GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN TOMATO (*Solanum lycopersicum* L.) GENOTYPES

EAPSHITA DEVI

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

DECEMBER, 2020

GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN TOMATO (*Solanum lycopersicum* L.) GENOTYPES

BY

Eapshita Devi

REGISTRATION NO. 19-10035

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, 2020

Approved by:

Prof. Dr. Naheed Zeba	**Prof. Dr.Firoz Mahmud**
Supervisor	**Co-Supervisor**

Prof. Dr. Md. Abdur Rahim
Chairman
Examination Committee

Prof. Dr. Naheed Zeba
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh

Phone: +8802-9180921-167 (Office), +8802-44814079 (Res.)
Mobile: +88 01913-091772
E-mail: zeban@sau.edu.bd

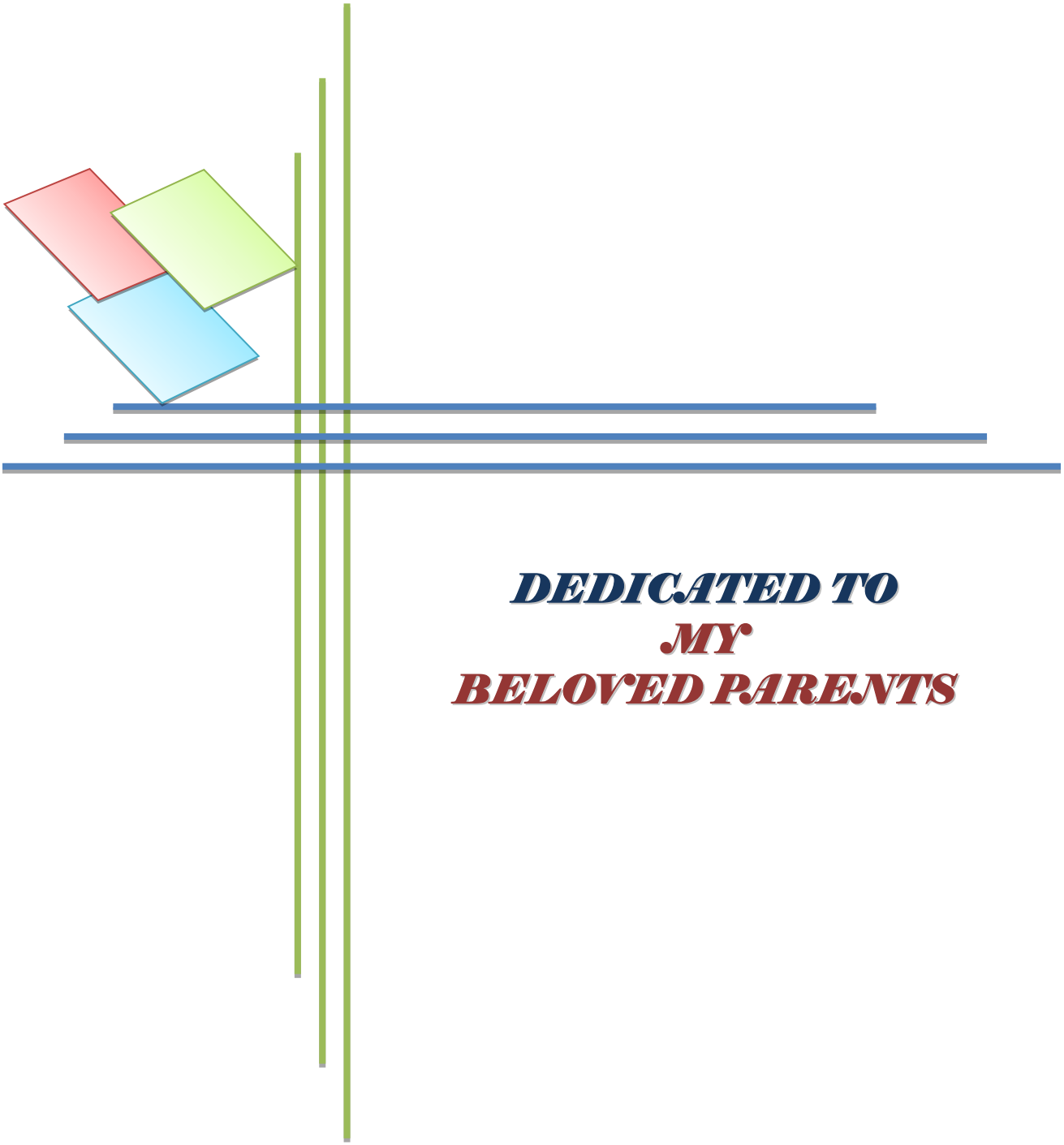
CERTIFICATE

This is to certify that thesis entitled, "GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN F2 GENERATION OF 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 Eapshita Devi, Registration number 19-10035 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, received during the course of this investigation has duly been acknowledged.

Dated: December, 2020
Dhaka, Bangladesh

(Prof. Dr. Naheed Zeba)
Supervisor



DEDICATED TO
MY
BELOVED PARENTS

Some commonly used abbreviations

Full word	Abbreviations	Full word	Abbreviations
Abstract	*Abstr*	International	*Intl.*
Advances/Advanced	*Adv.*	International Journal	*Intl. J.*
Agriculture	*Agric.*	Journal	*J.*
Agricultural	*Agril.*	Kilogram	Kg
Agronomy	*Agron.*	Limited	Ltd.
And others	*et al.*	Ministry	*Min.*
Analysis of Variance	ANOVA	Muriate of Potash	MP
Applied	*App.*	Negative logarithm of hydrogen ion concentration (-log $[H^+]$)	pH
Archives	*Arch.*		
Bangladesh Bareau of Statistics	BBS		
Biology	*Biol.*	Non-significant	^{ns}
Botany	*Bot.*	New South Wales	*NSW.*
Better parent	BP	Mid parent	MP
Breeding	*Breed.*	Parts per million	ppm
Centimeter	cm	Percentage	%
Component variance	CV	Plant	*PI.*
Cross between two dissimilar parents	X	Proceedings	*Proc.*
		Randomized Complete Block Design	RCBD
Degree celcious	°C		
Division	*Div.*	Research	*Res.*
Economic	*Econ.*	Review	*Rev.*
Environment	*Environ.*	Science	*Sci.*
Etcetera	etc.	Serial	Sl.
Experimental	*Expt.*	Society	*Soc.*
Food and Agricultural Organization	FAO	Specific combining ability	SCA
Gazette	*Gaz.*	Statistics	*Stat.*
General	*Gen.*	That is	i.e.
General combining ability (GCA)	GCA	The First Generation of a cross between two dissimilar parents	F_1
Genetics	*Genet.*		
Gram	G	Triple Super Phosphate	TSP
Heredity	*Hered.*	University	*Univ.*
Horticulture/ Horticultural	*Hort.*	Variety	*var.*
		Vegetable	*Veg.*
Incorporated	*Inc.*	Videlicet (namely)	*viz.*
Information	*Inf.*	Weight	wt.

ACKNOWLEDGEMENT

The author wishes to acknowledge the immense grace and implicit kindness of Almighty God, the one and only ruler of the universe, who give strength to the author to complete the research work and the thesis for the degree of Master of Science (M.Sc.) in Genetics and Plant Breeding.

The author would like to show her earnest respect, sincere appreciation and enormous thankfulness, heartiest gratitude and indebtedness to her honorable thesis supervisor Prof. Dr. Naheed Zeba, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for her congenial, endurance and effective cooperation, rousing counsel, appropriate guidance, valued support condign inspiration, and sincere advice throughout the research work, giving valuable suggestions fruitful discussion, timely instruction and for taking immense care just like a family during study and the preparation of this manuscript.

The author expresses her heartiest gratitude and respect to her honorable Co-Supervisor, Prof. Dr. Firoz Mahmud, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his guidance and suggestions encouragement and valuable teaching which was very helpful during the final stretch of his thesis writing.

The author is very much grateful to her honorable teacher Prof. Dr. Md. Abdur Rahim, Chairman, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his valued and knowledgeable teaching and guidance during his study period as well as constructive suggestions, encouragement and heartedly cooperation during the whole research period.

The author feels very grateful to Prof. Dr. Md. Shahidur Rashid Bhuiyan, Honourable Vice-chancellor, Sher-e-Bangla Agricultural University, Dhaka, and Professor Dr. Alok Kumar Paul, Dean, Post Gratuate Studies for giving every possible logistic support, valuable suggestions and cooperation during the whole study period.

The author perceive deep respect and thanks to her all respectable teachers, specially honourable Prof. Dr. Md. Sarowar Hossain, Prof. Dr. Jamilur Rahman, Dr. Md. Ashaduzzaman Siddikee, Dr. Kazi Md. Kamrul Huda , Dr. Md. Harun Ur Rashid, Dr. Shahanaz Parveen, Ms. Kamrunnahar and all other honourable course instructors of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for their valuable teaching, direct and indirect advices, encouragement and continuous support during the period of her study.

The author is very grateful to Mosammat Rexona Parvin and Shyamol Kumar Roy, academic officers and wants to give thanks to all the staff members of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for their continuous cooperation throughout the study period. It was also a great pleasure to work with her seniors Asmaul Husna, Abu Bakkar Siddique, and her classmates Nazmin Ara, and Mst Nusrat Jahan Upoma, students of the Department of Genetics and Plant Breeding and many of her classmates

and junior fellow MS students to whom the author was close throughout her institutional study and research period. It was an amazing experience to work with all of them.

Moreover the author impart her heartiest love and respect to her parents for their support continuous encouragement and inspiration who sacrificed much for her education and upbringing. She can never repay their debt.

The author wants to thanks those peoples who helped, supported, assisted and inspired the author in various ways with their valuable suggestions and directions to achieve her dream of higher education. She is unreservedly thankful and expresses her heartiest gratefulness to all of them as well as she regrets her inability for not to mention every one by name and heartedly requests for their forgiveness.

The Author

LIST OF CONTENTS

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF CONTENTS (CONT'D)

LIST OF TABLES

LIST OF PLATES

LIST OF FIGURE

LIST OF APPENDICES

GENETIC DIVERSITY AND CHARACTER ASSOCIATION IN TOMATO (*Solanum lycopersicum* L.) GENOTYPES

By

EAPSHITA DEVI

ABSTRACT

The experiment was conducted using thirty crossing genotypes and six parents in F_2 generation of tomato (*Solanum lycopersicum* L.) under field condition for identifying their inter genotypic variability, correlation, path co-efficient and genetic diversity by considering their nineteen yield contributing characters at the experimental field of Sher-e-Bangla Agriculture University, Dhaka, Bangladesh. For all the characters the genotypes significantly different from each other. PCV was always higher than GCV for all the traits. High heritability was observed for the number of flower per cluster (84.93%), number of fruit per cluster (90.30%), number of fruit per plant (99.77%), individual fruit weight (99.61%), fruit length (91.84%), and yield per plant (93.16%). Positive correlation co-efficient for both genotypic and phenotypic with yield was found for leaf width, individual fruit weight, fruit length, fruit width, skin diameter and locule number. A positive direct effect on yield per plant for the characters, leaf length, leaf width, number of cluster per plant, number of flower per plant, individual fruit weight, fruit length, fruit width, relative water content and P^H was identified through path co-efficient analysis. The highest inter-cluster distance was observed between II and IV (14.738) and the lowest inter-cluster distance was observed between I and V (3.681). The highest intra-cluster distances were observed in cluster III and the lowest intra-cluster distances were observed in cluster IV. Based on cluster mean and agronomic performance the genotypes G6×G1 showed the minimum days to first flowering and days to 50% flowering from cluster V. G6 showed the maximum number of cluster per plant from cluster II. G7×G1 showed maximum individual fruit weight from cluster IV. G6×G7 showed maximum fruit width and total soluble solids from cluster V and G9×G7 showed maximum yield per plant from cluster IV. Therefore, considering group distance and other agronomic performance these inter genotypic crosses might be suggested for future breeding program.

INTRODUCTION

CHAPTER I

INTRODUCTION

Vegetables has a profound effect on daily human diet which is well known since ancient era as they supply all major components of our balanced diet. Vegetables and spices are called the backbone of horticulture. As Bangladesh is entrusted with diverse favorable agro climatic zones and soils, which makes it enforceable to cultivate the largest number of vegetable crops in the world, all the year round and it is regarded as a "Horticulture Paradise" (Saravaiya and Patel, 2005).

Tomato ***(****Lycopersicon esculentum*) (2n=24) is an important nutritious vegetable which is grown widely in the world. It belongs to the family Solanaceae. In Bangladesh it is one of the most popular, nutritive and important vegetable crops which are receiving attention of the growers and consumers and made its position within few of the highest cultivated vegetables. The food value of Tomato is very high because of the greatest contents of Vitamins A, B and C and also minerals like Calcium which promote good health (Wilcox *et al*.2003) and is a self-pollinated crop. On account that it has achieved tremendous popularity over the last century. All over the world tomato is becoming a more important part of the food basket due to its nutritional value and delicious taste. Currently because of its higher consumption rate in developed countries, it has been considered as a luxury crop.

The soil and climatic condition of Bangladesh is very adaptive to tomato (Ahamed, 1995). Pertaining to production rate it ranks fourth and third as regard to area (BBS, 2013). In spite of being a tropical plant, it is broadly cultivated in tropical, sub-tropical and temperate climates and in this way tomato ranks third position in respect of world vegetable production (FAO, 2016).In the whole world, in total 4.79 million hectares of tomato was harvested in 2016 with a net production of 177.05 million Metric tons (http://www.faostat.fao.org.). The main tomato production countries are China, U.S.A., India, Turkey, Egypt, Italy and Iran.

All the year round tomato has a great demand in Bangladesh but as winter season is very favorable for its production, it is available and cheaper during that time. For this reason it

is cultivated as a winter vegetable covering an area of 27342.105 ha and the net production was 368.121 thousand metric tons (BBS, 2016) in Bangladesh. But unfortunately the mean yield rate of tomato in Bangladesh is considerably low compared to other countries like India (16.67 t ha-1), Japan (55.82 t ha-1), USA (66.22 t ha-1), China (31.39 t ha-1), Egypt (34.00 t ha-1) and Turkey (41.77 t ha-1) (FAO, 2016).Lycopene content of tomato is very high which is an antioxidant that reduces the risk of prostate cancer (Hossain *et al*., 2004) and also contains huge amount of nutritive elements nearly double compared to fruit apple (Barman, 2007). The food value of tomato is comprehensively dependent on its chemical composition such as ascorbic acid, titratable acidity, total sugar, dry matter, total soluble solids, etc. As per some studies in USA, the flavor and taste of tomato was associated to free sugars, organic acids and sugar acid ratios (Kader *et al*., 1978).As Bangladesh is a developing country where a huge amount of peoples are poor so malnutrition is a severe problem in Bangladesh, especially for women and children. Poverty and food insecurity is the main problem which limits one's ability to live on a diet that provides all the nutrients necessary for healthy living, leading to malnutrition. Hence, it is an urgent need of developing highly nutritious, health beneficial vegetables of which tomato is one of them that reduce malnutrition.

Whereas production of tomato seed is an immensely specialized activity, so growers cannot produce their own seed and they have to buy seed of unknown sources and quality. Continuous research to develop hybrids and open pollinated varieties in vegetable crops, particularly tomato, have yet to be made. Henceforth there is a large opportunity for vegetable breeding in general and for tomato in special, particularly by hybridization methods.

Weighing the potentiality of tomato, it is a badly needed to improve and develop varieties which suitable to specific agro-ecological situations and also for specific end use. A deep knowledge about the extent of genetic variability existing for several characters is important for starting the crop improvement program. Because of a systematic breeding program, to develop high yielding types, collection of information on genetic variability and inter relationship between different characters is prerequisite.

Yield which is a complex character considered as a function of several component characters and their relationship with environment. Substantiation of structure of yield involves the degree of mutual relationship between different characters contributing to the yield. In this case genotypic and phenotypic correlation express the degree of association among different characters and helps in selection the improvement of yield and yield contributing characters simultaneously. Also, path coefficient analysis helps in dividation of correlation coefficients into direct and indirect effects in the assessment of correlative contribution of each component character to the yield.

For crop improvement information considering genetic diversity and genetic relationships between different genotypes is very important. So for the selection of diverse parental combinations, reliable classification of accessions, and for exact identification of variety, genetic diversity of agro-morphogenic and nutritional traits analyzing is very important. Breeding and domestication has resulted in reduction of tomato genetic diversity. So, knowing about the genetic relationship between the tomato species is important.

Considering the above facts, the present study was therefore undertaken

1. To pursue the genetic variability in tomato genotypes in respect to fruit yield and its component characters.
2. To study the association between fruit yield and its components by estimating genotypic and phenotypic correlation coefficient.
3. To estimate the direct and indirect effects of fruit yield components by partitioning the total component through path coefficient analysis.
4. To know the extent of genetic distance among different genotypes within a group.

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

Tomato is a crop species which is involved in different studies of breeding, genetics, and genomics in plants. There are very researches which deals with tomato. And it can lead an uprising in the evaluation of tomato biology (Barone *et al*. 2008). To study tomato genomic diversity many studies have been done using different genes (Asamizu and Azure, 2009, Carelli *et al*. 2006, Martinez *et al*. 2006).

Away from the centre of origin domestication and also considerable genetic improvement influences the high degree of genetic uniformity in tomato cultivars, which, culminated in the achievement of uniformity, separated from the truth that only a limited number of genotypes were used for breeding. For the preservation of wild species, local varieties and traditional genotypes in gene banks the requirements is apparent, which have become a major frame of gene maintenance (Gepts, 2006). However, the accessions in gene banks should be characterized and evaluated in order to determine the magnitude of genetic diversity, which would allow the identification of redundant accessions and genotypes of interest in breeding programmes (Balestre *et al*. 2008; Terzopoulos and Bebeli, 2008).

2.1 Tomato

The tomato (*Solanum lycopersicum* L.) is an edible fruit which is an autogamous species with a narrow genetic base. Its height is around 1-3 m tall, with weak woody stem which usually scrambles over other plants and other supporting elements. The nomenclature, origin, distribution, nutritional and medicinal values of tomato are discussed and reviewed in below section.

2.1.1 Nomenclature, origin and distribution of tomato

Tomatoes were introduced into Europe from the Americas. After that it became known to botanists about the middle of the sixteenth century. After that the scientific naming of tomatoes, including wild species, is linked to the theory of diversity in *Solanum Iycopersicum*, which is the cultivated species. According to Pietro Andrea Matthioli (1544), tomatoes introduced for the first time with the common name "Pomi d'oro" (Golden Apples) in the first edition (written in Italian) of his 'Commentary' upon the work of the 1st

century Greek botanist Discords of Anazarbos. In the Latin edition, Matthioli (1554) referred to tomatoes as "Mala aurea" (the Latin equivalent of Golden Apple). Matthioli greatly enriched the tomato description with Italian traditional knowledge. He uses of plants previously not known in Europe, and many editions of Matthioli's work were translated in different languages throughout Europe (Watson, 1989).

Before standardized scientific naming different names in different languages were used to name tomatoes in the time. Pre-Linnaean botanists usually used polynomial, or phrase, names, consisting of several words and described the plant itself and distinguishing it from all others. They did not employ today's genus and species concepts, but did seek to name plants in a way that reflected their affinities. Interestingly, early botanists has found the close relationship of tomatoes with the genus *Solanum*, and after that they referred to them as *S. pomiferum* (Luckwill, 1943). Tournefort (1694) was the person who naming first the cultivated tomatoes as *Lycopersicon* ("wolf peach" in Greek). Tournefort placed forms with large multilocular fruits in the set of plants he called *Lycopersicon*, but kept the plants with bilocular fruits as *Solanum.* Linnaeus (1753) which began to consistently use Latin binomials in Species Plantarum, as polynomials were becoming too complicated. It also was difficult to memorize. He classified tomatoes in the genus *Solanum* and described *S. Iycopersicum* (the cultivated tomato) and *S. peruvianum*. The very next year Miller (1754) followed Tournefort (1694) and he formally described the genus *Lycopersicon*. Miller did not approve of Linnaeus's binomial system, and until 1768 he continued to use polynomial phrase names for all plants (Miller, 1768). Miller's circumscription of the genus *Lycopersicon* also included the vegetable potatoes as "*Lycopersicon radice* tuberose, *esculentum*" which was supported by the argument that "This Plant was always ranged in the Genus of *Solanum*, or Nightshade, and is now brought under that Title by Dr. Linnaeus; but as *Lycopersicon* has now been established as a distinct Genus, on account of the Fruit being divided into several Cells, by intermediate Partitions, and as the Fruit of this Plant [the potato] exactly agrees with the Characters of the other species of this Genus, I have inserted it here."

Later, Miller (1768) began to use Linnaeus' binomial system. He also published descriptions under *Lycopersicon* for several species, among them were *L. esculentum*, *L.*

peruvianum, L. Pimpinellifolium and *L. tuberosum* (potatoes). In the posthumously published edition of the gardener's and botanist's dictionary (Miller, 1807) the editor, Thomas Martyn, followed Linnaeus. They merged *Lycopersicon* back into *Solanum*. Following Miller's early work, a number of classical and modern authors recognized tomatoes under *Lycopersicon,* but other taxonomists included tomatoes in *Solanum.*

Today, based on evidence from phylogenetic studies by using DNA sequences and studies of plant morphology and distribution, there is general acceptance of the treatment of tomatoes in the genus *Solanum* by both taxonomists and breeders alike. For example, the use of *Solanum* names has obtained wide acceptance by the breeding and also by the genomics community such as the Solanaceae Genomics Network (SGN) and the International SOL 'Project (http://www.sqn.comell.edu/).

Lastly the generic status of tomatoes has been in flux since the eighteenth century, reflecting two main and competing goals in taxonomy, one is predictive natural classifications (treatment in *Solanum*) and second is the maintenance of nomenclatural stability (treatment in *Lycopersicon*).

The centre of origin of *Solanum lycopersicum*, (*S. Lycopersicon*) or natural geographic distribution has been localised in the narrow band between the Andes mountain ranges and the Pacific coast of western South America (WWF and IUCN, 1997). Including the Galapagos Islands this extends from southern Ecuador to northern Chile, (Peralta, Spooner and Knapp, 2008; Nuez *et al*., 1996; Jenkins, 1948).

During prehispanic times, Mesoamerica from South America there were various useful plants were introduced and domesticated. The original South American tomato fruit became a synanthrophyte and through trade between prehispanic cultures a plant species brought indirectly to Mexico. The characteristics of this wild fruit were different from the cultivated fruit which was small size (1-2 cm diameter), bilocular and acid taste (Jenkins, 1948). Upon its arrival in Mesoamerica, its similar morphology with the green tomato (*Physalis*) facilitated it’s adopted by Mexican cultures. Since those times, the use and diversification in morphotypes, dimensions, forms and colours of the fruits used as food by Mexican indigenous cultures were extraordinary (de Sahagún, 1979). Mexicobthe Andes zone, houses the largest morphological variability in tomato (Rick, 1978; Jenkins,

1948). It is considered as the centre of diversity and domestication of *S. lycopersicum* (Larry and Joanne, 2007; Nuez *et al*., 1996; Rick, 1990; Jenkins, 1948).

2.1.2 Nutritional and medicinal value of tomato

Tomatoes are now eaten freely overall the world. Their consumption is proved to benefit the heart among other organs. Lycopene is one of the most powerful natural antioxidants which is found in tomato. In some studies lycopene in cooked tomatoes has been found to help prevent prostate cancer and has also improve the skin's ability which is able to protect against harmful UV rays (World Cancer Research Fund,2007). Tomato (*Lycopersicon esculentum* Mill.) is termed as "the most popular vegetable fruit". It is a fruit of good source of good nutritive value such as vitamins (vitamin C), and other minerals like calcium, phosphorus and iron.

Sharon (2009) research concluded that against the risk of colorectal cancers lycopene provides a protective effect and may help reduce the risk of pancreatic cancer. In the area of food and phytonutrient research and experiment there is nothing has been hotter in the last several years than studies on the lycopene in tomatoes. This carotenoid found in tomatoes which is studied for antioxidant and cancer-preventing properties (and everything made from them). The antioxidant function of lycopene-its ability to help protect cells and other structures in the body from oxygen damage. It -has been linked in human research to the protection of DNA (our genetic material) inside of white blood cells. Lycopene also prevents heart disease which has been shown to be another antioxidant role played by against a growing list of cancers.

Tomato products is significantly reduced total and LDL cholesterol levels, while also increasing LDL's resistance to oxidation (damage by free radicals). A study involving 21 healthy subjects published in the British Journal of Nutrition. (Study volunteers followed a diet free of tomato products for 3 weeks, followed by a high tomato diet 13.5 ounces tomato juice and 1 ounce tomato ketchup daily).

Prostate cancer is the most known cancer among men in North America. A growing body of evidence has shown that tomato products helps to decrease the risk of prostate cancer. This is happened to be due to a high concentration of lycopene, a potent antioxidant. So

intake of lycopene supplements has become familiar among men who are concerned about their risk of prostate cancer. Although some observational studies and experiment have shown a protective effect (Tzonou *et al,*. 1999) by using of tomato products, others have failed to show this benefit (Cohen *et al*., 2000).

In recent years, especially in relation to prostate cancer l and tomato products have been the focus of intense investigation (Stacewicz-Sapuntzakis & Bowen, 2005). As Giovannucci (1999) reviewed the epidemiological literature on the relationship between intake of tomatoes and tomato-based products and plasma levels of lycopene and added the risks of various cancers. Among 72 studies identified, 57 reported inverse associations between tomato intake or blood lycopene level and the risk of cancer at defined anatomical sites, and 35 of these inverse associations were statistically significant. No study reported that higher tomato consumption or blood lycopene level can promote the risk of cancer at any of the sites investigated. The people who risks of atherosclerosis, or just trying to avoid it, is that tomatoes are a very good source of potassium and a good source of niacin, vitamin B6, and folate. Diets rich in potassium have been shown to lower high blood pressure and it reported that it can reduce the risk of heart disease (Sanjiv A and Rao AV, 2000).

The researchers examined a tracked close to 40,000 middle-aged and older women who were free of both cardiovascular disease and cancer when the study began. In that case more than 7 years of follow-up, those who consumed 7 to 10 servings each week of lycopene-rich foods (tomato-based products, including tomatoes, tomato juice, tomato sauce and pizza) were found to have a 29% lower risk of cardiovascular disease and) compared to women eating less than 1.5 servings of tomato products weekly. Women who ate more than 2 servings each week of oil-based tomato products, particularly tomato sauce and pizza, had an even found better result-a 34% lower risk of CVD.

Tomatoes and broccoli joined up to fight prostate cancer with further according to cardiac health, recent (2009) research from Cambridge University in the U.K., concluded that supplemental lycopene derived from Tomato can reduce the oxidation of harmful fats in the blood and can almost zero within eight weeks. Also added a natural supplement made from Tomatoes, taken daily, may stave off heart disease and strokes.

Natural chlorine which is found in tomato helps to stimulate the liver. Tomato also helps and assists the liver in removing the toxic waste products from the system. To protect the liver from cirrhosis and other debilitating conditions Sulphur plays a great role. Fresh tomato juice can help to regenerate the damaged, destroyed or surgically removed liver (International Cyber Business Services, 2000).

In the old Soviet Union, doctors usually prescribed and suggested Tomato to factory workers who were exposed to toxic chemical occupational environments. It is believed that the reason was due to the fact that Tomatoes have two very important detoxifying trace elements, they are chlorine and sulphur. Natural chlorine helps to stimulate liver function, and the sulphur is said to protect the liver from cirrhosis and other liver problems (http://www.holisticonline.com).

2.2 Variability

In breeding population the functional key to obtain the genetic improvement of a crop through a proper breeding programme and process is to assess the amount and nature of variation of plant characters. Variability is a useful thing that can help the breeder for improving the selection efficiency. Because of this many researchers already study about the variation of various characters in tomato.

When the genetic variability and the extent present, it becomes successful in case of crop improvement programme to which the desirable trait is heritable. In previous researchers it has shown that the presence of genetic variability in the breeding material has been emphasized (Naz *et al*., 2013; Reddy *et al*., 2013; Singh, 2009; Shuaib *et al*., 2007).

Naz *et al*. (2013) has conducted a field experiment which was about to study the genetic variation among twenty five tomato accessions that helped in the reliable varietal selection programme for breeding. Two parameters were used to analyse the all tomato accessions e.g. morphological and molecular parameters. The height of plant, fruit colour and fruit size show variability in this research.

In another case, Reddy *et al*. (2013) has used nineteen exotic collections of tomato which 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 shown the total variation.

Morphological trait measurements can provide a simple technique and it also quantifying genetic variation. It also simultaneously assessing genotypic performance and characters under relevant growing environments (Shuaib *et al.*, 2007). Some of the previous research reports which are related in this case are discussed here.

Mahesha *et al*. (2006), has figured out the significant variability for all the characters under study and marked 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. On the basis of phenotypic characters like color, size, taste etc. a number of germplasms are available in tomato.

Singh *et al*. (2005) was performed a field experiment on 15 advance generation breeding lines of tomato where he studied to the variation for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene content and dry matter content and figured out the significant differences among the genotypes under normal conditions. On the other hand the differences were not significant under high temperature conditions. During November than February planting the population mean was higher for all the characters except acid content and TSS.

Singh (2005) conducted a field experiment in where he used 30 tomato and five genotypes (DT-39, RHR-33-1, ATL-16, DARL-13 and RT-JOB-21) showed maximum number of primary branches than the control. From BT-117-5-3-1 the maximum number of fruits per plant was obtained. Fruit yield was higher (1.84 kg/plant) in DT-39. Total soluble solids content was higher in fruits in most of the cultivars compared to the control. The acidity percentage in fruits was highest in KS-60. The physiological loss in weight at seven days was highest in NDT-111 and lowest in Plant T-3. ATL-13 showed the highest lycopene content (59.67 mg/100 g).

Agong *et al*. (2001) has showed a large and significant variation in the quantitative traits between the accessions and evaluated the Kenyan tomato germplasm. 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. According to Mohanty and Prusti (2001) Research, a 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 finding out and 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 studies are presented here.

2.2.1 Plant height (cm)

Naz *et al*. (2013); has performed an experiment where he 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.

Kumari *et al*. (2007); conducted an experiment where the highest genotypic coefficient of variation for plant height was found.

Joshi *et al*. (2004) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and has found that plant height gave the highest heritability (78.82%). Shravan *et al*., (2004), Prasad and Mathura (1999) and Aditya and Phir (1995) reported significant variation for plant height.

Ravindra *et al*. (2003); has found significant genotype x environment interaction for plant height. Hannan *et al*., (2007) was held an experiment, where he estimated heterosis and character association in 45 single cross hybrids, obtained from 10 parental lines of tomato for yield and yield component traits. The characters studied were plant height, days to first flowering (DFF), number of flowers per cluster (NFPC), number of fruits per plant (NFPP), fruit weight per plant (FWPP) and days to first fruit ripening. They obtained significant differences among genotypes for all the traits and found positive high significant hererosis for FPP (72.9, 75.33 and 20.74), TFWPP (189, 172 and 187), NFPC (48.65, 44.14 and 37.86) over the mid parent, better parent and standard parent heterosis, respectively, and

significantly high percentage of positive heterosis for NFPP, TFWPP and NFC. They concluded that five hybrids possessed significant positive useful heterobeltiosis for TFWPP, positively correlated with FPP, NFPC and Plant height. They selected three single cross hybrids for their heterotic performance.

Parthasarathy and Aswath (2002), conducted a study with 23 genotypes of tomato and figured out 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 where 92 tomato genotypes were used 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), held an experiment where they 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 but in another experiment a narrow range of variations was observed by Ahmed *et al*. (1986).

Dev *et al.* (1994); reported that heterosis in tomato in a line × tester analysis. Appreciable heterosis was seen for the nine characters studied over their respective better parent. Heterosis over the better parent ranged from 0.05 to 115.7%, the minimum being for plant height and the maximum for number of fruits per plant. They concluded that the best F1 hybrid was EC156 × Marglove, which gave 83.18 and 29.23% greater yields than the better parent and the control variety, respectively.

Farkas (1993), figured out the problems in heterosis breeding of tomato. In a strain × 5 tester analysis in which the maternal parents had a morphological marker ah and positional sterility gene (ps2, s16). He found high GCA variances for early and total yield, mean fruit

weight and fruit firmness, but not for plant height and width. Estimation of GCA effects indicated that the maternal parent was superior in early and total yield. He also added that GCA and SCA effects were not directly related to the observed performance of hybrids for given characters. Moreover, heterosis effects compensated for a yield decrease in hybrids of the processing type.

Sonone *et al*. (1986) and Prasad and Prasad (1977) also reported in tomato high phenotypic and genotypic co-efficient of variation for plant height were seen.

Mallik (1985) stated that than genotypic co-efficient of variations for plant height lower than phenotypic co- efficient of variations in tomato.

2.2.2 Number primary and secondary branches plant^{-1}

Upadhyay *et al*. (2005); evaluated 34 genotypes of tomato where he found a range between 2.33-7.0 branches per plant. He stated that the PCV (35.93%) was higher than GCV (24.72%) for this character.

Singh *et al*. (2005); conducted a field experiment with 30 tomato and five genotypes (DT-39, RHR-33-1, ATL-16, DARL-13 and RT-JOB-21) Where higher number of primary branches than the control was shown. The maximum number of fruits per plant was obtained from BT-117-5-3-1. Fruit yield was maximum (1.84 kg/plant) in DT-39. Most of the cultivars showed higher total soluble solids content in their fruits compared to the control. The acidity percentage in fruits was highest in KS-60. The physiological loss in weight at 7 days was highest in NDT-111 and lowest in Plant T-3. ATL-13 showed the highest lycopene content (59.67 mg/100 g).

Singh (2005), Mohanty (2003) and Upadhaya *et al*. (2001) observed in their study that GCV was slightly lower than PCV for number of branches per plant.

Shravan *et al*. (2004) conducted an experiment where 30 tomato genotypes were used to study their genetic variability and reported significant difference for number of primary branches per plant among the genotypes.

Ravindra *et al*. (2003) observed remarkable genotype x environment interaction for number of primary branches.

Singh *et al.* (2002) carried out a field experiment where he worked with 92 tomato genotypes to study genetic variability and concluded 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.

Singh and Singh (1993), performed an experiment on heterosis breeding in tomato. In a diallel set eight cultivars with diverse values for quantitative characters were crossed. Data on yield and nine component traits were recorded for the 28 F_1 hybrids and parents. Hybrid Punjab Chhuhara × 84-8 showed the highest heterosis for fruit yield plant^{-1}(1200 g). Heterosis for this hybrid was also superior for number of fruits plant^{-1}and early yield over the mean parent, and number of branches plant $^{-1}$ over the better parent.

2.2.3 Days to first flowering

Farzaneh *et al.* (2013) showed earliness in a number of days to first flowering while studying combining ability from a 9x9 diallel cross. Whereas Monamodi *et al.*, (2013) had not found any significant differences in days to first flowering among tomato genotypes.

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

Matin *et al.* (2001) reported significant differences among the 26 tomato genotypes for days to first flowering ranging between 49.67 and 68.33 days. He also reported that the phenotypic variance was comparatively higher than the genotypic variance indicating high degrees of environmental effect for days to first flowering.

Singh *et al.* (1993) conducted an experiment on heterosis breeding in tomato. Eight cultivars with diverse values for quantitative characters were crossed in a diallel set. Data on yield and nine component traits were recorded for the 28 F_1 hybrids and parents. Hybrids

Punjab Chhuhara × 84-8, HS102 × Pusa Ruby, HS102 × 84-8 and Pusa Ruby × 84-10 showed significant negative heterosis for days to first flowering over the better parent, indicating their potential for producing an early crop. Hybrid Punjab Chhuhara × 84-8 showed the highest heterosis for fruit yield plant^{-1} (1200 g).

Biswas and Mallik (1989) observed that a minimum of 66 days was necessary for first flowering for cv. *Selection-7* and a maximum of 83 days for cv. *Mtuatham* in an experiment with 18 promising cultivars of tomato considering local cultivar Patharkutchi as control at Mymensingh reported significant variation for days to first flowering in six cultivars of tomato. The phenotypic variance was comparatively higher than the genotypic variance indicating high degrees of environmental effect for days to first flowering (Aditya, 1995 and Matin, 2001).

Geogieva *et al.* (1969) reported that pre-flowering periods of the varieties ranged from 56 to 76 days.

2.2.4 Days of Maturity

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

Pradeepkumar *et al.* (2001) conducted an experiment to quantify genetic variation in tomato for yield and resistance to Bacterial Wilt based on the idea that proper and systematic evaluation of genetic resources was essential to understand and estimate the genetic variability, heritability, and genetic advance. Data were recorded on plant height, days to maturity, number of fruits plant^{-1}, pericarp thickness, locule number, total soluble solids, average fruit weight, number of fruit plant^{-1} and plant yield. They observed highly significant differences among the genotypes for all the traits as well as the high genotypic coefficient of variation for all the characters. Higher heritability estimates and high genetic

advance for all the characters indicated the lesser influence of environment and higher role of additive gene action, respectively, so they suggested selection for rewarding improvement of these traits.

2.2.5 Number of cluster per plant

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

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

2.2.6 Number of fruits per cluster

Samadia *et al*. (2006); evaluated 14 cultivars of tomato where he found PCV and GCV for this character almost similar. In contrast Arun *et al*. (2003) evaluated 37 genotypes of tomato and observed the GCV was lower than PCV for Number of fruits per cluster. Similar result was observed by Aradhana and Singh (2003).

Singh *et al*. (1997) derived information on genetic variability, heritability and yield correlations from data on 14 agronomic and yield-related traits in 23 genotypes of tomato. They reported that based on heritability and genetic advance values, effective selection may be made for fruit weight and number of fruits plant-1 as fruit yield showed strong positive correlation with number of fruits plant^{-1}and number of fruits cluster^{-1}.They also recommended that number of fruits plant^{-1} and number of fruits cluster^{-1} are the most important character for consideration in a selection programme for improvement of yield.

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

2.2.7Average fruit weight

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

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

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

Singh *et al*. (2002) performed a field experiment to study genetic variability of fifteen heat tolerant tomato. He showed high phenotypic (PCV) and genetic (GCV) coefficients of variation for average fruit weight. Kumar and Tewari (1999) also got the similar results in their experiments with tomato.

Aditya (1995) said in his experiment that analysis of variances showed highly significant mean squares due to variety for average fruit weight among the 44 varieties of tomato. Phenotypic variance and phenotypic co-efficient of variation were bigger than genotypic variance associated with genotypic co-efficient of variation. In the study of genetic variability in 23 genotypes of tomato, Singh *et al*., (1997) concluded that phenotypic variation was quite large but genotypic variation was low.

Padmini and Vadivel (1997) performed an experiment where they studied genetic variability of six F_2 crosses and their parental cultivars and found that progeny of cross In Memory 5.30 p. m. X PKM-1 produced the highest mean values for individual. They also reported that fruit weight small difference was observed between genotypic and phenotypic variance for individual fruit weight.

Sahu and Mishra (1995), reported that in 16 lines of tomato, fruit weight had high genotypic co-efficient of variation.

Reddy and Reddy (1992) worked on phenotypic and genotypic variances, phenotypic and genotypic co-efficient of variation for individual fruit weight. For average individual fruit weight considerable variation was observed.

Ahmed (1987), reported that for individual & unit weight among 4 genotypes of tomato a wide range of variation was observed. He also reported that in four tomato varieties namely EC32099, HS102, HS107 and Columbia, genotypic co-efficient of variation was very high for individual fruit weight.

Sonone *et al*. (1986) reported that genotypic and phenotypic variances were high for individual fruit weight in the study of genetic variability with 13 genetically diverse tomato lines.

Arora *et al.* (1982) reported that a wide range of variation in fruit weight of four genotypes of tomato was observed. He also reported that in four tomato varieties, genotypic co-efficient of variation was very high for individual fruit weight.

2.2.8 Fruit length

Chishti *et al*. (2008); was performed an experiment where he worked on the analysis of combining ability for yield, yield components and quality characters in tomato (*Lycopersicon esculentum* Mill.), on plant material comprising 12 parental lines and their F1 hybrids (direct crosses). The data was recorded on days to flowering, number of flowers per cluster, number of fruits per cluster, number of marketable fruits per plant, fruit length, fruit width, and fruit weight, fruit yield per plant, pericarp thickness, and fruit firmness at red stage, total soluble solids and pH of juice. Analysis of variance revealed highly significant differences among genotypes, parents and hybrids and also shown highly significant mean squares due to GCA and SCA for all the characters.

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

2.2.9 Fruit diameter

Saleem *et al*. (2013), reported that twenty-five F1 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. In other hand fruit width was the most heritable trait.

Kumari *et al*. (2007) recorded data for fruit width and he figured out that there were highly significant differences among parents.

Anupam *et al*. (2002) evaluated 30 genotypes of tomato. Similar results for this character was found.

Singh *et al*. (2002) concluded that for this character phenotypic co-efficient of variation was greatest.

2.2.10 Fruit yield per plant

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

According to Matin and Kuddus (2001), for yield per plant among the genotypes, significant differences tested. He also added that phenotypic variance was little higher than genotypic variance indicating slight environmental influence on this trait.

Sachan (2001) conducted an experiment where he used certain tomato genotypes. He also reported among the genotypes for yield per plant significant differences were found.

Kumar and Tiwari (2002) studied that higher genotypic co-efficient of variation for average yield per plant among thirty two tomato genotypes.

Brar *et al*. (2000) reported for average yield per plant among the 186 genotypes, high degrees of variation 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) concluded that genotypic and phenotypic variances were high for average yield per plant.

2.3 Heritability and genetic advance

For all plant breeding practices, selection of plants on phenotypic characteristics is the most important task. In case of effectiveness of selection for yield depends upon heritability. A character with high heritability delivers better response to selection. Heritability and genetic advance are the most important parameters to judge the breeding potentiality of a population which is very important for future development through selection. Many researchers have studied heritability and genetic advance of yield and many yield contributing characters of tomato. The literature which is very relevant to the present study are reviewed below:

Saleem *et al.* (2013) conducted 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. On the other hand fruit width was the most heritable trait.

Buckseth *et al*. (2012) figured out throughout his experiment that high heritability with high genetic advance for number of fruits per plant, average fruit weight, and yield per plant and pericarp thickness indicating that most likely the heritability is due to additive gene effects and selection may be effective.

Narolia (2012) conducted an experiment where 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.

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

According to Ponnusviamy *et al*. (2010), 12 varieties of tomato were evaluated 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.

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

Golani *et al*. (2007) evaluated 20 tomato genotypes and observed high heritability with high genotypic coefficient of variation where genetic gain for 10-fruit weight, number of locules per fruit and fruit yield, could be improved by simple selection.

Kumari *et al.* (2007) reported that the estimates of heritability were high for all the characteristics and for plant height, moderate for total number of fruit bearing branches, weight per fruit and days to maturity, genetic advance was high while the remaining characteristics had low values of genetic advance.

Nardar *et al*. (2007) studied with 20 tomato genotypes and observed high heritability with high genotypic coefficient of variation and genetic gain for fruit weight and fruit yield, where through simple selection it could be improved.

According to Padda *et al.* (2007), broad sense heritability was highest for number of fruits per plant (96.56%), which was 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 for number of fruits per plant (96.56%), followed by number of flowers per plant (93.45%) broad sense heritability was highest which reflecting the effectiveness of selection in the present germplasm of tomato improvement.

Kumar *et al*. (2006) observed high genetic advance (35.55) and low heritability (4.40%) for plant height.

Mahesha *et al.* (2006) estimated expected genetic advance and heritability and 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.

According to Joshi *et al*. (2004); 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 were observed. Moderate heritability and low genetic gain for harvest duration suggests the presence of dominance and epistatic effects.

Kumar *et al*. (2004) estimated in 30 tomato genotypes heritability and genetic advance 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*. (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 for all characters except days from fruit setting to red ripe stage heritability was high. The highest genetic advance was predicted for average fruit weight, followed by shelf life of red ripe fruits.

High degrees of heritability and genetic advance for fruits per plant, individual fruit weight and number of seeds per fruit were reported by Matin (2001).

Matin and Kuddus (2001) reported heritability and genetic advance for fruits per plant, individual fruit weight and number of seeds per fruit were high.

Brar *et al*. (2000) figured out that low to moderate estimates of heritability shown on the number of fruits per plant, total yield per plant and marketable yield per plant had and genetic advance and number of marketable fruits per plant had high values of heritability and genetic advance.

Nessa *et al*. (2000) reported that for number fruits per plant, plant height had high heritability where moderate heritability for yield per plant.

Prasad and Mathura (1999) and Vikram and Kohli (1998) found very high heritability along with high genetic advance by fruit weight.

Phookan *et al*. (l998) studied and estimated that high heritability and genetic advance in percentage of mean were 4 estimated for fruits per plant and average fruit weight suggesting their importance in selection for tomato improvement.

Singh *et al.* (1997) estimated that in 23 genotypes of tomato heritability and genetic advance. 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); conducted an experiment where he studied heritability 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 in 27 genotypes of tomato with genetic advance. 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.

Aditya (1995), concluded that for number of fruits per plant, individual. Fruit weight and plant height high heritability (in broad sense) with high genetic advance in percentage of mean. However, moderate heritability had shown in case of yield per plant and low genetic advance but highest genetic advance as percentage of mean under selection.

According to Pujari *et al*., (1995), 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. Naidu (1993) reported number fruits per plant, plant height and moderate heritability for yield per plant shown high heritability.

Godekar *et al.* (1992) found high values for heritability along with high genetic advance by fruit weight. Reddy and Reddy (1992) performed an experiment where heritability and genetic advance studied 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) worked and studied with 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 where they figured out that heritability values were high for most of the characters but moderate for days to first flowering, maturity and plant height.

Kasrawi and Amr (1990) reported that in a study of seven quality characters using F2 populations, pH gave comparatively higher heritability estimates.

Singh *et al*. (1988) studied 32 genotypes for agronomic characters and obtained high heritability values for yield per plant only.

Abedin and Khan (1986) conducted a study where 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 in tomato, heritability estimates for fruit number, plant height and individual fruit weight were high. He also reported that in case of fruit yield, plant height, individual fruit weight and number of fruits per plant, high genetic advance was observed

Mallik (1985), reported high genetic advance for plant height, number of fruits per plant, individual fruit weight and yield per plant where in another hand low heritability for yield per plant.

Dudi *et al.* (1983) found that heritability and genetic advance-were high in case of number of fruits per plant, individual fruit weight and yield by per plant.

Singh and Singh (1980) concluded that high heritability for average fruit weight, total fruits and days to first picking.

Nandpuri *et al*. (1977) conducted an experiment and observed that heritability estimates were high for fruit size, plant height and yield per plant in tomato. Expected genetic advance was found high for fruit size, yield and number of fruits per plant.

2.4 Correlation and path co-efficient analysis

2.4.1 Correlation co-efficient analysis between yield and yield contributing characters

Between the characters correlation is an estimate to evaluate the inter-relationships between the characters. It will help the breeders to choose selection techniques. Because of yield is one of the main targets of most of the breeders for that in most cases, correlation between yield and yield contributing characters was studied. The yield contributing

characters are also interrelated among themselves. For planning effective selective breeding programme for maximization of yield, association of characteristics with yield and among its components is important. 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, in case of negative correlation co-efficient among yield components were generally observed indicating selection for any component might not bring improvement for yield. It has already found that many authors have studied correlation between yield and yield contributing characters of tomato. Some recent literatures which are related are reviewed in this section

Kumar *et al*. (2013) evaluated forty nine genotypes of tomato (*Solanum lycopersicum* L.) For various quantitative and quality traits by. 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) figured out that 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. 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 was observed.

Monamadi *et al*. (2013) found 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.

Buckseth *et al*. (2012) carried out an experiment by consisting of 40 genotypes of tomato to study the correlation among different quantitative and qualitative traits in tomato genotypes. The study showed highly significant differences among the genotypes for all the characters studied.

Rani *et al*. (2010) revealed that fruit weight, pericarp thickness, acidity, ascorbic acid and lycopene were positively and significantly associated with yield per plant and on another hand number of fruits per plant was associated negatively.

Ya Dong *et al.* (2010) figured out that the lycopene content is very significantly positively correlated with single inflorescence flower numbers, single inflorescence fruit numbers and soluble solids content. But with pedicel length and single fruit weight showed very significantly negative correlation. 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 fruit.

Ara *et al*. (2009) concluded that 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.

Anitha *et al.* (2007) reported that their corresponding phenotypic values and oxalate genotypic correlations were lower than content showed significant positive correlation with seediness and a non-significant positive correlation with lycopene, TSS and locule number.

Golani *et al.* (2007) observed that fruit weight had significant and as well as positive correlation with fruit length at both levels.

In thirty diverse tomato genotypes Correlation coefficient analysis was studied 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).

Wagh *et al*. (2007) performed Correlation analysis which 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.

According to Wright (2007) correlation analysis and observed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant.

Kumar *et al*. (2006) performed correlation coefficient analysis of 30 tomato genotypes and observed that number of fruits per plant had significant and fruit yield per plant shown positive correlation.

Megha *et al*. (2006) carried out a study in where 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.

Singh *et al.* (2005) performed correlation coefficient analysis on 15 advance generation breeding lines of tomato. He also observed that the phenotypic coefficients of variation were higher than genotypic coefficients of variation indicating that the genotypic effect is lessened under the influence of the given environment.

Manivannan *et al*. (2005); carried out an experiment in cherry to estimate correlation coefficient analysis and observed that fruit yield was significantly and positively correlated with the number of leaves and fruit weight.

According to Arun *et al*. (2004) observation 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 where he used 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.

Kumar *et al.* (2004) performed 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. Similarly, inter-relationships were studied in 92 tomato genotypes.

According to Singh *et al*. (2004), 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. Negative correlation was noticed between the number of primary branches per plant and number of fruits per plant.

Kumar *et al*. (2003) studied thirty diverse tomato genotypes for Correlation coefficient analysis 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. He also 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.

Dhaliwal *et al*. (2002) studied genetic parameters and correlations concerning fruit weight, yield plant-1. The correlation studies indicated that firm fruited - high yielding true breeding lines can be developed.

Harer *et al*. (2002) studied correlation where he used 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 fruit yield were significant in case of phenotypic and genotypic correlations 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.

Padma *et al*. (2002) found the negative correlation was observed between fruit weight and fruit number, plant height and fruit weight, fruit weight and fruit yield and plant height.

Susic *et al*. (2002); showed that a significant negative correlation was between mean fruit mass and number of fruits per plant. Between fruit length and fruit width a significant positive correlation was found.

Tiwari (2002) observed that between the yield and length of fruit there was highest positive and significant association. At the genotypic level, the highest positive association was observed between the yield and length of fruit.

Bhushana *et al.* (2001) conducted an experiment in correlation co-efficient in sixty genotypes of tomato and observed a positive and significant correlation between fruit yield per plant and total soluble solids, ascorbic acid, P^H and titratable acidity. A positive and significant correlation was recorded among rind thickness, ascorbic acid and P^H. They also found similar association between total soluble solids and ascorbic acid, and between titratable acidity and P^H.

According to Dhankar *et al*. (2001) study 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 in case of fruit yield improvement.

Kumar *et al.* (2001) reported that a positive genotypic correlation was found which significant bet is wean pericarp thickness and juice viscosity and between lycopene and ascorbic acid contents and locule number was negatively correlated with pericarp thickness.

Matin and Kuddus (2001), conducted an experiment in where they 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 added 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.

Sharma and Verma (2000) stated that Information on yield correlations is derived from data on eight yield components recorded in eighteen genetically diverse genotypes. 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 that between yield and fruit weight it had shown very high and significant positive correlation co-efficient.

Das *et al*. (1998) carried out an experiment in where correlation co-efficient estimated 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 figure out the associations between eight characters of 44 genotypes of tomato. He studied 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 and number of seeds per fruit.

Naidu (1993) performed an experiment and studied correlation coefficient analysis in 13 tomato genotypes. He 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 there was negative correlated between yield per plant and number of fruits per plant but positively and significantly correlated with individual fruit weight and plant height.

In an experiment Mallik (1985) studied phenotypic and genotypic correlations where 19 varieties of tomato was used and observed that individual fruit weight had positive significant correlations with plant height and yield.

Alvarez and Torres (1983) reported that correlation between ten characters including yield in 34 varieties/lines of tomato shown positive correlation between yield and plant height, yield and fruit number per plant also. All three were positively correlated with each other but negatively correlated with weight.

Dudi and Kalloo (1982) carried out a study in where they estimated 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

It becomes difficult when more characters are involved in correlation study to ascertain the traits which really contribute towards the yield. In this such situation the path analysis helps to determine the direct and indirect contribution of these traits towards the yield. Therefore, is a useful tool for understanding yield except chain of relationship between yield and yield contributing characters. 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.

Under open field condition Meena and Bahadur (2015), studied the character association for tomato germplasm. They worked with nineteen indeterminate tomato germplasm to estimate the nature and magnitude of associations of different characters with fruit yield and among themselves. In order to obtain a clear picture of the interrelationship between fruit yield per plant and its components, direct and indirect effects were measured using path coefficient analysis. Through selection the character showed high direct effect on yield per plant indicated that direct selection for these traits might be effective and there is a

possibility of improving yield per plant based on no. of flowers per plant, fruits per plant and fruit weight. Low residual effect indicates that the characters used explained almost all variability towards yield.

Monamodi *et al*. (2013); evaluated six determinate tomatoes. He reported 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.

Monamodi *et al*. (2013) carried out an experiment in where he used 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); performed an experiment to study path coefficient for yield components and quality traits in 23 hybrids of tomato. He also 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.

Anitha *et al*. (2007) performed path analysis and reported that oxalates, acidity, ascorbic acid and TSS showed positive and high direct effects on lycopene.

Golani *et al*. (2007) studied path analysis. He reported that the 10-fruit weight had the highest positive direct effect.

Dhankhar and Dhankhar (2006) resulted that number of fruits per plant had the maximum positive direct effect.

Marianna *et al.* (2005) conducted an experiment where he performed 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 the highest positive direct effect on fruit yield shown on the number of branches per plant. 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) conducted an experiment in where 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 reported that positive direct effect of number of fruits per plant on yield. Kumar *et al*. (2003) was also reported that. Through average fruit weight positive indirect effects mainly contributed towards its strong association with yield. The findings were on consonance with Mohanty (2002).

Singh *et al.* (2004) performed on 92 tomato genotypes where path analysis between yield and yield contributing characters were estimated 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) reported that the most important yield contributing character was the number of fruits per plant is followed by plant height through path co-efficient analysis.

Kumar *et al*. (2003); evaluated an experiment to estimate path analysis of thirty diverse tomato genotypes. He reported that fruit number per plant had the highest positive direct effect on yield per plant followed by average fruit weight.

Mohanty (2003) conducted a field experiment with eighteen tomato cultivars to study path coefficient analysis and reported 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.

Bodund (2002) carried out a field experiment on path coefficient analysis. According to his observation plant height and fruit diameter directly affected yield in tomato.

Harer *et al*. (2002); held a field experiment to study path analysis of thirty-seven tomato genotypes. He resulted 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 where he found that the number of branches per plant and average fruit weight exerted high positive direct effect on yield. And also reported that high positive indirect effect with each other.

Padma *et al*. (2002) performed path analysis. In this revelation it was said 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.

Bhushana *et al*. (2001) worked with sixty genotypes of tomato to estimate path analysis for fruit quality traits on fruit yield and showed that all the four variables (total soluble solids, ascorbic acid, pH and titratable acidity) exhibited low positive direct effects on fruit yield.

Matin and Kuddus (2001) found that the maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant. He also resulted 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) held an experiment to perform path analysis of yield components in thirty tomato genotypes. They reported 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) performed an experiment on 18 tomato varieties for the relationship of six yield components to yield in two different seasons. They added 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 an experiment in where genotypic and phenotypic path co-efficient analysis were done and reported 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.

McGiffen *et al*. (1994) reported that number of fruits was the most important yield component in where had direct effect on yield.

According to Supe and Kale (1992) study plant height had negative direct effect on yield per plant on twelve indigenous varieties of tomato.

Islam and Khan (1991) experimented on tomato and reported 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) evaluated 19 cultivars of tomato to estimate path co-efficient and found that maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant.

According to Gomez (1987) experiment, days to first flowering has negative direct effect on yield of tomato.

Highest direct effect of plant height and fruit weight on fruit yield of tomato were reported by Sonone *et al.* (l987).

Gorbatenko and Gorbatenko (1985) carried out an experiment where path co-efficient analysis of economically useful characters of tomato. In their findings they reported that individual fruit weight had an appreciable direct effect on yield per plant.

Path analysis in tomato was studied by Dudi and Kalloo (1982) and reported highest direct effects of early yield per plant, fruit weight and fruits per plant.

2. 5 Genetic divergence

According to Smith, (1984); Cox *et al*. (1986) in germplasm accurate assessment of the levels and patterns of genetic diversity can serve for the analysis of genetic variability, for further selection identification of diverse parental combinations to create segregating progenies with maximum genetic variability (Barrett & Kidwell, 1998) and introgression of desirable genes from wild germplasm into the adapted high yielding germplasm resource (Thompson *et al*., 1998).

To assess the potential of heterotic combinations before attempting crosses and hence saving time and resources such information is particularly useful (Hallauer & Miranda, 1988). For specific breeding purposes analysis of genetic diversity in germplasm collections can facilitate reliable classification of accessions and identification of subsets of core accessions with possible utility. Significant emphasis is being paid to comprehensive analysis of genetic diversity in numerous field crops for long-term success of breeding program and maximum exploitation of the genetic resources (Belaj *et al*., 2002). If the structure of the genetic diversity is known within a large collection of germplasm which may be of great help to make decisions on management procedures and breeding strategies to be used in breeding programs. With the development of advanced biometrical techniques such as multivariate analysis, quantification of degree of divergence among the biological populations and assessing the relative contribution of different components to the total divergence at intra- and inter-cluster levels have now become possible. Several researchers have been performed such studies on genetic divergence which are presented below:

Nalla *et al.* (2014) carried out an experiment where 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.

Reddy *et al.* (2013) reported that the percent contribution of eighteen characters for genetic divergence showed that fruit weight contributed maximum towards genetic divergence which was followed by plant height and number of fruits per plant.

Alam *et al*. (2012) concluded in his experiment that multivariate and biochemical analysis of genetic affinity among the tomato varieties are necessary before setting any program for their improvement. Many tomato accessions collected to judge the BARI released varieties and the other commercially available varieties on the basis of their genomic information.

Xiaorong *et al*. (2012) evaluated an experiment by 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 where genetic divergence of 30 tomato genotypes and grouped into 10 clusters was studied. He found that there was no parallelism between genetic diversity and geographical divergence in tomato. He also suggested that high diversity among the genotypes belonging to cluster VII and X can be selected in hybridization programmes to obtain good segregants.

According to Terzopoulos *et al*. (2009), landraces and local varieties contain much more genetic diversity than modern cultivars or hybrids. Therefore they are among the most important sources of genetic variation for breeders.

Kumari *et al*. (2007) recorded data for days to flowering, days to maturity, number of fruits per branch, plant height etc. and resulted 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) worked 30 tomato genotypes into nine clusters studied based on D2analysis. The cluster mean indicated that Days to 50% flowering, plant height, number of branches per plant, number of cluster per plant, number of fruit per cluster and fruit yield per plant were reported as chief contributors towards divergence.

Zhu *et al*. (2004) observed large morphological variations and great genetic diversity has been revealed by molecular markers in wild species. These variations provide great potential for crop improvement. Chen *et al*., (2009) also reported that genetic variation in modern cultivars or hybrids is limited.

Singh *et al*. (2004) reported that clustering pattern indicated no difference between geographical distribution of genotypes and genetic divergence.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.

Sharma *et al*. (2006) performed an experiment where 60 genotypes of tomato were studied for genetic divergence. The genotypes grouped into 10 clusters, maximum divergence within a cluster was exhibited by the cluster VIII (1.531), closely followed by cluster III (1.528) and cluster V (1.460), whereas, cluster VIII and II were the most divergent from each other followed by cluster VII and cluster VIII. Veer shetty (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.

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 were studied by Arun *et al*. (2003) 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.

Markovic *et al*. (2002) used 25 cultivars of tomato originating from the area of the former Yugoslavia and studied genetic divergence where the presence of a high degree of genetic divergence in different genotypes consisting of 5 clusters were recorded.

Singh *et al*. (2002) figured out 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. For indirect selection for yield in tomatoes this genetic variations offer an opportunity.

Dharmatti *et al.* (2001) conducted a field experiment in Dharwad, Kamataka, India during 1994-95 to assess genetic diversity where used 402 tomato population lines by using multivariate analysis based on plant height, number of branches, number of clusters per plant, fruits per cluster, number of fruits per plant, yield per plant, incidence tomato curl viruses and number of whiteflies per plant. They grouped the lines into 4 clusters based on the similarities of D^2values. Cluster-I was the biggest having 217 genotypes, which also consisted of commercial ToLCV susceptible genotypes, namely DWD^{-1}, DWD^{-2}, etc., cluster-II consisting of 51 genotypes / hybrids with potato leaf type and pink fruit, which exhibited field tolerance to ToLCV and cluster-III and IV had 99 and 35 genotypes respectively. Considerable diversity within and between cluster was noticed.

An experiment was carried out by Mohanty and Prusti (2001) on genetic diversity. In this experiment 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) worked on genetic divergence where 18 genotypes of tomato was used 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. He 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 shows 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) performed genetic divergence of 32 tomato genotypes and they could group them into 9 clusters based on D^2values. The magnitude of inter cluster distances showed lower than that of inter cluster distances.

55 tomato genotypes was grouped into nine clusters studied based on D^2 analysis in in Patil (1984) experiment. 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

Tomatoes are the most popular vegetable crop all over the world. It has an important and reliable source of antioxidants such as vitamin C and total soluble solids (% of brix) in human diet. It also decreases risk of heart diseases, diabetes, prostate and various forms of cancer. For new anticancer drugs current research 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 in another way

molecular targets involved in carcinogenesis and cardiovascular diseases. L-Ascorbic acid (AsA), which is an major and essential nutrient component for human health and plant metabolism where it plays key roles in diverse biological processes such as cell cycle, cell expansion, stress resistance, hormone synthesis, and signalling etc. Quality character as well as anti-carcinogenic properties of tomato on human and many animals has been studied by many scientists. Among them most relevant recent researches are reviewed below:

2.6.1 Total Soluble Solids (% of Brix)

In an aqueous solution brix percentage is the sugar content. One percent Brix is meant 1 gram of sucrose in 100 grams of solution. And it represents the strength of the solution as percentage by mass. If the solution contains dissolved solids other than pure sucrose, then the % Brix only approximates the dissolved solid content. There are various reports available on variation of Brix % for different genotypes of tomato. In respect to colour, texture, flavour, nutritive value, and wholesomeness the chemical constituents are concerned in the quality of tomato fruit. Overall high sugar contents, redness of colour, and firm texture are associated with prominence of rich flavour. Growth, maturation, and environment of tomato which are influenced by biochemical changes in fruit are discussed.

Nalla *et al*. (2014) conducted a field experiment where he used 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. There were no statistical differences between the averages of the F_1 and F_2 generations for total fruit number, total soluble solids content, fruit firmness, length and P^H, in a general way and for the majority of the genotypes, reported by Hernandez (2013). Panthee *et al.,* (2013) reported that 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).

Narolia *et al*. (2012) studied high estimates of genotypic coefficient of variation, heritability and genetic advance for acidity, total soluble solids, ascorbic acid content, and shelf life.

Silva *et al*. (2012) performed an experiment and evaluated the components of production and total soluble solids (Brix) of tomato cultivar Carolina. When the colour change from green to red fruits were begun to harvest; on the occasion were evaluated content of soluble solids, number, weight, length and diameter.

Chen *et al*. (2009) studied seven tomato lines. He reported that general heritability for vitamin C and total soluble solid content was high. Lines belonging to *L. esculentum* var. cerasiforme were better breeding materials in case of vitamin C, organic acid and total soluble solid content.

According to Krishna and Allolli (2005) highest fruit yield was (27.79 t/ha), total soluble solid content (6.11%), acidity (0.93%) and lycopene content (7.64 mg/100 g of juice).

A study was carried out by Cheema *et al.* (2003) where 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. It also included four commercial brands of tomato juices and ketchups. In overall experiment the 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) investigate and performed an experiment where he grown 37 tomato genotype. Correlation studies resulted that phenotypic correlation was lower than genotypic correlation for all characters examined. Among them the total soluble solid content had positive but there had low direct effects. But also positive association with fruit yield.

According to Dhaliwal *et al*. (1999) 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 in case of both general combining ability and specific combining ability effects for all characters studied.

2.6.2 P^H

Acid concentration and P^H are important quality and processing characteristics of tomatoes. Several studies have revealed that a proper sugar/acid ratio is paramount to good tomato flavor (Stevens, 1972; Simandle *et al*., 1966 Dennison, 1955). Both [H+] and potential acidity contribute to tartness (Harvey, 1920).The pH is important to process ability, as it should be lower than 4.4 to avoid problems with thermo phylic organisms (Rice and Pederson, 1954). Higher P^H values necessitate longer processing times, increasing the difficulty of obtaining a high quality product. Total acidity and P^H in a tomato should be closely related, but sometimes the relationship between these two factors is not good. Anderson (1957) found that P^H and acidity are not always inversely related, and that in some varieties both values are relatively high. Lower and Thompson (1967) also found poor correlation between pH and acidity in certain tomato lines and their progeny. Stevens (1972) found wide variation inthe $[H^+]$/titratable acidity (TA) ratio among 55 divergent accessions and obtain evidence indicating that variation in phosphorus concentration of the fruits is an important factor in the poor relationship between P^H and acidity. It should be possible to explain the relationship between TA and pH using model systems, as the TA is equal to the sum of TAs contributed by the buffers in the fruit. These buffers also establish the P^H.

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

This chapter illustrates the information that concerning the methodology in this experiment. This discussion emphasizes on methodologies related to the location of experimental site, planting materials, climate and soil, preparation of seed bed, experimental design and layout, pot preparation, transplantation of seedlings, fertilizing, intercultural operations, harvesting, data recording procedure, physiological, nutritional and statistical analyzing procedure.

3.1 Experimental site

The experiment was done in the experimental field, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from October 2019 to April 2020. Location of the experimental site was 23°74' N latitude and 90°35' E longitude with an elevation of 8 meters from sea level (Anon., 2004) in Agro-ecological zone of "Madhupur Tract" (AEZ-28) (Anon.1988). The experimental site is shown in the map of AEZ of Bangladesh in (Appendix I).

3.2 Soil and climate

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to Agro-ecological region of “Madhupur Tract” (AEZ No. 28). The texture of the soil was clay loam and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH was 5.47 to 5.63 and organic carbon content is 0.82% (Appendix II). The data of recorded air temperature, humidity and rainfall during the time of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Planting materials

For this research work thirty-six genotype were used. Among these genotypes six genotype was used as parents and thirty genotypes were the cross materials. The germination and purity percentage were 100%. The healthy seeds of this genotype were collected from the research supervisor Professor Dr. Naheed Zeba, Department of Genetics and Plant

Breeding, of Sher-e-Bangla Agricultural University Dhaka. The name and origin of these genotypes are presented in Table 1.

Table: 1 Name and origin of thirty six tomato genotypes used in the present study

Sl. No	Genotypes	Name/Accession No.	Source of collection
1	G_1	SAU tomato 1	GEPB, SAU
2	G_2	SAU tomato 2	GEPB, SAU
3	G_6	SL001	GEPB, SAU
4	G_7	SL002	GEPB, SAU
5	G_9	BARI Tomato 2	GEPB, SAU
6	G_{10}	SL003	GEPB, SAU
7	$G_1 \times G_2$	SAU tomato 1 × SAU tomato 2	GEPB, SAU
8	$G_1 \times G_6$	SAU tomato 1 × SL001	GEPB, SAU
9	$G_1 \times G_7$	SAU tomato 1×SL002	GEPB, SAU
10	$G_1 \times G_9$	SAU tomato 1 × BARI Tomato 2	GEPB, SAU
11	$G_1 \times G_{10}$	SAU tomato 1 × SL003	GEPB, SAU
12	$G_2 \times G_1$	SAU tomato 2 × SAU tomato 1	GEPB, SAU
13	$G_2 \times G_6$	SAU tomato 2 × SL001	GEPB, SAU
14	$G_2 \times G_7$	SAU tomato 2 × SL002	GEPB, SAU
15	$G_2 \times G_9$	SAU tomato 2 × BARI Tomato 2	GEPB, SAU
16	$G_2 \times G_{10}$	SAU tomato 2 × SL003	GEPB, SAU
17	$G_6 \times G_1$	SL001 × SAU tomato 1	GEPB, SAU
18	$G_6 \times G_2$	SL001 × SAU tomato 2	GEPB, SAU
19	$G_6 \times G_7$	SL001 × SL002	GEPB, SAU
20	$G_6 \times G_9$	SL001 × BARI Tomato 2	GEPB, SAU
21	$G_6 \times G_{10}$	SL001 ×SL003	GEPB, SAU
22	$G_7 \times G_1$	SL002 × SAU tomato 1	GEPB, SAU
23	$G_7 \times G_2$	SL002 × SAU tomato 2	GEPB, SAU
24	$G_7 \times G_6$	SL002 × SL001	GEPB, SAU
25	$G_7 \times G_9$	SL002 × BARI Tomato 2	GEPB, SAU
26	$G_7 \times G_{10}$	SL002 × SL003	GEPB, SAU
27	$G_9 \times G_1$	BARI Tomato 2 × SAU tomato 1	GEPB, SAU
28	$G_9 \times G_2$	BARI Tomato 2 × SAU tomato 2	GEPB, SAU
29	$G_9 \times G_6$	BARI Tomato 2 × SL001	GEPB, SAU
30	$G_9 \times G_7$	BARI Tomato 2 × SL002	GEPB, SAU
31	$G_9 \times G_{10}$	BARI Tomato 2 × SL003	GEPB, SAU
32	$G_{10} \times G_1$	SL003 × SAU tomato 1	GEPB, SAU
33	$G_{10} \times G_2$	SL003 × SAU tomato 2	GEPB, SAU
34	$G_{10} \times G_6$	SL003 ×SL001	GEPB, SAU
35	$G_{10} \times G_7$	SL003 × SL002	GEPB, SAU
36	$G_{10} \times G_9$	SL003 × BARI Tomato 2	GEPB, SAU

3.4 Seed bed preparation and seedling raising

Sowing of the tomato seeds was done in 25th October 2019. Before sowing all the seeds were treated with Bavistin for 5 minutes. All the seedlings of the genotypes were raised in the seed bed of Sher-e-Bangla Agricultural University, Dhaka-1207. Seeds were sown in rows spaced at 10 cm apart. The beds were watered regularly. Seedlings were raised using regular nursery practices. All the recommended cultural practices were taken to raising up the seedling properly. After 28 days, the seedlings were transplanted in the main field.

3.5 Design and layout

The experiment was carried out under field condition during rabi season 2019-2020 in Randomized Complete Block Design (RCBD) method. The genotypes were distributed randomly to every row within every line.

Genotype	:	36
Replications	:	3
Spacing	:	50 cm × 40 cm (row to row x plant to plant)
Plot size	:	18m × 10 m (length x width)
Date of transplanting	:	23th November 2019

3.6 Land preparation

Several ploughing and cross ploughing were used to prepared the land by using ladder, tractor, and power tiller. Cow dung were added for good tilth. All the weeds and stubbles were removed from the field and leveled carefully. The final land preparation was done on November 24, 2019.

3.7 Manure and fertilizer dose

One third of urea, total TSP Triple Super Phosphate), half of the MoP (Muriate of Potash), total Boric acid, Total Zinc, total Ghypsum and cowdung were used before one day of transplanting. Remaining Urea and MoP were used at the time of 15 DAYS of transplanting and 1st flowering. Fertilizer and manure doses are given in Table 2.

Table 2. Doses of fertilizer and manure

SL.No	Fertilizer/Manure	Doses per ha
1	Urea	8kg
2	TSP	6kg
3	MoP	4kg
4	Boric acid	500gm
5	Zinc	500gm
6	Ghypsum	5kg
7	Cowdung	200kg

3.8 Transplanting of seedlings

The seedlings were transplanted in the main field on 23th November 2019 when they were 28 days old. The seedlings were watered regularly so that the root could make a firm relation with soil to stand along.

3.9 Intercultural operations

After establishing of seedlings, 1st mulching and weeding were done. Then second weeding was done during the 2nd installment of urea after 15days. When the seedlings became large, bamboo sticks and ropes were used for supporting the plants. Some lateral branches and leaf were pruned out for obtaining proper sunlight and to reduce the infestation of insects.

I. Thinning and gap filling

After some days of transplanting when the seedlings became established, some new plants were planted at the place of dead seedlings to fill up the gap. Thinning was done to avoid the crowded of seedlings.

II. Weeding and mulching

Weeding and mulching were done several times after transplanting in the main field. Mulching was done for proper aeration and weeding was done to reduce the competition with the tomato plant.

III. Staking

Staking was done to keep the plants erect and for proper aeration. Staking was done by using bamboo stick and rope.

IV. Pesticide application

At the time of cropping period, "Ripcord" was used about 7 times at 7 day's interval during the sunny days in order to prevent the insect infestation. No herbicide was used to control the weeds, only hand weeding was done.

V. Irrigation and drainage

The seedlings were properly irrigated for consecutive 7 days after transplanting. The flood irrigation was done at the time of urea application. Final irrigation was done during fruiting stage. Drainage were done at the time of requirements.

3.10 Harvesting and Processing

All of the tomato varieties that were used in this experiment was different types. So, harvesting time was not same for all the varieties and it continued for about one and half month because fruits of different lines matured progressively at different dates. The fruits per entry were allowed to ripe and then seeds were collected and stored at $4^{o}C$ for future use. Harvesting was started from February 19, 2020 and completed by April 6, 2020. Raising of seedlings, an experimental field in growing condition of plants, intercultural operation, growth stage of a single tomato plant, flowering and fruiting stages of the tomato plant is displayed in **Plate 1** and **Plate 2**.

3.11. Data recording

Data were recorded from each pot based on different yield and yield contributing, physiological and nutritional traits. A view of data collection in the experimental site is shown in Plate 3A.

Plate 1. Different stages of tomato seedlings in the experimental Field. A. Seedling in the seed bed. B. Seedling in the main field after transplanting. C. Mature plant in the main field

Plate 2. Land preparation and intercultural operations. A. Final land preparation B. Weeding using a hook. C. Fertilizer application

3.11.1 Agro-morphological traits

Data for some physical parameters related to yield and yield contributing characters were recorded during the experiment. These traits are as following:

3.11.1.1 Plant height (cm)

Five plants from each genotype from each plot were selected at random and plant height was measured at maturity stage after 75 days of transplanting. Mean value of five plants were considered as the plant height for each plot.

3.11.1.2 Days to first flowering

The number of days was counted from the date of sowing to days to first flowering. . Mean value of five plants were considered as the days to first flowering for each plot.

3.11.1.3 Days to 50% flowering

Number of days when flower at 50% plant of each genotype was formed was counted as the days passed from seedling transplanting to flowering in half of the plants. Mean value of five plants were considered as the days to 50% flowering for each plot.

3.11.1.4 Number of branches per plant

Number of branches per plant was counted from each of the selected plant during maturity stage. Mean value of five plants were considered as the number of branches per plant for each plot.

3.11.1.5 Number of clusters per plant

At the time of harvesting number of clusters per plant was recorded. Mean value of five plants were considered as the number of cluster per plant for each plot.

3.11.1.6 Number of flower per clusters

The number of flower per plant was recorded at the time of flowering. Mean value of five plants were considered as the number of flower per clusters for each plot.

3.11.1.7 Leaf length (cm)

Leaf length was measured by picking a leaf randomly and measured its length from the petiole towards its tip. Mean value of five plants were considered as the leaf length for each plot.

3.11.1.8 Leaf width (cm)

Leaf width was measured by picking a leaf randomly and measured its width from the middle portion of the leaf. Mean value of five plants were considered as the leaf width for each plot.

3.11.1.9 Number of fruits per cluster

All fruits in one cluster were recorded by randomly selecting five clusters in every selected plant. Mean value of five plants were considered as the number of fruits per cluster for each plot.

3.11.1.10 Number of fruits per plants

Number of fruits per plant was recorded during maturity stage of plants from five plants from each genotype from each plot at random. Mean value of five plants were considered as the number of fruits per plants for each plot.

3.11.1.11 Individual Fruit weight (g)

Individual fruit weight was measured by picking a fruit from each genotype and measured its weight by electric precision balance and their mean value was calculated.

3.11.1.12 Fruit length (cm):

Fruit length was measured with a digital slide calipers from the neck of the fruit to the bottom of the same from five representative fruits of each genotype and their average was taken as the length of the fruit.

3.11.1.13 Fruit diameter (cm):

Fruit breadth was measured along the equatorial part of the same five representative fruits taken for fruit length by digital slide calipers and their average was taken as the breadth of the fruit.

3.11.1.14 Skin diameter of fruit (mm)

Five fruits of each replication of every genotype were cut into equal part horizontally and their skin diameter was measured by using slide calipers. Mean value of five representative fruits skin diameter of each genotype is calculated and considered as skin diameter of the fruit.

3.11.1.15 Number of locules per fruit

Five fruits of each replication of every genotype were cut into equal part horizontally and number of locules per fruit was recorded.

3.11.1.16 Yield per plant (kg)

As all the genotypes were indeterminate type, fruits ripped at different times in the same plant of same genotype. So, when harvested every time number of fruits harvested from each plant and their weight were recorded and finally after final harvest their average weight were calculated as yield per plant.

3.11.2 Physiological traits

Physiological traits *viz.* relative water content (RWC) in fruit was noted.

3.11.2.1 Relative Water Content (RWC)

Barrs and Weatherly (1962) method was followed to measure relative water content (RWC). Whole fresh plant was weighted. Then the plant was kept in emerged water under light until the weight stayed constant to attain full turgid and then turgid weight was recorded. Then the plant was kept in hot air oven at 60°C for 72 hours and the dry weight was recorded. Finally, the following formula was used to calculate relative water content (RWC),

$$\text{Relative water content (\%)} = \frac{(\text{Fresh weight} - \text{Dry weight})}{(\text{Turgid weight} - \text{Dry weight})} \text{x } 100$$

3.11.3 Nutritional traits

Some nutritional parameters of tomato named Brix (%), P^H of fruit were measured from ripe fruits.

3.11.3.1 Brix percentage (%)

With the help of portable Refractometer (ERMA, Tokyo, Japan) Brix percentages were measured at room temperature. Fruit juice was collected from a single fruit of each genotype by blending it to measure Brix percentage (%). Determination of Brix % is shown in Plate 3 (E-F).

3.11.3.2 Determination of Fruit P^H

Fruit juice was collected from a single fruit of each genotype by blending it to measure fruit P^H using REX P^H meter model –PHS-3C. The electrode was inserted into the juice to get P^H value. P^H determination is shown Plate 3 (D-E).

3.12 Statistical analysis

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and coefficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2016 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA). viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

Plate 3. Data collection and lab work. A. Data recording; B. Field visit of research supervisor; C. Explaining supervisor about the experiment; D. Determination of P^H; E. Samples for P^H and Brix% determination; F. Brix % determination

3.12.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance, $\sigma^2_P{}^H = \sigma^2_g + EMS$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

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

Where,

EMS = Mean Square Error

3.12.2 Estimation of genotypic and phenotypic coefficient of variation

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

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

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

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

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

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.12.3 Estimation of heritability

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

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.12.4 Estimation of genetic advance

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

Genetic advance, GA = K. h^2. σ_p

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

Where,

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

σ_{ph} = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.12.5 Estimation of genetic advance mean's percentage

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

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

3.12.6 Estimation of simple correlation coefficient

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

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

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.12.7 Estimation of genotypic and phenotypic correlation coefficient

For calculating the genotypic and phenotypic correlation coefficient for all possible combinations the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The covariance components were used to compute the genotypic and phenotypic correlation between the pairs of characters as follows:

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

Where,

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

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

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

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

Where,

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

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

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

3.12.8 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:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Where,

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

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

1 = Days to first flowering

2 = Plant Height

3 = Days to maturity

4 = Number of cluster per plant

5 = Number of flower per plant

6 = Number of fruit per cluster

7 = Number of fruits per plant

8 = Fruit weight (gm)

9= Fruit length (mm)

10 = Fruit diameter (mm)

11 = Fruit yield per plant (gm)

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Where,

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

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

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

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

Where,

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

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

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

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

3.12.9 Multivariate analysis

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

3.12.10 Principal Component Analysis (PCA)

Principal Component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. The contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.12.11 Principal Coordinate analysis (PCA)

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

3.12.12 Cluster analysis (CA)

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

3.12.13 Canonical Vector analysis (CVA)

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

3.12.14 Calculation of D^2 values

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

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

Where,

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

x = Number of characters.

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

3.12.15 Computation of average intra-cluster distances

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

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.

3.12.16 Computation of average inter-cluster distances

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

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

Where,

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

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

3.13 Selection of varieties for future hybridization programme

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by a largest

statistical distance (D^2) express the maximum divergence among the genotypes included in these different clusters. Variety (s) or line(s) were selected for efficient hybridization programme according to Singh and Chuadhury (1985). According to them the following points should be considered while selecting genotypes for hybridization programme:

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

RESULTS AND DISCUSSION

CHAPTER IV

RESULT AND DISCUSSION

The experiment was conducted to study the genetic variability, correlation, path coefficient analysis and genetic diversity of 36 tomato (*Solanum Lycopersicum* L.) accessions and identify the breeding values in respect of genotypic effects and comparative performances of different tomato genotypes. It also carried out the phenotypic and genotypic variability co-efficient of variation, heritability, genetic advance, and genetic advance of mean among different genotypes to estimate the direct and indirect effect of yield contributing traits on yield. Nineteen characters such as plant height (cm), days to first flowering, days to 50% flowering, number of branches per plant, number of cluster per plant, number of flower per cluster, leaf length (cm), leaf width (cm), number of fruit per cluster, number of fruits per plant, individual fruit weight (kg), fruit length (cm), fruit diameter (cm), skin diameter (mm) number of locules per fruit, yield per plant (kg), relative water content, total soluble solid and P^H were studied in respect of 36 genotypes. This chapter comprises the presentation and discussion of the findings obtained from the study. Data pertaining to 19 yield and yield contributing characters were calculated and statistically analyzed and the results of the present findings are presented under the following headings:

- Characterization
- Genetic variability
- Correlation coefficient analysis
- Path coefficient analysis
- Genetic diversity analysis

4.1 Morphological characterization

4.1.1 Fruits color

Fruit color is consider the important traits in tomato for consumer preference marketing. Generally dark red, orange, yellow, pink, pink, green and purple color fruits are commonly found in the market. In the present study, fruit color could be classified in distinct groups like red, yellow, pinkish red, brown or purple, and orange. Among the thirty six genotypes,

the color of the parents are yellow for G_1, red for G_2,G_6, G_9, G_{10} and pinkish red for G_7. But, different color had been noticed for some crossing genotypes which is not similar with the parents. Like pinkish red color was observed for $G_1 \times G_9$, $G_9 \times G_1$, $G_9 \times G_{10}$, brown or purple color fruits was observed for $G_6 \times G_{10}$, $G_7 \times G_1$,$G_7 \times G_{10}$, and orange color fruits was observed for $G_7 \times G_2$, $G_7 \times G_9$, $G_9 \times G_2$. Rest of the crossing genotypes produce a color which is similar to one of its parents except $G_1 \times G_2$, and $G_1 \times G_{10}$. These genotypes produce three types of fruits of different color yellow and red which are identical with their parents. But shape and size were different. (Table 3)

4.1.2 Fruit shape and size

For marketing preference fruit shape and size considered as an important perspective. Various types of tomato are found. Among the thirty six genotypes pear or oval, round, oblate, torpedo shaped, and three different size large, medium and small sized tomatoes were found. The shape and size of the parents are pear or oval and small for G_1 genotype, Round and small for G_2 and G_6 genotype, oblate and large for G_7 genotype, round and medium for G_9 genotype and round and large for G_{10} genotype are observed. Dissimilarities had been noticed in shape and size of some crossing genotypes from their parents like round shape and medium size were observed for $G_1 \times G_6$, $G_2 \times G_1$, $G_2 \times G_6$, $G_2 \times G_{10}$, and $G_6 \times G_1$, round shape and small size were observed for $G_1 \times G_7$, round shape and large size were observed for $G_6 \times G_2$ and $G_9 \times G_2$, oblate shape and large size were found for G6XG10, oblate shape and medium size were noticed for $G_9 \times G_1$ and $G_9 \times G_{10}$ genotype and torpedo shape and medium size were observed for $G_{10} \times G_1$, $G_{10} \times G_2$, $G_{10} \times G_6$, $G_{10} \times G_7$, $G_{10} \times G_9$ genotypes. All other crossing genotypes are same as their any of parents. But in case of $G_1 \times G_2$ and $G_1 \times G_{10}$ the observation is different. $G_1 \times G_2$ genotypes produced two type of fruits that are round and small and pear or oval and small. $G_1 \times G_{10}$ produced three types of fruits one was round and small and another two were torpedo shaped and small size but their color are different. (Table 3)

Table 3: Characterization of 36 tomato genotypes

No. of tomato genotypes	Fruit color	Fruit shape and size
G_1	Yellow	Pear or oval, small
G_2	Red	Round, small
G_6	Red	Round, small
G_7	Pinkish red	Oblate, large
G_9	Red	Round, medium
G_{10}	Red	Round, large
$G_1 \times G_2$	Red	Round, small
$G_1 \times G_2$	Yellow	Pear or oval, small
$G_1 \times G_6$	Red	Round, medium
$G_1 \times G_7$	Yellow	Round, Small
$G_1 \times G_9$	Pinkish red	Round, medium
$G_1 \times G_{10}$	Red	Round, small
$G_1 \times G_{10}$	Red	Torpedo, small
$G_1 \times G_{10}$	Yellow	Torpedo, small
$G_2 \times G_1$	Red	Round, Medium
$G_2 \times G_6$	Red	Round, Medium
$G_2 \times G_7$	Red	Round, small
$G_2 \times G_9$	Red	Round, small
$G_2 \times G_{10}$	Red	Round, medium
$G_6 \times G_1$	Red	Round, medium
$G_6 \times G_2$	Red	Round, large
$G_6 \times G_7$	Pinkish red	Oblate, large
$G_6 \times G_9$	Red	Round, medium
$G_6 \times G_{10}$	Brown/Purple	Oblate, large
$G_7 \times G_1$	Brown/Purple	Oblate, large
$G_7 \times G_2$	Orange	Round, medium
$G_7 \times G_6$	Pinkish red	Oblate, large
$G_7 \times G_9$	Orange	Round, medium
$G_7 \times G_{10}$	Brown/Purple	Oblate, large
$G_9 \times G_1$	Pinkish red	Oblate, medium
$G_9 \times G_2$	Orange	Round, large
$G_9 \times G_6$	Red	Round, medium
$G_9 \times G_7$	Red	Round, medium
$G_9 \times G_{10}$	Pinkish red	Oblate, medium
$G_{10} \times G_1$	Red	Torpedo, medium
$G_{10} \times G_2$	Red	Torpedo, medium
$G_{10} \times G_6$	Red	Torpedo, medium
$G_{10} \times G_7$	Red	Torpedo, medium
$G_{10} \times G_9$	Red	Torpedo, medium

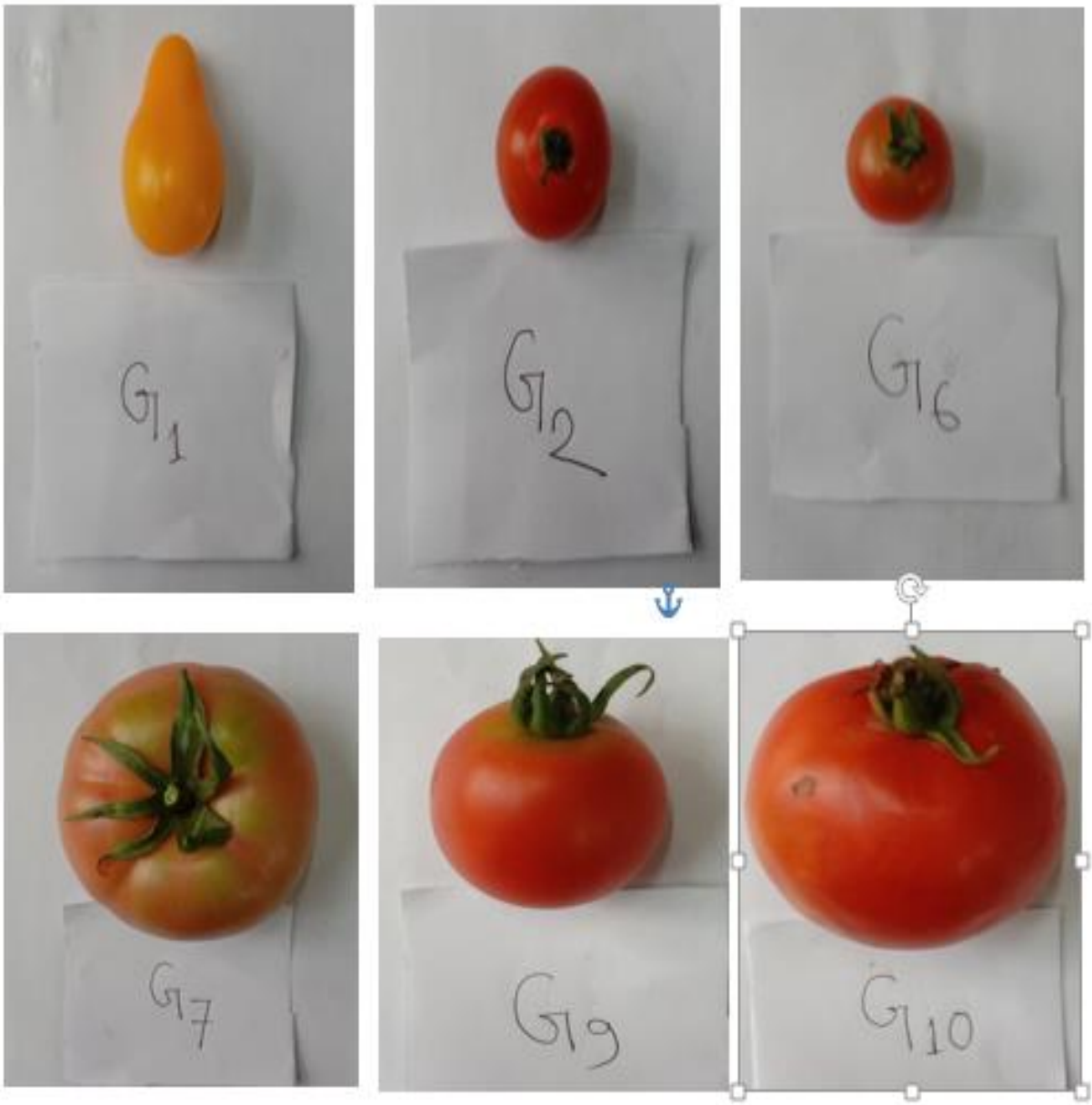


Plate 4. Parents (showing their color, shape and size)

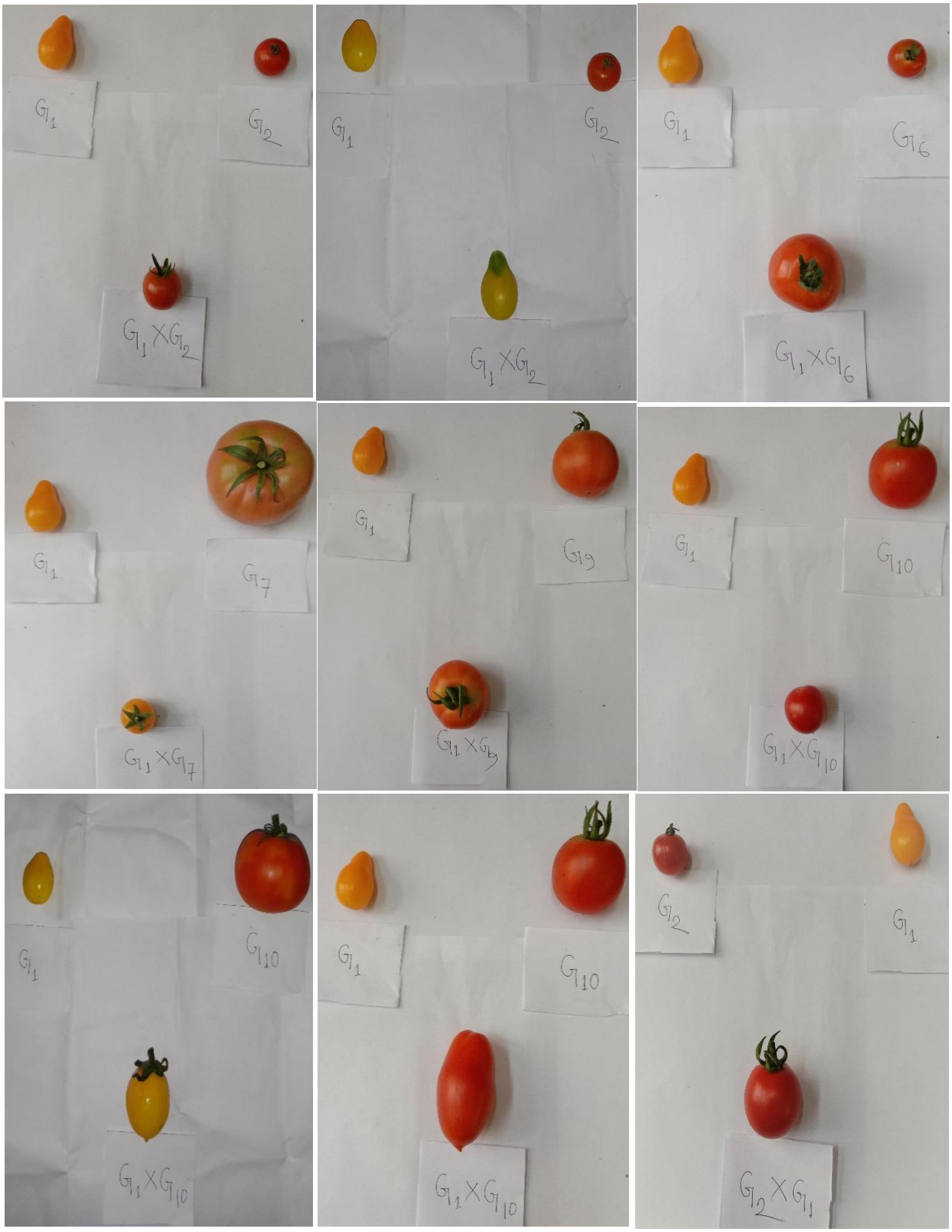


Plate 5. Offspring (showing their color, shape and size)

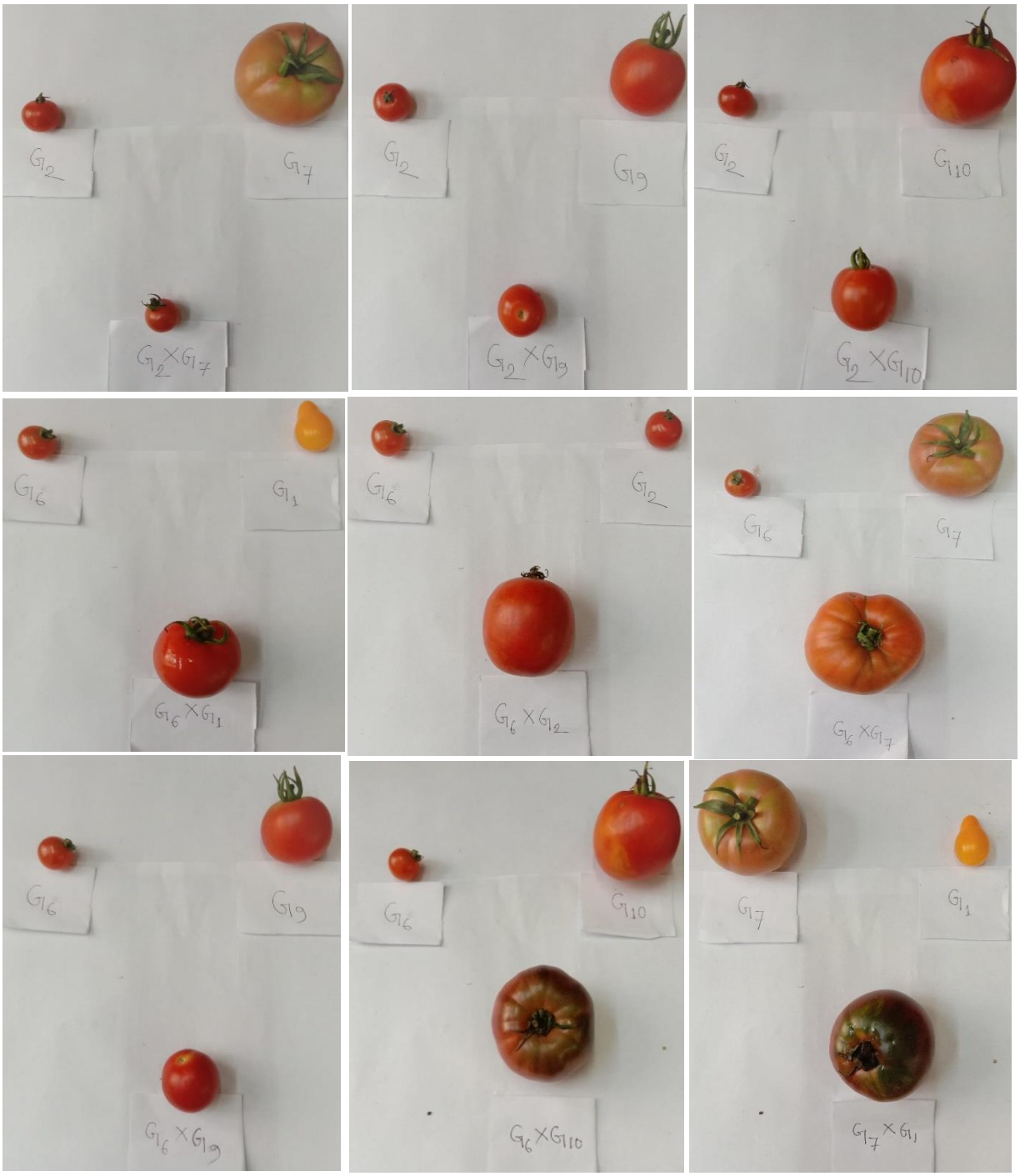


Plate 5. Cont'd

Plate 5. Cont'd

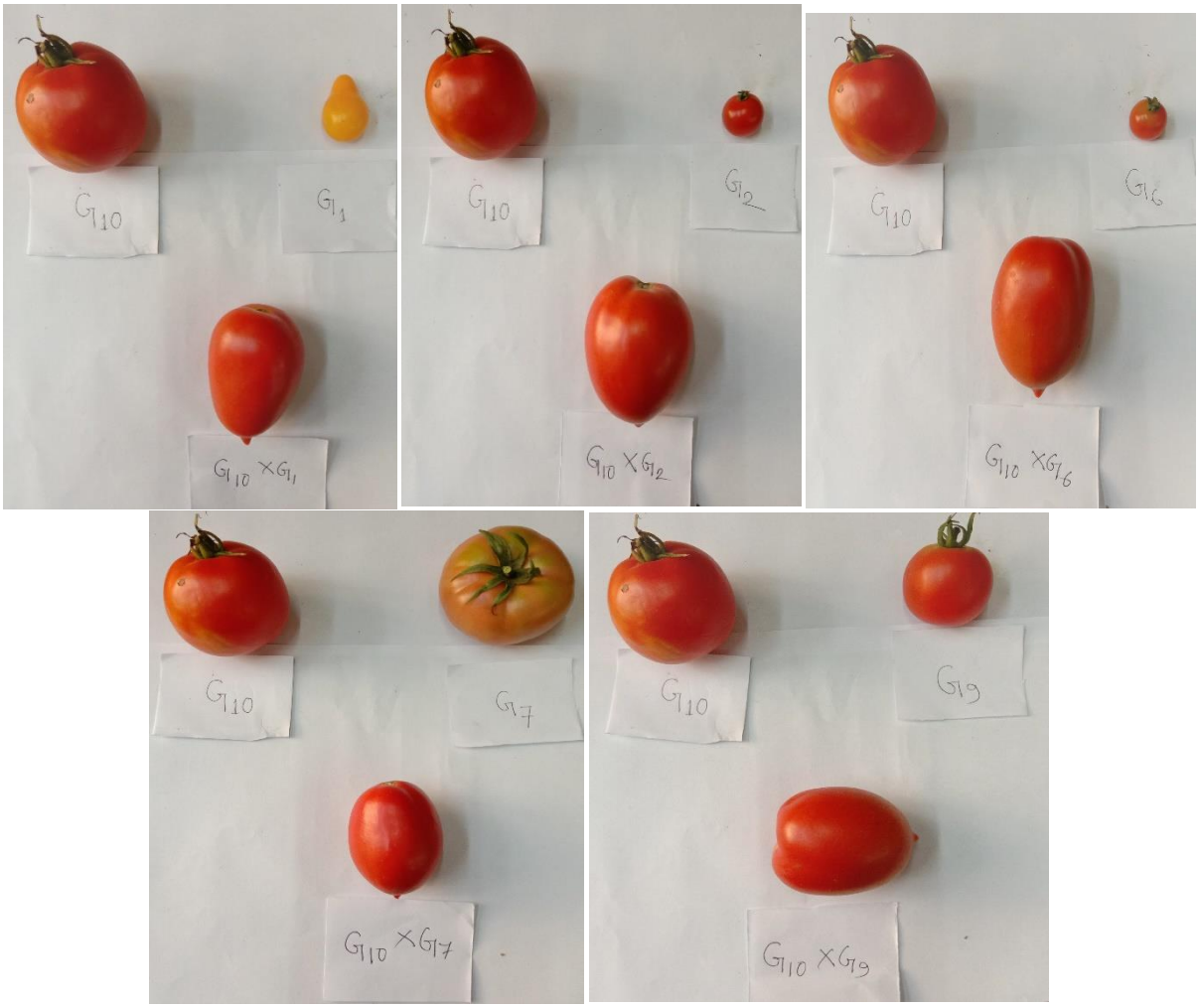


Plate 5. Cont'd

4.2. Genetic Variability

The analysis of variance indicated that the existence of highly significant variation among the genotype studied. The mean, mean sum of square, variance components, genotypic and phenotypic co efficient of variance, heritability, genetic advance, genetic advance in percent of mean are presented in Table 6.

4.2.1. Days to first flowering

The variance due to days to first flowering showed that the genotypes differed significantly and ranged from 52.00 days after transplanting (DAT) in ($G_6 \times G_1$) to 59.33 DAT in (G_7, $G_1 \times G_{10}$, $G_2 \times G_{10}$, $G_7 \times G_9$) with mean value 55.98 days after transplanting (DAT) (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 3.26 and 9.57, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (3.23) and PCV (5.53) were more or less similar to each other, indicated presence of low variability in this trait (Table 6).Similar result were recorded by Bhuiyan *et al (*2016) Singh *et al* (2002) for the character.

The heritability estimates for days to first flowering was moderate (34.08%) with low genetic advance (2.17%) and genetic advance in percentage of mean (3.88%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. A genetic advance in per cent of mean was low which is in accordance with the findings of Bhuiyan *et al (*2016)

4.2.2. Days to 50% flowering

The variance due to days to 50% flowering showed that the genotypes differed significantly and ranged from 68.00 days after transplanting (DAT) in ($G_6 \times G_1$) to 76.67 DAT in (G_7) with mean value 71.84 days after transplanting (DAT) (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 2.90 and 10.22, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The

GCV (2.37) and PCV (4.45) were more or less similar to each other, indicated presence of low variability in this trait (Table 6) which is same as the findings of Bhuiyan *et al (*2016) and Singh *et al* (2002).

The heritability estimates for days to 50% flowering was low (28.36%) with low genetic advance (1.87%) and genetic advance in percentage of mean (2.60%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. **(Table 6)**. According to Bhuiyan *et al (*2016) heritability, genetic advance and genetic advance in percent were low for lycopene and vitamin C content in tomato due to the effect of environment and presence of non-additive type of gene action.

Table 4. Analysis of variance for 19 characters in tomato genotype

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (36-1) = 35**	**Error (r-1)(g-1) = 70**
Days to first flowering	6.51	16.09**	6.31
Days to 50% flowering	0.84	16.01**	7.32
Plant height	3305.96	314.87*	192.84
Number of Branch per plant	1.51	1.30*	0.80
Leaf length	15.08	37.81**	14.61
Leaf width	3.40	56.57**	1.57
Number of Flower per cluster	1.79	21.09**	1.18
Number of Cluster per plant	14.33	44.57**	1.71
Number of fruit per cluster	4.11	45.10**	1.56
Number of fruit per plant	42.80	21267.30**	16.10
Individual Fruit weight	22.80	6493.63**	8.56
Fruit length	25.86	580.25**	16.68
Fruit width	14.40	726.67**	19.54
Skin diameter	0.22	5.98**	0.08
Relative water content	10.64	1171.35**	45.13
Locule number	0.10	1.26**	0.01
P^H	0.34	7.03**	0.56
Total soluble solids	0.05	4.04**	0.08
Yield per plant	1.736	22.504**	0.537

4.2.3. Plant Height (cm)

The variance due to plant height showed that the genotypes differed significantly and ranged from 67.03 cm in ($G_1 \times G_6$) to 105.03 cm in ($G_6 \times G_9$) with mean value 82.89 cm (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 40.68 and 233.52, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (7.69) indicated presence of low variability and PCV (18.44) indicated presence of Moderate variability in this trait (Table 6). Moderate PCV for plant height were also found by Aradhana and Singh (2003), Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi *et al*. (2004).

The heritability estimates for plant height was low (17.42%) with low genetic advance (5.48%) and genetic advance in percentage of mean (6.62%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. According to Bhuiyan *et al (*2016) reported the same findings for lycopene and vitamin C content in tomato due to the effect of environment and presence of non-additive type of gene action

4.2.4. Number of Branch per plant

The variance due to number of branch per plant showed that the genotypes differed significantly and ranged from 3.00 in ($G_7 \times G_9$, $G_{10} \times G_6$) to 6.33 in (G_1) with mean value 4.52 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 0.17 and 0.97, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (9.03) indicated presence of low variability and PCV (21.81) indicated presence of high variability in this trait (Table 6).

The heritability estimates for number of branch per plant was low (17.14%) with low genetic advance (0.35%) and genetic advance in percentage of mean (7.70%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were low which is in accordance with the findings of Bhuiyan *et al (*2016) for lycopene and vitamin C content in tomato.

4.2.5. Leaf length (cm)

The variance due to leaf length showed that the genotypes differed significantly and ranged from 20.10 cm in (G_1, $G_2 \times G_{10}$) to 33.63 cm in ($G_6 \times G_2$) with mean value 26.86 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 7.73 and 22.34, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (10.35) and PCV (17.60) were moderate and indicated presence of moderate variability in this trait (Table 6). Moderate PCV and GCV were also found by Aradhana and Singh (2003), Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi *et al*. (2004).

The heritability estimates for leaf length was moderate (34.61%) with low genetic advance (3.37%) and moderate genetic advance in percentage of mean (12.54%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective.

4.2.6. Leaf width (cm)

The variance due to leaf width showed that the genotypes differed significantly and ranged from 12.37 cm in (G_1) to 29.30 cm in ($G_6 \times G_2$) with mean value 19.85 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 18.33 and 19.91, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (21.57) and PCV (22.48) were more or less similar to each other, indicated presence of high variability in this trait (Table 6). Bhuiyan *et al (*2016) reported that, high phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for leaf length which indicating the higher magnitude of variability for these traits.

The heritability estimates for leaf width was higher (92.10%) with lower genetic advance (8.46%) and higher genetic advance in percentage of mean (42.64%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were higher which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for leaf width.

Table 5. Mean analysis of 19 yield contributing parameters

Genotype	DF	DFF	PH	NFB	LL	LW	NFF	NFC	NFFC
G_1	52.33	68.67	103.97	6.33	20.10	12.37	12.00	15.00	10.00
G_2	54.67	72.67	80.53	4.33	23.23	18.13	13.67	13.33	8.33
G_6	56.33	75.67	83.37	5.00	21.37	14.67	12.00	23.67	12.67
G_7	59.33	76.67	82.50	4.67	29.07	25.67	11.00	7.33	4.67
G_9	55.33	72.33	79.37	4.67	27.70	24.90	6.00	12.33	6.33
G_{10}	57.33	73.33	73.30	4.00	28.43	16.57	6.33	11.00	6.00
$G_1 \times G_2$	52.67	69.67	73.73	5.00	24.13	15.30	8.33	19.00	11.67
$G_1 \times G_6$	54.67	70.67	67.03	4.67	22.70	17.53	10.00	9.00	6.00
$G_1 \times G_7$	52.67	69.67	80.43	5.67	24.00	16.60	13.00	22.00	13.67
$G_1 \times G_9$	55.33	70.67	81.77	4.67	23.97	16.53	6.67	14.00	9.67
$G_1 \times G_{10}$	59.33	75.00	83.83	4.33	24.87	17.47	11.33	10.33	7.67
$G_2 \times G_1$	58.67	74.00	72.47	4.33	23.80	14.90	11.33	12.33	23.00
$G_2 \times G_6$	57.33	73.33	75.60	4.33	28.27	17.13	12.00	14.33	11.67
$G_2 \times G_7$	58.00	70.67	74.02	4.33	27.63	17.03	11.67	17.33	13.33
$G_2 \times G_9$	52.67	69.67	69.77	4.00	22.47	15.27	14.00	12.67	12.67
$G_2 \times G_{10}$	59.33	75.00	72.13	5.00	20.10	12.40	8.00	14.00	9.67
$G_6 \times G_1$	52.00	68.00	75.73	4.00	24.13	18.47	7.33	9.00	4.67
$G_6 \times G_2$	58.00	76.00	76.37	5.00	33.63	29.30	9.00	13.67	7.00
$G_6 \times G_7$	55.33	69.67	79.67	4.00	27.13	22.67	5.33	7.33	4.33
$G_6 \times G_9$	54.67	71.67	105.03	5.33	29.50	19.83	10.00	15.00	15.67

Table 5. Cont'd

Genotype	DF	DFF	PH	NFB	LL	LW	NFF	NFC	NFFC
$G_6 \times G_{10}$	53.33	70.00	82.80	4.33	24.60	15.00	11.00	7.00	6.00
$G_7 \times G_1$	58.67	74.00	79.60	4.00	24.60	23.50	7.00	10.33	6.33
$G_7 \times G_2$	52.67	70.00	75.07	4.00	25.23	20.70	6.67	9.33	7.67
$G_7 \times G_6$	58.00	70.00	97.50	5.00	30.87	26.73	5.67	11.67	7.33
$G_7 \times G_9$	59.33	74.00	71.73	3.00	30.80	18.17	6.33	7.33	5.67
$G_7 \times G_{10}$	57.33	73.00	92.08	4.33	29.30	18.73	8.67	11.00	4.67
$G_9 \times G_1$	53.33	69.00	103.60	4.67	28.27	23.70	8.00	11.00	4.33
$G_9 \times G_2$	54.00	69.00	88.87	5.33	32.23	25.67	7.00	11.33	8.00
$G_9 \times G_6$	56.67	72.33	74.13	4.33	24.90	17.77	7.00	12.67	6.33
$G_9 \times G_7$	54.67	69.00	87.97	4.67	30.33	23.70	6.00	11.67	8.33
$G_9 \times G_{10}$	56.67	72.33	100.73	4.33	29.17	23.90	6.67	8.00	7.67
$G_{10} \times G_1$	57.33	74.00	85.23	4.67	30.70	22.33	6.67	12.67	4.67
$G_{10} \times G_2$	55.33	71.33	93.73	5.33	30.40	22.40	5.67	7.67	6.67
$G_{10} \times G_6$	58.00	72.33	79.57	3.00	29.57	21.50	5.67	10.33	6.67
$G_{10} \times G_7$	56.00	70.33	86.60	4.33	31.57	26.43	6.00	12.00	6.33
$G_{10} \times G_9$	58.00	72.67	94.07	3.67	28.37	21.67	6.33	9.33	6.67
MIN	52.00	68.00	67.03	3.00	20.10	12.37	5.33	7.00	4.33
MAX	59.33	76.67	105.03	6.33	33.63	29.30	14.00	23.67	23.00
MEAN	55.98	71.84	82.89	4.52	26.86	19.85	8.59	12.11	8.39

DF= Days to first flowering, DFF= Days to 50% flowering, PH=Plant height, NFB=Number of flower branch^{-1}, LL=Leaf length, LW= Leaf width, NFF= Number of flower per cluster, NFC= Number of cluster per plant, NFFC= Number of fruit per cluster.

Table 5. Cont'd

Genotype	NFFP	IFW	FL	FW	SD	RWC	LNN	Ph	TSS	ypp
G_1	160.33	7.83	22.00	11.00	2.97	67.08	2.00	6.31	3.97	1.26
G_2	152.67	6.10	7.23	10.43	2.67	50.88	2.00	5.43	3.43	0.89
G_6	264.33	6.50	8.07	10.33	2.43	67.19	2.00	5.23	2.93	1.48
G_7	63.00	142.43	30.00	54.30	3.69	70.09	4.33	4.14	3.33	5.29
G_9	80.33	65.60	29.00	29.00	5.00	35.00	5.00	4.16	2.23	5.77
G_{10}	73.00	66.57	39.67	45.33	4.89	43.59	4.00	3.70	2.17	4.49
$G_1 \times G_2$	214.33	8.33	9.13	11.67	3.32	70.14	2.00	4.01	3.30	1.50
$G_1 \times G_6$	61.33	100.82	24.17	32.33	2.66	53.48	3.33	3.70	2.53	6.25
$G_1 \times G_7$	310.67	7.07	6.70	7.40	3.80	50.00	2.33	4.03	4.00	2.84
$G_1 \times G_9$	123.67	27.13	18.50	27.70	3.83	47.39	2.33	3.49	2.43	4.50
$G_1 \times G_{10}$	73.33	29.50	36.67	17.33	4.33	83.86	2.00	3.52	2.30	2.29
$G_2 \times G_1$	363.33	6.67	22.77	22.90	3.97	88.19	2.33	3.25	3.43	0.63
$G_2 \times G_6$	189.33	20.03	19.37	23.53	1.97	48.41	2.33	3.21	3.23	3.02
$G_2 \times G_7$	254.67	4.67	8.23	7.90	3.10	49.52	2.33	3.55	2.00	0.95
$G_2 \times G_9$	165.33	6.60	10.00	13.67	2.87	54.08	2.33	3.72	1.93	1.46
$G_2 \times G_{10}$	268.67	29.83	21.87	23.83	5.33	67.80	4.00	3.21	4.17	5.66
$G_6 \times G_1$	21.67	108.27	34.00	30.83	4.19	55.09	6.00	3.42	2.03	2.38
$G_6 \times G_2$	147.00	42.63	28.70	35.17	6.90	48.91	5.33	3.78	1.20	3.31
$G_6 \times G_7$	27.00	111.70	38.50	63.00	6.67	51.45	4.00	3.47	7.03	4.10
$G_6 \times G_9$	195.00	14.63	26.83	25.53	4.57	6.33	3.00	3.77	3.03	2.46

Table 5. Cont'd

Genotype	NFFP	IFW	FL	FW	SD	RWC	LNN	Ph	TSS	ypp
$G_6 \times G_{10}$	85.67	99.80	37.00	54.67	5.29	72.73	8.00	3.77	1.13	2.88
$G_7 \times G_1$	117.67	179.57	40.33	53.33	5.79	65.09	3.33	3.64	1.73	11.17
$G_7 \times G_2$	60.33	79.13	38.00	40.00	5.27	20.19	4.00	3.65	2.33	4.59
$G_7 \times G_6$	75.00	19.13	38.00	44.00	4.80	63.55	5.00	3.24	3.70	1.43
$G_7 \times G_9$	44.33	53.17	29.33	30.67	5.14	49.14	4.67	3.26	3.07	2.41
$G_7 \times G_{10}$	54.00	102.33	32.67	56.00	5.32	89.20	6.00	3.12	3.13	5.50
$G_9 \times G_1$	74.00	70.17	24.00	42.67	4.67	64.07	5.33	3.37	5.00	4.27
$G_9 \times G_2$	93.67	105.17	40.17	51.10	5.96	58.49	5.67	3.38	1.07	7.66
$G_9 \times G_6$	66.33	112.27	39.00	55.17	5.79	18.73	5.00	3.40	2.17	7.40
$G_9 \times G_7$	105.33	132.33	40.17	43.20	4.36	65.78	4.67	3.61	2.10	13.06
$G_9 \times G_{10}$	46.00	44.90	22.00	36.87	5.09	67.74	3.00	3.67	3.63	2.08
$G_{10} \times G_1$	94.67	99.83	59.33	37.07	7.78	7.76	2.33	3.70	2.03	4.74
$G_{10} \times G_2$	145.67	50.67	40.67	27.73	5.20	67.67	2.67	3.44	2.50	2.96
$G_{10} \times G_6$	122.67	54.93	57.33	37.80	6.14	75.84	2.00	3.89	2.17	3.00
$G_{10} \times G_7$	65.00	32.17	47.50	33.27	6.04	65.35	2.33	3.75	3.47	2.14
$G_{10} \times G_9$	55.33	70.37	52.60	38.83	7.17	41.70	2.33	3.77	4.00	2.87
MIN	21.67	4.67	6.70	7.40	1.97	6.33	2.00	3.12	1.07	0.63
MAX	363.33	179.57	59.33	63.00	7.78	89.20	8.00	6.31	7.03	13.06
MEAN	125.41	58.86	29.99	32.93	4.69	55.60	3.59	3.77	2.89	3.85

NFFP= Number of fruit per plant, IFW=Individual fruit weight, FL= Fruit length, FW= Fruit width, SD= Skin diameter, RWC= Relative water content, LNN=Locule number, TSS= Total soluble solids, ypp=yield plant^{-1}

Table 6. Estimation of genetic parameters in 19 characters of 36 genotypes in tomato

Parameters	Mean	σ^2p	σ^2g	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic Advance (%)	Genetic Advance (% of mean)	CV (%)
Days to first flowering	55.98	9.57	3.26	6.31	5.53	3.23	2.30	34.08	2.17	3.88	4.49
Days to 50% flowering	71.84	10.22	2.90	7.32	4.45	2.37	2.08	28.36	1.87	2.60	3.77
Plant height	82.89	233.52	40.68	192.84	18.44	7.69	10.74	17.42	5.48	6.62	16.75
Number of Branch per plant	4.52	0.97	0.17	0.80	21.81	9.03	12.78	17.14	0.35	7.70	19.85
Leaf length	26.87	22.34	7.73	14.61	17.60	10.35	7.24	34.61	3.37	12.54	14.23
Leaf width	19.85	19.91	18.33	1.57	22.48	21.57	0.91	92.10	8.46	42.64	6.32
Number of Flower per cluster	8.59	7.81	6.64	1.18	32.53	29.98	2.55	84.93	4.89	56.92	12.63
Number of Cluster per plant	12.11	16.00	14.29	1.71	33.03	31.21	1.82	89.29	7.36	60.75	10.81
Number of fruit per cluster	8.39	16.07	14.51	1.56	47.79	45.41	2.38	90.30	7.46	88.89	14.88
Number of fruit per plant	125.41	7099.83	7083.73	16.10	67.19	67.11	0.08	99.77	173.18	138.09	3.20
Individual Fruit weight	58.86	2170.25	2161.69	8.56	79.15	78.99	0.16	99.61	95.59	162.41	4.97
Fruit length	29.99	204.54	187.86	16.68	47.69	45.71	1.99	91.84	27.06	90.24	13.62
Fruit width	32.93	255.25	235.71	19.54	48.51	46.62	1.89	92.34	30.39	92.29	13.42
Skin diameter	4.69	2.05	1.97	0.08	30.48	29.87	0.61	96.04	2.83	60.31	6.06
Relative water content	55.60	420.54	375.41	45.13	36.88	34.85	2.04	89.27	37.71	67.83	12.08
Locule number	3.77	0.43	0.42	0.01	17.36	17.10	0.25	97.10	1.31	34.72	2.95
P^H	3.59	2.72	2.16	0.56	45.89	40.87	5.02	79.34	2.69	75.00	20.86
Total soluble solids	2.89	1.40	1.32	0.08	40.97	39.81	1.16	94.43	2.30	79.70	9.67
Yield per plant	3.86	7.86	7.32	0.54	72.68	70.15	2.53	93.16	5.38	139.48	19.00

σ^2p: Phenotypic variance **PCV: Phenotypic coefficient of variation**
σ^2g: Genotypic variance **GCV: Genotypic coefficient of variation**
σ^2e: Environmental variance **ECV: Environmental coefficient of variation** **CV (%) = coefficient of variation**

4.2.7. Number of Flower per cluster

The variance due to number of flower per cluster showed that the genotypes differed significantly and ranged from 5.33 in ($G_6 \times G_7$) to 14.00 in ($G_2 \times G_9$) with mean value 8.59 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 6.64 and 7.81, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (29.98) and PCV (32.53) indicated presence of high variability in this trait (Table 6).). High phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) was found for number of flower per cluster by Bhuiyan *et al (*2016).

The heritability estimates for number of flower per cluster was high (84.93%) with low genetic advance (4.89%) and higher genetic advance in percentage of mean (56.92%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for number of flower per cluster.

4.2.8. Number of Cluster per plant

The variance due to number of cluster per plant showed that the genotypes differed significantly and ranged from 7.00 in ($G_6 \times G_{10}$) to 23.67 in (G_6) with mean value 12.11 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 14.29 and 16.00, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (31.21) and PCV (33.03) were more or less similar to each other, indicated presence of high variability in this trait (Table 6) Many researchers found similar higher PCV than GCV in their experiment (Bhuiyan *et al* 2016; Manivannan et al., 2005; Singh, 2005; Samadia et al., 2006 and Singh et al., 2002).

The heritability estimates for number of cluster per plant was high (89.29%) with low genetic advance (7.36%) and high genetic advance in percentage of mean (60.75%). Thus

indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is the same findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for number of cluster per plant.

4.2.9. Number of fruit per cluster

The variance due to number of fruit per cluster showed that the genotypes differed significantly and ranged from 4.33 in ($G_6 \times G_7$, $G_9 \times G_1$) to 23.00 in ($G_2 \times G_1$) with mean value 8.39 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 14.51 and 16.07, respectively (Table 6).

The phenotypic variance $\sigma^2 p$ appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (45.41) and PCV (47.79) were more or less similar to each other, indicated presence of high variability in this trait (Table 6). It is the similar findings of (Bhuiyan *et al* 2016; Manivannan et al., 2005; Singh, 2005; Samadia et al., 2006 and Singh et al., 2002).

The heritability estimates for number of fruit per cluster was high (90.30%) with low genetic advance (7.46%) and high genetic advance in percentage of mean (88.89%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) indicated high heritability for number of fruit per cluster.

4.2.10. Number of fruit per plant

The variance due to number of fruit per plant showed that the genotypes differed significantly and ranged from 21.67 in ($G_6 \times G_1$) to 363.33 in ($G_2 \times G_1$) with mean value 125.41 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 7083.73 and 7099.83, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The

GCV (67.11) and PCV (67.19) were more or less similar to each other, indicated presence of high variability in this trait (Table 6). The finding is identical to the findings of Bhuiyan *et al.* (2016).

The heritability estimates for number of fruit per plant was high (99.77%) with high genetic advance (173.18%) and genetic advance in percentage of mean (138.09%). Thus indicating this trait was mostly controlled by additive gene and selection would be effective. Bhuiyan *et al* (2016), Kumari *et al.* (2007), Mahesha *et al.* (2006), Singh *et al.* (2006), Singh *et al.* (2005), Joshi *et al*. (2004) and Bai and Devi (1991) also reported similar results.

4.2.11. Individual Fruit weight (g)

The variance due to individual fruit weight showed that the genotypes differed significantly and ranged from 4.67 g in ($G_2 \times G_7$) to 179.57 g in ($G_7 \times G_1$) with mean value 58.86 g (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 2161.69 and 2170.25, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (78.99) and PCV (79.15) were more or less similar to each other, indicated presence of high variability in this trait (Table 6). Similar result was found by Bhuiyan *et al* (2016) for the same character.

The heritability estimates for individual Fruit weight was high (99.61%) with high genetic advance (95.59%) and genetic advance in percentage of mean (162.41%). Thus indicating this trait was mostly controlled by additive gene and selection would be effective. The findings is similar to the findings of Bhuiyan *et al* (2016), Kumari *et al.* (2007), Mahesha *et al.* (2006), Singh *et al.* (2006), Singh *et al.* (2005), Joshi *et al*. (2004) and Bai and Devi (1991).

4.2.12. Fruit length (cm)

The variance due to fruit length showed that the genotypes differed significantly and ranged from 6.70 cm in ($G_1 \times G_7$) to 59.33 cm in ($G_{10} \times G_1$) with mean value 29.99 cm (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 187.86 and 204.54, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (45.71) and PCV (47.69) were more or less similar to each other, indicated presence of high variability in this trait (Table 6) that is identical to the findings of Bhuiyan *et al* (2016).

The heritability estimates for fruit length was high (91.84%) with high genetic advance (27.06%) and genetic advance in percentage of mean (90.24%). Thus indicating this trait was mostly controlled by additive gene and selection would be effective.

4.2.13. Fruit width (cm)

The variance due to fruit width showed that the genotypes differed significantly and ranged from 7.40 cm in ($G_{1X}G_7$) to 63.00 cm in ($G_6 \times G_7$) with mean value 32.93 cm (Table 5). The σ^2g and σ^2p for this trait were 235.71 and 255.25, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (46.62) and PCV (48.51) were more or less similar to each other, indicated presence of high variability in this trait (Table 6) same as the result of Bhuiyan *et al* (2016) for the parameter fruit length.

The heritability estimates for fruit width was high (92.34%) with high genetic advance (30.39%) and genetic advance in percentage of mean (92.29%). Most likely the heritability of these traits is due to additive gene effects and selection may be effective in early generations for these traits.

4.2.14. Skin diameter (mm)

The variance due to skin diameter showed that the genotypes differed significantly and ranged from 1.97 cm in ($G_2 \times G_6$) to 7.78 cm in ($G_{10} \times G_1$) with mean value 55.60 cm (Table 5). The σ^2g and σ^2p for this trait were 1.97 and 2.05 respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The

GCV (29.87) and PCV (30.48) were more or less similar to each other, indicated presence of high variability in this trait (Table 6)

The heritability estimates for skin diameter was high (96.04%) with low genetic advance (2.83%) and genetic advance in percentage of mean (60.31%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is in accordance with the findings of Singh *et al*. (1973). Islam and Khan (1991) reported high heritability for skin diameter.

4.2.15. Relative water content

The variance due to relative water content showed that the genotypes differed significantly and ranged from 6.33 g in ($G_6 \times G_9$) to 89.20 g in ($G_7 \times G_{10}$) with mean value 4.69 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 375.41 and 420.54, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (34.85) and PCV (36.88) were more or less similar to each other, indicated presence of high variability in this trait (Table 6). Bhuiyan *et al* (2016) reported the same result for the parameter individual fruit weight, fruit length and number of fruit per plant.

The heritability estimates for relative water content was high (89.27%) with high genetic advance (37.71%) and genetic advance in percentage of mean (67.83%). Most likely the heritability of these traits is due to additive gene effects and selection may be effective in early generations for these traits.

4.2.16. Locule number

The variance due to locule number showed that the genotypes differed significantly and ranged from 2.00 in (G_1, G_2, G_6, $G_1 \times G_2$, $G_1 \times G_{10}$, $G_{10} \times G_6$) to 8.00 in ($G_6 \times G_{10}$) with mean value 3.59 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 0.42 and 0.43, respectively (Table 6).

The phenotypic variance appeared to be high than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The

GCV (17.10) and PCV (17.36) were more or less similar to each other, indicated presence of moderate variability in this trait (Table 6). Bhuiyan *et al* (2016) present similar result for plant height.

The heritability estimates for locule number was higher (97.10%) with low genetic advance (1.31%) and high genetic advance in percentage of mean (34.72%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for locule number.

4.2.17. P^H

The variance due to P^H showed that the genotypes differed significantly and ranged from 3.12 in ($G_7 \times G_{10}$) to 6.31 in (G_1) with mean value 3.77 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 2.16 and 2.72, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (40.87) and PCV (45.89) were more or less similar to each other, indicated presence of high variability in this trait (Table 6). High variability due to high GCV and PCV was also observed by Bhuiyan *et al* (2016) for the parameter individual fruit weight, fruit length and number of fruit per plant.

The heritability estimates for P^H was high (79.34%) with low genetic advance (2.69%) and high genetic advance in percentage of mean (75.00%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for P^H.

4.2.18. Total soluble solids

The variance due to total soluble solids showed that the genotypes differed significantly and ranged from 1.07 in ($G_9 \times G_2$) to 7.03 in ($G_6 \times G_7$) with mean value 2.89 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 1.32 and 1.40, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (39.81) and PCV (40.97) were more or less similar to each other, indicated presence of high variability in this trait (Table 6). Bhuiyan *et al* (2016) reported the same result for the parameter individual fruit weight, fruit length and number of fruit per plant.

The heritability estimates for total soluble solids was high (94.43%) with low genetic advance (2.30%) and high genetic advance in percentage of mean (79.70%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for total soluble solids.

4.2.19. Yield per plant (kg)

The variance due to yield per plant showed that the genotypes differed significantly and ranged from 0.63 kg in ($G_2 \times G_1$) to 13.06 kg in ($G_9 \times G_7$) with mean value 3.85 (Table 5). The $\sigma^2 g$ and $\sigma^2 p$ for this trait were 7.32 and 7.86, respectively (Table 6).

The phenotypic variance appeared to be higher than the genotypic variance suggested considerable influence of environment on the expression of genes controlling this trait. The GCV (70.15) and PCV (72.68) were more or less similar to each other, indicated presence of high variability in this trait (Table 6).

The heritability estimates for yield per plant was high (93.16%) with low genetic advance (5.38%) and high genetic advance in percentage of mean (139.48%). Thus indicating this trait was mostly controlled by non-additive gene and selection would be ineffective. Genetic advances in percent of mean were high which is in accordance with the findings of Singh *et al.* (1973). Islam and Khan (1991) reported high heritability for yield per plant.

4.3. Correlation

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the directly or indirectly influences of other yield components are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of character with yield and among themselves provides guidelines to the plant breeder for making improvement through selection provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors. Higher genotypic correlations than phenotypic one might be due to modifying or masking effect of environment in the expression of the character under study (Nandpuri *et al*. 1973). Results of genotypic and phenotypic correlation co-efficient of yield and its contributing traits of tomato were estimated separately as vegetative character and reproductive character with yield and shown in Table 7 and 8, which discussed character wise as follows:

4.3.1. Days to first flowering

Days to first flowering showed highly significant and positive correlation with days to 50% flowering (G=0.80, P=0.80), leaf length (G=0.42, P=0.21), leaf width (G=0.24), fruit length (G=0.36), fruit weight (G=0.27), skin diameter (G=0.36, P=0.20) and relative water content (G=0.021). It also observed that highly significant but negative correlation with plant height (G=-0.40), number of branch per plant (G=-0.71, P=-0.20), number of flower per cluster (G=-0.21), number of cluster per plant (G=-0.21) and P^H (G=-0.41, P=-0.22). Non-significant and positive correlation with number of fruit per plant (G=0.03, P=0.01), individual fruit weight (G=0.10,P=0.05), yield per plant (G=0.09), leaf width (P=0.11), fruit length (P=0.18), fruit weight (P=0.10), relative water content (P=0.13) and yield per plant (P=0.04) and non-significant but negative correlation number of fruit per cluster (G=-0.02,P=-0.05), locule number (G=-0.12, P=-0.09), total soluble solids (G=-0.00, P=-0.007), plant height (P=-0.01), number of flower per cluster (P=-0.11) and number of cluster per plant (P=-0.13)

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

	DF	DFF	PH	NFB	LL	LW	NFF	NFC	NFFC	NFFP	IFW	FL	FW	SD	RWC	LNN	P^H	TSS	ypp
DF	1																		
DFF	0.80**	1																	
PH	-0.40**	-0.62**	1																
NFB	-0.71**	-0.27**	0.91**	1															
LL	0.42**	0.11^{NS}	0.57**	-0.36**	1														
LW	0.24**	0.09^{NS}	0.54**	-0.13^{NS}	0.98**	1													
NFF	-0.21*	0.17^{NS}	-0.18^{NS}	0.46**	-0.70**	-0.56**	1												
NFC	-0.21*	0.03^{NS}	-0.10^{NS}	0.75**	-0.43**	-0.39**	0.48**	1											
NFFC	-0.02^{NS}	0.06^{NS}	-0.23*	0.41**	-0.46**	-0.48**	0.56**	0.60**	1										
NFFP	0.03^{NS}	0.21*	-0.29**	0.62**	-0.50**	-0.49**	0.58**	0.75**	0.88**	1									
IFW	0.10^{NS}	0.02^{NS}	-0.06^{NS}	-0.43**	0.29**	0.41**	-0.47**	-0.59**	-0.65**	-0.61**	1								
FL	0.36**	0.07^{NS}	0.33**	-0.57**	0.70**	0.51**	-0.73**	-0.62**	-0.56**	-0.59**	0.58**	1							
FW	0.27**	0.04^{NS}	0.24*	-0.50**	0.59**	0.52**	-0.62**	-0.68**	-0.63**	-0.67**	0.83**	0.67**	1						
SD	0.36**	0.18^{NS}	0.31**	-0.42**	0.70**	0.55**	-0.73**	-0.44**	-0.49**	-0.43**	0.45**	0.81**	0.63**	1					
RWC	0.21*	0.07^{NS}	0.10^{NS}	-0.08^{NS}	-0.17^{NS}	-0.11^{NS}	0.17^{NS}	-0.09^{NS}	0.07^{NS}	0.14^{NS}	-0.05^{NS}	-0.13^{NS}	-0.02^{NS}	-0.23*	1				
LNN	-0.12^{NS}	-0.20*	0.02^{NS}	-0.15^{NS}	0.33**	0.30**	-0.30**	-0.46**	-0.49**	-0.48**	0.57**	0.26**	0.70**	0.34**	0.03^{NS}	1			
P^H	-0.41**	-0.01^{NS}	0.34**	0.63**	-0.536**	-0.25**	0.44**	0.40**	0.10^{NS}	0.19*	-0.28**	-0.32**	-0.44**	-0.37**	0.008^{NS}	-0.37**	1		
TSS	-0.00^{NS}	-0.14^{NS}	0.43**	0.15^{NS}	-0.208*	-0.05^{NS}	-0.04^{NS}	0.02^{NS}	0.01^{NS}	0.03^{NS}	-0.18^{NS}	-0.16^{NS}	-0.001^{NS}	-0.03^{NS}	0.12^{NS}	-0.22*	0.08^{NS}	1	
ypp	0.09^{NS}	0.002^{NS}	-0.07^{NS}	-0.06^{NS}	0.19*	0.31**	-0.43**	-0.24*	-0.38**	-0.30**	0.79**	0.37**	0.58**	0.29**	-0.10^{NS}	0.39**	-0.27**	-0.25**	1

DF= Days to first flowering, DFF= Days to 50% flowering, PH=Plant height, NFB=Number of flower branch^{-1}, LL=Leaf length, LW= Leaf width, NFF= Number of flower per cluster, NFC= Number of cluster per plant, NFFC= Number of fruit per cluster, NFFP= Number of fruit per plant, IFW=Individual fruit weight, FL= Fruit length, FW= Fruit width, SD= Skin diameter, RWC= Relative water content, LNN=Locule number, TSS= Total soluble solids, ypp=yield plant^{-1}

Table 8. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of tomato

	DF	DFF	PH	NFB	LL	LW	NFF	NFC	NFFC	NFFP	IFW	FL	FW	SD	RWC	LNN	P^H	TSS	ypp
DF	1																		
DFF	0.80**	1																	
PH	-0.01^{NS}	-0.03^{NS}	1																
NFB	-0.20*	-0.15^{NS}	0.24**	1															
LL	0.21*	0.07^{NS}	0.17^{NS}	-0.07^{NS}	1														
LW	0.11^{NS}	-0.005^{NS}	0.20*	-0.02^{NS}	0.63**	1													
NFF	-0.11^{NS}	0.08^{NS}	-0.15^{NS}	0.19*	-0.34**	-0.47**	1												
NFC	-0.13^{NS}	0.01^{NS}	-0.03^{NS}	0.35**	-0.26**	-0.35**	0.42**	1											
NFFC	-0.05^{NS}	-0.01^{NS}	-0.03^{NS}	0.21*	-0.23*	-0.43**	0.50**	0.54**	1										
NFFP	0.01^{NS}	0.10^{NS}	-0.12^{NS}	0.27**	-0.30**	-0.48**	0.53**	0.71**	0.84**	1									
IFW	0.05^{NS}	0.00^{NS}	-0.03^{NS}	-0.17^{NS}	0.17^{NS}	0.40**	-0.43**	-0.56**	-0.62**	-0.61**	1								
FL	0.18^{NS}	0.01^{NS}	0.10^{NS}	-0.21*	0.36**	0.46**	-0.64**	-0.55**	-0.52**	-0.57**	0.56**	1							
FW	0.10^{NS}	-0.01^{NS}	0.05^{NS}	-0.20*	0.31**	0.50**	-0.54**	-0.63**	-0.58**	-0.65**	0.79**	0.64**	1						
SD	0.20*	0.07^{NS}	0.09^{NS}	-0.17^{NS}	0.41**	0.53**	-0.65**	-0.40**	-0.46**	-0.42**	0.44**	0.76**	0.59**	1					
RWC	0.13^{NS}	0.05^{NS}	0.01^{NS}	0.05^{NS}	-0.12^{NS}	-0.10^{NS}	0.14^{NS}	-0.08^{NS}	0.05^{NS}	0.13^{NS}	-0.05^{NS}	-0.12^{NS}	-0.02^{NS}	-0.22*	1				
LNN	-0.09^{NS}	-0.11^{NS}	0.04^{NS}	-0.02^{NS}	0.20*	0.24*	-0.25**	-0.40**	-0.44**	-0.43**	0.51**	0.22*	0.59**	0.27**	0.02^{NS}	1			
P^H	-0.22*	0.002^{NS}	0.13^{NS}	0.26**	-0.30**	-0.23*	0.42**	0.37**	0.10^{NS}	0.19*	-0.28**	-0.30**	-0.43**	-0.36**	0.01^{NS}	-0.33**	1		
TSS	-0.007^{NS}	-0.07^{NS}	0.18^{NS}	0.02^{NS}	-0.08^{NS}	-0.05^{NS}	-0.03^{NS}	0.01^{NS}	0.03^{NS}	0.03^{NS}	-0.17^{NS}	-0.15^{NS}	-0.002^{NS}	-0.03^{NS}	0.11^{NS}	-0.19*	0.08^{NS}	1	
ypp	0.04^{NS}	-0.006^{NS}	-0.05^{NS}	0.01^{NS}	0.12^{NS}	0.30**	-0.36**	-0.21*	-0.33**	-0.29**	0.76**	0.36**	0.54**	0.27**	-0.08^{NS}	0.31**	-0.24*	-0.242*	1

DF= Days to first flowering, DFF= Days to 50% flowering, PH=Plant height, NFB=Number of flower branch^{-1}, LL=Leaf length, LW= Leaf width, NFF= Number of flower per cluster, NFC= Number of cluster per plant, NFFC= Number of fruit per cluster, NFFP= Number of fruit per plant, IFW=Individual fruit weight, FL= Fruit length, FW= Fruit width, SD= Skin diameter, RWC= Relative water content, LNN=Locule number,TSS= Total soluble solids, ypp=yield plant^{-1}

4.3.2. Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with number of fruit per plant (G=0.21). It also observed that highly significant but negative correlation with plant height (G=-0.62), number of branch per plant (G=-0.27) and locule number (G=-0.20). Non-significant and positive correlation with leaf length (G=0.11, P=0.07), leaf width (G=0.09), number of flower per cluster (G=0.17, P=0.08), number of cluster per plant (G=0.03, P=0.01), number of fruit per cluster (G=0.06), individual fruit weight (G=0.02, P=0.00), fruit length (G=0.07, P=0.01), fruit weight (G=0.04), skin diameter (G=0.18, P=0.07), relative water content (G=0.07, P=0.05), yield per plant (G=0.002), number of fruit per plant (P=0.10) and P^H (0.002) and non-significant but negative correlation with P^H (G=-0.01),total soluble solids (G=-0.14), plant height (P=-0.03), number of Branch per plant (P=-0.15), leaf width (P=-0.005), number of fruit per cluster (P=-0.01), fruit weight (P=-0.01), locule number (P=-0.11), total soluble solids (P=-0.07) and yield per plant (P=-0.006)

4.3.3. Plant Height (cm)

Plant Height showed highly significant and positive correlation with number of branch per plant (G=0.91, P=0.24), leaf length (G=0.57), leaf width (G=0.54, P=0.20), fruit length (G=0.33), fruit weight (G=0.24), skin diameter (G=0.31), P^H (G=0.34) and total soluble solids (G=0.43). It also observed that highly significant but negative correlation with number of fruit per cluster (P=-0.23) and number of fruit per plant (P=-0.29). Non-significant and positive correlation with relative water content (G=0.10), locule number (G=0.02), leaf length (P=0.17), fruit length (P=0.10), fruit weight (P=0.05), skin diameter (P=0.09), relative water content (P=0.01), locule number (P=0.04), P^H (P=0.13) and total soluble solids (P=0.18) and non-significant but negative correlation with number of flower per cluster (G=-0.18, P=-0.15), number of cluster per plant (G=-0.10, P=-0.03), individual fruit weight (G=-0.06, P=-0.03), yield per plant (G=-0.07, P=-0.05), number of fruit per cluster (P=-0.03) and number of fruit per plant (P=-0.12).

4.3.4. Number of Branch per plant

Number of Branch per plant showed highly significant and positive correlation with leaf width (G=0.46), number of cluster per plant (G=0.75, P=0.35), number of fruit per cluster (G=0.41), number of fruit per plant (G=0.62), Ph (G=0.63, P=0.26), number of flower per cluster (P=0.19), number of cluster per plant (P=0.35) and number of fruit per plant (P=0.27). It also observed that highly significant but negative correlation with individual fruit weight (G=-0.43), fruit length (G=-0.57, P=-0.21), fruit weight (G=-0.50, P=-0.20), leaf length (G=-0.36) and skin diameter (G=-0.42). Non-significant and positive correlation with total soluble solids (G=0.15, P=0.02), relative water content (P=0.05) and yield per plant (P=0.01) and non-significant but negative correlation leaf width (G=-0.13), relative water content (G=-0.083), locule number (G=-0.15, P=-0.02), yield per plant (G=-0.06), leaf length (P=-0.07), leaf width (P=-0.02), individual fruit weight (P=-0.17) and skin diameter (P=-0.17).

4.3.5. Leaf length (cm)

Leaf length showed highly significant and positive correlation with leaf width (G=0.98, P=0.63), individual fruit weight (G=0.29), fruit length (G=0.70, P=0.36), fruit weight (G=0.59, P=0.31), SW (G=0.70, P=0.41), locule number (G=0.33, P=0.20) and yield per plant (G=0.19). It also observed that highly significant but negative correlation with number of flower per cluster (G=-0.70, P=-0.34), number of cluster per plant (G=-0.43, P=-0.26), number of fruit per cluster (G=-0.46, P=-0.23), number of fruit per plant (G=-0.50, P=-0.30), Ph (G=-0.536, P=-0.30) and total soluble solids (G=-0.208). Non-significant and positive correlation with individual fruit weight (P=0.17) and yield per plant (P=0.12) and non-significant but negative correlation with relative water content (G=-0.17, P=-0.12) and total soluble solids (P=-0.12).

4.3.6. Leaf width (cm)

Leaf width showed highly significant and positive correlation with individual fruit weight (G=0.41, P=0.40), fruit length (G=0.51, P=0.46), fruit weight (G=0.52, P=0.50), skin diameter (G=0.55, P=0.53), locule number (G=0.30, P=0.24) and yield per plant (G=0.31, P=0.30). It also observed that highly significant but negative correlation with number of

flower per cluster (G=-0.56, P=-0.47), number of cluster per plant (G=-0.39, P=-0.35), number of fruit per cluster (G=-0.48, P=-0.43), number of fruit per plant (G=-0.49, P=-0.48) and Ph (G=-0.25, P=-0.23) and non-significant but negative correlation with relative water content (G=-0.11, P=-0.10) and total soluble solids (G=-0.05, P=-0.05).

4.3.7. Number of Flower per cluster

Number of Flower per cluster showed highly significant and positive correlation with number of cluster per plant (G=0.48, P=0.42), number of fruit per cluster (G=0.56, P=0.20), number of fruit per plant (G=0.58, P=0.53) and Ph (G=0.44, P=0.42). It also observed that highly significant but negative correlation with fruit weight (G=-0.47, P=-0.43), fruit length (G=-0.73, P=-0.64), fruit weight (G=-0.63, P=-0.54), skin diameter (G=-0.73, P=-0.65), locule number (G=-0.530, P=-0.25) and yield per plant (G=-0.43, P=-0.36). Non-significant and positive correlation with relative water content (G=0.17, P=0.14) and non-significant but negative correlation with total soluble solids (G=-0.04, P=-0.03).

4.3.8. Number of Cluster per plant

Number of Cluster per plant showed highly significant and positive correlation with number of fruit per cluster (G=0.60, P=0.54), number of fruit per plant (G=0.75, P=0.71) and Ph (G=0.40, P=0.37). It also observed that highly significant but negative correlation with individual fruit weight (G=-0.59, P=-0.56), fruit length (G=-0.62, P=-0.55), fruit weight (G=-0.68, P=-0.63), skin diameter (G=-0.44, P=-0.40), locule number (G=-0.46, P=-0.40) and yield per plant (G=-0.24, P=-0.21). Non-significant and positive correlation with total soluble solids (G=0.02, P=0.01) and non-significant but negative correlation with relative water content (G=-0.09, P=-0.08).

4.3.9. Number of fruit per cluster

Number of fruit per cluster showed highly significant and positive correlation with number of fruit per plant (G=0.88, P=0.84). It also observed that highly significant but negative correlation with individual fruit weight (G=-0.65, P=-0.62), fruit length (G=-0.56, P=-0.52), fruit weight (G=-0.63, P=-0.58), skin diameter (G=-0.49, P=-0.46), locule number (G=-0.49, P=-0.44) and yield per plant (G=-0.38, P=-0.33). Non-significant and positive

correlation with relative water content (G=0.07, P=0.05), Ph (G=0.10, P=0.10) and total soluble solids (G=0.01, P=0.03).

4.3.10. Number of fruit per plant

Number of fruit per plant showed highly significant and positive correlation with P^H (G=0.19, P=0.19). It also observed that highly significant but negative correlation with individual fruit weight (G=-0.61, P=-0.61), fruit length (G=-0.59, P=-0.57), fruit weight (G=-0.67, P=-0.65), skin diameter (G=-0.43, P=-0.42), locule number (G=-0.48, P=-0.43) and yield per plant (G=-0.30, P=-0.29). Non-significant and positive correlation with relative water content (G=0.14, P=0.13) and total soluble solids (G=0.03, P=0.03).

4.3.11. Individual Fruit weight (g)

Individual Fruit weight showed highly significant and positive correlation with fruit length (G=0.58, P=0.56), fruit weight (G=0.83, P=0.79), skin diameter (G=0.45, P=0.44), locule number (G=0.57, P=0.51) and yield per plant (G=0.79, P=0.76). It also observed that highly significant but negative correlation with P^H (G=-0.28, P=-0.28) and non-significant but negative correlation with relative water content (G=-0.05, P=-0.05) and total soluble solids (G=-0.18, P=-0.17).

4.3.12. Fruit length (cm)

Fruit length showed highly significant and positive correlation with fruit weight (G=0.67, P=0.64), skin diameter (G=0.81, P=0.76), locule number (G=0.26, P=0.22) and yield per plant (G=0.37, P=0.36). It also observed that highly significant but negative correlation with Ph (G=-0.32, P=-0.30) and non-significant but negative correlation relative water content (G=-0.13, P=-0.12) and total soluble solids (G=-0.16, P=-0.15).

4.3.13. Fruit width (cm)

Fruit width showed highly significant and positive correlation with skin diameter (G=0.63, P=0.59), locule number (G=0.70, P=0.59) and yield per plant (G=0.58, P=0.54). It also

observed that highly significant but negative correlation with Ph (G=-0.44, P=-0.43) and non-significant but negative correlation relative water content (G=-0.02, P=-0.02) and total soluble solids (G=-0.001, P=-0.002).

4.3.14. Skin diameter (mm)

Skin diameter showed highly significant and positive correlation with locule number (G=0.34, P=0.27) and yield per plant (G=0.29, P=0.27). It also observed that highly significant but negative correlation with relative water content (G=-0.23, P=-0.22) and Ph (G=-0.37, P=-0.36) and non-significant but negative correlation with total soluble solids (G=-0.03, P=-0.03).

4.3.15. Relative water content

Relative water content showed non-significant and positive correlation with locule number (G=0.03, P=0.02), P^H (G=0.008, P=0.01) and total soluble solids (G=0.12, P=0.11) and non-significant but negative correlation with yield per plant (G=-0.10, P=-0.08)

4.3.16. Locule number

Locule number showed highly significant and positive correlation with yield per plant (G=0.39, P=0.31) and highly significant but negative correlation with P^H (G=-0.37, P=-0.33) and total soluble solids (G=-0.22, P=-0.19)

4.3.17. P^H

P^H showed highly significant and negative correlation with yield per plant (G=-0.27, P=-0.24) and non-significant but positive correlation total soluble solids (G=0.08, P=-0.08)

4.3.18. Total soluble solids

Total soluble solids showed highly significant but negative correlation with yield per plant (G=-0.25, P=-0.242).

4.4. Path Coefficient Analysis

Association of character determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on yield per plant. In order to find out a clear picture of the inter-relationship between yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at genotypic level which also measured the relative importance of each component. Though correlation analysis denotes the association pattern of components traits with yield, they basically represent the overall effect of a particular trait on yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the partioning of correlation coefficients into direct and indirect contribution of various characters on the yield. It is standardized partial regression coefficient analysis. As such, it measures the direct effect of one variable upon other. Such information would be of great value in enabling the breeder to exclusively identify the important component traits of yield and use the genetic resources for improvement in a planned way. In path coefficient analysis the direct effect of a trait on yield per plant and its indirect effect through other characters were calculated and the results are presented in Table 9.

4.4.1. Days to first flowering

Path co-efficient analysis revealed that days to first flowering had a negative direct effect (**-0.817**) on yield per plant. Days to first flowering had positive indirect effect on plant height (0.114), number of branch per plant (0.326) , leaf length (0.176), leaf width (0.036), number of flower per cluster (0.020), number of fruit per cluster (0.023), number of fruit per plant (0.051), individual fruit weight (0.039), fruit length (0.001), fruit width (0.332), relative water content (0.008), locule number (0.063) and total soluble solids (0.00005) while negative indirect effect on days to 50% flowering (-0.073), number of cluster per plant (-0.033), skin diameter (-0.113) and P^H (-0.064). It showed non-significant positive genotypic correlation (0.090) with yield per plant.

Table 9. Path coefficient analysis showing direct (bold) and indirect effects of different characters on yield of tomato

Direct Effect	DF	DFF	PH	NFB	LL	LW	NFF	NFC	NFFC	NFFP	IFW	FL	FW	SD	RWC	LNN	P^H	TSS	Genotypic Correlation withYPP
DF	**-0.817**	-0.073	0.114	0.326	0.176	0.036	0.020	-0.033	0.023	0.051	0.039	0.001	0.332	-0.113	0.008	0.063	-0.064	0.00005	0.090^{NS}
DFF	-0.658	**-0.091**	0.174	0.127	0.047	0.013	-0.016	0.005	-0.056	0.330	0.008	0.0003	0.053	-0.056	0.003	0.107	-0.003	0.015	0.002^{NS}
PH	0.333	0.056	**-0.280**	-0.418	0.243	0.078	0.017	-0.016	0.188	-0.452	-0.026	0.001	0.293	-0.098	0.004	-0.011	0.053	-0.047	-0.079^{NS}
NFB	0.584	0.025	-0.256	**-0.456**	-0.154	-0.019	-0.044	0.116	-0.333	0.961	-0.171	-0.002	-0.603	0.131	-0.003	0.078	0.099	-0.016	-0.063^{NS}
LL	-0.343	-0.010	-0.162	0.167	**0.420**	0.142	0.066	-0.066	0.375	-0.773	0.118	0.003	0.711	-0.217	-0.006	-0.172	-0.083	0.022	0.191*
LW	-0.204	-0.008	-0.152	0.061	0.415	**0.144**	0.053	-0.060	0.397	-0.764	0.164	0.002	0.633	-0.173	-0.004	-0.155	-0.039	0.006	0.316**
NFF	0.175	-0.016	0.051	-0.212	-0.295	-0.082	**-0.094**	0.075	-0.458	0.890	-0.185	-0.003	-0.746	0.226	0.006	0.159	0.070	0.005	-0.434**
NFC	0.178	-0.003	0.030	-0.346	-0.181	-0.056	-0.046	**0.153**	-0.494	1.150	-0.235	-0.002	-0.824	0.139	-0.004	0.241	0.062	-0.003	-0.241*
NFFC	0.023	-0.006	0.065	-0.187	-0.194	-0.070	-0.053	0.093	**-0.814**	1.353	-0.257	-0.002	-0.764	0.152	0.003	0.256	0.017	-0.002	-0.387**
NFFP	-0.027	-0.020	0.083	-0.286	-0.212	-0.072	-0.054	0.115	-0.719	**1.531**	-0.242	-0.002	-0.813	0.135	0.005	0.251	0.030	-0.004	-0.302**
IFW	-0.082	-0.002	0.019	0.199	0.126	0.060	0.044	-0.092	0.532	-0.941	**0.393**	0.002	0.997	-0.141	-0.002	-0.297	-0.045	0.020	0.790**
FL	-0.299	-0.007	-0.094	0.264	0.296	0.074	0.069	-0.095	0.463	-0.916	0.231	**0.004**	0.812	-0.252	-0.005	-0.135	-0.051	0.018	0.376**
FW	-0.227	-0.004	-0.069	0.230	0.249	0.076	0.058	-0.105	0.520	-1.039	0.327	0.002	**1.197**	-0.197	-0.001	-0.363	-0.069	0.000	0.587**
SD	-0.299	-0.016	-0.088	0.193	0.294	0.080	0.068	-0.069	0.400	-0.665	0.179	0.003	0.761	**-0.310**	-0.008	-0.177	-0.058	0.003	0.292**
RWC	-0.173	-0.006	-0.030	0.039	-0.073	-0.017	-0.016	-0.015	-0.061	0.225	-0.022	-0.001	-0.030	0.073	**0.036**	-0.018	0.001	-0.013	-0.101^{NS}
LNN	0.100	0.019	-0.006	0.069	0.140	0.043	0.029	-0.072	0.405	-0.746	0.226	0.001	0.843	-0.106	0.001	**-0.516**	-0.058	0.025	0.398**
P^H	0.338	0.002	-0.096	-0.292	-0.225	-0.036	-0.042	0.061	-0.089	0.299	-0.113	-0.001	-0.535	0.116	0.000	0.192	**0.155**	-0.009	-0.274**
TSS	0.0003	0.013	-0.123	-0.069	-0.087	-0.008	0.004	0.004	-0.011	0.059	-0.074	-0.0006	-0.0007	0.010	0.004	0.118	0.014	**-0.107**	-0.255**

Residual effects: 0.33

DF= Days to first flowering, DFF= Days to 50% flowering, PH=Plant height, NFB=Number of flower branch^{-1}, LL=Leaf length, LW= Leaf width, NFF= Number of flower per cluster, NFC= Number of cluster per plant, NFFC= Number of fruit per cluster, NFFP= Number of fruit per plant, IFW=Individual fruit weight, FL= Fruit length, FW= Fruit width, SD= Skin diameter, RWC= Relative water content, LNN=Locule number,TSS= Total soluble solids, ypp=yield plant

4.4.2. Days to 50% flowering

Path co-efficient analysis revealed that days to 50% flowering had a negative direct effect (**-0.091**) on yield per plant. days to 50% flowering had positive indirect effect on plant height (0.174), number of branch per plant (0.127) , leaf length (0.047), leaf width (0.013), number of cluster per plant (0.005), number of fruit per plant (0.330), individual fruit weight (0.008), fruit length (0.0003), fruit width (0.053), relative water content (0.003), locule number (0.107) and total soluble solids (0.015) while negative indirect effect on days to first flowering (-0.658), number of flower per cluster (-0.016), number of fruit per cluster (-0.056), skin diameter (-0.056) and P^H (-0.003). It showed non-significant positive genotypic correlation (0.002) with yield per plant.

4.4.3. Plant Height (cm)

Path co-efficient analysis revealed that plant height had a negative direct effect (**-0.280**) on yield per plant. plant height had positive indirect effect on days to first flowering (0.333), days to 50% flowering (0.056) , leaf length (0.243), leaf width (0.078), number of flower per cluster (0.017), number of fruit per cluster (0.188), fruit length (0.001), fruit width (0.293), relative water content (0.004) and P^H (0.053) while negative indirect effect on number of branch per plant (-0.418), number of cluster per plant (-0.016), number of fruit per plant (-0.452), individual fruit weight (-0.026), skin diameter (-0.098), locule number (-0.011) and total soluble solids (-0.47).. It showed non-significant negative genotypic correlation (-0.079) with yield per plant.

4.4.4. Number of Branch per plant

Path co-efficient analysis revealed that number of branch per plant had a negative direct effect (**-0.456**) on yield per plant. number of branch per plant had positive indirect effect on days to first flowering (0.584), days to 50% flowering (0.025), number of cluster per plant (0.116), number of fruit per plant (0.961), skin diameter (0.131), locule number (0.078) and P^H (0.099) while negative indirect effect on plant height (-0.256), leaf length (-0.154), leaf width (-0.019), number of flower per cluster (-0.044), number of fruit per

cluster (-0.333), individual fruit width (-0.171), fruit length (-0.002), fruit weight (-0.603), relative water content (-0.003) and total soluble solids (-0.016). It showed non-significant negative genotypic correlation (-.0063) with yield per plant.

4.4.5. Leaf length (cm)

Path co-efficient analysis revealed that leaf length had a positive direct effect (**0.420**) on yield per plant. leaf length had positive indirect effect on number of branch per plant (0.167), leaf width (0.142), number of flower per cluster (0.066), number of fruit per cluster (0.375), individual fruit weight (0.118), fruit length (0.003), fruit width (0.711) and total soluble solids (0.022) while negative indirect effect on days to first flowering (-0.343), days to 50% flowering (-0.010), plant height (-0.162), number of cluster per plant (-0.066), number of fruit per plant (-0.773), skin diameter (-0.217), relative water content (-0.006), locule number (-0.172) and P^H (-0.083). It showed significant positive genotypic correlation (0.191) with yield per plant.

4.4.6. Leaf width (cm)

Path co-efficient analysis revealed that leaf width had a positive direct effect (**0.144**) on yield per plant. leaf width had positive indirect effect on number of branch per plant (0.161), leaf length (0.415), number of flower per cluster (0.053), number of fruit per cluster (0.397), individual fruit weight (0.164), fruit length (0.002), fruit width (0.633) and total soluble solids (0.006) while negative indirect effect on days to first flowering (-0.204), days to 50% flowering (-0.008), plant height (-0.152), number of cluster per plant (-0.060), number of fruit per plant (-0.764), skin diameter (-0.173), relative water content (-0.004), locule number (-0.155) and P^H (-0.039). It showed highly significant positive genotypic correlation (0.316) with yield per plant.

4.4.7. Number of Flower per cluster

Path co-efficient analysis revealed that number of flower per cluster had a negative direct effect (**-0.094**) on yield per plant. number of flower per cluster had positive indirect effect

on days to first flowering (0.175), plant height (0.051), number of cluster per plant (0.075), number of fruit per plant (0.890), skin diameter (0.226), relative water content (0.006), locule number (0.159), P^H (0.070) and total soluble solids (0.005) while negative indirect effect on days to 50% flowering (-0.016), number of branch per plant (-0.212), leaf length.

4.4.8. Number of Cluster per plant

Path co-efficient analysis revealed that number of cluster per plant had a positive direct effect (**0.153**) on yield per plant. number of cluster per plant had positive indirect effect on days to first flowering (0.178), plant height (0.030), number of fruit per plant (0.150), skin diameter (0.139), locule number (0.241) and P^H (0.062) while negative indirect effect on days to 50% flowering (-0.003), number of branch per plant (-0.346), leaf length (-0.181), leaf width (-0.056), number of flower per cluster (-0.046), number of fruit per cluster (-0.494), individual fruit weight (-0.235), fruit length (-0.002), fruit width (-0.824), relative water content (-0.004) and total soluble solids (-0.003). It showed significant negative genotypic correlation (-0.241) with yield per plant.

4.4.9. Number of fruit per cluster

Path co-efficient analysis revealed that number of fruit per cluster had a negative direct effect (**-0.814**) on yield per plant. number of fruit per cluster had positive indirect effect on days to first flowering (0.023), plant height (0.065) , number of cluster per plant (0.093), number of fruit per plant (1.353), skin diameter (0.152), relative water content (0.003), locule number (0.256) and P^H (0.017) while negative indirect effect on days to 50% flowering (-0.006), number of branch per plant (-0.187), leaf length (-0.194), leaf width (-0.070), number of flower per cluster (-0.053), individual fruit weight (-0.257), fruit length (-0.002), fruit width (-0.764) and total soluble solids (-0.002). It showed highly significant negative genotypic correlation (-0.387) with yield per plant.

4.4.10. Number of fruit per plant

Path co-efficient analysis revealed that number of fruit per plant had a positive direct effect (**1.531**) on yield per plant. number of fruit per plant had positive indirect effect on plant height (0.083), number of cluster per plant (0.115) , skin diameter (0.135), relative water content (0.005), locule number (0.251) and P^H (0.030) while negative indirect effect on days to first flowering (-0.027), days to 50% flowering (-0.020), number of branch per plant (-0.286), leaf length (-0.212), leaf width (-0.072), number of flower per cluster (-0.054), number of fruit per cluster (-0.719), individual fruit weight (-0.242), fruit length (-0.002), fruit width (-0.813) and total soluble solids (-0.004). It showed highly significant negative genotypic correlation (-0.302) with yield per plant.

4.4.11. Individual Fruit weight (g)

Path co-efficient analysis revealed that individual fruit weight had a positive direct effect (**0.393**) on yield per plant. individual fruit weight had positive indirect effect on plant height (0.019), number of branch per plant (0.199), leaf length (0.126), leaf width (0.060), number of flower per cluster (0.044), number of fruit per cluster (0.532), fruit length (0.002), fruit width (0.997) and total soluble solids (0.020) while negative indirect effect on days to first flowering (-0.082), days to 50% flowering (-0.002), number of cluster per plant (-0.092), number of fruit per plant (-0.941), skin diameter (-0.141), relative water content (-0.002), locule number (-0.297) and P^H (-0.045). It showed highly significant positive genotypic correlation (0.790) with yield per plant.

4.4.12. Fruit length (cm)

Path co-efficient analysis revealed that fruit length had a positive direct effect (**0.004**) on yield per plant. fruit length had positive indirect effect on number of branch per plant (0.264), leaf length (0.296), leaf width (0.074), number of flower per cluster (0.069), number of fruit per cluster (0.463), individual fruit weight (0.231), fruit width (0.812) and total soluble solids (0.018) while negative indirect effect on days to first flowering (-0.299), days to 50% flowering (-0.007), plant height (-0.094), number of cluster per plant (-0.095), number of fruit per plant (-0.916), skin diameter (-0.252), relative water content (-0.005), locule number (-0.135) and P^H (-0.051). It showed highly significant positive genotypic correlation (0.376) with yield per plant.

4.4.13. Fruit width (cm)

Path co-efficient analysis revealed that fruit width had a positive direct effect (**1.197**) on yield per plant. Fruit width had positive indirect effect on number of branch per plant (0.230), leaf length (0.249), leaf width (0.076), number of flower per cluster (0.058), number of fruit per cluster (0.520), individual fruit weight (0.327), fruit length (0.002) and total soluble solids (0.00) while negative indirect effect on days to first flowering (-0.227), days to 50% flowering (-0.004), plant height (-0.069), number of cluster per plant (-0.105), number of fruit per plant (-1.039), skin diameter (-0.197), relative water content (-0.001),

locule number (-0.363) and P^H (-0.069). It showed highly significant positive genotypic correlation (0.587) with yield per plant.

4.4.14. Skin diameter (mm)

Path co-efficient analysis revealed that skin diameter had a nagetive direct effect (**-0.310**) on yield per plant. Skin diameter had positive indirect effect on number of branch per plant (0.193), leaf length (0.294), leaf width (0.080), number of flower per cluster (0.068), number of fruit per cluster (0.400), individual fruit weight (0.179), fruit length (0.003), fruit weight (0.761) and total soluble solids (0.003) while negative indirect effect on days to first flowering (-0.299), days to 50% flowering (-0.016), plant height (-0.088), number of cluster per plant (-0.069), number of fruit per plant (-0.665), relative water content (-0.008), locule number (-0.177) and P^H (-0.058). It showed highly significant positive genotypic correlation (0.292) with yield per plant.

4.4.15. Relative water content

Path co-efficient analysis revealed that relative water content had a positive direct effect (**0.036**) on yield per plant. Relative water content had positive indirect effect on number of branch per plant (0.039), number of fruit per plant (0.225) , skin diameter (0.073) and P^H (0.001) while negative indirect effect on days to first flowering (-0.173), days to 50% flowering (-0.006), plant height (-0.030), leaf length (-0.073), leaf width (-0.017), number of flower per cluster (-0.016), number of cluster per plant (-0.015), number of fruit per cluster (-0.061), individual fruit weight (-0.022), fruit length (-0.001), fruit width (-0.030), locule number (-0.018) and total soluble solids (-0.013). It showed non-significant genotypic correlation (-0.101) with yield per plant.

4.4.16. Locule number

Path co-efficient analysis revealed that locule number had a negative direct effect (**-0.516**) on yield per plant. Locule number had positive indirect effect on days to first flowering (0.100), days to 50% flowering (0.019), number of branch per plant (0.069), leaf length

(0.140), leaf width (0.043), number of flower per cluster (0.029), number of fruit per cluster (0.405), individual fruit weight (0.226), fruit length (0.001), fruit width (0.843), relative water content (0.001) and total soluble solids (0.025) while negative indirect effect on plant height (-0.006), number of cluster per plant (-0.072), number of fruit per plant (-0.746), skin diameter (-0.106) and P^H (-0.058). It showed highly significant positive genotypic correlation (0.398) with yield per plant.

4.4.17. P^H

Path co-efficient analysis revealed that P^H had a positive direct effect (**0.155**) on yield per plant. P^H had positive indirect effect on days to first flowering (0.338), days to 50% flowering (0.002) , number of cluster per plant (0.061), number of fruit per plant (0.299), skin diameter (0.116), relative water content (0.000) and locule number (0.192) while negative indirect effect on plant height (-0.096), number of branch per plant (-0.292), leaf length (-0.225), leaf width (-0.036), number of flower per cluster (-0.042), number of fruit per cluster (-0.089), individual fruit weight (-0.113), fruit length (-0.001), fruit width(-0.535) and total soluble solids (-0.009). It showed highly significant genotypic correlation (-0.274) with yield per plant.

4.4.18. Total soluble solids

Path co-efficient analysis revealed that total soluble solids had a negative direct effect (**-0.107**) on yield per plant. total soluble solids had positive indirect effect on days to first flowering (0.0003), days to 50% flowering (0.013) , number of flower per cluster (0.004), number of cluster per plant (0.004), number of fruit per plant (0.059), skin diameter (0.010), relative water content (0.004), locule number (0.118) and P^H (0.014) while negative indirect effect on plant height (-0.123), number of branch per plant (-0.069), leaf length (-0.087), leaf width (-0.008), number of fruit per cluster (-0.011), individual fruit weight (-0.074), fruit length (-0.0006) and fruit width(-0.007). It showed highly significant genotypic correlation (-0.255) with yield per plant.

4.5. Multivariate analysis

Genetic divergence in bottle gourd was analyzed by using GENSTAT software programme. Genetic diversity analysis involved several steps. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar. 2002; Uddin, 2001; Juned *et al*., 1988 and Aria, 1987). In the analysis of genetic diversity in tomato multivariate techniques were used.

4.5.1. Cluster analysis

The experiment was conducted to investigate the genetic diversity of thirty-six genotypes of tomato. The genotypes were divided into five cluster according to D^2 analysis (Table 10). The cluster I had the maximum number of genotypes (10) followed by cluster III which had 9 genotypes. Cluster IV, II and V had 6, 5 and 6 genotypes respectively. Remarkably cluster I had (G_9, G_{10}, $G_1 \times G_{10}$, $G_7 \times G_6$, $G_7 \times G_9$, $G_9 \times G_1$, $G_9 \times G_{10}$, $G_{10} \times G_6$, $G_{10} \times G_7$ and $G_{10} \times G_9$) whereas cluster II had (G_6, $G_1 \times G_7$, $G_2 \times G_1$, $G_2 \times G_7$ and $G_2 \times G_{10}$). Furthermore, cluster III had (G_1, G_2, $G_1 \times G_2$, $G_1 \times G_9$, $G_2 \times G_6$, $G_2 \times G_9$, $G_6 \times G_2$, $G_6 \times G_9$ and $G_{10} \times G_2$), cluster IV and cluster V both showed six genotypes (G_7, $G_6 \times G_{10}$, $G_7 \times G_1$, $G_7 \times G_{10}$, $G_9 \times G_2$ and $G_9 \times G_7$) and ($G_1 \times G_6$, $G_6 \times G_1$, $G_6 \times G_7$, $G_7 \times G_2$, $G_9 \times G_6$ and $G_{10} \times G_1$). Clustering was done at random that indicate a broad genetic base of the genotypes. Genetic variability in tomato was also found by Prasad *et al.* (2001). Joshi *et al*. (2003) assessed the nature and magnitude of genetic divergence using non hierarchical Euclidean cluster analysis in 73 tomato genotypes of diverse origin for different quantitative and qualitative traits. The maximum value of (53.208) was recorded for shelf life of fruits while the minimum value was 69.208 for days to first picking. The grouping of genotype into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes.

4.5.2. Principal component analysis (PCA)

Principal components were calculated from the correlation matrix from genotype scores obtained from first components and succeeding components with latent roots greater than

the unity. The Principal component analysis was studied with thirty-six genotypes of tomato. Eigen values and latent vectors of corresponding 19 principal component axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in (Table 11). It represents that the cumulative Eigen values of first five principal components accounted for 72.95% of the total variation; the first principle component accounted for 37.32% of the total variation; the second, third, fourth and fifth components accounted for 12.03%, 9.76%, 7.35% and 6.49% of the total variation, respectively. The rest of the components accounted for only 27.06% of the total variation.

Table 10. Distribution of 36 genotypes in different clusters

Cluster no.	Genotypes	No. of genotypes
I	G_9, G_{10}, $G_1 \times G_{10}$, $G_7 \times G_6$, $G_7 \times G_9$, $G_9 \times G_1$, $G_9 \times G_{10}$, $G_{10} \times G_6$, $G_{10} \times G_7$, $G_{10} \times G_9$	10
II	G_6, $G_1 \times G_7$, $G_2 \times G_1$, $G_2 \times G_7$, $G_2 \times G_{10}$,	5
III	G_1, G_2, $G_1 \times G_2$, $G_1 \times G_9$, $G_2 \times G_6$, $G_2 \times G_9$, $G_6 \times G_2$, $G_6 \times G_9$, $G_{10} \times G_2$	9
IV	G_7, $G_6 \times G_{10}$, $G_7 \times G_1$, $G_7 \times G_{10}$, $G_9 \times G_2$, $G_9 \times G_7$	6
V	$G_1 \times G_6$, $G_6 \times G_1$, $G_6 \times G_7$, $G_7 \times G_2$, $G_9 \times G_6$, $G_{10} \times G_1$	6
Total		36

Table 11. Eigen values and yield percent contribution of 36 characters of ten genotypes of tomato

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	7.091	37.32	37.32
II	2.286	12.03	49.35
III	1.855	9.76	59.11
IV	1.397	7.35	66.46
V	1.233	6.49	72.95
VI	1.082	5.69	78.64
VII	0.931	4.9	83.54
VIII	0.684	3.6	87.14
IX	0.594	3.13	90.27
X	0.453	2.39	92.66
XI	0.358	1.89	94.55
XII	0.271	1.43	95.98
XIII	0.207	1.09	97.07
XIV	0.161	0.85	97.92
XV	0.118	0.62	98.54
XVI	0.094	0.5	99.04
XVII	0.076	0.4	99.44
XVIII	0.066	0.35	99.79
XIX	0.042	0.22	100

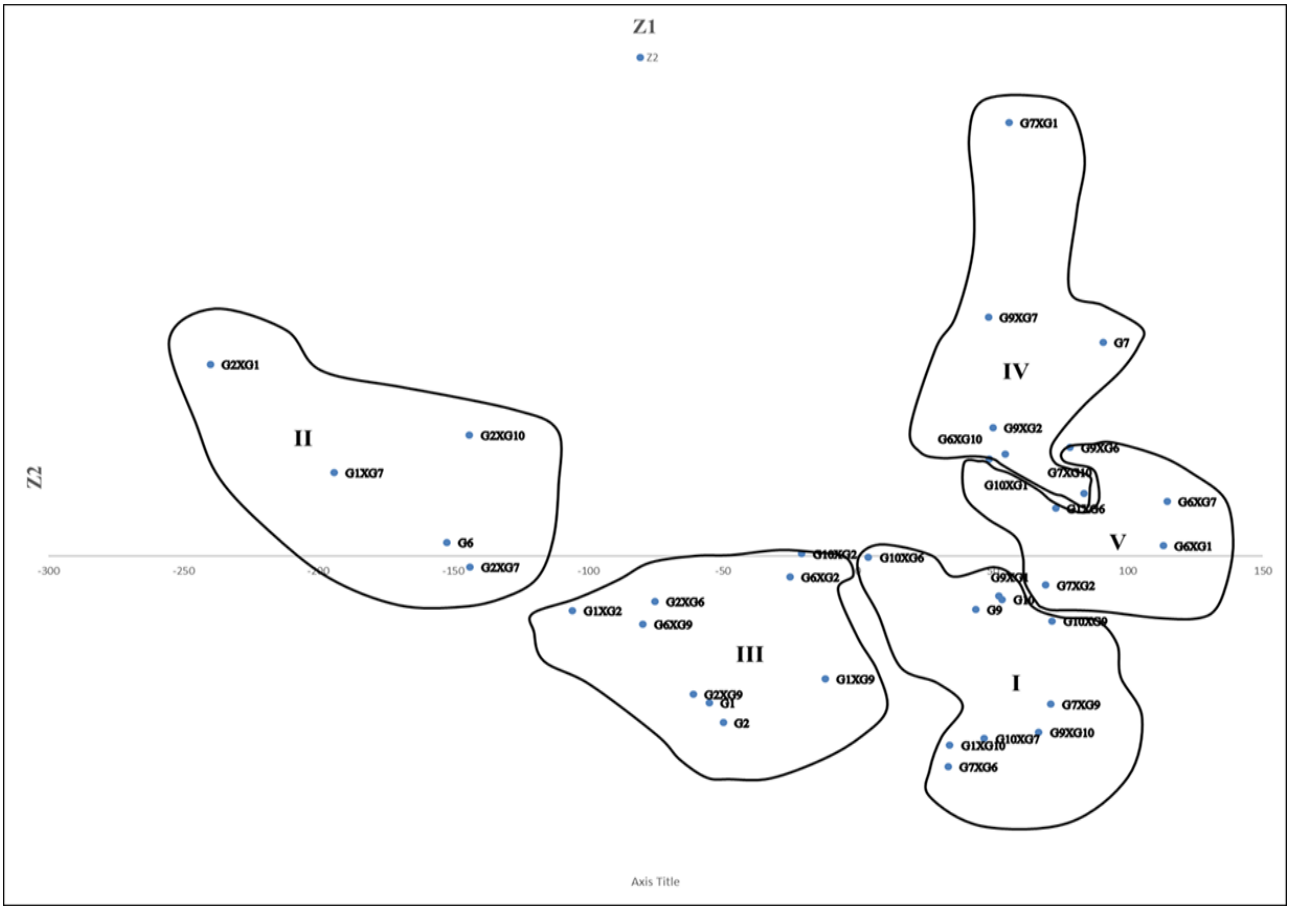


Figure 1. Cluster diagram showing genotypes grouping in different clusters of 36 genotypes of tomato

4.5.3. Construction of scatter diagram

In multivariate analysis, cluster analysis refers to methods used to divide up objects into similar groups, or more precisely, groups whose members are all close to one another on various dimensions being measured. Depending on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z1 - Z2) using component score 2 as X-axis and component score 1 as Y-axis was constructed, which has been presented in Figure 1. The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that there existed considerable diversity among the genotypes. The scattered diagram for the tomato genotypes of five cluster expressed that the genotypes $G_2 \times G_1$, $G_1 \times G_7$, $G_2 \times G_{10}$, $G_1 \times G_2$, $G_1 \times G_9$, $G_{10} \times G_6$, $G_9 \times G_7$, $G_7 \times G_1$, $G_6 \times G_7$, G_7 and $G_7 \times G_2$ were distantly located which suggesting more diverged from rest of the genotypes.

4.5.4. Principal coordinate analysis

Principal coordinate analysis (PCO) was estimated on auxiliary principal component analysis. This analysis helps in estimating distances. Principal coordination analysis (PCO) indicated that the highest inter genotypes distance (4.946) was observed between the tomato genotypes $G_2 \times G_7$ and $G_6 \times G_7$ followed by the genotypes $G_1 \times G_7$ and $G_6 \times G_7$. The highest pair distance was (4.527) observed between G_2 and $G_7 \times G_1$. The lowest distance (0.654) was observed between the genotypes G_6 and $G_1 \times G_2$ followed by the genotypes $G_7 \times G_1$ and $G_9 \times G_7$. The tenth lowest distance (0.844) was observed between the genotypes G_6 and G_9. The difference between the highest and the lowest inter-genotypes distance indicated the prevalence of variability among the 36 genotypes of tomato (Table 12). According to Rahman *et al*. (2011) who showed that the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. The maximum intra-cluster distance was presented in cluster III (2.023) which had ten genotypes (G_9, G_{10}, $G_1 \times G_{10}$, $G_7 \times G_6$, $G_7 \times G_9$, $G_9 \times G_1$, $G_9 \times G_{10}$, $G_{10} \times G_6$, $G_{10} \times G_7$ and $G_{10} \times G_9$). The minimum intra-cluster distance

was recorded in cluster IV (1.237) which containing six genotypes (G_7, $G_6 \times G_{10}$, $G_7 \times G_1$, $G_7 \times G_{10}$, $G_9 \times G_2$ and $G_9 \times G_7$). (Table 14)

4.5.5. Non-hierarchical clustering

Thirty-six *Solanum lycopersicum* L. genotypes were grouped into five different clusters non-hierarchical clustering (Table 13). These results confirmed the clustering pattern of the genotypes obtained through PCA. Shashikanth *et al.* (2010) reported ten clusters, Mahesha *et al.* (2006) reported nine clusters, Sharma and Verma (2001) reported five clusters in tomato. It indicated that cluster I contained ten genotypes, cluster II contained five genotypes, cluster III contained nine genotypes, cluster IV and cluster V contained six genotypes of tomato. From cluster mean (Table 13), cluster I had the maximum mean value for plant height (87.03) and the minimum mean value for yield per plant (3.08). Cluster II had the maximum mean value for number of fruit per plant (292.33) and minimum mean value for yield per plant (2.31). Cluster III had required maximum mean value for number of fruit per plant (165.93) and minimum mean value for yield per plant (2.38). Cluster IV had the lowest mean value for total soluble solids required (2.08), highest mean value for Individual Fruit weight (g) (126.94). Cluster V had required maximum mean value for plant height (g) (76.14) and minimum mean value for total soluble solids (3.02). These genotypes of cluster could be used for future hybridization program. Singh *et al*. (2013) reported that contribution of the characters to the divergence in tomato.

4.5.6. Conical variate analysis

Conical variate analysis (CVA) was done to identify the inter-cluster distance. (Table 14) (Table 15) were presented intra and inter-cluster distance (D^2) values. In this experiment the inter-cluster distances were higher from intra-cluster distances. It showed that the wide range of genetic variability among genotypes of tomato. Based on the result it indicated that the highest inter cluster distance was observed between II and IV (14.738), followed by II and V (14.497), I and II (11.189), III and IV (10.162) and III and V (8.372). The lowest inter-cluster distance was observed between I and V (3.681) followed by I and III

(4.882) and IV and V (5.845), whereas similar type of distance was found (II and IV) and (II and V). With the help of D^2 values within and between clusters, an arbitrary cluster diagram was constructed, which showed the relationship between different genotypes. Diagram also showed the intra and inter cluster distance of thirty-six genotype of tomato. However, the maximum inter-cluster distance was recorded between clusters II and IV followed by between II and V. Genotypes from these clusters can be used in hybridization programme. The intra-cluster divergence varied from 2.023 to 1.237, maximum for cluster III, which was comprised of nine genotypes of diverse origin, while the minimum distance was observed in cluster IV that comprised six genotypes. Results obtained from different multivariate techniques were superimposed in figure 2 from which it may be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one.

Table 12. Ten highest and ten lowest inter genotypic distance among the 36 genotypes of tomato

Highest Distance			Lowest Distance		
Genotypes		Distance	Genotypes		Distance
$G_2 \times G_7$	$G_6 \times G_7$	4.946	G_6	$G_1 \times G_2$	0.654
$G_1 \times G_7$	$G_6 \times G_7$	4.81	$G_7 \times G_1$	$G_9 \times G_7$	0.69
$G_2 \times G_7$	$G_7 \times G_1$	4.781	$G_7 \times G_2$	$G_9 \times G_6$	0.764
G_6	$G_6 \times G_7$	4.746	G_9	G_{10}	0.782
$G_2 \times G_7$	$G_6 \times G_7$	4.583	$G_9 \times G_2$	$G_9 \times G_7$	0.802
G_7	$G_2 \times G_7$	4.55	$G_{10} \times G_2$	$G_{10} \times G_6$	0.803
$G_2 \times G_7$	$G_9 \times G_7$	4.55	G_7	$G_7 \times G_{10}$	0.837
$G_2 \times G_7$	$G_9 \times G_6$	4.547	G_6	$G_2 \times G_7$	0.841
$G_1 \times G_7$	$G_6 \times G_1$	4.532	G_2	$G_2 \times G_9$	0.844
G_2	$G_7 \times G_1$	4.527	G_6	G_9	0.844

Table 13. Cluster mean for 19 yield and yield related characters in 36 genotype of tomato

Characters	I	II	III	IV	V
Days to first flowering	57.13	57	54.78	56.22	54.78
Days to 50% flowering	72.13	73	71.52	71.95	70.78
Plant height	87.03	76.48	84.5	85.64	76.14
Number of Branch per plant	4.1	4.87	4.92	4.55	4.28
Leaf length	28.96	23.38	26.19	28.35	25.8
Leaf width	22.1	15.12	18.47	22.05	19.91
Number of Flower per cluster	6.83	11.2	10.15	8.45	7.17
Number of Cluster per plant	10.33	17.87	13.85	9.78	10
Number of fruit per cluster	6.47	14.47	10.37	6.33	5.61
Number of fruit per plant	70.9	292.33	165.93	86.56	55.22
Individual Fruit weight	50.65	10.95	20.44	126.94	102
Fruit length	37.61	13.53	20.27	36.72	38.83
Fruit width	35.58	14.47	20.71	52.1	43.07
Skin diameter	5.33	3.73	3.81	5.07	5.39
Relative water content	58.98	64.54	51.21	70.23	34.45
Locule number	3.57	2.6	2.67	5.33	4.11
P^H	3.63	3.85	4.13	3.61	3.56
Total soluble solids	3.17	3.31	2.78	2.08	3.02
Yield per plant	3.08	2.31	2.38	7.6	4.91

Table 14. Intra (Bold) and inter cluster distances (D^2) for 10 genotypes of tomato

	I	II	III	IV	V
I	**1.343**				
II	11.189	**1.796**			
III	4.882	6.345	**2.023**		
IV	7.596	14.738	10.162	**1.237**	
V	3.681	14.497	8.372	5.845	**1.724**

Table 15. 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	V (3.681)	II (11.189)
2	II	III (6.345)	IV (14.738)
3	III	I (4.882)	IV (10.162)
4	IV	V (5.845)	II (14.738)
5	V	I (3.681)	II (14.738)

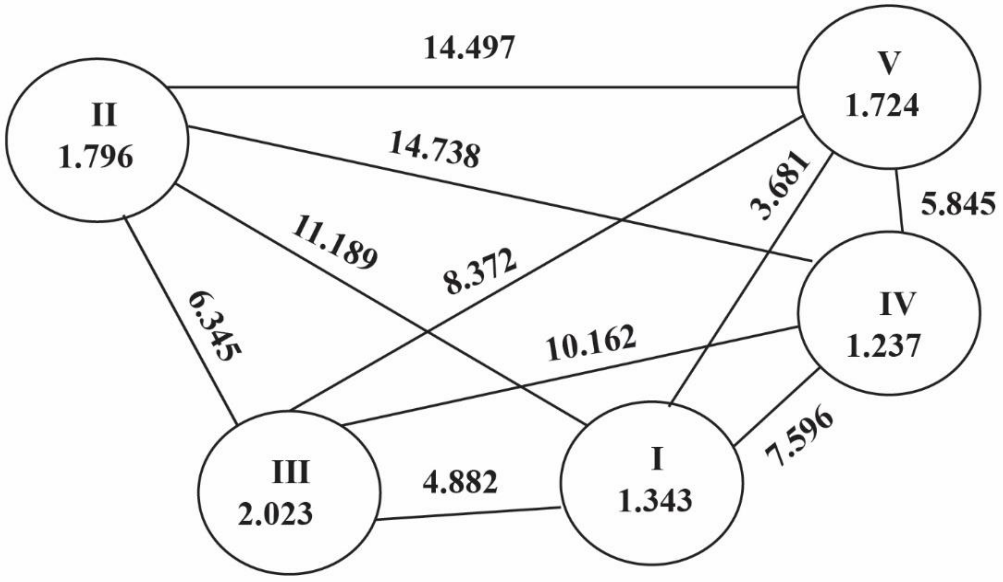


Figure 2. Cluster diagram showing the average intra and inter cluster distances of 36 tomato genotypes.

4.5.7. Contribution of characters towards divergence of the cultivars

For deciding on the cluster for the purpose of further selection and choice of parents for hybridization the character contributing maximum to the divergence were given greater emphasis (Jagadev *et al*. 1991).The PCA revealed that in vector I (Z1) the important characters responsible for genetic divergence in the major axis of differentiation were Days to first flowering, days to 50% flowering, plant height (cm), leaf width (cm), number of fruit per plant, skin diameter (cm), locule number, p^H and total soluble solids (Table 16). ln vector II (Z2) that was the second axis of differentiation Days to first flowering, plant height (cm), number of branch per plant, leaf length (cm), number of flower per cluster, number of cluster per plant, number of fruit per cluster, number of fruit per plant, individual fruit weight (g), fruit width (cm), skin diameter (cm), relative water content, locule number, p^H and yield per plant (g) were important. The role of Days to first flowering, plant height (cm), number of fruit per plant, skin diameter (cm), locule number and p^H in both the vectors were positive across two axes indicating the important components of genetic divergence in those materials.

Table 16. Latent vectors for 19 morphological characters in tomato

Characters	Vector 1	Vector 2
Days to first flowering	0.282	0.249
Days to 50% flowering	0.003	-0.249
Plant height	0.035	0.036
Number of Branch per plant	-0.172	0.167
Leaf length	-0.083	0.240
Leaf width	0.018	-0.164
Number of Flower per cluster	-0.289	0.310
Number of Cluster per plant	-0.121	0.064
Number of fruit per cluster	-0.303	0.060
Number of fruit per plant	0.049	0.017
Individual Fruit weight	-0.039	0.043
Fruit length	-0.097	-0.072
Fruit width	-0.042	0.042
Skin diameter	0.176	0.357
Relative water content	-0.015	0.044
Locule number	0.017	0.184
P^H	0.014	0.623
Total soluble solids	0.024	-0.451
Yield per plant	-0.090	0.150

4.5.8. Selection of genotypes for further trial

Identification and utilization of diverse germplasm is the main issue in plant breeding. Three factors (choice of particular cluster, selection of specific variety from a cluster and relative contribution of the character to the total divergence) should be considered for selecting parents for a breeding program (Chaudhary *et al.* 1977). Through knowledge of genetic diversity of the crop is necessary for parental selection that maximizes genetic improvement (Rahman *et al*. 2011). More accurate and complete description of genotypes and patterns of genetic diversity could help determinate future breeding strategies and facilitate introgression of diverse germplasm into the current commercial soybean genetic base (Baranek *et al.* 2002). Principal component analysis is useful as it gives information about the groups where certain traits are more important allowing the breeders to conduct specific breeding program (Salimi *et al*. 2012). Genetically distant parents are usually able to produce highest heterosis. Based on cluster mean and agronomic performance the genotypes $G_6 \times G_1$ minimum days to first flowering and days to 50% flowering from cluster V. G_6 maximum number of cluster per plant from cluster II. $G_7 \times G_1$ maximum individual fruit weight from cluster IV. $G_6 \times G_7$ maximum fruit width and total soluble solids from cluster V. $G_9 \times G_7$ maximum yield per plant from cluster IV. Therefore, considering group distance and other agronomic performance these inter genotypic crosses might be suggested for future trial program.

SUMMARY AND CONCLUSION

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted at the research field of the Sher-E-Bangla Agricultural University, Dhaka-1207 during the period from October 2019 to April 2020 for Genetic diversity, Correlation and path analysis in tomato. In this experiment 36 tomato genotypes were used as experimental materials. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Variability, mean performance, correlation matrix, path analysis and genetic diversity analysis on different yield and yield contributing characters of tomato genotypes was estimated and significant variation was observed for different tomato genotypes.

The longer period of days to first flowering was found in G_7, $G_1 \times G_{10}$, $G_2 \times G_{10}$, $G_7 \times G_9$ (59.33 DAT) and the earlier period of days to first flowering was found in $G_6 \times G_1$ (52.00 DAT). The highest days to 50% flowering was found in G_7 (76.67 DAT) and the lowest days to 50% flowering was found in $G_6 \times G_1$ (68.00 DAT). The highest plant height (cm) was found in $G_6 \times G_9$ (105.03) and the lowest plant height (cm) was found in $G_1 \times G_6$ (67.03). The highest number of branches per plant was found in G_1 (6.33) and the lowest number of branches per plant was found in $G_7 \times G_9$, $G_{10} \times G_6$ (3.00). The highest leaf length (cm) was found in $G_6 \times G_2$ (33.63) and the lowest leaf length (cm) was found in G_1, $G_2 \times G_{10}$ (20.10). The highest leaf width (cm) was found in $G_6 \times G_2$ (29.30) and the lowest leaf width (cm) was found in G_1 (12.37). The highest number of flower per cluster was found in $G_2 \times G_9$ (14.00) and the lowest number of flower per cluster was found in $G_6 \times G_7$ (5.33). The highest number of cluster per plant was found in G6 (23.67) and the lowest number of cluster per plant was found in $G_6 \times G_{10}$ (7.00). The highest number of fruit per cluster was found in G2XG1 (23.00) and the lowest number of fruit per cluster was found in $G_6 \times G_7$, $G_9 \times G_1$ (4.33). The highest number of fruit per plant was found in $G_2 \times G_1$ (363.33) and the lowest number of fruit per plant was found in $G_6 \times G_1$ (21.67). The highest individual fruit weight (g) was found in $G_7 \times G_1$ (179.57) and the lowest individual fruit weight (g) was found in

$G_2 \times G_7$ (4.67). The highest length (cm) of fruit was found in $G_{10} \times G_1$ (59.33) and the lowest length of fruit (cm) was found in $G_1 \times G_7$ (6.70). The highest width (cm) of fruit was found in $G_6 \times G_7$ (63.00 DAT) and the lowest width (cm) of fruit was found in $G_1 \times G_7$ (7.40). The highest skin diameter (cm) was found in $G_{10} \times G_1$ (7.78) and the lowest skin diameter (cm) was found in $G_2 \times G_6$ (1.97). The highest amount of relative water content was found in $G_7 \times G_{10}$ (89.20) and the lowest amount of relative water content was found in $G_6 \times G_9$ (6.33). The highest number of locule was found in $G_6 \times G_{10}$ (8.00). The lowest number of locule was found in G_1, G_2, G_6, $G_1 \times G_2$, $G_1 \times G_{10}$, and $G_{10} \times G_6$ (2.00). The highest P^H value was found in G1 (6.31) and the lowest P^H value was found in $G_7 \times G_{10}$ (3.12). The highest total soluble solids value was found in $G_6 \times G_7$ (7.03) and the lowest total soluble solids value was found in $G_9 \times G_2$ (1.07). The highest yield per plant (kg) was found in $G_9 \times G_7$ (13.06) and the lowest yield per plant (kg) was found in $G_2 \times G_1$ (0.63).

The phenotypic variance for all of the characters was considerably higher than the genotypic variance. In the case of genotypic co-efficient of variation was less than phenotypic co-efficient of variation for all the characters.

Leaf width, number of flower per cluster, number of cluster per plant, number of fruit per cluster, number of fruit per plant, individual fruit weight, fruit length, fruit width, skin diameter, relative water content, locule number, P^H, total soluble solids, and yield per plant showed high heritability whereas days to first flowering, leaf length showed moderate heritability and days to 50% flowering, plant height, and number of branches per plant showed low heritability.

Correlation co-efficient revealed that yield per plant had positive association with leaf width, individual fruit weight, fruit length, fruit width, skin diameter, locule number for both genotypic and phenotypic except leaf length.

Path analysis expressed a positive direct effect on yield per plant for the characters, leaf length, leaf width, number of cluster per plant, number of flower per plant, individual fruit weight, fruit length, fruit width, relative water content, P^H and indicating that these were

the main contributors to yield per plant and there is a great extent of possibility of improving seed yield through selection based on those characters.

Genetic diversity of thirty-six tomato genotypes based on nineteen characters was measured through Principal Component Analysis (PCA), Cluster Analysis, and Canonical Variate Analysis (CVA) using GENSTAT. According to PCA, PCO and Cluster analysis, the genotypes were grouped into five different clusters. The cluster I comprised the maximum number 10 of genotypes, followed by cluster III comprised of 9 genotypes. The cluster V, IV and II comprised 6, 6 and 5 genotypes, respectively. The highest inter-cluster distance was observed between II and IV (14.738) and the lowest inter-cluster distance was observed between I and V (3.681). The highest intra-cluster distances were observed in cluster III and and lowest intra-cluster distances were observed in IV. The inter-cluster distances were larger than the intra-cluster distances. The intra cluster distances in the entire five clusters were more or less low indicating that the genotypes within the same cluster were closely related. Though genotypically distant parents are able to produce higher heterosis but in different experiments it was also revealed that higher heterosis for yield and its components could be obtained from the crosses between the intermediate divergent parents than extreme ones.

In the morphological characterization it is found that $G_1 \times G_2$, and $G_1 \times G_{10}$. These genotypes produce three types of fruits of different color yellow and red which are identical with their parents. But shape and size were different.

Based on the results of the study, the following recommendations may be drawn

- Genotype G_6, $G_1 \times G_7$ and $G_2 \times G_7$ from cluster II. $G_7 \times G_1$, $G_9 \times G_7$ and G_7 from cluster IV. $G_6 \times G_7$, $G_6 \times G_1$ and $G_9 \times G_6$ from cluster V would be suitable for future selection.
- The genotypes of cluster II, IV and V could be used as parents for future breeding program to develop tomato variety.

REFERENCES

REFERENCES

Abedin, J. and Khan, S. H. (1986). Study of the morphogenetic divergence in tomato. *Bangladesh J. Agric. Res*. **11**(1): 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., Friedt, W. (2001). Genotypic variation of Kenyan tomato (*Lycopersicon esculentum* L.) germplasm. *J. Food Technol. Africa*. **6**(1): 13-17.

Ahamad, K. (1995). 'Phul Phal O Shak-Sabjee', 5th Edn. 414 Senpara, Parbata, Mirpur, Dhaka. p. 440.

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.

Anonymous. (1997). WWF and IUCN, Centres of Plant Diversity: Vol. 3, The Americas, IUCN Publications Unit, Cambridge, England.

Anonymous. (2007). World Cancer Research Fund / American Institute for Cancer Research. Food, Nutrition, Physical Activity, and the Prevention of Cancer: a Global Perspective.

Anupam B., Jain, B. P. and Verma, A. K., 2002, Genetic variability heritability and genetic advance in tomato (*Lycopersicon esculentum* (L.) Karst.). *J. Res. Birsa Agril.Uni.*, **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. *Indian. 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.

Ario, O.J. (1987). Multivariate analysis and choice of parents for hybridization in okra. *Theor.Appl. Genet.* **74**: 361-363.

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.). *Indian J. Agric. Sci.*, **73**(2): 110-113.

Asamizu, E. and Ezura, H. (2009). Inclusion of tomato in the genus Solanum as "*Solanum lycopersicum*" is evident from phylogenetic studies. *J. Japan. 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.

Balestre, M., Pinho, R.G.V., Souza, J.C. and Lima, J.I. (2008). Comparison of maize similarity and dissimilarity genetic coefficients based on microsatellite markers. *Genet. Mol. Res*. **7**: 695-705.

Baranek, M., Kadlec, M., Raddova, J., Vachun, M. and Pidra, M. (2002). Evaluation of genetic diversity in 19 Glycine max (L.) Merr. accessions included in the Czech National Collection of Soybean Genotypes. *Czech J. Genet. Plant Breed*. **38**(2): 69-74.

Barman, S. C. (2007). Real Adoption Impact Measure of Tomato Technologies on Production at Farmers' Level in Bangladesh. *Bangladesh J. Sci. Ind. Res.* **42**(1): 15-28.

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.

Bashar, M. K. (2002). Genetics and morpho-physiological basis of heterosis in rice. Ph.D. Thesis, BSMRU, Gazipur.

BBS. (2013). Statistical Pocket Book, Statistics Division, Ministry of Planning, Govt. of the People's Republic of Bangladesh, Dhaka. p. 62.

BBS. (2016). Statistical Pocket Book, Statistics Division, Ministry of Planning, Govt. of the People's Republic of Bangladesh, Dhaka. p. 58.

Bhuiyan, T.T.A., Rahman, M.M., Islam, M.R., Laylin, M.M.A. and Zeba, N. (2016). Estimation of genetic variability, heritability and genetic advance in agro-morphogenic and nutritional traits of tomato (*Solanum lycopersicum* L.) genotypes. *J. Expt. Biosci.* **7**(1):65-72.

Biswas, J. and S. C. Mallik. (1989). Days required for flowering and harvesting of some promising cultivars of tomato (*Lycopersicon esculentum)*. *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. 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.

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.

Chaudhary, B.D., Kakar S.N. and Singh, R.K. (1977). Estimation of genetic parameters in barley (Hordeum vulgare L.). *Theol. Appl. Genet*. **49**(4): 153-156.

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

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

Chishti, S.A.S., Khan, A.A., Sadia, B. and Khan, I.A. (2008). Analysis of combining ability for yield, yield components and quality characters in tomato (*Lycopersicon esculentum* Mill). *J. Agric. Res.* **46**(4): 325-332.

Cohen JH, Kristal AR, Stanford JL., (2000). Fruit and vegetable intake and prostate cancer risk. *J Natl Cancer Inst*, **92**:61 – 8.

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.

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

de Sahagún, B. (1979), Historia General de las Cosas de la Nueva España, Ed, Porrúa, Mexico.

Desai, N.C. and Jaimini, S.N. (1997). Studies on genetic divergence in potato. *J. Indian Potato Assoc*. **24** (3-4): 154-160.

Dev, H., Rattan, R.S., and Thakur, M.C. (1994). Heterosis in tomato. *Hort. J*. **7**(2): 125-132.

Dhaliwal, M.S., Singh, S., and Cheema, D.S. (2002). Estimating combining ability effects of the genetic male sterile lines of tomato for their use in hybrid breeding. *J. Genet. Breed*. **54**(3): 199-205.

Dhaliwal, M.S., Singh, S., and Cheema, D.S. (2002). Estimating combining ability effects of the genetic male sterile lines of tomato for their use in hybrid breeding. *J. Genet. Breed*. **54**(3): 199-205.

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). GENSTAT 5: A Second Course. Oxford Science. 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.

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* Mil1.). *Haryana Agric.Univ. 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.

FAO. (2006). FAO Production Yearbook, (1996). Basic Data Unit, Statistics Division, FAO, Rome, Italy, **55**:125-127.

Farzaneh, A., Nemati, H., Arouiee, H., 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 Plant. Improvement.* **29**(4): 693-710.

Geogieva, A. K., Dhanesh and Kulal, P.K., (1969) Path analysis in tomato. *J. Maharashti agric. Univ.*, **14:114**-116.

Gepts, P. (2006). Plant genetic resources conservation and utilization. *Crop Sci.* **46**: 2278-2292.

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

Giovannucci, E., Rimm, E. B., Wolk, A., Ascherio, A. Stampfer, M. J., Colditz, G. A., and Willett, W. C. 1998. Calcium and fructose intake in relation to risk of prostate cancer.

Godekar, D. A., Dhanukshe, B. L. and Patil, F. B. (1992). Studies on variability, heritability and genetic advance in tomato. *J. Maharasthra Agric. Univ*. **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. *Indian. J. Agril. Res*. **41**(2): 146-149.

Gomez, O. (1987). Correlations and path co-efficient analysis in tomato breeding lines. *Agrotecnia decuba*. **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.

Hannan, M.M., Ahmed, M.B.,.Razvy, M.A., Karim, R., Khatum, M., Hayder, A., Hussain, M., and Roy, U.K. (2007). Heterosis and correlation of yield and yield components in tomato. *Am-Eurasian J. Sci. Res*. **2**(2):146-150.

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.

Hossain, M. M., Khalequzzaman, K. M., Hossain, M. A., Mollah, M.R.A., Siddique, M. A. (2004). Influence of planting time on the extension of picking period of four Tomato varieties. *J Biol Sci.*, **4**: 616-619

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

Jagadev, P.N., Samal. K.M. and Lenka. L. (1991). Genetic divergence in rape mustard. *Indian journal of genetics and plant Breed* **51**: 465-466.

Jenkins, J.A. (1948), "The origin of the cultivated tomato", *Economic Botany*, Vol. 2/4, pp. 379-392.

Joshi, A. and Kohli, U.K. (2003). Genetic divergence for quantative and qualitative traits in tomato (Lycopersicon esculentum). *Indian J. Agric. Sci*. 73(2): 110-113.

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 stomato (*Solanum lycopersicum* L.). *Progr. Hort.* **36**(1):51-58.

Juned, S.A., Jackson, M.T. and Catty, J.P. (1988). Diversity in the wild potato species Chacoense Bitt. *Euphytica.* **37**(2): 149-156.

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

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

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., 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.). *Plant. Arc*. **4**(1): 191-193.

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.

Larry, R. and L. Joanne (2007), "Genetic resources of tomato", in: Razdan, M.K. and A.K. Mattoo (eds.), *Genetic Improvement of Solanaceous Crops, Vol. 2. Tomato*, Science Publishers,Enfield, New Hampshire.

Li, H., Deng, Z., Liu, R., Loewen, S. and Tsao, R. (2012). Ultra-performance liquid chromatographic separation of geometric isomers of carotenoids and antioxidant activities of 20 tomato cultivars and breeding lines. *Food Chem* **132**: 508-517.

Linnaeus, C. (1753). *Species Plantarum,* 1st ed. Stockholm: L.,Salvius.

Luckwill, L. C. (1943)a. The genus *Lycopersicon:* an historical, biological, and taxonomical survey of the wild and cultivated tomatoes. Aberdeen Univ. Stud. 120: 1-44.

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, 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. Rep.* **60**: 120-123.

Matthioli, P. A (1554). Commentarii, in libros sex Pedacci Dioscoricis Anazarbei, de medica materia.Venice: V. Valgrisi.

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

McCormick, S., Niedermeyer, J., Fry, J.J., Barnason, A., Worsch, R., and Fraley, R. (1986). Leaf disc transformation of cultivated tomato (*L. esculentum*) using *Agrobacterium tumifaciens*. *Plant Cell Rep.* **5**: 81-84.

Meena, O. P. and Bahadur, V (2015). Genetic Associations Analysis for Fruit Yield and Its Contributing Traits of Indeterminate Tomato (*Solanum lycopersicum* L.) Germplasm under Open Field Condition. *J. Agric. Sci.* **7**(3): 148-163.

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.

Miller, P. (1754). *The gardener's dictionary*, Abridged 4th ed. London: John and James Rivington.

Miller, P. (1768). *The gardener's dictionary*, Abridged 8th ed. London.

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. (2003). Genetic variability, correlation and path coefficient studies in tomato. *Indian 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.

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., 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.

Nandpuri. B. S., Singh, S. and Lal, T. (1973). Studies on the genetic variability and correlation of some economic characters in tomato. *J. Res*. **10**: 316-21.

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*). *Agric. Sci.Digest*. **32**(4): 281-285.

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). Comperative performance of ten genotypes of tomato in late planting. *Bangladesh J. Agric. Sci*. **27**(1): 121-124.

Nuez, F. et al. (1996), *Catálogo de Semillas de Tomate*, Banco de Germoplasma de la Universidad

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.

Padmini, K. and Vadivel, E. (1997). Studies on genetic variability and heritability in F2 generation of tomato (*Lycopersicon esculentum* Mill.). *South Indian Hort.* **45** (1-2): 1-4.

Pandit A, Rai V, Bal S. (2010). Combining QTL mapping and transcriptome profiling of bulked RILs for identification of functional polymorphism for salt tolerance genes in rice (*Oryza sativa* L.). *Mol. Genet. Genomics.* **284**:121-36.

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., D.M. Spooner and S. Knapp (2008), Taxonomy of wild tomatoes and their relatives *(Solanum sect. Lycopersicoides, sect. Juglandifolia, sect. Lycopersicon; Solanaceae)*, Systematic Botany Monographs, The American Society of Plant Taxonomists, **84**, 186.

Phookan, D. B., Talukdar, P., Shadeque A. and chakravarty, B. K. (1998). Genetic Variability and heritability in tomato (*Lycopersicon esculentum* Mill.) genotypes during summer season under plastic house condition. *Indian J. Agril Sci*. **68** (6): 304-306.

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.

Pradeepkumar, T., Joy, D.B.M., Radhakrishnan, N.V. and Aipe, K.C. (2001). Genetic variation in tomato for yield and resistance to Bacterial Wilt. *J. Trop. Agric*. **39**:157-158.

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. *Indian. 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., and Kale. P.N. (1994). Heterosis studies in tomato. *J. Mah. Agric. Univ.* **19** (1): 83-85.

Rahman, M.M., Rasul, M.G., Bashar M.K., Syed, M.A. and Islam, M.R. (2011). Parent selection for transplanted Aman rice breeding by morphological, physiological and molecular diversity analysis. *Libyan Agric. Res. Centre J. Int.* 2: 26-28.

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., 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.

Ravindra, M., Aravinda, S. and Kumar, J.S. (2003).Stability analysis for growth and earliness in tomato.*Indian 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, V.V.P. and Reddy, K.V. (1992). Studies in variability in tomato. *South Indian Hort*. **40**: 257- 260.

Rick, C.M. (1978), "The tomato", *Scientific American*, **239**, 77-87.

Rick, C.M. (1990), "Andean *Lycopersicon esculentum* var. cerasiforme genetic variation and its evolutionary significance", *Economic Botany*, **44**(3), 69-78.

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. *Intl. 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 f1 hybrids of tomato. *Pakistan J. Agri. Sci.* **50**(4): 649-653.

Salimi, S., Lahiji, H.S., Abadi, G.M., Salimi, S. and Moradi, S. (2012). Genetic diversity in soybean genotypes under drought stress condition using factor analysis and cluster analysis. *World Appl. Sci. J.* **16**(4): 474-478.

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.

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.

Sanjiv A and Rao AV. (2000). Tomato lycopene and its role in human health and chronic diseases. *Can Med Assoc J*.**163**:739-744.

Saravaiya, S. N. and Patel, M. B. (2005). DBM (Diamond Back Moth): The most notorious pest of cauliflower and its management strategies. *Agrobios Newsletter*, **3**(9):23-24.

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.

Sharon Palmer, R .(2009). Scanner. **2**(2):24

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

Shravan, K., Biswash, C. and Mollik, P. (2004) Heterosis and inbreeding depression in tomato. *Utter Pradesh Indian 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. *African J. Biotechnol*. **6:** 497-500.

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. N., Srivastava, J. P. and Prasad, R. (1977). Genetic variability and correlation studies in bitter gourd. *Indian J. Agri. Sci*. 47(12): 604-607.

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, P. K., Singh, B. and Pandey, S. (2006). Genetic variability and character association analysis in tomato. *Indian J. Plant Genet. Resour*. **19**:196-199.

Singh, R. R. and Singh, H. N. (1980). Correlation Studies in tomato. *Indian. J. Agric. Sci.*, **50**(8): 591-594.

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

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

Stacewicz-Sapuntzakis M & Bowen PE, (2005). Role of lycopene and tomato products in prostate health. Biochim Biophy Acta.; **1740**:202-5.

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., 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. and Bebeli, P.J. (2008). DNA and morphological diversity of selected Greek tomato landraces. *Sci. Horticultura*. **116**: 354-361.

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

Tournefort, J. P. de. (1694). *Elemens de Botanique.* Paris: I'lmprimerie Royale.

Tzonou A, Signorello LB, Laigou P, (1999). A diet and cancer of the prostate: a case-control study in Greece. *Int J Cancer*: **80**:704 –708.

Uddin, M.J. (2001). Morphogenetic diversity and gene antion in sesame (*Sesame indicum* L.). Ph.D. thesis, Department of Genetics and Plant Breeding, BSMRAU, Gazipur.

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

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.

Watson, W. P. (1989). The Matthioli woodblocks: a rare survival. In *The Matthioli woodblocks* (catalog with no pagination). London: B. Quaritch Ltd.

Wilcox, J.K. Gatignani, G.L. and Lazarus, C. (2003). Tomatoes and cardiovascular health. *Crit. Rev. Food Sci Nutr*. **43**(1): 1

World Cancer Research Fund / American Institute for Cancer Research.2007. *Food, Nutrition, Physical Activity, and the Prevention of Cancer: a Global Perspective.*

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

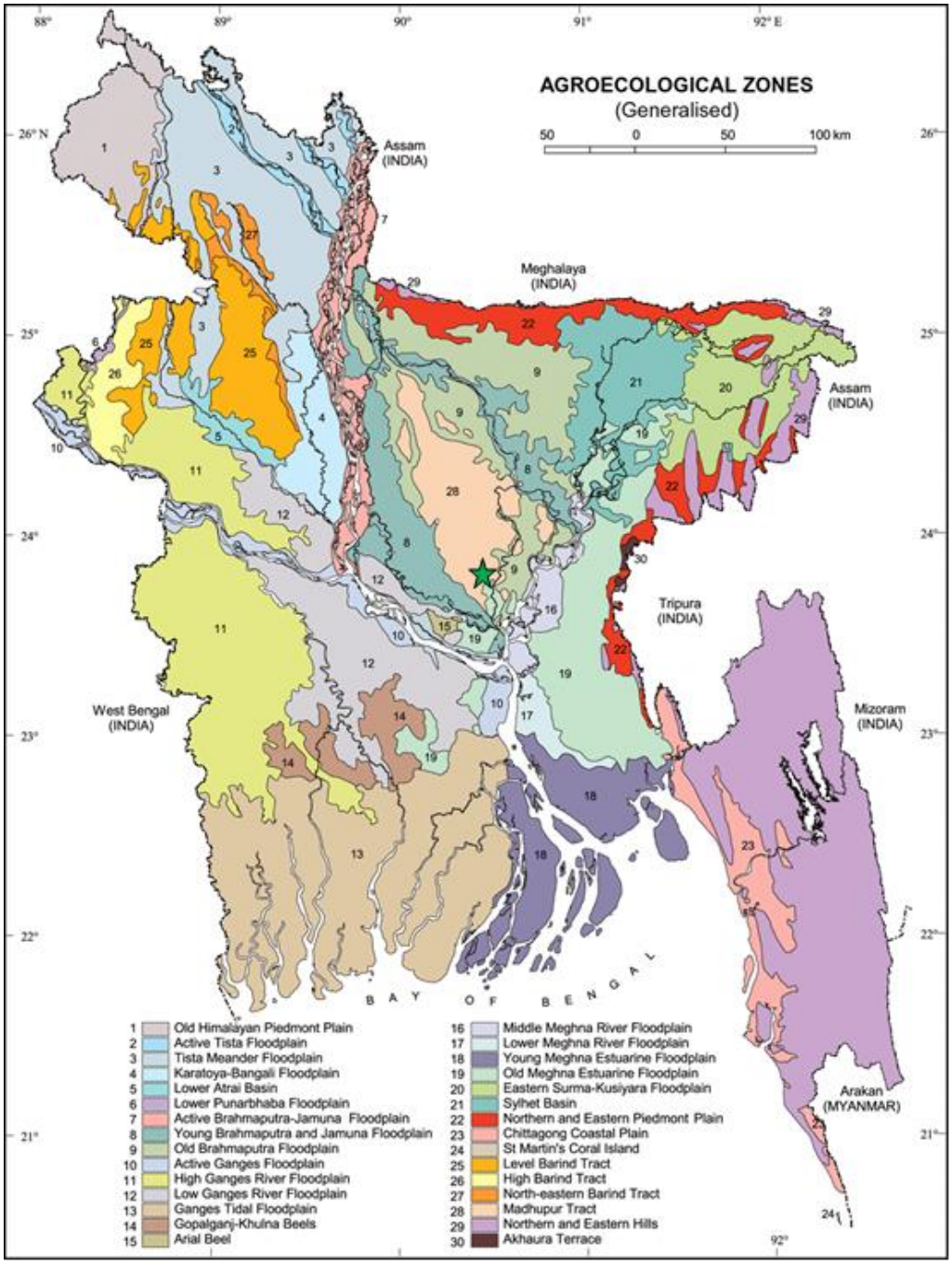
WWF and IUCN (1997), *Centres of Plant Diversity: Vol. 3, The Americas*, IUCN Publications Unit, Cambridge, England.

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. *Pakistan J. Bot*. **44**(2): 485-492.

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.

APPENDICES

Appendix I. Map showing the experimental site under the study



★ The experimental site under the study

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

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

Soil separates	%	Methods employed
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

Appendix II. (Cont'd)

C. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (me/100 g soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

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

Appendix III. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from November 2019 to March 2020

Month	Year	Monthly average air temperature (^{o}C)			Average relative humidity (%)	Total rainfall (mm)	Total sunshine (hours)
		Maximum	Minimum	Mean			
Nov	2019	31	18	24	63	Trace	216.4
Dec	2019	27.12	11.56	19.34	61	Trace	212.50
Jan.	2020	28	10	14	65	Trace	212.50
Feb	2020	32	12	22	73.23	4.0	195.00
Mar.	2020	34	16	25	67.23	4.5	225.50

Source: Bangladesh Meteorological Department (Climate division), Agargaon, Dhaka-1212.

Appendix IV. Pictorial views of the experimental field.

Visit of research supervisor in the field