GENETIC DIVERSITY ANALYSIS OF TOMATO (*Solanum lycopersicum* L.) GENOTYPES BASED ON YIELD AND YIELD COMPONENTS

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CERTIFICATE

This is to certify that the thesis entitled, "Genetic diversity analysis of tomato (Solanum lycopersicum L.) genotypes based on yield and yield components" 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 Mahima Akter, Registration No. 11-04545 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2017
Place: Dhaka, Bangladesh

Prof. Dr. Naheed Zeba
Supervisor

DEDICATED TO

CHAPTER I

INTRODUCTION

Vegetables are the cheapest source of vitamins and minerals and are considered as protective food. In Bangladesh, more than 70 varieties of vegetable are grown round the year in varied seasons (Parvin, 2017). Doctors have been known to promote the consumption of vegetables to alleviate malnutrition and vitamin deficiencies. Production of tomato is mainly done through synthetic farming technique. It is being increasingly realized that enhancing vegetable production especially tomato would ensure the fulfillment of the objective of household food, nutritional and economic security in a single go. Tomato (*Solanum lycopersicum L.*) is one of the most important solanaceous vegetable crops in the world in terms of both production and harvested area (FAOSTAT, 2015). It is an important and widely cultivated food crop in our country in terms of nutritional value. It is used to make soups, conserves, pickles, ketchup's, sauces, juices etc. and is one of the most important popular salad vegetables. It is also excellent source of vitamin C and is commonly referred to as poor man's orange. It is a good source of vitamins (A, C and Calcium) fiber and minerals (Kallo, 1989). More than 7% of total vitamin of vegetable source comes from tomato in Bangladesh. It contains 94 g water, 0.5 g minerals, 0.8 g fiber, 0.9 g protein, 0.2 g fat and 3.6 g carbohydrate and other elements like 48 mg calcium, 0.4 mg iron, 356 mg carotene, 0.12 mg vitamin B-1, 0.06 mg vitamin B-2 and 27 mg vitamin C in 100 g edible ripen tomato (Anonymous, 2010a). Tomato is rich in antioxidant called Lycopene. Now Bangladesh is producing a good amount of tomatoes. It has great demand in Bangladesh throughout the year but it is available and cheaper in winter season. In Bangladesh it is cultivated as winter vegetable, which occupied an area of 67535 acres and total production was 368121 metric tons in 2015-16 (Anonymous, 2016). The average tomato yield in Bangladesh is 50-90 tons/ha (Anonymous, 2010b).

According to FAO report world dedicated 4.8 million hectares of land in 2012 for tomato cultivation and the total production was about 161.8 million tones. The average world farm yield for tomato was 33.6 ton per hectare. In Bangladesh about 6.10 % area is under tomato cultivation both in winter and summer and tomato is grown on an area of 26300 million hectares with an average production of 251 thousand metric tons which is very low (0.2 %) to other countries

(FAO, 2013). Popular tomato growing areas in Bangladesh are Dinajpur, Rajshahi, Dhaka, Cumilla and Chattagram.

Growers cannot produce their own seed because tomato seed production is a highly specialized activity therefore growers are forced to purchase seed of unknown sources and quality. Consistent efforts for developing hybrid varieties in vegetable crops, especially tomato, have yet to be made. Hence there exists a lot of scope for vegetable breeding particularly for tomato breeding, especially through hybridization programs. For basic and applied research tomato is an excellent model crop. This is due to many reasons, including ease of culture, short life cycle, high self-fertility and homozygosity, great reproductive potential, ease of use for controlled pollination and hybridization, availability of a wide array of mutants and genetic stocks (Miller and Tanksley, 1990), diploid with a rather small genome (0.86 pg, 950 kb) (Amaral *et al*., 1997), and amenability to asexual propagation and protoplast, cell and tissue cultures and whole plant regeneration (McCormick, *et al*., 1986).

Parameters of genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in available genotypes. Heritability and genetic advance help in determining the influence of environmental expression of characters and the extent to which improvement is possible after selection (Robinson *et al.*, 1949). Crop improvement depends on the magnitude of genetic variability and the extent to which desirable characters are heritable. High heritability alone is not enough to make efficient selection in segregating generation, unless the information is accompanied for substantial amount of genetic advance (Johnson *et al.,* 1995). Hybridization is one of the tools for achieving variability aiming at the improvement of the crop. Before hybridization genetic diversity of existing materials or entries needs to be known. Information about genetic diversity in available germplasm is important for optimal design of any breeding program. This helps to choose desirable parents for establishing new breeding population. Besides, better knowledge on genetic diversity could help to sustain long term selection gain (Chowdhury and sharma, 2002).

The knowledge of association between yield and its contributing traits is of great importance in planning a breeding program. As yield is one of the main objectives if a breeder, so it is important to know the relationship between various characters that have direct and indirect effect on yield. The correlation studies provide under complex characters but sometimes may not give a

clear picture under complex situations. The direct effect of a trait and indirect influences of it through other characters on yield would provide a clear picture of relationship that would definitely help the breeder to choose the ideal character for selective breeding program (Khanom *et al.*, 2008). According to Burton (1952), for the improvement of any character through breeding, it is essential to know the extent of variability present in that species, nature of association among the characters and the contribution of different characters towards yield. The success of a plant breeding program depends on the amount of genetic variability exists in nature or the skill of a plant breeder to create variability in the target population so as to perform effective selection.

Now-a-days several seed companies are importing different tomato verities from other countries and supplying to local seed market which fulfill a large demand of seeds among farmers. However, Bangladesh Agricultural Research Institute has (BARI) released 17 open pollinated and eight hybrid tomato varieties so far (some of them already obsolete).

Analysis of genetic diversity of agro-morphogenic traits is useful in selecting diverse parental combinations, reliable classification of accessions, and for exact identification of variety. Therefore an experiment was conducted to get information regarding genetic diversity and genetic relationships among different genotypes on variability, correlation, path co-efficient and genetic diversity analysis between agro-morphogenic traits of tomato, considering the above scheme, to fulfill the following objectives:

(1) To understand the genetic diversity among various tomato genotypes.
(2) To study the genetic relationship between yield and yield contributing characters among the various tomato genotypes.
(3) To assess the correlation among the yield and yield contributing traits.
(4) To know the yield potential genotypes.

CHAPTER II

REVIEW OF LITERATURE

Since tomato is an introduced crop in Bangladesh, being diploid with 12 pairs of chromosoms (2n=24) provides less genetic variability. Tomato is a well-studied crop species for breeding, genetics and genomics in plants. Various resources are accessible now for its research, which can lead to uprising in evaluation of tomato biology (Barone *et al*., 2008). Many studies have been done using different genes to examine its genetic diversity (Carelli *et al*., 2006, Asamizu and Ezura, 2009, Martinez *et al*., 2006). The high degree of genetic uniformity in tomato cultivars is not only strongly influenced by domestication away from the center of origin, but above all by the considerable genetic improvement which, culminated in the achievement of uniformity, apart from the fact that only a limited number of genotypes were used for breeding.

To estimate the genetic variation and diversity in plant germplasm, different methods can be applied such as morphological, biological and molecular markers. Among them morphological markers are used plentifully to study genetic diversity in plant. Use of morphological markers for genetic diversity study is direct, inexpensive and easy (Bernousi *et al.,* 2011). An important form of gene maintenance is the preservation of wild species, local varieties and traditional genotypes in gene banks (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 programs (Balestre *et al.,* 2008; Terzopoulos and Bebel, 2008). Some of the important research findings have been reviewed in this chapter under the following headlines:

2.1 Nomenclature, Origin and distribution of tomato

Well known scientific name of tomato for most of the scientific community is *Solanum lycopersicum* L. the old scientific name of the tomato was *Lycopersicon esculentum* Mill. and widely used from 1768 to 2005. According to “International Plant Name Index” and “Slow Food ® Upstate”, in 1753, Linnaeus placed the tomato in the genus *Solanum* as *Solanum lycopersicum* and in 1768 Philip Miller moved it to its own genus, naming it

Lycopersicon esculentum. This name came into wide use, but was in violating of the plant naming rules. Genetic evidence has now shown that Linnaeus was correct to put the tomato in the genus *Solanum*, making *Solanum lycopersicum* the correct name (Peralta and Spoonar, 2001). However, both names will probably be found in the literature for some time.

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

Tomato originated from south part of America which includes Peru, Bolivia, Chile and Ecuador, where they usually grew wild. Aztecs and Incas were first cultivated tomatoes about 700AD. Tomatoes didn't arrive in Europe until 16^{th} century although it is not known how. It has been said that Spanish Conquistadors brought back tomato in Europe from America. Some legends said that two Jesuit priests brought them to Italy from Mexico. Another group suggested that Columbus brought first tomato to Europe (Anonymous, 2014).

The tomato is native to western South America and Central America (Filippone, 2014). Tomato (*Solanum lycopersicum L.*), is an autogamous species with a narrow genetic base, is a tropical plant and grown in almost every corner of the world. Mexico has been considered the most likely center of domestication of tomato. Italy and Spain are considered secondary centers of diversification (Gentilcore, 2010; Smith, 1994). The cultivated tomato originated in the Peru-Ecuador-Bolivia area of the South American (Vavilov, 1951). Major tomato producing countries are Spain, Brazil, Iran, Mexico, Greece, Russia, China, USA, India, Turkey, Egypt and Italy. The introduction of the species in Europe, from Mexico, was pivotal in the reduction of genetic variability, since in the European habitat tomatoes were generally cultivated in protected environments.

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

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

2. 2 Variability

To achieve the genetic improvement of a crop through a proper breeding program the fundamental key is to assess the amount and nature of variation of plant characters in breeding population. It helps the breeder for improving the selection efficiency. For this reason, many researchers studied variation of various characters in tomato.

The success of any crop improvement program depends on the presence of genetic variability and the extent to which the desirable trait is heritable. Genetic diversity can be estimated using both morphological and molecular markers. The presence of genetic variability in the breeding material has been emphasized by previous researchers (Naz *et al*., 2013; Reddy *et al*., 2013). Some of the previous research reports are discussed here.

Naz *et al*. (2013) conducted a field experiment on the basis of two parameters such as morphological and molecular parameters to study the genetic variation among twenty five tomato accessions that helped in the reliable varietal selection for breeding program. This study revealed that height of plant, fruit color and fruit size show variability. On the other hand by using nineteen exotic collections of tomato, Reddy *et al*. (2013) revealed considerable genetic variability for all the eighteen quantitative characters which was pertaining to the growth, earliness, yield and quality. Fruit weight, plant height and number of fruits per plant contributed to the total variation.

Paul *et al.* (2014) found significant differences among genotypes while working with the genetic variability among the yield contributing traits nand their direct and indirect contribution of these parameters towards the yields and identify better combination as selection criteria for developing high yielding tomato genotypes.

Bhuiyan (2014) conducted an experiment on 18 genotypes to analyze genetic variayion and stated that the number of fruit yield per plant showed highest range of variation with the highest mean value. In case of days to maturity, plant height, number of cluster per plant, number of fruits per cluster, number of fruits per plant and yield per plant showed higher influence of environment for the expression of these characters.

To study genetic variability Mahesh *et al.* (2006) carried out an experiment in 30 genotypes of tomato revealed significant difference for all the characters under study and observed a wide range of variation for plant height, number of branches per plant, fruit weight, fruit length, fruit diameter, fruit set percentage, fruits per plant, fruit yield per plant, ascorbic acid content and total soluble solids. Again, Alam *et al*. (2012) collected many tomato accessions to judge the BARI released varieties and the other commercially available varieties on the basis of their genomic information. They also suggested that Multivariate and biochemical analysis of genetic affinity among the tomato varieties are necessary before setting any program for their improvement.

Morphological trait measurements can provide a simple technique of quantifying genetic variation and simultaneously assessing genotype performance under relevant growing environments (Shuaib *et al*., 2007). Data recorded by Kumari *et al*. in 2007 for days to flowering, days to maturity, number of fruits per branch, plant height etc. and found that there were highly significant differences for all the characters among parents except early yield, total yield and days to flowering. Similarly, A field experiment on 15 advance generation breeding lines of tomato conducted by Singh *et al.* (2005) to study the variation for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene content and dry matter content and observed significant differences among the genotypes under normal conditions, whereas differences were not significant under high temperature conditions. The population mean was higher during November than February planting for all the characters except acid content and TSS.

Mohanty and Prusti (2001) showed considerable genetic variability among 18 indigenous and exotic tomato cultivars for five economic characters (plant height, number of branches per plant, number of fruits per plant, average fruit weight and yield) in Orissa, India during rabi 1998-99.

Agong (2001) found a large and significant variation in the quantitative traits between the accessions while working with 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. The fundamental key to achieve the genetic improvement of a crop through a proper breeding programme is to calculate the amount and nature of variation of plant characters in breeding population.

Shashikanth *et al.* (2010) carried out a field experiment to study the genetic variation among 30 tomato germplasm lines and observed that the range of variation and mean values were high for plant height, days to 50% flowering and average fruit weight. He also observed that high genotypic variance was for most of the characters indicating a high contribution of the genetic component for the total variation. The assessment helps breeder for improving the selection efficiency. Many researchers studied variation of various characters in tomato. Some of those are presented her

2.2.1 Plant height

Ravindra *et al.* (2003) observed significant genotype x environment interaction for plant height. Naz *et al*. (2013) used 25 tomato germplasam to characterize morphologically by comparing the height of plant, leaf length, shape and arrangement, fruit shape and size. This study revealed that height of plant show highest variability. Parthasarathy and Aswath (2002) conducted a study with 23 genotypes of tomato and observed a considerable variability among genotypes for 8 morphological characters. Plant height, fruit number, fruit size were contribute higher variability among them. Kumari *et al*. (2007) observed the highest genotypic coefficient of variation for plant height. Joshi *et al*. (2004) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and noticed that plant height gave the highest heritability (78.82%). Shravan *et al*. (2004) reported significant variation for plant height.

Naime (2016) conducted an experiment on fifteen genotypes of tomato to analyze their diversity and she revealed that plant height showed higher influence of environment for the expression of this character.

Singh *et al*. (2002) carried out a field experiment with 92 tomato genotypes to study genetic variability and reported that the analysis of variance revealed highly significant genetic variation for plant height. The traits characterized by adequate variability may be considered in a hybridization program for yield improvement in tomato. Matin and Kuddus (2001) also reported that phenotypic variance was relatively higher than genotypic variance for plant height. They again observed that genotypic co-efficient of variation was lowering than phenotypic co-efficient of variation indicating influence of environment for expression of this character.

Hannan *et al*. (2007) conducted an experiment, to estimate heterosis and character association in 45 single cross hybrids, obtained from 10 parental lines of tomato for yield and yield component traits. The characters studied were plant height, days to first flowering (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.

2.2.2 Number of branches per plant

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

Singh and Singh (1993) conducted an experiment on heterosis breeding in tomato. Eight cultivars with diverse values for quantitative characters were crossed in a diallel set. Data on yield and nine component traits were recorded for the 28 F1 hybrids and parents. 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.

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) showed higher number of primary branches than the control.

2.2.3 Days to first flowering

Matin and Kuddus (2001) reported significant differences among the 26 tomato genotypes for days to first flowering ranging between 49.67 and 68.33 days. He also reported that the phenotypic variance was comparatively higher than the genotypic variance indicating high degrees of environmental effect for days to first flowering. Farzaneh *et al.* (2013) showed earliness in number of days to first flowering while studying combining abilty from a 9x9 diallele cross. Whereas Monamodi *et al.* (2013) 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, reducing sugars, titratable acidity, ascorbic acid, lycopene, days to flowering, days to maturity, number of fruits per bunch, weight per fruit, fruit length, fruit width, number of fruit bearing branches, 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 acidity, early yield, total yield, and days to flowering.

Biswas and Mallik (1989) observed that a minimum of 66 days was necessary for first flowering for cv. Selectim-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.

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

2.2.4 Number of clusters per plant

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

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

2.2.5 Number of Fruits per cluster

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

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

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 concluded that based on heritability and genetic advance values, effective selection may be made for fruit weight and number of fruits plant -1as fruit yield showed strong positive correlation with number of fruits plant -1 and number of fruits cluster -1. They recommended that number of fruits plant -1 and number of fruits cluster -1 are the

most important character for consideration in a selection program for improvement of yield.

2.2.6 Number of Fruits per plant

Islam *et al.* (1996) reported wide range of genotypic variation for number of fruits per plant. Singh *et al*. (1997) studied variability for yield related characters in 23 genotypes of tomato and reported that phenotypic variation was quite large but genotypic variation was low. The phenotypic and genotypic co-efficient of variation indicated that selection may be made for number of fruits per plant.

Joshi and Singh (2003) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and observed the number of fruits per plant which provide the highest phenotypic and genotypic coefficient of variation. Saeed *et al*. (2007) observed the variation among the accessions. The coefficient of variation was greater in traits such as number of fruits per plant followed by number of flowers per plant and yield per plant.

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

Brar *et al*. (2000) estimated phenotypic and genotypic co-efficient of variation and observed high variability in the characters of number of fruits per plant of 186 genotypes of tomatoes.

Bhutani *et al.* (1989) suggested that maximum genetic improvement would be possible by genetic variability for number of fruits. Sonone *et al.* (1986) estimated the high genotypic and phenotypic co-efficients of variation for fruits per plant.

Reddy and Reddy (1992) evaluated 139 tomato genotypes and estimated phenotypic and genotypic variances, phenotypic and genotypic co-efticients of variation. Considerable variation was observed for number of fruits per plant (4.0—296.5). Islam and Khan

(1991) and Sharma and Rastogi *et al.* (1993) reported significant variations for number of fruits per plant.

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

Mohanty (2003) observed that the number of fruits per plant had positive direct effects on the yield and negative indirect effects on average fruit weight. Saeed *et al*. (2007) observed that the variation between the accessions based on the coefficient of variation was greater in traits such as number of fruits per plant (13.92%), followed by number of flowers per plant (10.75%) and yield per plant (9.99%).

2.2.7 Fruit weight

Kumar *et al.* (2004) and Shravan *et al.* (2004) studied genetic variability with 30 tomato genotypes in Utter Pradesh of India and reported significant difference for average fruit weight among the genotypes. Sahu and Mishra (1995) reported that fruit weight had high genotypic co-efficient of variation in 16 lines of tomato.

Padmini and Vadivel (1997) performed an experiment to study genetic variability of six F2 crosses and their parental cultivars and reported that progeny of cross In Memory 5.30 p. m. X PKM-1 produced the highest mean values for individual. They also reported that fruit weight small difference was observed between genotypic and phenotypic variance for individual fruit weight.

Farzaneh *et al.* (2013) conducted a study and found significant variation due to general combining ability (GCA) as well as specific combining ability (SCA) indicated the importance of additive and non-additive types of gene action in inheritance of all characters except number of fruits per plants Reddy and Reddy (1992) estimated

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

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. Ahmed (1987) reported that a wide range of variation was observed for individual & unit weight among 4 genotypes of tomato. He also reported that genotypic co- efiicient of variation was very high for individual fruit weight in four tomato varieties namely EC32099, HS102, HS107 and Columbia respectively. Kumar and Tewari (1999) also obtained similar results in their experiments with tomato.

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

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

Brar *et al*. (2000) reported that varietal differences were significant among 20 cultivars of tomato for average fruit weight ranged between 24.1g and 76.6g. Matin and Kuddus (2001) reported similar results for average fruit weight in an experiment with 26 tomato genotypes. Singh *et al.* (2002) carried out a field experiment to study genetic variability of fifteen heat tolerant tomato and showed that phenotypic (PCV) and genetic (GCV) coefficients of variation were high for average fruit weight.

2.2.8 Yield per plant

Aditya and Phir (1995) observed highly significant differences for average yield per plant among 44 genotypes of tomato. She also reported that phenotypic variance and

phenotypic co- efficient of variation were higher than genotypic variance and genotypic co-efticient of variation respectively. Ghosh *et al*. (1995) observed highest variation for yield per plant. Singh *et al.* (1997) observed that phenotypic variation was quite higher than genotypic variation for this trait in 27 genotypes of tomato.

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

Dudi *et al*. (1983) reported that genotypic and phenotypic variances were high for average yield per plant. Kumar and Tewari (1999) reported higher genotypic co-efficient of variation for average yield per plant among thirty two tomato genotypes. Brar *et al*. (2000) reported high degrees of variation for average yield per plant among the 186 genotypes tested.

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

Reddy and Reddy (1990) observed considerable variations for yield per plant in 139 tomato varieties. Singh (2009) assessed 48 genotypes for their genetic divergence using Mahalar statistics. They observed that clustering pattern indicated no difference between geographical distribution of genotypes and genetic divergence. They concluded that characters like number of fruits plant -1, average fruit weight, plant height and fruit yield contributed maximum to genetic divergence.

2.3 Heritability and genetic advance

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

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

While working with fifteen genotypes of tomato Naime (2016) found all the characters of her study such as plant height, number of branches per plant, number of flowers per plant, number of fruits per plant etc exhibited the highest value of heritability.

Nur-unnahar (2015) revealed high heritability along with high genetic advance as percent of mean in plant height, individual fruit weight and fruit yield per plant during her working with 28 tomato genotypes to study diversity.

Buckseth *et al*. (2012) found 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. According to Saleem *et al.* (2013) a study of quantitative genetics of yield and some yield related traits. The highest estimates of genotypic and phenotypic coefficients of variability (GCV and PCV) were recorded for number of fruits per plant while fruit width was the most heritable trait. By Narolia (2012) thirteen quantitative characters were studied in 55 genotypes of tomato. High heritability coupled with high genetic advance as per cent of mean was observed for all the characters except days to 50% flowering indicating the presence of additive gene action in the expression of these characters. Shashikanth *et al.* (2010) observed the range of variation and mean values were high for plant height, days to 50% flowering and average fruit weight. He also observed high genotypic variance for most of the characters indicating a high contribution of the genetic component for the total variation.

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

Padda *et al*. (2007) observed that broad sense heritability was highest for number of fruits per plant (96.56%), followed by number of flowers per plant (93.45%), reflecting the

effectiveness of selection in the present germplasm of tomato improvement. Nardar *et al.* (2007) evaluated 20 tomato genotypes and observed high heritability with high genotypic coefficient of variation and genetic gain for fruit weight and fruit yield, which could be improved by simple selection.

Paul *et al.* (2014) found in an experiment that the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for days to germination, fruits per brunch, harvest index and yield per plant of tomato. All characters were highly heritable in broad sense.

Nandpuri *et al*. (1974) observed that heritability estimates were high for fruit size, plant 2 heights and yield per plant in tomato. Expected genetic advance was also high for fruit size, yield and number of fruits per plant. Dudi *et al*. (1983) reported that heritability and a genetic advance-were high for number of fruits per plant, individual fruit weight and yield by per plant. Mallik (1985) reported high genetic advance for plant height, number of fruits per plant, individual fruit weight and yield per plant but low heritability for yield per plant. Abedin and Khan (1986) also reported high values of heritability in broad sense and high genetic advance for plant height, number of fruits per plant and individual fruit weight.

Sonone *et al*. (1986) reported that heritability estimates for fruit number, plant height and individual fruit weight were high in tomato. He also reported that high genetic advance (>30%) was observed for fruit yield, plant height, individual fruit weight and number of fruits per plant. Estimates of high heritability and high genetic advance for number of fruits per plant, individual fruit weight and plant height indicated control by additive genetic effects.

Kasrawi and Amr (1990) reported that pH gave comparatively higher heritability estimates in a study of seven quality characters using F_2 populations. Singh *et al*. (1988) evaluated 32 genotypes for agronomic characters and obtained high heritability values for yield per plant only.

Bai and Devi (1991) evaluated five varieties and nine hybrids of tomato. Heritability estimates of 90% were obtained for plant height, number of fruits per plant and individual fruit weight. Islam and Khan (1991) studied 12 tomato genotypes and reported that

heritability values were high for most of the characters but moderate for days to first flowering, maturity and plant height.

Pujari *et al*. (1995) observed high heritability coupled with high genetic advance for number of fruits per plant, plant height and average fruit weight which indicated additive gene action. Reddy and Reddy (1992) studied heritability and genetic advance in 139 tomato varieties. Heritability values for yield per plant, number of fruits per fruits per plant and average individual fruit weight were 97.99%, 95.96% and 98.46% respectively.

Mittal *et al*. (1996) estimated heritability and genetic advance in 27 genotypes of tomato. High heritability associated with high genetic advance was observed by them indicating the character, predominantly under the control of additive gene, could be improved through selection. Aditya (1995) reported high heritability (in broad sense) with high genetic advance in percentage of mean for number of fruits per plant, individual fruit weight and plant height. However, yield per plant showed moderate heritability and low genetic advance but highest genetic advance as percentage of mean under selection.

Singh *et al*. (1997) estimated heritability and genetic advance in 23 genotypes of tomato. High values of heritability and genetic advance indicated that effective selection may be made for fruit weight and number of fruits per plant. Phookan *et al*. (l998) observed 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.

Vikram and Kohli (1998) reported high heritability and genetic advance for mean fruit weight which suggested that improvement for this character should be fairly straight forward. lslam *et al.* (1996) studied heritabiltiy and genetic advance in 26 diverse genotypes of tomato. High heritability and genetic advance was observed in number of fruits per plant, plant height, fruit yield and individual fruit weight. Prasad *et al*. (1999) estimated heritability in 75 exotic genotypes of tomato and reported very high heritability along with high genetic advance by fruit weight. Brar *et al*. (2000) reported that the number of fruits per plant, total yield per plant and marketable yield per plant had low to

moderate estimates of heritability and genetic advance and number of marketable fruits per plant had high values of heritability and genetic advance.

Mohanty (2003) evaluated 18 genotypes of tomato and revealed high heritability with moderate to high genetic gain for average fruit weight, number of fruits per plant and plant height. Singh *et al.* (2002) reported that heritability was high for all characters except days from fruit setting to red ripe stage and the highest genetic advance was predicted for average fruit weight, followed by shelf life of red ripe fruits.

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

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

Singh *et al.* (2005) estimated heritability and showed that heritability estimates (in the broad sense) were high for all the characters for November planting except for lycopene content. Mahesh *et al.* (2006) estimated heritability and expected genetic advance in 30 genotypes of tomato and observed that fruit weight, fruits per plant and plant height exhibited very high heritability values along with high genetic gain. It indicated the importance of considerable additive gene effects and therefore greater emphasis should be given on these characters while selecting the better genotypes in tomato.

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

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

Pandit *et al.* (2010) evaluated12 varieties of tomato to estimate heritability and reported that high heritability coupled with high genetic advance as percentage of mean for average fruit weight, indicating the control of such character by additive gene. He also recorded that high heritability coupled with low genetic advance as percentage of mean for rest of the characters except pericarp thickness, indicating most of the characters were governed by non-additive genetic components.

Nessa *et al*. (2000) reported high heritability for number fruits per plant, plant height and moderate heritability for yield per plant. Matin and Kuddus (2001) reported high degrees of heritability and genetic advance for fruits per plant, individual fruit weight and number of seeds per fruit. Godekar *et al*. (1992) obtained high values for hetitability along with high genetic advance by fruit weight.

2.4 Correlation and path co-efficient analysis

2.4.1 Correlation between the characters

Since yield is one of the main target for the breeders correlation between yield and yield contributing characters was studied by many breeder. Correlation between the characters is an estimate to evaluate the inter-relationships between the characters which will help the breeders to choose selection techniques. The yield contributing characters are also interrelated among themselves. So, association of characteristics with yield and among its components is important for planning effective selective breeding program for maximization of yield. Such correlation studies may vary due to agro-climatological variations from year to year. If any component of yield has higher heritability than yield itself and there is positive correlation between these, then there may be some possibility to increase in the total yield by selecting that component. But, negative correlation co-efficient among yield components were generally observed indicating selection for any component might not bring improvement for yield. Correlation analysis in tomato revealed that the percent fruit set, average fruit weight, number of primary branches and number of fruit per plant were positively and significantly associated with yield per plant. Many authors have studied correlation between yield and yield contributing characters of tomato. Some pertinent recent literatures are reviewed in this section.

The experiment also carried out by Naime (2016) consisting fifteen genotypes of tomato to study genetic diversity and a significant positive correlation with yield per plant was found in number of branches per plant, number of flowers per plant, number of fruits per plant, single fresh fruit weight at genotypic and phenotypic level while a significant negative correlation was found in the number of fruits per cluster at genotypic and phenotypic level.

Nur-unnahar (2015) conducted an experiment on 28 tomato genotypes to study character association and found significant positive correlation positive direct effect in plant height, number of primary and secondary branches per plant, average fruit weight and width of fruit.

Bhuiyan (2014) conducted an experiment on 18 genotypes and got significant positive correlation with fruit yield per plant in single fruit weight, number of branches per plant

and number of fruits per plant at genotypic and phenotypic level. Non-significant negative correlation with seed yield per plant was also found in plant height while the high significant negative correlation was found in days to maturity, fruits per cluster and % brix content at genotypic and phenotypic level.

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

Mahapatra *et al.* (2013) found fruit yield had positive and significant correlation with plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, and average fruit weight. It was observed that with increase in plant height, there was corresponding increase in number of primary branches per plant, days to 50% flowering and number of flower clusters per plant. Forty nine genotypes of tomato (*Solanum lycopersicum* L.) were evaluated for various quantitative and quality traits by Kumar *et al.* (2013).The character association analysis indicated that total numbers of fruits/plant were significantly and positively correlated with gross yield (g/plant), marketable yield (g/plant), number of marketable fruits/plant and plant height (cm).

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

resulting in more fruit weight. This is supported by the observed strong positive association between fruit number per plant and fruit weight per plant.

Correlation analysis performed by Wagh *et al*. (2007) showed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant along with fruit quality characters such as lycopene, beta -carotene, ascorbic acid and titratable acidity. Kumar *et al*., (2011) studied correlation coefficient analysis for thirty diverse tomato genotypes and noticed that correlation coefficients at the genotypic level were generally higher than the corresponding phenotypic ones and yield per plant was positively and significantly associated with plant height, fruit number per plant, fruit shape index and pericarp thickness. Kumar *et al.* (2006) performed correlation coefficient analysis of 30 tomato genotypes and observed that number of fruits per plant had significant and positive correlation with fruit yield per plant.

Megha *et al*. (2006) studied correlation in exotic tomato cultivars to determine the correlation of 26 tomato cultivars for number of flowers per cluster, flower clusters at first picking, number of fruits per cluster, weight per fruit, yield per plant and total yield. They observed that improvement in yield could be managed by selection for number of flowers per cluster, flower clusters at first picking, number of fruits per cluster and weight per fruit.

Kumar *et al*. (2004) analyzed correlation coefficient of 30 tomato genotypes 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. Highly significant positive correlation was observed between the number of fruits per plant and yield and between plant height and number of fruits per plant while negative correlation was noticed between the number of primary branches per plant and number of fruits per plant (Singh *et al*., 2005).

Mohanty (2003) studied correlation coefficient analysis of 18 tomato cultivars and reported that yield was significantly and positively correlated with number of fruits per plant and number of day to harvest, and significantly but negatively correlated with plant height, number of branches per plant and average fruit weight and the number of fruits

per plant was inversely related to average fruit weight. He also reported that most early cultivars were small fruited and low yielders.

Mohanty and Prusti (2001) reported that the phenotypic and genotypic correlations of fruit yield were significant and positive with days to first harvest, number of branches and fruits/plant, significant and negative with plant height and average fruit weight and number of fruits per plant was inversely related with average fruit weight. Harer *et al*. (2002) studied correlation of thirty-seven tomato genotypes and showed that the number of fruits per cluster and number of fruits per plant were significantly and positively correlated with fruit yield per plant, whereas the number of primary branches per plant, fruit weight had negative association with fruit yield. The negative correlation was observed between fruit weight and fruit number, plant height and fruit weight, fruit weight and fruit yield and plant height by Padma *et al.* (2002). Tiwari *et al*. (2002) observed that the highest positive and significant association was between the yield and length of fruit. At the genotypic level, the highest positive association was observed between the yield and length of fruit. 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.

Dhankar *et al*. (2001) reported the average fruit weight under normal condition showed the highest positive effect on yield, therefore selection for average fruit weight, number of fruits per plant and number of fruits per cluster is important for improvement of fruit yield. Dhaliwal *et al*. (2002) studied genetic parameters and correlations concerning fruit weight, yield plant^{-1}. The correlation studies indicated that it would be possible to develop firm fruited - high yielding true breeding lines. Matin and Kuddus (2001) studied phenotypic and genotypic correlations of 13 qualitative and quantitative characters of 26 genotypes of tomato and found that individual fruit weight had significant positive correlations with plant height and yield per plant. Sharma *et al*. (1993) concluded from the data on eight yield components which he recorded in eighteen genetically diverse genotypes that when selection 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.

Anitha *et al.* (2007) found that genotypic correlations were higher than their corresponding phenotypic values and oxalate content showed significant positive correlation with seediness and a non-significant positive correlation with lycopene, TSS and locule number. Naidu *et al*. (1993) studied correlation coefficient analysis in 13 tomato genotypes and revealed that plant height, number of branches per plant, plant spread, fresh plant weight, number of fruiting clusters, number of days to 50% flowering, number of fruits per cluster, and number of fruits per plant should be considered for the enhancement of the yield of tomato. Prasad *et al.* (1999) observed very high and significant positive correlation co-efficient were between yield and fruit weight. Das *et al.* (1998) studied correlation co-efficient in fruit characters of tomato. They observed significant positive correlation of fruit yield per plant with number of fruits per plant. Aditya *et al.* (1995) studied phenotypic and genotypic correlation co-efficient to find out the associations between eight characters of 44 genotypes of tomato. He reported that yield of fruits per plant showed significant positive correlations with plant height and number of fruits per plant; and insignificant positive correlation with weight of individual fruit (phenotypically) and number of seeds per fruit. Abedin and Khan (1986) studied correlation of 20 cultivars of tomato and found that yield per plant was negatively correlated with number of fruits per plant but positively and significantly correlated with individual fruit weight and plant height. Mallik (1985) studied phenotypic and genotypic correlations in an experiment with 19 varieties of tomato and observed that individual fruit weight had positive significant correlations with plant height and yield.

Manivannan *et al*. (2005) carried out correlation coefficient analysis in cherry and observed that fruit yield was significantly and positively correlated with the number of leaves and fruit weight. Arun *et al.* (2003) observed that in case of tomato yield per plant was positively and significantly correlated with average fruit weight and plant height. Joshi *et al*. (2004) performed correlation analysis of 37 tomato genotypes and showed that yield per plant was positively and significantly correlated with average fruit weight, fruit length, plant height and harvest duration. The average fruit weight was positively correlated with fruit length, fruit breadth. However, fruit weight was negatively

correlated with the number of fruits per plant, number of fruits per cluster and ascorbic acid content.

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

Path co-efficient analysis provides an exact picture of relative importance of direct and indirect influence of each of the component character towards the desired character. It also helps in further partitioning the correlation coefficient into direct and indirect effects. Path co-efficient is a standard tool which measures the direct influence of one character upon another and permits the separation of correlation co-efficient into components of direct and indirect effects. Path co-efficient between yield and yield contributing characters provides an exact picture of the relative importance of direct and indirect influences of each other component characters on fruit yield. It also provides valuable additional information for improving fruit yield via selection for its yield components. Recent publications involving path co-efficient analysis between yield and components of yield relevant to the present study are reviewed in this section:

The experiment also carried out by Naime (2016) consisting fifteen genotypes of tomato to study genetic diversity. This experiment revealed that path coefficient analysis showed single fruit weight had the positive correlation with fruit yield per plant. Positive direct effect was also found in plant height, number of branches per plant, number of flower per plant, days to first flowering, number of clusters per plant and number of fruits per plant.

The germination percent, height of first leaf appearance, days to first flowering and harvest index exhibited direct effect on fruit yield of tomato by a field experiment with 30 genotypes which is conducted by Paul *et al.* (2014).

Bhuiyan (2014) conducted an experiment on 18 genotypes and estimate that plant height, number of cluster per plant and number of fruit per cluster had negative direct effect with fruit yield per plant. Number of fruit per cluster had a high negative correlation to fruit yield per plant Fruits per plant had positive direct effect on yield and it had a positive correlation to fruit yield per plant.

Meena and Bahadur (2015) evaluated nineteen indeterminate tomato germplasm to estimate the nature and magnitude of associations of different characters with fruit yield

and among themselves. 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 through selection based on no. of flowers per plant, fruits per plant and fruit weight. Low residual effect indicates that the characters used explained almost all variability towards yield. Monamodi *et al.* (2013) used six determinate tomatoes. Results obtained suggest that fruit number and single fruit weight are relevant components to use as selection criteria for improving tomato yield. Path coefficient analysis results showed that marketable fruit number and single fruit weight were directly related to yield. Golani *et al.* (2007) performed path analysis and confirmed that the 10-fruit weight had the highest positive direct effect. Rani *et al*. (2010) conducted a field experiment to study path coefficient for yield components and quality traits in 23 hybrids of tomato and exhibited that fruit weight had the highest positive direct effect on yield per plant, while, fruit weight was also having high positive indirect effect on yield per plant.

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

Singh *et al*. (2005) performed path analysis between yield and yield contributing characters of 92 tomato genotypes and reported that number of fruits per plant exerted the high positive direct effect on yield followed by average weight per fruit, number of primary branches per plant, plant height, days to 50% flowering, number of fruits per cluster and days to first fruit harvest. However, days to first fruit set, number of primary branches per plant, plant height, number of fruit clusters per plant. Singh (2005) reported that the genotypic and phenotypic path coefficient studies described that number of fruits per plant had the maximum positive effect on yield followed by average fruit weight. Regarding indirect effects, it was observed that number of fruits per plant exhibited positive indirect effect towards fruit yield via number of branches per plant; it was negative via plant height, days to 50 per cent flowering. Singh and Cheema (2006) have revealed that positive direct effect of number of fruits per plant on yield. It was also

reported by Kumar *et al*. (2004). Its positive indirect effects through average fruit weight mainly contributed towards its strong association with yield.

Mayavel *et al.* (2005) reported that number of branches per plant had the highest positive direct effect on fruit yield. Whereas, plant height, number of fruits per cluster, number of fruits per plants and number of locules per fruit had negative direct effects on fruit yield. Arun *et al*. (2003) revealed that the number of fruits per plant is the most important yield contributing character followed by plant heighst through path co-efficient analysis. Mohanty (2003) conducted a field experiment to study path coefficient analysis of eighteen tomato cultivars and observed that the number of fruits per plant and average fruit weight had positive direct effects on the yield and negative indirect effects on each other. Kumar *et al*. (2004) performed path analysis of thirty diverse tomato genotypes and indicated that fruit number per plant had the highest positive direct effect on yield per plant followed by average fruit weight. Bodunde (2002) carried out a field experiment on path coefficient analysis and observed that plant height and fruit diameter directly affected yield in tomato.

Verma and Sarnaik (2000) conducted a field experiment to perform path analysis of yield components in thirty tomato genotypes and observed that total number of fruits per plant, average weight of fruit and number of branches per plant exhibited positive as well as high direct effects. Harer *et al*. (2002) carried out a field experiment to study path analysis of thirty-seven tomato genotypes and reported that number of fruits per cluster; average fruit weight and number of fruits per plant had direct maximum effects on fruit yield. Mohanty (2003) performed path analysis and showed that the number of branches per plant and average fruit weight exerted high positive direct effect on yield and high positive indirect effect with each other. Padma *et al.* (2002) performed path analysis and revealed that number of branches, fruit weight, fruit length and number of fruits per plant exhibited positive effect on yield per plant at the genotypic and phenotypic levels. Matin and Kuddus (2001) observed that the maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant. He also reported that days to first flowering, plant height and number of seeds per fruit had negative direct effect on yield per plant. Domini and Maya (1997) evaluated 18 tomato varieties for the

relationship of six yield components to yield in two different seasons. They reported that fruit number per plant was the most important character having a direct effect on yield either in early sowing.

Supe and Kale (1992) studied path analysis of seven different characters of twelve indigenous varieties of tomato and observed that plant height had negative direct effect on yield per plant. Islam and Khan (1991) observed that fruits per plant, average fruit weight, plant height and days to first flowering had positive direct effects on yield of tomato. Gomez (1987) reported that days to first flowering has negative direct effect on yield of tomato. Gorbatenko and Gorbatenko (1985) carried out path co-efficient analysis of economically useful characters of tomato and found that individual fruit weight had an appreciable direct effect on yield per plant.

CHAPTER III

MATERIALS AND METHODS

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

3.1 Experimental site

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

3.2 Planting materials

A total of fifteen genotypes of tomato were used in this experiment. The materials were collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultureal University, Dhaka and Plant Genetic Resource Centre (PGRC) and Horticulture Research Centre (HRC) at Bangladesh Agricultural Research Institute (BARI), Gazipur. The name and source of collection of these genotypes are presented in Table 1.

3.3 Climate and soil

Experimental site was located in the subtropical climatic zone, set aparted by plenty of sunshine and moderately low temperature prevails during October to March (Rabi season) which is suitable for tomato growing in Bangladesh. The soil was sandy loam in texture having pH 5.46- 5.62. Weather information and physicochemical properties of the soil are presented in (Appendix II and Appendix III respectively).

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

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Origin
1	G_1	SAU Tomato-1	SAU
2	G_2	SAU Tomato-2	SAU
3	G_3	SAU Tomato-3	SAU
4	G_4	SAU Tomato-4	SAU
5	G_5	Sl005	GEPB, SAU
6	G_6	Sl006	GEPB, SAU
7	G_7	Sl007	GEPB, SAU
8	G_8	BARI Hybrid-4	PGRC, BARI
9	G_9	BARI Hybrid-5	PGRC, BARI
10	G_{10}	BARI Tomato-14	PGRC, BARI
11	G_{11}	BARI Tomato-16	PGRC, BARI
12	G_{12}	BARI Tomato-2	PGRC, BARI
13	G_{13}	BARI Tomato-3	PGRC, BARI
14	G_{14}	BARI Tomato-11	PGRC, BARI
15	G_{15}	BARI Tomato-15	PGRC, BARI

SAU= Sher-e-Bangla Agricultural University, PGRC=Plant Genetic Research Centre, BARI=Bangladesh Agricultural Research Institute

3.4 Seed bed preparation and raising of seedling

The sowing was carried out on November 02, 2016 in the seedbed. Before sowing, seeds were treated with Bavistin for 5 minutes. Seedlings of all genotypes were raised in seedbeds in the Sher-e-Bangla Agricultural University, Dhaka-1207 farm unit. Seeds were sown in rows spaced at 10 cm apart, beds were watered regularly. Seedlings were raised using regular nursery practices. Recommended cultural practices were taken up before and after sowing the seeds. When the seedlings become 27 days old, those were transplanted in the main field.

3.5 Design and layout of the experiment

The experiment was laid out and evaluated under field condition during Rabi 2016- 17 in Randomized Complete Block Design (RCBD). There were 15 genotypes and three replications. The spacing was 60 cm × 60 cm. The plot size was 14 m × 20 m. The date of transplanting was 29th November 2016.

3.6 Land preparation

The experimental plots were ploughed and brought into a fine tilth and raised the nursery bed, applied the recommended dose of fertilizers and farm yard manures (FYM). Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on November 20, 2016.

3.7 Transplanting of seedlings

The seedlings were raised in the seedbed in usual way and 27 days old seedlings were transplanted in the main field on November 29, 2016. The transplanted seedlings were watered regularly to make a firm relation with roots and soil to stand along.

3.8 Manure and fertilizers application

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

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

Sl. No.	Fertilizers/ Manures	Dose	
		Applied in the plot	**Quantity/ha**
1.	Urea	15.5 kg	550 kg
2.	TSP	12 kg	450 kg
3.	MOP	7 kg	250 kg
4.	Cow dung	280 kg	10 ton

3.9 Intercultural operations

When the seedlings were well established, first weeding was done uniformly in all the plots. Second weeding was done after 20 days of the first one. Mechanical support was provided to the growing plants by bamboo sticks to keep them erect. During early stages of growth, pruning was done by removing some of the lateral branches to allow and plants to get more sunlight and to reduce the self-shading and incidence of increased insect infestation. Thinning and gap filling, staking, pesticide application, irrigation and after-care were also done as per requirement (Plate 1).

3.10 Harvesting and processing

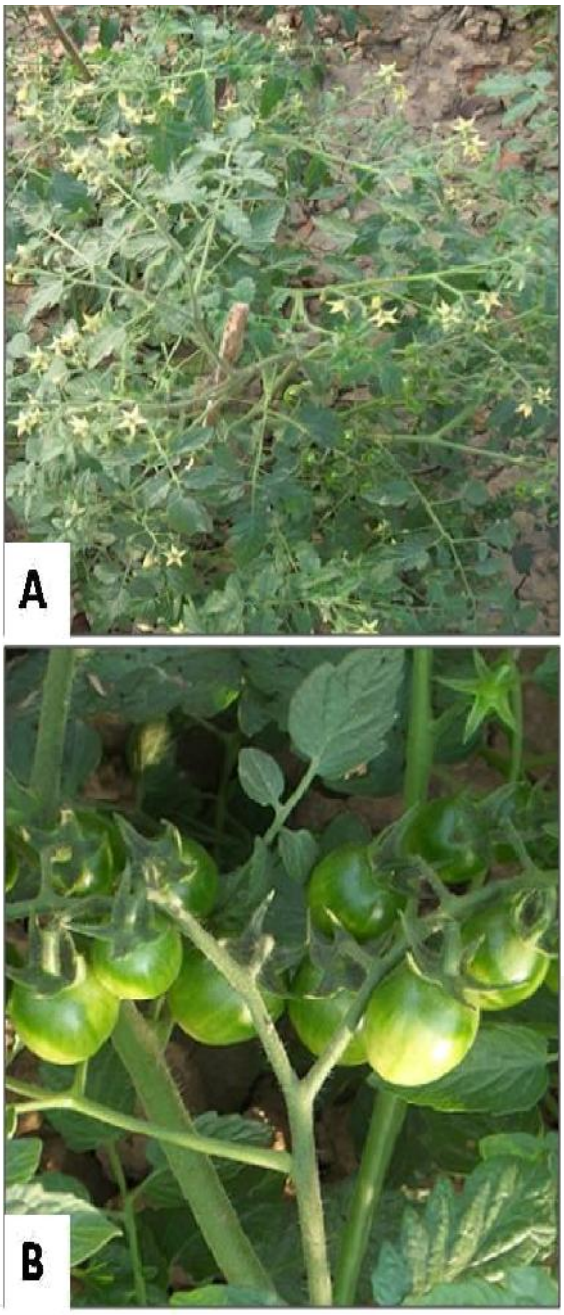
All of the tomato varieties used in this experiment was indeterminate types. So, harvesting continued for about one and half month because fruits of different lines matured progressively at different dates and over long time. The fruits per entry were allowed to ripe and then seeds were collected and stored at 4^{o}C for future use. Harvesting was started from March 2, 2017 and completed by April 26, 2017. Raising of seedlings, growing condition of plants, flowering and fruiting stages of tomato plant are displayed in Plate 2 and Plate 3. A view of the experiment in the field with ripen fruits in plant is illustrated in Plate 4.

3.11 Data recording

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

Plate 1. Different Intercultural operations A. tagging B. manuring

Plat 2. Different stages of tomato plant in the experimental site A. Raising seedlings in seed bed B. Growing condition of tomato plant



Plat 3. Different stages of the mature tomato plant in the experimental field. A. Flowering stage of tomato plants B. Fruiting stage of a single tomato plant

Plate 4. Ripen fruits in the experimental plot in the farm of Sher-e-Bangla Agricultural University

3.11.1 Plant height (cm)

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

3.11.2 Days to first flowering

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

3.11.3 Number of branches per plant

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

3.11.4 Number of clusters per plant

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

3.11.5 Number of fruits per cluster

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

3.11.6 Number of fruits per plant

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

3.11.7 Fruit weight (g)

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

3.11.8 Fruit yield per plant (kg)

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

3.11.9 Total yield per hector (ton)

Total yield per plot was calculated first from the data yield per plant. Than the result converted to total yield per hector and expressed in ton.

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 program. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.12.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of square

r = number of replications

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

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

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

Where,

EMS = Mean Square Error

3.12.2 Estimation of genotypic and phenotypic co-efficient of variation

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

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

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, $GA = K. h^2. \sigma_p$

Or Genetic advance, GA = K. $\frac{\pm^2 g}{\pm^2 ph}$.$\pm ph$

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 percentage of 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 co-efficient:

Simple correlation co-efficient (r) was estimated with the following formula (Singh and Chaudhary, 1985).

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

Where,

$\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

3.12.7 Estimation of genotypic and phenotypic correlation co-efficient

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

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

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

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 (eight equations in this example) is required to be formulated as shown below:

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

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

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

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

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

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

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

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

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

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,….9)

1 = Plant Height (cm)

2 = Days to first flowering (DAT)

3 = Number of branches per plant

4 = Number of clusters per plant

5 = Number of fruit per cluster

6 = Number of fruits per plant

7 = Fruit weight (gm)

8 = Fruit yield per plant (kg)

9= Yield per hectare (ton)

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

Where,

$P_{1.y}$, $P_{2.y}$,$P_{3.y}$. ……. $P_{9.y}$ = Path coefficient of the independent variables 1, 2, 3,….,9 on the dependent variable y, respectively.

$r_{1.y}$, $r_{2.y}$, $r_{3.y}$, …., $r_{9.y}$ = Correlation coefficient of 1, 2, 3,…., 9 with y, respectively.

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

$P^2_{RY} = 1- (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} +……..+ r_{9.y}P_{9.y})$

Where,

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

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 parent selection in hybridization program 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 program. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.12.10 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. 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)

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

3.12.14 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

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

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).

$$\text{Average intra-cluster distance} = \frac{\sum D_{i2}}{n}$$

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).

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

Where,

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in clusters 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 program

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

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

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

CHAPTER I

RESULTS AND DISCUSSION

The experiment was conducted for genetic diversity analysis of different genotypes of tomato (*Solanum lycopersicum* L.) using yield contributing traits. This chapter comprises the presentation and discussion of the findings obtained from this experiment. The fruits were harvested when they began the color change from green to red. Fruits of the studied genotypes are presented in Plate 5. The data pertaining to nine characters have been presented and statistically analyzed with the possible interpretations given under the following headings:

4.1 Analysis of variance

Analysis of variance showed significantly high variability among the genotypes for all the character studied such as plant height (PH), number of branches per plant (NBP), days of first flowering (DFF), number of cluster per plant (NCP), number of fruits per cluster (NFC), number of fruits per plant (NFP), fruit weight (FW), yield per plant (YPP), and total yield (YPH) (Appendix IV). The variation due to replication was non-significant for all the characters studied.

4.2 Genetic variability, heritability and genetic advance

The mean values for each character of all the genotypes are shown in Table 3. Performance of the genotypes is described below for each character. The extent of variation among the genotypes in respect of nine characters was studied and mean sum of square, phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2b), genetic advance (GA), genetic advance in percent of mean and coefficient of variation (CV) presented in Table 4.

4.2.1 Plant height (cm)

Significant differences were observed among the genotypes for plant height which ranged from 118.33 cm (G_{15}) to 54.00 cm (G_4) with mean value 85.76 cm. (Table 3). Naz *et al*. (2013), Ravindra *et al*. (2003), Shravan *et al*. (2004) and Prasad *et al*. (1999) were also found similar significant variation for plant height. The phenotypic and genotypic

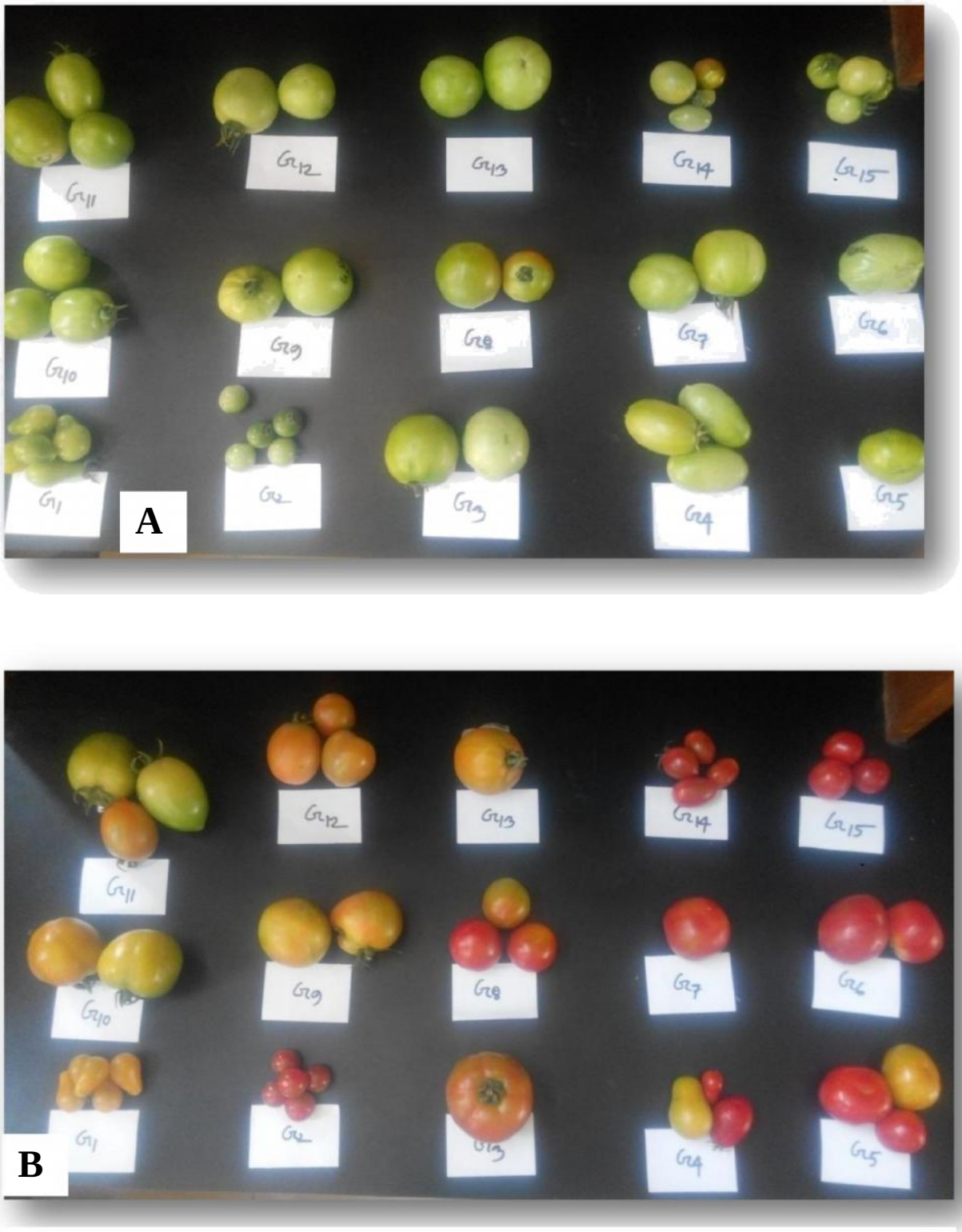


Plate 5. Studied genotypes of tomato A. Green stage B. Ripen stage

Table 3: Mean performance of growth, yield and yield contributing parameters

Genotypes	PH	NOB	DFF	CPP	FPC	FPP	FW	YPP	YH
G_1	100.00	11.33	43.00	18.00	7.67	196.00	14.94	2.04	35.96
G_2	92.67	8.00	34.33	14.00	11.00	199.67	10.00	1.45	32.58
G_3	94.33	9.33	44.33	4.00	3.00	36.00	109.55	4.50	85.42
G_4	54.00	6.67	47.33	4.67	3.67	105.00	58.43	5.20	85.46
G_5	85.33	6.67	34.00	6.67	3.00	20.00	84.52	1.69	29.72
G_6	100.00	7.67	37.00	5.00	3.33	16.33	97.17	1.58	27.85
G_7	99.00	8.00	32.00	8.00	2.67	20.67	98.75	2.05	36.18
G_8	58.67	7.67	31.00	14.67	5.33	77.33	76.30	4.48	84.00
G_9	62.67	8.67	35.33	9.33	4.00	36.33	109.35	3.97	70.07
G_{10}	80.33	10.00	36.00	10.00	5.67	57.00	100.61	4.32	84.91
G_{11}	86.00	8.33	37.00	8.33	4.33	35.33	100.00	4.44	83.61
G_{12}	69.67	10.67	36.00	9.00	3.67	55.00	88.08	5.20	85.26
G_{13}	70.33	9.00	38.00	8.33	3.33	27.33	99.51	2.73	48.20
G_{14}	115.00	12.67	36.00	20.00	11.33	184.00	9.50	1.12	25.63
G_{15}	118.33	10.00	28.67	12.33	6.00	72.33	26.95	1.94	34.28
Mean	**85.76**	**8.98**	**36.67**	**10.16**	**5.20**	**75.89**	**72.24**	**3.11**	**56.61**
$LSD_{0.05}$	**30.950**	**5.561**	**7.218**	**10.376**	**2.424**	**24.669**	**24.851**	**1.567**	**27.654**
CV(%)	**12.07**	**18.37**	**6.75**	**32.28**	**15.33**	**12.99**	**10.70**	**16.84**	**16.85**

PH- Plant height(cm), **NOB**- number of branches, **DF**- Days to first flowering (DAT), **CPP**-Clusters per plant, **FPC**- fruits per cluster, **FPP**- Fruits per plant, **FW**- Fruit weight(g), Y**PP**-Yield per plant (kg) and **YH**- Yield per hectare (ton).

Table 4: Estimation of genetic parameters in nine characters of fifteen genotypes of tomato

Traits	GenMS	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA	GA (% mean)	CV(%)
PH	1161.68**	352.36	104.59	456.95	22.15	12.07	25.23	77.11	33.96	40.08	12.07
NOB	9.10**	1.91	3.38	5.28	13.81	18.37	22.98	36.09	1.71	17.09	18.37
DF	39.97**	11.43	5.69	17.12	9.57	6.75	11.72	66.77	5.69	16.12	6.75
CPP	101.57**	29.94	11.76	41.69	51.52	32.28	60.80	71.80	9.55	89.93	16.83
FPC	23.56**	7.64	0.64	8.28	52.94	15.34	55.12	92.25	5.47	104.76	15.33
FPP	11811.26**	3914.94	66.44	3981.38	99.70	12.99	100.54	98.33	127.81	203.65	12.99
FW	4757.66**	1563.41	67.42	1630.84	51.50	10.69	52.60	95.87	79.75	103.87	10.70
YPP	405.81**	132.05	9.65	141.70	62.28	16.84	64.52	93.19	22.85	123.86	16.84
YH	3513.83**	1143.44	83.50	1226.94	62.34	16.85	64.58	93.19	67.25	123.98	16.85

PH- Plant height(cm), **NOB**- number of branches, **DF**- Days to first flowering (DAT), **CPP**-Clusters per plant, **FPC**- fruits per cluster, **FPP**- Fruits per plant, **FW**- Fruit weight(g), Y**PP**-Yield per plant (kg) and **YH**- Yield per hectare (ton).

variance was observed 456.95 and 352.36, respectively (Table 4) with large environmental influence. The phenotypic co-efficient of variation (25.23) and genotypic co-efficient of variation (22.15) were revealed higher influence of environment for plant height (Table 4 and Figure 1). Kumari *et al*. (2007) obtained highest genotypic coefficient of variation which disagree with this result. Singh *et al.* (2002) showed that the phenotypic coefficient of variation was greatest for this character. Similar observations were made by Matin and Kuddus (2001). The heritability estimates for this trait was high (77.11%) with high genetic advance (33.96%) and genetic advance in percent of mean (40.08%) (Table 4 and Figure 2) indicated that most likely the heritability was due to additive gene effects and selection for this character might be effective. Bai and Devi (1991), Kumari *et al.* (2007), Mahesha *et al.* (2006), Singh *et al.* (2006), Singh *et al.* (2005) and Joshi *et al*. (2004) also reported similar results.

4.2.2 Number of branches per plant

Number of branches per plant in tomato showed significant difference where the highest number of branches was found 12.67 in G_{14} and the lowest was recorded 6.67 in G_4 and G_5 with mean value 8.98 (Table 3). The phenotypic variance (5.28) was much higher than the genotypic variance (1.91). The genotypic co-efficient of variation and phenotypic co-efficient of variation were 13.81 and 22.98 respectively (Table 4) indicating that the phenotypic expression of this trait is highly governed by the environment. Singh *et al*. (2002) also showed that the PCV was higher than GCV for number of primary branches per plant. The heritability estimates for this trait was moderate (36.09), genetic advance was low (1.71%) and genetic advance in per cent of mean (17.09) (Table 4 and Figure 2) were found moderate, revealed that this trait was governed by non-additive gene action. Moderate heritability and low genetic advance for this character was also observed by Kumar *et al.* (2004).

4.2.3 Days to first flowering

The variance due to days to first flowering showed that the genotypes differed significantly and ranged from 28.67 days after transplanting (DAT) in G_{15} to 44.33 DAT in G_3 with mean value 36.67 days after transplanting (DAT) (Table 3). The genotypic variance and phenotypic variance for this trait were 11.43 and 17.12, respectively (Table 4). The phenotypic variance appeared to be high than the genotypic variance

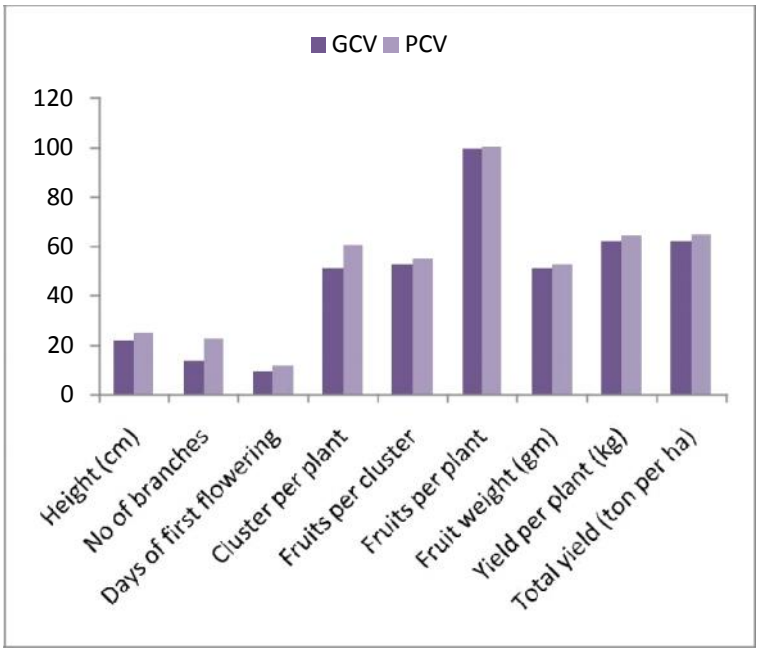


Figure 1. Genotypic co-efficient of variation and genotypic co- efficient of variation

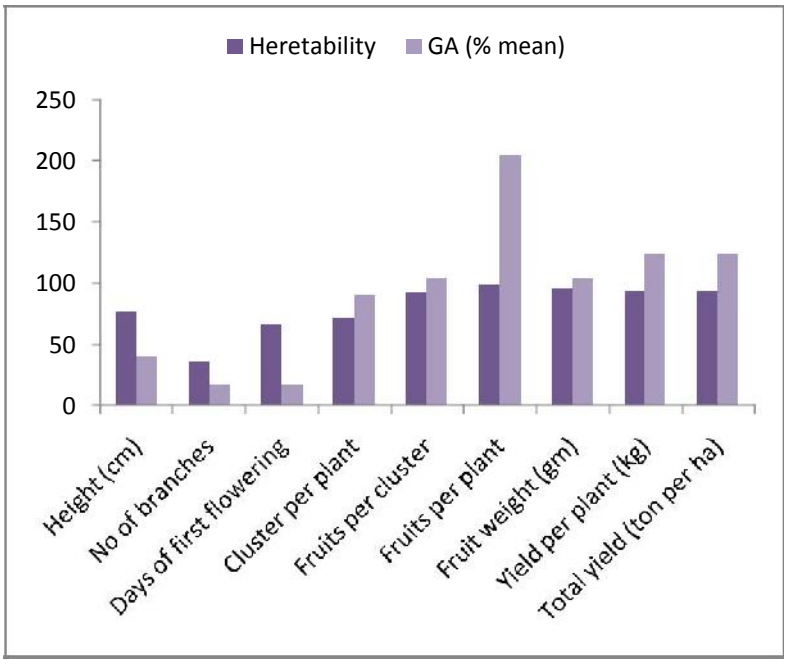


Figure 2. Heritability and genetic advance at percent mean of different genotypes

suggested considerable influence of environment on the expression of genes controlling this trait. The genotypic co-efficient of variation (GCV) (9.57) was less than phenotypic co-efficient of variation (PCV) (11.72) but difference was not so high which indicated presence of negligible variability in this trait (Table 4). Therefore, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Similar findings were reported by Farzaneh *et al.* (2013) and Kumari *et al.* (2007). Matin and kuddus (2001) also found similar results in tomato. In contrast Monamodi *et al.* (2013) and Aditya *et al*. (1995) found insignificant difference in days to first flowering. The heritability estimates for days to first flowering was high (66.77 %) with low genetic advance (5.69 %) and genetic advance in percentage of mean
(16.12 %) which was indicative of no-additive gene action and high heritability exhibited due to favorable environment not genotypes. Selection for this character might not be effective. Islam and Khan (1991) reported high heritability for days to first flowering.

4.2.4 Number of clusters per plant

Cluster per plant showed significant difference among the genotypes which was ranged from 4.00 in G_3 to 20 in G_{14} their mean was 10.16. Genotypic variance and phenotypic variance were 29.94 and 41.69, respectively. GCV (51.52) and PCV (60.80) values revealed that the influence of environment was high. Similar PCV and GCV were also observed by Singh *et al.* (2002). Heritability (71.80%) for this trait was high with low genetic advance (9.55%) and high percent mean of genetic advance (89.93%) which indicated non-additive gene action. High heritability due to good environment and selection for this character might not be good. In contrast, high heritability coupled with high genetic advance was obtained by Singh *et al*. (2002).

4.2.5 Number of fruits per cluster

Number of fruits per cluster showed significant difference among the genotypes which was ranged from 2.67 in G_7 to 11.33 in G_{14} their mean was 5.20. Genotypic variance and phenotypic variance were 7.64 and 8.28, respectively with very low environmental influence. GCV (52.94) and PCV (55.12) values revealed that the influence of environment was low. The observations found by Singh *et al*. (2002) were not similar. Moderate PCV and GCV were found by Aradhana and Singh (2003) also. Heritability (92.25%) for this trait was high with low genetic advance (5.47%) and high percent mean

of genetic advance (104.76%) which indicated non-additive gene action. High heritability due to good environment and selection for this character might not be rewarding. Moderate heritability and moderate genetic gain for this character were also observed by Joshi *et al.* (2004).

4.2.6 Number of fruits per plant

From the current study we observed that the maximum range for number of fruits per plant was found 199.00 in G_2 and the minimum was recorded 16 in G_6 and mean was 75.89 (Table 3). The difference between genotypic (3914.94) and phenotypic (3981.38) variances indicated a very high environmental influence (Table 4). The difference between phenotypic coefficient of variation (100.54) and genotypic coefficient of variation (99.70) was low, which indicated presence of low variability among the genotypes (Table 4). Singh *et al.* (2002), Saeed *et al.* (2007) and Joshi and Singh (2003) found same result in case of number of fruits per plant. The heritability estimated for this trait was high (98.33%) accompanied with high genetic advance (127.81%) and genetic advance in percent of mean (203.65%), revealed that this character was governed by additive gene and selection for this character would be effective. This character showed high heritability coupled with high genetic gain which is supported by Ara *et al.* (2009) and Saeed *et al.* (2007).

4.2.7 Fruit weight (g)

A significant difference were found within fifteen genotypes of tomato for the character single fruit weight where the maximum single fruit weight was recorded 109.55 g in G_3 and the minimum was recorded 9.50 g in G_{14} with mean value 72.24 g (Table 3). The genotypic variance (1563.41) and phenotypic variance (1630.84) for fruit weight was very high (Table 4). The difference between genotypic co-efficient of variation (51.50) and phenotypic co-efficient of variation (52.60) was close to each other, proved that environment has little influence for the expression of this character. Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. High GCV and PCV for average fruit weight were also noticed by Singh *et al*. (2002) and Manivannan *et al*. (2005). High heritability (95.87%) associated with high genetic advance in percent of mean (103.87%) and moderated Genetic advance (79.75%) (Table 4) was observed indicating fruit weight governed by

additive gene and selection would be effective. Ara *et al.* (2009), Pandit *et al.* (2010) and Singh *et al.* (2006) also supported the findings.

4.2.8 Yield per plant (g)

Highest fruit yield per plant was found 5.20 kg in G_4 and in G_{12} and the lowest was recorded 1.12 kg in G_{14} with mean value 3.11 kg (Table 3). The phenotypic variance (5317.03) found higher than genotypic variance (5256.49) (Table 4), suggested considerable influence of environment on the expression of the genes controlling this character. The phenotypic coefficient of variation and genotype coefficient of variation were 6.30 and 6.26, respectively for fruit yield per plant, which indicating that significant variation exists among different genotypes which made the trait effective for selection. Similar findings supported by Singh *et al.* (2006) and Manivannan *et al*. (2005). Estimation of high heritability (98.86%) for fruit yield per plant with high genetic advance (148.50 %) and low Genetic advance of % mean (12.83 %) (Table 4) revealed that this character was governed by additive gene and provides opportunity for selecting high valued genotypes for breeding program. High heritability and high genetic advance was also observed by Anupam *et al.* (2002).

4.2.9 Yield per hectare (ton)

Total yield per hector (ton) showed significant difference among the genotypes which was ranged from 25.63 ton in G_{14} to 85.46 in G_4 their mean was 56.61. Genotypic variance and phenotypic variance were 1143.44 and 1226.94, respectively with very high environmental influence. GCV (62.34) and PCV (64.58) values revealed low to moderate environment influence. Heritability (93.19%) for this trait was high with high genetic advance (67.25%) and high percent mean of genetic advance (123.98%) which indicated additive gene action. High heritability was due to additive gene effect and selection would be effective. Ara *et al.* (2009) also found the same result.

4.3 Correlation Co-efficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with fruit yield. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by Singh and Chaudhary (1985). As we know yield

is a complex product being influence by several inter-dependable quantitative characters. So selection may not be effective unless the other contributing components influence the yield directly or indirectly. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). Phenotypic and genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of tomato are given in Table 5 and Table 6.

4.3.1 Plant height (cm)

Plant height had a significant positive correlation with both no. of branch and fruits per plant at genotypic level (0.5915 and 0.4814) but at phenotypic level both the character had a non-significant positive correlation (0.4582 and 0.4749) (Table 5 and Table 6 and Figure 3). Again plant height had non-significant negative correlation with days to first flowering (DAT) (-0.2921), fruit weight (-0.4375) and yield per hectare (-0.1028) at genotypic level and at phenotypic level found the same result for those characters which is supported by Mohanty (2003). Plant height had also non significant positive correlation with number of clusters per plant, number of fruits per cluster.

4.3.2 Number of branches per plant

The number of branches per plant had highly significant positive correlation with clusters per plant (0.812) and fruits per plant (0.7971) at genotypic level (Table 5). At phenotypic level clusters per plant (0.6499), fruits per cluster (0.5264) and fruits per plant (0.632) were found in a significant positive correlation with no. of branch (Table 6). Monamodi *et al*. (2013) found more branch number in a plant will produce more fruits. But a negative correlation between the number of branches per plant and number of fruits per plant was noticed by Singh *et al*. (2005). Yield per plot (0.4949), yield per hectare (0.4949) and fruits per cluster (0.695) gave a significant positive correlation with no. of branches per plant at genotypic level. Yield per plant and yield per hectare gave a non-significant positive correlation with this character at phenotypic level (table 6). A positive

Table 5: Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of tomato

	PH	NOB	DF	CPP	FPC	FPP	FW	YPP	YH
PH		0.5915*	-0.2921	0.3581	0.4681	0.4814*	-0.4375	-0.1025	-0.1028
NOB			-0.1266	0.812**	0.695*	0.7971**	-0.438	0.4949*	0.4949*
DF				-0.6074*	-0.4009	-0.4253	0.483*	-0.2794	-0.2789
CPP					0.8941**	0.9355**	-0.6946**	0.4976*	0.4976*
FPC						0.978**	-0.7672**	0.3151	0.3152
FPP							-0.7491**	0.3805	0.3804
FW								0.2146	0.2146
YPP									1

PH- Plant height(cm), **NOB**- number of branches, **DF**- Days to first flowering (DAT), **CPP**-Clusters per plant, **FPC**- fruits per cluster, **FPP**- Fruits per plant, **FW**- Fruit weight(g), Y**PP**-Yield per plant (kg) and **YH**- Yield per hectare (ton).

Table 6: Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of tomato

	PH	NOB	DF	CPP	FPC	FPP	FW	YPP	YH
PH		0.4749	-0.2714	0.3517	0.4258	0.4582	-0.4025	-0.0975	-0.0975
NOB			-0.0956	0.6499*	0.5264*	0.6302*	-0.3253	0.4112	0.4112
DF				-0.5786*	-0.3531	-0.3951	0.4513	-0.2613	-0.2612
CPP					0.8446**	0.9214**	-0.6796*	0.4851*	0.485*
FPC						0.9658**	-0.7529**	0.3147	0.3147
FPP							-0.7438**	0.3794	0.3794
FW								0.2163	0.2163
YPP									1

PH- Plant height(cm), **NOB**- number of branches, **DF**- Days to first flowering (DAT), **CPP**-Clusters per plant, **FPC**- fruits per cluster, **FPP**- Fruits per plant, **FW**- Fruit weight(g), Y**PP**-Yield per plant (kg) and **YH**- Yield per hectare (ton).

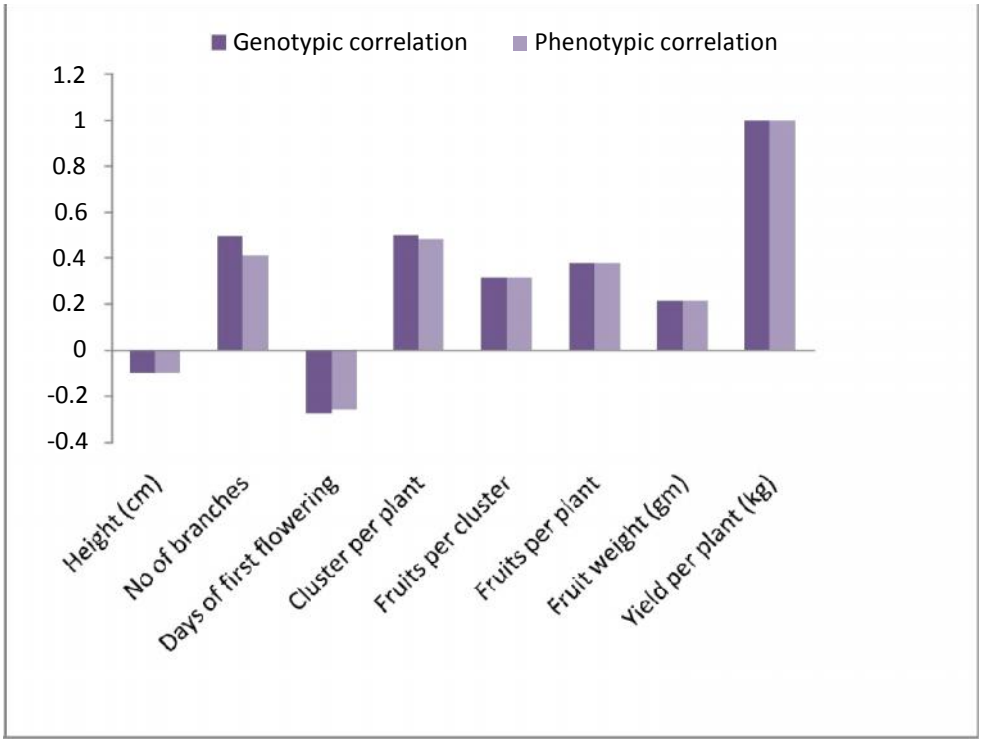


Figure 3. Genotypic and phenotypic correlation

correlation between yield of fruits per plant and number of branches per plant was observed by Singh *et al*. (2006) and Ara *et al*. (2009). There was a non-significant negative correlation of no. of branches with days to first flowering (-0.1266 and -0.0956) and fruit weight (-0.438 and -0.3253) at genotypic and phenotypic level Table 5 and Table 6).

4.3.3 Days to first flowering (DAT)

Days to first flowering showed a significant positive correlation with fruit weight (0.483) at genotypic level and a positive correlation at phenotypic level (0.4513) (Table 5 and Table 6 and Figure 3). It had significant negative correlation with cluster per plant (-0.6074 and -0.5786) both at phenotypic and genotypic level. Days to first flowering also had a non-significant negative correlation with fruits per cluster (-0.4009 and -0.35310), fruits per plant (-0.4253 and -0.3951), yield per plant (-0.2794 and -0.2613) and yield per hectare (-0.2789 and -0.2612) both at genotypic and phenotypic level (Table 5 and Table 6). But Mayavel *et al.* (2005) found a significant positive correlation with fruit yield plant which disagreed with my result.

4.3.4 Number of clusters per plant

Number of cluster per plant had a highly significant positive correlation with fruits per cluster (0.8941and 0.8446) and fruits per plant (0.9355 and 0.9214) both at genotypic and phenotypic level. This trait also had a positive significant correlation with yield per plant (0.4976 and 0.4851) and yield per hectare (0.4976 and 0.485) both at genotypic and phenotypic level. A positive correlation between number of clusters per plant and fruit yield per plant was also observed by Prasanth (2003). Nesgea *et al*. (2002) also found similar results for this trait in tomato. Fruit weight had a highly significant negative correlation with this trait both genotypic and phenotypic level (-0.6946 and -0.6796).

4.3.5 Number of fruits per cluster

Number of fruits per cluster had a highly significant positive association with number of fruits per plant both at genotypic and phenotypic level (0.978 and 0.9658). This trait also had a highly significant but negative correlation with fruit weight (-0.7672 and -0.7529) both at genotypic and phenotypic level. The findings of Nesgea *et al.* (2002) and Megha *et al* (2006) supported my result. Yield per plant and yield per hectare were non-

significantly but positively correlated with this trait both at genotypic level (0.3151 and 0.3152) and phenotypic level (0.3147 and 0.3147) (Table 5 and Table 6).

4.3.6 Number of fruits per plant

The number of fruits per plant had a highly significant but negative association with fruit weight both genotypic and phenotypic level (-0.7491 and -0.7438) (Table 5 and Table 6 and Figure 3). Joshi *et al.* (2004) showed that number of fruits per plant was negatively correlated with fruit weight. Both yield per plant and yield per hectare were found non-significantly but positively correlated with this trait at both genotypic (0.3805 and 0.3804) and phenotypic (0.3794 and 0.3794). But Rani *et al.* (2010) found negative association between those traits.

4.3.7 Fruit weight (g)

Fruit weight showed a positive non-significant correlation with both yield per plant and yield per hectare at both genotypic (0.2146 and 0.2146) and phenotypic (0.2163 and 0.2163) level (Table 5 and Table 6 and Figure 3). Arun *et al*. (2003) and Joshi *et al.* (2004) observed that in case of tomato yield per plant was positively and significantly correlated with average fruit weight. Matin and Kuddus (2001) found that individual fruit weight had significant positive correlations with yield per plant.

4.3.8 Yield per plant (kg)

Fruit yield is the ultimate target any plant breeding program. So its correlation study is very important. Type of association of this trait with other characters has already discussed. From above discussion we found a positive correlation and significant relation of fruit yield per plant with no. of branches and cluster per plant at both the level. Again it showed negative non-significant relation with plant height and days to first flowering at both genotypic and phenotypic level (Table 5 and Table 6 and Figure 3). A non-significant but positive correlation was found between fruit yield per plant and fruits per cluster, fruits per plant and fruit weight both at genotypic level and genotypic level. Rani *et al*. (2010) found during an experiment that fruit yield per plant was positively and significantly associated with fruit weight. Weber and Moorthy (2010) also found the evidence of positive and strong association between yield per plant and fruit yield.

4.3.9 Yield per hectare (ton)

Yield per hectare is simply the conversion of the yield per plant to hectare which is expressed in ton. This parameter is highly associated with yield per plant. Association of yield per hectare with other traits has already discussed which expressed that no. of branches and cluster per plant had a significant positive association with this trait where height and days to first flowering had negative association (Table 5 and Table 6). Other characters had a positive non-significant correlation.

4.4 Path coefficient analysis

Path analysis paved the direction of effects of yield contributing characters on yield whether they direct or indirect. Here yield per hectare was considered as effect (dependent variable) and plant height (cm), days to first flowering, no. of branches per plant, number of cluster per plant, fruits per cluster, fruits per plant, fruit weight (g) and yield per plant (kg) were treated as independent variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of tomato in Table 7.

4.4.1 Plant height

Path analysis revealed that plant height had direct negative effect (-0.0073) on yield per hectare (YH). It had indirect positive effect on YH through cluster per plant (0.0028), fruits per plant (0.0010) and fruit weight (0.0007) (table 7). It had also indirect negative effect on YH through no. of branches (-0.0062), days to first flowering (-0.0013) and fruits per cluster (-0.0019) (Table 7). Matin and Kuddus (2001) found that plant height had negative direct effect on yield per plant.

4.4.2 Number of branches per plant

Number of branches per plant had a negative direct effect on yield per hectare (-0.0182). It had also negative but indirect effect on days to first flowering (-0.0005) and fruits per cluster (-0.0020). It had a significant positive correlation with yield per hectare (0.4949) (Table 7). It had positive indirect effect on plant height (0.1668), cluster per plant (0.0051), fruits per plant (0.0011), fruit weight (0.0005) and yield per plant (0.3421). Singh *et al.* (2005) also reported that number of branches per plant had direct negative effects on yield which is supported by present findings.

Table 7: Path coefficient analysis showing direct and indirect effects of different characters on yield of tomato

Characters	Direct effect	Indirect effect								Genotypic correlation with yield
		PH	NOB	DF	CPP	FPC	FPP	FW	YPP	
PH	-0.0073		-0.0062	-0.0013	0.0028	-0.0019	0.0010	0.0007	-0.0906	-0.1028
NOB	-0.0182	0.1668		-0.0005	0.0051	-0.0020	0.0011	0.0005	0.3421	0.4949*
DF	0.0054	-0.0302	0.0016		-0.0041	0.0016	-0.0009	-0.0008	-0.2516	-0.2789
CPP	0.0092	0.1792	-0.0100	-0.0024		-0.0037	0.0018	0.0013	0.3220	0.4976*
FPC	-0.0055	0.0171	-0.0067	-0.0016	0.0062		0.0022	0.0016	0.3019	0.3152
FPP	0.0024	0.0027	-0.0087	-0.0019	0.0072	-0.0052		0.0016	0.3824	0.3804
FW	-0.0022	-0.0073	0.0040	0.0020	-0.0056	0.0040	-0.0017		0.2214	0.2146
YPP	1.0063*	-0.0005	-0.0062	-0.0013	0.0029	-0.0017	0.0009	-0.0005		1.0000*

PH- Plant height(cm), **NOB**- number of branches, **DF**- Days to first flowering (DAT), **CPP**-Clusters per plant, **FPC**- fruits per cluster, **FPP**- Fruits per plant, **FW**- Fruit weight(g), Y**PP**-Yield per plant (kg) and **YH**- Yield per hectare (ton).

4.4.3 Days to first flowering

Days to first flowering had a positive direct effect on yield per plant (0.0054) and a non-significant negative genotypic correlation with yield per hectare (-0.2789). Matin and kuddus (2001) reported dissimilar result with the present study and they stated that days to first flowering had negative direct effect on yield per plant. On the other hand findings of Bhuiyan (2014) supported my result. It had negative indirect effect on plant height (-0.0302), cluster per plant (-0.0041), fruits per plant (-0.0009), fruit weight (-0.0008) and yield per plant (-0.2516) (Table 7). Bhuiyan (2014) also found negative indirect effect plant height, cluster per plant and fruits per plant. It had indirect positive effect on no. of branches (0.0016) and fruits per cluster (0.0016).

4.4.4 Number of clusters per plant

Number of clusters per plant had direct positive effect (0.0092) on yield per hectare and significantly positively correlated with yield per hectare (0.4976) (Table 7). It had indirect positive effect on height (0.1792), fruits per plant (0.0018), fruit weight (0.0013) and yield per plant (0.3220). It showed negative indirect effect on days to first flowering (-0.0024), fruits per cluster (-0.0037) and no. of branches (-0.0100). Singh *et al.* (2005) found negative indirect effect of this trait on fruits per cluster.

4.4.5 Number of fruits per cluster

Number of fruits per cluster expressed direct negative effect on yield per hectare (-0.0055). It was also positively correlated with YH at genotypic level. It had negative indirect effect on no. of branches (-0.0067) and days to first flowering (-0.0016). Again fruits per plant had positive indirect effect on yield per hectare through plant height (0.0171), clusters per plant (0.0062), fruits per plant (0.0022), fruit weight (0.0016) and yield per plant (0.3019) (Table 7). Mayavel *et al.* (2005) and Bhuiyan (2014) also reported that number of fruits per cluster had negative direct effects on fruit yield.

4.4.6 Number of fruits per plant

Number of fruits per plant had positive direct effect (0.0024) on yield per hectare and positively correlated with yield per hectare (0.3804). Bhuiyan (2014) found same result. It was also positive indirect effect on plant height (0.0027), cluster per plant (0.0072), fruit weight (0.0016) and yield per plant (0.3824). Again it had negative indirect effect on

no. of branches (-0.0087), days to first flowering (-0.0019) and fruits per cluster (-0.0052) (Table 7). Singh *et al.* (2006) and Kumar *et al.* (2013) also observed fruits per plant had direct positive effects on fruit yield at the genotypic and phenotypic levels.

4.4.7 Fruit weight (g)

Fruit weight had direct negative effect on yield per hectare (-0.0022) but it had positively correlated with yield per hectare (0.2146) at genotypic level. Rani *et al.* (2010), Singh *et al.* (2006) and Manivannan *et al.* (2005) also reported positive direct effects on fruit yield This is not similar to my result this might be due to environmental influence. Path analysis revealed that single fruit weight had negative indirect effect on plant height (-0.0073), cluster per plant (-0.0056) and fruits per plant (-0.0017). Again it had positive indirect effect on no. of branches (0.0040), days to first flowering (0.0020), fruits per cluster (0.0040) and yield per plant (0.2214) (Table 7). Bhuiyan (2014) also found indirect positive effect on no. of branches and fruits per cluster.

4.4.8 Yield per plant (kg)

Path analysis revealed that yield per plant had significant direct positive effect on yield per hectare (1.0063) and had significant positive correlation with YH (1.0000) at genotypic level. It had also positive but indirect effect on cluster per plant (0.0029) and fruits per plant (0.0009). Again it had indirect negative effect on YH through plant height (-0.0005), no. of branches (-0.0062), days to first flowering (-0.0013), fruits per cluster (-0.0017) and fruit weight (-0.0005) (Table7).

4.5 Multivariate analyses

The genetic diversity of tomato advanced lines is presented in Table 8 to 12.

4.5.1 Principal component analysis (PCA)

Principal component analysis was done with fifteen genotypes of tomato which gives Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes. First three Eigen values for three principal coordination axes of genotypes accounted for 86.92 % variation (Table 8).

4.5.2 Non-Hierarchical Clustering

Fifteen genotypes were grouped into three different clusters non-hierarchical clustering (Table 9 and Figure 4 and Figure 5). These results confirmed the clustering pattern of the

Table 8: Eigen values and yield percent contribution of 9 characters of fifteen genotypes

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Plant Height (cm)	4.6936	52.15	52.15
Number of Branches	2.146	23.84	75.99
Days to first Flowering (DAT)	0.9837	10.93	86.92
Clusters per Plant	0.7333	8.15	95.07
Fruits per Cluster	0.3353	3.73	98.8
Fruits per Plant	0.0613	0.68	99.48
Fruit Weight (g)	0.0352	0.39	99.87
Yield per Plant (kg)	0.0116	0.13	100
Yield per hactor (ton)	0	0	100

Table 9: Distribution of fifteen genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G_1 G_2 G_{14}	3	SAU Tomato-1 SAU Tomato-2 BARI Tomato-11
II	G_3 G_4 G_5 G_6 G_7 G_{12} G_{13} G_{15}	8	SAU Tomato-3 SAU Tomato-4 Sandwich slicer Mortgage lifter Black cream BARI Tomato-2 BARI Tomato-3 BARI Tomato-15
III	G_8 G_9 G_{10} G_{11}	4	BARI Hybrid-4 BARI Hybrid-5 BARI Tomato-14 BARI Tomato-16

Table 10. Cluster mean values of nine different characters of fifteen genotypes

Character	I	II	III
Plant Height (cm)	102.56	86.37	71.92
Number of Branches	10.67	8.5	8.67
Days to first Flowering (DAT)	34.11	36.04	34.83
Clusters per Plant	17.33	7.25	10.58
Fruits per Cluster	10	3.58	4.83
Fruits per Plant	172.56	27.17	51.5
Fruit Weight (g)	17.61	82.87	109.07
Yield per Plant (kg)	19.85	11.34	31.65
Yield per Hectare (ton)	58.39	33.35	93.08

Table 11. Intra (Bold) and inter cluster distances (D^2) for fifteen genotypes of tomato

Cluster	I	II	III
I	**1.665**	13.176	14.561
II		**1.268**	5.748
III			**0.867**

Table 12. The nearest and farthest clusters from each cluster between D^2 values in tomato

Sl. No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**II** (13.176)	**III** (14.561)
2	**II**	**III** (5.748)	**I** (13.176)
3	**III**	**II** (5.748)	**I** (14.561)

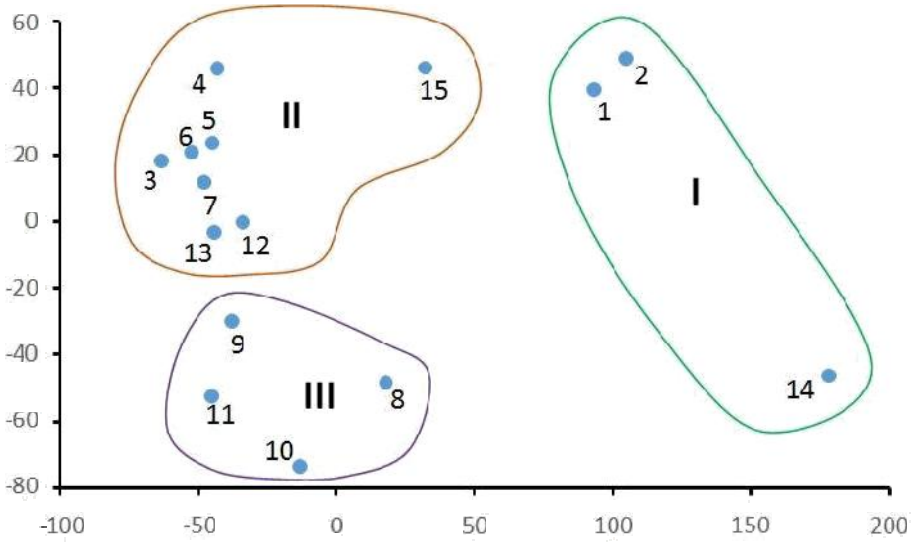


Figure 4. Distribution of different clusters

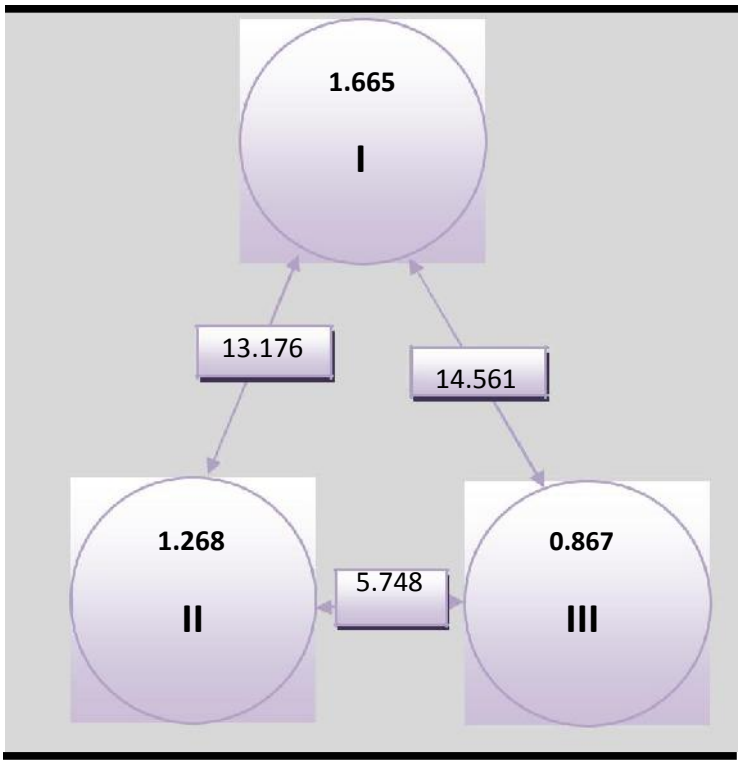


Figure 5. Intra and inter cluster distances of different clusters

genotypes obtained through principal component analysis. Naime (2016), Bhuiyan (2014) and Sharma and Verma (2001) reported five clusters, Shashikanth *et al.* (2010) reported ten clusters, Mahesh *et al.* (2006) reported nine clusters tomato. Cluster II had highest number of eight genotypes followed by cluster I had three and cluster III constituted by four genotypes (Table 9).

Cluster I had G_1, G_2 and G_{14} and cluster III had G_8, G_9, G_{10} and G_{11}. On the other hand cluster II had highest genotypes which comprised G_3, G_4, G_5, G_6, G_7, G_{12}, G_{13} and G_{15} (Table 9). Cluster I had highest mean value for five characters such as Plant height (102.56), Number of branches (10.67), Cluster per plant (17.33), Fruits per cluster (10) and Fruits per plant (172.56). This result indicated that cluster I could be used as parent in future hybridization program for these five characters. On the other hand it had lowest mean value of days to first flowering (34.11) which is good sign for breeding program (Table 10). Cluster II had highest mean value for days to first flowering (36.04) (Table 10). It had a moderate mean value for all other characters. It could be used in future breeding program for morphological parameters studied in this research. Cluster III had highest cluster mean value for Fruit weight (109.07), Yield per plant (31.65) and Yield per hectare (93.08) (Table 10). This result indicated that cluster III could be used as parent in future hybridization program for these three characters.

4.5.3 Canonical variate analysis

Canonical Variate Analysis (CVA) was done to calculate the inter-cluster distances. Table 11 represents the intra and inter-cluster distance (D^2) values. This experiment expressed that the inter-cluster distances were higher than the intra-cluster distances which means a broader genetic diversity among the genotypes of different groups. Bhuiyan (2014) and Naime (2016) also reported that the inter-cluster distances were larger than the intra-cluster distances.

The highest inter-cluster distance was observed between clusters I and III (14.561), than between cluster I and II (13.176) and lowest inter cluster distance were found between II and III (5.748). However, the maximum inter-cluster distance indicated that genotypes from these two clusters may produce a wide spectrum of segregating population in hybridization program. On the other hand highest intra-cluster distance was found in

cluster I (1.665) which had 4 genotypes. Inter and intra cluster distances were showed in table 11. Cluster I consists of nearest cluster with D^2 values cluster II (13.176) and farthest cluster with D^2 values III (34.75) (Table 12).

4.5.4 Selection of genotypes as parent for hybridization program

Ultimate goal of any breeding program is the selection of genetically diverse parents. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distance parents.

Considering the cluster mean value and agronomic performance the genotype G_{14} for maximum plant height, number of branches per plant, number of cluster per plant and number of fruits per cluster was found promising. Maximum number of fruits per plant was found G_2. G_3 was found promising for highest fruit weight (g). G_4 was best for yield per plant (kg) and yield per hectare (ton) as it had maximum fruit yield per plant and yield per hectare. G_{15} was good for lowest days to first flowering (DAT). Therefore considering group distance and other agronomic performance the inter-genotypic crosses between G_1, G_2, G_3, G_4, G_{14} and G_{15} also other improved variety and/or high yielding variety might be suggested for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The present research was done at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207, Bangladesh with fifteen genotypes of tomato *(Solanum lycopersicum* L.) during November 2016 to April 2017. Seeds were sown in seed bed then transferred to the main field in Randomized Complete Block Design (RCBD) with three replications. Data on various yield contributing characters such as plant height (cm), number of branch per plant, days to first flowering, number of cluster per plant, number of fruit per cluster, number of fruit per plant, fruit weight (g), yield per plant (kg) and yield per hectare (ton) were recorded. Analysis of variance expressed significant differences among all the genotypes for all the characters under study.

The analysis of variances showed significant mean squares for different characters indicated the presence of sufficient variation among the genotypes for all the characters. The number of fruit yield per plant showed highest range of variation that means wide range of variation present for this character.

In case of plant height, number of branches per plant and number of cluster per plant showed higher influence of environment for the expression of these characters. On the other hand, days to first flowering, fruits per cluster, fruits per plant, fruit weight, yield per plant and yield per hectare showed least difference in phenotypic and genotypic variance suggesting additive gene action for the expression of the characters. All the characters under the present study exhibit the highest value of heritability except number of branches and days to first flowering.

Correlation coefficients among the characters were studied to define the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study. The significant positive correlation with yield per hectare was found in number of branches and cluster per at genotypic level. In addition, there were non-significant positive correlation with fruit yield per hectare was also found in fruits per

cluster, fruits per plant, fruit weight and yield per plant at genotypic and phenotypic level, respectively. On the other hand, the non-significant negative correlation also found in plant height and days to first flowering. Again non-significant positive correlation was found between yield per hectare and number of branches at phenotypic level.

Path coefficient analysis showed that days to first flowering, cluster per plant fruits per plant and yield per plant had direct positive effect on yield per hectare while yield per plant showed significant positive effect. Number of branches had a significant positive correlation with yield per hectare but it had negative direct effect on yield. There was a significant positive correlation of yield per plant with clusters per plant and yield per plant that's also had a positive direct effect on yield per hectare indicating selection will be judicious and more effective for these characters in future breeding program. Days to first flowering and fruits per plant had a positive direct effect on yield per hectare. Negative direct effects of plant height, number of branches, fruits per cluster and fruit weight on yield per hectare were found.

Genetic diversity among tomato genotypes was performed through Principal Component Analysis (PCA), Cluster Analysis, Canonical Variate Analysis (CVA) using GENSTAT computer program. The first three principal component axes accounted for 86.92% variation towards the divergence. Among three clusters cluster II contained maximum number of genotypes (8) while cluster I had three genotypes and cluster III had four genotypes. According to PCA, D^2 and cluster analysis, the genotypes grouped into three divergent clusters obtained from principal component scores. The highest inter-cluster distance was observed between clusters I and III (14.561) indicating genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and II (5.748). On the other hand, the maximum intra-cluster distance was found in cluster I (1.665) which contained of three genotypes, whereas the minimum distance was found in cluster III (0.867) that comprises 4 genotypes. Considering the cluster mean value and agronomic performance the genotype G_{14} for maximum plant height, number of branches per plant, number of cluster per plant and number of fruits per cluster was found promising. Maximum number of fruits per plant was found G_2. G_3 was found promising for highest fruit weight (g). G_4 was best for yield per plant (kg) and

yield per hectare (ton) as it had maximum fruit yield per plant and yield per hectare. G_{15} was good for lowest days to first flowering (DAT). Therefore considering group distance and other agronomic performance the inter-genotypic crosses between G_1, G_2, G_3, G_4, G_{14} and G_{15} also other improved variety and/or high yielding variety might be suggested for future hybridization program.

From the findings of the present study, the following conclusions could be drawn:

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

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

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

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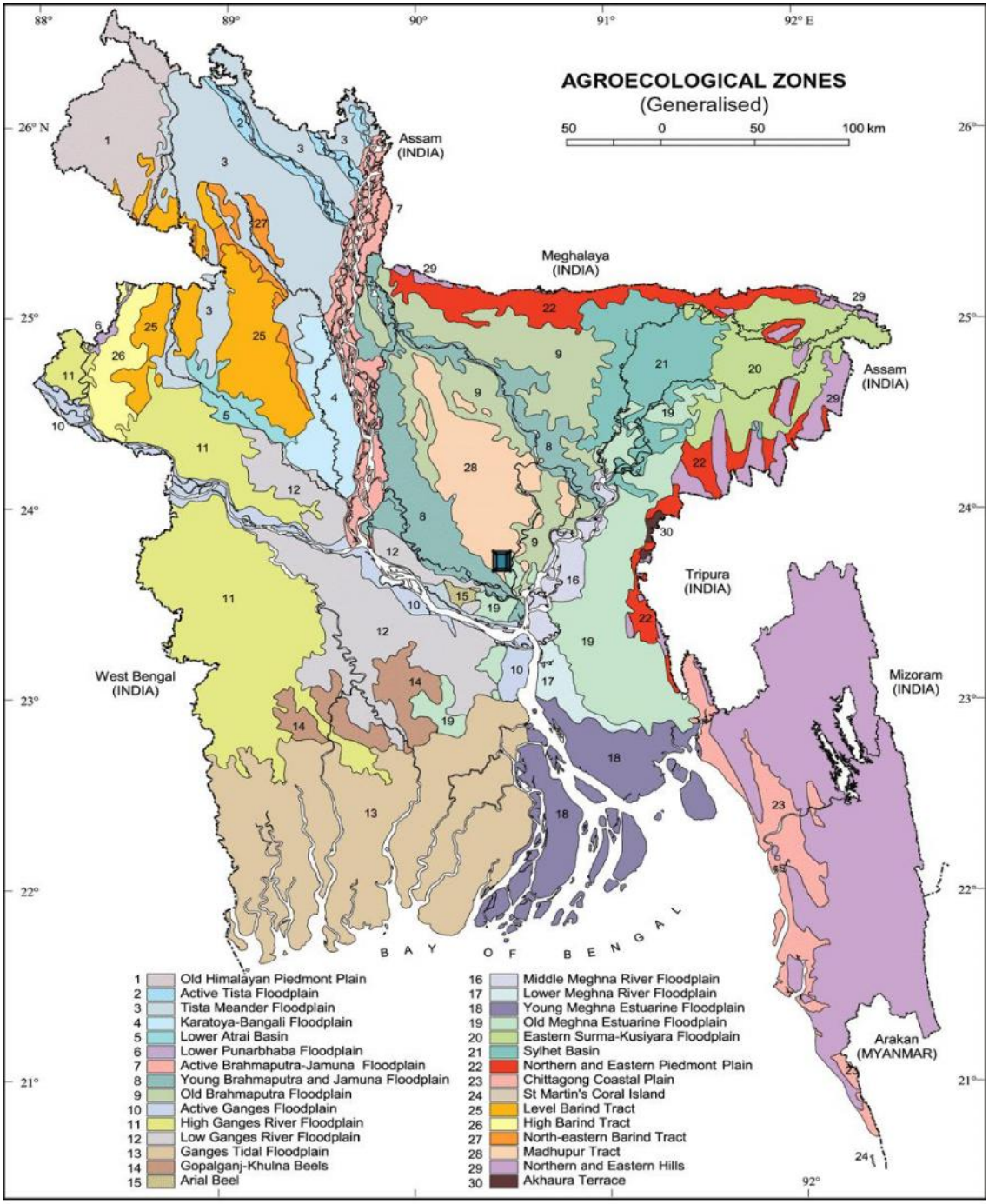
APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from October 2013 to May 2014

Month	Year	Monthly average air temperature (^{o}C)			Average relative humidity (%)	Total rainfall (mm)	Total sunshine (hours)
		Maximum	Minimum	Mean			
Oct.	2016	29.36	18.54	23.95	74.80	Trace	218.50
Nov.	2016	28.52	16.30	22.41	68.92	Trace	216.50
Dec.	2016	27.19	14.91	21.05	70.05	Trace	212.50
Jan.	2017	25.23	18.20	21.80	74.90	4.0	195.00
Feb.	2017	31.35	19.40	25.33	68.78	3.0	225.50
Mar.	2017	32.22	21.25	26.73	72.92	4.0	235.50
April	2017	33.21	22.25	27.23	70.05	5.0	236.50

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

Appendix III. **The mechanical and chemical characteristics of soil of the experimental site as observed prior to experimentation (0 - 15 cm depth).**

A. Mechanical composition:

Particle size constitution		
Sand	:	40%
Silt	:	40%
Clay	:	20%
Texture	:	Loamy

B. Chemical composition:

Soil characters	:	Value
Organic matter	:	1.44 %
Potassium	:	0.15 meq/100 g soil
Calcium	:	3.60 meq/100 g soil
Magnesium	:	1.00 meq/100 g soil
Total nitrogen	:	0.072
Phosphorus	:	22.08 µg/g soil
Sulphur	:	25.98 µg/g soil
Boron	:	0.48 µg/g soil
Copper	:	3.54 µg/g soil
Iron	:	262.6 µg/g soil
Manganese	:	164 µg/g soil
Zinc	:	3.32 µg/g soil

Source: Soil Resources Development Institute (SRDI), Khamarbari, Dhaka.

Appendix IV. Analysis of variance of nine important characters in respect of yield and yield components

Source of variation	df	PH	NOB	DFF	CPP	FPC	FPP	FW	YPP	YH
Replication	14	1161.676**	9.095**	39.975**	101.565**	23.556**	11811.260**	4757.665**	405.808**	**3513.828****
Genotypes	2	147.467	6.067	3.356	26.756	0.022	126.156	226.061	27.461	**234.731**
Error	28	104.586	3.376	5.689	11.756	0.641	66.441	67.424	9.652	**83.497**

** Significant at 1% level of significance

* Significant at 5% level of significance

PH	**Height (cm)**
NOB	No of Branches
DFF	Days of first flowering(DAT)
CPP	Cluster per plant
FPC	Fruits per cluster
FPP	Fruits per plant
FW	Fruit weight(gm)
YPP	Yield per plot(kg)
YH	Total yield (ton per ha)