CHARACTER ASSOCIATION AND GENETIC DIVERSITY IN TOMATO

(*Solanum lycopersicum* L.)

BY

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CERTIFICATE

This is to certify that thesis entitled, **"CHARACTER ASSOCIATION AND GENETIC DIVERSITY IN TOMATO (Solanum lycopersicum L.)"** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **Tasnia Taiana**, Registration No. **08-03087** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2014
Place: Dhaka, Bangladesh

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DEDICATED TO

MY

BELOVED PARENTS

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ABSTRACT

The experiment was conducted with twenty one genotypes of tomato at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period of November 2013 - April 2014 to estimate the variability, heritability, correlation, path coefficient and genetic diversity among the genotypes. All the genotypes varied significantly with each other for all the studied characters indicating the presence of considerable variations among the genotypes. The Phenotypic Coefficient of Variation (PCV) values were slightly higher than the respective Genotypic Coefficient of Variation (GCV) values for all the characters under study indicating that the characters were less influenced by the environment. Plant height and number of fruits per plant showed high heritability along with high genetic advance indicating them to be helpful in predicting the genetic gain under selection. Moderate heritability for primary branches per plant indicated favorable influence of environment rather than genotypes. Correlation analysis revealed that fruit yield per plant was highly significant and positively associated with secondary branches per plant and number of fruits per plant at both genotypic and phenotypic level. On the other hand, both genotypic and phenotypic level fruit yield per plant had highly significant and negative correlation with days to 50% flowering and days to maturity. Path analysis revealed that secondary branches per plant, number of fruits per cluster, days to first flowering, days to maturity, fruits per plant, average fruit weight and fruit diameters had positive direct effects on yield per plant. Significant difference among the clusters was observed through multivariate analysis, clusters analysis and canonical vector analysis. Based on D^2 analysis the genotypes were grouped into five different clusters. Clusters I had the maximum seven and cluster V had the minimum a single genotype. The highest inter-cluster distance was observed between III and V and the lowest distance was in between III and IV. The highest and lowest intra-cluster distance was observed in III and V respectively. Genotypes included in cluster II were important for secondary branches per plant, days to first flowering, fruit yield per plant whereas number of flowers per cluster, number of fruits per cluster and number of fruits per plant were remarkable feature for cluster V. Considering the above findings and other agronomic performances, the genotypes BD-7748, Local Jessore-3 and Local Kushtia-1, BD-7762, BD-7285, BARI hybrid-4, BD-7290, BD-9011 and BARI Tomato-3 might be considered as better parents for efficient hybridization programme in future.

TABLE OF CONTENTS

TABLE OF CONTENTS (Cont'd.)

TABLE OF CONTENTS (Cont'd.)

TABLE OF CONTENTS (Cont'd.)

TABLE OF CONTENTS (Cont'd.)

LIST OF TABLES

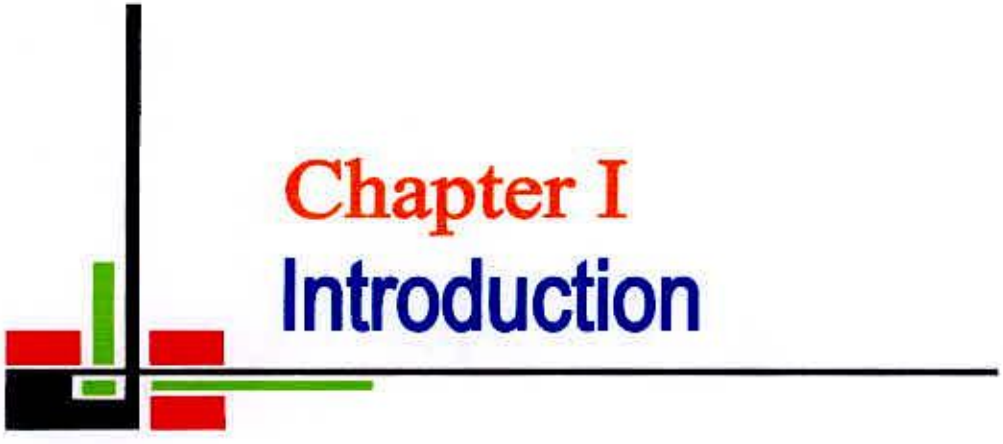
LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL WORD
AEZ	Agro- Ecological Zone
et al	And others
ACC	Accessions
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co- efficient of Variation
etc	Etcetera
Fig	Figure
G	Genotype
GA	Genetic advance
GCV	Genotypic Co- efficient of Variation
$\square^2g$	Genotypic Variance
g	Gram
j.	Journal
Kg	Kilogram
MSS	Mean Sum of Square
mm	Millimeter
MP	Muriate of potash
No.	Number
PCV	Phenotypic Co- efficient of Variation
$\square^2P$	Phenotypic Variance
RCBD	Randomized Complete Block Design
R	Replication
Res	Research
SAU	Sher-e-Bangla Agricultural University
SE	Standard Error
m^2	Square meter
TSP	Triple Super Phosphate



Chapter I
Introduction

CHAPTER I

INTRODUCTION

Tomato is an herbaceous, usually sprawling plant in the order solanales and nightshade family, solanaceae. Tomato (*Solanum lycopersicum* L.) is one of the most important vegetable crops of both tropics and subtropics of the world. It is an excellent source of lycopene, a powerful antioxidant and reduces the risk of prostate cancer (Hossain *et al.* 2004).

Tomato has an excellent nutritional profile owing largely to its balanced mixture of minerals (potassium, calcium, phosphorus, iron and zinc), vitamins (A, B1, B2, B6, biotine, folic acid, nicotinic acid, pantothenic acid, C, E and K), antioxidants such as carotenoids, polyphenolic compounds and carbohydrates. No doubt, because of its exceptional nutritive value, tomato is the world's major vegetable crop. Fresh ripe tomatoes are prevalently consumed raw in salad as well as curried in combination with variety of vegetables. Tomato can also be processed and canned into a wide range of value added products like soups, juices, pastes, sauces, ketchups and purees. Tomato is also having medicinal value. The pulp and juice are digestible and blood purifier (Frasher *et al.* 1991). It's centre of origin is presumed to be in the present state of Mexico. It is believed that the tomato was introduced in subcontinent during the British regime. It is popular for its taste, nutritional status and various uses. The crop is adapted to a wide variety of climates ranging from the tropics to a few degree of the Arctic Circle. In 2009 the world's total cultivated area under tomato was 4.98 million ha, with a production quantity of 141.14 million tons (FAOSTAT, 2011).

Now Bangladesh is producing a good amount of tomatoes. In Bangladesh tomato has great demand throughout the year but is available and cheaper during the winter season. Tomato was cultivated in 61213 acre of land and its record production was 232459 metric tons during 2010-2011 (BBS, 2011). Now-a-days, tomatoes are grown round the year. Due to increasing consumption of tomato products, the crop is becoming promising. The best tomato growing areas in Bangladesh are Dinajpur, Rajshahi, Dhaka, Comilla and Chittagong.

Parameters of genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in predicting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment expression of the characters and the extent to which improvement is possible after selection (Robinson *et al.* 1949). Crop improvement depends upon the magnitude of genetic variability and extent to which the desirable characters are heritable. The total variability can be partitioned into heritable and non-heritable components with the help of genetic parameters like genotypic and phenotypic coefficients of variation, heritability and genetic advance (Johnson *et al.* 1955).

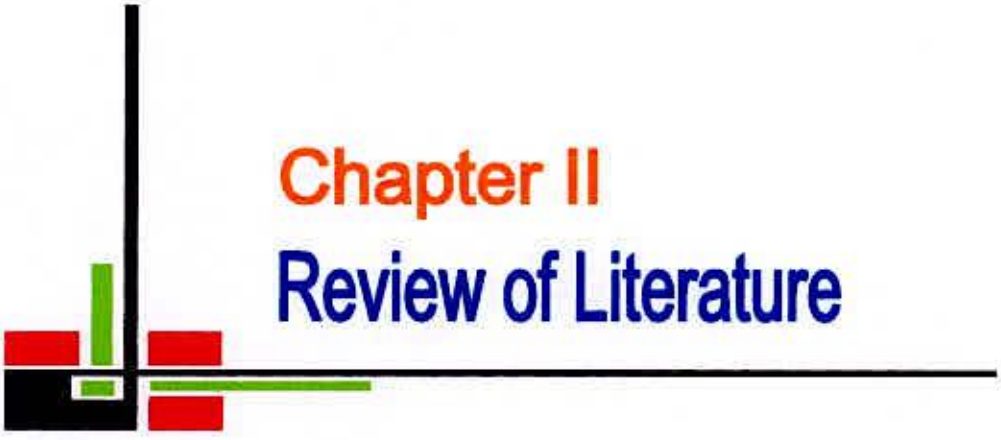
The knowledge of association between yield and its contributing traits is of great values in planning a breeding programme. Thus determination of correlation among the characters is a matter of considerable importance in selection of correlated response. The degree of relationship or association of these characters with yield can be ascertained by correlation studies. This would aid in formulation an efficient breeding program for improving the yield potential via its components. But it does not give the exact information of the relative importance of direct and indirect effects of various yield attributes. Path analysis facilitates the partitioning of correlation coefficients into direct and indirect effects of various characters on yield or any other attribute. Hybridization is one of the major tools for achieving variability aiming at the improvement of a crop. Before hybridization genetic diversity of the existing materials or entries needs to be known. Information about genetic diversity in available germplasm is important for the 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).

Diverse breeding lines including specific genetic stocks are the most precious basic materials for crop breeders to meet the current and future needs. Characterization of genetic stocks and varieties by morphological is obligatory for the purpose of selection of new varieties for direct production or for use in hybridization program. Crops as manifested in morphological or molecular diversity are essential for crop improvement, leading to the production of preferred crop types. The importance of genetic diversity in the improvement of a crop has been emphasized in both self and cross pollinated crops (Gadekar *et al.* 1992).

According to Burton (1952), for the improvement of any character through breeding, it is essential to know the extent of variability present in that species, nature of association among the characters and the contribution of different characters towards yield. The efficiency of a plant breeding program depends on the amount of genetic variability exist in nature or how much a plant breeder can create variability in the population so as to perform effective selection. However, knowledge on genetic information obtained through the analysis of genetic diversity and relatedness between or within different species, population and individuals is a pre-requisite towards effective utilization and conservation of plant genetic resources (Chaudhury *et al.* 1976, Weising *et al.* 1995). Therefore, characterization and analysis of genetic similarity/dissimilarity among the tomato varieties are necessary before setting any program for their improvement.

The germplasm were collected from the Plant Genetic Resource Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur. Information about species as well as their identifying characters for most of the germplasms collected was unknown. So, it is an opportunity to characterize the germplasms morphologically under different species for future utilization in breeding program to develop short durated and high yielding genotype of tomato. With conceiving the above idea in mind, the present research work has been undertaken in order to fulfilling the following objectives:

1. To know the yield potentiality of the genotypes.
2. To assess the genetic variability among the tomato genotypes in respect of different morphological characters.
3. To determine the nature of association, direct and indirect relation between yield and yield contributing characters; and
4. To assess the genetic diversity among the tomato genotypes for identifying the genetically divergent parents and to use those in the further improvement of tomato.



Chapter II
Review of Literature

CHAPTER II

REVIEW OF LITERATURE

Tomato *(Solanum lycopersicum* L.*)* is one of the most important vegetable crops grown throughout the world because of its wider adaptability, high yielding potential and suitability for variety of uses in fresh as well as processed food industries. At present tomato ranks, second next to potato in terms of global vegetable production. Morphological characterization of any agricultural crop is a valuable tool, which can utilize for crop improvement program.

The present research work has aimed to study the variability, heritability, genetic advance, correlation, path coefficient analysis and genetic diversity among different yield contributing characters. Different workers in different institutions of the world have already performed related works. Some of the most relevant literatures are cited here on objective basis.

2.1 Variability

The fundamental key to achieve the genetic improvement of a crop through a proper breeding program 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.

Ahirwar *et al.* (2013) carried out a field experiment in nineteen genotypes of tomato to study the genetic variability, heritability; genetic advance and correlation for different yield contributing characters. Significant differences were observed among the genotypes for all the traits. The phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) for all the traits. Traits like plant height 120 DAT, number of branches 120DAT, number of fruits per plant, average fruit weight, number of cluster per plant, fruit set (%), radial diameter and polar diameter (mm), ascorbic acid (vitamin C), TSS (brix), showed positive correlation with fruit yield per ha, plant height after 120 DAT, days to 50 per cent flowering, leaf curl incidence and intensity showed negative correlation at both phenotypic and genotypic level.

Al-Aysh *et al.* (2012) reported that the genotypes exhibited a wide range of variation for all the characters. Phenotypic coefficient of variation and genotypic coefficient of variation were the highest for number of fruits per plant whereas the lowest ones were for harvest index.

Kaushik *et al.* (2011) evaluated ten genotypes of tomato. They observed that the variation was maximum (424 to 825 qtl/ha) for fruit yield and minimum for fruit width (4.1 to 5.6 cm). The magnitude of genotypic and phenotypic coefficient of variation was higher for number of leaves (21.2 and 22.3), fruit length (19.6 cm and 19.7 cm) and fruit yield (19.6 kg and 19.6 kg).

Shashikanth *et al.* (2010) carried out a field experiment to study the genetic variation among thirty 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 variation was for most of the characters indicating a high contribution of the genetic component for the total variation.

Kumari and Subramanian (2007) recorded data for total soluble solids, dry matter content, reducing sugars, titratable acidity, ascorbic and 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 plants, plant height, early 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.

Mahesh *et al.* (2006) carried out an experiment to study genetic variability in thirty genotypes of tomato and reported significant difference for all the characters under study and observed a wide range of variability for plant height, number of branches per plant, fruit weight, fruit length, fruit diameter, number of locules per fruit, fruit set percentage, fruits per plants, fruit yield per plant, ascorbic acid content and total soluble solids.

Singh *et al.* (2005a) conducted a field experiment on fifteen advance generation breeding lines of tomato, to study the variation for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity, lycopene content and dry matter and observed significant difference 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.

Singh *et al.* (2005b) conducted a field experiment with thirty tomato cultivars 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. The maximum number of fruits per plants was obtained from BT-117-5-3-1. Fruit yield was maximum (1.84 kg/plant) in DT-39. Most of the cultivars showed higher total soluble solids content in their fruits compared to the control. The acidity percentage in fruits was highest in KS-60. The physiological loss in weight at seven days was highest in NDT-111 and lowest in plant T-3. ATL-13 showed the highest lycopene content (59.67 mg/100g).

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

2.1.1 Plant Height

Golani *et al.* (2007) observed that the phenotypic and genotypic association of fruit yield was significant and negative with plant height. Kumari *et al.* (2007) observed the highest genotypic coefficient of variation for plant height followed by early yield, lycopene content, number of fruit bearing branches and titratable acidity.

Joshi and Choudhury (2003) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and noticed that plant height gave the highest heritability (78.82%). Matin *et al.* (2001) also reported that phenotypic variance was relatively higher than genotypic variance for this trait. They again observed that genotypic coefficient of variance was lower than phenotypic coefficient of variance indicating influence of environment for expression of this character.

Prasad and Mathura (1999) found high degrees of phenotypic and genotypic co-efficient of variance for plant height in 75 exotic genotypes of tomato. Aditya (1995) and Matin *et al.* (2001) reported significant variation for plant height.

According to Aditya (1995) plant height ranged between 48.8 and 104.2 cm while Matin *et al.* (2001) reported that it ranged between 70.70 and 103.80 cm.

2.1.2 Primary branches per plant

Shravan *et al.* (2004) conducted an experiment with 30 tomato genotypes in Utter Pradesh of India during 2001/02 winter to study their genetic variability and reported significant difference for number of primary branches per plant among the genotypes.

2.1.3 Secondary branches per plant

Chernet *et al.* (2013) evaluated 36 varieties of tomato to estimate genetic variability and its association among characters. Based on the mean value, the average mean value was more than twice of the minimum mean value for traits days to 50% flowering, number of primary and secondary branches, number of flower per plant, number of matured fruits per plant, fruit set percentage, weights of fruit per plant, single fruit weight, number of seeds per fruit and total fruit yield per hector indicating their maximum contribution to the total variability observed among the tomato genotypes.

2.1.4 Number of flower per cluster

Tasisa *et al.* (2011) evaluated 23 varieties of tomato to estimate variability, heritability and genetic advance in yield and yield components. Higher values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed fruits per plant, seeds per fruit, flower per cluster, fruit yield per plot, fruit cluster per plant, and plant height indicating the existence of higher magnitude of variability among the test genotypes for effective selection in respect of the above characters.

Haydar *et al.* (2007) conducted an experiment to study the genetic parameters, character association and path coefficient analysis between yield and yield contributing characters of different tomato genotypes. High genetic advance as percentage of mean was exhibited for fruit weight/plant followed by number of fruits in three cluster/plant and number of flowers in three clusters per plant.

2.1.5 Number of fruit per cluster

Samadia *et al.* (2006) evaluated 14 cultivars of tomato and found a range between 1.48-4.51 fruits per cluster. They reported almost similar estimates of PCV (41.86%) and GCV (41.83%) for this character.

Arun and Veeraragavathatham (2005) evaluated 37 genotypes of tomato and observed a range between 2.33-6.63 fruits per cluster. They reported the PCV (22.65%) was higher than GCV (15.93%) for this character. Aradhana and Singh (2003) evaluated 40 genotypes of tomato and found a range between 2.67-4.47 fruits per cluster. He reported the PCV (19.98%) was higher than GCV (10.54%).

2.1.6 Days to first flowering

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

Aditya (1995) reported that there were no significant differences in days to first flowering among the 44 tomato genotypes which ranged between 52.67 and 58.87 days.

Biswas and Mallik (1989) observed that a minimum of 66 days was necessary for first flowering for cv. Selectim-7 and maximum of 89 days for cv. Geogieva (1969) reported that pre-flowering periods of the varieties ranged from 56 to 76 days.

2.1.7 Days to 50% flowering

Samadia *et al.* (2006) evaluated 14 cultivars of tomato and observed a range between 52.1-67.10 days to 50% flowering. They reported the PCV (7.12%) was slightly higher than GCV (7.05%).

Singh *et al.* (2005) evaluated 10 genotypes of tomato and observed a range between 34-41 days to 50% flowering. They reported the PCV (6.21%) was higher than GCV (5.42%) for this character.

2.1.8 Days to maturity

Singh *et al.* (2005) evaluated 10 genotypes of tomato and reported that phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for this character. Prasanth and Aswanth (2003) evaluated 67 genotypes of tomato and found similar results for this character.

2.1.9 Number of fruits per plant

Joshi and Choudhury (2003) conducted a field experiment with forty tomato genotypes to evaluate their genetic variability and observed the number of fruits per plant gave the highest phenotypic and genotypic coefficient of variation (61.21 and 44.05, respectively) and genetic advance as percentage of mean (65.24).

Brar *et al.* (1998) estimated phenotypic and genotypic coefficient of variation and observed high variability in the characters of number of fruits per plant of 186 genotypes of tomatoes.

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

Islam *et al.* (1996) recorded highest genetic variability for number of fruits per plant in 26 diverse genotypes of tomato. Sahu and Mishra (1995) also reported wide range of genotypic variation for number of fruits per plant and they found high genotypic variation for number of fruits per plant.

Reddy and Reddy (1992) evaluated 139 tomato genotypes and estimated phenotypic and genotypic coefficient of variation. Considerable variation was observed for number of fruits per plant (4.0-296.5). Islam and Khan (1991) also reported significant variations for number of fruits per plant.

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

2.1.10 Average fruit weight

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.

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

Brar *et al.* (1998) reported that varietal differences were significant among 20 cultivars of tomato for average fruit weight ranged between 24.1 and 76.6 g. Singh *et al.* (1997) studied genetic variability of 23 genotypes of tomato and reported that phenotypic variation was quite large but genotypic variation was low for this character.

Sahu and Mishra (1995) reported that fruit weight had high genotypic coefficient of variation in 16 lines of tomato grown during the winter season of 1986 at Bhubaneswar, India.

Reddy and Reddy (1992) estimated phenotypic and genotypic variation, phenotypic and genotypic coefficient of variation for individual fruit weight. Considerable variation was observed for average individual fruit weight (1.25-158.87).

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

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

2.1.11 Fruit length

Singh *et al.* (2002) reported that phenotypic coefficient of variation was greatest for fruit length. Mohanty (2002) evaluated 18 genotypes of tomato and also found that phenotypic coefficient of variation was greatest for fruit length.

2.1.12 Fruit diameter

Singh *et al.* (2002) reported that phenotypic coefficient of variation was the greatest for fruit diameter. Anupam *et al.* (2002) evaluated 30 genotypes of tomato and also found that phenotypic co-efficient of variation was greatest for fruit diameter.

2.1.13 Fruit yield per plant

Matin *et al.* (2001) reported significant differences for yield per plant among the genotypes tested. They also reported that phenotypic variance was little higher than genotypic variance indicating slight environmental influence on this trait.

Brar *et al.* (1998) reported high degrees of variation for average yield per plant among the 186 genotypes tested. Kumar and Tewari (1999) reported genotypic coefficient of variation was higher for average yield per plant among the 32 tomato genotypes. Singh *et al.* (1997) observed that phenotypic variation was quite higher than genotypic variation for these traits in 27 genotypes of tomato.

Aditya (1995) observed highly significant differences for average yield per plant among 44 genotypes of tomato. He also reported that phenotypic variance and phenotypic coefficient of variation were higher than genotypic variance and genotypic coefficient of variation respectively.

Reddy and Reddy (1992) observed considerable variations for yield per plant in 139 tomato varieties. Sonone *et al.* (1986) reported that genotypic and phenotypic variances were high for average yield per plant. Dudi *et al.* (1983) reported that phenotypic and genotypic coefficient of variation was high for average yield per plant. Sachan and Sharma (1982) performed an experiment with certain tomato genotypes at south Guzrat, India and reported significant differences among the genotype for yield per plant.

2.2 Heritability and genetic advance

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. Heritability and genetic advance are the most important parameters to judge the breeding potentiality of a population for future development through selection. Many researchers have studied heritability and genetic advance of yield and many yield contributing characters of tomato. The literatures very relevant to the present study are reviewed below:

Patel *et al.* (2013) evaluated thirteen tomato genotypes to estimate variability, heritability and genetic advance in yield and yield contributing characters. A high degree of significant variation was observed for all the characters studied except pericarp thickness and number of locules. High heritability with high genetic advance as percent of mean was observed for fruit yield per plant and average fruit weight which could be improved by simple selection.

Al-Aysh *et al.* (2012) reported that high heritability coupled with high genetic advance as percentage over mean were observed for number of primary branches per plant, number of fruits per plant, number of fruits per cluster, average fruit weight and fruit yield per plant indicating that selection for these characters would give good response.

Tasisa *et al.* (2011) evaluated 23 varieties of tomato to estimate variability, heritability and genetic advance in yield and yield components. High heritability values coupled with high genetic advance were observed in respect of seeds per fruit, fruits per plant, plant height and fruit cluster per plant, indicating selection for these traits would be most likely effective in tomato improvement.

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

Kumari and Subramanian (2007) reported that the estimates of heritability were high for all 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 co-efficient of variation and genetic gain for fruit weight, number of locules per fruit and fruit yield, which could be improved by simple selection.

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 selection of the better genotypes in tomato.

Singh *et al.* (2005) estimated heritability and showed that heritability estimates were high for all the characters for November planting except for lycopene content.

Shravan *et al.* (2004) 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 fruit, 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.

Joshi *et al.* (2004) observed moderate heritability and moderate genetic gain for number of fruits per cluster, fruit length, fruit breadth, stem and 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.

Arun (2005) reported that moderate heritability associated with moderate genetic advance for plant height of 37 genotypes of tomato. Mohanty (2003) observed that

high heritability with high genotypic co-efficient of variation was for fruit weight, plant height, number of fruits, number of branches per plant.

Singh *et al.* (2002a) reported that heritability was high for all the characters except days from fruit setting to red ripe stage and the highest genetic advance was predicted for average fruit weight, followed by shelf life of red ripe fruits. Matin *et al.* (2001) reported high degrees of heritability and genetic advance for fruits per plant, individual fruit weight and number of seeds per fruit.

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

Nessa *et al.* (2000) reported high heritability for number of fruits per plant, plant height and moderate heritability for yield per plant. Prasad *et al.* (1999) estimated heritability for 75 exotic genotypes of tomato and reported very high heritability along with high genetic advance by fruit weight.

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.

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, number of fruits per plant. Islam *et al.* (1996) studied heritability and genetic advance in 26 diverse genotypes of tomato. High heritability and genetic advance was observed in number of fruits per plant, plant height, fruit yield and individual fruit weight.

Mittal *et al.* (1996) estimated heritability 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.

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.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.

Godekar *et al.* (1992) obtained high values of heritability along with high genetic advance by fruit weight. Reddy and Reddy (1992) studied heritability and genetic advance in 139 tomato varieties. Heritability values for yield per plant, number of fruits per plant, average individual fruit weight were 97.99%, 95.96% and 98.46% respectively.

Bai and Devi (1991) evaluated five varieties and nine hybrids of tomato and 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 heritability values were high for most of the characters but moderate for days to 1st flowering, maturity and plant height.

Kasrawi and Amr (1990) reported that plant height gave comparatively higher heritability estimates in a study of seven quality characters using F_2 populations. 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. They also reported 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. Mallik (1985) reported high genetic advance in plant height, number of fruits per plant and individual fruit weight and yield per plant but low heritability for yield per plant. Dudi *et al.* (1983) reported that heritability and genetic advance were high for number of fruits per plant and individual fruit weight and yield per plant.

2.3 Correlation coefficient:

Correlation between the characters is an estimate to evaluate the inter-relationships between the characters which helps the breeders to choose selection techniques. In most cases, correlation between yield and yield contributing characters was studied as increased yield is one of the main targets of most of the breeders. Fruit yield of tomato is the final character which is contributed by a complex chain of interrelating effects of different yield contributing characters. The yield contributing characters are also interrelated among themselves. So, association of characteristics with yield and among its components is important for planning effective selective breeding programme for maximization of yield. Such correlation studies may vary due to agro-climatologically 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 of increase in the total yield by selecting that component. But, negative correlation coefficient among yield components was generally observed indicating selection for an increase in any component might not bring improvement for yield. Many authors have studied correlation between yield and yield contributing characters of tomato. Some pertinent recent literatures are reviewed in this section.

Reddy *et al.* (2013) were carried out an experiment to study correlation and path analysis in nineteen tomato genotypes for yield and quality characters. The association studies showed that fruit yield per plant was positively and significantly correlated with number of fruits per plant and fruit width. However, fruit yield per plant was negatively and significantly correlated with days to last fruit harvest and shelf life.

Rani *et al.* (2010) revealed that fruit weight, pericarp thickness, acidity, ascorbic acid and lycopene were positively and significantly associated with yield per plant, while number of fruits per plant was associated negatively. YaDong *et al.* (2010) showed that the lycopene content is very significantly and positively correlated with single inflorescence flower numbers, single inflorescence fruit numbers and soluble solids content, but very significantly and negatively correlated with pedicel length and single fruit weight. They also reported that the lycopene content is significantly and positively correlated with fruit shape index, but significantly and negatively correlated with fruit firmness, flesh thickness, longitudinal diameter fruit.

Anitha *et al.* (2007) reported 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. Golani *et al.* (2007) observed that fruit weight had significant and positive correlation with fruit length, fruit girth and number of locules per fruit at both levels.

Wagh *et al.* (2007) performed correlation analysis and observed that yield improvement can be achieved by selection for 50% flowering, plant height, number of fruits per plant along with fruit quality characters such as lycopene, beta -carotene, ascorbic acid and titratable acidity.

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, total yield, total soluble solids and juice percentage observed that improvement in yield could be managed by selection for number of flowers per cluster, flower clusters at first picking, number of fruits per cluster and weight per fruit.

Manivannan *et al.* (2005) carried out correlation coefficient analysis in cherry and observed that the phenotypic and genotypic correlation coefficient was the highest for the number of fruits per plant, fruit weight and fruit yield. Fruit yield was significantly and positively correlated with the number of leaves, fruit weight and juice content.

Arun *et al.* (2003) observed that yield per plant of tomato 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, stem end scar size, pericarp thickness, whole fruit firmness and shelf life of the fruits. However, fruit weight was negatively correlated with the number of fruits per plant, number of fruits per cluster and ascorbic acid content.

Kumar *et al.* (2004) performed correlation coefficient analysis of 30 tomato genotypes and observed that number of fruits per plant had significant and positive correlation with fruit yield per plant, whereas fruit acidity had significant and positive correlation with number of locules per fruit.

Singh *et al.* (2004) studied genetic parameters, inter-relationships and path co-efficient 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.

Kumar *et al.* (2003) carried out correlation coefficient analysis of thirty diverse tomatoes and observed that the number of fruits per plant had significant and positive correlation with fruit yield per plant, whereas fruit acidity had significant and positive correlation with number of locules per fruit and average fruit weight was significantly correlated with physiological weight loss. They also observed that correlation coefficients at the genotypic level were generally higher than the corresponding phenotypic ones. They found that yield per plant was positively and significantly associated with plant height, fruit number per plant, fruit shape index and pericarp thickness.

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

Bodunde (2002) studied path coefficient analysis in tomato and reported that the number of leaves at flowering, plant height and fruit diameter directly affected yield and results showed that the 5 traits were directly responsible for the determination of yield in tomato.

Harer *et al.* (2002) studied correlation of thirty-seven tomato genotypes and showed that genotypic correlation was higher than phenotypic correlation for all characters examined. 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 and ascorbic acid content had negative association with fruit yield.

Nesgea *et al.* (2002) studied correlation coefficient analysis in 13 tomato genotypes and revealed that plant height, number of branches per plant, plant spread, fresh plant weight, number of fruiting clusters, number of days to 50% flowering, number of fruits per cluster and number of fruits per plant should be considered for the enhancement of the yield of tomato.

Singh *et al.* (2002) showed that total yield was significantly and positively correlated with marketable yield, average fruit weight, and days from fruit setting to red ripe stage. They also reported that the phenotypic coefficient of variation was the largest for fruit length, number of fruits per plant, plant height, fruit weight per plant, fruit yield and number of fruit clusters per plant and moderate for number of fruits per cluster, number of primary branches per plant, fruit diameter and total soluble solid content.

Susic *et al.* (2002) showed that a significant negative correlation was between mean fruit mass and number of fruits per plant and a significant positive correlation was found between fruit length and fruit width. The number of locules per fruit was significantly and positively correlated with fruit weight, fruit length, fruit width and number of fruits per plant. Tiwari (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.

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

Matin *et al.* (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. They also reported that number of fruits per plant also had significant positive correlations with fruit dry matter content and found significant negative correlations between number fruits per plant and individual fruit weight; and dry matter was negatively correlated with individual fruit weight.

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 (1995) studied phenotypic and genotypic correlation co-efficient to find out the associations between eight characters of 44 genotypes of tomato. She 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. Islam and Khan (1991) observed high positive phenotypic and genotypic correlation with individual fruit weight, fruits per plant, plant height and days to flowering on yield.

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/lines of tomato and observed that individual fruit weight had positive significant correlations with plant height and yield.

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

2.4 Path coefficient:

Path coefficient 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 coefficient between yield and yield contributing characters provides an exact picture of the relative importance of direct and indirect influences of each other component characters on fruit yield. Path analysis, therefore, is a useful tool for understanding yield except chain of relationship between yield and yield contributing characters. It also provides valuable additional information for improving fruit yield via selection for its yield components. Recent publications involving path co-efficient analysis between yield and components of yield relevant to the present study are reviewed in this section.

Reddy *et al.* (2013) were carried out an experiment to study correlation and path analysis in nineteen tomato genotypes for yield and quality characters. Path analysis studies depict the cause and effect relationship revealed that plant height, number of fruits per plant, fruit length, fruit width and ascorbic acid had high positive direct effects on fruit yield per plant. Hence, direct selection for these traits is done for improving fruit yield per plant. 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.

Anitha *et al.* (2007) performed path analysis and revealed that oxalates, acidity, ascorbic acid and TSS had positive and high direct effects on lycopene. Golani *et al.* (2007) performed path analysis and confirmed that the 10-fruit weight had the highest positive direct effect, followed by the number of locules per fruit. Manivannan *et al.* (2005) carried out path coefficient analysis in cherry tomato and showed that fruit weight had the highest direct effect on fruit yield.

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

Arun *et al.* (2003) revealed that the number of fruits per plant is the most important yield contributing character followed by plant height through path coefficient analysis. Joshi *et al.* (2004) carried out path coefficient analysis and showed that the number of fruits per plant is the most important yield contributing trait followed by fruit length, fruit breadth and plant height.

Singh *et al.* (2004) performed path analysis between yield and yield contributing characters of 92 tomato genotypes and reported that number of fruits per plant exerted the high positive direct effect on yield followed by average weight per fruit, number of primary branches per plant, plant height, days to 50% flowering, number of fruits per cluster and days to first fruit harvest. However, days to first fruit set, number of primary branches per plant, plant height, number of fruit clusters per plant and total soluble solids had direct negative effects on yield.

Kumar *et al.* (2003) performed path analysis of thirty diverse tomato genotypes and indicated that fruit number per plant had the highest positive direct effect on yield per plant followed by average fruit weight. Mohanty (2003) conducted a field experiment to study path coefficient analysis of 18 tomato cultivars and observed that the number of fruits per plant and average fruit weight had positive direct effects on the yield and negative indirect effects on each other.

Bodunde (2002) carried out a field experiment on path coefficient analysis and observed that the number of leaves at flowering, plant height and fruit diameter directly affected yield. Results showed that the 5 traits (number of leaves at first flowering, plant height at first harvest, fruit length, fruit diameter and days to maturity) were directly responsible for the determination of yield in tomato.

Harer *et al.* (2002) carried out a field experiment to study path analysis of thirty-seven tomato genotypes and reported that number of fruits per cluster; average fruit weight and number of fruits per plant had direct maximum effects on fruit yield. Mohanty (2002) performed path analysis and showed that the number of branches per plant and average fruit weight exerted high positive direct effect on yield and high positive indirect effect with each other.

Padma *et al.* (2002) performed path analysis and revealed that number of branches, dry matter production, fruit weight, fruit length, fruit volume, TSS content, juice

percentage, and number of fruits per plant exhibited positive effect on yield per plant at the genotypic and phenotypic levels. Matin *et al.* (2001) observed that the maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant. He also reported that days to first flowering, plant height and number of seeds per fruit had negative direct effect on yield per plant.

Verma and Sarnaik (2000) conducted a field experiment to perform path analysis of yield components in thirty tomato genotypes and observed that total number of fruits per plant, average weight of fruit, thousand seed weight and number of branches per plant exhibited positive as well as high direct effects. Vikram and Kohli (1998) carried out an experiment with 25 genotypes of tomato and accomplished path co-efficient analysis and revealed that mean fruit weight is the most important yield contributing trait following fruits per plant.

Aditya (1995) carried out genotypic and phenotypic path co-efficient analysis and revealed that plant height and number of fruits per plant had high positive direct effect on yield and on the other hand, weight of individual fruit had positive indirect effect on yield per plant. McGiffen *et al.* (1994) revealed that number of fruits was the most important yield component which had direct effect on yield.

Supe and Kale (1992) studied correlation and 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 though its correlation co-efficient with yield was positive.

Islam and Khan (1991) observed that fruits per plant, average fruit weight, plant height and days to first flowering had positive direct effects on yield of tomato. Alam *et al.* (1988) studied path coefficient in 19 cultivars of tomato and found that maximum direct contribution towards yield was through individual fruit weight followed by number of fruits per plant.

Gomez (1987) reported that days to first flowering has negative direct effect on yield of tomato. Sonone *et al.* (1986) reported highest direct effect of plant height and fruit weight on fruit yield of tomato.

Gorbatenko and Gorbatenko (1985) carried out path coefficient analysis of economically useful characters of tomato and found that individual fruit weight had an appreciable direct effect on yield per plant. Dudi and Kalloo (1982) studied path analysis in tomato and reported highest direct effects of early yield per plant, fruit weight and fruits per plant.

2.5 Genetic diversity

The assessment of genetic diversity using quantitative traits has been of prime importance in many contexts particularly in differentiating well defined populations. The germplasm in a self- pollinated crop can be considered as a heterogeneous set of groups, since each group being homozygous within itself. Selecting the parents for breeding program for such crops is critical because, the success of such program depends upon the seggregants of hybrid derivatives between the parents, particularly when the aim is to improve the quantitative characters like yield. To help the breeder in the process of identifying the parents, that need better, several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives. Among them, Mahalanobis's generalized distance occupies a unique place and an efficient method to gauge the extent of diversity among genotypes, which quantify the differences among several quantitative traits. In crop improvement program, genetic divergence has been considered as an important parameter to identify most diverse parents for obtaining highly heterotic F_1 generation through selection. Many scientists have studied genetic divergence of tomato on the basis of Mahalanobis's D^2 –statistic based on multivariate analysis. Among them most relevant recent publications are reviewed below:

Meena and Bahadur (2013) were carried out an experiment at Vegetable Research Farm, Department of Horticulture, SHIATS and Allahabad during 2012-13. All the genotypes were grouped into six clusters based on D^2 values, which exhibited no association between geographical and genetic divergence. The intra-cluster distance was maximum for cluster V (10192.68) and minimum for cluster III (0.0). The maximum distance at inter-cluster level was between cluster III and cluster VI (47922.37) followed by clusters I and VI (44098.14) which may serve as a potential stocks of genotypes for hybridization programme.

Shashikanth *et al.* (2010) carried out a field experiment to study genetic divergence of 30 tomato genotypes and observed that analysis of variance of the genotypes were significantly different for all the characters studied indicating the existence of genotypic variation; there was no parallelism between genetic diversity and geographical divergence in tomato and suggested that high diversity among the genotypes belonging to cluster VII and X can be selected in hybridization programs to obtain good seggregants.

Mahesh *et al.* (2006) grouped 30 tomato genotypes into nine clusters studied based on D^2 analysis. The cluster mean indicating that days to 50% flowering, plant height, number of branches per plant, number of cluster per plant, number of fruits per cluster and fruits yield per plant were reported as chief contributors towards divergence.

Sharma *et al.* (2006) conducted an experiment with 60 genotypes of tomato genetic divergence. The genotypes grouped into 10 clusters, maximum divergence within a cluster was exhibited by the cluster VIII (1.513), closely followed by cluster III (1.528) and cluster V (1.460), whereas, cluster VIII and II were the most divergent from each other followed by cluster VII and cluster VIII.

Veershetty (2004) grouped 32 tomato genotypes into 10 clusters based on D^2 analysis. Number of fruits per cluster, plant height, number of branches, pericarp thickness, average fruit weight and TSS content of fruit were reported as chief contributors towards divergence.

Arun *et al.* (2003) studied the nature and magnitude of genetic divergence in 73 tomato genotypes of different origin for quantitative characters and grouped the genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes in cluster 5 having 6 genotypes. The mean fruits yield per plant (1034 g/plant) and average fruit weight (102.76 g/plant) were the highest in cluster 5 and 3 respectively. The plant height (135.91 cm), harvest duration (37.77 days) were maximum in cluster 15 and the lowest number of leaves (2,0280) was recorded in cluster 9 and cluster 6 consisted of the highest number of fruits per cluster (4.90).

Markovic *et al.* (2002) studied genetic divergence of 25 entirely reward cultivars and local populations of tomato originating from the area of the former Yugoslavia and

recorded the presence of a higher degree of genetic divergence in different genotypes consisting of 5 clusters.

Dharmatti *et al.* (2001) carried out a field experiment in Dharwad, Kamataka, India during 1994-95 to assess genetic diversity in a population of 402 tomato lines by using multivariate analysis based on plant height, number of branches, number of cluster per plant, fruits per cluster, number of fruits per plant, yield per plant, incidence of tomato curl viruses and number of white flies per plant. They grouped the lines into 4 clusters based on the similarities of D^2 values. Cluster –I was the biggest having 217 genotypes, which also consisted of commercial ToLCV and cluster –II and IV had 99 and 35 genotypes respectively. Considerable diversity within and between cluster was noticed.

Mohanty and Prusti (2001) carried out a study on genetic diversity among 18 indigenous and exotic tomato cultivars for five economic characters (plant height, number of branches, number of fruits per plant, average fruit weight and yield per plant) in Orissa, India during rabi 1998-99 and found considerable variations among the accessions. They could group the genotypes into 5 clusters indicating two solitary groups and reported that genetic diversity was not associated with geographical distribution. Maximum inter cluster distance (D^2=1289.31) was observed between the cluster I and V. The distance between cluster I and III, III and IV, IV and V was moderate. They also reported that number of fruits per plant and average fruit weight contributed predominantly towards the total divergence.

Sharma and Verma (2001) studied genetic divergence of 18 genotypes of tomato and grouped them into 5 clusters irrespective of geographic divergence indicating no parallelism between genetic diversity and geographical divergence. Fruit yield was one of the three characters which played an important role in divergence between the populations. Kumar and Tewari (1999) studied genetic divergence of 32 tomato genotypes and could group them into 9 clusters based on D^2 values. The magnitude of inter cluster distance was comparatively lower than that of inter cluster distances.

Rai *et al.* (1998) studied 37 tomato genotypes and could able to group them into four clusters using a non-hierarchical clustering approach with the help of Mahalanobis's D^2 –statistic for yield and yield contributing characters. The population was grouped into 4 clusters. The clustering pattern indicates that there was no association between

geographical distribution of genotype and genetic divergence characters namely number of primary branches, days to first flowering, plant height and average fruit weight contributed to maximum divergence. Patil (1984) grouped 55 tomato genotypes into nine clusters studied based on D^2 analysis. A maximum of 16 genotypes entered cluster I, followed by 15 in cluster IV, 9 in cluster III, 7 in cluster II, 4 in cluster V and remaining four clusters consisted of solitary genotype.

Chapter III

Materials and Methods

CHAPTER III

METERIALS AND METHODS

An experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during the period from November 2013 to April 2014 to select short durated and high yielding genotypes of tomato (*Solanum lycopersicum* L.). A brief description about the location of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizer, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc. are presented as follows:

3.1 Experimental site

The research work was conducted at the Sher-e-Bangla Agricultural University farm, Dhaka, Bangladesh during the period from November 2013 to April 2014.

3.2 Geographical Location

The experimental area was situated at 23°77'N latitude and 90°33'E longitude at an altitude of 8.6 meter above the sea level. The experimental field belongs to the Agro-ecological zone of "The Modhupur Tract", AEZ-28. This was a region of complex relief and soils developed over the Modhupur clay, where floodplain sediments buried the dissected edges of the Modhupur Tract leaving small hillocks of red soils as 'islands' surrounded by floodplain. The experimental site was shown in the map of AEZ of Bangladesh (Appendix I).

3.3 Climate

Area has subtropical climate, characterized by high temperature, high relative humidity and heavy rainfall in Kharif season (April-September) and scanty rainfall associated with moderately low temperature during the Rabi season (October-March). Weather information regarding temperature, relative humidity, rainfall and sunshine hours prevailed at the experimental site during the study period was presented (Appendix II).

3.4 Characteristics of soil

Soil of the experimental site belongs to the general soil type, shallow red brown terrace soils under Tejgaon series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0-6.6 and had organic matter 0.84%. Experimental area was flat having available irrigation and drainage system and above flood level. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physiochemical properties of the soil are presented (Appendix III).

3.5 Planting materials

Twenty one (21) genotypes of tomato were used for the present research work. Among these genotypes three land races, seven popular varieties, eleven advanced lines were included. The genetically pure and physically healthy seeds of these genotypes were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur and land races were collected from farmer's field. The name and origin of these genotypes are presented in Table 1.

Table 1. Name and origin of twenty one tomato genotypes used in the present study

Genotypes No.	Name/Acc No. (BD)	Origin
G1	Local Jessore-2	Farmer's field
G2	Local Jessore-3	Farmer's field
G3	BARI Tomato-7	PGRC, BARI
G4	BARI Tomato-9	PGRC, BARI
G5	BD-7281	PGRC, BARI
G6	Local Kushtia-1	Farmer's field
G7	BARI Tomato-15	PGRC, BARI
G8	BD-9960	PGRC, BARI
G9	BD-7289	PGRC, BARI
G10	BD-7279	PGRC, BARI
G11	BD-7290	PGRC, BARI
G12	BARI Tomato-8	PGRC, BARI
G13	BARI Tomato-3	PGRC, BARI
G14	BD-10321	PGRC, BARI
G15	BD-7762	PGRC, BARI
G16	BD-7276	PGRC, BARI
G17	BD-7748	PGRC, BARI
G18	BARI Hybrid-4	PGRC, BARI
G19	BD-7285	PGRC, BARI
G20	BARI Tomato-11	PGRC, BARI
G21	BD-9011	PGRC, BARI

Here, PGRC= Plant Genetic Research Centre, BARI= Bangladesh Agricultural Research Institute.

3.6 Design and layout of the experiment

The study was laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 195 m^2 (13m x15m). A distance of 1m from block to block, 60 cm from row to row and 50 cm from plant to plant was maintained. The genotypes were randomly distributed to each row within each line.

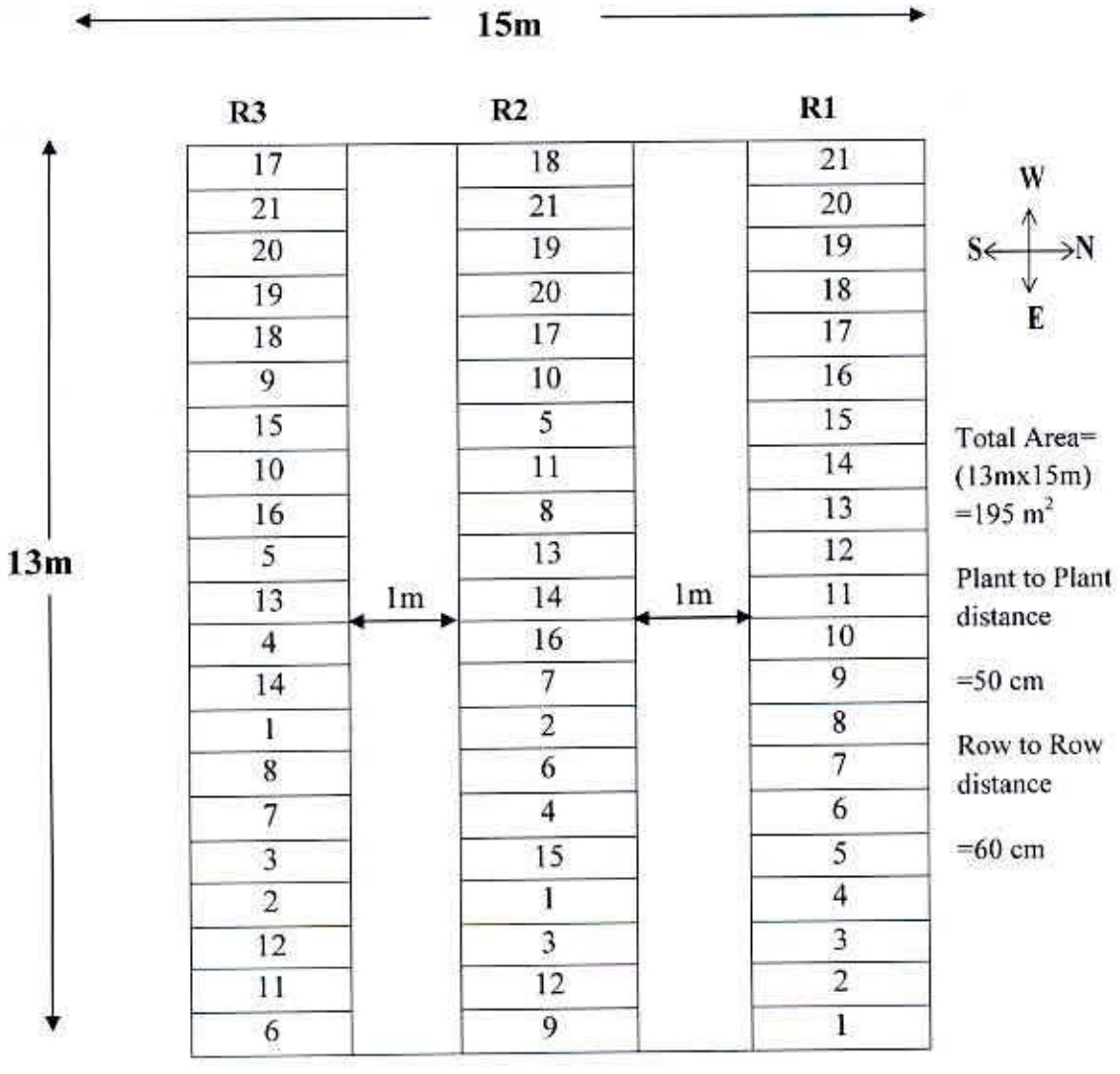


Figure 1. Showing the layout of the experimental plot

3.7 Seedbed preparation and raising seedling

The seeds were sown on 13 November 2013 in the seedbed. Seedlings of all genotypes were raised in seedbeds in the farm of Sher-e-Bangla Agricultural University, Dhaka-1207. Recommended cultural practices were taken up before and after sowing the seeds. When the seedlings become 25 days old; those were transplanted into the main field.

3.8 Land preparation

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth in the last week of November 2013. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.9 Manure and fertilizer application

Total cowdung and triple super phosphate (TSP) were applied in the main 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 half muriate of potash (MOP) were applied in the plot after five weeks of transplanting. Doses of manure and fertilizers used in the study are showing in Table 2.

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

Sl. No.	Name of the fertilizer	Dose	
		Applied in the plot	Quantity/ha
01	Urea	12 kg	550 kg
02	TSP	10 kg	450 kg
03	MP	7 kg	250 kg
04	Cow dung	200 kg	10 ton

3.10 Transplanting of seedlings into the main field

The seedlings were raised in the seedbed in usual way and 25 days old seedlings were transplanted in the main field on 8 December, 2013. The transplanted seedlings were watered regularly for the faster establishment in the soil.

3.11 Intercultural operation

When the seedlings were well established, 1st mulching and weeding were done uniformly in all the plots. 2nd weeding was done after 20 days of the first one. Mechanical support was provided to the growing plants with bamboo sticks to keep them erect. During early stages of growth, pruning was done by removing some leaves to allow the plants to get more sunlight and to reduce the self-shading and incidence of increased insect infestation.

3.11.1 Thinning and gap filling

When the seedlings were well established, the soil around the base of each seedling was pulverized. A few gaps filling was done with healthy seedlings of the same stock where initial planted seedlings failed to survive. Thinning was done for the proper development and avoid crowd environment.

3.11.2 Staking

When the plants were well established, staking was done using bamboo sticks to keep the plan erect.

3.11.3 Weeding and mulching

Weeding and mulching were done as per requirement. At the very first stage weeding was done for ease of aeration and less competition seedling growth and mulch was provided after an irrigation to prevent crust formation and facilitate good aeration.

3.11.4 Irrigation and after care

After transplanting the seedlings were properly irrigated for 3 consecutive days. Then flood irrigation was given to the plants after each top dressing of urea. Final irrigation was given during active fruiting stage.

3.11.5 Pesticide application

During the cropping period, there was no significant pest infestation in the field, hence no control measure was undertaken. In order to prevent disease infestation, 'Ripcord 10EC' was used for 6 times at an interval of 7 days from 06 January to 11 February 2014. There were different types of weeds which were controlled effectively by hand weeding.

3.12 Harvesting

Harvesting continued for about one and half month because fruits of different lines matured progressively at different dates and over long time. Fruits were picked on the basis of maturity, size, color and age being determined for the purpose of consumption as the fruit grew rapidly and soon get beyond the marketable stage. Frequent picking was done throughout the harvesting period. Harvesting was started from 04 March to 20 April, 2014. The fruits per entry were allowed to ripe and then seeds were collected for future use. Photograph showing one replication view of the experimental field in Plate 1, a single tomato plant in the experimental field in Plate 2, a tomato plant with flower in Plate 3 and a tomato plant with a cluster of tomatoes in Plate 4.

Plate 1: View of the experimental field

Plate 2: A single tomato plant in the experimental plot

Plate 3: A tomato plant with flower

Plate 4: A tomato plant with a cluster of tomatoes

3.13 Data recording

Three plants in each line were selected randomly and were tagged. These tagged plants were used for recording observation for the following characters.

3.13.1 Plant height (cm)

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

3.13.2 Primary branches per plant

The number of branches arising from the main stem above the ground was recorded.

3.13.3 Secondary branches per plant

The number of branches arising from the primary branches was recorded.

3.13.4 Number of flower per cluster

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

3.13.5 Number of fruit 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.

3.13.6 Days to first flowering

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

3.13.7 Days to 50 percent flowering

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

3.13.8 Days to maturity

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

3.13.9 Number of fruits per plant

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

3.13.10 Average fruit weight (g)

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

3.13.11. Fruit length (mm)

It was measured from stalk end to blossom end by using slide calipers.

3.13.12. Fruit diameter (mm)

It was measured from fruit breadth at highest bulged portion of the fruit by using slide calipers.

3.13.13. Fruit yield per plant (kg)

The weight of fruits from each picking was recorded from the three labeled plant of each line 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.

3.14.1 Statistical analysis:

Mean data of the characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using the mean values (Singh and Chaudhary, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.14.1.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

$$\text{Phenotypic variance } (\sigma^2_{ph}) = \sigma^2_g + EMS$$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

3.14.1.2 Estimation of genotypic and phenotypic coefficient of variation

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

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

The phenotypic coefficient of variation was calculated from the following formula.

$$\text{Phenotypic coefficient variation (PCV)} = \frac{\sqrt{\sigma^2 ph}}{\bar{x}} \times 100$$

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.14.1.3 Estimation of heritability

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

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.14.1.4 Estimation of genetic advance

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

Genetic advance (GA) = K. h^2. σ_{ph}

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

Where,

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

σ_{ph} = Phenotypic standard deviation

h^2_b= Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_{ph} = Phenotypic variance

3.14.1.5 Estimation of genetic advance mean's percentage

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

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

3.14.2 Estimation of simple correlation coefficient:

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

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

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observations

3.14.2.1 Estimation of genotypic and phenotypic correlation coefficient

For calculating the genotypic and phenotypic correlation coefficient for all possible combinations the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted.

The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The covariance components were used to compute 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 covariance 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 traits x and y

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

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

3.14.3 Estimation of path coefficient

Path coefficient analysis 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 grain yield. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3.....and 13 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

$r_{1.y} = r_{1.1} P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y} + r_{1.9} P_{9.y} + r_{1.10} P_{10.y} + r_{1.11} P_{11.y} + r_{1.12} P_{12.y}$

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

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

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

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

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

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

$r_{8.y} = r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + r_{8.8} P_{8.y} + r_{8.9} P_{9.y} + r_{8.10} P_{10.y} + r_{8.11} P_{11.y} + r_{8.12} P_{12.y}$

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

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

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

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

Where,

r_{iy} = Genotypic correlation coefficients between y and i th character (y = Grain yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,……,13)

1 = Plant Height

2 = Primary branches per plant

3 = Secondary branches per plant

4 = Number of flower per cluster

5= Number of fruit per cluster

6= Days to first flowering

7= Days to 50% flowering

8= Days to maturity

9= Number of fruits per plant

10= Average fruit weight (g)

11= Fruit length (mm)

12= Fruit diameter (mm)

13= Fruit yield per plant

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

$r_{1.1}P_{1.y}$ = the direct effect of 1 on y

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

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

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

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

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

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

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

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

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

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

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

Where,

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

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

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

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

Where,

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

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

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

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

3.14.4 Multivariate analysis

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

3.14.4.1 Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying

most of the original variability in a smaller number of dimensions. Therefore, principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity. Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.14.4.2 Principal Coordinate Analysis (PCO)

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).

3.14.4.3 Cluster Analysis (CA)

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

3.14.4.4 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.

3.14.4.5 Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhury

(1985).The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

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

Where,

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

x = Number of characters

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

3.14.4.6 Computation of average intra-cluster distances

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

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

Where,

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

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

3.14.4.7 Computation of average inter-cluster distances

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

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

Where,

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

n_i = Number of populations in cluster i

n_j = Number of populations in cluster j

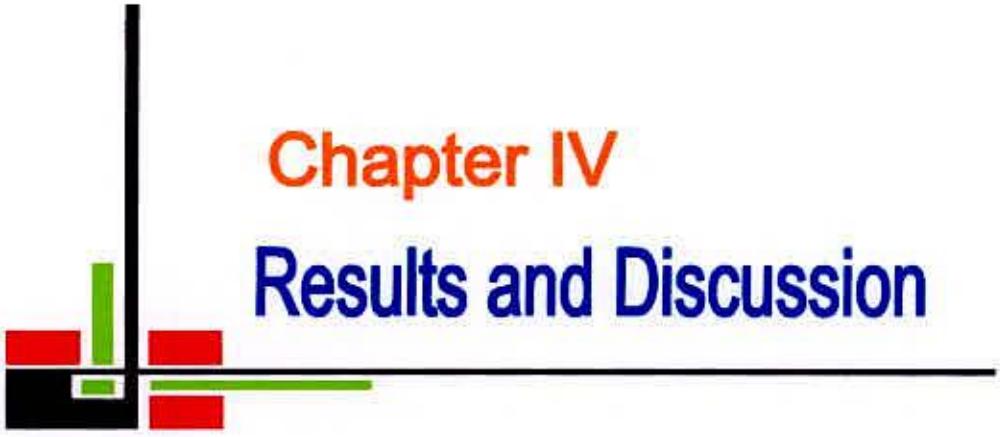
3.14.4.8 Cluster diagram

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

3.14.4.9 Selection of varieties for future hybridization programme

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

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



Chapter IV

Results and Discussion

CHAPTER IV

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Diversity is the function of parent selection and also heterosis. The availability of transgressive segregants in a breeding programme depends upon the divergence of parents. Thus, the accurate information on the nature and degree of diversity of the parents is the prerequisite of an effective breeding programme. The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to screen better genotypes for hybridization programme. The data on plant height, primary branches per plant, secondary branches per plant, number of flower per cluster, number of fruit per cluster, days to first flowering, days to 50% flowering, days to maturity, single fruit weight, fruit length, fruit diameter, number of fruit per plant, fruit yield per plant etc were recorded. Genetic diversity was analyzed using GENSTAT software programme. Therefore, genetic parameters and more than one multivariate technique were required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001).

4.1 Genetic parameters

The analysis of variance indicated the existence of highly significant variability for all the characters studied. The mean sum of square, mean, range, variance components, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in Table 3 and Table 4.

4.1.1 Plant height (cm)

The grand mean of plant height was recorded 100.05 cm. It ranged from 61 cm to 160.78 cm (Table 3). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (160.78 cm) was recorded by the "BD-7279" and the lowest plant height (61.00 cm) was recorded by "BD-7748" (Appendix- IV). The PCV and GCV were 31.23% and 30.40% respectively (Table 4). There was little difference between the phenotypic and genotypic coefficient of variation indicating little environmental influence in the expression of this character. In the present study, the genotypic and phenotypic

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Table 3. Estimation of genetic parameters in thirteen characters of 21 genotypes in tomato

Parameters	Range	Mean	MS	CV (%)
PH	61.00-160.78	100.05	2,826.50**	7.13
PBP	5.80-12.55	9.61	8.55**	14.01
SBP	3.33-14.00	7.18	22.64**	21.52
NFC	6.37-15.93	8.52	16.63**	13.23
FPC	3.07-10.78	4.47	8.39**	19.07
DFF	46.00-61.67	52.00	56.10**	4.45
D50%F	52.00-67.33	58.41	80.66**	3.83
DM	82.33-124.45	113.74	364.17**	2.43
FPP	28.55-415.00	124.83	23,105.76**	15.49
AFW	6.93-73.97	34.45	1,013.50**	19.28
FL	23.32-52.76	35.22	213.74**	10.92
FD	5.51-16.06	11.92	23.50**	9.71
FYP	1.02-3.46	1.79	1.18**	15.59

** Mean square is significant at the 0.01 level.

PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flowers per cluster, FPC = Number of fruits per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm), FYP = Fruit yield per plant (Kg), MS = mean sum of square, CV (%) = Coefficient of variation.

Table 4. Estimation of genetic parameters in thirteen characters of 21 genotypes in tomato

Parameters	σ^2 p	σ^2g	σ^2 e	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
PH	976.14	925.18	50.96	31.23	30.40	7.13	94.78	61.00	60.97
PBP	4.06	2.25	1.81	20.98	15.61	14.01	55.37	2.30	23.93
SBP	9.14	6.75	2.39	42.10	36.19	21.52	73.87	4.60	64.07
NFC	6.39	5.12	1.27	29.66	26.55	13.23	80.12	4.17	48.96
FPC	3.29	2.56	0.73	40.51	35.73	19.07	77.83	2.91	64.94
DFF	22.26	16.92	5.34	9.07	7.91	4.45	76.00	7.39	14.21
D50%F	30.23	25.22	5.02	9.41	8.60	3.83	83.41	9.45	16.17
DM	126.47	118.85	7.62	9.89	9.59	2.43	93.97	21.77	19.14
FPP	7951.26	7577.25	374.01	71.43	69.73	15.49	95.30	175.05	140.23
AFW	367.26	323.12	44.14	55.63	52.18	19.28	87.98	34.73	100.82
FL	81.10	66.32	14.78	25.57	23.13	10.92	81.78	15.17	43.08
FD	8.73	7.39	1.34	24.78	22.80	9.70	84.66	5.15	43.22
FYP	0.45	0.37	0.08	37.36	33.95	15.59	82.58	1.14	63.55

PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flowers per cluster, FPC = Number of fruits per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm), FYP = Fruit yield per plant (Kg), σ^2 p = Phenotypic variance, σ^2g = Genotypic variance σ^2 e = Environmental variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, ECV= Environmental coefficient of variation.

coefficient of variation was moderate for plant height. Similar observations were made by Marine *et al.* (2003). Singh *et al.* (2002) showed that the phenotypic coefficient of variation was the largest for this character. The estimate of heritability was as high as 94.78% with an expected genetic advance 61.00% (Table 4). Genotypic and phenotypic variability in tomato are showing in Figure 2. Heritability and genetic advance over different yield contributing characters in tomato are showing in Figure 3.

4.1.2 Primary branches per plant

The grand mean number of primary branches per plant was registered 9.61. It ranged from 5.80 to 12.55 (Table 3). The maximum number of primary branches (12.55) was recorded in the genotype "BD-7279" and the minimum number of primary branches (5.80) was recorded by the "BARI Tomato-9" (Appendix- IV). The PCV and GCV were 20.98 and 15.61 percent respectively (Table 4).The PCV values were slightly higher than the respective GCV for all the characters denoting little influence of environmental factors on their expression. Singh *et al.* (2002) also showed that phenotypic coefficient of variation was the largest for primary branches per plant. This indicated that it may be attributed to non-additive gene effects controlling its expression and selection would not be rewarding. The estimate of heritability was moderate at 55.37 % with low genetic advance 2.30% (Table 4). Photographs are showing variation in leaves among different genotypes of tomato in plate 5a and 5b.

4.1.3 Secondary branches per plant

The grand mean number of secondary branches per plant was recorded 7.18. It ranged from 3.33 to 14.00 (Table 3). The maximum number of secondary branches (14.00) was recorded in the genotype "BD-7285" and the minimum (3.33) was recorded with "BARI Tomato-8" (Appendix- IV). The PCV and GCV were 42.10 and 36.19 percent, respectively (Table 4). Coefficient of variation studies indicated that thischaracter was slightly influenced by the environment. Therefore, selection as the basis of phenotype alone cannot be effective for the improvement of the trait. The estimates of heritability was high at 73.87 % with low genetic advance (4.60%) (Table 4).

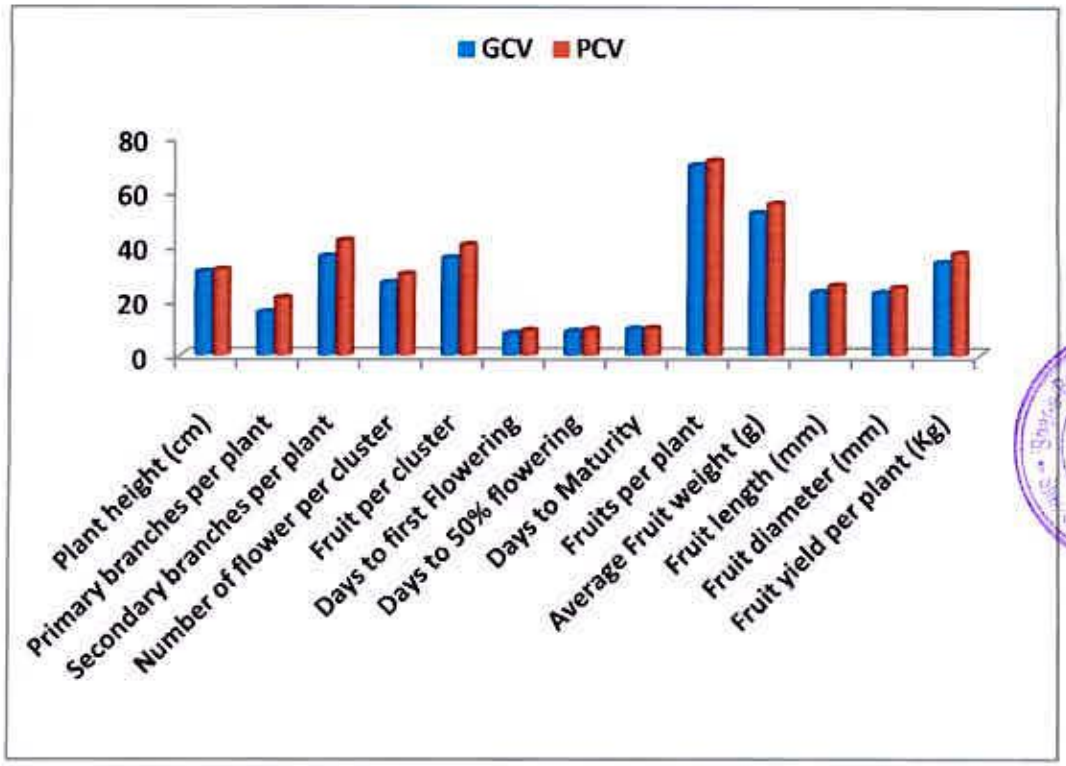


Figure 2. Genotypic and phenotypic variability in yield and yield contributing traits in tomato

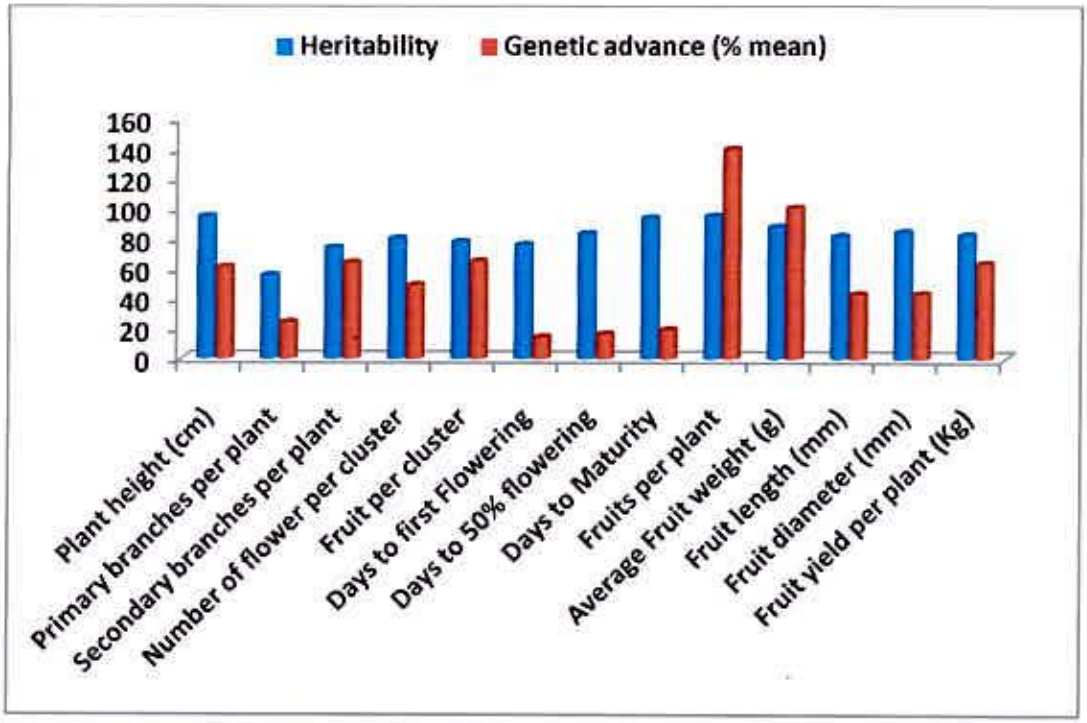


Figure 3. Heritability and genetic advance over different yield contributing characters in tomato

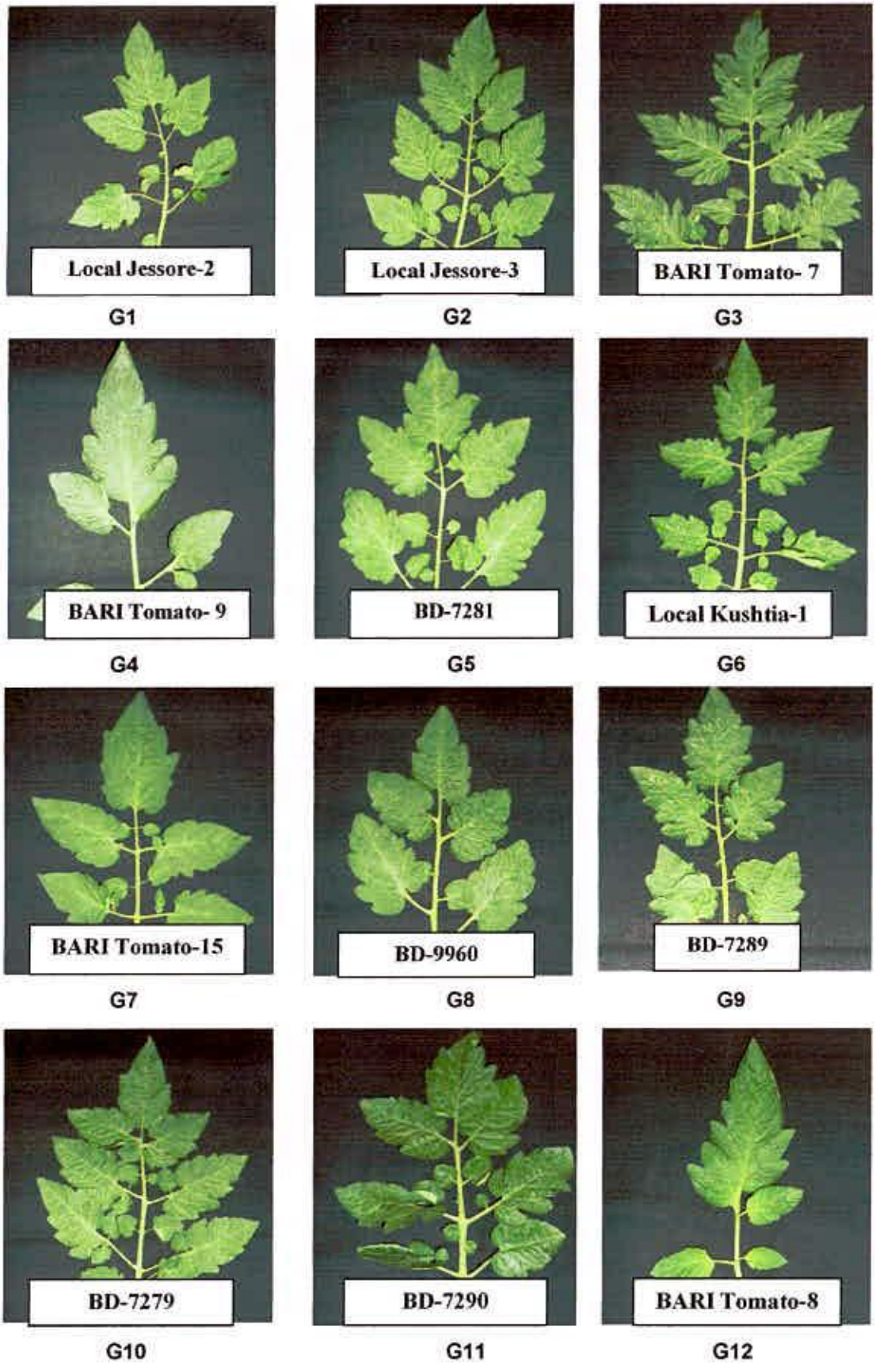


Plate 5a. Showing phenotypic variation in leaves among different genotypes of tomato (G1-G12)

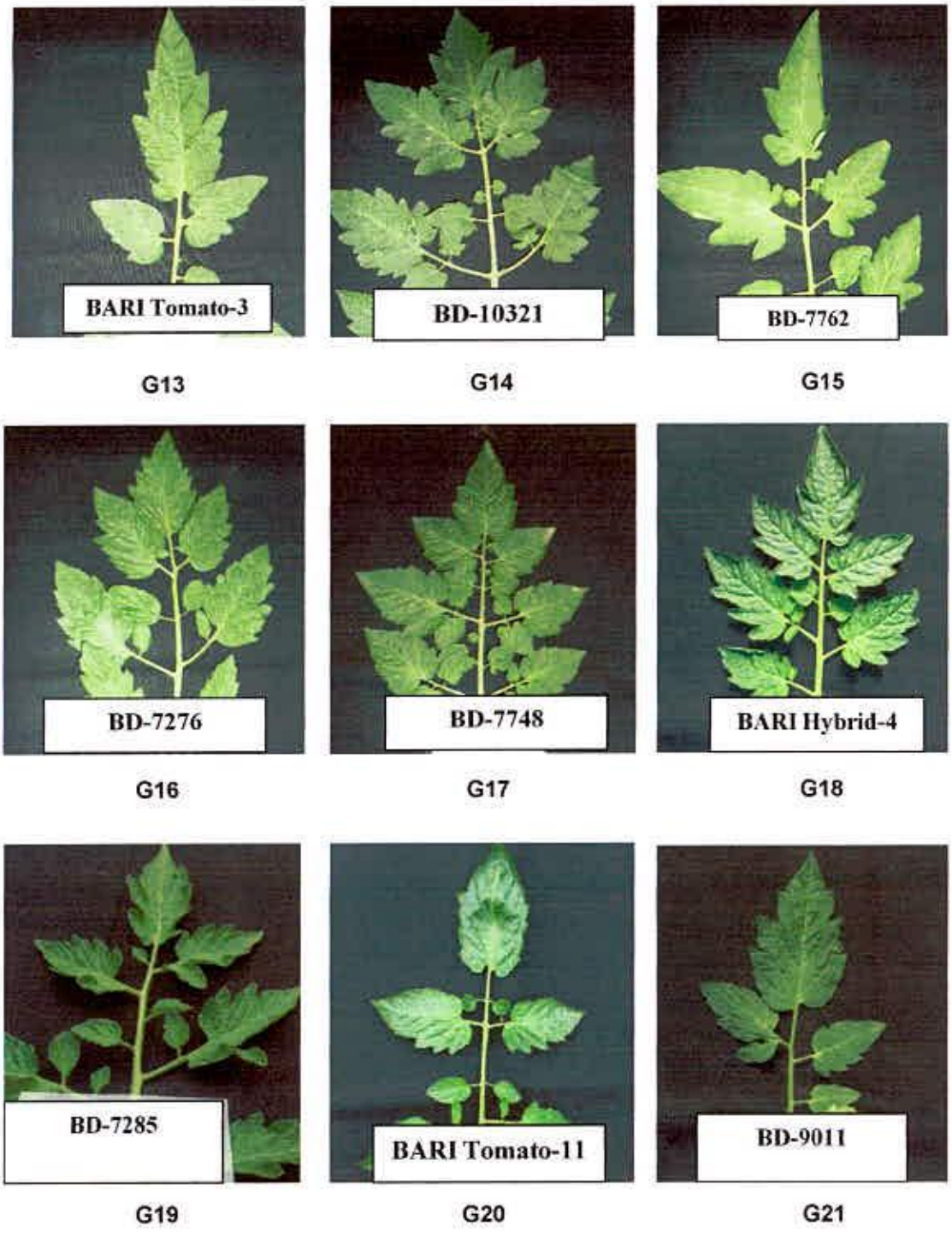


Plate 5b. Showing phenotypic variation in leaves among different genotypes of tomato (G13-G21)

4.1.4 Number of flowers per cluster

The grand mean number of flower per cluster was 8.52. It ranged from 6.37 to 15.93 (Table 3). The maximum number of flower per cluster (15.93) was recorded in the genotype "BARI Tomato-11" and the minimum number of flower per cluster (6.37) was recorded in the genotype "BD-7285" (Appendix- IV). The PCV and GCV were 29.66 and 26.55 percent, respectively (Table 4). There was little difference between the phenotypic and genotypic coefficient of variation indicating little environmental influence in the expression of this character. The estimates of heritability was as high as 80.12% with low genetic advance (4.17%) (Table 4).

4.1.5 Number of fruits per cluster

The grand mean number of fruit per cluster was 4.47. It ranged from 3.07 to 10.78 (Table 3). The maximum number of fruit per cluster (10.78) was recorded in the genotype "BARI Tomato-11" and the minimum (3.07) was in the genotype "BD-7748" (Appendix- IV). The PCV and GCV were 40.51 and 35.73 percent, respectively (Table 4).The PCV was a bit higher than the GCV indicating that no.of fruits per cluster was influenced by the environment to some extent. The estimate of heritability was as high as 77.83 % with low genetic advance 2.91% (Table 4). This indicated the predominance of additive gene action in expression of this trait that is expected to be effective. Photographs are showing variation in fruits per cluster among different genotypes of tomato in plate 6a and 6b.

4.1.6 Days to first flowering

The grand mean number of days to first flowering was recorded as 52.00. It ranged from 46.00 to 61.67 (Table 3). The maximum number of days to first flowering (61.67) was obtained by the "BARI Tomato-3" and the minimum (46.00) was scored by the "BD-7748" (Appendix- IV). The PCV and GCV were 9.07 and 7.91 percent, respectively (Table 4). There was little difference between the phenotypic and genotypic coefficient of variation indicating little environmental influence in the expression of this character. Such value of GCV with least difference was observed by Singh *et al.* (1973) and Korla *et al.* (1998). The estimate of heritability was high (76.00%) coupled with low genetic advance 7.39% (Table 4).

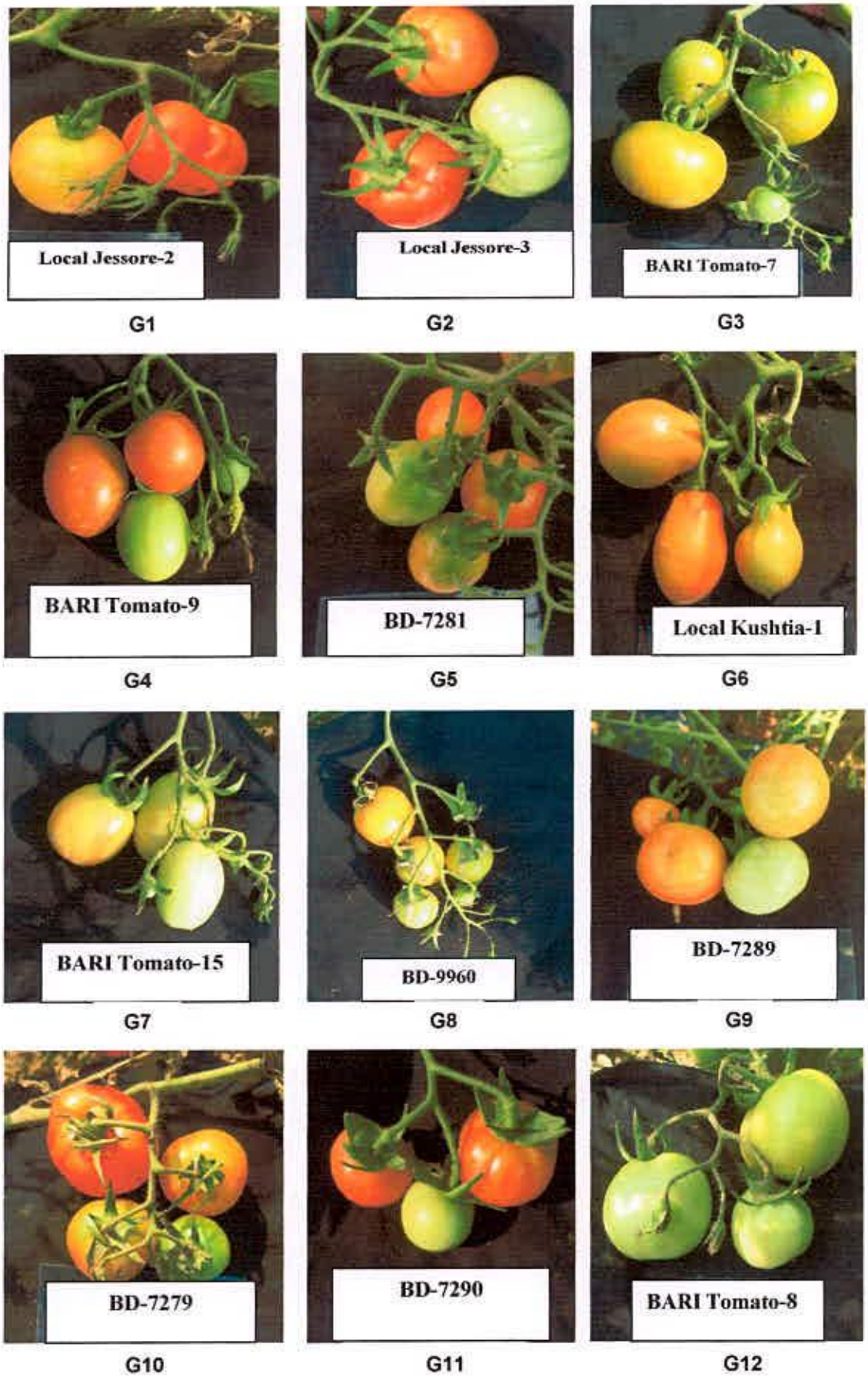


Plate 6a. Showing phenotypic variation in fruits per cluster among different genotypes of tomato (G1-G12)

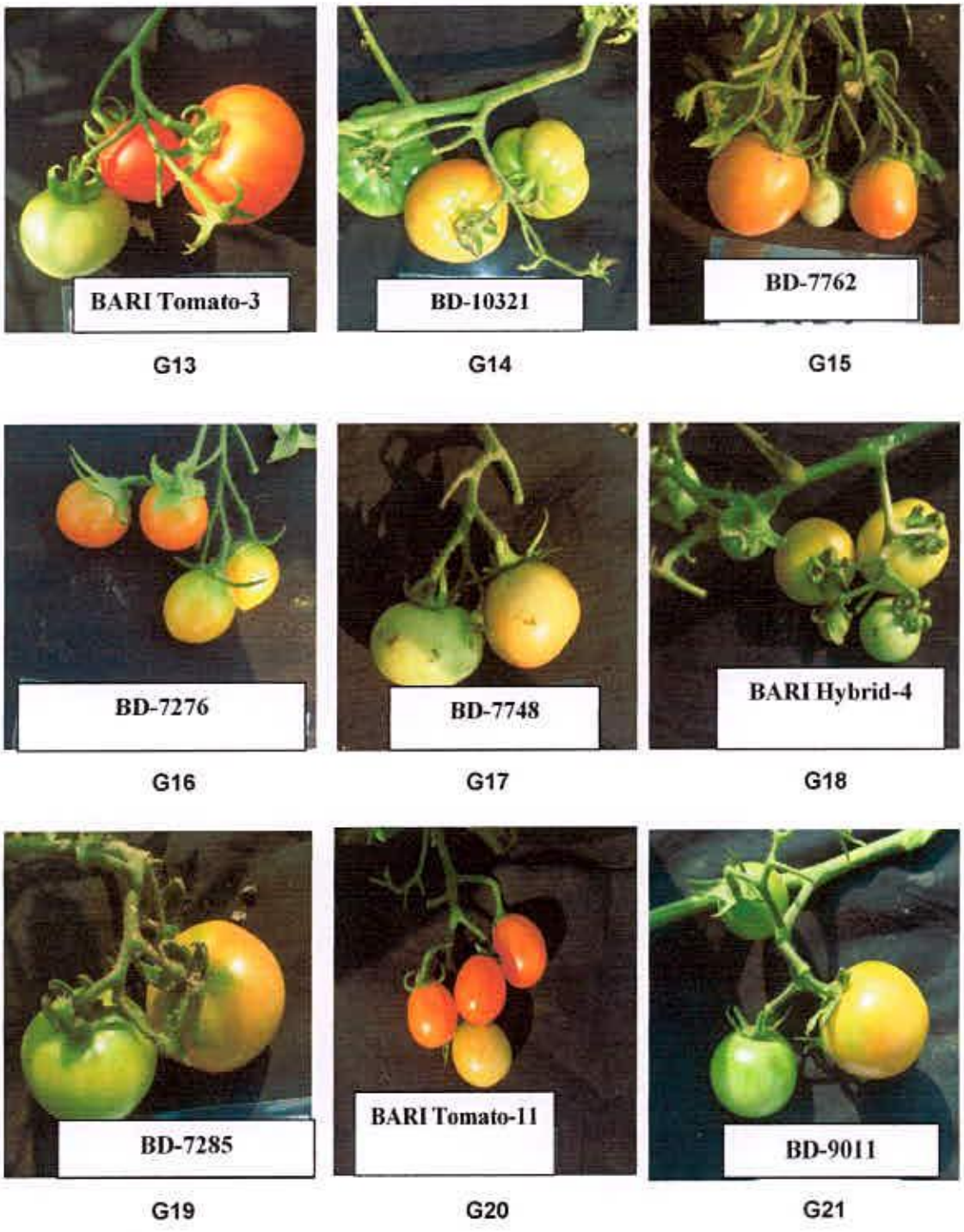


Plate 6b. Showing phenotypic variation in fruits per cluster among different genotypes of tomato (G10-G21)

4.1.7 Days to 50% flowering

The grand mean number of days to 50% flowering was 58.41. It ranged from 52.00 to 67.33 (Table 3). The maximum number of days to 50% flowering (67.33) was obtained by the "BARI Tomato-3" and the minimum number of days to 50% flowering (52.00) was recorded with the "Local Jessore 3" (Appendix- IV). The PCV and GCV were 9.41 and 8.60 percent, respectively (Table 4). The PCV were slightly higher than the respective GCV denoting environmental factors had minor influence in the expression of this trait. The estimate of heritability was high (83.41%) along with low genetic advance 9.45% (Table 4). High heritability coupled with low genetic advance was observed for days to 50 % flowering by Singh *et al.* (1973) and Kumar *et al.* (1980).

4.1.8 Days to maturity

The grand mean number of days to maturity was recorded as 113.74. It registered from 82.33 to 124.45 (Table 3). The maximum number of days to maturity (124.45) was recorded with the "BD-7279" and the minimum with "BARI Tomato-11" (Appendix- IV). The PCV and GCV were 9.89 and 9.59 percent, respectively (Table 4). Narrow difference between the values of PCV and GCV indicating that they were less influenced by the environment and can be convinced by looking of low values of ECV. The works of Hayder *et al.* (2007), Mohamed *et al.* (2012) and Pradeepkumar *et al.* (2001) support the present findings. The estimate of heritability was as high as 93.97% with moderate genetic advance 21.77% (Table 4). This indicates the influence of non-additive gene action and considerable influence of environment in the expression of this trait contradictory findings with that obtained through GCV and PCV value. This trait could be exploited through manifestation of dominance and epistatic components through heterosis.

4.1.9 Number of fruits per plant

The grand mean number of fruit per plant was recorded as 124.83. It ranged from 28.55 to 415.00 (Table 3). The maximum number of fruits per plant (415.00) was recorded with the "BARI Tomato-11" and the minimum number of fruits per plant (28.55) was recorded with the "BARI Tomato-8" (Appendix- IV). The PCV and GCV were 71.43 and 69.73 percent, respectively (Table 4). There was little difference between the phenotypic and genotypic coefficient of variation indicating little environmental influence in the expression of this character. The estimate of

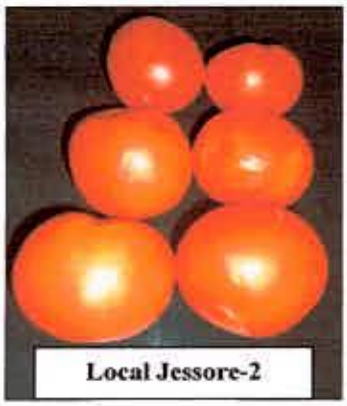
heritability was high (95.30%) with high genetic advance 175.05% (Table 4). This indicates the predominance of additive gene effects and suggesting that effective selection may be done for the character and the findings are in agreement with the observations of Ara *et al.* (2009), and Singh *et al.* (2001).

4.1.10 Average fruit weight (g)

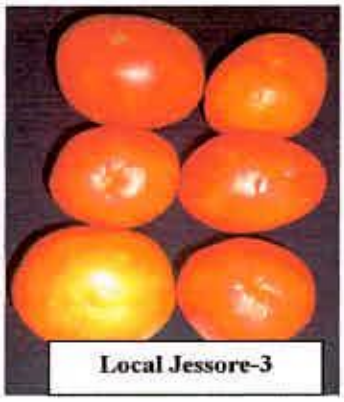
The average fruit weight over all genotypes was 34.45 g. It ranged from 6.93 g to 73.97 g (Table 3). The maximum average fruit weight (73.97 g) was recorded in the genotype "BARI Tomato-15" and the minimum (6.93 g) was in the genotype "BARI Tomato-11" (Appendix- IV). The PCV and GCV were 55.63% and 52.18%, respectively (Table 4). There was little difference between the phenotypic and genotypic coefficient of variation indicating little environmental influence in the expression of this character. The estimate of heritability was as high as 87.98% with moderate genetic advance 34.73% (Table 4). High estimates of heritability coupled with moderate genetic advance observed for this character is in accordance with earlier findings of Mohanty (2003).

4.1.11 Fruit length (mm)

The grand mean fruit length was 35.22 mm. It ranged from 23.32 -52.76 mm (Table 3). The maximum (52.76 mm) and the minimum (23.32 mm) were recorded with the "BARI Tomato-15" and "BARI Tomato-11", respectively (Appendix- IV). The PCV and GCV were 25.57 and 23.13 percent respectively (Table 4). There was little difference between the phenotypic and genotypic coefficient of variation indicating little environmental influence in the expression of this character. The estimate of heritability was high as (81.78%) along with low genetic advance, 15.17% (Table 4).Photographs are showing phenotypic variation in fruits among different genotypes of tomato in Plate 7a and 7b.



G1

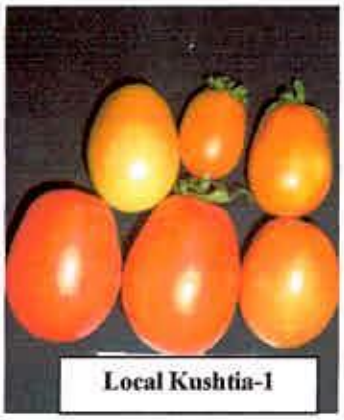


G2

G3

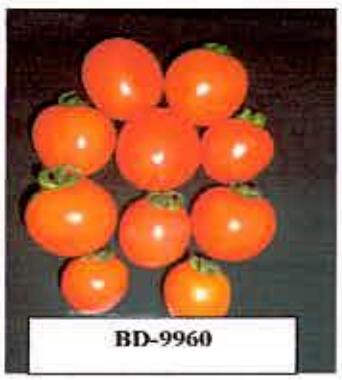
G4

G5



G6

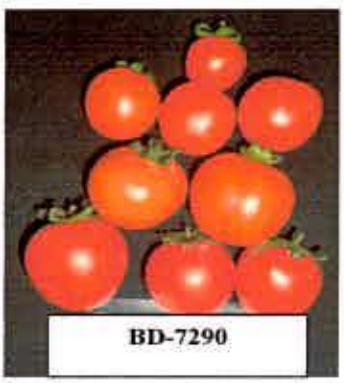
G7



G8

G9

G10



G11

G12

Plate 7a. Showing phenotypic variation in fruits among different genotypes of tomato (G1-G12)

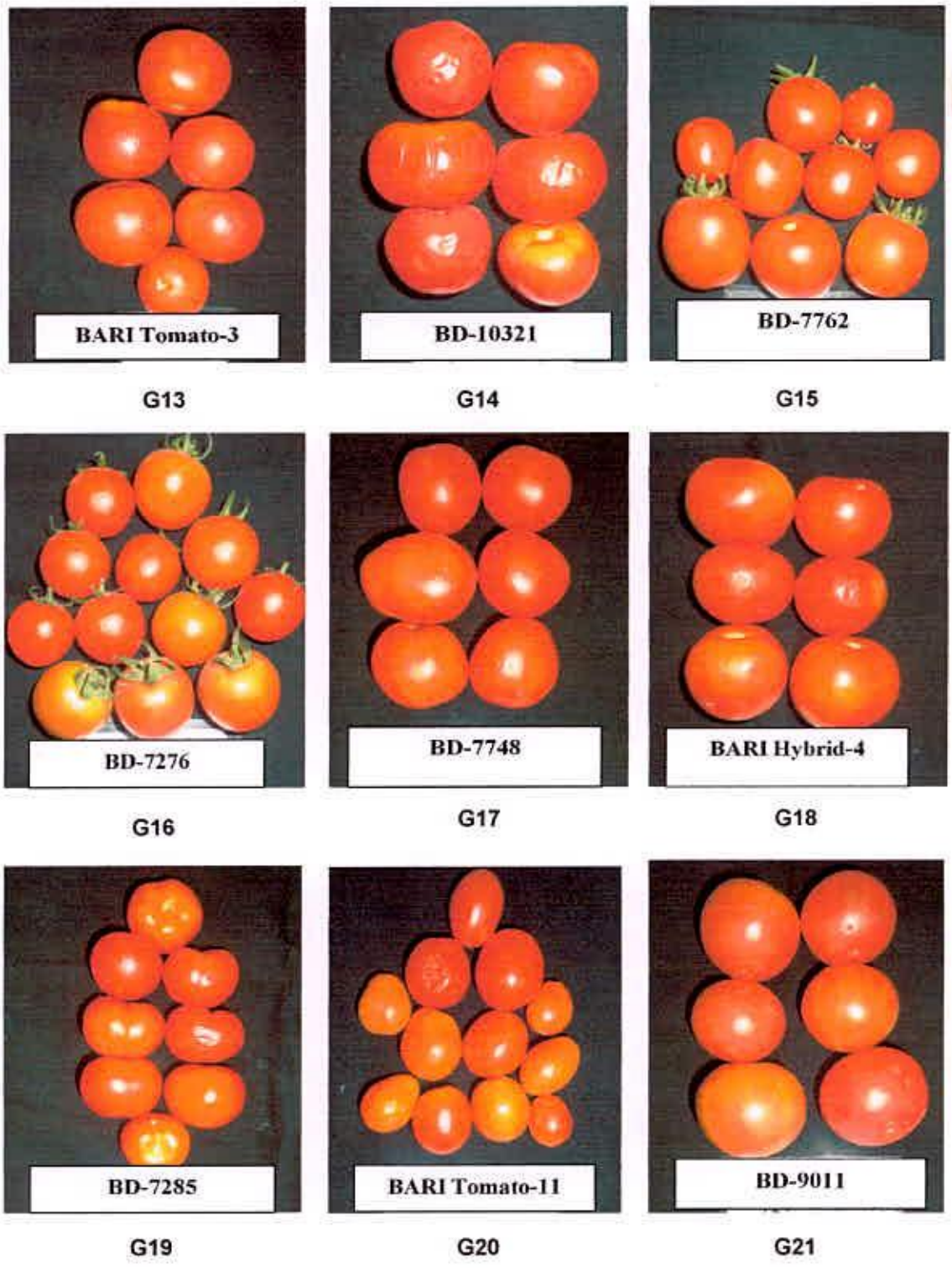


Plate 7b. Showing phenotypic variation in fruits among different genotypes of tomato (G13-G21)

4.1.12 Fruit diameter (mm)

The grand mean fruit diameter was 11.92 mm. It ranged from 5.51 mm to 16.06 mm (Table 3). The maximum fruit diameter (16.06 mm) was recorded by the "BD-7748" and the minimum (5.51 mm) was in the "BARI Tomato-11" (Appendix- IV). The PCV and GCV were 24.78% and 22.80%, respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The estimate of heritability was high at 84.66% with low genetic advance 5.15% (Table 4).

4.1.13 Fruit yield per plant (kg)

The grand mean fruit yield per plant was found as 1.79 kg. It ranged from 1.02 kg to 3.46 kg (Table 3). The maximum fruit yield per plant (3.46 kg) was recorded with the "BD-7285" and the minimum fruit yield per plant (1.02 kg) was recorded with the "BD-7279" (Appendix- IV). The PCV and GCV were 37.36 and 33.95 percent respectively (Table 4). There was little difference between the phenotypic and genotypic coefficient of variation indicating little environmental influence in the expression of this character. The estimate of heritability was high at 82.58 percent with low genetic advance 1.14% (Table 4).

4.2 Correlation coefficient

Knowledge of correlation between yield and its contributing characters are basic and foremost endeavor to find out guidelines for plant selection. The existing relationships between traits are generally determined by the genotypic and phenotypic correlations. The phenotypic correlation measures the degree of association of two variables and is determined by genetic and environmental factors. The genotypic correlation on the other hand, which represents the genetic portion of the phenotypic correlation, is the only one of inheritable nature and therefore, is used to orient breeding programs (Falconer, 1989). However, the correlation coefficient between two characters does not necessarily imply a cause and effect relationship. The inter-relationship could be grasped best if a coefficient could be assigned to each path in the diagram designed to measure the direct influence on it. Before placing strong emphasis on breeding for yield improvement trait, the knowledge on the association between yield and yield attributes will enable the breeder in the improvement of yield. The correlation coefficient may also help to identify characters that have little or no importance in the selection programme. The existence of correlation may be attributed to the presence

of linkage or pleiotropic effect of genes or physiological and developmental relationship or environmental effect or in combination of all (Oad *et al.*, 2002). The basic objective of most of the crop improvement programs is to realize a marked improvement in crop yield. But yield is a complex character which is controlled by association of various characters. Thus, information on association of yield attributes and their direct and indirect effects on grain yield are of paramount significance.

4.2.1 Plant height (cm)

Plant height was found to display highly significant positive relationships with primary branches per plant (0.468, 0.409), days to maturity (0.340, 0.319) and days to first flowering (0.332, 0.288) at genotypic and phenotypic level, respectively (Table 5 and Table 6). The character showed highly significant negative association with fruit length (-0.384, -0.303) at genotypic and phenotypic level (Table 5 and Table 6) and also showed significant negative association with average fruit weight (-0.282), fruit yield per plant (-0.179) at genotypic level (Table 5). This finding is in contrast to Singh *et al.* (2006), Sivapraasad (2008) and Gosh *et al.* (2010). Plant height also showed non-significant positive correlation with secondary branches per plant (0.058, 0.158), days to 50% flowering (0.219, 0.163), fruit diameter (0.032, 0.040) at genotypic and phenotypic level (Table 6). It also showed non-significant negative correlation with number of flower per cluster (-0.129), number of fruit per cluster (-0.171) and fruits per plant (-0.130) at genotypic level (Table 5) and also showed non significant negative correlation with number of flower per cluster(-0.091), number of fruit per cluster (-0.100), average fruit weight (-0.242), number of fruits per plant (-0.105) and fruit yield per plant (-0.179) at phenotypic level (Table 6).

Table 5. Genotypic correlation coefficients among yield and yield contributing characters for 21 different genotypes of tomato

	PBP	SBP	NFC	FPC	DFF	D50%F	DM	FPP	AFW	FL	FD	FYP
PH	0.468**	0.058	-0.129	-0.171	0.332**	0.219	0.340**	-0.130	-0.282*	-0.384**	0.032	-0.245*
PBP		0.568**	0.112	0.006	0.149	-0.350**	-0.364**	0.466**	-0.751**	-0.699**	-0.516**	0.233
SBP			-0.114	-0.060	-0.080	-0.431**	-0.606**	0.496**	-0.388**	-0.457**	-0.320**	0.709**
NFC				0.920**	0.220	0.130	-0.426**	0.693**	-0.445**	-0.444**	-0.699**	-0.260*
FPC					0.133	0.150	-0.578**	0.794**	-0.435**	-0.342**	-0.697**	-0.113
DFF						0.783**	0.192	0.033	-0.156	-0.155	-0.128	0.025
D50%F							0.384**	-0.189	0.079	0.021	0.008	-0.336**
DM								-0.844**	0.428**	0.386**	0.505**	-0.630**
FPP									-0.701**	-0.594**	-0.822**	0.318**
AFW										0.876**	0.893**	0.079
FL											0.680**	0.115
FD												0.154

Here, ** = Significant at 1%.,* = Significant at 5%, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flowers per cluster, FPC =Number of fruits per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm), FYP = Fruit yield per plant (Kg).

Table 6. Phenotypic correlation coefficients among yield and yield contributing characters for 21 different genotypes of tomato

	PBP	SBP	NFC	FPC	DFF	D50%F	DM	FPP	AFW	FL	FD	FYP
PH	0.409**	0.158	-0.091	-0.100	0.288*	0.163	0.319**	-0.105	-0.242	-0.303*	0.040	-0.179
PBP		0.564**	0.154	0.040	0.044	-0.335**	-0.261*	0.380**	-0.530**	-0.542**	-0.422**	0.222
SBP			-0.054	-0.013	-0.080	-0.422**	-0.455**	0.451**	-0.338**	-0.344**	-0.211	0.632**
NFC				0.773**	0.179	0.102	-0.350**	0.612**	-0.408**	-0.388**	-0.570**	-0.174
FPC					0.195	0.173	-0.507**	0.747**	-0.356**	-0.272*	-0.509**	-0.057
DFF						0.731**	0.191	0.026	-0.146	-0.073	-0.037	-0.054
D50%F							0.361**	-0.169	0.125	0.107	0.122	-0.373**
DM								-0.780**	0.349**	0.351**	0.441**	-0.579**
FPP									-0.598**	-0.546**	-0.696**	0.342**
AFW										0.780**	0.767**	0.075
FL											0.658**	0.019
FD												0.005

Here, ** = Significant at 1%,* = Significant at 5%,PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flowers per cluster, FPC =Number of fruits per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm), FYP = Fruit yield per plant (Kg).

4.2.2 Primary branches per plant

The character showed highly significant positive relationship with secondary branches per plant (0.568, 0.564), fruits per plant (0.466, 0.380) at genotypic and phenotypic level (Table 5 and Table 6). The character showed highly significant negative association with days to 50% flowering (-0.350, -0.335), days to maturity (-0.364, -0.261), average fruit weight (-0.751, -0.530), fruit length (-0.699, -0.542) and fruit diameter (-0.516, -0.422) at genotypic and phenotypic level. Highly significant positive association between numbers of primary branches per plant and number of secondary branches per plant indicates that the traits are governed by same gene by pleiotropic effect and simultaneous improvement would be effective. It also showed non significant positive genotypic correlation with number of flower per cluster (0.112, 0.1554), fruit per cluster (0.006, 0.040), days to first flowering (0.149, 0.044) and fruit yield per plant (0.233, 0.222) at genotypic and phenotypic level.

4.2.3 Secondary branches per plant

Secondary branches per plant showed highly significant positive relationship with number of fruits per plant (0.496, 0.451) and fruit yield per plant (0.709, 0.632) and also showed highly significant negative association with days to 50% flowering (-0.431, -0.422), days to maturity (-0.606, -0.455), average fruit weight (-0.388, -0.338) and fruit length (-0.457, -0.344) at genotypic and phenotypic level (Table 5 and Table 6). The character showed highly significant negative association with fruit diameter (-0.516) at genotypic level (Table 5). It showed non significant negative correlation with fruit diameter (-0.211) at phenotypic level (Table 6). It also implied non significant negative correlation with number of flower per cluster (-0.114, -0.054), number of fruit per cluster (-0.060, -0.013) and days to first flowering (-0.080, -0.080) at genotypic and phenotypic level. According to NeWall and Eberhart (1961) when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise simultaneous selection for these characters in the development of a variety. Hence, under such situations, judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters.

4.2.4 Number of flowers per cluster

Number of flowers per cluster showed highly significant positive relationship with number of fruits per cluster (0.920, 0.773), fruits per plant (0.693, 0.612) and it also showed highly significant negative association with days to maturity (-0.426, -0.350), average fruit weight (-0.445, -0.408), fruit length (-0.444, -0.388) and fruit diameter (-0.699, -0.570) at genotypic and phenotypic level (Table 5 and Table 6). The character showed significant and non-significant negative relationship with fruit yield per plant (-0.260, -0.174) at genotypic and phenotypic level, respectively (Table 5 and 6). It also showed non significant positive correlation with days to first flowering (0.220, 0.179) and days to 50% flowering (0.130, 0.102) at genotypic and phenotypic level. The estimates of correlation coefficients revealed that, in general, the genotypic and the phenotypic correlation coefficients followed similar trend but genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients, which might be due to masking or modifying effect of environment (Singh, 1980). Very close values of genotypic and phenotypic correlations were also observed between some character combinations, which might be due to reduction in error (environmental) variance to minor proportions as reported by Dewey and Lu (1959).

4.2.5 Number of fruits per cluster

The character showed highly significant positive relationship with fruits per plant (0.794, 0.747) at genotypic and phenotypic level (Table 5 and Table 6). Number of fruit per cluster showed highly significant negative association with days to maturity (-0.578, -0.507), average fruit weight (-0.435, -0.356), fruit length (-0.342, -0.272) and fruit diameter (-0.697, -0.509) at genotypic and phenotypic level and it also showed non-significant positive correlation with days to first flowering (0.133, 0.195), days to 50% flowering (0.150, 0.173) number of fruits per cluster also showed non-significant negative correlation with fruit yield per plant (-0.113, -0.057) at genotypic and phenotypic level.

4.2.6 Days to first flowering

Days to first flowering showed highly significant positive relationship with days to 50% flowering (0.783, 0.731) and non-significant positive correlation with days to maturity (0.192, 0.191), number of fruits per plant (0.033, 0.026) at genotypic and phenotypic level (Table 5 and Table 6). It also showed non-significant positive correlation with fruit yield per plant (0.025) at genotypic level (Table 5) showed non-significant negative correlation with average fruit weight (-0.156, -0.146), fruit length (-0.156, -0.073) and fruit diameter (-0.128, -0.037) at genotypic and phenotypic level. It also showed non-significant negative correlation with fruit yield per plant (-0.054) at phenotypic level (Table 6).

4.2.7 Days to 50% flowering

Days to 50% flowering showed highly significant positive correlation with days to maturity (0.384, 0.361) and significant negative association with fruit yield per plant (-0.336, -0.373) at genotypic and phenotypic level (Table 5 and Table 6). It also showed non-significant positive correlation with average fruit weight (0.079, 0.125), fruit length (0.021, 0.107) and fruit diameter (0.008, 0.122) and non-significant negative correlation with number of fruits per plant (-0.189, -0.169) at genotypic and phenotypic level.

4.2.8 Days to maturity

Days to maturity showed highly significant positive correlation with average fruit weight (0.428, 0.349), fruit length (0.386, 0.351) and fruit diameter (0.505, 0.441) and highly significant negative association with number of fruits per plant (-0.844, -0.780) and fruit yield per plant (-0.630 and -0.579) at genotypic and phenotypic level, respectively (Table 5 and Table 6).

4.2.9 Number of fruits per plant

Number of fruits per plant showed highly significant positive correlation with fruit yield per plant (0.318, 0.342) at genotypic and phenotypic level (Table 5 and Table 6). The character also reflected highly significant negative association with average fruit weight (-0.701,-0.598), fruit length (-0.594, -0.546) and fruit diameter (-0.822, -0.696) at genotypic and phenotypic level.

4.2.10 Average fruit weight (g)

Average fruit weight showed highly significant positive correlation with fruit length (0.876, 0.780), fruit diameter (0.893, 0.767) at genotypic and phenotypic level (Table 5 and Table 6). It also showed non-significant positive correlation with fruit yield per plant (0.079, 0.075) at genotypic and phenotypic level respectively.

4.2.11 Fruit length (mm)

Fruit length showed highly significant positive correlation with fruit diameter (0.680, 0.658) at genotypic and phenotypic level (Table 5 and Table 6). It also showed non-significant positive correlation with fruit yield per plant (0.115, 0.019) at genotypic and phenotypic level respectively.

4.2.12 Fruit diameter (mm)

The character showed positive correlation with fruit yield per plant (0.154, 0.005) at genotypic and phenotypic level (Table 5 and Table 6).

4.3 Path coefficient analysis

4.3.1 Plant height (cm)

Plant height employed direct negative effect (-0.349) on yield per plant as well as indirect positive effect via secondary branches per plant, number of flower per cluster, days to first flowering, fruit length and fruit diameter. It also showed negative indirect effect of primary branches per plant, fruit per cluster and days to maturity, number of fruits per plant and average fruit weight. The result was in line to Singh *et al.* (2006) and Hayader *et al.* (2007) who reported positive direct effect on plant height on yield per plant in tomato. The direct and indirect effects of different characters on yield are presented in table 7.

4.3.2 Primary branches per plant

Primary branches per plant had negative direct effect (-0.041) and positive indirect effects by means of secondary branches per plant, fruit per cluster, days to first flowering, days to 50 % flowering, days to maturity, number of fruits per plant and fruit length on yield per plant however, negative indirect effect of plant height, number of flower per cluster, average fruit weight and fruit diameter curtailed it.

4.3.3 Secondary branches per plant

Secondary branches per plant showed positive direct effect (0.281) on yield per plant and positive indirect effect via number of flower per cluster, days to 50 % flowering, days to maturity, number of fruits per plant and fruit length on yield per plant. However, this trait had negative indirect effect of plant height, primary branches per plant, fruit per cluster, days to first flowering, average fruit weight and fruit diameter on fruit yield per plant.

4.3.4 Number of flowers per cluster

This character showed negative direct effect (-1.195) on yield per plant and positive indirect effect through plant height, fruit per cluster, days to first flowering, days to maturity, number of fruits per plant and fruit length on yield per plant. It also showed negative indirect effect is a primary branches per plant, secondary branches per plant, days to 50 % flowering, average fruit weight and fruit diameter on yield.

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

	Direct effect	Indirect effect											Genotypic correlation with yield
		PH	PBP	SBP	NFC	FPC	DFF	D50%F	DM	FPP	AFW	FL	FD	
PH	**-0.349**	-	-0.019	0.016	0.154	-0.171	0.351	-0.185	-0.073	-0.036	-0.010	0.056	0.021	-0.245*
PBP	**-0.041**	-0.163	-	0.160	-0.134	0.006	0.158	0.296	0.078	0.129	-0.026	0.103	-0.332	0.233
SBP	**0.281**	-0.020	-0.023	-	0.136	-0.060	-0.085	0.365	0.130	0.137	-0.013	0.067	-0.206	0.709**
NFC	**-1.195**	0.045	-0.005	-0.032	-	0.920	0.233	-0.110	0.092	0.191	-0.015	0.065	-0.449	-0.260*
FPC	**1.000**	0.060	0.000	-0.017	-1.099	-	0.141	-0.127	0.124	0.219	-0.015	0.050	-0.448	-0.113
DFF	**1.058**	-0.116	-0.006	-0.022	-0.263	0.133	-	-0.662	-0.041	0.009	-0.005	0.023	-0.082	0.025
D50%F	**-0.846**	-0.076	0.014	-0.121	-0.155	0.150	0.828	-	-0.083	-0.052	0.003	-0.003	0.005	-0.336**
DM	**0.011**	-0.119	0.015	-0.170	0.509	-0.578	0.203	-0.325	-	-0.233	0.015	-0.057	0.325	-0.630**
FPP	**0.276**	0.045	-0.019	0.139	-0.828	0.794	0.035	0.160	0.181	-	-0.024	0.087	-0.529	0.318**
AFW	**0.034**	0.098	0.031	-0.109	0.532	-0.435	-0.165	-0.067	-0.092	-0.193	-	-0.129	0.574	0.079
FL	**-0.147**	0.134	0.029	-0.128	0.531	-0.342	-0.164	-0.018	-0.083	-0.164	0.030	-	0.437	0.115
FD	**0.643**	-0.011	0.021	-0.090	0.835	-0.697	-0.135	-0.007	-0.109	-0.227	0.030	-0.100	-	0.154

Residual effect: 0.226, ** = Significant at 1%, * = Significant at 5%, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flowers per cluster, FPC = Number of fruits per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm).

4.3.5 Number of fruits per cluster

Number of fruits per cluster showed positive direct effect (1.000) on yield per plant and positive indirect effect by means of plant height, primary branches per plant, days to first flowering, days to maturity, number of fruits per plant and fruit length on yield per plant. It also showed negative indirect effect of secondary branches per plant, number of flower per cluster, days to 50 % flowering, average fruit weight and fruit diameter.

4.3.6 Days to first flowering

Days to first flowering showed positive direct effect (1.058) on yield per plant and positive indirect effect by means of fruit per cluster, number of fruits per plant, fruit length on yield per plant however, negative indirect effect of plant height, primary branches per plant, secondary branches per plant, number of flower per cluster, days to 50 % flowering, days to maturity, average fruit weight and fruit diameter.

4.3.7 Days to 50% flowering

This character showed negative direct effect (-0.846) on yield per plant and positive indirect effect by means of primary branches per plant, fruit per cluster, days to first flowering, average fruit weight and fruit diameter on yield per plant however, negative indirect effect of plant height, secondary branches per plant, number of flower per cluster, days to maturity, number of fruits per plant, fruit length on yield per plant.

4.3.8 Days to maturity

Days to maturity showed positive direct effect (0.011) on yield per plant and positive indirect effect by means of primary branches per plant, number of flower per cluster, days to first flowering, average fruit weight and fruit diameter on yield per plant however, negative indirect effect of plant height, secondary branches per plant, fruit per cluster, days to 50 % flowering, number of fruits per plant, fruit length on yield per plant.

4.3.9 Number of fruits per plant

This character showed positive direct effect (0.276) on yield per plant and positive indirect effect by means of plant height, secondary branches per plant, fruit per cluster, days to first flowering, days to 50 % flowering, days to maturity, fruit length

on yield per plant. It also showed negative indirect effect of primary branches per plant, number of flower per cluster, average fruit weight and fruit diameter.

4.3.10 Average fruit weight (g)

This character showed positive direct effect (0.034) on yield per plant and positive indirect effect by means of plant height, primary branches per plant, number of flower per cluster, fruit diameter on yield per plant. It also showed negative indirect effect of secondary branches per plant, fruit per cluster, days to first flowering, days to 50 % flowering, days to maturity, number of fruits per plant, fruit length on yield per plant.

4.3.11 Fruit length (mm)

This character showed negative direct effect (-0.147) on yield per plant and positive indirect effect by means of plant height, primary branches per plant, number of flower per cluster, average fruit weight and fruit diameter on yield per plant. It also showed negative indirect effect of secondary branches per plant, fruit per cluster, days to first flowering, days to 50 % flowering, days to maturity, number of fruits per plant on yield per plant.

4.3.12 Fruit diameter (mm)

This character showed positive direct effect (0.643) on yield per plant and positive indirect effect by means of primary branches per plant, number of flower per cluster, average fruit weight. It also showed negative indirect effect of plant height, secondary branches per plant, fruit per cluster, days to first flowering, days to 50 % flowering, days to maturity, number of fruits per plant, fruit length on yield per plant.

4.4 Multivariate Analysis

Diversity is the function of parent selection and also heterosis. The availability of transgressive segregants in a breeding programme depends upon the divergence of the parents. Thus, the accurate information on the nature and degree of diversity of the parents is the pre-requisite of an effect breeding programme. The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to screen better genotypes for hybridization programme.

4.4.1 Principal Component Analysis (PCA)

Principal components were computed from the correlation matrix and genotype scores obtained from first components (which had property of accounting for maximum variance) and succeeding components with latent roots greater than the unity. Contributions of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal components.

The principal component analysis yielded values of each principal component axes of coordination of genotypes in which the first axes totally accounting for the variation among the genotypes, whereas four of these given values above unity accounted for 87.93 %. The first two principal axes accounted for 60.99% of the total variation among the thirteen characters describing in 21 tomato genotypes (Table 8).

4.4.2 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional (Z_1-Z_2) scatter diagram was constructed, using component score 1 as X-axis and component score 2 as Y-axis, which is presented in figure 5. The position of the genotypes in the scatter diagram was random, which indicated the considerable diversity among the genotypes included in a cluster. Some distantly located genotypes of different clusters were the genotypes number G10, G14, G17, G12, G13, G3, G9, G11, and G20. The scatter diagram (Figure 6) represented apparently five clusters of the genotypes and they were distantly located from each other.

Table 8. Eigen values and yield percent contribution of thirteen characters of twenty one germplasm of tomato

Characters	Eigen values	% variation	Cumulative variation (%)
Plant height (cm)	5.181	39.86	39.86
Primary branches per plant	2.747	21.13	60.99
Secondary branches per plant	2.118	16.29	77.28
Number of flower per cluster	1.385	10.65	87.93
Number of fruit per cluster	0.515	3.96	91.89
Days to first flowering	0.376	2.89	94.78
Days to 50% flowering	0.233	1.79	96.57
Days to maturity	0.219	1.68	98.25
Number of fruits per plant	0.103	0.79	99.04
Average fruit weight (g)	0.053	0.40	99.44
Fruit length (mm)	0.043	0.33	99.77
Fruit diameter (mm)	0.015	0.12	99.89
Fruit yield per plant (Kg)	0.013	0.11	100.00

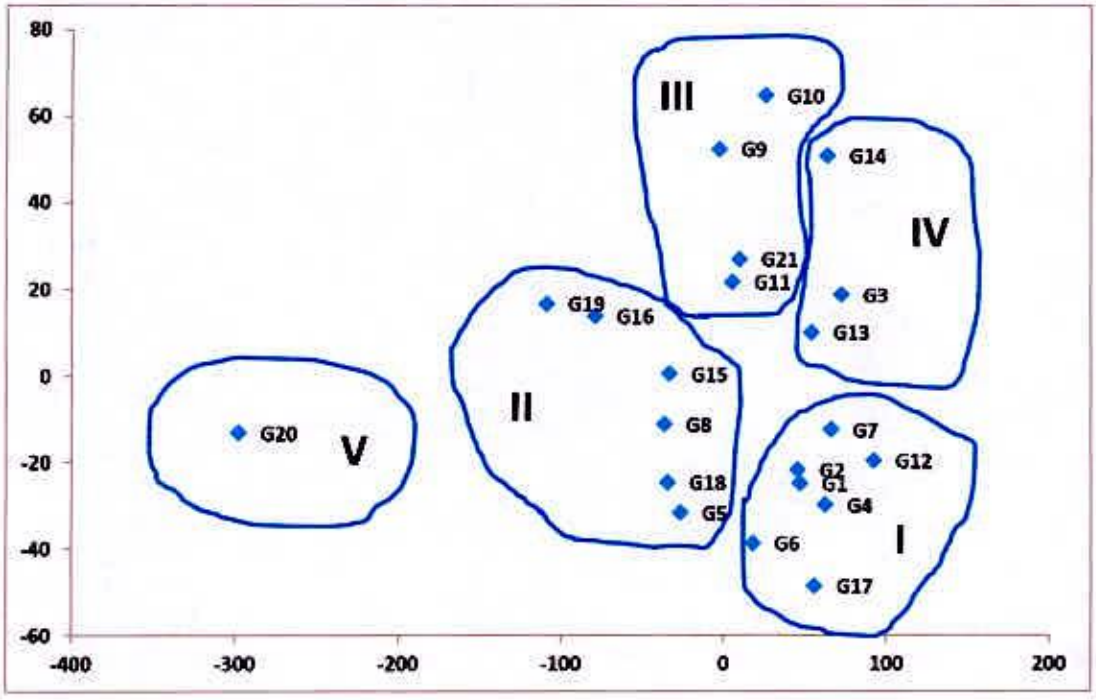


Figure 4. Scatter distribution of tomato genotypes of based on their principal component scores superimposed with clustering

4.4.3 Non-hierarchical clustering

On the basis of D^2 values, the 21 genotypes were grouped into five highly divergent clusters (Table 9).The clusters divergence was proved by the high inter-cluster and low intra clusters D^2 values. Cluster I had maximum number (seven) of genotypes followed by cluster II with six genotypes, Clusters III, IV and V had 4, 3 and 1 genotypes respectively. The grouping pattern did not show any relationship between genetic divergence and geographical diversity which has been a point of debate in the past. Table 9 clearly showed the genotypes did not cluster according to geographical distributions. This is an agreement with results of Meena and Bahadur (2013), Basavaraj *et al.* (2010), Joshi and Kohli (2003) and Mohanty and Prusti (2001). One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of genetic material among the crop improvement programmes in the country makes it difficult to maintain the real identify of the genotypes. Moreover, breeding programmes incorporate genes from varied sources, thus losing the basic geographical identity of the genotype. The absence of relationship between genetic diversity and geographical distance indicates that forces others than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection are responsible for genetic diversity, It may also be possible that causes for clustering pattern were much influenced by environment and (genotype x environment) interaction resulting in differential gene expression. Another possibility may be that estimates that might not have been sufficient to account for the variability caused by some other traits of physiological or biochemical nature which might have importance in depicting the total genetic diversity in the population

4.4.4 Principal Coordinates Analysis (PCO)

By using this inter-genotypic distances intra-cluster genotypic distances were calculated (Table 10) as suggested by Singh and Chaudhary (1985). Cluster III that was composed of four genotypes showed the highest intra-cluster distance (0.275) and cluster V showing the lowest intra-cluster distance (0.00) composed of one genotype, which indicated within group diversity of the genotypes was maximum in cluster III and minimum in cluster V.

Table 9. Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	G1, G2, G4, G6, G7, G12, G17	7	Local Jessore-2, Local Jessore-3, BARI Tomato-9, Local Kustia-1, BARI Tomato-15, BARI Tomato-8, BD-7748
II	G5, G8, G15, G16, G18, G19	6	BD- 7281, BD- 9960, BD-7762, BD-7276, BARI Hybrid-4, BD-7285
III	G9, G10, G11, G21	4	BD-7289, BD-7279, BD-7290, BD-9011
IV	G3, G13, G14	3	BARI Tomato-7, BARI Tomato-3, BD-10321
V	G20	1	BARI Tomato-11

Table 10. Intra (Bold) and inter cluster distances (D^2) for twenty one genotypes

Cluster	I	II	III	IV	V
I	**0.105**	5.43	11.76	6.43	10.56
II		**0.14**	8.43	5.65	6.54
III			**0.275**	4.54	15.23
IV				**0.73**	14.34
V					**0.00**

Table 11. Cluster mean values of thirteen different characters of twenty one genotypes

Characters	I	II	III	IV	V
Plant height (cm)	77.62	89.29	138.81	130.59	75.00
Primary branches per plant	8.03	10.50	10.80	9.67	10.25
Secondary branches per plant	5.59	9.24	8.45	4.81	8.00
Number of flower per cluster	7.53	9.22	7.42	8.46	15.93
Number of fruit per cluster	3.94	4.64	3.97	3.95	10.78
Days to first flowering	49.62	54.39	52.00	54.11	48.00
Days to 50% flowering	58.19	59.11	57.25	60.55	54.00
Days to maturity	117.68	107.09	119.25	120.96	82.33
Number of fruits per plant	67.60	181.52	113.75	63.04	415.00
Average fruit weight (g)	51.85	23.23	22.38	41.57	6.93
Fruit length (mm)	43.62	30.04	30.81	35.79	23.32
Fruit diameter (mm)	13.62	10.12	11.52	14.22	5.51
Fruit yield per plant (Kg)	1.66	2.21	1.54	1.59	1.76

The cluster mean (Table 11) for all thirteen characters varied in magnitude. Genotypes in cluster I showed maximum performance for average fruit weight (51.85) and fruit length (43.62). Cluster II showed maximum performance for secondary branches per plant (9.24), days to first flowering (54.39), fruit yield per plant (2.21). Cluster III recorded high mean performance for plant height (138.81), primary branches per plant (10.80) and cluster IV showed minimum performance for secondary branches per plant (4.81), fruits per plant (63.04). Cluster V showed maximum performance for number of flowers per cluster (15.93), fruit per cluster (10.78) and fruits per plant (415.00).

4.4.6 Canonical Vector Analysis (CVA)

Canonical vector analysis was performed to compute the inter-cluster Mahalanobis's values. Statistical distances represent the index of genetic diversity among the clusters. The divergence within the cluster (intra-cluster distance) indicates the divergence among the genotypes falling in the same cluster. On the other hand, inter cluster divergence suggest the distance (divergence) between the genotypes of different clusters. The intra and inter clusters D^2 values among 21 genotypes presented in Table 10 revealed that cluster V showed minimum intra cluster D^2 value (0.00) distance followed by cluster I (0.105), whereas, maximum intra cluster D^2 value (0.73) was shown by cluster IV followed by cluster III (0.275), which indicated that genotypes included in this cluster were very diverse and was due to both natural and artificial selection forces among the genotypes. Minimum inter cluster D^2 value was observed between the clusters III and IV (4.54) indicating close relationship among the genotypes included in these clusters. Maximum inter–clusters D^2 value was observed between the clusters III and V (15.23) that indicated the genotypes belongings to these groups were genetically most divergent and the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregating population (Mehta and Asati, 2008). Several authors also reported profound diversity in the germplasm of tomato by assessing genetic divergence on the basis of quantitative traits following Mahalanobis D^2 statistic (Basavaraj *et al.* 2010 and Evgenidis *et al.* 2011). Average inter and intra-cluster distance revealed that, in general inter-cluster distance were much higher than those of intra-cluster distances, suggesting homogenous and heterogenous nature of the germplasm lines within and between the clusters, respectively. These results are in accordance with the findings of Mahesh *et al.* (2006) and Meena and Bhadur (2013)

in tomato. Results obtained from different multivariate techniques from which it may be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one.

The clustering pattern of the genotypes revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure. This indicated that geographic diversity was not related to genetic diversity that might be due to continuous exchange of genetic materials among the countries of the world. Same results have been reported by Murty and Anand (1966); Anand and Rawat (1984) in brown mustard; It had been observed that geographic diversity was not always related to genetic diversity and therefore, it was not adequate as an index of genetic diversity. Murty and Arunchalam (1966) studied that genetic drift and selection in different environment could cause greater diversity than geographic distance. Furthermore, there was a free exchange of seed material among different region, as a consequence, the characters constellation that might be associated with particular region in nature, lose their individually under human interference, and however, in some cases effect of geographic origin influenced clustering that was why geographic distribution was not the sole criterion of genetic diversity. The free clustering of the genotypes suggested dependence upon the directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices would favor constancy of the associated characters would thus indiscriminate clustering. This would be suggested that it was not necessary to choose diverse parents for diverse geographic regions for hybridization.

4.4.7 Contribution of characters towards divergence of the cultivars

The character contributing maximum to the divergence were given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization. The PCA in vector I (Z1) revealed that the important characters responsible for genetic divergence in the major axis of differentiation were days to 50% flowering, days to maturity, average fruit weight, fruit length and fruit diameter (Table 12). In vector II (Z2) that was the second axis of differentiation, plant height, no. of flowers per cluster, fruits per cluster, days to first flowering, days to 50% flowering and days to maturity were important. The role of days to 50% flowering, days to maturity in both the vectors were positive across two axes indicating the important components of genetic divergence in the materials under this study.

Table 12. Relative contributions of the thirteen characters of twenty one varieties of tomato to the divergence

Characters	Vector-1	Vector-2
Plant height (cm)	-0.0213	0.1458
Primary branches per plant	-0.2802	-0.1115
Secondary branches per plant	-0.2376	-0.3867
Number of flower per cluster	-0.2848	0.3008
Number of fruit per cluster	-0.2897	0.2530
Days to first flowering	-0.0335	0.3496
Days to 50% flowering	0.1030	0.4828
Days to maturity	0.3304	0.2440
Number of fruits per plant	-0.4103	-0.0110
Average fruit weight (g)	0.3717	-0.1226
Fruit length (mm)	0.3400	-0.0939
Fruit diameter (mm)	0.3817	-0.1406
Fruit yield per plant (Kg)	-0.1040	-0.4513

Table 13. Principle component score twenty one genotypes of tomato

Genotypes	Z_1	Z_2
G1	47.26	-24.81
G2	45.78	-21.72
G3	72.25	18.73
G4	62.68	-29.8
G5	-26.53	-31.57
G6	18.24	-38.72
G7	66.18	-12.42
G8	-36.33	-11.17
G9	-2.92	52.36
G10	25.66	64.84
G11	5.27	21.66
G12	92.44	-19.62
G13	54.12	9.99
G14	63.46	50.84
G15	-33.34	0.51
G16	-78.9	13.76
G17	55.96	-48.6
G18	-34.43	-24.61
G19	-108.86	16.57
G20	-297.68	-13.12
G21	9.7	26.91

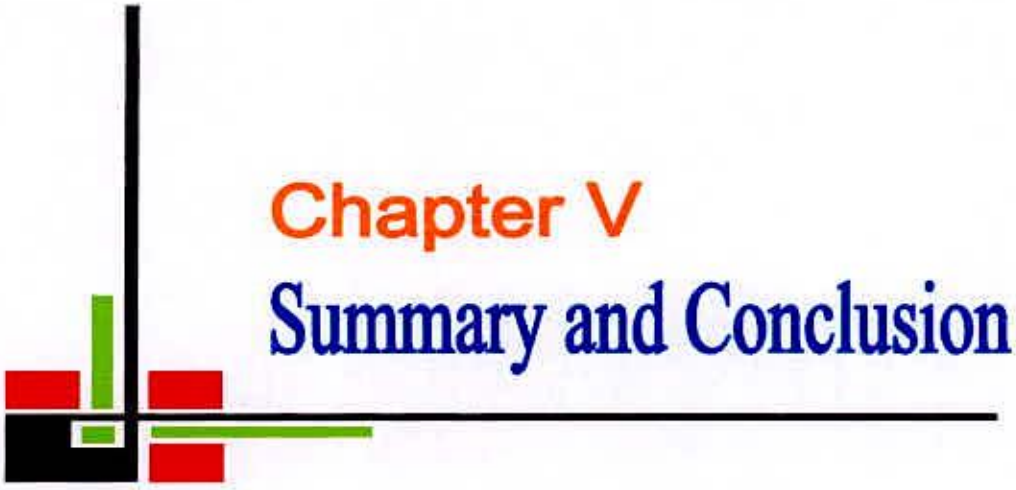
4.4.8 Comparison of different multivariate techniques

The clustering pattern of D^2 analysis through non-hierarchical clustering had taken care of simultaneous variation in all the characters under study. However, the distribution of genotypes in different clusters of the D^2 analysis had followed more or less similar trend of the Z1 and Z2 vector of the principal component analysis (Figure 4). The D^2 and principal component analysis was found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However, the principal component analysis provided information regarding the contribution of characters towards divergence of tomato.

4.4.9 Selection of cultivars for future hybridization

Genotypically distant parents were able to produce higher heterosis (Falconer, 1960; Arunachalam 1981; Ghaderi *et al.*, 1984; Mian and Bhal, 2001). Beside this, Arunachalam (1981) reported in groundnut that the higher heterosis for yield and its components could be obtained from the crosses between the intermediate divergent parents than extreme ones. Mian and Bahl (2001) also reported the same in chick pea that medium divergent genotypes showed higher heterosis in crosses for different yield contributing characters. Arunachalam (1981) reported in triticale that very high or very low parental divergent failed result in heterosis.

Considering this idea and other agronomic performances, the genotypes BD-7748, Local Jessore-3 and Local Kushtia-1 form cluster I, BD-7762, BD-7285 and BARI hybrid-4 form cluster II, BD-7290 and BD-9011 form cluster III, BARI Tomato-3 form cluster IV, might be considered as better parents for efficient hybridization programme.



Chapter V

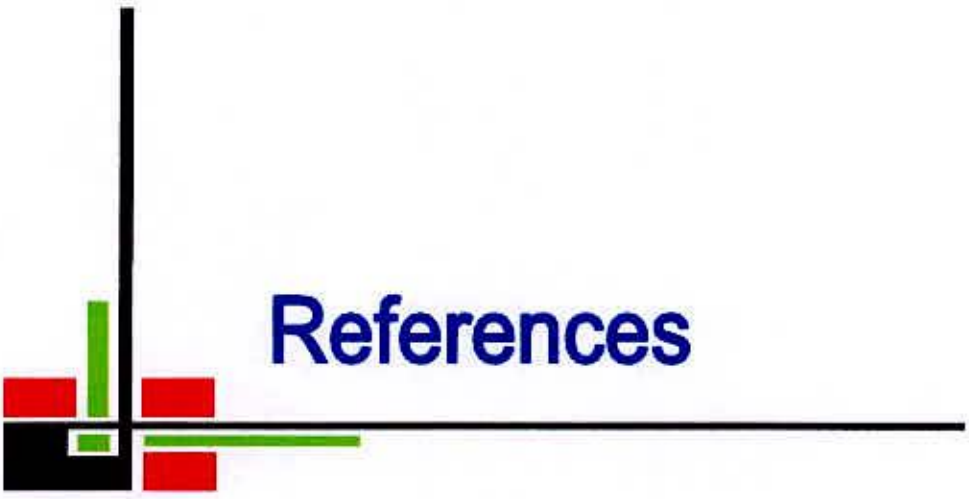
Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The twenty one genotypes were used to show variation, heritability, genetic advance and genetic advance in percentage of mean, genetic diversity, character associations and direct and indirect effect of different traits on yield. All the genotypes varied significantly with each other for most of the studied characters indicated the presence of considerably variations among the genotypes studied. The PCV values were slightly higher than the respective GCV values for all the characters under study indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of the traits. Plant height and number of fruits per plant showed high heritability along with high genetic advance were normally more helpful in predicting the genetic gain under selection. Therefore, these characters were most likely to be influenced by additive gene effects and selection for the improvement of these traits would be effective in early generations (F_2-F_3) for the development of superior genotypes. Moderate heritability for primary branches per plant indicated favorable influence of environment rather than genotypes and selection of superior genotypes to develop branching habit would not be rewarding in early genotypes. The phenomenon can be explained in a way that total fluctuations in yield are governed principally by changes in one or more component; though all fluctuations in components as in or case were not expressed in yield due to indecisive ratings of desirable and undesirable associations among yield and yield related traits. Correlation analysis revealed that fruit yield per plant showed highly significant positive association with secondary branches per plant and fruits per plant at both genotypic and phenotypic level. On the other hand, both genotypic and phenotypic level fruit yield per plant employed highly significant and negative correlation with days to 50% flowering and days to maturity. It also showed significant and negative association with plant height and number of fruit per cluster at genotypic level only. Path analysis revealed that secondary branches per plant, number of fruits per cluster, days to first flowering, days to maturity, fruits per plant, average fruit weight and fruit diameters had positive direct effects on yield per plant. Significant difference among the clusters was observed through multivariate analysis, clusters analysis and canonical vector analysis. Based

on D^2 analysis the genotypes were grouped into five different clusters. Clusters I had the maximum seven and cluster V had the minimum one genotype. The highest inter-cluster distance was observed between III and V and the lowest distance was in between III and IV. The highest and lowest intra-cluster distance was observed in III and V, respectively. Genotypes included in cluster II were important for secondary branches per plant, days to first flowering, fruit yield per plant, whereas number of flowers per cluster, number of fruits per cluster and number of fruits per plant were remarkable feature for cluster V. Considering moderate magnitude of divergence and agronomic performances, the genotypes BD-7748, Local Jessore-3, Local Kushtia-1, BD-7762, BD-7285, BARI hybrid-4, BD-7290, BD-9011 and BARI Tomato-3 might be considered as better parents for efficient hybridization programme.



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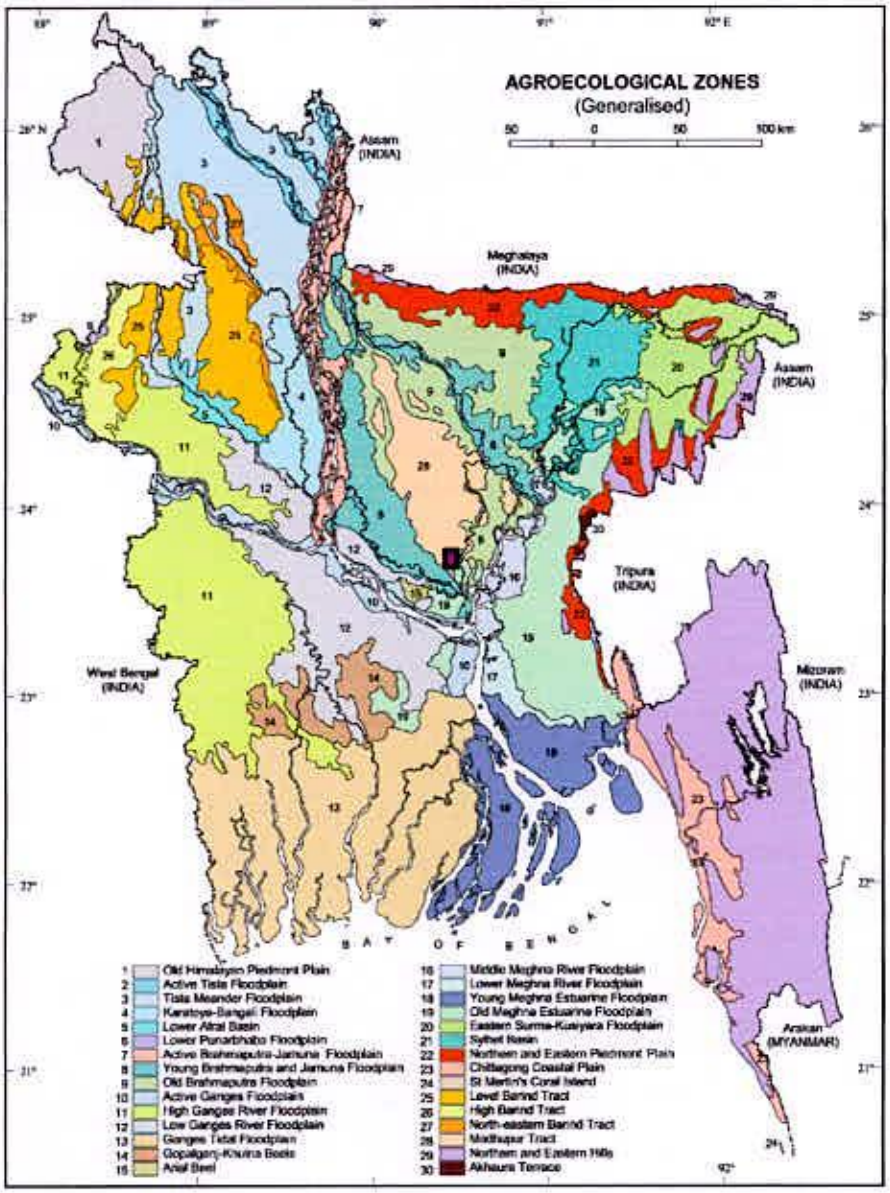
Appendices

APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site under study

Appendix II. Monthly average Temperature, Relative Humidity and Total Rainfall and sunshine of the experimental site during the period from October,2010 toMarch, 2011

Month	Air temperature (ºc)		Relative humidity (%)	Rainfall (mm) (total)
	Maximum	Minimum		
November, 2013	28.10	6.88	58.18	0.52
December, 2013	25.36	5.21	54.3	0.21
January, 2014	21.17	15.47	64.03	0.00
February, 2014	24.31	19.11	52.0	65.6
March, 2014	29.84	22.38	48.91	0.00
April, 2014	33.87	22.91	51.08	65.6

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka -1207.

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

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

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

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

Sl No.	Genotypes	PH	PBP	SBP	NFC	FPC	DFF	D50%F	DM	FPP	AFW	FL	FD	FYP
1	Local Jessore-2	75.11	9.89	6.33	7.20	3.34	48.67	53.33	113.56	63.22	35.67	34.40	12.97	1.46
2	Local Jessore-3	83.67	10.11	5.89	6.93	3.22	46.33	52.00	115.00	79.11	49.73	38.77	14.27	2.10
3	BARI Tomato-7	124.78	10.00	4.43	7.45	3.37	47.67	56.00	123.33	60.33	45.00	36.58	14.71	1.44
4	BARI Tomato-9	71.33	5.80	3.48	8.04	5.70	51.00	65.00	121.11	57.89	39.70	43.95	11.97	1.07
5	BD- 7281	62.33	9.72	9.89	9.08	3.52	50.33	55.00	113.00	145.44	20.80	24.73	8.89	1.72
6	Local Kushtia-1	63.11	9.33	4.25	7.82	3.78	47.67	54.00	115.11	115.89	35.20	49.69	10.13	1.57
7	BARI Tomato-15	97.00	7.55	5.85	8.93	5.08	57.33	65.00	124.11	60.55	73.97	52.76	14.61	1.85
8	BD- 9960	82.44	10.33	4.99	12.59	5.63	59.33	62.00	115.78	158.56	20.67	31.52	9.89	1.60
9	BD-7289	148.11	10.67	7.78	7.44	4.11	49.00	53.33	117.44	129.00	15.50	26.71	10.30	1.38
10	BD-7279	160.78	12.55	8.48	7.56	3.89	54.67	62.00	124.45	97.33	16.47	27.44	10.43	1.02
11	BD-7290	118.67	10.78	8.89	7.89	4.19	52.67	59.67	114.11	115.00	24.23	29.64	11.10	1.72
12	BARI Tomato-8	92.11	5.89	3.33	6.89	3.41	50.33	66.00	121.11	28.55	58.27	38.32	15.34	1.09
13	BARI Tomato-3	113.00	8.67	3.56	7.56	4.55	61.67	67.33	120.00	69.45	45.27	39.40	14.95	2.02

Here, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flower per cluster, FPC = Number of fruit per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm), FYP = Fruit yield per plant (Kg)

Appendix IV. Mean performance of various growth parameter and yield components (cont'd)

14	BD-10321	154.00	10.33	6.44	10.37	3.93	53.00	58.33	119.56	59.33	34.43	31.40	13.00	1.30
15	BD-7762	87.11	11.11	8.55	7.89	4.33	54.00	59.67	114.67	152.67	24.30	33.20	10.38	1.89
16	BD-7276	113.55	9.83	7.33	11.93	6.11	57.33	65.67	113.33	217.56	17.33	24.67	7.76	1.42
17	BD-7748	61.00	7.67	10.00	6.89	3.07	46.00	52.00	113.78	68.00	70.40	47.48	16.06	2.47
18	BARI Hybrid-4	77.67	10.70	10.67	7.44	4.30	50.67	53.67	92.67	154.22	43.10	38.18	13.84	3.18
19	BD-7285	112.67	11.33	14.00	6.37	3.96	54.67	58.67	93.11	260.67	13.20	27.92	9.97	3.46
20	BARI Tomato-11	75.00	10.25	8.00	15.93	10.78	48.00	54.00	82.33	415.00	6.93	23.32	5.51	1.76
21	BD-9011	127.67	9.21	8.67	6.81	3.70	51.67	54.00	121.00	113.67	33.33	39.45	14.27	2.05
	Mean	100.05	9.61	7.18	8.52	4.47	52.00	58.41	113.74	124.83	34.45	35.22	11.92	1.79
	Min.	61.00	5.80	3.33	6.37	3.07	46.00	52.00	82.33	28.55	6.93	23.32	5.51	1.02
	Max.	160.78	12.55	14.00	15.93	10.78	61.67	67.33	124.45	415.00	73.97	52.76	16.06	3.46

Here, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flowers per cluster, FPC = Number of fruits per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm), FYP = Fruit yield per plant (Kg)

Appendix V. Analysis of variance of twelve yield and yield related characters of tomato

Source of variation	df	Mean sum of square											
		PH	PBP	SBP	NFC	FPC	DFF	D50%F	DM	FPP	AFW	FL	FD	FYP
Replication	2	113.05	0.15	0.44	1.85	0.77	8.14	0.68	9.68	2408.44	77.81	23.24	0.60	0.32
Genotype	20	2,826.50**	8.55**	22.64**	16.63**	8.39**	56.10**	80.66**	364.17**	23,105.76**	1,013.50**	213.74**	23.50**	1.18**
Error	40	50.96	1.81	2.38	1.27	0.72	5.34	5.01	7.62	374.01	44.13	14.77	1.33	0.07

Here, ** indicates significant at the 0.01 level, df = Degrees of freedom, PH = Plant height (cm), PBP = Primary branches per plant, SBP = Secondary branches per plant, NFC = Number of flower per cluster, FPC = Number of fruit per cluster, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to Maturity, FPP = Number of fruits per plant, AFW = Average fruit weight (g), FL = Fruit length (mm), FD = Fruit diameter (mm), FYP = Fruit yield per plant (Kg)