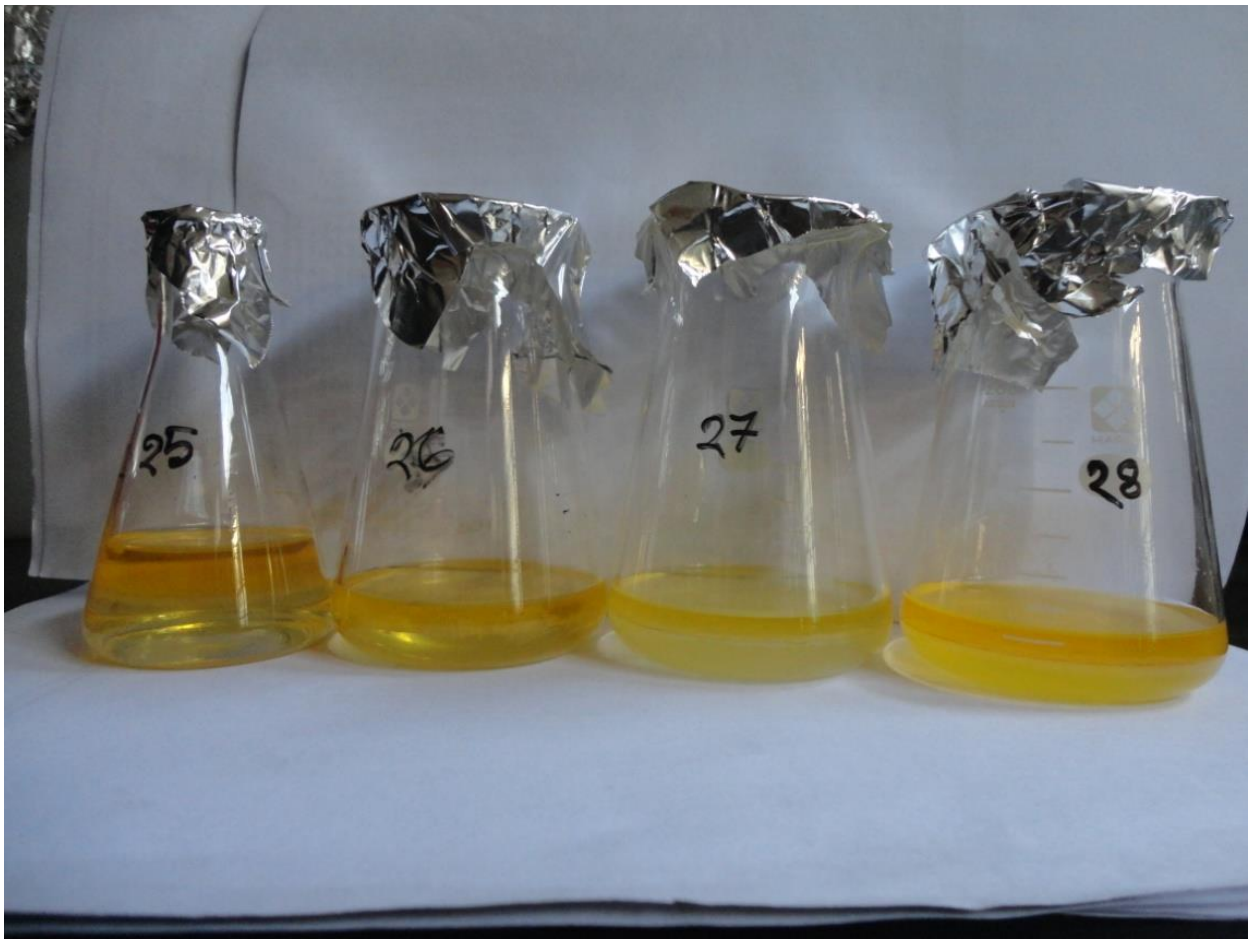

Plate 6. Extraction of lycopene content. The upper dark orange color layer is lycopene.

3.2.5 Determination of moisture percentage

The moisture percentage was estimated as described by Isbat (1996) 5 g of pulp was taken in a porcelain crucible and oven dried at 80^{o} C until the weight became constant. Three samples were used for each variety. Percent of moisture was calculated according to the following formula:

$$\% \text{ Moisture} = \frac{I-F}{I} \times 100$$

Where,

I= Initial weight of pulp

F= Final weight of pulp

3.2.6 Determination of dry matter

It was calculated from the data to obtain from percent moisture contain (F).

3.2.7 Measuring of chlorophyll content

Leaf chlorophyll content was measured by using SPAD-502 plus Portable Chlorophyll meter. The chlorophyll content was measured from four different portion of the leaf and then averaged for analysis.

CHAPTER IV
RESULTS AND DISCUSSION

The experiment was conducted to perform the diversity analysis of different genotypes of tomato (*Solanum Lycopersicum* L.) using yield contributing and nutritional traits. This chapter comprises the presentation and discussion of the findings obtained from the experiment. The fruits were harvested when they began the color change from green to red; on the occasion were evaluated days to first flowering, fruit number, weight, length and diameter. The data pertaining to eleven characters have been presented and statistically analyzed with the possible interpretations given under the following headings:

4.1 Experiment 1: Evaluation of tomato genotypes based agromorphogenic traits

This part of the chapter opened the results and their interpretation in order to, evaluation of tomato genotypes based on their agromorphogenic traits.

4.1.1 Genetic parameters

The analysis of variance indicated significantly higher amount of variability present among the genotypes for all the characters studied viz., Days to 1st flowering, plant height (cm), days to maturity, no. of cluster per plant, flower per cluster, no. of Fruit per cluster, fruit per plant, fruit weight (g), fruit length (mm), fruit diameter (mm), fruit yield per plant (g) (Table 3). The results clearly indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore, there is a lot of scope for selection for majority of the traits in the genotypes. The mean sum of squares of all the 11 characters is presented in (Table 4).

4.1.2 Genetic variability, heritability and genetic advance

The mean values for each character of all the genotypes are shown in (Table 3). Performance of the genotypes is described below for each character. The extent of variation among the genotypes in respect of fifteen characters was studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation

(GCV), heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in (Table 5).

The data were analyzed and possible interpretations are given here based on established scales. According to Deshmukh *et al.* (1986) PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%). Wide difference between PCV and GCV for the traits implies their susceptibility to environmental fluctuation, whereas narrow difference suggested their relative resistant to environmental alteration. Heritability is the percentage of phenotypic variance that is attributed to genetic variance. According to Singh (2009), heritability of a trait is considered as vary high or high when the values is 80% or more and moderate when it ranged from 40-80% and when it is less than 40%, it is low. The estimates of heritability alone fail to indicate the response to selection (Johnson *et al.*, 1955). Therefore, the heritability estimates appears to be more meaningful when accompanied by estimates of genetic advance and the genetic advance at percentage of mean. Deshmukh *et al.* (1986) classified genetic advance as percentage of mean as low (<10%), moderate (10-20%) and high (>20%).

4.1.2.1 Days to first flowering

The variance due to days to first flowering showed that the genotypes differed significantly and ranged from 22.67 days after transplanting (DAT) in (G6) to 30.33 DAT in (G3) with mean value 26.51 days after transplanting (DAT) (Table 4). The σ^2g and σ^2p for this trait were 3.08 and 6.08, respectively (Table 5). The σ^2p appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (6.62) and PCV (9.30) were more or less similar to each other, indicated presence of low variability in this trait (Table 4). Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop.

Table 3. Analysis of variance for eleven agromorphogenic characters in tomato genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (g-1) = 18**	**Error (r-1)(g-1) = 36**
Days to 1st flowering	7.07	12.23**	2.99
Plant height (cm)	13.47	670.75**	3.90
Days to maturity	19.80	29.07**	7.25
No. of cluster per plant	2.33	16.86**	1.85
Flower per cluster	0.91	4.42**	1.11
No. of Fruit per cluster	11.17	160.66**	2.23
Fruit per plant	26.01	1,517.68**	6.57
Fruit weight (g)	6.70	129.54**	4.21
Fruit Length (mm)	7.17	67.66**	0.65
Fruit diameter (mm)	4.70	47.76**	2.07
Fruit Yield per plant (g)	38,695.68	145,058.99**	4,648.13

** Denote Significant at 1% level of probability

Similar findings were reported by Farzaneh *et al.* (2013) and Kumari *et al.* (2007). Matin *et al*. (2001) also found similar results in tomato. In contrast, Monamodi *et al.* (2013) and Aditya *et al*. (1995) found in significant difference in days to first flowering. The heritability estimates for days to first flowering was moderate (50.69%) with low genetic advance (2.57%) and genetic advance in percentage of mean (9.71%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were low which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for days to first flowering.

4.1.2.2 Plant height (cm)

Significant differences were observed among the genotypes for plant height which ranged from 56.50 cm (G2) to 113.06 cm (G6) with mean value 85.81 cm (Table 4) Naz *et al*. (2013), Ravindra *et al*. (2003), Shravan *et al*., (2004) and Prasad *et al*., (1999) were also found similar significant variation for plant height. The σ^2p and σ^2g was observed 226.19 and 222.28, respectively (Table 4) with large environmental influence. The PCV (17.53) and GCV of variation (17.37) were moderate for plant height. Kumari *et al*. (2007) obtained highest GCV, which disagree with this result. Singh *et al.* (2002) showed that the PCV was greatest for this character. Similar observations were made by Matin *et al.* (2001). The heritability estimates for this trait was high (98.27%) with high genetic advance (30.45%) and genetic advance in percent of mean (35.48%) (Table 5) revealed that this trait was governed by additive gene and selection is effective for this trait. Bai and Devi (1991), Kumari *et al.* (2007), Mahesha *et al.* (2006), Singh *et al.* (2006), Singh *et al.* (2005) and Joshi *et al*. (2004) also reported similar results.

Table 4: Mean performance of growth, yield and yield contributing parameters

Genotypes	Days to first flowering	Plant height (cm)	Days to maturity	No. of cluster/plant	No. of flower/cluster	No. of fruit/cluster	No. of fruit/plant	Fruit weight (g)	Fruit length (mm)	Fruit diameter (mm)	Fruit yield/plant (g)
G1	28.33	86.30	77.33	7.67	6.33	5.00	31.67	19.79	24.00	25.00	627.35
G2	29.33	56.50	83.33	5.33	5.00	4.67	19.00	20.75	28.00	28.00	392.75
G3	30.33	103.94	79.33	6.67	4.67	4.00	16.00	19.24	23.00	28.00	308.47
G4	24.33	107.13	82.67	8.33	7.00	5.00	34.33	21.35	22.00	28.00	731.11
G5	28.33	96.15	80.00	9.33	5.33	6.00	26.00	25.76	21.00	26.00	665.97
G6	22.67	113.06	76.33	10.00	6.67	5.00	24.00	18.38	26.00	25.00	443.00
G7	26.67	85.91	79.00	6.00	7.00	4.33	21.67	21.61	26.67	24.00	467.11
G8	27.67	73.66	76.00	9.67	5.00	24.67	31.67	37.83	37.67	34.67	1196.70
G9	26.67	84.77	78.33	11.67	8.33	31.67	28.33	27.10	24.00	20.67	768.24
G10	27.33	105.64	79.33	16.00	7.67	6.00	58.00	10.24	22.00	21.33	595.03
G11	28.67	77.01	74.33	6.67	8.00	7.00	33.00	18.10	31.00	26.33	599.33
G12	23.33	75.81	72.67	8.00	8.00	6.33	39.33	17.38	27.00	26.00	680.96
G13	25.67	65.58	83.33	9.33	7.00	6.00	37.00	18.96	21.00	20.33	701.13
BARI Hybrid 4	26.33	93.35	77.67	10.00	6.33	4.33	24.67	23.37	28.00	30.00	577.23
BARI Hybrid 5	25.33	74.25	76.00	8.00	5.67	4.00	20.00	28.84	32.00	32.67	577.64
BARI Tomato-2	24.33	75.72	74.00	7.33	4.00	5.00	27.00	30.13	26.00	24.33	814.90
BARI Tomato-3	25.67	84.30	78.33	8.33	6.00	6.00	25.67	19.73	24.00	22.33	502.31
BARI Tomato-11	26.67	78.27	82.00	9.00	6.67	7.33	118.67	9.45	16.00	20.67	1121.11
BARI Tomato-15	26.00	93.05	76.33	7.00	7.00	8.00	30.33	22.40	26.33	23.00	680.43
Min	**22.67**	**56.50**	**72.67**	**5.33**	**4.00**	**4.00**	**16.00**	**9.45**	**16.00**	**20.33**	**308.47**
Max	**30.33**	**113.06**	**83.33**	**16.00**	**8.33**	**31.67**	**118.67**	**37.83**	**37.67**	**34.67**	**1196.70**
Mean	**26.51**	**85.81**	**78.23**	**8.65**	**6.40**	**7.91**	**34.02**	**21.60**	**25.56**	**25.60**	**655.30**

Table 5: Estimation of genetic parameters in eleven characters of nineteen genotypes in tomato

Parameters	Mean	σ^2p	σ^2g	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic Advance (5%)	Genetic Advance (% of mean)	CV (%)
Days to 1st flowering	26.51	6.08	3.08	3.00	9.30	6.62	6.53	50.69	2.57	9.71	6.53
Plant height (cm)	85.81	226.19	222.28	3.90	17.53	17.37	2.30	98.27	30.45	35.48	2.30
Days to maturity	78.23	14.53	7.27	7.25	4.87	3.45	3.44	50.08	3.93	5.03	3.44
No. of cluster per plant	8.65	6.86	5.01	1.85	30.28	25.87	15.73	73.00	3.94	45.53	15.73
Flower per cluster	6.40	2.22	1.10	1.12	23.27	16.41	16.50	49.74	1.53	23.84	16.50
No. of Fruit per cluster	7.91	55.04	52.81	2.23	93.77	91.85	18.88	95.95	14.66	185.33	18.88
Fruit per plant	34.02	510.28	503.70	6.57	66.40	65.98	7.54	98.71	45.93	135.03	7.54
Fruit weight (g)	21.60	45.99	41.78	4.21	31.40	29.92	9.50	90.84	12.69	58.75	9.50
Fruit Length (mm)	25.56	22.99	22.34	0.66	18.76	18.49	3.17	97.14	9.60	37.54	3.17
Fruit diameter (mm)	25.60	17.30	15.23	2.07	16.25	15.25	5.62	88.02	7.54	29.47	5.62
Fruit Yield per plant (g)	655.30	51451.76	46803.62	4648.14	34.61	33.01	10.40	90.97	425.06	64.86	10.40

σ^2p: Phenotypic variance
σ^2g: Genotypic variance
σ^2e: Environmental variance
PCV: Phenotypic coefficient of variation
GCV: Genotypic coefficient of variation
ECV: Environmental coefficient of variation
GA (5%): Genetic advance
GAM: Genetic advance (% of mean)
CV (%) = coefficient of variation

4.1.2.3 Days to maturity

The studied genotypes showed significant difference in case of duration for days to maturity. Maximum was found 72.67 DAT in (G12) and the minimum was recorded 62 DAT in (G13) with mean value 78.23 (Table 4). The σ^2g (7.27) was lower than σ^2p (14.53). The GCV (3.45) and PCV (4.87) were also close to each other (Table 4). Suggesting environmental influence is minor on the expression of the genes controlling this trait. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The results of Prashanth (2003) disagree with this result with high phenotypic coefficient of variation. The heritability estimates for this trait was moderate (50.08%) with low genetic advance (3.93%) and genetic advance in percent of mean (5.08%) (Table 5). It indicates that the character was governed by non-additive gene and influenced by environmental effect and selection would be non-significant. High heritability and moderately high genetic advance for days to maturity was also found by Kumari *et al*. (2007).

4.1.2.4 Number of clusters per plant

Number of clusters per plant was ranged from 5.33 in G2 and 16.00 in G10 with mean value 8.65 (Table 3). The σ^2g and σ^2p for this trait were 5.01 and 6.86, respectively (Table 4). The σ^2p appeared higher than the σ^2g suggested influence of environment on the expression of the genes controlling this character. The GCV was low (25.87) than PCV (30.28) which was not desirable for the improvement of this crop. Singh et al. (2002) also observed similar PCV and GCV. The heritability estimates moderate (73.00%) for this trait was moderate with low genetic advance (3.94%) and high genetic advance in percent of mean (45.53%) (Table 5) indicated that this trait was governed by additive gene. The low heritability is being exhibited due to high environmental effects and selection for this character would take long time. In contrast, high heritability coupled with high genetic advance was obtained by Singh *et al*. (2002) and Kumar *et al.* (1980).

4.1.2.5 Number of flower per cluster

Number of flower per cluster was ranged from 4.00 in (BARI Tomato-2) and 16.00 in (G9) with mean value 6.40 (Table 4). The σ^2g and σ^2p for this trait were 1.10 and 2.22, respectively (Table 4). The σ^2p appeared higher than the σ^2g suggested influence of environment on the expression of the genes controlling this character. The GCV was low (16.41) than PCV (23.27) which was not desirable for the improvement of this crop. Singh et al. (2002) also observed similar PCV and GCV. The heritability was moderate (49.74%) for this trait with low genetic advance (1.53%) and high genetic advance in percent of mean (23.84%) (Table 5) indicated that this trait was controlled by non-additive gene and selection for this character would take long time. In contrast, high heritability coupled with high genetic advance was obtained by Singh *et al*. (2002) and Kumar *et al.* (1980).

4.1.2.6 Number of fruits per cluster

Significant differences were observed among the genotypes for number of fruits per cluster which ranged from 4.00 (G3) and 31.67 (G9) with mean value 7.91(Table 4). The σ^2g and σ^2p for this trait were 52.81 and 55.04; the σ^2p appeared higher than the σ^2g. The PCV and GCV were high (93.77 and 91.85 respectively) (Table 5),which indicated presence of low variability among the genotypes. The observations found by Singh *et al*. (2002) were not similar. Aradhana and Singh (2003) also found moderate PCV and GCV. The heritability estimates for this trait was very high (95.95%), genetic advance moderate (14.66%) and genetic advance in percent of mean was found high (185.33%), revealed that this character was governed by additive gene and selection for this character would be effective. Moderate heritability and moderate genetic gain for this character were also observed by Joshi *et al.* (2004).

4.1.2.7 Number of fruits per plant

From the current study we observed that the minimum was recorded 16.00 in (G3) and the maximum range for number of fruits per plant was 118.67 found in (BARI tomato-11) (Table 4). The difference between σ^2g (503.70) and σ^2p (510.28) variances indicate high environmental influence (Table 5). The PCV (93.77) and GCV (91.85) was high, which indicated presence of low variability among the genotypes (Table 4). Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi *et al*. (2003) supported the findings. The heritability estimates for this trait was high (98.71%), high genetic advance (45.93%) and genetic advance in percent of mean (135.03%) were found high, revealed that this character was governed by additive gene and selection for this character would be effective. This character showed high heritability coupled with high genetic gain, which is supported by Ara et al. (2009), and Saeed *et al.* (2007).

4.1.2.8 Single fruit weight (g)

The maximum single fruit weight was recorded 6.70g in (BARI tomato-11) and where the minimum was recorded 37.83g in (G8) with mean value 31.65 g (Table 4). The σ^2g (41.78) and σ^2p (45.99) for fruit weight was moderate (Table 5). The GCV and PCV were high (29.92 and 31.40 respectively) and close to each other, proved that environment has little influence of the expression of this character. Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Manivannan et al. (2005) and Singh et al. (2002) also noticed high GCV and PCV for average fruit weight. High heritability (90.84%) associated with high genetic advance in percent of mean (58.75%) and moderated Genetic advance (12.69%) (Table 4) was observed indicating fruit weight governed by additive gene and selection may be effective. Pandit *et al.* (2010), Ara *et al.* (2009) and Singh *et al.* (2006) also supported the present findings.

4.1.2.9 Fruit length (mm)

The mean fruit length was noticed as 25.56 mm with a range of 16.00 mm to 37.67 mm. The line (BARI Tomato-11) showed the minimum fruit length and the maximum fruit length was recorded in the accession (G8) (Table 4). The σ^2g and σ2p were high (22.34 and 22.99 respectively) and GCV (18.49) and PCV (18.76) were close to each other (Table 5), indicating minor environmental influence on this character that would be effective for the improvement of this crop. Singh *et al*. (2002) showed that the phenotypic coefficient of variation was greatest for this character, which does not support the present study. High heritability estimates (97.14%) with low genetic advance (9.60%) and high genetic advance over percent of mean (37.54%) (Table 5) indicative of non-additive gene action. The high heritability is being exhibited due to influence of environmental rather than genotypes effective selection may not be rewarding for this trait. Joshi et al observed moderate heritability and moderate genetic gain for this character. (2004).

4.1.2.10 Fruit diameter (mm)

The mean fruit diameter was 25.60 mm with a minimum range of 20.33 mm (G13) to 34.67 mm (G13) (Table 4). The σ^2p and σ^2g were low (17.30 and 15.23 respectively) and GCV (15.25) and PCV (16.25) (Table 5) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato. Singh *et al*. (2002) showed that the PCV was greatest for this character, which does not support the present study. High heritability estimate (88.02%) with low genetic advance (7.54%) over high genetic advance percent of mean (29.47%) (Table 5) indicate that effective selection may not be made for fruit dia. Pandit et al observed high heritability coupled with low genetic gain for this character. (2010).

4.1.2.11 Fruit yield per plant (g)

Fruit yield per plant was found 308.47 g in (G3), which is lowest and the highest was recorded 1196.70 g in (G7) with mean value 655.30 g (Table 4). The σ^2p (51451.76) found higher than σ^2g (46803.62) (Table 5), suggested considerable influence of environment on the expression of the genes controlling this character. The phenotypic coefficient of variation and genotype coefficient of variation were 34.61 and 33.01, respectively for fruit yield per plant, which indicating that significant variation exists among different genotypes, which made the trait effective for selection. Similar findings supported by Singh *et al.* (2006) and Manivannan *et al*. (2005). Estimation of high heritability (90.97%) for fruit yield per plant with high genetic advance (425.06%) and high Genetic advance of % mean (64.86%) (Table 5) revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding programme. Ara et al. (2009) and Anupam et al. (2002) also observed high heritability and high genetic advance.

4.1.3 Correlation Coefficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by (Singh and Chaudhary, 1985). As we know yield is a complex product being influence by several inter-dependable quantitative characters. Therefore, selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence, knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection

Table 6. Pearson correlation coefficients among different pairs of yield and yield contributing characters for different genotype of tomato

	DFF	PH	DM	CPP	FPC	NFPC	FPP	FW	FL	FD
PH	-0.152									
DM	0.306	-0.013								
CPP	-0.150	0.399	0.064							
FPC	-0.252	0.158	-0.058	0.361						
NFPC	0.088	-0.146	-0.112	0.335	0.215					
FPP	-0.054	-0.053	0.250	0.315	0.273	0.019				
FW	-0.017	-0.241	-0.321	-0.190	-0.477*	0.473*	-0.565*			
FL	0.026	-0.310	-0.570*	-0.221	-0.183	0.269	-0.521*	0.671**		
FD	0.140	-0.088	-0.257	-0.263	-0.465*	0.010	-0.419	0.607 **	0.749**	
FYP	-0.147	-0.265	-0.065	0.241	0.016	0.527*	0.595**	0.276	0.052	0.035

*p<0.05, **p<0.01

DFF : days to 1st flowering, **PH :** plant height (cm), **DM :** days to maturity, **CPP :** no. of cluster per plant, **FPC :** flower per cluster, **NFPC :** no. of Fruit per cluster, **FPP :** fruit per plant, **FW :** fruit weight (g), **FL :** fruit Length (mm), **FD :** fruit diameter (mm) and **FYP :** Fruit Yield per plant (g)

Table 7. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of tomato

		PH	DM	CPP	FPC	NFPC	FPP	FW	FL	FD	FYP
DFF	G	-0.183	0.465*	-0.175	-0.383*	0.097	-0.056	-0.027	0.032	0.187	-0.171
	P	-0.111	0.147	-0.122	-0.120	0.077	-0.053	-0.003	0.017	0.080	-0.118
PH	G		-0.009	0.428*	0.168	-0.147	-0.051	-0.247	-0.312	-0.091	-0.267
	P		-0.020	0.354*	0.150	-0.144	-0.057	-0.232	-0.306	-0.082	-0.261
DM	G			0.089	-0.039	-0.147	0.291	-0.413	-0.665**	-0.351	-0.105
	P			0.036	-0.078	-0.066	0.200	-0.205	-0.456*	-0.140	-0.013

CPP	G				0.420*	0.352	0.334	-0.219	-0.240	-0.265	0.251
	P				0.292	0.308	0.286	-0.143	-0.190	-0.262	0.225
FPC	G					0.252	0.327	-0.557**	-0.221	-0.531**	0.043
	P					0.173	0.205	-0.379*	-0.135	-0.388*	0.020
NFPC	G						0.019	0.481*	0.271	0.013	0.536**
	P						0.018	0.460*	0.263	0.004	0.512**
FPP	G							-0.574**	-0.522**	-0.428*	0.600**
	P							-0.550**	-0.519**	-0.402*	0.584**
FW	G								0.687**	0.631**	0.262
	P								0.641**	0.565**	0.300
FL	G									0.762**	0.060
	P									0.725**	0.037
FD	G										0.037
	P										0.031

*p<0.05, **p<0.01

DFF- Days to 1st flowering, **PH**- Plant height (cm), **DM**- Days to maturity, **CPP**- No. of cluster/plant, **FPC**- Number of fruits/cluster, **NFPC**- No. of fruit/cluster, **FPP**-No. of fruits/plant, **FW**- Fruit weight (g), **FL**- fruit length (cm), **FD**- fruit diameter (cm), **FYP**- Fruit yield/plant (g).

with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). Pearson correlation analysis among yield and its contributing characters are shown in (Table 6). For clear understanding, correlation coefficients are separated into genotypic and phenotypic level in (Table 7). The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. While phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level. The depicted of genotypic and phenotypic correlation coefficient among yield and yield contributing characters of tomato are shown in (Table 7).

4.1.3.1 Days to first flowering

Days to first flowering had significant positive correlation with days to maturity at genotypic level (0.465) (Table 7). Patil and Bojappa (1993), Mayavel *et al.* (2005) and Samadia *et al.* (2006) observed positive correlation which support the present findings. It had negatively significant correlation at genotypic level with fruits per cluster (-0.383). Days to first flowering had positive but non-significant correlation with number of fruit per cluster, fruit length and fruit diameter at both level. This trait had non-significant negative correlation at both levels for plant height, cluster per plant, number of fruits per plant, single fruit weight and fruit yield per plant.

4.1.3.2 Plant height

Plant height had significant positive correlation with cluster per plant per plant (0.428 and 0.354) at genotypic and phenotypic levels (Table 7) which is supported by Mohanty (2003). Plant height had also non-significant positive correlation with number of flower per cluster at both levels. It had non-significant negative correlation with days to maturity, number of fruit per cluster, fruit per plant, fruit weight, fruit length, fruit diameter and fruit yield per plant both levels.

4.1.3.3 Days to maturity

Days to maturity had highly significant negative correlation with fruit length (-0.665 and -0.456) at genotypic and phenotypic levels (Table 7). It had also non-significant negative association with fruit per cluster, number of fruit per cluster, fruit weight fruit diameter and fruit yield per plant at both levels.

Days to maturity had positive non-significant association with cluster per plant and fruit per plant. A significant and positive correlation observed by Singh *et al.* (2002) and Mohanty (2003) between days to maturity and fruit yield per plant and. This does not support the present findings.

4.1.3.4 Number of clusters per plant

The number of clusters per plant had significant and positive association with fruit yield per plant (0.420) at genotypic level (Table 7). Number of clusters per plant had non-significant positive association with number of fruit per cluster, number fruit per plant and fruit yield per plant both at the genotypic and phenotypic levels. It also had non-significant negative association with fruit weight, fruit length and fruit diameter both at genotypic and phenotypic level. A positive correlation between number of clusters per plant and fruit yield per plant was also observed by Prasanth (2003). Nesgea *et al*. (2002) also found similar results for this trait in tomato.

4.1.3.5 Number of fruits per cluster

The number of fruits per cluster had highly significant but negative association with fruit weight (-0.557 and -0.379), fruit diameter (-0.531 and -0.388) at genotypic level and significant at phenotypic level (Table 7). The number of fruits per cluster showed non-significant and positive association with number of fruits per cluster, number of fruit plant and fruit yield per plant at genotypic and phenotypic levels. It also exhibited non-significant negative association with fruit length at the genotypic and phenotypic level, respectively. The findings also supported by Nesgea *et al.*

(2002) and Megha *et al* (2006). However, Joshi *et.al* (2004) found number of fruits per cluster showed negative association.

4.1.3.6 Number of fruits per cluster

The number of fruits per cluster had highly significant and positive association with fruit yield per plant (0.536 and 0.512) at genotypic and phenotypic levels respectively. This trait has also positively significant association with fruit weight at genotypic and phenotypic level (Table 7). Rani *et al.* (2010) reported that the number of fruits per plant was negatively associated with yield per plant. It had also positive non-significant correlation with number of fruit per plant, fruit length and fruit diameter at both level. Joshi *et al.* (2004) showed that number of fruits per plant was negatively correlated with fruit weight.

4.1.3.7 Number of fruits per plant

The number of fruits per plant had highly significant and positive association with yield per plant (0.600 and 0.584) at genotypic and phenotypic levels respectively (Table 7). Rani *et al.* (2010) reported that the number of fruits per plant was negatively associated with yield per plant. It had also highly significant negative correlation single fruit weight (-0.574 and -0.550), fruit length (-0.522 and -0.519) at both level and significant negative correlation with fruit diameter (-0.428 and -0.402) at genotypic levels. Joshi *et al.* (2004) showed that number of fruits per plant was negatively correlated with fruit weight.

4.1.3.8 Single fruit weight (g)

Fruit weight showed highly significant and positive correlation with fruit length (0.687 and 0.641), fruit diameter(0.631 and 0.565) for both genotypic and phenotypic levels (Table 7). Matin *et al*. (2001) found that individual fruit weight had significant positive correlations with yield per plant. Arun *et al*. (2004) and Joshi *et al.* (2004) observed that in case of tomato yield per plant was positively and

significantly correlated with average fruit weight. Megha *et al*. (2006) also found similar results for this trait in tomato. It had non-significant positive effect with fruit yield per plant at both levels.

4.1.3.9 Fruit length (mm)

Fruit length was significantly positively correlated with fruit yield (0.105) at genotypic level) and non-significant positive correlation (0.096) at phenotypic level (Table 7). Fruit length (FL) also showed highly negative correlation with fruit diameter (0.645 and 0.518) and vitamin C content (0.102 and 0.062) at both the levels. It had strong significant negative correlation with days to maturity (-0.468 and -0.355). It had also non-significant positive correlation with % brix (0.122 and 0.106) and lycopene content (0.223 and 0.189).

4.1.3.10 Fruit diameter (mm)

Fruit diameter showed significant positive relation with fruit yield per plant (0.110) at genotypic level but non-significant positive correlation at phenotypic level (0.105) (Table 7). It had also strong positive association with vitamin C content (0.113 and 0.093) at both the levels. Fruit diameter also showed significant positive relation with days to 50% flowering, number of cluster per plant and fruit length at genotypic level and phenotypic levels. On other hand, fruit diameter was highly negatively associated with date of maturity, plant height and number of fruits per cluster at both the levels. It was insignificantly positively correlated with yield per plant at genotypic level. So, it was unlikely to combine high fruit diameter with high plant height and short maturity date. And if the number of fruits per cluster was high then it is expected that fruit diameter will decreased in size.

4.1.4 Path coefficient analysis

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield

rather than providing cause and effect relationship. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way. The direct and indirect effects of yield contributing characters on yield were worked out by using path analysis. Here yield per plant was considered as effect (dependent variable) and days of first flowering, plant height (cm), days to maturity, number of cluster per plant, number of flower per cluster, fruits per cluster, fruits per plant, fruit weight (g), fruit length (mm), fruit diameter (mm) were treated as independent variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of tomato in (Table 8).

4.1.4.1 Days to first flowering

Days to first flowering had negative direct effect (-0.0220) on yield per plant (Table 8) which is contributed to result non-significant negative genotypic correlation with yield per plant (-0.171). Matin *et al*. (2001) reported dissimilar result with the present study and they stated that days to first flowering had negative direct effect on yield per plant. It had positive indirect effect on FL (0.0008. Negative indirect effect was also found on PH (-0.0001), DM (-0012), CPP (-0.0026), FPC (-0.0401), NFPC (-0.0004) and FPP (-0.0593), FW (-0.0167) and FD (-0.0062).

4.1.4.2 Plant height

Plant height had positive direct effect (0.0004) on yield per plant (Table 8), which is contributed to result non-significant negative genotypic correlation with yield per plant (-0.267). It had positive indirect effect through DFF (0.0033), DM (0.0001), CPP (0.0068), FPC (0.0251), NFPC (0.0006) and FD (0.0113). On the other hand, plant height showed negative indirect effect on yield per plant through FPP (-0.0582), FW (-0.2369) and FL (-0.0090). Matin *et al*. (2001) reported that plant height had negative direct effect on yield per plant.

4.1.4.3 Days to maturity

Days to maturity had negative direct effect on yield per plant (-0.0040) and it had also non-significant negative correlation with yield per plant (-0.105) at genotypic level. Singh *et al.* (2005) also reported that days to maturity had high negative direct effects on yield in tomato. Days to maturity had positive indirect effect on CPP (0.0011), NFPC (0.0004), FPP (0.2748) and FD (0.0113). This trait had also negative indirect effect on DFF (-0.0067), FPC (-0.0092), FW (-0.3155) and FL (-0.0165) (Table 8).

4.1.4.4 Number of clusters per plant

Number of fruits per cluster showed positive direct effect (0.0170) on yield per plant and non-significant positive correlation (0.251) at genotypic level. It also showed positive indirect effects through DFF (0.0033), PH (0.0002), FPC (0.0574), FPP (0.3462) and FD (0.0116) (Table 8). It also showed negative indirect effects on DM (-0.0003), NFPC (-0.0013), FW (-0.1868) and FL (-0.0064). Mayavel *et al.* (2005) also reported that number of fruits per cluster had negative direct effects on fruit yield.

4.1.4.5 Number of flower per cluster

Number of flower per cluster showed positive direct effect (0.1590) on yield per plant. It had also highly significant positive correlation with yield per plant (0.043) at genotypic level (Table 8).

Table 8. Path coefficient analysis showing direct (bold) and indirect effects of different characters on yield of tomato

Character	DFF	PH	DM	CPP	FPC	NFPC	FPP	FW	FL	FD	Genotypic correlation with yield
DFF	**-0.0220**	-0.0001	-0.0012	-0.0026	-0.0401	-0.0004	-0.0593	-0.0167	0.0008	-0.0062	-0.171
PH	0.0033	**0.0004**	0.0001	0.0068	0.0251	0.0006	-0.0582	-0.2369	-0.0090	0.0039	-0.267
DM	-0.0067	0.0000	**-0.0040**	0.0011	-0.0092	0.0004	0.2748	-0.3155	-0.0165	0.0113	-0.105
CPP	0.0033	0.0002	-0.0003	**0.0170**	0.0574	-0.0013	0.3462	-0.1868	-0.0064	0.0116	0.251
FPC	0.0055	0.0001	0.0002	0.0061	**0.1590**	-0.0009	0.3000	-0.4689	-0.0053	0.0205	0.043
NFPC	-0.0019	-0.0001	0.0004	0.0057	0.0342	**-0.0040**	0.0209	0.4650	0.0078	-0.0004	0.536**
FPP	0.0012	0.0000	-0.0010	0.0054	0.0434	-0.0001	**1.0990**	-0.5554	-0.0151	0.0184	0.600**
FW	0.0004	-0.0001	0.0013	-0.0032	-0.0758	-0.0019	-0.6209	**0.9830**	0.0195	-0.0267	0.262
FL	-0.0006	-0.0001	0.0023	-0.0038	-0.0291	-0.0011	-0.5726	0.6596	**0.0290**	-0.0330	0.060
FD	-0.0031	0.0000	0.0010	-0.0045	-0.0739	0.0000	-0.4605	0.5967	0.0217	**-0.0440**	0.031

Residual effect: 0.259 ** = Significant at 1%. * = Significant at 5%.

DFF : days to 1st flowering, PH : plant height (cm), DM : days to maturity, CPP : no. of cluster per plant, FPC : flower per cluster, NFPC : no. of Fruit per cluster, FPP : fruit per plant, FW : fruit weight (g), FL : fruit Length (mm), FD : fruit diameter (mm) and FYP : Fruit Yield per plant (g)

Number of flower per cluster had positive indirect effects on DFF (0.0055), PH (0.0001), DM (0.0002), CPP (0.0061), FPP (0.3000) and FD (0.0205). It had negative indirect effect on NFPC (-0.0009), FW (-0.4689) and FL (-0.0053). Singh *et al.* (2006) and Kumar *et al.* (2003) also observed fruits per plant had direct positive effects on fruit yield at the genotypic and phenotypic levels. Ara *et al.* (2009) also found similar results for this trait in tomato. This is not supported by present findings. This discrepancy with present findings might be due to environmental variation.

4.1.4.6 Number of fruits per cluster

Number of fruits per cluster showed negative direct effect (-0.0040) on yield per plant. It had also highly significant positive correlation with yield per plant (0.536) at genotypic level (Table 8). Number of fruits per cluster had positive indirect effects on DM (0.0004), CPP (0.0057), FPC (0.0342), FPP (0.0209), FW (0.4650) and FL (0.0078). It had negative indirect effect on DFF (-0.0019), PH (-0.0001) and FD (-0.0004). Singh *et al.* (2006) and Kumar *et al.* (2003) also observed fruits per plant had direct positive effects on fruit yield at the genotypic and phenotypic levels. Ara *et al.* (2009) also found similar results for this trait in tomato. This is not supported by present findings. This discrepancy with present findings might be due to environmental variation.

4.1.4.7 Number fruit per plant

Path analysis revealed that single fruit per plant had direct positive effect (1.0990) on yield per plant and highly significant positive correlation with yield per plant (0.600) at genotypic level (Table 8). Further, fruit weight showed indirect positive effect on DFF (0.0012), CPP (0.0054), FPC (0.0434) and FD (0.0184). This trait had also indirect negative effect on DM (-0.0010), NFPC (-0.0001), FW (-0.5554) and FL (-0.0151). Significant genotypic correlation between fruit weight and yield further strengthened their reliability in the process of selection for higher yield. Rani *et al.* (2010), Singh *et al.* (2006) and Manivannan *et al.* (2005) also reported positive direct effects on fruit yield

4.1.4.7 Single fruit weight

Path analysis revealed that single fruit weight had direct positive effect (0.9830) on yield per plant and non-significant positive correlation with yield per plant (0.262) at genotypic level (Table 8). This trait had also indirect positive effect on DFF (0.0004), DM(0.0013) and FL(0.0195). Further, fruit weight showed indirect negative effect on PH (-0.0001), CPP (-0.0032), FPC (-0.0758), NFPC (-0.0019), FPP (-0.6209) and FD (-0.0267). Significant genotypic correlation between fruit weight and yield further strengthened their reliability in the process of selection for higher yield. Rani *et al.* (2010), Singh *et al.* (2006) and Manivannan *et al.* (2005) also reported positive direct effects on fruit yield

4.1.4.8 Fruit length

Fruit length had positive direct effect (0.0290) on yield per plant. It had also non-significant positive correlation with yield per plant (0.060) at genotypic level (Table 8). . This trait had also indirect positive effect on DM (0.0023) and FW (0.6596). Fruit length showed indirect negative effect on DFF (-0.0006), PH (-0.0001), CPP (-0.0038), FPC (-0.0291), NFPC (-0.0011), FPP (-0.5726) and FD (-0.330) (Table 6). Padda *et al.* (2007), Singh *et al.* (2004) revealed that fruit length exhibited positive effect on yield per plant at the genotypic and phenotypic levels.

4.1.4.9 Fruit diameter

Fruit diameter showed negative direct effect (-0.0440) on yield per plant. It had also non-significant positive correlation with yield per plant (0.037) at genotypic level (Table 8). It had positive indirect effect on DM (0.0010), FW (0.5967) and FL (0.0217.Fruit diameter had negative indirect effects on DFF (-0.0031), CPP (-0.0045), FPC (-0.0739) and FPP (-0.4605) (Table 6). Padma *et al.* (2002) found that fruit diameter had high positive direct effect on fruit yield at the genotypic and phenotypic levels. This is supported by present findings.

4.1.5 Multivariate analysis

4.1.5.1 Cluster analysis

The experiment was conducted to investigate the genetic diversity of nineteen genotypes of tomato. The genotypes were divided into four cluster according to D^2 analysis (Table 9). The cluster IV had maximum number of genotypes (7) followed by cluster III which had 6 genotypes. Cluster I and II had 4 and 2 genotypes respectively. Remarkably cluster I had (G2, G3, G6 and G7) where as cluster II had (G8 and G18). Furthermore cluster III had (G1, G10, G11, G14, G15 and G17), cluster IV showed seven genotypes (G4, G5, G9, G12, G13, G16 and G19). Clustering was done at random that indicate a broad genetic base of the genotypes. Genetic variability in tomato was also found by Prasad *et at.* (2001).

4.1.5.2 Principal component analysis (PCA)

Proper idea about genetic divergence is an important tool for breeding program. The diversity analysis is useful to determine the magnitude of divergence among population (Murthy and Quadri, 1966). Principal component analysis was studied with nineteen genotypes of tomato. First three Eigen values for three principal co-ordination axes of genotypes accounted for 79.68% variation (Table 10). Based on principal component scores (Appendix IV) I and II obtained from the Principal component analysis (Table 10), a two-dimensional scatter diagram (Z1-Z2) using component score I as X axis and component score II as Y axis was Constructed, which has been presented in Figure 1.

4.1.5.3 Principal coordination analysis

Principal coordination analysis (PCO) indicated that the maximum inter genotypic distance between genotype G3 and G18 (2.574), the minimum distance was showed between genotype G1 and genotype G4 (Table 11). There was moderate level of variation present among nineteen genotypes of tomato due

Table 9. Distribution of nineteen genotypes in different clusters

Cluster no.	Genotypes	No. of population	Name of Genotypes
I	G2, G3, G6, G7	4	SL-006, SL-007, SL-011, SL-012
II	G8, G18	2	SL-013, BARI Tomato-11
III	G1, G10, G11, G14, G15, G17	6	SL-006, SL-015, SL-016, BARI Hybrid 4, BARI Hybrid 5, BARI Tomato-3
IV	G4, G5, G9, G12, G13, G16, G19	7	SL-009, SL-010, SL-014, SL-018 BARI Tomato-2, BARI Tomato-15
Total		19	

Table 10. Eigen values and yield percent contribution of eleven characters of nineteen genotypes of tomato

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
Days of first flowering	3.459	31.45	31.45
Plant height	2.157	19.61	51.06
Days of Maturity	1.598	14.53	65.59
Number of cluster per plant	1.133	10.30	75.89
Number of flower per cluster	0.931	8.46	84.35
Fruits per cluster	0.685	6.23	90.58
Number of fruits per plant	0.467	4.25	94.83
Individual Fruit Weight (g)	0.371	3.37	98.19
Fruit length (mm)	0.108	0.98	99.17
Fruit Diameter (mm)	0.073	0.66	99.83
Fruit yield per plant (g)	0.018	0.17	100

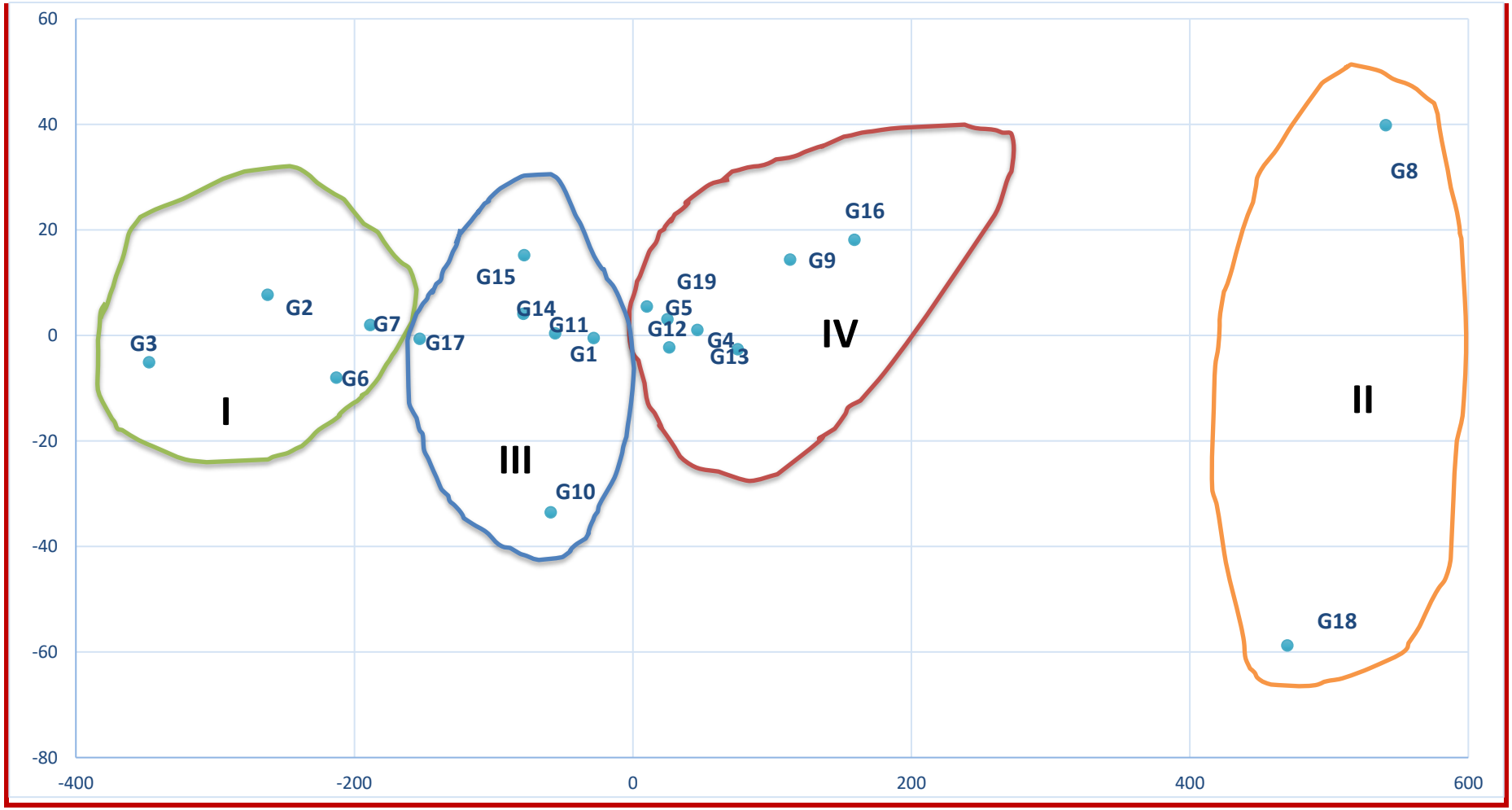

Figure 1. Cluster diagram showing genotypes grouping in different clusters of 19 genotypes of tomato

to low inter genotypic distance. The maximum intra-cluster distance was presented in cluster IV (0.938) which had seven genotypes (G4, G5, G9, G12, G13, G16 and G19). The minimum intra-cluster distance was recorded in cluster II which containing two genotypes (G8, G18) (Table 12). Khan *et al.* (2008) reported twelve clusters in tomato. Quaruzzaman *et al*. (2008) reported six clusters in tomato.

4.1.5.4 Non-hierarchical clustering

Nineteen *Solanum lycopersicum* L.genotypes were grouped into four different clusters non-hierarchical clustering (Figure 1). These results confirmed the clustering pattern of the genotypes obtained through PCA (Appendix 1). Shashikanth *et al.* (2010) reported ten clusters, Mahesha *et al.* (2006) reported nine clusters, Sharma and Verma (2001) reported five clusters in tomato. It indicated that cluster I contained four genotypes, cluster II contained two genotypes, cluster III contained six genotypes and cluster IV presented seven genotypes of tomato (Table 9). From cluster mean (Table 14), cluster II had the maximum mean value for six characters namely number of fruit per cluster (16), fruit per plant (75.17), fruit weight (23.64), fruit length (26.83 mm), fruit diameter (27.67 mm) and fruit yield per plant (1158.91 g). This cluster mean gives idea about the cluster II could be used for future hybridization program for fruit per cluster, fruit per plant, fruit weight (g), fruit length (mm), fruit diameter (mm) and fruit yield per plant (g). Cluster III had required for number of cluster per plant (9.44) and number of flower per cluster (6.67). Cluster IV had lowest mean value for days to first flower required (25.52) days, Days to maturity (78.19) days. cluster I and cluster IV had moderate mean value for all character. These genotypes of cluster could be used for future hybridization program. Singh *et al*. (2013) reported that contribution of the characters to the divergence in tomato.

Table 11. Ten highest and ten lowest inter genotypic distance among the nineteen genotypes of tomato

Highest Distance			Lowest Distance		
Genotypes		Distance	Genotypes		Distance
G2	G8	2.138	G1	G4	0.372
G3	G18	2.574	G11	G12	0.372
G3	G8	2.422	G1	G17	0.378
G2	1G8	2.395	G11	G19	0.424
G8	G18	2.383	G6	G17	0.448
G15	G18	2.346	G12	G13	0.455
G3	G9	2.324	G1	G5	0.458
G8	G10	2.243	G14	G15	0.459
G7	G18	2.173	G1	G12	0.468
G2	G9	2.164	G1	G14	0.474

Table 12. Intra (Bold) and inter cluster distances (D^2) for 19 genotypes of tomato

Cluster	I	II	III	IV
I	**2.85**	140.75	317.88	440.83
II		**0.00**	177.45	580.30
III			**3.79**	758.30
IV				**4.73**

Table 13. The nearest and farthest clusters from each cluster between D^2 values in tomato

Sl. No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	II (140.75)	IV (440.83)
2	**II**	I (140.75)	IV (580.30)
3	**III**	II (177.45)	IV (758.30)
4	**IV**	I (440.83)	III (758.30)

Table 14. Cluster mean for 11 yield and yield related characters in 19 genotypes of tomato

Characters	I	II	III	IV

Days to 1st flowering	27.25	27.17	26.94	25.52
Plant height (cm)	89.85	75.96	86.81	85.46
Days to maturity	79.5	79	77.17	78.19
No. of cluster per plant	7	9.34	9.44	8.71
Flower per cluster	5.84	5.84	6.67	6.67
No. of Fruit per cluster	4.5	16	5.39	9.71
Fruit per plant	20.17	75.17	32.17	31.76
Fruit weight (g)	19.99	23.64	20.01	23.3
Fruit Length (mm)	25.92	26.83	26.83	23.9
Fruit diameter (mm)	26.25	27.67	26.28	24.05
Fruit Yield per plant (g)	402.83	1158.91	579.82	720.39

4.1.5.5 Conical variate analysis

Conical variate analysis (CVA) was done to calculate the inter-cluster distance. Table (12) were presented intra and inter-cluster distance (D^2) values. In this study the inter-cluster distances were more than the intra-cluster distances. It proved that the wide range of genetic variability among genotypes of tomato. Intra and inter-cluster distances were indicated in (Table 12). On the basis of intra and inter cluster (D2) value, the close cluster of cluster IV was cluster I (440.83) and distant cluster was cluster III (758.30). Cluster III consists of nearest cluster with D2 values was II (177.45) and distant cluster was cluster I (317.88). In case of cluster II the nearest cluster was III (177.45) and the distant cluster was IV (440.83). In case of cluster I the nearest cluster was II (145.75) and the distant cluster was IV (440.83). With the help of D^2 values within and between clusters, an arbitrary cluster diagram (Figure 2) was constructed, which showed the relationship between different genotypes. Diagram also showed the intra and inter cluster distance of fifteen genotype of tomato. Shanmugam and Rangasamy(1982) stated that genotypes distributed in different clusters are sign of broad genetic base of diversity.

4.1.5.6 Selection of genotypes as parent for hybridization programme

Genetically dissimilar parent selection is the fundamental works for hybridization programme. So the genotypes were chosen according to specific trait, maximum heterosis could be shown in offspring from the crosses between genetically diverse parents. Based on cluster mean and agronomic performance the genotype G8 for maximum fruit weight (gm), fruit length (mm) and fruit diameter (mm), G6 for days to first flowering and plant height found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G3, G18, G2 and G8 and other improved variety and might be suggested for future hybridization program.

Figure 2. Intra and inter cluster distances (D^2) of 19 genotypes in tomato

4.2 Experiment 2: Evaluation of tomato genotypes based on nutritional traits

It comprises a brief description of nutritional traits. The nutritional traits included lycopene content, vitamin C content, pH, moisture %, dry matter %, SPAD % and brix %. This part of the chapter opened the results and their interpretation in order to, evaluation of tomato genotypes based on their nutrational traits

4.2.1 Genetic variability, heritability and genetic advance

4.2.1.1 brix %

Brix % is primarily a measure of the carbohydrate level of tomato. Significant differences were observed among the genotypes for Brix % which ranged from 2.77 (G6) to 5.23 (G9) with mean value 3.82 (Table 16). The σ^2p and σ^2g was observed 0.72 and 0.74, respectively (Table 17) with large environmental influence. The PCV (22.49) and GCV (22.17) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato. The heritability estimates for this trait was high (97.22%) with low genetic advance (1.72%) over high genetic advance in percent of mean (45.04%) (Table 17) revealed that this trait was governed by additive gene and selection is effective for % of brix content.

4.2.1.2 pH

pH is primarily a measure of the acidic level of tomato. Significant differences were observed among the genotypes for pH which ranged from 4.10 (G5) to 4.53 (G7) with mean value 4.34 (Table 16). The σ^2p and σ^2g was observed 0.02 and 0.01, respectively (Table 17). The PCV (22.49) and GCV (22.17) were close to each other, indicating high environmental influence on this character that would be effective for the improvement of tomato. The heritability estimates for this trait was moderate (41.97%) with low genetic advance (0.11%) over low genetic advance in percent of mean (2.57%) (Table 17) revealed that this trait was governed by environmental effects selection would be ineffective.

Table 15. Analysis of variance for different fruit quality characters in tomato genotypes

Characters	Mean sum of square	
	Genotype (g-1) = 18	Error (n-t) = 38
Brix%	2.173**	0.020
pH	0.031**	0.010
Lycopene (472nm)	19.558**	0.323
Lycopene (502nm)	15.471**	0.448
Vitamin C (mg/100gm)	45.770**	0.420
Moisture%	916.390**	15.684
SPAD%	75.738**	0.637
Dry matter content%	981.409**	17.316

** Denote Significant at 1% level of probability

Table 16. Mean performance of eight qualitative characters of 19 tomato genotypes

Genotypes	Brix%	pH	Lycopene (472 nm)	Lycopene (502 nm)	Vitamin C (mg/100gm)	Moisture%	SPAD%	Dry matter content%
G1	4.53	4.30	10.70	7.62	13.67	13.69	51.00	86.31
G2	2.83	4.20	15.13	12.96	9.91	32.34	48.48	67.66
G3	4.80	4.30	7.54	4.72	17.44	36.95	44.62	63.05
G4	4.47	4.27	6.55	4.99	20.25	54.19	54.72	45.81
G5	4.70	4.10	9.83	7.95	19.84	37.24	48.55	75.40
G6	2.77	4.37	12.51	10.96	9.91	69.30	40.56	30.70
G7	4.60	4.53	9.22	7.90	10.80	65.57	43.62	34.42
G8	4.73	4.43	8.15	6.86	11.49	29.34	52.66	70.66
G9	5.23	4.37	7.95	6.90	15.41	35.16	38.78	64.84
G10	4.12	4.40	7.78	6.91	11.99	36.38	49.08	63.62
G11	2.77	4.33	9.03	7.94	9.70	62.52	38.72	37.48
G12	2.80	4.33	5.57	5.04	14.19	34.46	42.83	65.54
G13	2.77	4.47	9.89	8.97	13.03	33.41	43.70	66.59
BARI Hybrid 4	3.40	4.43	8.33	6.20	16.71	55.81	51.93	44.19
BARI Hybrid 5	3.73	4.30	4.20	3.86	7.25	49.38	47.63	50.62
BARI Tomato-2	4.30	4.27	5.76	4.98	8.62	80.73	47.83	19.27
BARI Tomato-3	3.50	4.27	9.63	8.75	8.14	43.44	42.97	56.56
BARI Tomato-11	2.83	4.37	5.98	4.90	17.19	73.31	54.70	26.69
BARI Tomato-15	3.70	4.43	8.13	6.97	14.74	43.49	50.73	56.51
Min	**2.77**	**4.10**	**4.20**	**3.86**	**7.25**	**13.69**	**38.72**	**19.27**
Max	**5.23**	**4.53**	**15.13**	**12.96**	**20.25**	**80.73**	**54.72**	**86.31**
Mean	**3.82**	**4.34**	**8.52**	**7.13**	**13.17**	**46.67**	**47.01**	**54.00**

Table 17. Estimation of genetic parameters for eight qualitative characters in tomato

Parameters	Mean	σ^2p	σ^2g	$\sigma^2 e$	PCV	GCV	ECV	Heritability	GA (5%)	GAM	CV (%)
Brix%	3.82	0.74	0.72	0.02	22.49	22.17	3.75	97.22	1.72	45.04	3.75
pH	4.34	0.02	0.01	0.01	2.97	1.92	2.26	41.97	0.11	2.57	2.26
Lycopene (472nm)	8.52	6.73	6.41	0.32	30.46	29.72	6.67	95.20	5.09	59.74	6.67
Lycopene (502nm)	7.13	5.46	5.01	0.45	32.78	31.41	9.39	91.79	4.42	61.98	9.39
Vitamin C (mg/100gm)	13.17	15.54	15.12	0.42	29.93	29.52	4.92	97.29	7.90	59.98	4.92
Moisture%	46.67	315.92	300.24	15.68	38.09	37.13	8.49	95.04	34.80	74.56	8.49
SPAD%	47.01	25.67	25.03	0.64	10.78	10.64	1.70	97.52	10.18	21.65	1.70
Dry matter content%	54.00	338.68	321.36	17.32	34.08	33.20	7.71	94.89	35.97	66.62	7.71

σ^2p: Phenotypic variance
σ^2g: Genotypic variance
σ^2e: Environmental variance

PCV: Phenotypic coefficient of variation
GCV: Genotypic coefficient of variation
ECV: Environmental coefficient of variation

GA (5%): Genetic advance
GAM: Genetic advance (% of mean)
CV (%) = coefficient of variation

4.2.1.3 Lycopene

The lycopene was extracted from ripe tomatoes using the method by Alda *et al*.(2009). Significant differences were observed among the genotypes for lycopene which ranged from 4.20 mg (BARI Hybrid 5) to 15.13 mg (G2) with mean value 8.52 mg (Table 16) in case of 472 nm. In case of 502 nm highest lycopene content of fruit was observed in genotype BARI Hybrid 5 (12.96 mg) and the lowest was observed in the genotype G2 (3.86 mg) (Table 17). The σ^2p and σ^2g was observed 6.73 and 6.41, respectively (Table 17). The PCV (30.46) and GCV of variation (29.72) were close to each other, indicating high environmental influence on this character that would be effective for the improvement of tomato in case of 472 nm. The σ^2p and σ^2g was observed 5.46 and 5.01, respectively (Table 17). The PCV (32.78) and GCV (31.41) were close to each other, indicating high environmental influence on this character that would be effective for the improvement of tomato in case of 502 nm. The heritability estimates for this trait was High (95.20%) with low genetic advance (5.09%) over high genetic advance in percent of mean (59.74%) in case of 472 nm (Table 17). The heritability estimates for this trait was High (91.79%) with low genetic advance (4.42%) over high genetic advance in percent of mean (61.98%) in case of 502 nm (Table 14) revealed that this trait was governed by additive gene selection would be effective.The variation in lycopene content is presented in genotypes. Colour of fruit is an important quality parameter both for table purpose and processing varieties. Potaczek and Michalik (1998) have observed that environmental factors especially temperature and light intensity exerted a great influence on lycopene level than on carotene contents in tomato fruits. Red-fruiting cultivars also have higher lycopene content than yellow, orange and black- fruiting cultivars (Cox *et al.*, 2003).

4.2.1.4 Vitamin C (mg/100 gm)

The studied genotypes showed significant difference in case of Vitamin C content (Table 13). Maximum was found 20.25 mg in (BARI Hybrid 5) and the minimum was recorded 7.25 in (G4) with mean value 13.17 (Table 16). The σ^2g

(15.12) was lower than σ^2p (15.54). GCV (29.52) and PCV (29.93) were also close to each other (Table 17) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (97.29%) with low genetic advance (7.90%) over high genetic advance in percent of mean (59.98%) (Table 17) revealed that this trait was governed by additive gene and selection is effective for vitamin C content.

4.2.1.5 Moisture %

Significant differences were observed among the genotypes for moisture % which ranged from 13.69 (G1) to 80.73 (BARI Tomato-2) with mean value 46.67 (Table 16). The σ^2p and σ^2g was observed 315.92 and 300.24, respectively (Table 17) with large environmental influence. The PCV (38.09) and GCV (37.13) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato. The heritability estimates for this trait was high (95.04%) with high genetic advance (34.80%) over high genetic advance in percent of mean (74.56%) (Table 17) revealed that this trait was governed by additive gene and selection is effective for moisture %.

4.2.1.6 SPAD %

Significant differences were observed among the genotypes for SPAD % which ranged from 38.72 (G11) to 54.72 (G4) with mean value 47.01 (Table 16). The σ^2p and σ^2g was observed 25.67 and 25.03, respectively (Table 17) with large environmental influence. The PCV (10.78) and GCV (10.64) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato. The heritability estimates for this trait was high (97.52%) with low genetic advance (10.18%) over moderate genetic advance in percent of mean (74.56%) (Table 17) revealed that this trait exhibited due to favorable influence of environment rather than genotype and selection for this trait may not be rewarding.

4.2.1.7 Dry matter content %

Significant differences were observed among the genotypes for dry matter content % which ranged from 19.27 (BARI Tomato-2) to 86.31 (G1) with mean value 54.00 (Table 16). The σ^2p and σ^2g was observed 338.8 and 321.36, respectively (Table 17) with large environmental influence. The PCV (34.08) and GCV (33.20) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato. The heritability estimates for this trait was high (94.89%) with high genetic advance (35.97%) over high genetic advance in percent of mean (66.62%) (Table 17) revealed that this trait was governed by additive gene and selection is effective for % of brix content.

4.2.2 Correlation coefficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by (Singh and Chaudhary, 1985). As we know yield is a complex product being influence by several inter-dependable quantitative characters. Therefore, selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence, knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). Phenotypic and genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of tomato are given in Table18 and Table 19.

4.2.2.1 Brix %

Brix % had significant positive correlation with vitamin C content at phenotypic (0.309) and genotypic level (0.292) (Table 19). It had also positive correlation with dry matter content at phenotypic (0.294) and genotypic (0.284) level. It had negatively significant correlation with moisture % at phenotypic (-0.262) and genotypic (-0.254). It had also negative significant correlation with lycopene content at phenotypic (-0.342) and genotypic (-0.336) level in case of 502 nm. Brix % had positive but non-significant correlation with SPAD %. This trait had non-significant negative correlation at both levels for pH, lycopene content inn case of 472 nm.

4.2.2.2 pH

pH had significant negative correlation dry matter content % at phenotypic (-0.294) level (Table 19). It had positive but non-significant correlation with moisture %. This trait had non-significant negative correlation at both levels for lycopene content in case of (472 nm and 502nm), vitamin C content and SPAD %.

4.2.2.3 Lycopene content

Lycopene content in case of 472 nm had highly significant positive correlation with lycopene content in case of 502 nm both at genotypic (0.975) and phenotypic (0.933) level. It had also positive significant correlation with dry matter content % both at genotypic (0.278) and phenotypic (0.268) level (Table 19). Lycopene content in case of 472 nm had negative but non-significant correlation with vitamin C content, moisture % and SPAD %.

Lycopene content in case of 502 nm had significant negative correlation with vitamin C content both at genotypic (-0.315) and phenotypic (-0.302) level. It had also negative significant correlation with SPAD % both at genotypic (-0.309) and phenotypic (-0.304) level (Table 19). Lycopene content in case of 502 nm had negative but non-significant correlation with moisture % and dry matter content %.

Table 18. Pearson correlation coefficient for different traits

Traits	Brix	pH	Lycopene (472 nm)	Lycopene (502 nm)	Vitamin C (mg/100gm)	Moisture	SPAD	Dry matter content
Brix	1							
pH	-0.082	1						
Lycopene (472 nm)	-0.213	-0.097	1					
Lycopene (502 nm)	-0.334*	0.004	0.918**	1				
Vitamin C (mg/100gm)	0.291*	-0.122	-0.156	-0.287*	1			
Moisture	-0.250	0.109	-0.254	-0.166	-0.166	1		
SPAD	0.147	-0.033	-0.200	-0.272*	0.402**	-0.044	1	
Dry matter content	0.283*	-0.160	0.267*	0.187	0.224	-0.935**	0.060	1

*p<0.05, **p<0.01

Table 19. Genotypic (G) and phenotypic (P) correlations among different pairs of qualitative traits for different genotype of tomato

Traits		pH	Lycopene (472 nm)	Lycopene (502 nm)	Vitamin C (mg/100gm)	Moisture%	SPAD%	Dry matter content %
Brix%	G	-0.091	-0.228	-0.342*	0.309*	-0.262*	0.152	0.294*
	P	-0.078	-0.212	-0.336*	0.292*	-0.254*	0.151	0.284*
pH	G		-0.163	-0.105	-0.163	0.162	-0.096	-0.273*
	P		-0.106	-0.045	-0.134	0.108	-0.058	-0.170
Lycopene (472 nm)	G			0.975**	-0.157	-0.266*	-0.205	0.278*
	P			0.933**	-0.158	-0.259*	-0.205	0.268*
Lycopene (502 nm)	G				-0.315*	-0.182	-0.309*	0.192
	P				-0.302*	-0.180	-0.304*	0.186
Vitamin C (mg/100gm)	G					-0.173	0.406**	0.234
	P					-0.167	0.401**	0.227
Moisture%	G						-0.048	-0.995**
	P						-0.049	-0.972**
SPAD%	G							0.059
	P							0.057

*p<0.05, **p<0.01

4.2.2.4 Vitamin C

Vitamin C had highly significant positive correlation with SPAD % both at phenotypic (0.406) level and genotypic (0.401) level (Table 19). It had positive but non-significant correlation with dry matter content %. This trait had non-significant negative correlation at both levels for moisture %.

4.2.2.5 SPAD %

This trait had non-significant negative correlation at both levels for dry matter % (Table 19)

4.2.3 Path coefficient analysis

Though correlation analysis indicates the association pattern of components traits with yield, they simply represent the overall influence of a particular trait on yield rather than providing cause and effect relationship. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

In path coefficient analysis the direct effect of a trait dry matter content % of plant and its indirect effect through other characters were computed and the results are presented in (Table 20).

4.2.3.1 Brix content %

Brix content % had positive direct effect (0.0690) on dry matter content % (Table 20) which is contributed to result significant positive genotypic correlation with dry matter content % (0.294). It had positive indirect effect on pH (0.0047), lycopene content 472 nm (0.0230), vitamin C content (0.0244), moisture %

(0.2233) and SPAD % (0006). Negative indirect effect was also found on lycopene content 502nm (-0.0625).

4.2.3.2 pH

pH had negative direct effect (-0.0570) on dry matter content % (Table 20) which is contributed to result significant negative genotypic correlation with dry matter content % (-0.273). It had positive indirect effect on lycopene content 472 nm (0.0105), lycopene content 502 nm (0.0007). Negative indirect effect was also found on Brix % (-0.0057), vitamin C content (-0.0102), moisture % (-0.0973) and SPAD % (-0.0001).

4.2.3.3 Lycopene content 472 nm

Lycopene content 472 nm had negative direct effect (-0.1080) on dry matter content % (Table 20) which is contributed to result significant positive genotypic correlation with dry matter content % (0.278). It had positive indirect effect on pH (0.0055) lycopene content 502 nm (0.1717), moisture % (0.2268). Negative indirect effect was also found on Brix % (-0.0147), vitamin C content (-0.0131) and SPAD % (-0.0008).

4.2.3.4 Lycopene content 502 nm

Lycopene content 502 nm had positive direct effect (0.1870) on dry matter content % (Table 20) which is contributed to result non-significant positive genotypic correlation with dry matter content % (0.192). It had positive indirect effect on moisture % (0.1482). Negative indirect effect was also found on Brix % (-0.0230), pH (-0.0002) lycopene content 472 nm (-0.0991), vitamin C content (-0.0241) and SPAD % (-0.0011).

Table 20. Path analysis showing direct (bold) and indirect effects of ten traits by path analysis of tomato

Traits	Brix	pH	Lycopene (472 nm)	Lycopene (502 nm)	Vitamin C (mg/100gm)	Moisture	SPAD	Genotypic correlation with Dry matter content %
Brix	**0.0690**	0.0047	0.0230	-0.0625	0.0244	0.2233	0.0006	0.294
pH	-0.0057	**-0.0570**	0.0105	0.0007	-0.0102	-0.0973	-0.0001	-0.273
Lycopene (472 nm)	-0.0147	0.0055	**-0.1080**	0.1717	-0.0131	0.2268	-0.0008	0.278
Lycopene (502 nm)	-0.0230	-0.0002	-0.0991	**0.1870**	-0.0241	0.1482	-0.0011	0.192
Vitamin C (mg/100gm)	0.0201	0.0070	0.0168	-0.0537	**0.0840**	0.1482	0.0016	0.234
Moisture	-0.0173	-0.0062	0.0274	-0.0310	-0.0139	**-0.8930**	-0.0002	0.995
SPAD	0.0101	0.0019	0.0216	-0.0509	0.0338	0.0393	**0.0040**	0.059

Residual effect: 0.333 ** = Significant at 1%. * = Significant at 5%.

4.2.3.5 Vitamin C (mg/100gm)

Vitamin C (mg/100gm) had positive direct effect (0.0840) on dry matter content % (Table 20) which is contributed to result non-significant positive genotypic correlation with dry matter content % (0.234). It had positive indirect effect on Brix % (0.0201), pH (0.0070) lycopene content 472 nm (0.0168), moisture % (0.1482) and SPAD % (0.0016). Negative indirect effect was also found on lycopene content 502 nm (-0.0537).

4.2.3.6 Moisture %

Moisture % had negative direct effect (-0.8930) on dry matter content % (Table 20) which is contributed to highly significant negative result on genotypic correlation with dry matter content % (-0.995). It had positive indirect effect on lycopene 472 nm (0.0274). Negative indirect effect was also found on Brix % (-0.0173), pH (-0.0062) lycopene content 502 nm (-0.0310), vitamin C content (-0.0139) and SPAD % (-0.0002).

4.2.3.7 SPAD %

SPAD % had positive direct effect (0.0040) on dry matter content % (Table 20) which is contributed to result non-significant positive genotypic correlation with dry matter content % (0.059). It had positive indirect effect on Brix % (0.0101), pH (0.0019) lycopene content 472 nm (0.0216), vitamin C content (0.0338) and moisture % (0.0393). Negative indirect effect was also found on lycopene content 502 nm (-0.0509).

4.2.4 Genetic diversity:

The knowledge of available genetic diversity is an important factor for any heritable improvement and its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. There is still much scope for improving of genetic architecture desirable for hybrid through heterosis breeding. Its magnitude in desirable direction is preferable. The success

of hybridization depends upon the selection of suitable parental genotypes and performance of their cross combinations.

The amount of diversity available in the crop decides the success of any crop improvement programme with manifested objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. In the present investigation, 19 genotypes of tomato were considered for the assessments of genetic diversity by multivariate analysis as per Mahalanbis's (1936) concept of generalize distance D^2 considering eight important qualitative characters. Based on value, the genotypes were grouped in four cluster (Table 21)

4.2.4.1 Nonhierarchical clustering

Nineteen *Solanum lycopersicum* L. Genotypes were grouped into four different clusters through non-hierarchical clustering (Table 21). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Cluster II had highest number of eight genotypes followed by cluster III and cluster IV constituted by five genotypes, respectively. On the other hand, cluster I constituted by one genotypes G1. Cluster II had maximum eight genotypes namely G2, G3, G5, G8, G9, G10, G12 and G13. Cluster III represents 5 genotypes namely G4, G14, G15, G17 and G19. Last of all, cluster IV had 5 genotypes G6, G7, G11, G16 and G18. The results confirmed the clustering pattern of the genotypes according to the principal component analysis. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. For that reason it can be said that the results obtained through PCA were established by nonhierarchical clustering. Clustering pattern of 19 genotypes of tomato is presented in Figure 3.

Table 21. Distribution of 19 genotypes in different clusters

Cluster no.	Genotypes	No. of populations	Name of Genotypes
I	G1	1	SL-006
II	G2, G3, G5, G8, G9, G10, G12, G13	8	SL-007, SL-008, SL-010, SL-013, SL-014, SL-015, SL-017, SL-018
III	G4, G14, G15, G17, G19	5	SL-009, BARI Hybrid 4, BARI Hybrid 5, BARI Tomato-3, BARI Tomato-15
IV	G6, G7, G11, G16, G18	5	SL-011, SL-012, SL-016 BARI Tomato-2, BARI Tomato-11
Total		19	

Table 22. Eigen values and yield percent contribution of eight characters of 19 genotype

Principal component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	2.517	31.46	31.46
II	2.336	29.20	60.66
III	1.049	13.11	73.77
IV	0.859	10.73	84.50
V	0.660	8.25	92.75
VI	0.551	6.89	99.64
VII	0.023	0.29	99.93
VIII	0.005	0.07	100

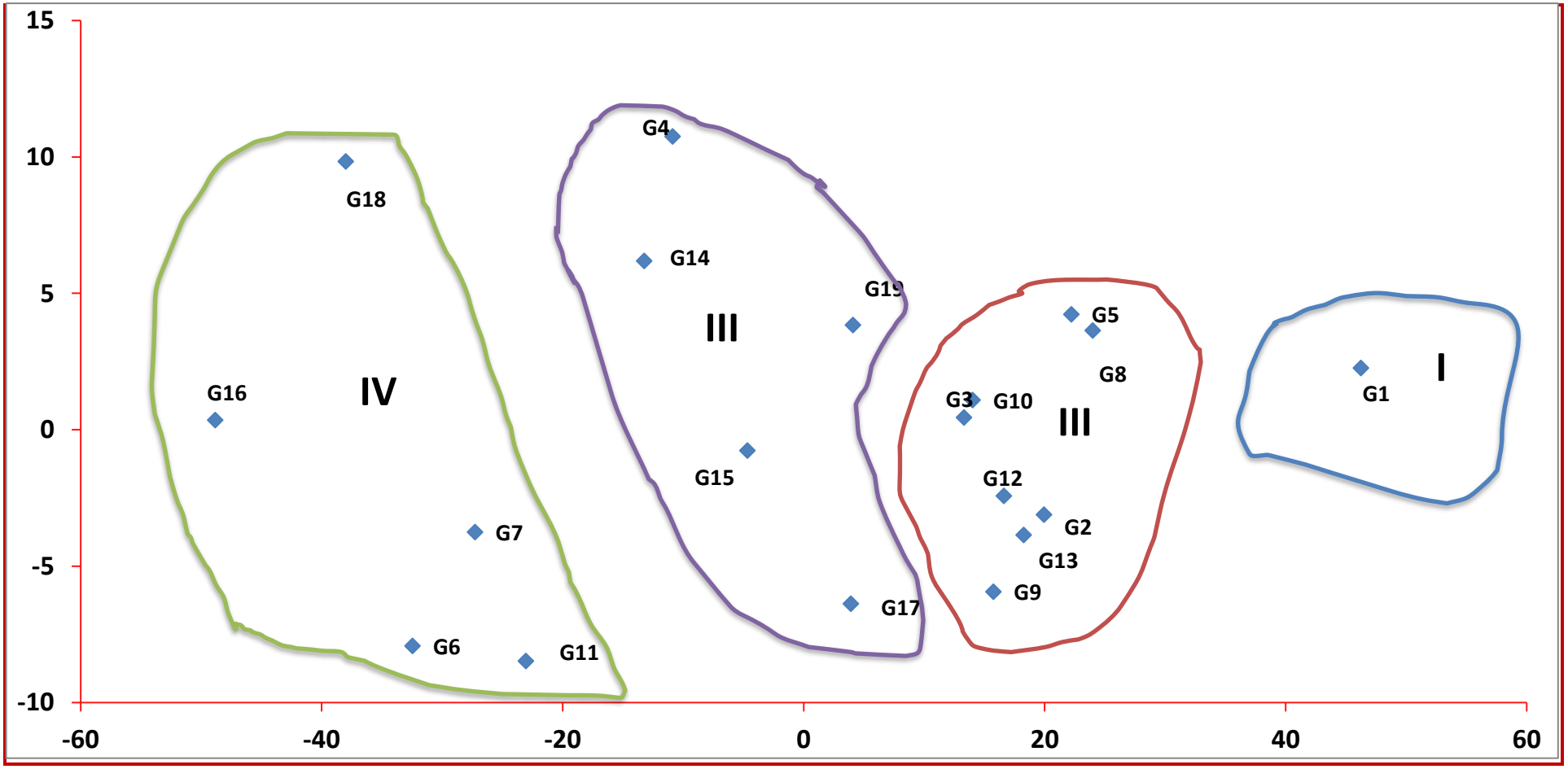

Figure 3. Cluster diagram-showing genotypes grouping in different clusters of 19 genotypes of tomato

4.2.4.2 Principal component analysis (PCA)

Principal component analysis was carried out with nineteen genotypes of tomato, which gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes. First four Eigen values for four principal coordination axes of genotypes accounted for 84.5% variation showed in (Table 22). Based on principal component scores I and II obtained from the Principal component analysis (Appendix V), a two-dimensional scatter diagram (Z1-Z2) using component score I as X axis and component score II as Y axis was Constructed, which has been presented in Figure 3. The scatter diagram revealed that there were four apparent clusters. The genotypes were distantly located from each other, which indicated that considerable diversity existed among the genotypes.

4.2.4.3 Canonical variate analysis

Canonical Variate Analysis (CVA) was done to compute the inter-cluster distances. The intra and inter-cluster distance (D^2) values were shown in (Table 23). In this experiment, the inter-cluster distances were higher than the intra-cluster distances thus indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between clusters I and IV (16.462), followed by between clusters I and III (10.286), II and IV (9.906). In contrast, the lowest inter-cluster distance was observed between cluster II and III (3.660).

However, the maximum inter-cluster distance was observed between the clusters I and IV (16.462) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of segregating population. On the other hand, the minimum intra-cluster distance was found in cluster II (7.125), which contained of 8 genotypes, while the minimum distance was found in cluster I (0.79)

Table 23. Intra (Bold) and inter cluster distances (D^2) for 19 genotypes

Cluster	I	II	III	IV
I	**0.00**	7.125	10.286	16.462
II		**0.34**	3.660	9.906
III			**0.87**	6.476
IV				**2.23**

Table 24. The nearest and farthest clusters from each cluster between D^2 values in tomato

Sl. No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	II (7.125)	IV (16.462)
2	**II**	III (3.660)	IV (9.906)
3	**III**	II (3.660)	I (10.286)
4	**IV**	III (6.476)	I (16.462)

that comprises 5 genotypes. Inter and intra cluster distances were showed in (Table 23). Cluster I consists of nearest cluster with D^2 values cluster II (7.125) and farthest cluster with D^2 values IV (16.462) (Table 24). Cluster II consists of nearest cluster with D^2 values cluster III (3.660) and farthest cluster with D^2 values IV (9.906). Cluster III consists of nearest cluster with D^2 values cluster II (3.660) and farthest cluster with D^2 values I (10.286). Cluster IV consists of nearest cluster with D^2 values cluster III (6.476) and farthest cluster with D^2 values I (16.462). A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, showing in the relative position. According to scatter diagram all the genotypes were apparently distributed into four clusters (Figure 3). It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. Furthermore, for a practical plant breeder, the objective is to achieve high-level production in addition to high heterosis. In the present, study the maximum distance existence between cluster I and IV. Therefore, the crosses between the genotypes belonging cluster I with cluster IV might produce high heterosis. In addition, the crosses between genotypes from cluster I with IV might produce high level of segregating population. So the genotypes belonging to cluster I and cluster IV might be selected for future hybridization program.

4.2.4.4 Cluster mean analysis

The cluster means of 8 different characters (Table 25) were compared and indicated considerable differences between clusters for all the characters studied. Maximum brix % were observed in cluster I (4.53), whereas minimum brix % in cluster IV (3.45). Then maximum pH were observed in IV (4.37) whereas minimum plant height were observed in cluster I (4.30). Lycopene content at 472 nm was observed in cluster I (10.70) and minimum (7.37) in cluster III. Lycopene content at 502 nm was observed maximum in cluster I (7.62) and minimum to cluster III (6.15). Cluster II showed highest vitamin C content (14.16) and cluster IV showed lowest (11.24).

Table 25. Cluster mean for eight qualitative trait in 19 tomato genotypes

Characters	I	II	III	IV
Brix%	4.53	4.00	3.76	3.45
pH	4.30	4.33	4.34	4.37
Lycopene (472nm)	10.70	8.98	7.37	8.50
Lycopene (502nm)	7.62	7.54	6.15	7.34
Vitamin C (mg/100gm)	13.67	14.16	13.42	11.24
Moisture%	13.69	34.41	49.26	70.29
SPAD%	51.00	46.09	49.60	45.09
Dry matter content%	86.31	67.17	50.74	29.71

Maximum (70.29) and minimum (13.69) moisture % were observed in cluster IV and I, respectively. Maximum SPAD % was observed in cluster I (51.00), whereas minimum SPAD % was observed in cluster IV (45.09). Maximum (86.31) and minimum (29.71) dry matter content % were observed in cluster I and IV, respectively. Cluster I has late flowering, maximum plant height, maximum number of main branches, maximum number of leaf and leaf area index, maximum number of pod and highest yield among the genotypes studied. Again, cluster II was matured early, lowest leaf area index and minimum number of flower per plant. The genotypes belonging to the cluster III were minimum of yield and pod length. To develop high yielding varieties these groups can be used in hybridization program.

4.2.4.5 Contribution of characters towards divergence of the genotypes

Contribution of characters towards the divergence obtained from canonical variate analysis is presented in (Table 26). In this method vectors was calculated to represent the varieties in the graphical form (Rao, 1952). This is helpful in cluster analysis as it facilitated the study of group constellation and also serves as a pictorial representation of the configuration of various groups.

The latent vectors (Z_1 and Z_2) obtained from principal component analysis (PCA) (Appendix V). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z_1) were pH (4.9332), lycopene content 502 nm (0.4520), moisture % (0.134) and dry matter % (0.0817), leaf area index (33.087), number of flower per plant (0.107) and yield (1.512). These characters were important because all these characters had positive signs in first axis. Brix % (0.2350), lycopene content at 502 nm (2.1923) and vitamin C content (0.2587) had positive sign in vector II (Z2), second axis of differentiation. On the other hand, brix %, lycopene content at 472 nm, vitamin C content and SPAD % possessed the negative sign in the first axis of differentiation and pH, lycopene content at 472 nm, moisture %, SPAD %, and dry matter % possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence. Lycopene content at 502 nm had positive sign in both the.

Table 26. Relative contributions of the eleven characters of 19 varieties to the total divergence

Characters	Principal Component	
	Vector-1	**Vector-2**
Brix%	-0.1326	0.2350
pH	4.9332	-1.7909
Lycopene (472nm)	-0.2606	-1.9205
Lycopene (502nm)	0.4520	2.1923
Vitamin C (mg/100gm)	-0.0648	0.2587
Moisture%	0.3436	-0.0373
SPAD%	-0.0644	-0.0505
Dry matter content%	0.0817	-0.0249

axis, which indicated that they were the important component characters having higher contribution to genetic divergence among the genotypes studied

4.2.4.7 Selection of genotypes as parent for hybridization program

Selection of genetically diverse parents is an urgent step for hybridization program. Therefore, in the present study genotypes were to be selected on the basis of specific objectives. From the crosses between genetically distance parents, a high heterosis could be produced. Considering the magnitude of cluster mean and qualitative performance the genotype G1 for brix % from cluster I; for maximum lycopene content G1 from cluster I and G2 from cluster II, G4 and G5 for vitamin C content from cluster II and Cluster III were found promising. Therefore considering group distance and other qualitative performance the inter-genotypic crosses might be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The present study was undertaken at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207, Bangladesh with nineteen genotypes of tomato *(Solanum lycopersicum* L.) during November 2016 to April 2017. Seeds were sown in seedbed then transferred to the main field in Randomized Complete Block Design (RCBD) with three replications. Data on various agromorphogenic traits such as, days to first flowering, plant height, days to maturity, (cm), number of cluster per plant, number of flower per cluster, number of fruit per cluster, number of fruit per plant, fruit weight (g) fruit length (mm), fruit diameter (mm), yield per plant (g). Data on various qualitative traits such as brix %, pH, lycopene content at 472 nm, lycopene content at 502 nm, vitamin C content, moisture %, SPAD %. Dry matter content %. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

The analysis of variances showed significant mean squares for different characters indicated the presence of sufficient variation among the genotypes for all the characters. The number of fruit yield per plant showed highest range of variation in agromorphogenic traits (1196.70-308.47) that means wide range of variation present for this character. The dry matter content % showed highest range of variation in qualitative traits (981.409-17.316) that means wide range of variation present for this character.

In case of days to days to first flowering, days to maturity, flower per cluster, fruit length (mm) and fruit diameter (mm) showed higher influence of environment for the expression of these characters. On the other hand, plant height, number of fruit per cluster, fruit weight (gm), fruit yield per plant (gm) diameter showed least difference in phenotypic and genotypic variance suggesting additive gene action for the expression of the characters. In case of qualitative traits pH and SPAD % showed higher influence of environment for the expression of these characters. Instead brix %, lycopene content, vitamin C,

Moisture % and dry matter content % showed least difference in phenotypic and genotypic variance suggesting additive gene action for the expression of the characters. All the characters under the present study exhibit the highest value of heritability.

Correlation coefficients among the characters were studied to define the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study. In case of agromorphogenic traits, the highly significant positive correlation with no. of fruit per cluster, no. of fruit per plant at genotypic and phenotypic level. In addition, there were non-significant positive correlation with no. of cluster per plant, flower per cluster, fruit length, and fruit diameter at genotypic and phenotypic level, respectively. On the other hand, the non-significant negative correlation with days of first flowering, plant height, and days to maturity was also found in at genotypic and phenotypic level, respectively. In case of qualitative traits, positive significant correlation was found in brix % and lycopene content at 472nm at both level. Negative highly significant correlation was revealed in moisture %, pH at genotypic and phenotypic level. There were non-significant positive correlation was found in lycopene content at 502nm, vitamin C content and SPAD % at both level.

Path coefficient analysis showed that no. of fruit per plant had the positive correlation with fruit yield per plant. Coherently, this trait contributes to the yield through direct effect (1.0990) indicating selection will be judicious and more effective for these characters in future breeding program. Days to first flowering, plant height, number of cluster per plant and number of fruit per cluster had negative direct effect with fruit yield per plant. No. of fruit per cluster had negative direct effect on yield (-0.0040)) and it had a positive correlation to fruit yield per plant as (0.536). Positive direct effect was also found in PH, CPP, FPC, FW and FL. In case of qualitative traits, moisture % had direct negative effect (-

.8930) on dry matter content % and had highly significant negative relation at genotypic level (-0.995). There were also some traits had direct negative effect on dry matter content % such as lycopene content at 472 nm, pH. Positive direct effect was also found in brix %, vitamin C content, lycopene content at 502 nm and SPAD %.

Genetic diversity among tomato genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. The first five principal component axes accounted for 84.35% variation towards the divergence in agromorphogenic traits and 92.75% in qualitative traits. In agromorphogenic traits among four clusters cluster IV contained maximum number of genotypes seven while cluster II had only two genotypes. On the other hand, four cluster were also obtained in qualitative traits, where cluster II contained eight genotypes whereas cluster I contained single genotypes. According to PCA, D^2 and cluster analysis, the genotypes grouped into four divergent clusters obtained from principal component scores. In agromorphogenic traits the highest inter-cluster distance was observed between clusters IV and III (758.30) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster I and II (140.75). In qualitative traits the highest inter cluster distance was observed between clusters IV AND III. On the other hand, for agromorphogenic traits the maximum intra-cluster distance was found in cluster IV (4.73), which contained of seven genotypes, whereas the minimum distance was found in cluster II (0.00) that comprises 2 genotype. Whereas cluster IV (2.23) containing eight genotypes and cluster I (0.00) containing one genotype have maximum and minimum intra-cluster distance respectfully. Therefore, in agromorphogenic traits crossing between the genotypes belonging cluster I with cluster IV, cluster II with cluster I, cluster III with cluster IV and cluster I with cluster IV might produce high heterosis in respect of yield, single fruit weight and higher number of fruit per plant. In addition, the crosses between genotypes

from cluster IV with cluster III might produce high level of segregating population. Therefore, the genotypes belonging to cluster I and cluster IV, cluster II and cluster I, cluster III and cluster IV and cluster IV and cluster I have been selected for future hybridization program. In case of qualitative traits crossing between cluster IV with I, II with IV, III with I and IV with I produce high heterosis in respect of Brix %, lycopene content, vitamin C content. Considering the magnitude of cluster mean and agromorphogenic performance the genotype G8 for fruits per plant, fruit weight, fruit yield per plant and G18 for maximum fruit per plant, fruit weight, fruit diameter, fruit yield per plant found promising. In case of qualitative traits G2 for lycopene content, G4 for maximum vitamin C content, G1 for dry matter % and G9 for maximum % Brix content were found promising. Therefore, considering group distance and other agronomic performance the inter-genotypic crosses between G8, G18, G9, G2, G1 and G18 and also other improved variety and/or high yielding variety might be suggested for future hybridization program.

In qualitative traits, lycopene content of samples from nineteen genotype, G2 showed very high lycopene content at 472 nm as compared to those of the other genotypes. Significant genotypic variation for Vitamin C was observed among the nineteen genotypes of tomato. G4 (20.25 mg/100g) and G5 (19.84 mg/100g) genotypes having very high Vitamin C content indicated that they could be recommend to the farmers for cultivation and could be used for future breeding program for nutrition and for protection of various diseases. G9 contained high brix percentage and it could be recommended for high Brix percentage. From the findings of the present study, the following conclusions could be drawn:

i. Technique of selection would be applied for desired characters such as lowest days to first flowering and increase number of clusters per plant, number of fruits per cluster, number of fruits per plant, fruit weight, fruit diameter, biochemical properties to develop high yielding varieties.

ii. Genetic diversity existed at wide range among the tomato genotypes. That variability could be used for future breeding programme of tomato in Bangladesh.

iii. Comparatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

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APPENDICES

Appendix I. Map showing the experimental site under the study

The experimental site under study

Appendix II. Monthly average Temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2016 to February, 2017.

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (h)
	Maximum	Minimum			
November, 2016	34.8	18.0	77	227	5.8
December, 2016	32.3	16.3	69	0	7.9
January, 2017	29.0	13.0	79	0	3.9
February, 2017	28.1	11.1	72	1	5.7

Source: Bangladesh Meteorological Department (Climate and Weather Division), Agargoan, Dhaka - 1212

Appendix III. Morphological, physical and chemical characteristics of initial soil (0- 15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data
1	Organic carbon (%)	0.82
2	Total N (kg/ha)	1790.00
3	Total S (ppm)	225.00
4	Total P (ppm)	840.00
5	Available N (kg/ha)	54.00
6	Available P (kg/ha)	69.00
7	Exchangeable K (kg/ha)	89.50
8	Available S (ppm)	16.00
9	pH (1:2.5 soil to water)	5.55
10	CEC	11.23

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix IV. Z1-Z2 score of agromorphogenic traits of 19 genotypes of tomato

Genotypes	PCA 1	PCA 2
G1	-28.12	-0.50
G2	-262.44	7.71
G3	-347.59	-5.06
G4	75.22	-2.59
G5	9.96	5.48
G6	-213.00	-7.99
G7	-188.60	1.97
G8	540.72	39.83
G9	112.82	14.38
G10	-59.15	-33.54
G11	-55.80	0.41
G12	26.05	-2.27
G13	46.21	1.05
G14	-78.65	4.08
G15	-78.14	15.22
G16	159.02	18.12
G17	-153.19	-0.66
G18	469.95	-58.73
G19	24.72	3.08

Appendix V. Z1-Z2 score of qualitative traits of 19 genotypes of tomato

Genotypes	PCA 1	PCA 2
G1	46.24	2.26
G2	19.94	-3.11
G3	13.30	0.45
G4	-10.87	10.75
G5	22.21	4.23
G6	-32.45	-7.92
G7	-27.26	-3.75
G8	24.00	3.64
G9	15.75	-5.94
G10	14.02	1.09
G11	-23.05	-8.48
G12	16.62	-2.42
G13	18.27	-3.86
G14	-13.24	6.19
G15	-4.67	-0.76
G16	-48.83	0.35
G17	3.93	-6.38
G18	-38.00	9.84
G19	4.09	3.84

Appendix VI

Experiment in the field of Sher-e-Bangla Agricultural University

A close view of the research field