GENETIC VARIABILITY FOR MORPHO-AGRONOMIC AND NUTRITIONAL TRAITS IN TOMATO (*Solanum lycopersicum* L.)

BY

INEEN NAYEEM FIMA

REGISTRATION NO. 07-02545

A Thesis
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

SEMESTER: JULY-DECEMBER, 2013

Approved by:

Naheed Zeba

(Dr. Naheed Zeba)
Professor
Supervisor

(Dr. Md. Sarowar Hossain)
Professor
Co-supervisor

(Dr. Md. Sarowar Hossain)
Chairman
Examination Committee

Prof. Dr. Naheed Zeba
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Mob: +8801913091772
e-mail: naheed0359@hotmail.com

CERTIFICATE

This is to certify that thesis entitled, " ***GENETIC VARIABILITY FOR MORPHO-AGRONOMIC AND NUTRITIONAL 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* ***INEEN NAYEEM FIMA,*** *Registration No.* ***07-02545*** *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 duly been acknowledged.

Naheed Zeba

Dated: December, 2013
Place: Dhaka, Bangladesh

(Prof. Dr. Naheed Zeba)
Supervisor


DEDICATED TO
MY
BELOVED PARENTS

ACKNOWLEDGEMENTS

At first I express my best gratitude to Almightly Allah for his never-ending blessing to complete this work successfully. It is a great pleasure to express profound gratitude to my respected parents, who entiled much hardship inspiring for prosecuting my studies, thereby receiving proper education.

I would like to to express my earnest respect, sincere appreciation and enormous thankfulness to my reverend supervisor, Prof. Dr. Naheed Zeba, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for her scholastic supervision, helpful commentary and unvarying inspiration throughout the research work and preparation of the thesis.

I wish to express my gratitude and best regards to my respected Co-Supervisor and Chairman Prof. Dr. Md. Sarowar Hossain, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his continuous direction, constructive criticism, encouragement and valuable suggestions in carrying out the research work and preparation of this thesis.

I am grateful to Prof. Md. Shadat Ulla, Honourable Vice Chancellor, Sher-e-Bangla Agricultural University, Dhaka for providing me with all possible help during my studies.

It is great pleasure for me to express my sense of gratitude to the Honourable Minister of Science and Technology of People's Republic of Bangladesh to give me the opportunity of M.S. study under the National Science and Technology Scholarship.

I am also highly grateful to my honorable teachers Prof. Dr. Md. Shahidur Rashid Bhuiyan, Prof. Dr. Firoz Mahmood, Dr. Md. Ashaduzzaman Siddikee and

Dr. Md Abdur Rahim, Associate Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for their valuable teaching, direct and indirect advice, encouragement and cooperation during preparation of this thesis.

I am also thankful to my honorable teachers Prof. Dr.A.F.M. Jamal Uddin Department of Horticulture and Post Harvest Management, and Prof. Md. Kamal Uddin Ahmed, Department of Biochemistry, Sher-e-Bangla Agricultural University, for providing me Lab facilities in my biochemical research.

I feel to expresses my heartfelt thanks to all the teachers and staff of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for their valuable suggestions and encouragement during the period of the study.

I would like to thank Zahirullah who helped me with technical support to prepare this thesis paper. I also thank to my friends Momtaz Begum, Mst. Moka Shefa, Nibedita Chakma, Farzana Aktar, Afrin Aktar Faria, Takia Tanzina and my sister Ramisha Tabassum for their help and inspiration in preparing my thesis.

December, 2013 **The Author**

SAU, Dhaka

GENETIC VARIABILITY FOR MORPHO-AGRONOMIC AND NUTRITIONAL TRAITS IN TOMATO (*Solanum lycopersicum* L.)

ABSTRACT

A field experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during November 2012 to April 2013. Nineteen genotypes of tomato (*Solanum lycopersicum L.*) were studied in the present study. The objectives of the study were diversity and biochemical analysis of tomato to assess the magnitude of genetic divergence in genotypes, association among the characters and their contribution to yield and quality. The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for average fruit weight, fruit per cluster, fruit per plant and fruit yield per plant whereas days to first flowering, days to 50% flowering and days to maturity showed low GCV. High heritability with high genetic advance in percent of mean was observed for number of fruits per cluster, number of fruits per plant, average fruit weight and fruit yield per plant indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. The results obtained, showed that fruit yield per plant had high positive significant relation with fruit weight, but high negative significant relation with days to first flowering, days to maturity, number of fruit per clusters and number of fruit per plant. Days to 50% flowering, number of branches per plant, fruit weight and fruit length had high positively direct effect on yield of tomato. So, these are found to be important characters and could be used on direct selection for yield. Considering all the characters, G_4, G_6, G_9, G_{18} and G_{19} can be selected for future breeding program. Lycopene content of samples from genotype G_2, G_4, G_5, G_8 and G_{18} showed very high lycopene content at both absorbance 472 nm and 502 nm. G_1 and G_{18} genotype have very high Vitamin C content. G_5 and G_{19} genotypes having high brix content indicated that they could be recommending to the farmers for cultivation and could be used for future breeding program to obtain healthy and for protective tomatoes against diseases

TABLE OF CONTENTS

TABLE OF CONTENTS

TABLE OF CONTENTS

TABLE OF CONTENTS

TABLE OF CONTENTS

LIST OF TABLES

LIST OF PLATES

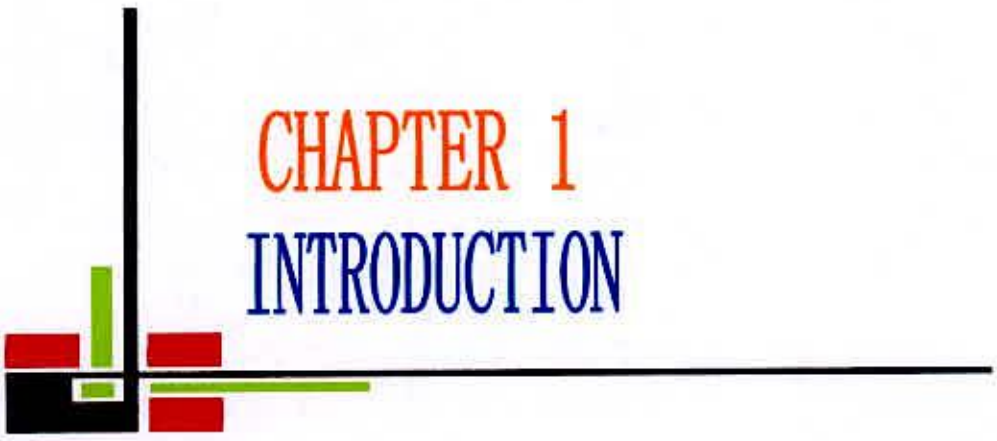
LIST OF FIGURE

LIST OF APPENDICES

LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL NAME
AEZ	Agro-Ecological Zone
Agricl.	Agricultural
et al.	And others
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co-efficient of Variation
DAS	Days After Sowing
°C	Degree Celsius
etc.	Etcetera
FAO	Food and Agriculture Organization
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
δ^2_g	Genotypic Variance
g	Gram
ha	Hectare
h^2b	Heritability in broad sense
j.	Journal
Kg	Kilogram
m	Meter
MSS	Mean Sum of Square
mm	Millimeter
MP	Muriate of Potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
δ^2_p	Phenotypic variance
RCBD	Randomized Complete Block Design

ABBREVIATION	FULL NAME
Res.	Research
SAU	Sher-e-Bangla Agricultural University
m^2	Square meter
Sci.	Science
TSP	Triple Super Phosphate
Uni.	University



CHAPTER 1
INTRODUCTION

CHAPTER I

INTRODUCTION

The cultivated tomato is the second most consumed vegetable and a well-studied crop species in terms of genetics, genomics and breeding. Right now the accepted scientific name for most of the scientific community is *Solanum lycopersicum* L. *Lycopersicon esculentum* Mill. is the old scientific name used from 1768 to 2005. In 2005 Spooner *et al.* proposed a change back to the original nomenclature used by Linnaeus (1753). Tomato is a self-pollinated annual crop and belongs to the family Solanaceae. Tomato species are diploid (2n=2x=24). Tomato has been an excellent model system for both basic and applied plant research due to many reasons, including ease to culture under a wide range of environments, short life cycle, photoperiod insensitivity, high self-fertility and homozygosity, great reproductive potential, ease of controlled hybridization etc. (Foolad, 2007).

Tomato is important vegetable crops in the world in terms of both production and harvested area (FAOSTAT, 2005). It is popular for its taste, nutritional status and various uses. It is extensively used in salad as well as for culinary purposes and a unique crop which provides a variety of processed products, namely, juice, paste, puree, soup, ketchup etc. It is a good source of vitamins (A, C and Calcium), fiber and minerals (Kalloo, 1989). More than 7% of total vitamin C of vegetable origin comes from tomato in Bangladesh. It contain 94 g water, 0.5 g minerals, 0.8 g fibre, 0.9 g protein, 0.2 g fat and 3.6 g carbohydrate and other elements like 48 mg calcium, 0.4 mg iron, 356 mg carotene, 0.12 mg vitamin B_1, 0.06 mg vitamin B_2 and 27 mg vitamin C in 100 g edible ripen tomato (Anon., 2010). It has antioxidant properties and potential beneficial health effects (Zhang *et al.*, 2009). Tomato intake reduce entire cholesterol, LDL cholesterol and triglyceride levels in white blood cells which reduce cardiovascular risk related with type 2 diabetes, also decrease risk of breast cancer, neck cancers and strongly protect against neurodegenerative

diseases (Freedman *et al.*, 2008). The fruit also contains significant amounts of lycopene, beta-carotene, magnesium, iron, phosphorus, potassium, riboflavin, niacin, sodium and thiamine. Tomatoes are rich in the antioxidant Lycopene which has anti-diabetes and anti-cardiovascular function. Determination of the degree of lycopene isomerization during processing would provide a measure of the potential health benefits of tomato-based foods (Dubey *et al.*, 2014). The total production of tomato was 339 lac tons in China, 137 lac tons in USA, 109 lac tons in Turkey, 103 lac tons in India and 92 lac tons in Egypt (Anon., 2010). Now Bangladesh is producing a good amount of tomatoes. It 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, which occupied an area of 23828 ha and total production was 190 thousand metric tons in 2009-10 (BBS, 2010). The average tomato yield in Bangladesh is 50-90 tons/ha (Anon., 2010). Due to increasing consumption of tomato products, the crop is becoming promising. The best tomato growing areas in Bangladesh are Dinajpur, Rajshahi, Dhaka, Comilla and Chittagong.

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). Genetic analysis of tomato is essential to enhance the genetic yield potential and maximum utilization of the desirable characters for synthesizing of any ideal genotypes (Kumar *et al.*, 2003). Evaluation of germplasm is of immense importance in genetic improvement of the crop. Crop improvement depends upon the magnitude of genetic variability and extent to which the desirable character are heritable. The assessment of the relative genetic diversity within and between populations of tomato varieties can be estimated using various approaches including pedigree information, morphological, biochemical and molecular characterization (Garcia *et al.*, 2004). Knowledge of genetic

variation has important implications for the conservation of genetic resources and breeding programs. 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.*, 1955). Hybridization is one of the major tools for achieving variability aiming at the improvement of a crop. Before hybridization genetic diversity of the existing materials or entries needs to be known. Information about genetic diversity in available germplasm is important for optimal design of any breeding programme. This help to choose desirable parents for establishing new breeding population. Besides, better knowledge on genetic diversity could help to sustain long term selection gain (Chowdhury and Sharma, 2002).

The knowledge of association between yield and its contributing traits is of great values in planning a breeding programme. As yield is the main object of a breeder, so it is important to know the relationship between various characters that have direct and indirect effect on yield. According to Burton (1952), for the improvement of any character through breeding, it is essential to know the extent of variability present in that species, nature of association among the characters and the contribution of different characters towards yield. The efficiency of a plant breeding programme depends on the amount of genetic variability exists in nature or how much a plant breeder can create variability in the target population so as to perform effective selection. Genetic diversity analysis assists in interpreting the genetic background and breeding value of the germplasm. It was also said that plant breeders use a much less diverse genetic pool than the overall available genetic diversity within the crop (Joshi *et al.*, 2012). Multivariate analysis provides valuable information on the extent of variation present in the crop under improvement and usually helps a plant breeder in choosing desirable parents for breeding programme. Also inclusion of genetically diverse parents in any breeding programme is essential to generate new variability and desirable recombinants. To meet all the requirements of successful hybrids, it is necessary to be familiar with the

detailed genetic makeup of the selected material to be used in hybrid breeding. Genetic variability among the parents is a prerequisite to develop new cultivar and select better segregants for various economic characters. Knowledge of correlations is equally important for simultaneous and/ or indirect improvement of characters that are difficult to quantify especially for those traits, which exhibit low heritability (Buckseth *et al.*, 2012). A study was, therefore, conducted on the genetic diversity, correlation and path co-efficient analysis between yield and yield contributing characters of tomato. Biochemical analyses were also performed to screen out quality tomatoes. Information about species as well as their identifying characters for most of the germplasms collected was unknown. So, it is an opportunity to categorize the germplasm morphologically under different species for future utilization. With conceiving the above scheme in mind, the present research work has been undertaken in order to fulfill the following objectives:

1. To assess the magnitude of genetic divergence in genotypes for identifying the genetically divergent parents to use them in future breeding programme.
2. To know the nature of association of traits, direct and indirect relation between yield contributing characters through correlation coefficient and path coefficient analysis.
3. To assess the bio-chemical compound among the genotypes.

CHAPTER 2
REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Adequate knowledge of genetics of various traits is very essential in vegetable breeding programme for obtaining desired results in the generation. However, the success of vegetable breeding depends on the extent and the magnitude of variability existing in the germplasm. At the same time, improvement is possible on the basis of heritable variation. Tomato obtained second position after potato in the world ranking. Tomato is a well-studied crop species for breeding, genetics and genomics in plants. Various resources are accessible now for its research, which can lead to uprising in 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 Ezura, 2009, Martinez *et al.*, 2006; Benor *et al.*, 2008).

Morphological characters were studied in selected tomato accessions by already set standards for morphological characters by IPGRI (International Plant Genetic Resources Institute) tomato descriptor (Darwin *et al.*, 2003). These Characterizations include the plant growth type and size, leaf shape, size and arrangement, plant height and fruit morphology i.e number of fruits per plant. Morphological marker is a valuable tool, which can utilize in crop improvement programme. Identification of phenotypic marker is essential to sort out the segregating generation and subsequent selection. However, knowledge on genetic information obtained through the analysis of genetic diversity and relations between or within different species, population and individuals is a pre-requisite towards effective utilization and conservation of plant genetic resources (Weising *et al.*, 1995).

Selection for yield, based on multiple traits is always better than selection based on yield alone. Yield is a quantitative character controlled by many genes (Lungu, 1978). Adequate knowledge about the magnitude and degree of

association of yield with its attributing characters or components is of great importance to breeders. Using these components, breeders would understand strength of correlated traits that would assists in decision making process to select for simultaneous improvement of more than one character (Sivaprasad, 2008). Keeping in view the objectives of the present research work, the review of literature concerning to the studies conducted for this dissertation is discussed below.

2.1 Nomenclature, Origin and distribution of tomato

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). Both names, however, will probably be found in the literature for some time.

Tomato translates to *"wolfpeach"* -- 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*. 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 considered 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 (Anon., 2010). It is believed that the tomato was introduced in 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.

2.2 Variability

The success of any crop improvement programme depends on the presence of genetic variability and the extent to which the desirable trait is heritable. Genetic diversity can be estimated 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 plant, fruit colour and fruit size show variability (Naz *et al.*, 2013). On the other hand 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 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 on the basis of their genomic information.

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.* in 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. Mahesha *et al.* (2006) exposed significant variability for all the characters under study and detected a wide range of variation for plant height, number of branches per plant, fruit weight, fruit length, fruit diameter, fruit set percentage, fruits per plant, fruit yield per plant. A number of germplasms on the basis of phenotypic characters like color, size, taste etc. are available in tomato. The evaluation of the Kenyan tomato germplasm by Agong (2001) showed a large and significant variation in the quantitative traits between the accessions. The average fresh and dry fruit weight varied notably among the accessions. Most of the landraces gave lower fresh and dry fruit yields than the market cultivars. Mohanty and Prusti (2001) showed considerable genetic variability among 18 indigenous and exotic tomato cultivars for five economic characters (plant height, number of branches per plant, number of fruits per plant, average fruit weight and yield) in Orissa, India during rabi 1998-99. The fundamental key to achieve the genetic improvement of a crop through a proper breeding programme is to calculate the amount and nature of variation of plant characters in breeding population. The

assessment helps breeder for improving the selection efficiency. Many researchers studied variation of various characters in tomato. Some of those are presented here.

2.2.1 Days to first flowering

Farzaneh *et al.* (2013) showed earliness in number of days to first flowering while studying combining abilty from a 9x9 diallele cross. Whereas Monamodi *et al.* (2013) and Aditya and Phir (1995) had not found any significant differences in days to first flowering among tomato genotypes. Kumari *et al.* (2007) recorded data for days to flowering and for some other traits and found that there were highly significant differences for all the characters among parents. Matin and Kuddus (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.

2.2.2 Days of 50% flowering

Nalla *et al.* (2014) done a field experiment using 27 tomato genotypes and reported days to 50% flowering (1.14%) contributed very little for variability. Thirteen quantitative characters were studied in 55 genotypes of tomato by Narolia (2012) and found high variability for all the characters studied except number of branches per plant and days to 50% flowering for which variability was moderate and low, respectively. The stability of 5 cultivars of tomatoes for growth and earliness was determined in a field experiment by Ravindra *et al.* (2003). Significant genotype x environment interaction was observed for number of days to 50% flowering.

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 favourable 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 phenotypic coefficient of variation was higher than genotypic coefficient of variation for days to maturity.

2.2.4 Plant height (cm)

Naz *et al.* (2013) used 25 tomato germplasam to characterize morphologically by comparing the height of plant, leaf length, shape and arrangement, fruit shape and size. This study revealed that height of plant show highest variability. Ravindra *et al.* (2003) observed significant genotype x environment interaction for plant height. Kumari *et al.* (2007) observed the highest genotypic coefficient of variation for 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%). Shravan *et al.* (2004), Prasad *et al.* (1999) and Aditya and Phir (1995) reported significant variation for 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 contribute 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 and Kuddus (2001) also reported that phenotypic variance was relatively higher than genotypic variance for plant height. They again observed that genotypic co-efficient of variation was lowering than phenotypic co-efficient of variation indicating 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 a narrow range of variations was observed by Ahmed *et al.* (1986). Sonone *et al.* (1986) and Prasad and Prasad (1977) also reported high phenotypic and genotypic co-efficient of variation for plant height in tomato. But Mallik *et al.* (1985) reported that phenotypic co-efficient of variations were higher than genotypic co-efficient of variations for plant height in tomato.

2.2.5 Branches per plant

Singh (2005), Mohanty (2003) and Upadhaya *et al.* (2001) observed PCV was slightly higher than GCV for number of branches per plant. Shravan *et al.* (2004) conducted an experiment with 30 tomato genotypes to study their genetic variability and reported significant difference for number of primary branches per plant among the genotypes. Ravindra *et al.* (2003) observed significant genotype x environment interaction for number of primary branches.

2.2.6 Number of clusters per plant

Dufera (2013) conducted an experiment using twenty one tomato germplasms. Higher genotypic and phenotypic coefficients variation values were recorded by the character fruit clusters per plant, indicating the presence of variability among the genotypes and the scope to improve these characters through selection. Singh *et al.* (2006) observed considerable range of genetic variability for yield and yield components in the materials under study and maximum genotypic coefficient of variation was recorded for number of clusters per plant.

2.2.7 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 per cluster. Similar result was observed by Aradhana and Singh (2003).

2.2.8 Fruits per plant

Seventeen diverse genotypes of tomato were evaluated by Thakur (2009) for their performance and interaction with changing environments through the characters like fruit yield, number of fruits/plant. 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 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 number of fruits per plant followed by number of flowers per plant and yield per plant. Joshi and Singh (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.

Brar *et al.* (2000) estimated phenotypic and genotypic co-efficient of variation and observed high variability in the characters of number of fruits per plant of 186 genotypes of tomatoes. Das *et al.* (1998) and Islam *et al.* (1996) reported wide range of genotypic variation for 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 co-efficient of variation indicated that selection may be made for number of fruits per plant. Sidhu and Singh (1989) and Bhutani and Kallo (1989) suggested that maximum genetic improvement would be possible by genetic variability for number of fruits. Prasad and Prasad (1977), Dudi *et al.* (1983) and Sonone *et al.* (1986) estimated the high genotypic and phenotypic co-efficients of variation for fruits per plant.

2.2.9 Average fruit weight (g)

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. Singh *et al.* (2002) carried out a field experiment to study genetic variability of fifteen heat tolerant tomato and showed high phenotypic (PCV) and genetic (GCV) coefficients of variation for average fruit weight. Brar *et al.* (2000) reported significant varietal differences among 20 cultivars of tomato for average fruit weight. Sahu and Mishra (1995) reported that fruit weight had high genotypic co-efficient of variation in 16 lines of tomato. 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 palnts. Reddy and Reddy (1992) estimated phenotypic and genotypic variances, phenotypic and genotypic co-efficient of variation for individual fruit weight. Considerable variation was observed for average individual fruit weight. 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 co-efficient of variation was very high for individual fruit weight in four tomato varieties.

2.2.10 Fruit length (cm)

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 high phenotypic coefficient of variation for this character.

2.2.11 Fruit diameter (cm)

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 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 co-efficient of variation was greatest for this character.

2.2.12 Fruit yield per plant (g)

Matin and Kuddus (2001) reported significant differences for yield per plant among the genotypes tested. He also reported that phenotypic variance was little higher than genotypic variance indicating slight environmental influence on this trait. Sachan (2001) performed an experiment with certain tomato genotypes and he also reported significant differences among the genotypes for yield per plant. Kumar and Tiwari (2002) reported higher genotypic co-efficient 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 Gulshanlal (1990) observed considerable variations for yield per plant in 139 tomato varieties. 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

The effectiveness of selection for yield depends upon heritability. A character with high heritability gives 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 genetic advance of yield and yield contributing characters of tomato. The literatures which are relevant to the present study are reviewed below:

According Saleem *et al.* (2013) a study of 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 number of fruits per plant while fruit width was the most heritable trait. Buckseth *et al.* (2012) found high heritability with high genetic advance for 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. By Narolia (2012) thirteen quantitative characters were studied in 55 genotypes of tomato. High heritability coupled with high genetic advance as per cent of 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. In 2010, Shashikanth *et al.* 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 percentage of mean for average fruit weight, indicating the control of such character by additive gene. He also recorded that high heritability coupled with low genetic advance as percentage of mean for rest of the characters except pericarp thickness, indicating most of the characters were governed by non-additive genetic components. Kumari *et al.* (2007) reported that the estimates of heritability were high for all the characteristics and genetic advance was high for plant height, moderate for total number of fruit bearing branches, weight per fruit and days to maturity, while the remaining characteristics had low values of genetic advance. Nardar *et al.* (2007) evaluated 20 tomato genotypes and observed high heritability with 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 number of fruits per plant (96.56%), followed by number of flowers per plant (93.45%), reflecting the

effectiveness of selection in the present germplasm of tomato improvement. Saeed *et al.* (2007) observed that broad sense heritability was highest for number of fruits per plant (96.56%), followed by number of flowers per plant (93.45%), reflecting the effectiveness of selection in the present germplasm of tomato improvement. Kumar *et al.* (2006) observed low heritability (4.40%) and high genetic advance (35.55) for plant height. Mahesha *et al.* (2006) estimated heritability and expected 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 on these characters while selecting the better genotypes in tomato.

Heritability for nineteen genotypes of tomato and were estimated and found high heritability for ascorbic acid content, average weight of fruits and number of fruits per plant. Estimates of high heritability with high genetic advance was recorded in case of number of leaves per plant, average weight of fruits, number of fruits per plant and plant height, whereas high heritability with low genetic advance was recorded for number of locules per fruit, dry matter content, pericarp thickness and yield per plant (Singh *et al.*, 2006). Heritability was estimated by Singh *et al.* (2005) and showed that heritability estimates (in the broad sense) were high for all the characters. Kumar *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. Heritability and genetic advance estimated by Shravan *et al.* (2004) 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 .The rest of the characters showed moderate

heritability and low genetic advance. Moderate heritability associated with moderate genetic advance for plant height of 37 tomato genotypes of tomato were reported by Arun *et al.* (2004).

Joshi *et al.* (2004) observed moderate heritability and moderate genetic gain for 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. Moderate heritability and low genetic gain for harvest duration suggests the presence of dominance and epistatic effects. Joshi *et al.* (2003) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and noticed that plant height gave the highest heritability. Mohanty (2003) observed that high heritability with high genotypic coefficient of variation was for fruit weight, plant height, number of fruits and number of branches per plant. Hanson *et al.* (2002) proposed heritability as the ratio of genotypic variance to the total variance in a non-segregating population. Since, the estimate of heritability gives indication of the amount of progress expected from selection, as they are most meaningful when accompanied by estimate of genetic advance. Genetic advance is the measure of improvement that can be achieved by practicing selection in a population.

Singh (2002) reported that heritability was high for all characters except days from fruit setting to red ripe stage and the highest genetic advance was predicted for average fruit weight, followed by shelf life of red ripe fruits. Matin and Kuddus (2001) reported high degrees of heritability and genetic advance for fruits per plant, individual fruit weight and number of seeds per fruit. Brar *et al.* (1998) reported that the number of fruits per plant, total yield per plant and marketable yield per plant had low to moderate estimates of heritability and genetic advance and number of marketable fruits per plant had high values of heritability and genetic advance. Nessa *et al.* (2000) reported high heritability for number fruits per plant, plant height and moderate

heritability for yield per plant. Prasad and Mathura (1999) and Vikram and Kohli (1998) estimated very high heritability along with high genetic advance by fruit weight. Singh *et al.* (1997) estimated heritability and genetic advance in 23 genotypes of tomato. High values of heritability and genetic advance indicated that effective selection may be made for fruit weight and number of fruits per plant. Islam *et al.* (1996) studied heritabiltiy and genetic advance in 26 diverse genotypes of tomato. High heritability and genetic advance was observed in number of fruits per plant, plant height, fruit yield and individual fruit weight. Mittal *et al.* (1996) estimated heritability and genetic advance in 27 genotypes of tomato. High heritability associated with high genetic advance was observed by them indicating the character, predominantly under the control of additive gene, could be improved through selection.

High heritability coupled with high genetic advance was observed for number of fruits per plant, plant height and average fruit weight which indicated additive gene action (Pujari *et al.*, 1995). Naidu (1993) reported high heritability for number fruits per plant, plant height and moderate heritability for yield per plant. Reddy and Reddy (1992) studied heritability and genetic advance in 139 tomato varieties. Heritability values were high for yield per plant, number of fruits per fruits per plant and average individual fruit weight. Bai and Devi (1991) evaluated five varieties and nine hybrids of tomato. Heritability estimates high for plant height, number of fruits per plant and individual fruit weight. Islam and Khan (1991) studied 12 tomato genotypes and reported that heritability values were high for most of the characters but moderate for days to first flowering, maturity and plant height. Singh *et al.* (1988) evaluated 32 genotypes for agronomic characters and obtained high heritability values for yield per plant only. Abedin and Khan (1986) also reported high values of heritability in broad sense and high genetic advance for plant height, number of fruits per plant and individual fruit weight. Sonone *et al.* (1986) reported that heritability estimates for fruit number, plant height and individual fruit weight were high in tomato. He also reported that high genetic

advance was observed for fruit yield, plant height, individual fruit weight and number of fruits per plant. Mallik (1985) reported high genetic advance for plant height, number of fruits per plant, individual fruit weight and yield per plant but low heritability for yield per plant. Dudi *et al.* (1983) reported that heritability and genetic advance-were high for number of fruits per plant, individual fruit weight and yield by per plant. Singh and Singh (1980b) reported high heritability for average fruit weight, total fruits and days to first picking. Nandpuri *et al.* (1977) observed that heritability estimates were high for fruit size, plant height and yield per plant in tomato. Expected genetic advance was also high for fruit size, yield and number of fruits per plant.

2.4 Correlation and path co-efficient 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, 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. So, 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 positive correlation between these, then there may be some possibility to increase in the total yield by selecting that component. But, negative correlation co-efficient among yield components were generally observed indicating selection for any component might not bring improvement for yield. Many authors have studied correlation between yield and yield contributing characters of tomato. Some pertinent recent literatures are 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 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 increase in plant height, there was corresponding increase in number of primary branches per plant, days to 50% flowering and number of flower clusters per plant.

According to Monamadi *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 were positively and significantly associated with yield per plant, while number of fruits per plant was 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 significant and positive correlation with fruit length at both levels.

Correlation coefficient analysis was studied for thirty diverse tomato genotypes and noticed that correlation coefficients at the genotypic level were generally higher than the corresponding phenotypic ones and yield per plant was positively and significantly associated with plant height, fruit number per plant, fruit shape index and pericarp thickness (Kumar *et al.*, 2007). 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 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 number of flowers per cluster, flower clusters at first picking, 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 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. Arun *et al.* (2004) observed that in case of tomato yield per plant was positively and significantly correlated with average fruit weight and plant height. Joshi *et al.* (2004) performed 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 number of fruits per plant had significant and positive correlation

with fruit yield per plant Kumar *et al.* (2004). Similarly, inter-relationships were studied in 92 tomato genotypes. 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.*, 2004). Correlation coefficient analysis carried out by Kumar *et al.* (2003) for thirty diverse tomato genotypes and observed that correlation coefficients at the genotypic level were generally higher than the corresponding phenotypic ones. He also observed that yield per plant was positively and significantly associated with plant height, fruit number per plant, fruit shape index and pericarp thickness. 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 correlation of thirty-seven tomato genotypes and showed that the number of fruits per cluster and number of fruits per plant were significantly and positively correlated with fruit yield per plant, whereas the number of primary branches per plant, fruit weight had negative association with fruit yield. Mohanty (2002) reported that the phenotypic and genotypic correlations of fruit yield were significant and positive with days to first harvest, number of branches and fruits/plant, significant and negative with plant height and average fruit weight and number of fruits per plant was inversely related with average fruit weight. 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. The negative correlation was observed between fruit weight and fruit number, plant height and fruit weight, fruit weight and fruit yield and plant height Padma *et al.* (2002). Susic (2002) showed that a significant negative correlation was between mean fruit mass and number of fruits per plant and a significant positive correlation was 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, number of fruits per plant and number of fruits per cluster is important for improvement of fruit yield. Kumar *et al.* (2001) reported that a significant positive genotypic correlation was found bet wean pericarp thickness and juice viscosity and between lycopene and ascorbic acid contents and locule number was negatively correlated with pericarp thickness. Matin and Kuddas (2001) studied phenotypic and genotypic correlations of 13 qualitative and quantitative characters of 26 genotypes of tomato and found that individual fruit weight had significant positive correlations with plant height and yield per plant. He also reported that number of fruits per plant also had significant positive correlations with fruit dry matter content and found significant negative correlations between number fruits per plant and individual fruit weight. Dry matter was negatively correlated with individual fruit weight. Information on yield correlations is derived from data on eight yield components recorded in eighteen genetically diverse genotypes by Sharma and Verma (2000). It is concluded that when selected for high yield in tomato, the main emphasis

should be placed on number of fruits/plant. Fruit diameter and average fruit weight are also important components.

Prasad and Mathura (1999) observed very high and significant positive correlation co-efficient were between yield and fruit weight. Das *et al.* (1998) studied correlation co-efficient in fruit characters of tomato. They observed significant positive correlation of fruit yield per plant with number of fruits per plant. Aditya and Phir (1995) studied phenotypic and genotypic correlation co-efficient to find out the associations between eight characters of 44 genotypes of tomato. He reported that yield of fruits per plant showed significant positive correlations with plant height and number of fruits per plant; and insignificant positive correlation with weight of individual fruit (phenotypically) and number of seeds per fruit. Naidu (1993) 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.

Abedin and Khan (1986) studied correlation of 20 cultivars of tomato and found that yield per plant was negatively correlated with number of fruits per plant but positively and significantly correlated with individual fruit weight and plant height. Mallik (1985) studied phenotypic and genotypic correlations in an experiment with 19 varieties of tomato and observed that individual fruit weight had positive significant correlations with plant height and yield. Alvarez and Torres (1983) studied correlation between ten characters including yield in 34 varieties/lines of tomato and observed positive correlation between yield and plant height, yield and fruit number per plant also. All three were positively correlated with each other and negatively correlated with weight. Dudi and Kalloo (1982) investigated yield per plant and seven yield related characters in 40 lines of tomato and observed that yield per plant and fruits per plant are positively correlated with total yield at the phenotypic level.

2.4.2 Path co-efficient analysis between yield and yield contributing characters

The study of correlation does not provide an exact picture of relative importance of direct and indirect influence of each of the component character towards the desired character. So, this can be overcome by following path coefficient analysis technique by further partitioning the correlation coefficient into direct and indirect effects. Path co-efficient is a standard tool which measures the direct influence of one character upon another and permits the separation of correlation co-efficient into components of direct and indirect effects. Path co-efficient 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 co-efficient analysis between yield and components of yield relevant to the present study are reviewed in this section:

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. The direct effects of marketable fruit number and fruit weight on fruit yield were positive and large. A field experiment was carried out by Monamodi *et al.* (2013) using six determinate tomatoes. 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 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 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. Mayavel *et al.* (2005) reported that number of branches per plant had the highest positive direct effect on fruit yield. Whereas, plant height, number of fruits per cluster, number of fruits per plants and number of locules per fruit had negative direct effects on fruit yield. Singh (2005) reported that the genotypic and phenotypic path coefficient studies described that number of fruits per plant had the maximum positive effect on yield followed by average fruit weight. Regarding indirect effects, it was observed that number of fruits per plant exhibited positive indirect effect towards fruit yield via number of branches per plant; it was negative via plant height, days to 50 per cent flowering.

Singh and Cheema (2006) have revealed that positive direct effect of number of fruits per plant on yield. It was also reported by Kumar *et al.* (2003). Its positive indirect effects through average fruit weight mainly contributed towards its strong association with yield. The findings were on consonance with Mohanty (2002). Singh *et al.* (2004) 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. However, days to first fruit set, number of primary branches per plant, plant height, number of fruit clusters per plant. Arun *et al.* (2003) revealed that the number of fruits per plant is the most important yield contributing character followed by plant height through path co-efficient analysis. 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. Kumar *et al.* (2003) 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.

Bodund (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 number of fruits per cluster, average fruit weight and number of fruits per plant had direct maximum effects on fruit yield. Mohanty (2002) performed path analysis and showed that the number of branches per plant and average fruit weight exerted high positive direct effect on yield and high positive indirect effect with each other. Padma *et al.* (2002) performed path analysis and revealed that number of branches, fruit weight, fruit length and number of fruits per plant exhibited positive effect on yield per plant at the genotypic and phenotypic levels.

Matin and Kuddus (2001) observed that the maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant. He also reported that days to first flowering, plant height and number of seeds per fruit had negative direct effect on yield per plant. Verma and Sarnaik (2000) conducted a field experiment to perform path analysis of yield components in thirty tomato genotypes and observed that total number of fruits per plant, average weight of fruit and number of branches per plant exhibited positive as well as high direct effects. Domini and Maya (1997) evaluated 18 tomato varieties for the relationship of six yield components to yield in two different seasons. They reported that fruit number per plant was the most important character having a direct effect on yield either in early sowing.

Aditya and Phir (1995) carried out genotypic and phenotypic path co-efficient analysis and revealed that plant height and number of fruits per plant had high positive direct effect on yield and on the other hand, weight of individual fruit had positive indirect effect on yield per plant. Supe and Kale (1992) studied

path analysis of seven different characters of twelve indigenous varieties of tomato and observed that plant height had negative direct effect on yield per plant. Islam and Khan (1991) observed that fruits per plant, average fruit weight, plant height and days to first flowering had positive direct effects on yield of tomato. Alam *et al.* (1988) studied path co-efficient in 19 cultivars of tomato and found that maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant. Gomez (1987) reported that days to first flowering has negative direct effect on yield of tomato. Gorbatenko and Gorbatenko (1985) carried out path co-efficient analysis of economically useful characters of tomato and found that individual fruit weight had an appreciable direct effect on yield per plant. Dudi and Kalloo (1982) studied path analysis in tomato and reported highest direct effects of early yield per plant, fruit weight and fruits per plant.

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 them 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 number of flower clusters per plant and days to 50% flowering contributed very little for 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. A study done by Xiaorong *et al.* (2012) using twenty six morphological traits 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 great genetic diversity has been revealed by molecular markers in wild species (Zhu *et al.*, 2004). These variations provide great potential for crop improvement. However, genetic variation in modern cultivars or hybrids is limited (Chen *et al.*, 2009).

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 geographical distribution of genotypes and genetic divergence observed by Singh *et al.* (2004). They assessed 48 genotypes for their genetic divergence using Mahalar statistics. They concluded that characters like number of fruits plant $^{-1}$, average fruit weight, plant height and fruit yield contributed maximum to genetic divergence. Veershetty (2004) grouped 32 tomato genotypes into 10 cluster based on D^2 analysis number of fruits per cluster, plant height, number of branches, pericarp thickness, average fruit weight and TSS content of fruit were reported as chief contribution towards divergence. Arun *et al.* (2003) studied the nature and magnitude of genetic divergence in 73 tomato genotypes of different origin for quantitative characters and they grouped genotypes into 15 cluster 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 highest number of fruits/cluster. Singh *et al.* (2002) observed high genetic variation in tomato for plant height, number of days to fruit set, number of fruit clusters per plant, number of fruits per plant, fruit weight per plant and fruit yield per plant. This genetic variations offer an opportunity for indirect selection for yield in tomatoes.

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. Maximum intercluster distance was observed between the clusters I and V. The distance between clusters I and II, III and IV, IV and V was moderate. They also reported that 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.

Rai *et al.* (1998) studied 37 tomato genotypes and could able to group them into four clusters using a non-heritable clustering approach with the help of Mahalanobis' D^2 statistics for yield and yield contributing characters. The clustering pattern indicates that there was no association between geographical distribution of genotype and genetic divergence characters namely number of primary branches, days to first flowering, plant height and average fruit weight contributed to maximum divergence. Kumar and Tiwari (1999) studied genetic divergence of 32 tomato genotypes and could group them into 9 clusters based

on D^2 values. The magnitude of inter cluster distances was comparatively lower than that of inter cluster distances. Patil (1984) grouped 55 tomato genotypes into nine clusters studied based on D^2 analysis. A maximum of 16 genotypes entered cluster I, followed by 15 in cluster IV, 9 in cluster III, 7 in cluster II, 4 in cluster V and the remaining four clusters consisted of solitary genotype.

2.6 Biochemical 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 human diet and has been linked with decreases 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 epidermiological and intervention studies have demonstrated that dietary intake of LYC-rich foods result 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. Majid Foolad 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 un-substituted alkene). Some of the previous reports on Lycopene experiment are discussed here (Datta *et al.*, 2013; Dong *et al.*, 2010; Alda *et al.*, 2009; Moigrădean *et al.*, 2007; Cucu and Loco, 2011).

According to Datta, *et. 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 (TJ) 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 piror 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 was recorded for lycopene content. Mendelova *et al.* (2013) conducted a work 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 F_1, Diana F_1, Denar, Milica F_1, Orange F_1 Paulina F_1, Sejk F_1. 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 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 being a potent antioxidant has been found to inhibit proliferation of several types of human cancer cells, including endometrial, prostate, breast, upper aero digestive 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 (Louis *et al.*, 2010). 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 very 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 mean was higher during November than February planting for all the characters except acid content and TSS. Jones *et al.* (2003) 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 petunidine, followed by malvidine and delphinidinin, 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.

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 R_2=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 colour 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.

2.6.2 Vitamin-C

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 (Supera, 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 done by Schulzova and Hajslova (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, dehydrotomatine). 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 phenotypic correlation for all characters examined. Among them the ascorbic acid content had negative direct effects and association with fruit yield.

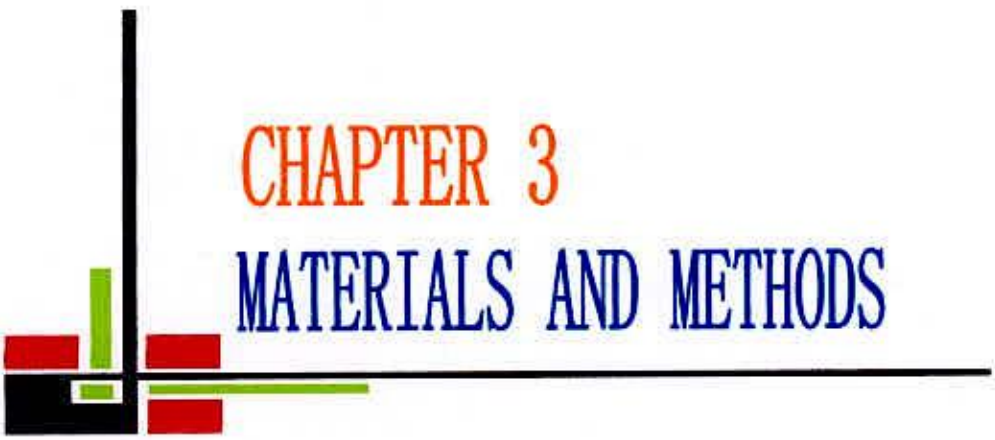
2.6.3 Total Soluble Solids (% of Brix)

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 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 content of soluble solids, number, weight, length and diameter. Krishna and Allolli (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). Seven tomato lines studied by Chen (2004) 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. 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 ketchups 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 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.* (1999) 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 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.



CHAPTER 3

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

This chapter illustrates information concerning methodology that was used in execution of the experiment. It comprises a brief description of locations of experimental site, planting materials, climate and soil, seed bed preparation, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data collection procedure, statistical and biochemical analysis procedure etc., which are presented as follows:

3.1 Experimental site

The experiment was accomplished at experimental field, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from November 2012 to April 2013. Location of the site is 23°74' N latitude and 90°35' E longitude with an elevation of 8 meter 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).

3.2 Planting materials

A total of nineteen genotypes of tomato collected from different places of Bangladesh were used in this experiment. The materials were collected from Plant Genetic Resource Centre (PGRC) and Horticulture Research Centre (HRC) at Bangladesh Agricultural Research Institute (BARI), Gazipur. The name and origin of these genotypes are presented in Table 1.

3.3 Climate and soil

Experimental site was located in the subtropical climatic zone, set aparted by plenty of sunshine and moderately low temperature prevails during October to

Table 1. Name and place of collection of nineteen tomato genotypes used in the present study

Sl. No.	Genotypes No.	Name/Acc. No. (BD)	Place of collection
1	G_1	BD-7258	PGRC, BARI
2	G_2	BD-7270	PGRC, BARI
3	G_3	BD-7276	PGRC, BARI
4	G_4	BD-7279	PGRC, BARI
5	G_5	BD-7281	PGRC, BARI
6	G_6	BD-7285	PGRC, BARI
7	G_7	BD-7286	PGRC, BARI
8	G_8	BD-7289	PGRC, BARI
9	G_9	BD-7290	PGRC, BARI
10	G_{10}	BD-7759	PGRC, BARI
11	G_{11}	BD-7762	PGRC, BARI
12	G_{12}	BD-9010	PGRC, BARI
13	G_{13}	BD-9011	PGRC, BARI
14	G_{14}	BD-9960	PGRC, BARI
15	G_{15}	BD-10321	PGRC, BARI
16	G_{16}	BARI Tomato-7	HRC, BARI
17	G_{17}	BARI Tomato-11	HRC, BARI
18	G_{18}	BARI Tomato-14	HRC, BARI
19	G_{19}	BARI Tomato-15	HRC, BARI

PGRC = Plant Genetic Research Centre, HRC = Horticulture Research Centre
BARI = Bangladesh Agricultural Research Institute

March (Rabi season). The soil was sandy loam in texture having pH 5.46- 5.62. Weather information and physicochemical properties of the soil are presented in (Appendix II and Appendix III, respectively).

3.4 Seed bed preparation and raising of seedling

Seed sowing was carried out on November 19, 2012 in the seedbed (Plate 1A). 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.

3.5 Design and layout of the experiment

The experiment was laid out and evaluated under field condition during Rabi 2012- 13 in Randomized Complete Block Design (RCBD).

Genotype	:	19
Replications	:	3
Spacing	:	40 cm × 60 cm
Plot size	:	6 × 37 m
Date of transplanting	:	14th December 2012

3.6 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 farm yard manures (FYM). Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on December 12, 2012.

3.7 Transplanting of seedlings

The seedlings were raised in the seedbed in usual way and 25 days old seedlings were transplanted in the main field on December 14, 2012. The transplanted seedlings were watered regularly to make a firm relation with roots and soil to stand along.

3.8 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.

3.9 Intercultural operations

When the seedlings were well established, 1st 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.

3.10 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 long time. The fruits per entry were allowed to ripe and then seeds were collected and stored at 4°C for future use. Harvesting was started from March 2, 2013 and completed by April 26, 2013.

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

Seed bed preparations, raising of seedlings, experimental field in growing condition of plants, intercultural operation, growth stage of a single tomato plant, flowering and fruiting stages of tomato plant are displayed in Plate 1 (A-D) and Plate 2 (A-D).

3.11 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.

3.11.1 Days to first flowering

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

3.11.2 Days to 50% flowering

The number of days was counted from the date of sowing to 50 per cent of plants flowered.

3.11.3 Days to maturity

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

3.11.4 Plant height (cm)

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

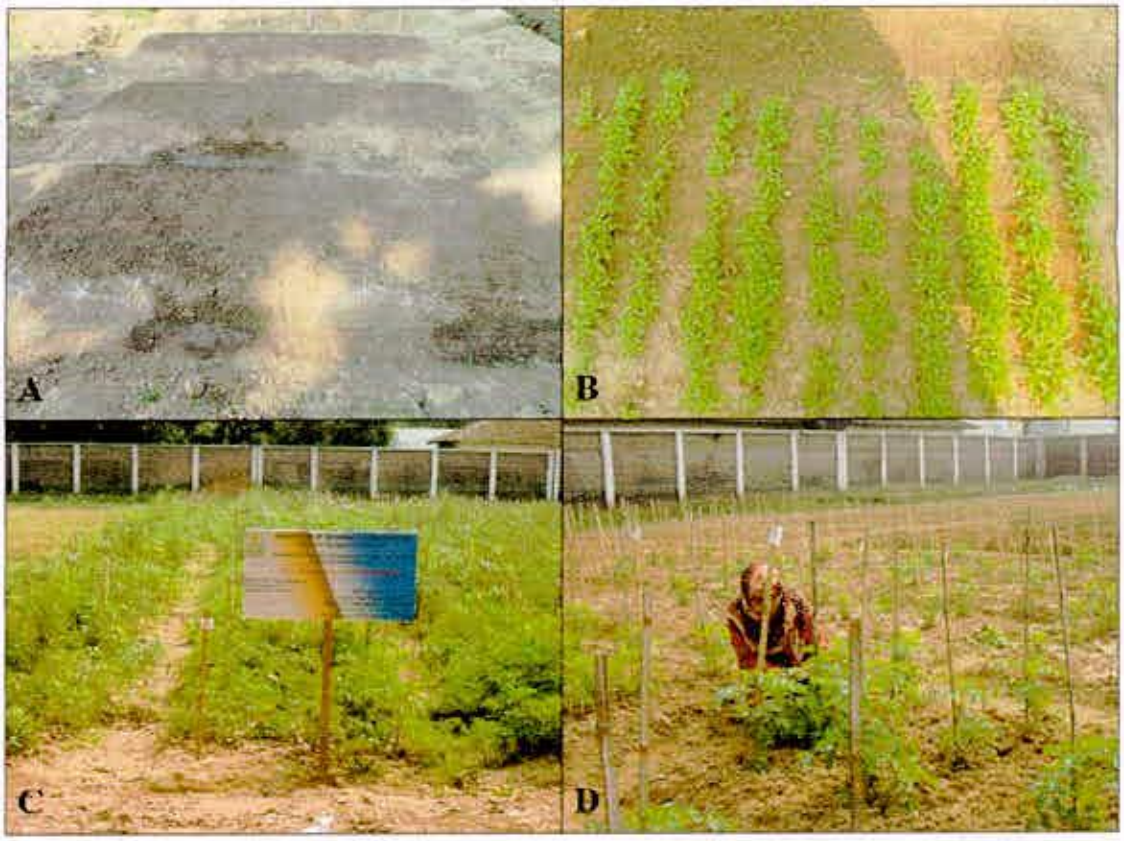


Plate 1. Sowing, transplanting and intercultural operation during the growth stage of tomato plant. Seed bed preparation (A), raising of seedling (B), growing condition in the field after transplantation (C), mechanical support by bamboo sticks (D).

Plate 2. Growing to ripening stages of tomato plant/s in the field. Growing stage (A), Flowering stage (B), Fruiting stage (C), Ripening stage (D).

3.11.5 Branches per plant

The number of branches arising from the main stem above the ground was recorded at 70 days after transplanting.

3.11.6 Number of clusters per plant

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

3.11.7 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.

3.11.8 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.

3.11.9 Average Fruit weight (g)

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

3.11.10 Fruit length (cm)

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

3.11.11 Fruit Diameter (cm)

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

3.11.12 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.

3.12.1 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 co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.12.1.1 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

3.12.1.2 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation, GCV % = $\frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 10$

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

3.12.1.3 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

3.12.1.4 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

3.12.1.5 Estimation of genetic advance mean's percentage

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

$$\text{Genetic advance (\% of mean)} = \frac{\text{Gene c Advance (GA)}}{\text{Popula on mean } (\bar{x})} \text{ X } 100$$

3.12.1.6 Estimation of simple correlation co-efficient:

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

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

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.12.1.7 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation co-efficient 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 co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

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

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

3.12.1.8 Estimation of path co-efficient

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:

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

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

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

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

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

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

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

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

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

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

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

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

Where,

r_{iy} = 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 = Plant Height

2 = Days to first flowering

3 = Days to 50% flowering

4 = Days to maturity

5 = Number of branches per plant

6 = Number of clusters per plant

7 = Number of fruit per cluster

8 = Number of fruits per plant

9 = Fruit weight (gm)

10 = Fruit length (cm)

11 = Fruit diameter (cm)

12 = Fruit yield per plant (kg)

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

Where,

$P_{1.y}, P_{2.y}, P_{3.y}, \ldots\ldots\ldots P_{8.y}$ = Path coefficient of the independent variables 1, 2, 3,….,12 on the dependent variable y, respectively.

$r_{1.y}, r_{2.y}, r_{3.y}, \ldots., r_{12.y}$ = Correlation coefficient of 1, 2, 3,…., 12 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 :

$P^2_{RY} = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots\ldots\ldots\ldots + r_{12.y}P_{12.y})$

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.

3.12.2 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 efficient method of evaluating genetic diversity. These are as follows:

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

3.12.2.2 Principal Coordinate analysis (PCA)

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).

3.12.2.3 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.

3.12.2.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds 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 of the ratio of among groups to the within group variations. The canonical vector are 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.

3.12.2.5 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.

3.12.2.6 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.

3.12.2.7 Computation of average inter-cluster distances

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

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

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. and n_j = Number of populations in cluster j.

3.12.2.8 Cluster diagram

Using the values of intra and inter-cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.12.2.9 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 largest statistical distance (D^2) express the maximum divergence among the genotypes included into 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 cluster from which genotypes are selected for use as parent (s)
2. Selection of particular genotype(s) from the selected cluster(s)
3. Relative contribution of the characters to the total divergence
4. Other important characters of the genotypes performance

3.13 Biochemical Analysis

3.13.1 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 the each sample were homogenized with 25 ml of hexane:ethanol:acetone, which were 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 4). 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 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)

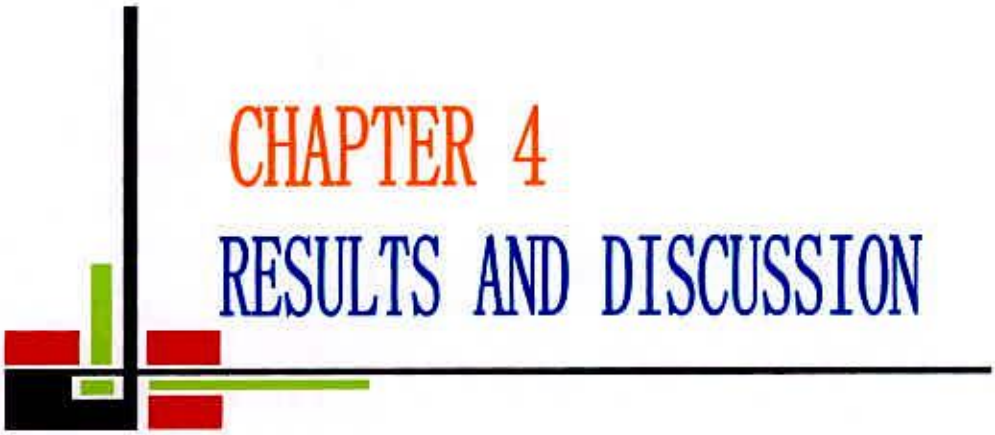
E = extinction coefficient

3.13.2 Determination of Vitamin-C

Vitamin-C was measured by Oxidation Reduction Titration Method (Tee *et al.*, 1988). Single fruit was blend and tomato exactract 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-dichlorophenol indophenol). 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 known sample.

3.13.3 Determination of Brix percentage

Brix percentages were measured by portable refractometer (ERMA, Tokyo, Japan) (Plate 3). 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.



CHAPTER 4
RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted to execute the multivariate and biochemical analysis in tomato (*Solanum lycopersicum* L.) genotypes using morpho-agronomic 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 (Plate 3-5). The data pertaining to twelve characters have been presented and statistically analyzed with the possible interpretations given under the following headings:

4.1 Genetic variability, heritability and genetic advance

The extent of variation among the genotypes in respect of twelve 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 3. The mean value of all genotypes for each character is shown in Appendix IV. Performance of the genotypes is described below for each character.

4.1.1 Days to first flowering

The variance due to days to first flowering showed that the genotypes differed significantly and ranged from 67.00 days after sowing (DAS) in BD-10321 to 60.67 DAS in BD-7270 with mean value 63.53 days after sowing (DAS) (Appendix IV). The genotypic variance and phenotypic variance for this trait were 1.99 and 3.12, respectively (Table 3). The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. Phenotypic variation in fruits of different genotypes ($G_1 - G_{19}$) is shown in Plate 3a-3c.

Table 3. Estimation of genetic parameters in twelve characters of nineteen genotypes in tomato

Parameters	MS	σ^2 p	σ^2g	σ^2 e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)	CV (%)
DFF	7.08**	3.12	1.99	1.13	2.78	2.22	1.67	63.74	2.32	3.65	1.67
D50%F	6.78**	3.08	1.85	1.23	2.41	1.87	1.52	60.09	2.17	2.98	1.52
DM	15.88**	6.85	4.52	2.33	2.59	2.11	1.51	65.97	3.56	3.52	1.51
PH	742.57**	320.96	210.81	110.15	22.29	18.06	13.06	65.68	24.24	30.15	13.06
BPP	17.34**	6.39	5.48	0.91	26.48	24.52	9.99	85.78	4.47	46.81	9.99
NCP	29.86**	12.33	8.77	3.56	26.44	22.29	14.21	71.10	5.14	38.73	14.21
FPC	5.01**	2.14	1.44	0.70	36.43	29.84	20.89	67.11	2.02	50.33	20.89
FPP	1,354.51**	563.86	395.33	168.52	31.80	26.63	17.39	70.11	34.30	45.93	17.39
AFW	922.64**	312.07	305.29	6.78	77.22	76.37	11.38	97.83	35.60	155.59	11.38
FL	1.30**	0.49	0.41	0.09	19.39	17.62	8.08	82.64	1.19	33.02	8.08
FD	1.25**	0.47	0.40	0.07	19.22	17.72	7.45	84.96	1.20	33.67	7.45
FYP	228,330.82**	88421.07	69954.88	18466.18	35.09	31.21	16.03	79.12	484.63	57.18	16.03

**, * significant at the 1% and 5% level, respectively.

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to Maturity, PH = Plant height (cm), BPP = Branches per plant, NCP = Number of cluster per plant, FPC = Fruits per cluster, FPP = Fruits per plant, AFW = Average Fruit Weight (g), FL = Fruit length (cm), FD = Fruit Diameter (cm), FYP = Fruit yield per plant (g), MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2 e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation.

Plate 3a. Phenotypic variation in fruits of different genotypes of tomato (G_1 - G_9)

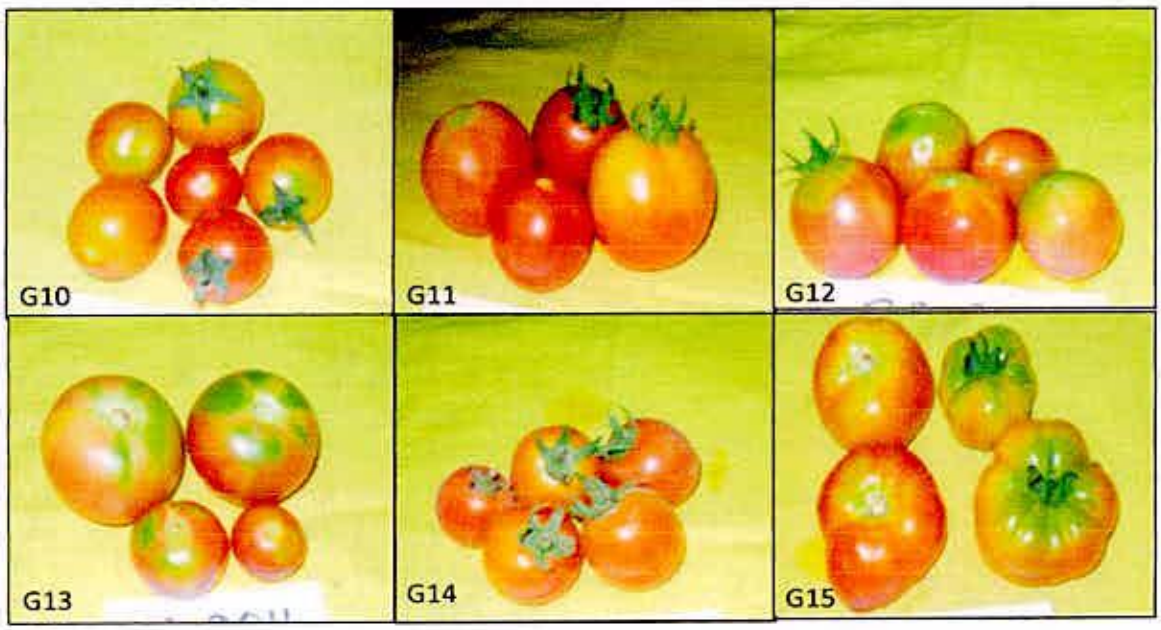


Plate 3b. Phenotypic variation in fruits of different genotypes of tomato (G_{10} - G_{15})

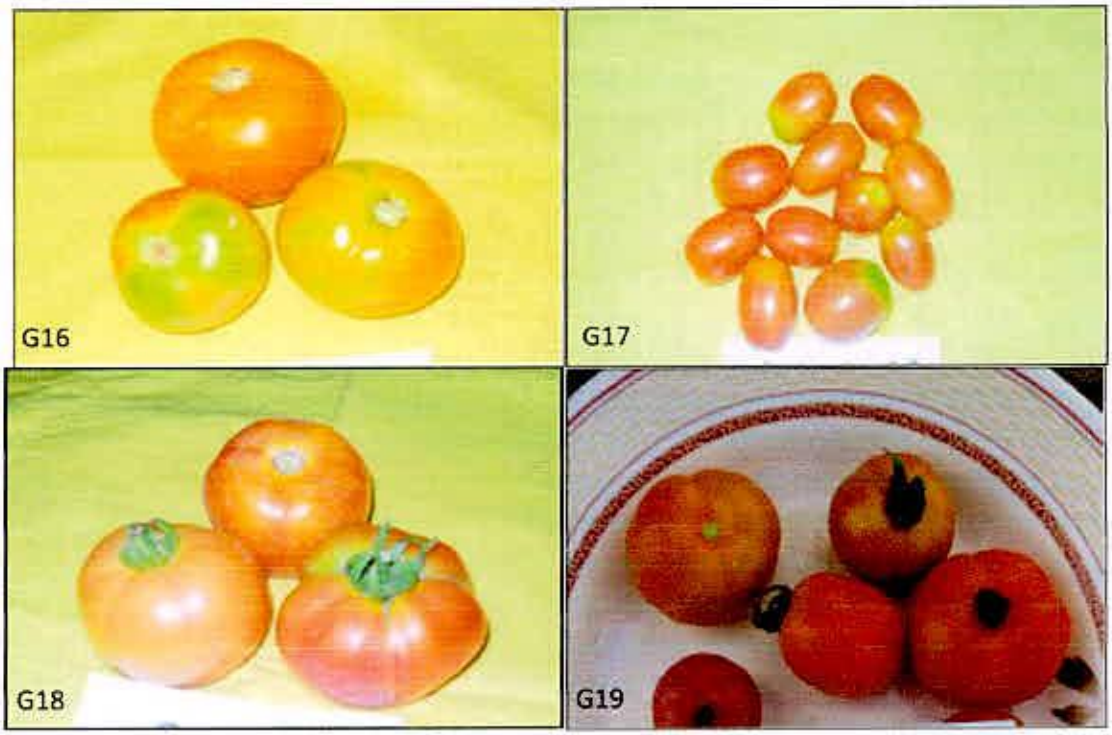


Plate 3c. Phenotypic variation in fruits of different genotypes of tomato (G_{16} - G_{19})

The difference between the genotypic co-efficient of variation (GCV) (2.22) and phenotypic co-efficient of variation (PCV) (2.78) were more or less similar to each other, indicated the variability not only for genotype but also influence of environment. Therefore, such selection sometimes is misleading (Table 3). Similar findings were reported by Farzaneh *et al.* (2013) and Kumari *et al.* (2007). Matin and Kuddus (2001) also found similar results in tomato. In contrast Monamodi *et al.* (2013) and Aditya and Phir (1995) found in significant difference in days to first flowering. The heritability estimates for days to first flowering was high with low genetic advance and genetic advance in percentage of mean. Thus indicating this trait was mostly controlled by non-additive gene. Genetic advances in per cent 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 Days to 50% flowering

Present study observed low variance for days to 50% flowering. Similar findings for days to 50% flowering were also observed by Narolia (2012). On the other hand Nalla *et al.*, (2014) found dissimilar result with very low variability for this trait. Genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) were found low. Significant differences were observed among the genotypes for days to 50% flowering which ranged from 75.33 DAS in BD-10321 to 70.00 DAS in BD-7290 with mean value 72.88 DAS (Appendix IV). The phenotypic variance appeared to be high than the genotypic variance advised significant influence of environment on the expression of genes governing days to 50% flowering (Table 3). Many author also found higher PCV than GCV (Singh, 2005 and Samadia *et al.*, 2006). Therefore, it can be referring that selection based upon phenotypic expression of this character wouldn't be productive for the improvement of tomato. The heritability estimates for this trait was high with low genetic advance and genetic advance in per cent of mean, indicating this

trait was controlled by non-additive gene. Singh *et al.* (1973) and Kumar *et al.* (1980) support the findings.

4.1.3 Days to maturity

The studied genotypes showed significant difference in case of duration for days to maturity. Maximum was found 105.67 DAS in BD-9960 and the minimum was recorded as 97.33 DAS in BD-7285 with mean value of 100.91 (Appendix IV). The genotypic variance was lower than phenotypic variance (Table 3). Genotypic co-efficient of variation and phenotypic co-efficient of variation were also close to each other. 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 results of Prashanth (2003) disagree with this result with high phenotypic coefficient of variation. The heritability estimates for this trait was high. In contrast genetic advance and genetic advance in per cent of mean were found low, indicated that this trait was controlled by non-additive gene. High heritability and moderately high genetic advance for days to maturity was also found by Kumari *et al.* (2007), Islam and Khan (1991).

4.1.4 Plant height (cm)

Significant differences were observed among the genotypes for plant height which ranged from 111.10 cm (BD-7279) to 52.00 cm (BD-7270) with mean value of 80.39 (Appendix IV). Naz *et al.* (2013), Ravindra *et al.* (2003), Shravan *et al.*, (2004) and Prasad *et al.*, (1999) also found similar significant variation for plant height. The genotypic and phenotypic variance was observed as 210.81 and 320.96, respectively with large environmental influence (Table 3). The phenotypic co-efficient of variation (22.29) and genotypic co-efficient of variation (18.06) were moderate for plant height. Kumari *et al.* (2007) obtained highest genotypic coefficient of variation which disagree with this result. Singh *et al.* (2002) showed that the phenotypic coefficient of variation was greatest for this character. Similar observations were made by Matin and

Kuddus (2001). The heritability estimates for this trait was high with moderate genetic advance and genetic advance in per cent of mean revealed that this trait was governed by additive gene. 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.

4.1.5 Branches per plant

Number of branches per plant in tomato showed significant difference where maximum number of branches was found as 16.00 in BD-7279 and the minimum was recorded as 5.67 in BD-7289 with mean value of 9.54 (Appendix IV). The phenotypic variance was higher than the genotypic variance. The genotypic co-efficient of variation and phenotypic co-efficient of variation were 22.52 and 26.48, respectively indicating that the phenotypic expression of this trait is highly governed by the environment (Table 3). Singh *et al.* (2002) also showed that the PCV was higher than GCV for number of primary branches per plant. The heritability estimates for this trait was high, genetic advance was low and genetic advance in per cent of mean were found moderate, revealed that this trait was governed by non-additive gene. Moderate heritability and low genetic advance for this character was also observed by Kumar *et al.* (2004).

4.1.6 Number of clusters per plant

Number of clusters per plant was ranged from 23.00 in BD-7285 and 9.00 in BD-7285 with mean value of 13.28 (Appendix IV). The genotypic variance and phenotypic variance for this trait were 8.77 and 12.33, respectively (Table 3). The phenotypic variance appeared higher than the genotypic variance which suggested influence of environment on the expression of the genes controlling this character. The genotypic co-efficient of variation was low than phenotypic co-efficient of variation which was not desirable for the improvement of this crop. Similar PCV and GCV were also observed by Singh *et al.* (2002). The heritability estimates for this trait was high with low genetic advance and

moderate genetic advance in per cent of mean 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).

4.1.7 Fruits per cluster

Significant differences were observed among the genotypes for number of fruits per cluster which ranged from 9.00 (in BARI Tomato-11) and 2.67 (in BARI Tomato-14) with mean value of 4.02 (Appendix IV). The genotypic variance and phenotypic variance for this trait were 1.44 and 2.14, respectively (Table 3). Phenotypic and genotypic coefficients of variation were moderate but the phenotypic variance appeared higher than the genotypic variance. The genotypic coefficient of variation and phenotypic coefficient of variation for were 29.84 and 36.43, respectively, which indicated presence of high variability among the genotypes. Similar observations found by Singh *et al.* (2002). Moderate PCV and GCV were found by Aradhana and Singh (2003) also. The heritability estimates for this trait was very high, genetic advance was low and genetic advance in per cent of mean was found moderately high, 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).

4.1.8 Fruits per plant

From the current study we observed that the maximum range for number of fruits per plant was found 104.00 in BD- 7290 and the minimum was recorded as 40.67 in 'BARI Tomato-14 (Appendix IV). The difference between genotypic (395.33) and phenotypic (563.86) variances indicate high environmental influence (Table 3). The phenotypic coefficient of variation and genotypic coefficient of variation was moderate, which indicated presence of low variability among the genotypes. Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi *et al.* (2003) supported the findings. The heritability estimates for this trait was high, genetic advance and genetic advance in per cent of mean were

found moderate, 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).

4.1.9 Average Fruit weight (g)

The maximum fruit weight was recorded as 66.93 g in BARI Tomato-14 and BARI Tomato-15 where minimum was recorded as 3.10g in BARI Tomato-11 with mean value of 22.88g (Figure 1) (Appendix IV). The genotypic variance and phenotypic variance for fruit weight was high (Table 3). The genotypic co-efficient of variation and phenotypic co-efficient of variation were high and close to each other, proved that environment has little influence on the expression of this character. Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. High GCV and PCV for average fruit weight were also noticed by Manivannan *et al.* (2005) and Singh *et al.* (2002). High heritability associated with high genetic advance in per cent of mean was observed indicating fruit weight governed by additive gene. Pandit *et al.* (2010), Ara *et al.* (2009) and Singh *et al.* (2006) also supported the present findings.

4.1.10 Fruit Length (cm)

The mean fruit length was noticed as 3.619 cm with a range of 4.93 cm to 2.63 cm. (Appendix IV). The line BD-7285 showed the minimum fruit length and the maximum fruit length was recorded in the accession BD-9011 (Figure 2). The phenotypic and genotypic variance were very low and genotypic co-efficient of variation (17.62) and phenotypic co-efficient variation were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of this crop (Table 3). 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 estimate with moderate genetic advance over percent of mean indicate that effective

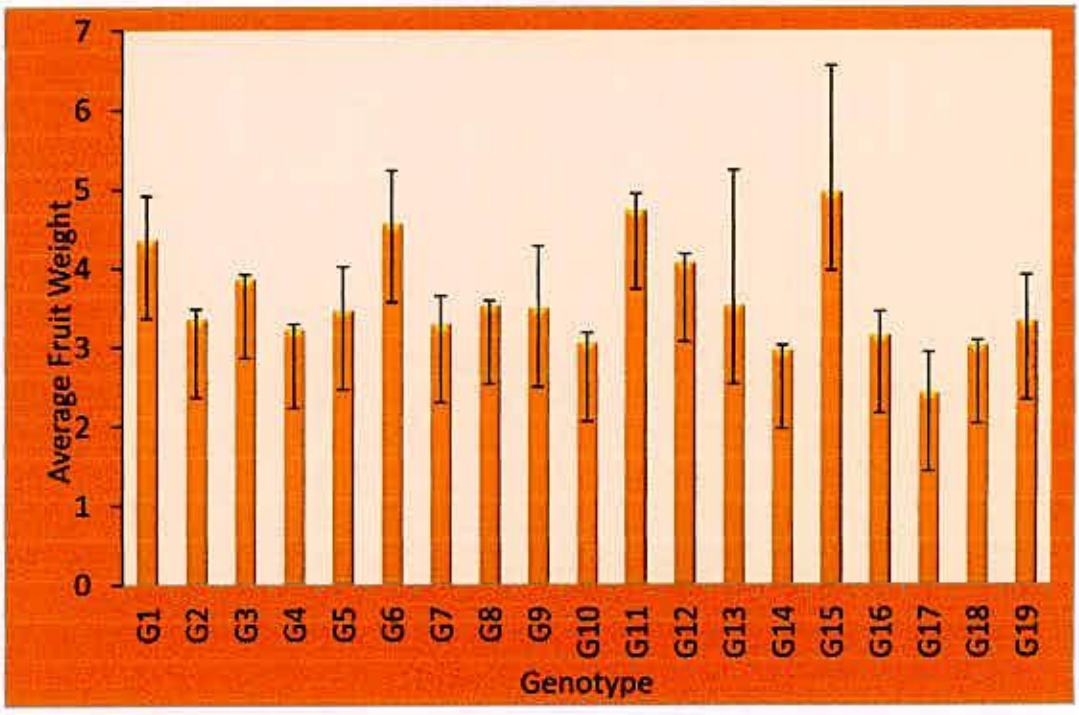


Figure 1. Comparison of Average fruit weight among nineteen genotypes of tomato

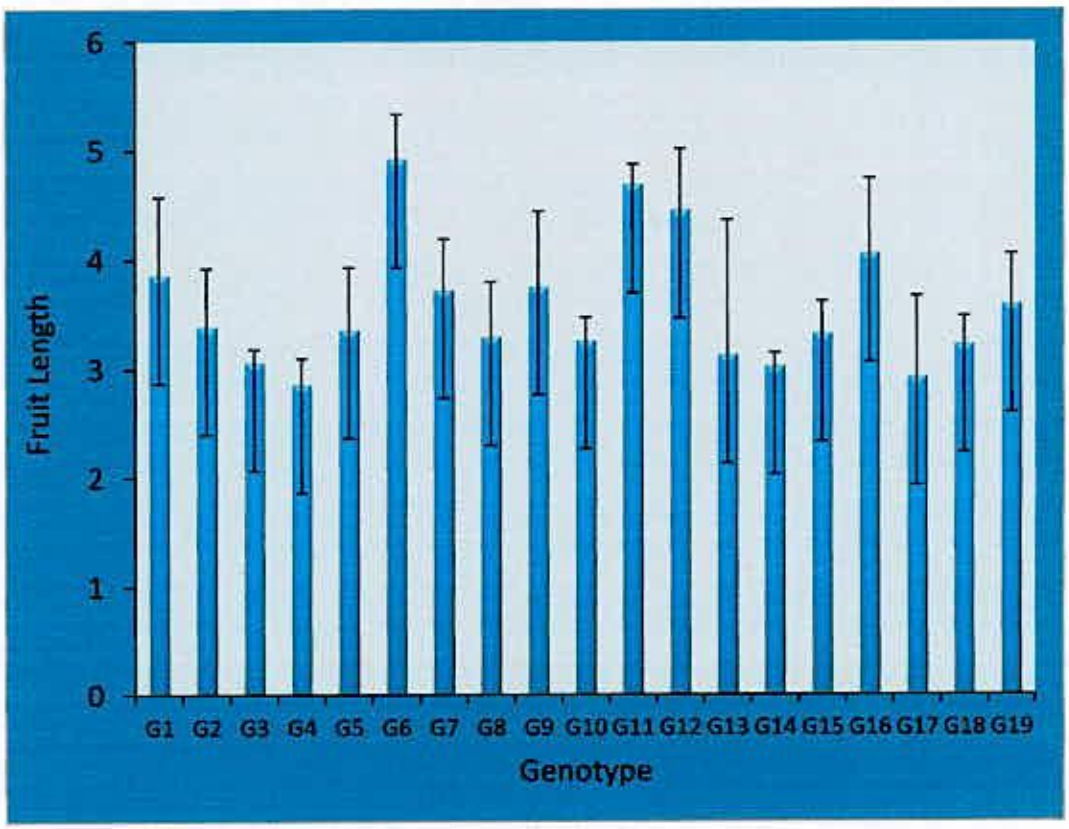


Figure 2. Comparison of fruit length among nineteen genotypes of tomato

selection may be made for fruit length. Moderate heritability and moderate genetic gain for this character was observed by Joshi et al. (2004).

4.1.11 Fruit Diameter (cm)

Fruit Diameter showed the mean fruit diameter was 3.55 cm with a range of 4.83 cm (in BD-7285) to 2.50 cm (in BARI Tomato-11) (Figure 3) (Appendix IV). The phenotypic and genotypic variance were very low and genotypic co-efficient of variation (17.62) and phenotypic co-efficient variation were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of tomato (Table 3). 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 estimate with moderate genetic advance over percent of mean indicate that effective selection may be made for fruit length. High heritability coupled with low genetic gain for this character was observed by Pandit *et al.* (2010).

4.1.12 Fruit yield per plant (g)

Fruit yield per plant was found 1356.33 g in BARI Tomato-14 which is highest and the lowest was recorded as 402.67 g in BARI Tomato-11 with mean value of 847.51 g (Figure 4) (Appendix IV). The phenotypic variance found higher than genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this character (Table 3). The phenotypic coefficient of variation and genotype coefficient of variation were 35.09 and 31.21, respectively for fruit yield per plant, which indicating that significant variation exists among different genotypes which made the trait effective for selection. Similar findings were recorded by Singh *et al.* (2006) and Manivannan *et al.* (2005). Estimation of high heritability for fruit yield per plant with high genetic advance revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding programme. High heritability and high genetic advance was also observed by Ara *et al.* (2009) and Anupam *et al.* (2002).

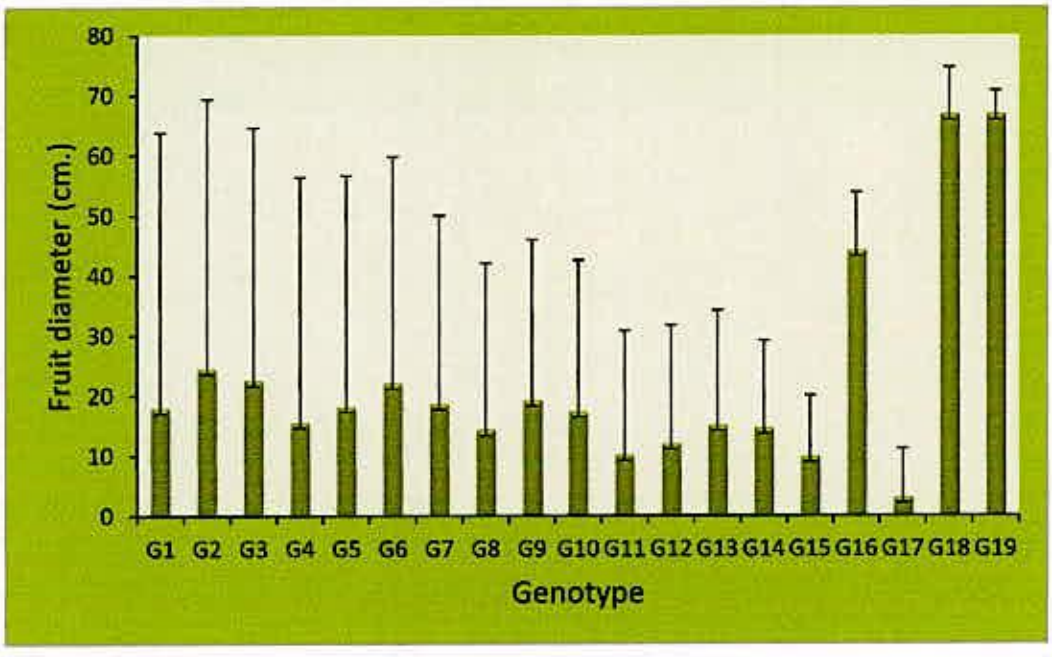


Figure 3. Comparison of fruit diameter among nineteen genotypes of tomato

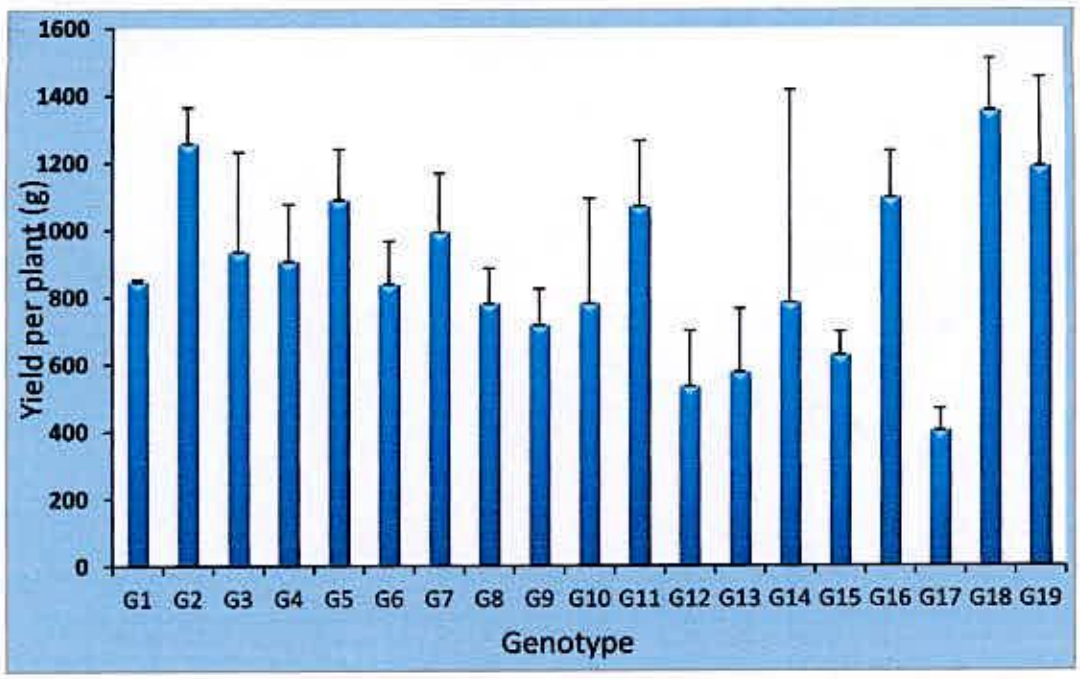


Figure 4. Comparison of yield per plant among nineteen genotypes of tomato

4.2 Correlation Co-efficient

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. So 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 genotype of tomato are given in Table 4 and Table 5.

4.2.1 Days to first flowering

Days to first flowering had significant negative correlation with fruit yield per plant (-0.260) at genotypic level. Patil and Bojappa (1993), Mayavel *et al.* (2005) and Samadia *et al.* (2006) observed positive correlation which doesn't support the present findings (Table 4). This character also showed highly significant positive association with days to 50% flowering and branches per plant at both genotypic and phenotypic levels (0.600, 0.578 and 0.547, 0.342, respectively). It had highly negative significant correlation at genotypic level with fruits per cluster (-0.341) and fruit length (0.287) at genotypic level. Days to first flowering had positive but non-significant correlation with days to maturity, plant height and fruit diameter at both level. The trait had Non-significant negative correlation at both levels for average fruit weight and fruit per cluster and fruit length at phenotypic level.

Table 4. Genotypic correlation coefficients among different pairs of yield and yield contributing characters in different genotypes of tomato

Characters	D50%F	DM	PH	BPP	NCP	FPC	FPP	AFW	FL	FD	FYP
DFF	0.600**	0.144	0.240	0.547**	0.070	-0.341**	-0.029	-0.188	-0.287*	0.172	-0.260*
D50%F		0.045	0.100	0.355**	0.133	-0.415**	0.163	-0.461**	0.177	0.332**	-0.241
DM			0.236	-0.083	-0.368**	-0.049	-0.334**	-0.136	-0.587**	-0.456**	-0.438**
PH				0.376**	-0.014	-0.054	-0.179	0.109	-0.251	-0.455**	-0.143
BPP					0.559**	-0.222	0.275*	-0.120	-0.095	0.245	-0.047
NCP						-0.083	0.454**	-0.052	0.200	0.380**	0.026
FPC							0.269*	-0.304**	-0.111	-0.386**	-0.537**
FPP								-0.399**	-0.111	0.038	-0.323**
AFW									-0.029	-0.190	0.744**
FL										0.744**	0.123
FD											0.099

** = Significant at 1%. * = Significant at 5%.

DFF = Days to First Flowering, D50%F = Days to 50% Flowering, DM = Days to Maturity, PH = Plant Height (cm), BPP = Branches Per Plant, NCP = Number of Cluster per Plant, FPC = Fruits Per Cluster, FPP = Fruits Per Plant, AFW = Average Fruit Weight (g), FL = Fruit Length (cm), FD = Fruit Diameter (cm), FYP = Fruit Yield per Plant (g).

Table 5. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters in different genotypes of tomato

Characters	D50%F	DM	PH	BPP	NCP	FPC	FPP	AFW	FL	FD	FYP
DFF	0.578**	0.177	0.208	0.342**	0.011	-0.239	-0.039	-0.150	-0.155	0.123	-0.207
D50%F		0.101	0.037	0.197	0.024	-0.306**	0.037	-0.608**	0.115	0.274*	-0.154
DM			0.128	-0.051	-0.220	-0.059	-0.144	-0.118	-0.377**	-0.332**	-0.302*
PH				0.269*	-0.051	0.007	-0.121	0.092	-0.154	-0.317**	-0.204
BPP					0.566**	-0.147	0.294*	-0.117	-0.108	0.203	-0.041
NCP						-0.011	0.459**	-0.044	0.157	0.265*	0.041
FPC							0.270*	-0.234	-0.080	-0.276*	-0.349**
FPP								-0.321**	-0.027	0.045	-0.265*
AFW									-0.017	-0.166	0.650**
FL										0.701**	0.128
FD											0.099

** = Significant at 1%. * = Significant at 5%.

DFF = Days to First Flowering, D50%F = Days to 50% Flowering, DM = Days to Maturity, PH = Plant Height (cm), BPP = Branches per Plant, NCP = Number of Cluster per Plant, FPC = Fruits Per Cluster, FPP = Fruits Per Plant, AFW = Average Fruit Weight (g), FL = Fruit Length (cm), FD = Fruit Diameter (cm), FYP = Fruit Yield per Plant (g).

4.2.2 Days to 50% flowering

Days to 50% flowering showed non-significant negative association with fruit yield per plant (-0.241 and -0.154) at both levels (Table 4). Dhankhar *et al.* (2006) and Samadia *et al.* (2006) observed positive correlation. It showed highly significant positive association with fruit diameter (0.332 and 0.274) at genotypic and phenotypic level and with branch per plant at genotypic level. Days to 50% flowering exhibited strongly significant negative relationship with fruit weight and fruit per cluster at genotypic and phenotypic level. The character revealed non-significant positive relation with plant height, number of cluster per plant, and fruits per plant at genotypic level and for fruit length at genotypic and phenotypic level. Non- significant association of this trait with yield indicated that the association was largely influenced by environment. Yield improvement can be achieved by selection for days to 50% flowering were reported by Wright *et al.* (2007).

4.2.3 Days to maturity

Days to maturity had highly significant negative correlation with fruit yield per plant (-0.438 and -0.302) at genotypic and phenotypic levels (Table 4). It had highly significant negative association with fruit length (-0.587, -0.377) and fruit diameter (-0.456, -0.332) at both levels and with number of cluster per plant and fruits per plant only genotypic level. Days to maturity had positive association with plant height. A significant and positive correlation was observed by Singh *et al.* (2002) and Mohanty (2002) between days to maturity and fruit yield per plant. This doesn't support the present findings.

4.2.4 Plant height (cm)

Plant height had non-significant negative correlation with fruit yield per plant (-0.143 and -0.204) at genotypic and phenotypic levels which is supported by Mohanty (2002) (Table 4). Plant height had significant positive correlation with

branches per plant (0.376 and 0.269) at both levels. However, it had strong negative correlation with fruit diameter (-0.455 and -0.317) at genotypic and phenotypic levels respectively. Plant height had non-significant negative relation with fruit per plant and fruit length at both levels and non-significant positive relation with average fruit weight.

4.2.5 Branches per plant

The number of branches per plant had positive and highly significant correlation with plant height (0.376 and 0.269), number of clusters per plant (0.559, and 0.566) at genotypic and phenotypic levels, respectively and number of fruits per plant (0.294) in phenotypic level (Table 4). Monamadi *et al.* (2013) found more branch number in a plant which produced more fruits. But a negative correlation between the number of branches per plant and number of fruits per plant was noticed by Singh *et al.* (2004). It had non-significant positive correlation with fruit diameter at both levels. The number of branches per plant showed non-significant negative relation for fruits per cluster, fruit weight and fruit length at both levels which results negative correlation with fruit yield per plant at both levels indicated that the association between these traits is largely influenced by environmental factors. A positive correlation between yield of fruits per plant and number of branches per plant was observed by Singh *et al.* (2006) and Ara *et al.* (2009).This doesn't support the present findings.

4.2.6 Number of clusters per plant

The number of clusters per plant had highly significant and positive association with number of branches per plant (0.559 and 0.556), number of fruits per plant (0.454 and 0.459) and fruit diameter (0.380 and 0.265) at the genotypic and phenotypic levels (Table 4). It also had highly significant negative association with days to maturity (-0.368) at genotypic level. It had significant and positive association with fruit length for both levels and days to 50% flowering at both at

genotypic and phenotypic levels. A non-significant positive correlation with fruit yield per plant (0.026, 0.041) was also observed. A positive correlation between number of clusters per plant and fruit yield per plant was also observed by Prasanna *et al.* (2005). Nesgea *et al.* (2002) also found similar results for this trait in tomato.

4.2.7 Fruits per cluster

The number of fruits per cluster showed highly significant and positive association with number of fruits per plant (0.269, 0.270) both at genotypic and phenotypic levels (Table 4). It had highly significant but negative association with days to 50% flowering (-0.415 and -0.306) and fruit diameter (-0.386 and -0.276) at both levels and at genotypic level for days to first flowering (-0.381) and average fruit weight -0.304). It also exhibited highly significant negative association with fruit yield per plant (-0.537, -0.349) at the genotypic and phenotypic level, respectively. The findings also supported by Nesgea *et al.* (2002) and Megha *et al* (2006). But Joshi *et.al* (2004) found number of fruits per cluster showed negative association

4.2.8 Fruits per plant

The number of fruits per plant had highly significant but negative association with yield per plant (-0.323 and -0.265) at genotypic and phenotypic levels respectively (Table 4). Rani *et al.* (2010) reported that the number of fruits per plant was negatively associated with yield per plant. It had significant negative correlation average fruit weight (-0.399 and -0.321) at both level and for days to maturity at genotypic levels. Joshi *et al.* (2004) showed that number of fruits per plant was negatively correlated with fruit weight. It had positive significant effect on number of cluster per plant (0.454 and 0.459) at genotypic and phenotypic level, respectively and at genotypic level for fruit per cluster (0.269).

4.2.9 Average fruit weight (g)

Fruit weight showed highly significant and positive correlation with fruit yield per plant (0.744 and 0.650) for both levels (Table 4). Matin and Kuddus (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 highly significant negative effect at both levels for days to 50% flowering and fruits per plant and for fruit per cluster only at genotypic level. Matin and Kuddus (2001) found significant negative correlations between number fruits per plant and individual fruit weight.

4.2.10 Fruit length (cm)

Fruit length was insignificantly positively correlated with fruit yield (0.123 at genotypic level). Fruit length (FL) also showed highly negative correlation with fruits per plant (-0.287) and date of maturity (-0.587) (Table 4). It evidenced no significant positive relation with any of the yield contributing characters. But, it was insignificantly and positively associated with number of cluster per plant (0.20, at genotypic level).

4.2.11 Fruit diameter (cm)

Fruit diameter showed significant positive relation with days to 50% flowering, number of cluster per plant and fruit length at genotypic level (Table 4). The genotypic correlation coefficients were 0.332, 0.380 and 0.744, respectively (all significant at 1% level). On other hand, fruit diameter was highly negatively associated with date of maturity, plant height and number of fruits per cluster. It was insignificantly positively correlated with yield per plant. 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.

4.2.12 Fruit yield per plant (g)

In general, fruit yield is the main target of improvement. Thereby its correlation study is utmost important. From Table 4 and 5 it was observed that, fruit yield per plant was strongly and positively correlated with average fruit weight at both genotypic and phenotypic level (genotypic correlation coefficient 0.744 and phenotypic correlation coefficient 0.650), significant at 1% level of significance. Similar result was also reported by several authors. Rani *et al.* (2010) conducted an experiment with tomato and found average fruit weight along with some other fruit quality (like pericarp thickness and lycopene content) was positively and significantly associated with fruit yield per plant. Findings' of Weber *et al.* (2010) also evidenced the positive and strong association between fruit yield per plant and average fruit weight. Singh and Cheema (2006) reported positive indirect effects through average fruit weight mainly contributed towards its strong association with yield. This study also revealed positive but insignificant correlation between fruit yield per plant and fruit length and fruit diameter at genotypic level (0.123 and 0.099, respectively). Though, strong association between fruit yield per plant and fruit diameter and fruit length were reported earlier (Susic. 2002). Again, fruit yield per plant showed strong negative association with date of maturity, fruits per cluster and fruits per plant at both genotypic and phenotypic level. Genotypic correlation coefficients of date of maturity, fruit per cluster and number of fruit per plant were -0.438, -0.537 and -0.323, respectively. Inconsistently, fruits per plant manifested strong positive association with fruit yield per plant in several earlier investigations (Kumar *et al.*, 2004; Kumar *et al.*, 2003 and Singh *et al.*, 2004). Dhankar (2006) reported number of fruits per plant had the highest direct effect on yield per plant. But, in more recent study, Rani *et al.* (2010) investigated negative association between numbers of fruit per plant with fruit yield. It is assumed that,

less fruit number enabled high average fruit weight and thereby high positive correlation between average fruit weight and fruit yield per plant had already been established in the present study.

4.3 Path coefficient analysis

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 plant height (cm), days of first flowering, days 50% flowering, days to maturity, branches per plant, number of clusters per plant, fruits per cluster, fruits per plant, individual fruit weight (g), fruit length (cm) and fruit diameter (cm)were treated as independent variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of tomato in Table 6.

4.3.1 Days to first flowering

Days to first flowering had negative direct effect on yield per plant which is contributed to result non-significant negative genotypic correlation with yield per plant (-0.189). Matin and Kuddus (2001) reported that days to first flowering had negative direct effect on yield per plant. It had positive indirect effect on days to 50% flowering (0.096), number of branches per plant (0.049), number of fruits per cluster (0.043) and fruit length (0.100). Negative indirect effect was found via days to maturity (-0.039) plant height (-0.050), average fruit weight (-0.076), fruit diameter (-0.003).

4.3.2 Days to 50% flowering

Days to 50% flowering had positive direct effect (0.165) on yield per plant. Days to 50% flowering had positive indirect effect on number of branches per plant (0.030), number of fruits per cluster (0.053) and fruit length (0.030). But it had negative indirect effect on, days to first flowering (-0.128), days to maturity

Table 6. Path coefficient analysis showing direct and indirect effects of different characters on yield of tomato

Characters	Direct effect	Indirect effect											Genetic correlation with yield
		DFF	D50%F	DM	PH	BPP	NCP	FPC	FPP	AFW	FL	FD	
DFF	-0.221	-	0.096	-0.039	-0.050	0.049	0.002	0.043	0.009	-0.076	0.002	-0.003	-0.189
D50%F	0.165	-0.128	-	-0.023	-0.009	0.030	-0.030	0.053	-0.004	-0.224	0.030	-0.009	-0.149
DM	-0.223	-0.039	0.017	-	-0.030	-0.007	0.006	0.010	0.020	-0.068	-0.001	0.011	-0.304**
PH	-0.256	-0.043	0.006	-0.026	-	0.040	0.001	-0.002	0.018	0.052	0.002	0.010	-0.198
BPP	0.158	-0.069	0.031	0.009	-0.065	-	-0.015	0.024	-0.044	-0.069	-0.001	-0.006	-0.047
NCP	-0.027	0.017	0.001	0.048	0.013	0.089	-	-0.001	-0.068	-0.032	0.001	-0.009	0.032
FPC	-0.168	0.057	-0.052	0.014	-0.003	-0.022	-0.010	-	-0.040	-0.144	-0.010	0.009	-0.349**
FPP	-0.146	0.014	0.004	0.031	0.032	0.048	-0.012	-0.046	-	-0.193	0.001	-0.001	-0.270*
AFW	0.602	0.028	-0.061	0.025	-0.022	-0.018	0.001	0.040	0.047	-	0.001	0.006	0.647**
FL	0.623	0.001	-0.070	-0.029	-0.062	-0.036	-0.046	0.019	-0.022	-0.034	-	0.001	0.021
FD	-0.033	-0.023	0.044	0.076	0.078	0.031	-0.007	0.045	-0.006	-0.102	-0.068	-	0.101

Residual effect: 0.209

*** = Significant at 5%. ** = Significant at 1%.**

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to Maturity, PH = Plant Height (cm), BPP = Branches per plant, NCP = Number of cluster per plant, FPC = Fruits per cluster, FPP = Fruits per plant, AFW = Average Fruit Weight (g), FL = Fruit length (cm), FD = Fruit Diameter (cm).

(-0.023), plant height (-0.009), number of fruits per plant (-0.004), average fruit weight (-0.224) and fruit diameter (-0.009). Number of cluster per plant (0.000) contributed to result no genotypic correlation with yield per plant. Singh *et al.* (2004) showed that days to 50% flowering had high positive direct effect on yield, which is supported by present findings.

4.3.3 Days to maturity

Days to maturity had negative direct effect on yield per plant (-0.223) and it had also significant negative correlation with yield per plant (-0.304). Singh *et al.* (2004) also reported that days to maturity had high negative direct effects on yield in tomato. Days to maturity had positive direct effect on yield through days to first flowering (0.067), days to 50% flowering (0.781), number of cluster per plant (0.163), plant height (0.037), number of fruits per cluster (0.077), fruit diameter (0.414). This trait had also negative indirect effect on number of branches per plant (-0.175), number of fruits per plant (-0.195), individual fruit weight (-0.022) at genotypic level (Table 6).

4.3.4 Plant height (cm)

Plant height had negative direct effect on yield per plant (Table 6). It had positive indirect effect through days to 50% flowering (0.006), branches per plant (0.040), fruits per plant (0.018), average fruit weight (0.052) and fruit length (0.020). On the other hand, plant height showed negative indirect effect on yield per plant via days to first flowering (-0.043), days to maturity (-0.026), number fruits of per cluster (-0.002), fruit diameter (-0.300) which resulted non-significant negative genotypic correlation with yield per plant (-0.198). Matin and Kuddus (2001) reported that plant height had negative direct effect on yield per plant.

4.3.5 Branches per plant

Number of branches per plant had positive direct effect on yield per plant (0.158) and it had also negative correlation with yield per plant (-0.047). This

trait had positive indirect effect on days to 50% flowering (0.031), days to maturity (0.009), number of fruits per clusters (0.024) and fruit length (0.007). On the other hand negative indirect effect was found on days to first flowering (-0.069), plant height (-0.065), number of clusters per plant (-0.015), number of fruits per plant (-0.044), average fruit weight (-0.069) and fruit diameter (-0.006) (Table 6). Singh *et al.* (2004) also reported that number of branches per plant had direct negative effects on yield which is not supported by present findings. This disagreement with present findings might be due to environmental variation.

4.3.6 Number of clusters per plant

Number of clusters per plant had negative direct effect (-0.027) on yield per plant and non-significant positive correlation with yield per plant (0.032). It had positive indirect effect on days to first flowering (0.017), days to 50% flowering (0.001), days to maturity (0. 048), plant height (0.013), number of branches per plant (0.089). This trait showed negative indirect effect on number of fruits per clusters (-0.001), number of fruits per plant (-0.068), average fruit weight (-0.032) and fruit diameter (-0.009) (Table 6). Similar findings reported by Singh *et al.* (2004).

4.3.7 Fruits per cluster

Number of fruits per cluster showed negative direct effect (-0.168) on yield per plant at genotypic level. It also showed positive indirect effects through days to first flowering (0.057), days to maturity (0.014), fruit diameter (0.009). It had negative indirect effect on days to 50% flowering (-0.052), plant height (-0.003), number of branches per plant (-0.022), number of fruits per plant (-0.040) average fruit weight (-0.144) and fruit length (-0.020) (Table 6). It had also significant negative correlation with yield per plant (-0.349). Mayavel *et al.* (2005) also reported that number of fruits per cluster had negative direct effects on fruit yield.

4.3.8 Fruits per plant

Number of fruits per plant showed negative direct effect (-0.146) on yield per plant. It had also significant negative correlation with yield per plant (-0.270). Number of fruits per plant had positive indirect effects on days to first flowering (0.014), days to 50% flowering (0.004), days to maturity (0.031), plant height (0.032), and number of branches per plant (0.048). It had negative indirect effect on number of clusters per plant (-0.012), number of fruits per cluster (-0.046), average fruit weight (-0.193) and fruit diameter (-0.001) (Table 6). 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.

4.3.9 Average fruit weight (g)

Path analysis revealed that fruit weight had direct positive effect (0.602) on yield per plant and significant positive correlation with yield per plant (0.647). This trait had also indirect positive effect on days to first flowering (0.028), days to maturity (0.025), number of clusters per plant (0.001), number of fruits per cluster (0.040), number of fruits per plant (0.047) and fruit diameter (0.006). Further, fruit weight showed indirect negative effect on days to 50% flowering (-0.061), plant height (-0.022) and number of branches per plant (-0.018) (Table 6). 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.

4.3.10 Fruit length (cm)

Fruit length (0.623) had positive direct effect on yield per plant. It had also non-significant positive correlation with yield per plant (0.021). This trait had also indirect positive effect on number of branches per plant (0.006) and

number of fruits per cluster (0.019). Fruit length showed indirect negative effect on days to 50% flowering (-0.240), plant height (-0.26) and average fruit weight (-0.034) (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.

4.3.11 Fruit diameter (cm)

Fruit diameter showed highly negative direct effect (-0.033) on yield per plant. It had also non-significant positive correlation with yield per plant (0.101). It had positive indirect effect on days to 50% flowering (0.044), days to maturity (0.076), plant height (0.078), number of branches per plant (0.031), number of fruits per cluster (0.045) and fruit length (0.053). Fruit diameter had negative indirect effects on days to first flowering (-0.023), number of clusters per plant (-0.007), fruits per plant (-0.006) and average fruit weight (-0.102) (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 not supported by present findings. This discrepancy with present findings might be due to environmental variation. The genotypic residual effect was 0.380, which indicated that there were other responsible traits for contribution to yield per plant but not taken into consideration in the present study.

4.4 Multivariate analyses

The genetic diversity of tomato advanced lines is presented in Table 7 to 12 and Figure 5 & 6.

4.4.1 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 three Eigen values for three principal coordination axes of genotypes accounted for 61.55% variation (Table 7).

Table 7. Eigen values and yield percent contribution of 12 characters of nineteen genotypes

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Days of first flowering	2.755	22.96	22.96
Days 50% flowering	2.586	21.55	44.51
Days of maturity	2.045	17.04	61.55
Plant height (cm)	1.559	12.99	74.54
Branches per plant	0.895	7.46	82.00
Number of clusters per plant	0.646	5.38	87.38
Fruits per cluster	0.523	4.36	91.64
Fruits per plant	0.327	2.72	94.36
Average fruit weight (g)	0.299	2.49	96.85
Fruit length (cm)	0.223	1.86	98.71
Fruit diameter (cm)	0.084	0.70	99.41
Fruit yield per plant (g)	0.057	0.59	100.00

A two dimensional scattered diagram was developed (Figure 5). According to the principal axes I and II, a two dimensional chart (Z1-Z2) (Appendix V) of the genotypes. The scatter diagram revealed that there were five apparent clusters. The genotypes were distantly located from each other (Figure 6).

4.4.2 Non-Hierarchical Clustering

Nineteen *Solanum lycopersicum* L. genotypes were grouped into five different clusters through non-hierarchical clustering (Table 8). These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Shashikanth *et al.* (2010) reported ten clusters, Mahesha *et al.* (2006) reported nine clusters, Sharma and Verma (2001) reported five clusters in tomato. Cluster I had highest number of six genotypes followed by cluster II and cluster III constituted by four genotypes, respectively. On the other hand, cluster IV constituted by three genotypes and cluster I had two genotypes (Table 7). Interestingly, cluster V have G_{18} and G_2 (BARI Tomato-14, BD-7270) whereas cluster IV composed of G_{12} (BD-9010), G_{14} (BD-9960) and G_{17} (BARI Tomato-11). Furthermore, cluster III constitute with G_9 (BD-7290), G_{10} (BD-7759), G_{13} (BD-9011) and G_{15} (BD-10321). Cluster II represents 4 genotypes namely G_5 (BD-7281), G_{11} (BD-7762), G_{16} (BARI Tomato-7) and G_{19} (BARI Tomato-15). Last of all cluster I had six genotypes G_1 (BD-7258), G_3 (BD-7276), G_4 (BD-7279), G_6 (BD-7285), G_7 (BD-7286), G_8 (BD- 7289). According to the cluster means (Table 8), cluster I had the highest cluster mean value for five characters namely days to maturity (98.8), branch per plant (10.6), cluster per plant (14.7), fruits per plant (82.8) and fruit diameter (3.8). This indicates that, genotype of cluster I could be used for parent in future hybridization program for days to maturity, branch per plant, cluster per plant, fruits per plant and fruit diameter. Cluster II had high value for number of plant height (86.6) and fruit length (3.9) than other cluster. In cluster III had moderate mean value for all character. Highest cluster mean value was achieved for fruits per cluster (5.6) in cluster IV.

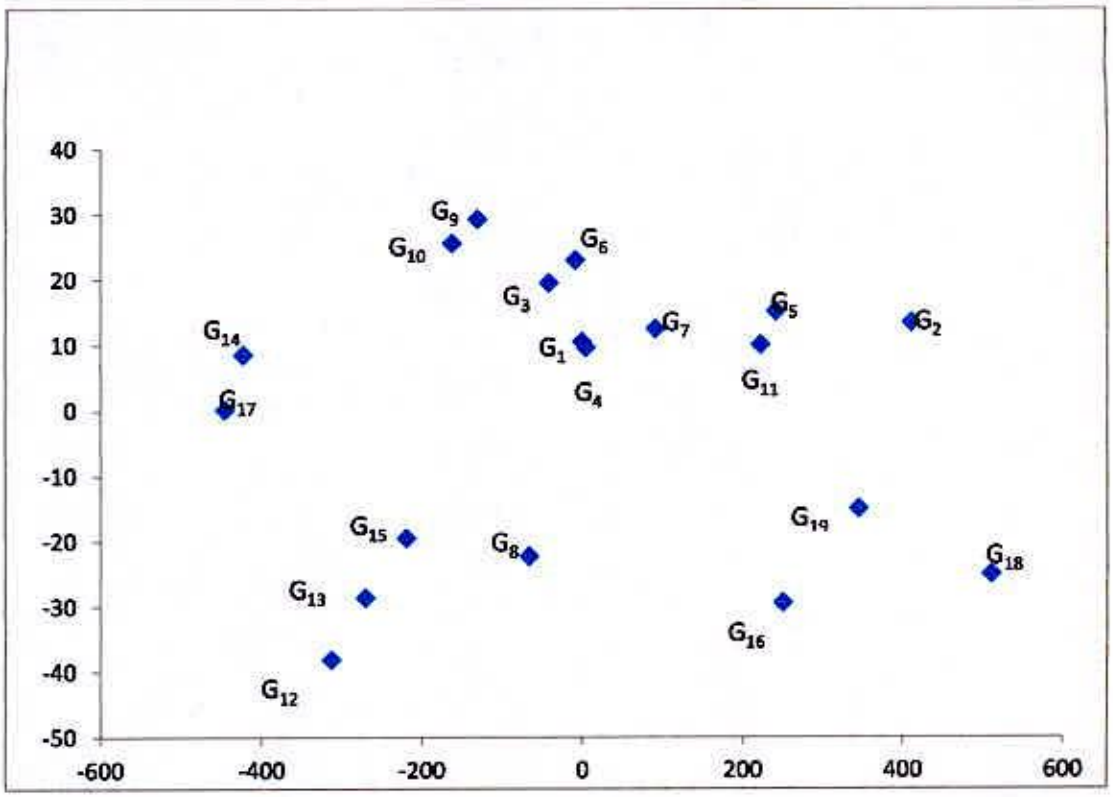


Figure 5. Scatter diagram of nineteen tomato genotypes based on their principle component scores

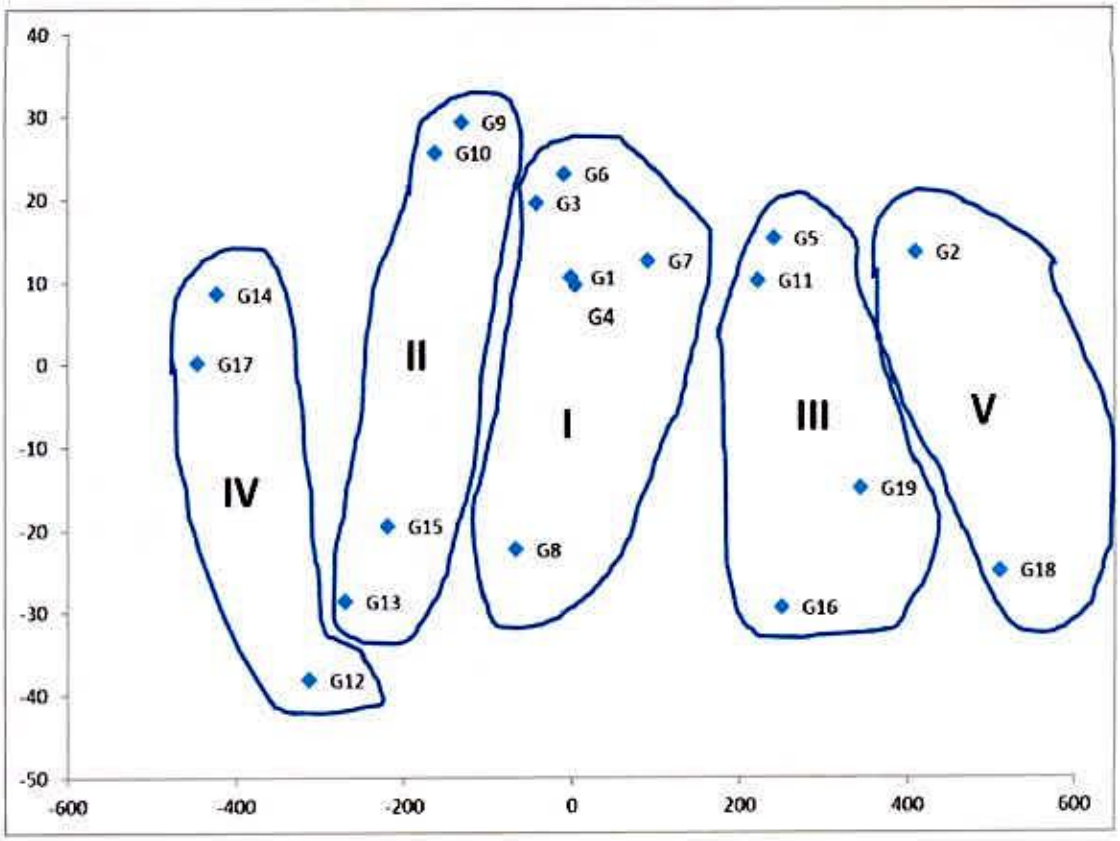


Figure 6. Scatter diagram of nineteen genotypes of tomato based on their principal component scores superimposed with clustering

Table 8. Distribution of nineteen genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G_1, G_3, G_4, G_6, G_7, G_8	6	BD-7258, BD-7276, BD-7279, BD-7285, BD-7286, BD-7289
II	G_5, G_{11}, G_{16}, G_{19}	4	BD-7281, BD-7762, BARI Tomato-7, BARI Tomato-15
III	G_9, G_{10}, G_{13}, G_{15}	4	BD-7290, BD-7759, BD-9011, BD-10321
IV	G_{12}, G_{14}, G_{17}	3	BD-9010, BD-9960, BARI Tomato-11
V	G_2, G_{18}	2	BD-7270, BARI Tomato-14

Cluster mean value was achieved high for fruit weight (45.80) and fruit yield per plant (1.38) and minimum requirement for days to first flowering (62.0) and for days to 50% flowering in cluster V. Genotype of cluster III could be used for parent in future hybridization program for all morphological character in this experiment studied.

4.4.3 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 9. 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. Islam and Islam (2000) reported that the inter-cluster distances were larger than the intra-cluster distances. The highest inter-cluster distance was observed between clusters IV and V (45.95), followed by between clusters II and V (41.92), III and V (39.26) and I and IV (34.75). In contrast, the lowest inter-cluster distance was observed between cluster I and III (7.11), followed by III and IV (8.43).

However, the maximum inter-cluster distance was observed between the clusters IV and V (45.95) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population. On the other hand, the maximum intra-cluster distance was found in cluster IV (0.78), which contained of 3 genotypes, while the minimum distance was found in cluster V (0.00) that comprises 2 genotypes. Inter and intra cluster distances were showed in table 10. Results of different multivariate analysis were superimposed in Figure 1 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another. Cluster I consists of nearest cluster with D^2 values cluster III (7.11) and farthest cluster with D^2 values V (34.75) (Table 11). Cluster II consists of nearest cluster with D^2 values cluster I (15.54) and farthest cluster with D^2 values V (41.92). Cluster III consists of nearest cluster

with D^2 values cluster I (7.11) and farthest cluster with D^2 values V (45.95). Cluster IV consists of nearest cluster with D^2 values cluster III (8.43) and farthest cluster with D^2 values V (45.95). Cluster V consists of nearest cluster with D^2 values cluster I (34.75) and farthest cluster with D^2 values IV (45.95). 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 five clusters.

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 IV and V. So the crosses between the genotypes belonging cluster I with cluster II, cluster II with cluster III and cluster IV with cluster V might produce high heterosis. Also the crosses between genotypes from cluster IV with cluster V might produce high level of segregating population. So the genotypes belonging to cluster I and cluster II, cluster II and cluster III and cluster IV and cluster V have been selected for future hybridization program.

4.3.3 Contribution of traits towards divergence of the genotypes

The latent vectors (Z1 and Z2) obtained from principal component analysis (PCA). The important characters responsible for genetic divergence in the axis of differentiation in vector I (Z1) were number of cluster per plant (0.012), Individual fruit Weight (g) (0.042) and branches per plant (4.135) were major characters that contribute to the genetic divergence. In vector II days to first flowering (1.270), days to 50% flowering (0.317), plant height (0.415), date of Maturity (1.647), fruits per cluster (3.637), fruits per plant (0.136), fruit Diameter (cm) (9.480) and fruit yield per plant (g) (0.041) showed their important role toward genetic divergence. The value of Vector I and Vector II

Table 9. Cluster mean values of twelve different characters of nineteen genotypes

Characters	I	II	III	IV	V
Days of first flowering	64.4	63.0	63.7	63.3	62.0
Days 50% flowering	73.4	72.7	73.1	72.8	71.3
Days of Maturity	98.8	100.6	102.3	103.4	101.3
Plant height	79.5	86.6	81.7	83.6	63.3
Branches per plant	10.6	8.6	9.5	9.0	9.3
Number of cluster per plant	14.7	12.9	11.9	12.9	13.0
Fruits per cluster	3.8	3.8	3.8	5.6	3.2
Fruits per plant	82.8	66.7	81.4	74.1	53.3
Average Fruit Weight (g)	18.6	34.9	15.5	10.0	45.8
Fruit length (cm)	3.7	3.9	3.3	3.6	3.2
Fruit Diameter (cm)	3.8	3.7	3.5	3.2	3.2
Fruit yield per plant (g)	844.5	1112.4	652.2	454.1	1307.4

Table 10. Intra (Bold) and inter cluster distances (D^2) for nineteen genotypes of tomato

Cluster	I	II	III	IV	V
I	**0.07**	15.54	7.11	14.91	34.75
II		**0.25**	16.92	19.90	41.92
III			**0.23**	8.43	39.26
IV				**0.78**	45.95
V					**0.00**

Table 11. 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	III (7.11)	V (34.75)
2	II	I (15.54)	V (41.92)
3	III	I (7.11)	V (39.26)
4	IV	III (8.43)	V (45.95)
5	V	I (34.75)	IV (45.95)

Table 12. Relative contributions of the twelve characters of nineteen genotypes to the total divergence

Characters	Vector-1	Vector-2
Days of first flowering	-3.210	1.270
Days 50% flowering	-0.527	0.317
Days of Maturity	-2.456	1.647
Plant height	-0.782	0.415
Branches per plant	4.135	-2.322
Number of cluster per plant	0.012	0.316
Fruits per cluster	-5.342	3.637
Fruits per plant	-0.368	0.136
Individual Fruit Weight (g)	0.042	-0.095
Fruit length (cm)	-2.044	-0.898
Fruit Diameter (cm)	-15.988	9.480
Fruit yield per plant (g)	-0.005	0.041

(Table 12) revealed that both Vectors had positive values for number of cluster per plant indicating the highest contribution of these traits towards the divergence among nineteen genotypes of tomato. Negative values in both vectors for fruit length had lower contribution towards the divergence.

4.4.5 Selection of genotypes as parent for hybridization programme

Selection of genetically diverse parents is the prime task for any plant breeding activities. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distance parents (Ghaderi *et al.*, 1984). Considering the magnitude of cluster mean and agronomic performance the genotype G_4 for maximum branches per plant, G_6 for maximum number of cluster per plant; G_9 for number of fruits per plant; G_{18} and G_{19} for maximum fruit weight, G18 for maximum fruit yield per plant were found promising. Therefore considering group distance and other agronomic performance the inter-genotypic crosses betweenG_4 and G_9; G_6 and G_9; G_{19} and G_9; G_{18} and G_6 might be suggested for future hybridization program.

4.5 Biochemical analysis

Regular consumption of tomatoes has been associated with decreased risk of chronic degenerative diseases. Epidemiological findings confirm the observed health effects are due to the presence of different antioxidant molecules such as carotenoids, particularly lycopene and ascorbic acid. Brix is primarily a measure of the carbohydrate level tomato. High brix foods have greater mineral density and taste better. In this work, three components contributing to the healthy quality of tomato (i. e. lycopene, Vitamin C and Brix) were studied in the framework of breeding programs aiming to develop nutritional superior genotypes. The lycopene content, vitamin C content and Brix percentage were estimated and the mean value is presented in Appendix VI and Appendix VII.

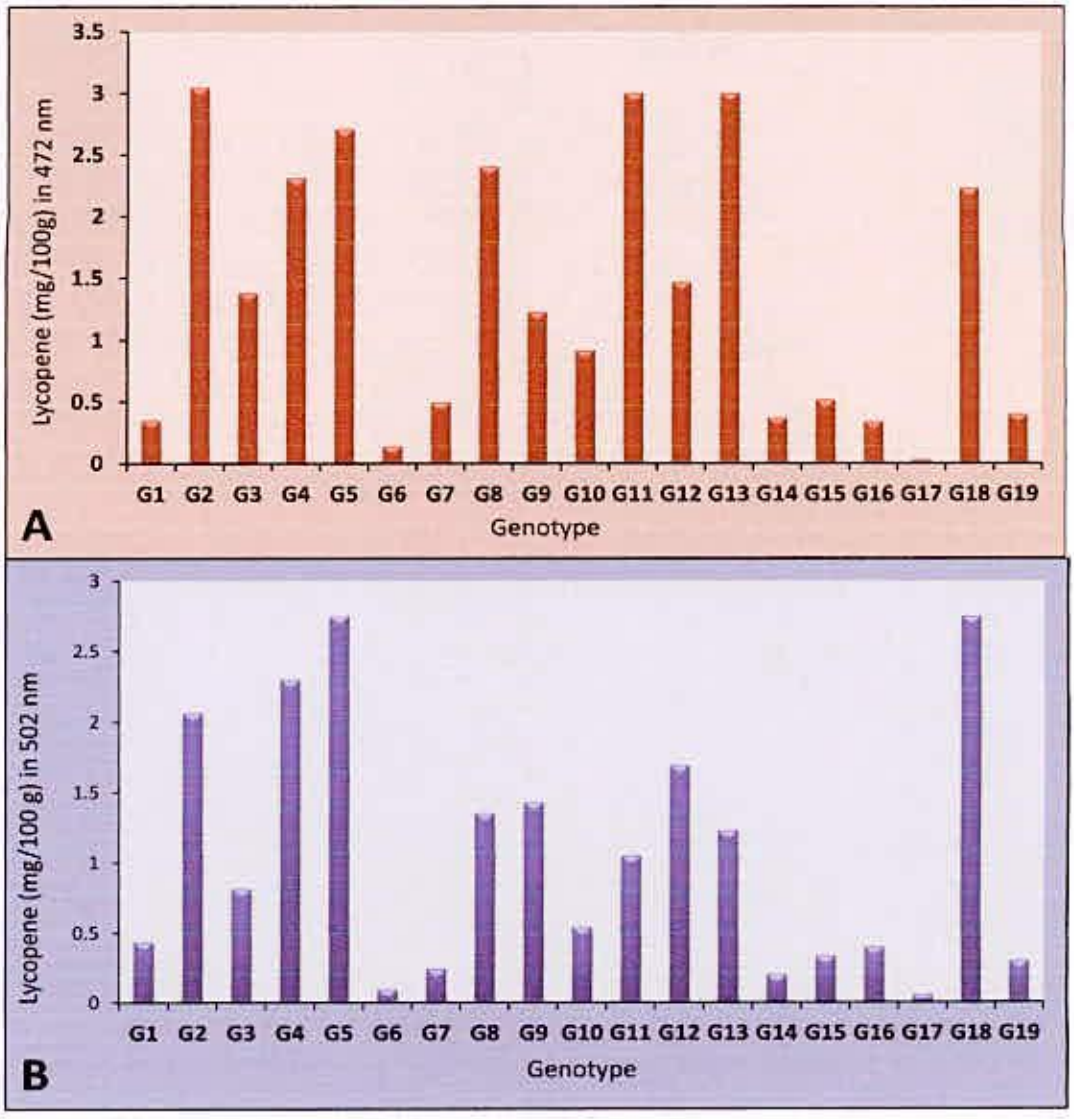


Figure 7. Lycopene content in nineteen genotypes of tomato. A) Lycopene content at the absorbance of 472 nm and B) lycopene content at the absorbance of 502 nm

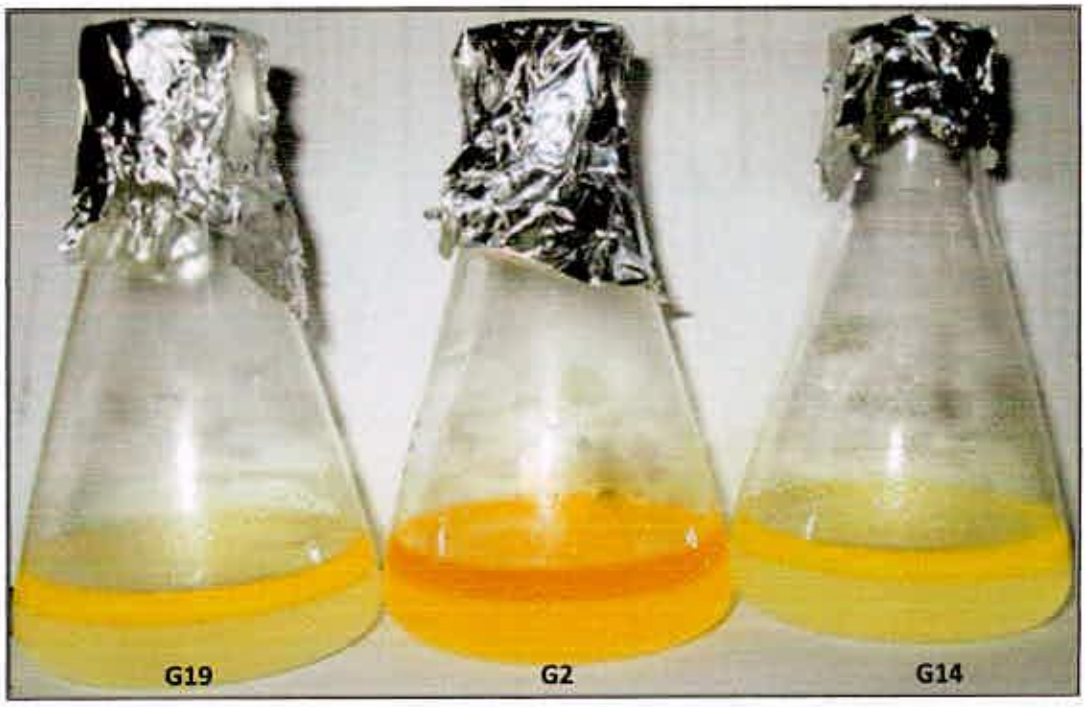


Plate 4. Variation in lycopene content in different genotypes of tomato

4.5.1 Lycopene

The lycopene content of nineteen genotypes of tomato was determined. The result was observed among nineteen genotypes of tomato (Plate 4; Figure 7). The upper layer which is lycopene were isolated with micropipette and measured with the spectrophotometer. The products studied were presented in mg /100 g Figure 7. Illustrates the significant variability for lycopene content among the genotypes. The result showed that lycopene content of samples from genotype G_2 (3.0468 mg /100 g at 472 nm and 2.067 mg / g at 502 nm), G_4 (2.31 mg /100 g at 472 nm and 2.3 mg /100 g at 502 nm), G_5 (2.71 and 2.75 mg /100 g at 472 and 502 nm respectively), G_8 (2.404 and 1.356 mg /100 g at 472 and 502 nm respectively) and G_{18} (2.228 and 2.75 mg /100 g at 472 and 502 nm respectively) showed very high lycopene content at both absorbance 472 nm and 502 nm as compared to those of the other genotypes. Lycopene is an important intermediate in the biosynthesis of many carotinoids including beta carotene, responsible for yellow, orange or red pigmentation, photosynthesis and photo-protection. Due to its strong colour and non-toxicity lycopene is a useful food coloring. For these reasons, these five genotypes could be selected for cultivation as well as for future breeding program. Follad (2013), Alda *et al.* (2009), Moigrădean *et al.* (2007), Cucu and Loco, (2011) found similar variability for lycopene in their experiments.

4.5.2 Vitamin C

Vitamin C, more properly called ascorbic acid, is an essential antioxidant needed by the human body. In this experiment, the Vitamin C content of nineteen genotypes of tomato was determined by oxidation reduction titration method. The result for Vitamin C was observed among the nineteen genotypes of tomato (Figure 8A). G_1(1.26 mg /100 g), G_{10} (1 mg /100 g) and G_{14} (1.2 mg /100 g) 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.

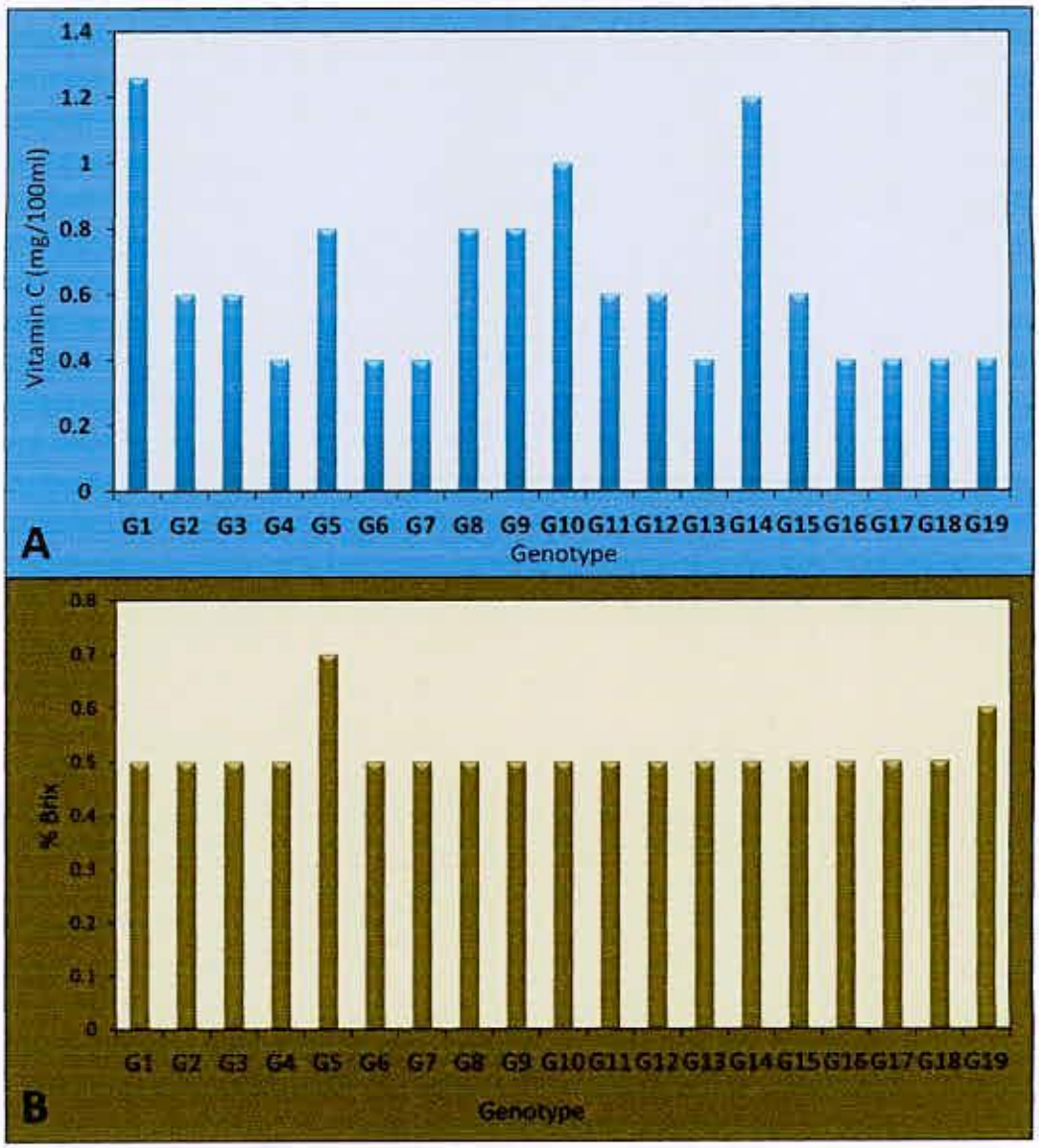
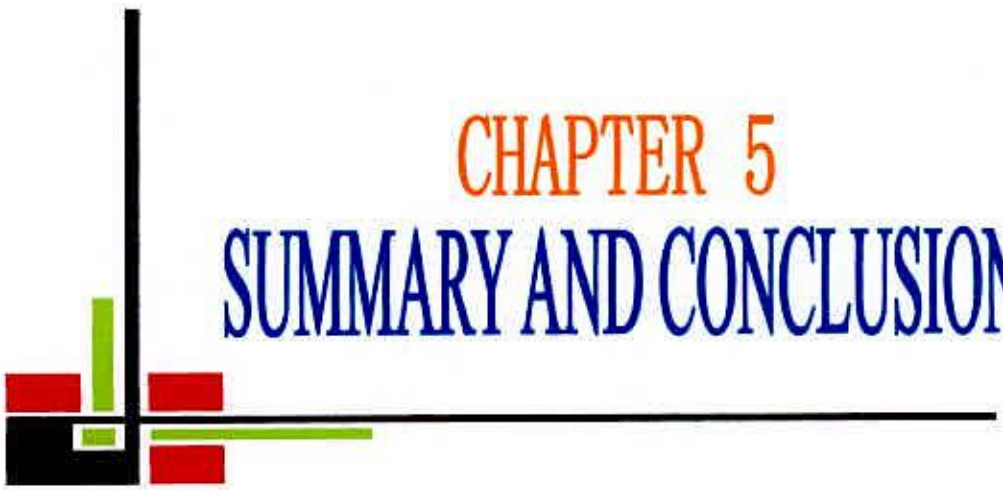


Figure 8. Vitamin C content and % of Brix in nineteen genotypes of tomato A) Vitamin C content B) % of Brix

4.5.3 % of Brix

In this experiment, the % of Brix of nineteen genotypes of tomato was determined by refractometer. Very little variability was observed among the genotypes for percent of Brix (Figure 8B). G_5 and G_{19} contained high brix percentage.



CHAPTER 5
SUMMARY AND CONCLUSION

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 2012 to April 2013. Seeds were sown in seed bed then transferred to the main field in Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, days to first flowering, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of fruits per cluster, number of fruits per plant, fruit weight (g) fruit length (cm), fruit diameter (cm) and yield per plant (g) were recorded. 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 (1356.33-402.67) that means wide range of variation present for this character. This character also showed the highest mean value (847.51). However, the phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient variation for all the characters under study. In case of days to maturity, plant height, number of cluster per plant, number of fruits per cluster, number of fruits per plant and yield per plant showed higher influence of environment for the expression of these characters. On the other hand, branch per plant, fruit per cluster, fruit length and fruit diameter showed least difference in phenotypic and genotypic variance suggesting additive gene action for the expression of the characters. All the characters under 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 and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with seed yield per plant was found in average fruit weight (0.744 and 0.650). In addition, there were non-significant positive correlation with fruit yield per plant was also found in number of cluster per plant (0.026 and 0.041), fruit length (0.123 and 0.128) and fruit diameter (0.099 and 0.099) at genotypic and phenotypic level, respectively. On the other hand, the non-significant negative correlation was also found in days to 50% flowering (-0.241, -0.154), plant height (-0.143 and -0.204), branches per plant (-0.047 and -0.041) while the highest significant negative correlation was found in days to maturity (-0.438 and -0.302), fruits per cluster (-0.537 and -0.349) and fruits per plant (-0.323 and -0.265) at genotypic and phenotypic level, respectively.

Path coefficient analysis showed that average fruit weight had the highest positive correlation with fruit yield per plant. Coherently, this trait contributes to the yield through high direct effect (0.602) indicating selection will be judicious and more effective for these characters in future breeding program. Days to maturity had negative indirect effect on fruit yield via days to first flowering (-0.039), plant height (-0.030), average fruit weight (-0.068) and finally make significant negative correlation with fruit yield (-0.304) though it had some positive indirect effect. Number of fruit per cluster had a high negative correlation to fruit yield per plant as (-0.349). Its direct effect was (-

0.168) which was more increased by the negative indirect contribution of average fruit weight (-0.144). Fruits per plant had negative direct effect on yield (-0.146) and it had a high negative correlation to fruit yield per plant as (-0.270). It had positive indirect effect on days to first flowering (0.014), days to maturity (0.031), plant height (0.032), and branches per plant (0.048).

Genetic diversity among tomato genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. The first three principal component axes accounted for 61.55% variation towards the divergence. Among five clusters cluster I contained maximum number of genotypes (6) while cluster V had only two genotypes. According to PCA, D2 and cluster analysis, the genotypes grouped into five divergent clusters using Z1 and Z2 values obtained from principal component scores. The highest inter-cluster distance was observed between clusters IV and V (45.95) 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 III (7.11).

On the other hand, the maximum intra-cluster distance was found in cluster IV (0.78), which contained of 3 genotypes, whereas the minimum distance was found in cluster V (0.00) that comprises 2 genotypes. Therefore, crossing between the genotypes belonging cluster I with cluster II, cluster II with cluster III, cluster III with cluster IV and cluster I with cluster V might produce high heterosis in respect of yield, average fruit weight and higher number of fruit per plant. Also the crosses between genotypes from cluster IV with cluster V might produce high level of segregating population. So the genotypes belonging to cluster I and cluster II, cluster II and cluster III, cluster III and cluster IV and cluster IV and cluster V have been selected for future hybridization program. The role of number of cluster per plant in both the vectors was important components for genetic divergence in these materials. On the other hand, the

role of fruit length had a minor role in the genetic divergence. Considering the magnitude of cluster mean and agronomic performance the genotype G_4 and G_6 from cluster I, for maximum branches per plant and number of cluster per plant respectively; G_9 from cluster III, for number of fruits per plant; G_{18} and G_{19} from cluster V and II, respectively for maximum fruit weight, G_{18} from cluster V for maximum fruit yield per plant were found promising. Therefore considering group distance and other agronomic performance the inter-genotypic crosses between G_4 and G_9, G_6 and G_9, G_{19} and G_9; G_{18} and G_6 might be suggested for future hybridization programme.

lycopene content of samples from genotype G_2 (3.0468 mg /100 g at 472 nm and 2.067 mg /g at 502 nm), G_4 (2.31 mg /100 g at 472 nm and 2.3 mg /100 g at 502 nm), G_5 (2.71 and 2.75 mg /100 g at 472 and 502 nm respectively), G_8 (2.404 and 1.356 mg /100 g at 472 and 502 nm respectively) and G_{18} (2.228 and 2.75 mg /100 g at 472 and 502 nm respectively) showed very high lycopene content at both absorbance 472 nm and 502 nm as compared to those of the other genotypes. G_1(1.26 mg /100 g), G_{10} (1 mg /100 g) and G_{14} (1.2 mg /100 g) 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. G_1 (1.26 mg /100 g), G_{10} (1 mg /100 g) and G_{14} (1.2 mg /100 g) 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. G_5 and G_{19} could be recommended for high Brix percentage. From the findings of the present study, the following conclusions could be drawn:

i. Selection procedure 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, and fruit diameter to develop high yielding varieties.

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

iii. Relatively higher value and lower differences between genotypic co-efficient of variation and phenotypic coefficient of variation of different yield contributing characters like fruit weight, number of fruits per plant, yield per plant were observed which indicates high potentiality to select these traits in future which were less affected by environmental influence.

REFERENCES

REFFERENCES

Abedin, J. and Khan, S. H. (1986). Study of the morphogenetic divergence in tomato. *Bangladesh J. Agric. Res.* **11** (11): 39-47.

Aditya, P.M. and Phir, K. (1995). Studied on genetic variability in tomato. *Progr. Hort.* **32** (2): 172-182.

Agong, S.G., Schittenhelm, S. and Friedt, W. (2001). Genotypic variation of Kenyan tomato (*Lycopersicon esculentum* L.) germplasm. *J. Food Technol. Afr.* **6** (1): 13-17.

Ahmed, S.U., Saha, H.K., Rahman, L. and Sharfuddin, A.F.M. (1986). Performance of some advance lines of tomato. *Bangladesh Hort.* **14** (1): 47-48.

Alam, M.S., Ahmed, Q.N. and Ali, M.N. (1988). Correlation and path co-efficient analysis for some characters in tomato. *Bangladesh J. Genet. Pl. Breed.* **1** (1&2): 42-46.

Alam, K.S., Ishrat, E., Zaman, M.Y. and Habib, M.A. (2012). Comparative karyotype and RAPD analysis for characterizing three varieties of (*Solanum lycopersicum* L.). *Bangladesh J. Bot.* **41** (2): 149-154.

Alda, L.M., Gogoasa, I., Bordean, D.M., Gergen, I., Alda, S., Moldovan, C. and Nita, L. (2009). Lycopene content of tomatoes and tomato products. *J. Agroali. Proc. techonol.* **15** (4): 540-42.

Alvarez, M. and Torres, V. (1983). Correlation analysis in a collection of varieties and lines of tomato (*Lycopersicon esculentum* Mill). *Cultivos Tropicals*. **5** (1): 49-59.

Anandgowda, N. (1997). Variability and gene action- studies for characteristics related to processing in tomato *(Lycopersicon esculentum* Mill.). M.Sc. (Agri.) Thesis, Univ. Agric. Sci., Dharwad (India).

Anitha, P., Sharma, R.R., Tiwari, R.N. and Surja, A.K. (2007). Correlation and path analysis for some horticultural traits in tomato. *Ind. J. Hort.* **64** (1): 90-93.

Anonymous, (1988). Crop Status Report. Christian Reformed Worlds Relief Committee, Bogra. Pp. 124-127

Anonymous, 2010. www.faostat.fao.org, FAO Static Division. Rome, Italy.

Anupam, B., Jain, B.P. and Verma, A.K. (2002). Genetic variability heritability and genetic advance in tomato (*Lycopersicon esculentum* L.). *J. Res. Birsa Agril. Univ.* **14** (2): 249-252.

Ara, A.R., Narayan, N. and Khan, S.H. (2009). Genetic variability and selection parameters for yield and quality attributes in tomato. *Ind. J. Hort.* **66**: 73-78.

Aradhana, J.C. and Singh, J.P. (2003). Studied on genetic variability in tomato. *Progr. Hort.* **35** (2): 179-182.

Arora, S.K., Pandita, M.L. and Pratap, P.S. (1982). Genetic variability and heritability studies in tomato in relation to quality characters under high temperature conditions. *Haryana Agril. Univ. J. Res.* **12** (4): 583-590.

Arun, J., Kohil, U.K. and Joshi, A. (2003). Genetic divergence for quantitative and qualitative traits in tomato (*Lycopersicon esculentum* Mill.). *Ind. J. Agric. Sci.* **73** (2): 110-113.

Arun, K., Veera, R. and Ragavathatham, K. (2004). Variability studies in tomato (*Solanum lycopersicum* L.) genotypes under green house and open conditions in different seasons. *South Indian Hort.* **53** (1-6): 18-24.

Asamizu, E. and Ezura, H. (2009). Inclusion of tomato in the genus Solanum as "*Solanum lycopersicum*" is evident from phylogenetic studies. *J. Jpn. Soc. Hort. Sci.* **78**: 3–5.

Bai, N.R. and Devi, D.S. (1991). Study on genetic parameters in tomato hybrids. *Orissa J. Agric. Res.***4**: 27-29.

Baishya, K.C., Syamal, M.M. and Singh, K.P. (2000). Diallel analysis in tomato. J. *Agril. Sci. Soc. North East Ind.* **13** (2): 225-228.

Barone, A., Chiusano, M.L., Ercolano, M.R., Giuliano, G., Grandillo, S. and Frusciante, L. (2008). Structural and functional genomics of tomato. *Int. J. Plant Genomics.* Article ID 820274, 12p.

BBS (Bangladesh Bureau of Statistics). (2005). Compendium of Environment Statistics of Bangladesh. Government of Bangladesh, Dhaka.

BBS (Bangladesh Bureau of Statistics). (2010). Year Book of Agricultural Statistics of Bangladesh. Bangladesh Bureau of Statistics, Planning Division, Ministry of Planning, Govt. of the Peoples Republic of Bangladesh, Dhaka. p. 163.

Benor, S., Zhang, M.Y., Wang Z.F. and Zhang, H.S. (2008). Assessment of genetic variation in tomato (*Solanum lycopersicum* L.) inbred lines using SSR molecular markers. *J. Genet. Genomics.* **35**: 373-379.

Bhusana, H.O., Kulkarni, R.S., Basavarajaiah, D., Helaswamy, B.H. and Halesh, G.K. (2001). Correlation and path analysis for fruit quality traits on fruit yield in tomato (*Lycopersicon esculentum* Mill.). *Crop Res. Hissar.* **22** (1): 107-109.

Bhutani, R.D. and Kalloo, G. (1989). Correlation and path coefficient analysis of some quality traits in tomato (*Lycopersicon esculentum* Mill). *Haryana J. Hort. Sci.* **18**: 130-135.

Biswas, J. and Mallik, S.C. (1989). Days required for flowering and harvesting of some promising cultivars of tomato (*Lycopersicon esculentum* Mill). *Environ. Ecol.* 7 (4): 1003-1095.

Bodunde, J.G. (2002). Path co-efficient and correlation studies in tomato (*Lycopersicon esculentum* Mill.). *Moor J. Agric. Res.* **3** (2): 195-198.

Borguini, ,R.G., Bastos, D.H.M. Neto, J.M. Capasso, F.S. and Torres, E. (2013). Antioxidant potential of tomatoes cultivated in organic and conventional systems. *Brazilian Arch. Bio.* Tech. **56** (4): 521-529.

Brar, G.S., Singh, S., Chima, D.S. and Dhariwal, M.S. (2000). Studies on variability, heritability, genetic advance for yield and components characters in tomato (*Lycopersicon esculentum* Mill). *J. Res. Punjab Agric. Univ.* **37** (3-4): 190-193.

Buckseth, T., Sharma, K.M. and Thakur, K.S. (2012). Genetic diversity and path analysis in tomato (*Solanum lycopersicum* L.). *Veg. Sci.* **39** (2): 221-223.

Burton, G.W. (1952). Quantitative interaction in grasses. In: Proc. Int. Grassland Congr. **1**: 277-283.

Camara, M., Matallana, M.C., Sanchezmata, M.C., Lilloayue, R. and Labra, E. (2003). Lycopene and hydroxyl methyl furfural (HMF) evaluation in tomato products. *Acta Hort.* **613**: 365-371.

Carelli, B.P., Gerald, L.T.S., Grazziotin, F.G. and Echeverrigaray, S. (2006). Genetic diversity among Brazilian cultivars and landraces of tomato *Solanum lycopersicum* L. revealed by RAPD markers. *Genet. Resour. Crop. Ev.* **53**: 395–400.

Cheema, D.S., Kumar, D. and Kaur, R. (2003). Diallel analysis for combining ability involving heat tolerant lines of tomato (*Lycopersicon esculentum* Mill). *Crop Improvement.* **30** (1): 39-44.

Chen, J., Wang, H., Shen, H.L., Chai, M., Li, .J.S., Qi, M.F. and Yang, W.C. (2009). Genetic variation in tomato populations from four breeding

programs revealed by single nucleotide polymorphism and simple sequence repeat markers. *Sci. Hort.* **122**: 6-16.

Chen, X., Yang, D., Yang, Z., Li Y.Y. and Zhang, H. (2009). The genetic analysis of quality of fruit of 7 tomato breeding lines. *J. Yunnan Agril. Uni.* **19** (5): 518-523.

Chowdhury, D. and Sharma, K.C. (2002). Studies on variability, heritability genetic advance and correlation in ridge gourd (*Luffa acutangula* Roxb.) *Hort. J.* **15** (3): 53-58.

Clarke G.M. (1973). Statistics and Experimental Design. Edward Arnold. London.

Comstock, R.E. and Robinson, H.F. (1952). Genetic Parameters their estimation and significance. Proc. Of 6th Int. Grassland Cong. **1**: 128-291.

Cramer, C.S. and Wehner, T.C. (1998). Fruit yield and yield component means and correlations of four slicing cucumber populations improved through six to ten cycles of recurrent selection. *J. Am. Soc. Hort. Sci.* **123**: 388-395.

Cucu, T. and Loco, J.V. (2011). Assessment of dietary intake of lycopene by the Belgian adult population. Wetens chapel ijk Instituut Volksgezondheid and Institut Scientifique De Sante Publique. *J. Wytsman straat Bru.* Belgium.

Darwin, S.C., Knapp, S. and Peralta, I.E. (2003). Taxonomy of tomatoes in the Galapagos Islands: Native and introduced species of *Solanum* section *Lycopersicon* (*Solanaceae*). *Syst. Biodivers.* **12**: 29–53.

Das, B., Hazarika, M.H. and Das, P.K. (1998). Genetic variability and correlation in fruit characters of tomato (*Lycopersicon esculantum* Mill.). *Ann. Agril. Res.* **19** (1):77-80.

Datta, M., Taylor, M.L. and Frizzell, B. (2013). Dietary and serum lycopene levels in prostate cancer patients undergoing intensity-modulated radiation therapy. *J. Med. Food.* **16** (12): 1131-1137.

Davis, A.R., Fish, W.W. and Veazie, P. (2003). A rapid spectrophotometric method for analyzing lycopene content in tomato and tomato products. *Postharvest Bio. Technol.* **28** (3): 425-430.

Deway, D.R. and Lu, K.N. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* **51:** 515-518.

Dhaliwal, M.S., Kaur, A. and Singh, S. (2002). Genetic analysis and correlations involving populations derived from *L. esculentum* x *L. pimpinellifolium* crosses of tomato. *J. Genetics Breed.* **56** (4): 345-351.

Dhaliwal, M.S., Singh S., Badhan, B.S. and Cheema, D.S. (1999). Diallel analysis for total soluble solids content, pericarp thickness and locule number in tomato. *Veg. Sci.* **26** (2): 120-122.

Dhankar, S.K., Dhankar, B.S. and Sharma, N.K. (2001) Correlation and path analysis in tomato under normal and high temperature conditions. *Haryana J .Hort. Sci.* **30** (1-2): 89-92.

Dhankhar, S.K. and Dhankar, S.S. (2006). Variability, heritability, correlation and path coefficient studies in tomato. *Haryana J. Hort. Sci.* **35** (1&2): 179-181.

Digby P. Galway N. and Lane P. (1989). GENESTST 5: A Second Course. Oxford Science Publications, Oxford. P: 103-108.

Domini, M. R. and Maya, C. (1997). Correlation and path coefficient estimates of different tomato seedlings stage. *Cult. Trop.* **18** (3): 63-65.

Dubey, R., Ojha, M.D., Prabhakar, M.K., Singh, P.K. and Saha, B. (2014). The generation mean analysis for quality and value added traits in tomato (*Lycopersicon esculentum* Mill.). *Ann. Agric. Bio Res.* **19** (1): 128-133.

Dudi, B.S. and Kalloo, G. (1982). Correlation and path analysis studies in tomato. *Haryana J. Hort. Sci.* **11**: 122-126.

Dudi, B.S., Dixit, J. and Partap, P.S. (1983). Components of variability, heritability and genetic advance studies in tomato (*Lycopersicum esculentum* Mill.). *Haryana Agric. Uni. J. Res.* **13**: 135-139.

Dufera, J.T. (2013). Evaluation of agronomic performance and lycopene variation in Tomato (*Lycopersicon esculantum* Mill.) genotypes in Mizan, southwestern Ethiopia. *World App. Sci. J.* **27** (11): 1450-1454.

Elumalai, M., Karthika, B. and Usha, V. (2013). Lycopene role in cancer prevention. *Int. J. Phar. Bio. Sci.* **4** (3): 371-378.

FAO. (2010). Plant genetic resource for food and agriculture. Rome, Food and Agriculture Organisation of the United Nations.

FAOSTAT. (2005). Food and Agricultural Organization of the United Nations, Statistics. Available from http: //faostat.fao.org/site/408/default.aspx.

Farzaneh, A., Nemati, H., Arouiee, H. and Kakhki, A.M. (2013). Genetic analysis of traits associated with yield and earliness in nine tomato (*Lycopersicon esculentum* Mill.) lines using diallel crossing method. *J. Seed Pl. Improv.* **29** (4): 693-710.

Filippone, P.T. (2014). Tomato History - The history of tomatoes as food. Once considered poisonous. The tomato is now a favorite food. Home Cooking Expert. (http://homecooking.about.com/od/foodhistory/a/tomatohistory.htm).

Foolad, M.R. (2007). Genome Mapping and Molecular Breeding of Tomato. *Iny. J. Plant Genomics.* Article ID 64358, pp: 52. doi: 10.1155/6435864358.

Freedman, N.D., Park, Y. and Subar, A.F. (2008). Fruit and vegetable intake and head and neck cancer risk in a large United States prospective cohort study. *Intl. J. Cancer.* **122** (10): 2330-2336.

Garcia, A.A.F., Benchimol, L.L., Barbosa, A.M.M., Geraldil, O. and Souza, C.L. (2004). Comparison of RAPD, RFLP, AFLP, and SSR markers for diversity studies in tropical maize inbred lines. *Genet. Mol. Biol.*, **27:** 579–588.

Garcia, E.M., Jamilena, J.I., Alvarez, T., Arnedo, J.L. and Lozano, R. (1998). Genetic relationships among melon breeding lines revealed by RAPD markers and agronomic traits. *Theor. App. Genet.* **96**: 878-885.

Gentilcore, D. (2010). A History of the Tomato in Italy Pomodoro. New York, NY: Columbia University Press, ISBN 023115206X.

Geogieva, A.K., Dhanesh and Kulal, P.K. (1969). Path analysis in tomato. *J. Maharasthra Agric. Uni.* **14**:114-116.

Ghosh, P.K., Syamai, M.M., Rai, N. and Joshi. A.K. (1995). Improvement of hybrid tomatoes. *Adv. Pl. Sci.* **2**(1): 207-213.

Godekar, D.A., Dhanukshe, B.L. and Patil, F.B. (1992). Studies on variability, heritability and genetic advance in tomato. *J. Maharasthra Agric. Uni.* **17**: 305-306.

Golani, I.J., Mehta, D.R., Purohit, V.L., Pandya, H.M. and Kanzariya, M.V. (2007). Genetic variability, correlation and path coefficient studies in tomato. *Ind. J. Agril. Res.* **41**(2): 146-149.

Gomez, O. (1987). Correlations and path co-efficient analysis in tomato breeding lines. *Agrotecnia de cuba.* **20** (2): 252-256.

Gorbatenko, E.M. and Gorbatenko, I.Y.U. (1985). Path analysis of economically usefull characters in tomato, *Tsitologiya Genetica*. **19** (3): 206-210.

Gosselin, A. and Trudel, M.J. (1984). Interactions between root-zone temperature and light levels on growth, development and photosynthesis of *Lycopersicon esculentum* Mill. Cultivar 'vendor'. *Sci. Hort.* 23: 313-321.

Hallmann, E. and Rembiakowska, E. (2007). Comparison of the nutritive quality of tomato fruits from organic and conventional production in Poland. University of Hohenheim, Germany. 131-134.

Hanson, C.M., Robinsen, R.R. and Comstock, R.R. (2002). Biometrical studies on yield in segregating population of Kotean. *Lespedeza. Agron. J.* **48**: 268-272.

Harer, P.N., Lad, D.B. and Bhor, T.J. (2002). Correlation and path analysis studies in tomato. *J. Maharashtra Agric. Univ.* **27** (3): 302-303.

Hernandez, L.E., Lobato, O.R., Garcia, Z.J.J., Lopez, D. and Hernandez, B.A. (2013). Agronomic performance of F_2 populations from tomato hybrids (*Solanum lycopersicum* L.). *Rev. Fit. Mexicana*. **36** (3): 209-215.

"International Plant Name Index". (1753). Sp. Pl. 1: 185. (http://web.archive.org/web/20110606004439/http://www.ipni.org/ipni/idPlantNameSear ch.do?id=146898-2).

Islam, M.S. and Khan, S. (1991). Variability and character association in tomato (*Lycopersicon esculentum* Mill). *Bangladesh J. Pl. Breed. Genet.* **4** (1&2): 49-53.

Islam, P., Prakash, S. and Singh, A.K. (1996). Variability studies in tomato (*Lycopersicon esculentum* Mill). *Bangladesh J. Pl. Breed. Genet.* **4** (1&2): 49-53.

Jain, V. (2013). http://www.researchgate.net/post/What is the current valid name of tomato *Lycopersicon esculentum* or *Solanum lycopersicon* Both genera are different.

Johnson, H.W., Robinson, H.F. and Comstock, R.E., (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**: 477-483.

Joshi, A. and Singh, J.P. (2003). Studies on genetic variability in tomato. *Progr. Hort.* **35** (2): 179-182.

Joshi, A., Vikram, A. and Thakur, M.C. (2004). Studies on genetic variability, correlation and path analysis for yield and physico- chemical traits in tomato (*Solanum lycopersicum* L.). *Progr. Hort.* **36** (1): 51-58.

Joshi, B.K., Randy, G., Gardner, S. and Dilip, R.P. (2012). Diversity Analysis of Tomato Cultivars Based on Coefficient of Parentage and RAPD Molecular Markers. *J. Crop Imp.* **26**: 177–196.

Kallo, G. (1989). Correlation and path coefficient analysis of some quality traits in tomato (*Lycopersicon esculentum* Mill.). *Haryana J. Hort. Sci.* **18**: 130-135.

Kasrawi, M.A. and Amr, A.S. (1990). Genotypic variation and correlation for quality characteristics in processing tomatoes. *J. Genet. Pl. Breed.* **44**: 85-99.

Kochieva, E.Z., Ryzhova, N.N., Khrapalova, I.A. and Phukhaskyi, V.A. (2002). Using RAPD for estimating genetic polymorphism in and phylogenetic relationships among species of genus. *Russian J. Genet.* **38** (9): 1104-1108.

Krishna, B.E. and Allolli, T.B. (2005). Influence of cropping system and source of nutrients in Leucaena-based alley cropping system on yield and quality of tomato. *Karnataka J. Agril. Sci.* **18** (2): 464-468.

Kumar, S., Rattan, P. and Sharma, J.P. (2013). Genetic variation and character interrelationship studies for identification of selection parameters in tomato (*Solanum lycopersicum* L.). *Ind. J. Agril. Sci.* **83** (11): 1149-1152.

Kumar, P. and Tewari, R.N. (1999). Studies on genetic variability for processing characters in tomato. *Ind. J. Hort.* **56** (4): 332-336.

Kumar, P., Dijee B., Joy, M., Radhakrishnan, N. and Aipe, K.C. (2001). Genetic variation in tomato for yield and resistance to bacterial wilt. *J. Trop. Agric.* **39**: 157-158.

Kumar, R., Kumar, N., Singh, J., and Rai, G.K. (2006). Studies on yield and quality traits in tomato. *Veg. Sci.* **33** (2): 126-132.

Kumar, S., Kumar, M., Singh, M., Banerjee, K. and Rai, M. (2003). Hybrid seed production of Solanaceous vegetables. A Practical Manual, II VR Technical Bulletin. **9**: 1-34.

Kumar, S., Singh, T., Singh, B. and Singh, J.P. (2004). Studies on correlation coefficient and path analysis among the different characters including fruit yield of tomato (*Lycopersicon esculentum* Mill.). *Pl. Arc.* **4** (1): 191-193.

Kumar, T. and Tewari, R.N. (2003). Studies on genetic variability for processing characters in tomato. *Ind. J. Hort.* **56** (4): 332-336.

Kumar, V.R.A., Thakur, M.C. and Hedau, N.K. (2003). Correlation and path coefficient analysis in tomato (*Lycopersicon esculentum* Mill.). *Ann. Agric. Res.* **24** (1): 170-177.

Kumari, A. V. and Subramanian, M. (2007). Genetic variability in tomato. *Madras Agric. J.* **8**: 657-653.

Kumari, N., Srivastava, J.P., Shekhavat, A.K.S., Yadav, J.R. and Singh, B. (2007). Genetic variability and heritability of various traits in tomato (*Lycopersicon esculentum* Mill.). *Progr. Agric.* **7** (1/2): 80-83.

Lee, M. and Media, D. (2014). Do tomatoes have more vitamin C than oranges? (healthy eating.sfgate.com/tomatoes vitamin-c oranges 3711.html.)

Linnaeus, C. (1753). Species plantarum, exhibentesplantas rite cognitas, ad genera relatas, cum differentiisspecificis, nominibustrivialibus, synonymisselectis, locisnatalibus, secundum system asexual digestas. Holmiae, Impensis Laurentii Salvii. L. Salvius, Stockholm.

Lungu, M.D. (1978). Classifying winter wheat environments into adaptive zones as a basis for recommending a reduction in the number of international winter wheat. *South Ind. Hort.* **34**: 70-73.

Lush, J.L. (1943). Heritability of qualitative characters in farm animals. Pro. of 8th Cong. Genetics and Hereditist Supplement. pp. 356-375.

Mahalanobis, P.C. (1936). On the generalized distance in statistic. *Proc. National acad. Sci.* **2**: 79-85.

Mahapatra, A.S., Singh, A.K., Vani, V.M., Mishra, R., Kumar, H. and Rajkumar, B.V. (2013). Inter-relationship for various components and path coefficient analysis in tomato (*Lycopersicon esculentum* Mill). *Int. J. Current Microbiology. App. Sci.* **2** (9): 147-152.

Mahesha, D.K., Apte, Y.B. and Jadhav, B.B. (2006). Studies on genetic divergence in tomato (*Solanum lycopersicum* L.). *Crop Res.* **32** (2): 401-402.

Mallik, A.K. (1985). Study on genetic parameters and character association of tomato. M.S. Thesis, Dept. Genet. Pl. Breed. BAU, Mymensingh.

Manivannan, K., Natarajan, J. and Irulappan, I. (2005). Correlation studies in tomato. *South Indian Hort.* **34**: 70-73.

Markovic, Z., Zdravkovic, J., Mijatovic, M., Danjanovic, M., Paroussi, G., Voyiatzis, D. and Paroussis, E. (2002). Breeding potential of local tomato populations for beta-carotene and vitamin C. Proceedings of the Second Balkan Symposium on Vegetables and Potatoes, Thessaloniki, Greece. *Acta-Hort.* 579: 157-161.

Martinez, G., Andreani, S., Gusano, L.G., Geuna, M. and Ruiz, F.J.J. (2006). Evolution of amplified length polymorphism and simple sequence repeats for tomato germplasm fingerprinting: Utility for grouping closely related traditional cultivars. *Genome.* **49**: 648–656.

Matin, K. and Kuddus, M. (2001). Varietal resistance to bacterial wilt in tomato. *Plant Disease.* **60**: 120-123.

Mayavel, A., Balakrishnamurthy, G. and Natarajan, S. (2005). Variability and heritability studies in tomato hybrids. *South Indian Hort.* **53** (1-6): 262-266.

Megha, U., Singh, J.P., Singh, A. and Joshi, A. (2006). Studies on genetic variability in tomato (*Solanum lycopersicum* L.). *Progr. Hort.* **3** (2): 463- 465.

Mendelova, A., Fikselova, M. and Mendel, L. (2013). Carotenoids and lycopene content in fresh and dried tomato fruits and tomato juice. *Acta Uni. Agril. Silvi. Mend. Bru.* **61** (5): 1329-1337.

Mew, T.W. and Ho, W.C. (1976). Varietal resistance to bacterial wilt in tomato. *Plant Disease.* **60** : 264-268.

Millar, P.A., Williams, J.C., Robinsen, H.F. and Comstock, R.E. (1958). Estimates of genotypic and environmental variance and covariance and their implication in selection. *Agron. J.* **50**: 126-131.

Miller, J.C. and Tanksley, S.D. (1990). RFLP analysis of phylogenetic relationships and genetic variation in the genus *Lycopersicon*. *Theor. Appl. Genet.* **80**: 437-448.

Mittal, P., Prakash, S. and Singh, A.K. (1996). Variability studies in tomato (*Lycopersicon esculentum* Mill.) under sub-humid condition of Himachal pradesh. *South Ind. Hort.* **44**: 132-148.

Mohanty, B.K. (2002). Studies on variability, heritability, interrelationship and path analysis in tomato. *Ann. Agric. Res.* **2** (1): 65-69.

Mohanty, B.K. (2002). Variability, heritability, correlation and path coefficient studies in tomato. *Haryana J. Hort. Sci.* **31** (3/4): 230-233.

Mohanty, B.K. (2003). Genetic variability, correlation and path coefficient studies in tomato. *Ind. J. Agril. Res.* **37** (1): 68-71.

Mohanty, B.K., and Prusti, A.M. (2001). Analysis of genetic distance in tomato. *Res. Crops.* **2** (3): 382-385.

Moigrădean, D., Lăzureanu, A., Poiană, M.A., Gogoaşă, I., Hărmănescu, M. and Gergen, I. (2007). Sunlight influence of lycopene content in tomatoes varieties. *J. Agroalimentary Processes techonol.* **13** (2): 369-372.

Monamodi, E.L., Lungu, D.M. and Fite, G.L. (2013). Analysis of fruit yield and its components in determinate tomato (*Lycopersicon lycoperscicum*) using correlation and path coefficient. *Bots. J. Agric. Appl. Sci.* **9** (1): 29-40.

Naidu, D.Y. (1993). Study of segregating populations in tomato (*Solanum lycopersicum* L.). M. Sc. (Agril.). Thesis, Uni. Agric. Sci. Dharwad (India).

Nalla, M.K., Rana, M.K., Singh, S.J., Sinha, A.K., Reddy, P.K. and Mohapatra, P.P. (2014). Assessment of genetic diversity through D^2 analysis in

tomato (*Solanum lycopersicon* .L) *Intl. J. Innovation and App. Studies*. **6** (3): 431-438.

Nandpuri, K.S., Kanwar, J.S. and Roshanlal, J.K. (1977). Variability path analysis and discriminate function selection in tamato (*Solanum lycopersicum* L.). *Haryana J. Hort. Sci*. **6**: 73-78.

Nandpuri, K.S., Singh, S. and Tarsemlal, L. (1974). Studies on the genetic variability and correlation of some economic characters in tomato. *J. Res. Punjab Agric. Univ*. **10** (3): 36-321.

Nardar, C.R., Muthukrishnan, C.R., Irulappan, I. and Shanmugusubramanian, A. (2007). Variability studies in tomato (*Solanum lycopersicum* L.). *South Indian Hort.* **28**: 123-127.

Narolia, R.K., Reddy, R.V., Sujatha, M. (2012). Genetic architecture of yield and quality in tomato (*Solanum lycopersicum* L.). *Agric. Sci. Digest*. **32** (4): 281-285.

Natural History Museum. (2014). "Solanaceae Source: Phylogeny of the genus Solanum". "Molecular phylogenetic analyses have established that the formerly segregate genera *Lycopersicon*, *Cyphomandra*, *Normania*, and *Triguera* are nested within *Solanum*, and all species of these four genera have been transferred to *Solanum*".

Naz, S., Zafrullah, A., Shahzadhi, K. and Munir, N. (2013). Assessment of genetic diversity within germplasm accessions in tomato using morphological and molecular markers. *J. Animal Plant Sci.* **23** (4): 1099-1106.

Nesgea, S., Krishnappa, K.S. and Raju, T.B. (2002). Correlation coefficient analysis in tomato. *Current Res. Univ. Agric. Sci*. **31** (7/8): 127-130.

Nessa, J., Rahman, L. and Alam, M.S. (2000). Comparative performance of ten genotypes of tomato in late planting. *Bangladesh J. Agric. Sci.* **27** (1): 121-124.

Padda, D.S., Saibhi, M.S. and Singh, S. (2007). Genotypic and phenotypic variabilities and correlations in quality characters of tomato (*Solanum lycopersicum* L.). *Indian J. Agric. Sci.* **41**: 199-202.

Padma, E., Ravisankar, C. and Srinivasulu, R. (2002). Correlation and path coefficient studies in tomato (*Lycopersicon esculentum* Mill). *J. Res. Angrau.* **30** (4): 68-71.

Panthee, D.R., Labate, J.A., McGrath, M.T., Breksa, A.P. and Robertson, L.D. (2013). Genotype and environmental interaction for fruit quality traits in vintage tomato varieties. *Euphytica.* **193** (2): 169-182.

Parthasarathy, V.A. and Aswath, E. (2002). Genetic diversity among tomato genotype. *South Indian J. Hort.* **59** (2): 162-166.

Patil, A.A. (1984). Studies on correlation, path analysis, genetic divergence, Heterosis and combining ability in ten parent diallel cross of tomato (*Lycopersicum esculentum* Mill.). Ph.D. Thesis, Univ. Agric. Sci., Dharwad (India).

Peralta, I.E., Knapp, S. and Spooner, D.M. (2006). Nomenclature for wild and cultivated tomatoes. Rpt. Tomato. *Genet. Coop.* **56**: 6-12.

Peralta, I.E., Spooner, D.M. (2001). Granule bound starch synthase (GBSSI) gene phylogeny of wild tomatoes (*Solanum* L. section *Lycopersicon* (Mill.) Wettst. Subsection *Lycopersicon*)". *Amer. J. Bot.* **88** (10): 1888–1902.

Ponnusviamy, V. and Muthukrishnan, E.R. (2010). A study of inter and intra generation correlation coefficients in F_2 and F_3 generation of tomato. *South Indian Hort.* **25**: 39-43.

Prasad, A. and Prasad, R.A. (1977). Variability and correlation studies in tomato. *Ind. J. Agric. Sci.* **47**: 77-80.

Prasad, V.S.R. and Mathura, R. (1999). Genetic variability, components association and direct and indirect selection in some exotic tomato germplasm. *Ind. J. Hort.* **56** (3): 262-266.

Prashanth, S.J. (2003). Genetic variability and divergence study in tomato (*Lycopersicon esculentum* Mill). M. Sc. (Agri.) Thesis, Univ. Agric. Sci. Dharwad (India).595-598.

Pujari, C.V., Wagh, R.S. and Kale, P.N. (1995). Genetic variability and heritability in tomato. *J. Maharashtra Agric. Uni.* **20** (1): 15-17.

Rai, N., Rajput, Y.S. and Singh, A.K. (1998). Genetic divergence in tomato using non-hierarchical clustering approach. *Veg. Sci.* **25** (2): 133-135.

Ramirez R.G., Bennett, A., McDonald, M.B. and Francis, D. (2005). Total antioxidant capacity of fruit and seeds from normal and enhanced lycopene tomato (*Lycopersicon esculentum* Mill.) genotypes. *Seed Tech.* **27** (1): 66-75.

Rani, C.I., Muthuvel, I. and Veer, D. (2010). Correlation and path coefficient for yield components and quality traits in tomato (*Lycopersicon esculentum* Mill.). *Agric. Sci. Digest.* **30** (1): 11-14.

Rani, I., Veeraragavathatham D. and. Sanjutha, D. (2008). Studies on Correlation and Path Coefficient analysis on Yield Attributes in Root Knot Nematodes Resistant F_1 Hybrids of Tomato. *J. App. Sci. Res.* **4**: 287-295.

Rao, C.R. (1952). Advanced statistical methods in biometrics research, John Wiley and Sons, New York. Pp. 357-369.

Ravindra, M., Aravinda, S. and Kumar, J.S. (2003). Stability analysis for growth and earliness in tomato. *Ind. J. Hort.* **60** (4): 353-356.

Reddy B.R., Reddy, M.P., Begum, H. and Sunil, N. (2013). Genetic diversity studies in tomato (*Solanum lycopersicum* L.). *J. Agric. Vet. Sci.* **4** (4): 53-55.

Reddy, M.L.N. and Gulshanlal, K. (1990). Genetic variability and path co-efficient analysis in tomato. *Progr. Hort.* **19**: 284-288.

Reddy, V.V.P. and Reddy, K.V. (1992). Studies in variability in tomato. *South Ind. Hort.* **40**: 257- 260.

Robinson, H.F., Comstock, R.E. and Harvey, V.H. (1949). Estimates of heritability and degree of dominance in corn. *Agron. J.* **41**: 353-359.

Sachan, M.N. (2001). Heterosis, combining ability, RAPD analysis and resistance breeding to leaf curl viruses and bacterial wilt in tomato (*Solanum lycopersicum* L). M. Sc. (Agri.) Thesis, Uni. Agric. Sci. Dharwad (India).

Saeed, A., Hayat, K., Khan, A.A., Iqbal, S. and Abbas, G. (2007). Assessment of genetic variability and heritability in *Lycopersicon esculentum* Mill. *Int. J. Agric. Bio.* **9** (2): 375-377.

Sahu, G.S. and Mishra, R.S. (1995). Genetic divergence in tomato. *Mysore J. Agric. Sci.* **29**: 5-8.

Saleem, M.Y., Iqbal, Q. and Asghar, M. (2013). Genetic variability, heritability, character association and path analysis in F_1 hybrids of tomato. *Pak. J. Agri. Sci.* **50** (4):649-653.

Samadia, D.K., Aswani, R.C. and Dhandar, G. (2006). Genetic analysis for yield components in tomato land races. *Haryana J. Hort. Sci.* **35** (1&2): 116-119.

Schulzova, V. and Hajslova, J. (2007). Biologically active compounds in tomatoes from various fertilisation systems. Int. Congr. Eur. Integ. Project Quality. Uni. Hohenheim, Germany. 144-147.

Schwarz, K. Resende, J.T., Preczenhak, A.P, Paula, J.T. Faria, M.V. and Dias, D.M. (2013). Agronomic performance and physico-chemical quality in tomato hybrids grown without guiding. *Hort. Brasileira.* **31** (3): 410-418.

Sekar, K. (2001). Genetic analysis in tomato (*Lycopersicon esculentum* Mill.). *Madras Agril. J.* **88** (1/3): 43-45.

Sharma, H.R., Sharma, D. and Thakur, A.K. (1993). Studies on analysis of genetic divergence in tomato (*Solanum lycopersicum* L.). *J. Hort. Sci.* **1** (1): 19-22.

Sharma, K.C. and Verma, S. (2000). Path coefficient analysis in tomato (*Lycopersicon esculentum* Mill.). *Ind. J. Agri. Sci.* **70** (10): 700-702.

Sharma, K.C. And Verma, S. (2001). Analysis of genetic divergence in tomato. *Annals Agric. Res.* **22** (1): 71-73.

Shashikanth, P., Das, K. and Mulal, K. (2010). Studies on tomato leaf curl virus. *Ind. J. Virol.* **15**: 115-117.

Shravan, K., Biswash, C. and Mollik, P. (2004). Heterosis and inbreeding depression in tomato. *Utter Pradesh Ind. J.*, **60**: 139-144.

Shuaib, M., Alam, Z., Zahir,A., Waqar,A., Taufiq, A. and Ikhtiar, K. (2007). Characterization of wheat varieties by seed storage protein electrophoresis. *Afr. J. Biotechnol.* **6:** 497-500.

Sidhu, A.S. and Singh, S. (1989). Genetic variability and correlation for yield and quality characters in tomato (*Lycopersicon esculentum* Mill.). *Ind. J. Agric. Sci* .**59** (12): 810- 812.

Silva, P.F., Silva, A.C., Tavares, K.N. and Santos, D.P. (2012). Production and brix degrees content of tomato irrigated with water of different saline concentrations. *Rev. Verde Agroe. Des. Sust.* 7 (4):85-89.

Singh, A.K. (2005). Genetic variability, correlation and path coefficient studies in tomato (*Solanum lycopersicum* L.) under cold arid region. *Progr. Hort.* **37** (2): 437-443.

Singh, B.D. (2009). Plant Breeding Principles and Methods, Kalyani Publisher, New Delhi India

Singh, D.N., Sahu, A. and Parida, A.K. (1997). Genetic variability and correlation studies in tomato (*Lycopersicon esculentum* Mill). *Env. Ecol.* **15** (1): 117-121.

Singh, H. and Cheema, D.S. (2006). Correlation and path coefficient studies in tomato (*Lycopersicon esculentum* Mill.). *Haryana J. Hort. Sci.* **35** (1&2): 126-129.

Singh, J.K., Singh, J.P., Jain, S.K. and Joshi, A. (2004). Correlation and path coefficient analysis in tomato. *Progr. Hort.* **36** (1): 82-86.

Singh, J.K., Singh, J.P., Jain, S.K., Joshi, A. and Joshi, K. (2002). Studies on genetic variability and its importance in tomato (*Solanum lycopersicum* L.). *Progr. Hort.* **34** (1): 77-79.

Singh, J.P., Singh, A. and Joshi, A. (2005). Studies on genetic variability in tomato (*Lycopersicon esculentum* Mill.). *Prog. Hort.* **37** (2): 463-465.

Singh, J.P., Singh, D.K. and Gulshanlal. (2000). Variability pattern in Agromorphological characters in tomato (*Solanum lycopersicum* L.). *Pro. Hort.* **32** (1): 79-81.

Singh, K.P., Mandal, G. and Saha, B.C. (2006). Genetic variability of yield components and biochemical characters in spring season tomato (*Lycopersicon esculentum* Mill). *J. Interacade.* **10** (3): 314-318.

Singh, P., Singh, S., Cheema, D.S., Dhaliwal, M.S. and Singh, S. (2002). Genetic variability and correlation study of some heat tolerant tomato genotypes. *Veg. Sci.* **29** (1): 68-70.

Singh, R.R. and Singh, H.N. (1980). Correlation Studies in tomato. *Indian J. Agric. Sci.* **50** (8): 225-235.

Singh, R.K. and Choudhary, B.D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci.* **12** (2):151-156.

Singh, R.R., Singh, J.P. and Singh, H.N. (1988). Genetic Divergence in tomato. *Indian J. Agric. Sci.* **50** (8): 591-594.

Sivaprasad, K. (2008) Genetic variability and correlation studies in biparental mating populations of tomato (*Lycopersicon esculentum* Mill.). M.Sc. (Agri.) Thesis, University of. Agril. Sci., Dhanwad, India.

"Slow Food® Upstate". (2014). Renato Vicario. Retrieved 1 January 2014. (http://renatovicario.com/pdf/tomato.pdf)

Smith, A.F. (1994). The Tomato in America: Early History, Culture, and Cookery. Columbia SC, USA: University of South Carolina Press. ISBN 1-57003-000-6.

Sonone, A.H., More, D.C. and Thombre, M.V. (1987). Path analysis in tomato. *J. Maharashtra Agric. Uni.* **12**: 115-116.

Sonone, A.H., More, D.C. and Thombre, M.V. (1986). Path analysis in tomato. *J. Maharashtra Agric. Univ.* **12**: 115-116.

Supe, V.S. and Kale, P.B. (1992). Correlation and path analysis in tomato. *J. Maharashtra Agric. Univ.* **17**: 331-333.

Susic, Z., Pavlovic, N., Cvikic, D. and Rajicic, S.T. (2002). Studies of correlation between yield and fruit characteristics of (*Lycopersicon esculentum* Mill.) hybrids and their parental genotypes. *Acta Hort.* **579**: 163-166.

Terzopoulos, P.J., Walter, S.A. and Bebeli, P.J. (2009). Evaluation of Greek tomato landrace populations for heterogeneity of horticultural traits. *Eur. J. Hort. Sci.* **74**: 24-29.

Thakur, B.S. (2009). Adaptability of tomato genotypes under mid-hill conditions of Himachal Pradesh. *Haryana J. Hort. Sci.* **38** (1/2): 93-95.

Tiwari, J.K. (2002). Correlation studies in tomato. *Haryana J. Hort. Sci.* **31** (1&2): 146-147.

Upadhay, R., Lal, G. and Ram, H.H. (2001). Genotype environment interaction and stability analysis in tomato. *Prog. Hort.* **33** (2): 190-193.

Vavilov, N.I. (1951). The origin, variation, immunity and breeding of cultivated plants. *Chronica Bot.* **13**: 1-366.

Veershety. (2004). Studies on variability, character association and genetic diversity in tomato (*Lycopersicon esculentum* Mill.). M. Sc. (Agri.) Thesis, Univ. Agric. Sci., Dharwad (India).

Verma, S.K. and Sarnaik, D.A. (2000). Path analysis of yield components in tomato (*Lycopersicon esculentum* Mill). *J. App. Bio.* **10** (2): 136-138.

Vikram, A. and Kohli, U.K. (1998). Genetic variability, correlation and path analysis in tomato. *J. Hill. Sci.* **11** (1): 107-111.

Wagh, R.S., Bharud, R.W., Patil, R.S. and Bhalekar, M.N. (2007). Correlation analysis of growth, yield and fruit quality components in tomato. *J. Mahar. Agric. Uni.* **32** (1): 29-31.

Wang, R.S., Li, Y.R., Yang, L.T. and Li, W.J. (2006). Analysis of genetic diversity based on SSR and morphological markers among tomato cultivars. *J. Trop. Subtrop. Bot.* **14** (2): 120-125.

Weber, C.R. and Moorthy, H.R. (2010). Heritable and non-heritable relationship and variability of oil content and agronomic characters in the F_2 generation of soybean crosses. *Agron. J.* **44**: 202-209.

Weising, K., Atkinson, R.G. and Gardner, R.C. (1995) Genomic finger priniting by microsatellite primed PCR: A critical evaluation. *PCR Meth. Appl.* **4**: 249-255.

Wright, S. (2007). Correlation and causation. *J. Agric. Res.* **20**: 202-209.

Xiaorong, H.U., Hui, W., Jia, C. and Yang, W. (2012). Genetic Diversity of Argentina Tomato Varieties Revealed by Morphological traits, simple sequence repeat and single Nucleotide polymorphism markers. *Pak. J. Bot.* **44** (2): 485-492.

Yi, S.S., Jatoi, S.A., Fujimura, T., Yamanaka, S. and Watanabe, K.N. (2008). Potential loss of unique genetic diversity in tomato landraces by genetic colonization of modern cultivars at a non-center of origin. *Plant Breed.* **127**: 189-196.

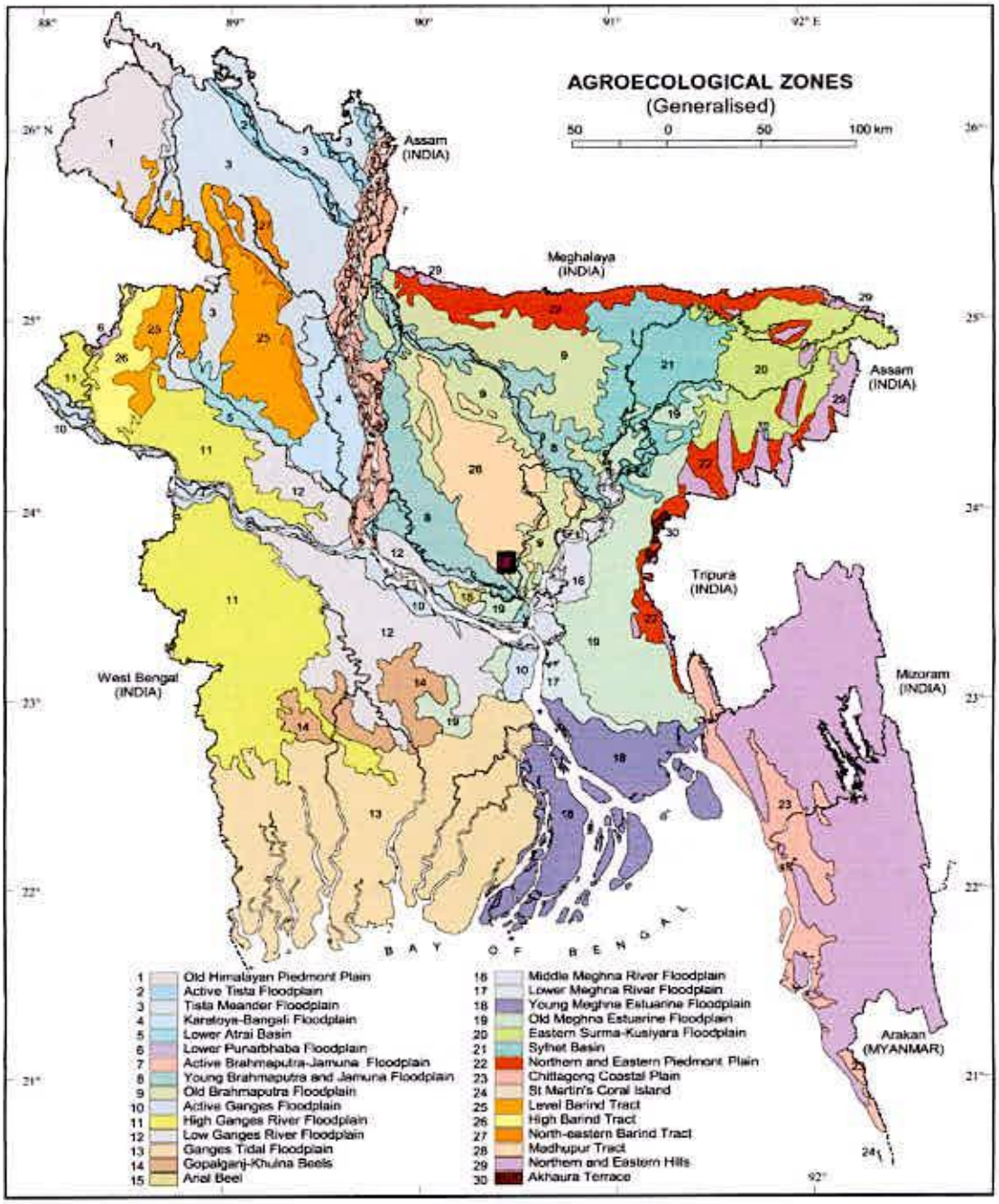
Zhang, C.X., Fu, J.H., Cheng, S.Z. and Lin, F.Y. (2009). Greater vegetable and fruit intake is associated with a lower risk of breast cancer among Chinese women. *Intl. J. Cancer.* **125** (1): 181-8.

Zhu, H.S., Zhang, H., Mao, M.K., Li, H.T. and Wang, A.Y. (2004). The genetic diversity of Yunnan local varieties and wild species of tomato. *J. Yunnan Agric. Univ.* **19**: 373-377.

Zhu, J.X., Hao, W., Wang, C.R. and Shaolan, Y. (2013). Technology optimization of ultrasonic-assisted extraction for lycopene from lyophilized tomato powder. *Tansactions Chi. Soc. Agrl. Eng.* **29** (18): 284-291.


APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly average temperature, relative humidity, total rainfall and sunshine of the experimental site during the period of November, 2012 to April, 2013

Month	Air temperature (°C)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (h)
	Maximum	Minimum			
November, 2012	34.8	18.0	77	227	5.8
December, 2012	32.3	16.3	69	0	7.9
January, 2013	29.0	13.0	79	0	3.9
February, 2013	28.1	11.1	72	1	5.7
March, 2013	33.9	12.2	55	1	8.7
April, 2013	34.6	16.5	67	45	7.3

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

Appendix III. Physical characteristics and chemical composition of soil of the experimental plot

Soil characteristics	Analytical results
Agrological Zone	Madhupur Tract
P^H	6.00 – 6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq / 100 g soil

Source: Soil Resource and Development Institute (SRDI), Dhaka.

Appendix IV. Mean performance of various growth parameter and yield components

G	DFF	D50%F	DM	PH	BPP	NCP	FPC	FPP	AFW	FL	FD	FYP
BD-7258	64.00	73.33	97.33	66.00	9.00	12.33	4.33	79.33	18.05	4.23	4.27	847.33
BD-7270	60.67	71.67	101.00	52.00	9.00	14.00	3.67	66.00	24.59	3.23	3.37	1258.50
BD-7276	65.00	72.33	98.33	73.33	11.00	18.00	4.33	94.33	22.67	3.07	3.87	806.33
BD-7279	65.00	73.00	100.67	111.10	16.00	15.67	3.33	95.00	15.62	2.93	3.23	853.21
BD-7281	65.00	74.33	102.33	82.33	10.00	16.33	3.33	83.33	18.29	3.20	3.37	1090.00
BD-7285	63.00	73.67	97.33	72.67	12.67	23.00	3.67	96.33	22.17	4.93	4.83	839.33
BD-7286	64.00	75.00	97.67	86.33	9.00	10.33	3.33	87.00	18.73	3.87	3.30	939.67
BD-7289	65.33	73.00	101.33	67.39	5.67	9.00	3.67	45.00	14.33	3.40	3.53	781.00
BD-7290	62.00	70.00	100.33	64.00	8.00	12.00	4.33	104.00	19.33	3.93	3.90	717.33
BD-7759	63.33	75.00	102.00	71.33	8.00	12.67	4.00	103.33	17.48	3.27	3.07	685.67
BD-7762	61.67	73.33	100.00	66.33	8.00	11.33	3.67	70.00	10.20	4.70	4.73	1070.90
BD-9010	64.00	74.00	103.67	87.00	9.00	13.00	3.33	42.00	12.12	4.57	4.07	534.33
BD-9011	62.33	72.00	103.67	106.00	8.00	11.67	3.67	59.67	15.17	2.63	2.73	577.67
BD-9960	64.00	73.33	105.67	80.67	9.33	13.33	4.33	95.67	14.67	3.03	2.97	425.33
BD-10321	67.00	75.33	103.33	85.67	14.00	11.33	3.33	58.67	9.96	3.33	4.23	628.33
BARI Tomato-7	62.33	72.00	99.00	108.54	8.33	12.67	4.00	51.00	44.33	4.33	3.17	1097.67
BARI Tomato-11	62.00	71.00	101.00	83.00	8.67	12.33	9.00	84.67	3.10	3.27	2.50	402.67
BARI Tomato-14	63.33	71.00	101.67	74.67	9.67	12.00	2.67	40.67	66.93	3.23	3.03	1356.33
BARI Tomato-15	63.00	71.33	101.00	89.00	8.00	11.33	4.33	62.67	66.93	3.47	3.33	1191.00
Mean	**63.53**	**72.88**	**100.91**	**80.39**	**9.54**	**13.28**	**4.02**	**74.67**	**22.88**	**3.61**	**3.55**	**847.51**
Min.	**60.67**	**70.00**	**97.33**	**52.00**	**5.67**	**9.00**	**2.67**	**40.67**	**3.10**	**2.63**	**2.50**	**402.67**
Max.	**67.00**	**75.33**	**105.67**	**111.10**	**16.00**	**23.00**	**9.00**	**104.00**	**66.93**	**4.93**	**4.83**	**1356.33**

DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to Maturity, PH = Plant height (cm), BPP = Branches per plant, NCP = Number of Clusters per Plant, FPC = Fruits per Cluster, FPP = Fruits per Plant, AFW = Average Fruit Weight (g), FL = Fruit length (cm), FD = Fruit Diameter (cm), FYP = Fruit Yield per Plant (g).

Appendix V. Lycopene content (mg/100g), Vitamin C content (mg/100ml) and % of Brix

Genotype No.	Lycopene (mg/100g)		Vitamin C (mg/100ml)	% of Brix
	472nm	502nm		
G_1	0.352	0.436	1.26	0.5
G_2	3.0468	2.0676	0.6	0.5
G_3	1.382	0.816	0.6	0.5
G_4	2.31	2.3	0.4	0.5
G_5	2.71	2.75	0.8	0.7
G_6	0.1434	0.09523	0.4	0.5
G_7	0.499	0.2436	0.4	0.5
G_8	2.404	1.356	0.8	0.5
G_9	1.23	1.43	0.8	0.5
G_{10}	0.91866	0.5403	1	0.5
G_{11}	3	1.05	0.6	0.5
G_{12}	1.47	1.697	0.6	0.5
G_{13}	3	1.23	0.4	0.5
G_{14}	0.37308	0.201	1.2	0.5
G_{15}	0.5185	0.33606	0.6	0.5
G_{16}	0.34	0.4	0.4	0.5
G_{17}	0.03109	0.055	0.4	0.5
G_{18}	2.228	2.75	0.4	0.5
G_{19}	0.4	0.304	0.4	0.6

Appendix VI. Principal component score nineteen genotypes of tomato

Genotypes	Z_1	Z_2
G_1	-0.4	10.5
G_2	411.0	13.5
G_3	-41.5	19.5
G_4	4.6	9.6
G_5	241.7	15.2
G_6	-8.6	23.0
G_7	91.5	12.5
G_8	-66.0	-22.3
G_9	-130.7	29.3
G_{10}	-162.4	25.6
G_{11}	222.8	10.1
G_{12}	-312.6	-38.1
G_{13}	-269.7	-28.6
G_{14}	-422.5	8.6
G_{15}	-219.2	-19.5
G_{16}	251.1	-29.4
G_{17}	-445.4	0.2
G_{18}	511.0	-25.0
G_{19}	345.2	-15.0

Plate 5. Working in Laboratory for Biochemical analysis