GENETIC DIVERSITY ANALYSIS IN TOMATO
(Solanum lycopersicon)

BY

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CERTIFICATE

This is to certify that thesis entitled, **"Genetic Diversity Analysis in Tomato (Solanum lycopersicon)"** 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 **Manjur Hossain**, Registration No. **05-01646** 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.

.....

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Dated: June, 2011
Place: Dhaka, Bangladesh

DEDICATED TO

MY

BELOVED PARENTS

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ABSTRACT

Thirty five genotypes of Tomato (*Solanum lycopersicon*) were studied in a field experiment conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka, during November 2010 to March 2011. The objectives of the study were to identify divergent parents for hybridization programme, to identify the characters contributing to genetic diversity, to assess the magnitude of genetic divergence in genotypes, to screen out the suitable parents group which are likely to provide superior segregants on hybridization. The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters. Different multivariate analysis techniques were used to classify 35 tomato genotypes. Diversity was estimated by cluster distance. All the genotypes were grouped into four clusters. Principal Component Analysis, Cluster Analysis and Canonical Variate Analysis exhibited similar results. Significant variations were observed among the tomato genotypes for all the parameters under study. Cluster IV had the maximum (16) and cluster II had the minimum (1) number of genotypes. The highest intra-cluster distance was observed in cluster III followed by IV. The highest inter-cluster distance was observed between cluster II and III and the lowest inter-cluster distance was found between the clusters I and IV. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for number of fruits per cluster, number of fruits per plant, fruit weight and fruit yield per plant whereas days to first flowering, days to 50% flowering and days to maturity showed low GCV. In all cases, phenotypic variances were higher than the genotypic variance. High heritability with low genetic advance in percent of mean was observed for days to 50% flowering, number of fruits per cluster, fruit length, and fruit yield per plant which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance in percent of mean was observed for number of fruits per plant and fruit weight indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Considering all the characters G24 (BD-7761); G27 (BARI Tomato-3); G29 (BARI Tomato-6); G31 (BARI Tomato-8); G33 (BARI Tomato-11) can be selected for future breeding programme.

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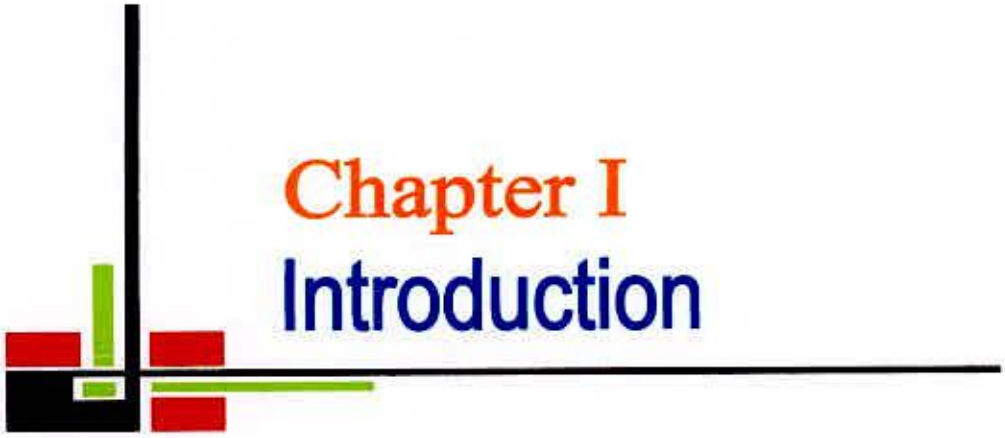
LIST OF ABBREVIATED TERMS

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
δ^2_g	Genotypic Variance
g	Gram
h^2b	Heritability in broad sense
j.	Journal
Kg	Kilogram
MSS	Mean Sum of Square
mm	Millimeter
MP	Muriate of Potash
No.	Number
PCV	Phenotypic Co-efficient of Variation
δ^2_p	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 (*Solanum lycopersicon*) belongs to the family Solanance and is a self crossing annual crop. It is a good source of vitamins (A and C) and minerals (Kalloo and Pardita, 1989). It is also the dependable source of vitamin A, B, C and D, minerals, Ca, P and Fe. More than 7% of total vitamin-C of vegetable origin comes from tomato in Bangladesh. Tomato is used as a fresh vegetable and can be processed and as paste, juice, ketch-up, sauce, powder or as a whole. World volume has increased approximately 10 % since 1985, reflecting a substantial increase in dietary use of the tomato. Nutritional, tomato is a significant dietary source of minerals, vitamin A and C, organic acid and essential amino acids. Its 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. The present leading tomato producing countries of the world are China, United States of America, Turkey, India, Egypt, Italy, Iran, Spain, Brazil Mexico, and Russia (FAO, 2010). 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. In Bangladesh it is cultivated as winter vegetable, which occupies an area of 58854 acres in 2009-10 (BBS, 2010). The tomato production was 339 lac tons in China, 137 lac tons in USA, 109 lac tons in Turkey, 103 lac tons in India and 92 lac tons in Egypt in 2008 (FAO, 2010). The total production of tomatoes were 190 thousands metric tons in Bangladesh in the year of 2009-2010 (BBS, 2010). Nowadays, 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.

Diversity in tomato is expected to be immense as the fruits vary greatly in shape and size studies on genetic parameters and character associations provide information about the expected response of various traits to selection and help in developing optimum breeding procedure. 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 target population so as to perform effective selection.

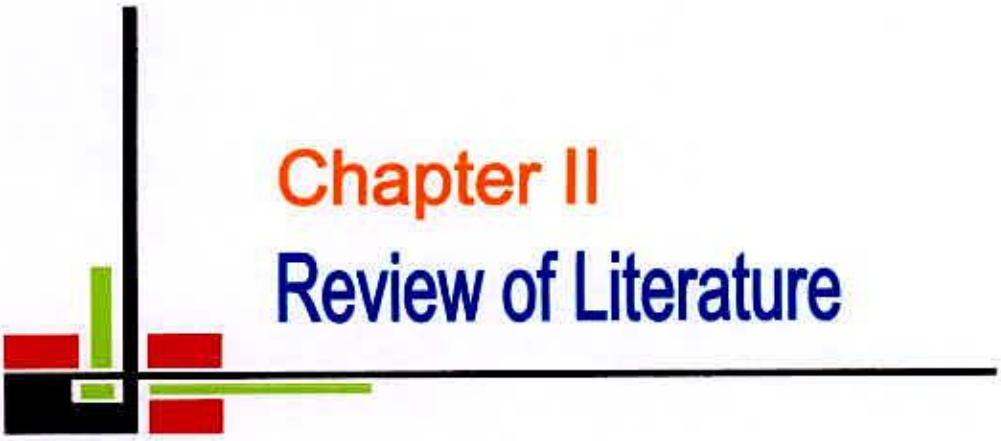
Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregates and/or to produce high heterotic crosses. More diverse the parents, greater are the chances of obtaining high heterotic and broade spectrum of variability in segregating generations (Arunachalam, 1981). The parents identified on the basis of divergence analysis would be more promising in selecting genotypes with desirable character combinations from the segregating generations obtained through hybridization. Furthermore, genetic divergence as a function of heterosis, is one of the criteria of parent selection. Therefore, the availability of transgressive segregants in any breeding programme depends upon the divergence of test parents. Precise information on the nature and degree of genetic divergence of the parents is the prerequisite of an effective breeding programme. The quantification of genetic diversity through biometrical procedures (Rao, 1952) has made it possible to choose genetically diverged parents for a successful breeding programme. The importance of genetic diversity in the improvement of a crop has been stressed

in both self and cross-pollinated crops (Gadekar *et al.*, 1992). Moreover, evaluation of genetic diversity is important to know the sources of genes for a particular trait within the available germplasm (Dharmatti, 1995).

The germplasms were received 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 were unknown. So, it is an opportunity to categorize the germplasm morphologically under different species for future utilization.

A study was conducted on the genetic diversity of tomato. With conceiving the above scheme in mind, the present research work has been undertaken in order to fulfilling the following objectives:

- To estimate the nature and magnitude of genetic divergence of among the tomato genotypes.
- To identify the most divergent parents or genotypes for further breeding programme.
- To know the yield potentiality of genotypes.
- To screen out the suitable parents group which are likely to provide superior segregants on hybridization.



Chapter II

Review of Literature

CHAPTER II

REVIEW OF LITERATURE

Tomato is one of the most popular and widely grown vegetable in the world ranking second in importance to potato in many countries. Morphological marker of any agricultural crop is a valuable tool, which can utilize for crop improvement program. Identification of phenotypic marker is essential to sort out the segregating generation and subsequent selection.

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

2.1.1 Variability

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

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

Kumari *et al.* (2007) recorded data for total soluble solids, dry matter content, reducing sugars, titratable acidity, ascorbic acid, lycopene, days to flowering, days to maturity, number of fruits per bunch, weight per fruit, fruit length, fruit width, number of fruit bearing branches, total number of fruits per plant, plant height, early yield and total yield and found that there were highly significant differences for all the characters among parents except acidity, early yield, total yield, and days to flowering.

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

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

Singh *et al.* (2005) conducted a field experiment with 30 tomato and five genotypes (DT-39, RHR-33-1, ATL-16, DARL-13 and RT-JOB-21) showed higher number of primary branches than the control. The maximum number of fruits per plant was obtained from BT-117-5-3-1. Fruit yield was maximum (1.84 kg/plant) in DT-39. Most of the cultivars showed higher total soluble solids content in their fruits compared to the control. The acidity percentage in fruits was

highest in KS-60. The physiological loss in weight at seven days was highest in NDT-111 and lowest in Plant T-3. ATL-13 showed the highest lycopene content (59.67 mg/100 g).

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.

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

2.1.1 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. He also reported that the phenotypic variance was comparatively higher than the genotypic variance indicating high degrees of environmental effect for days to first flowering .

Aditya *et al.* (1995) reported that there was no it significant difference in days to first flowering among the 44 genotypes which ranged between 52.67 and 58.87.

Sharma, (2001) reported significant variation for days to first flowering in six cultivars of tomato.

Biswas and Mallik (1989) observed that a minimum of 66 days was necessary for first flowering for cv. Selectim-7 and a maximum of 83 days for cv.

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

2.1.2 Days to 50% flowering

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

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

2.1.3 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.

Prashanth (2003) evaluated 67 genotypes of tomato and found similar results for this character.

2.1.4 Plant Height

Golani *et al.* (2007) observed that the phenotypic and genotypic associations 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 co-efficient of variation was lower than phenotypic co-efficient of variation indicating influence of environment for expression of this character.

Prasad *et al.* (1999) found high degrees of phenotypic and genotypic co-efficient of variation for plant height in 75 exotic genotypes of tomato.

Ghosh *et al.* (1995) and Nandpuri *et al.* (1974) reported a high degree of variation for plant height while a narrow range of variations was observed by Ahmed (1987).

Aditya (1995) and Matin (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.

Sonone *et al.* (1986) and Prasad and Prasad (1977) also reported high phenotypic and genotypic co-efficient of variation for plant height in tomato. But Mallik *et al.* (1985) reported that phenotypic co- efficient of variations were higher than genotypic co-efficient of variations for plant height in tomato.

2.1.5 Number of branches per plant

Singh *et al.* (2005) evaluated 10 genotypes of tomato and observed a range between 3.40-7.47 branches per plant. He reported the PCV (23.49%) was slightly higher than GCV (22.58%) for this character.

Mohanty and prusti (2003) evaluated 18 cultivars of tomato and observed a range between 4.97-13.73 branches per plant. He reported the PCV (32.35%) was higher than GCV (30.62%).

2.1.6 Number of clusters per plant

Singh *et al.* (2001) observed considerable range of genetic variability for yield, yield components and biochemical characters in the materials under study and maximum genotypic coefficient of variation was recorded for number of leaves per plant, followed by number of clusters per plant.

2.1.7 Number of fruits per cluster

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

Arun *et al.* (2004) evaluated 37 genotypes of tomato and observed a range between 2.33-6.63 fruits per cluster. He 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%).

2.1.8 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 co-efficient of variation and observed high variability in the characters of number of fruits per plant of 186 genotypes of tomatoes.

Das *et al.* (1998) reported wide range of genotypic variation for number of fruits per plant. They also reported high genotypic variation for number of fruits per plant.

Phookan *et al.* (1998) reported that is the estimation of genotypic and phenotypic co-efficient of variation were high for fruits per plant.

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

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 variances, phenotypic and genotypic co-efficient 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.

Bhutani *et al.* (1989) performed a varietal trial of 84 genotypes and reported that Set-23, Growthens Globe, Punjab Chhuhara, VSII-2, Pusa Red Plum and HS 102 were the best 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-efficients of variation were estimated for fruits per plant.

2.1.9 Fruit weight (gm)

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 a field experiment to study genetic variability of fifteen heat tolerant tomato and showed that phenotypic (PCV) and genetic (GCV) coefficients of variation were high for average fruit weight.

Matin (2001) reported similar results for average fruit weight in an experiment with 26 tomato genotypes.

Brar *et al.* (1998) reported that varietal differences were significant among 20 cultivars of tomato for average fruit weight ranged between 24.1g and 76.6g.

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

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.

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

with genotypic co-efficient of variation were smaller than phenotypic variance and phenotypic co-efficient of variation respectively.

Sahu and Mishra (1995) reported that fruit weight had high genotypic co-efficient 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 variances, phenotypic and genotypic co-efiicient 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 co- efiicient 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.

2.1.10 Fruit length

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

Mohanty (2002) evaluated 18 genotypes of tomato and also found similar results for this character

2.1.11 Fruit diameter

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

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

2.1.12 Yield per plant

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

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 co-efficient of variation was higher for average yield per plant among 32 tomato genotypes.

Singh *et al.* (1997) observed that phenotypic variation was quite higher than genotypic variation for this trait in 27 genotypes of tomato.

Aditya *et al.* (1995) observed highly significant differences for average yield per plant among 44 genotypes of tomato. She also reported that phenotypic variance and phenotypic co- efficient of variation were higher than genotypic variance and genotypic co-efticient of variation respectively.

Ghosh *et al.* (1995) observed highest variation for yield per plant. Pujari *et al.* (1995) also observed highest variation for yield per plant.

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 co-efficient of variation were 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 genotypes 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:

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

Kumari and Subramanian (2007) reported that the estimates of heritability were high for all the characteristics and genetic advance was high for plant height, moderate for total number of fruit

bearing branches, weight per fruit and days to maturity, while the remaining characteristics had low values of genetic advance.

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

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

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

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

Joshi *et al.* (2004) observed moderate heritability and moderate genetic gain for number of fruits per cluster, fruit length, fruit breadth, stem end scar size, number of locules per fruit, whole fruit firmness, ascorbic acid content and plant height indicating additive gene effects. Low heritability

and low genetic gain was observed for pericarp thickness. Moderate heritability and low genetic gain for harvest duration suggests the presence of dominance and epistatic effects. High heritability combined with high genetic gain was observed for shelf life indicating additive gene action.

Arun *et al.* (2004) reported that moderate heritability associated with moderate genetic advance for plant height of 37 tomato genotypes of tomato.

Mohanty (2003) observed that high heritability with high genotypic coefficient of variation was for fruit weight, plant height, number of fruits and number of branches per plant.

Singh (2002) reported that heritability was high for all characters except days from fruit setting to red ripe stage and the highest genetic advance was predicted for average fruit weight, followed by shelf life of red ripe fruits.

Matin (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 the number of fruits per plant, total yield per plant and marketable yield per plant had low to moderate estimates of heritability and genetic advance and number of marketable fruits per plant had high values of heritability and genetic advance.

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

Prasad *et al.* (1999) estimated heritability in 75 exotic genotypes of tomato and reported very high heritability along with high genetic advance by fruit weight.

Phookan *et al.* (1998) observed high heritability and genetic advance in percentage of mean were 4 estimated for fruits per plant and average fruit weight suggesting their importance in selection for tomato improvement.

Vikram and Kohli (1998) reported high heritability and genetic advance for mean fruit weight which suggested that improvement for this character should be fairly straight forward.

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

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

Mittal *et al.* (1996) estimated heritability and genetic advance in 27 genotypes of tomato. High heritability associated with high genetic advance was observed by them indicating the character, predominantly under the control of additive gene, could be improved through selection.

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 but highest genetic advance as percentage of mean under selection.

Gadekar *et al.* (1992) obtained high values for 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 fruits per plant and 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. Heritability estimates of 90% were obtained for plant height, number of fruits per plant and individual fruit weight.

Islam and Khan (1991) studied 12 tomato genotypes and reported that heritability values were high for most of the characters but moderate for days to first flowering, maturity and plant height.

Kasrawi and Amr (1990) reported that pH 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. He also reported that high genetic advance (>30%) was observed for fruit yield, plant height, individual fruit weight and number of fruits per plant. Estimates of high heritability and high genetic advance for number of fruits per plant, individual fruit weight and plant height indicated control by additive genetic effects.

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

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

2.3 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 in such crops is critical because, the success of such program depends upon the segregants 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 programme, genetic divergence has been considered as an important parameter to identity most diverse parents for obtaining highly heterotic F_1 generation through selection. Many scientists have studied genetic divergence of tomato on the basis of Mahalanobis' D^2-statistics based on multivariate analysis. Among them most relevant recent publications are reviewed below:

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 showed significant differences 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 programmes to obtain good seggregants.

Mahesh *et al.* (2006) grouped 30 tomato genotypes into nine clusters studied based on D2 analysis. The cluster mean indicated that Days to 50% flowering, plant height, number of branches per plant, number of cluster per plant, number of fruit per cluster and fruit yield per plant were reported as chief contributors towards divergence.

Sharma *et al.* (2006) reported 60 genotypes of tomato were studied for genetic divergence. The genotypes grouped into 10 clusters, maximum divergence within a cluster was exhibited by the cluster VIII (1.531), closely followed by cluster III (1.528)and cluster V (1.460), where as, 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 cluster based on D2 analysis number of fruits per cluster, plant height, number of branches, pericarp thickness, average fruit weight and TSS content of fruit were reported as chief contribution towards divergence.

Arun *et al.* (2003) studied the nature and magnitude of genetic divergence in 73 tomato genotypes of different origin for quantitative characters and they grouped genotypes into 15 cluster indicated the presence of wide range of genetic diversity among the genotypes, cluster 5 having 6 genotypes. The mean fruit yield/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 lowest number of leaves (2,0280) was recorded in cluster 9 and cluster 6 consist of highest number of fruits/cluster (4.90).

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

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 clusters per plant, fruits per cluster, number of fruits per plant, yield per plant, incidence tomato curl viruses and number of whiteflies per plant. They grouped the lines into 4 clusters based on the similarities of D^2 values. Cluster-I was the biggest having 217 genotypes, which also consisted of commercial ToLCV susceptible genotypes, namely DWD-1, DWD-2, *etc.*, cluster-II consisting of 51 genotypes / hybrids with potato leaf type and pink fruit, which exhibited field tolerance to ToLCV and cluster-III and IV had 99 and 35 genotypes respectively. Considerable diversity within and between cluster was noticed.

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 per plant, number of fruits per plant, average fruit weight and yield) in Orissa, India during rabi 1998-99 and found considerable variations among the accessions. They could group the genotypes into 5 clusters including two solitary groups and reported that genetic diversity was not associated with geographic distribution. Maximum inter cluster distance (D^2=l289.31) was observed between the clusters I and V. The distance between clusters I and Ill, Ill 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 distances 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-heritable clustering approach with the help of Mahalanobis' D2 statistics 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 cluster studied based on D^2 analysis. A maximum of 16 genotypes entered cluster I, followed by 15 in cluster IV, 9 in cluster III, 7 in cluster II, 4 in cluster V and the remaining four cluster consisted of solitary genotype.

Chapter III

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

An experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from November 2010 to March 2011 to study on the genetic diversity analysis in tomato *(Solanum lycopersicon*). A brief description about the locations of the experimental site, characteristics of soil, climate, materials, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural operations, harvesting, data recording procedure, economic and statistical analysis etc., which are presented as follows:

3.1. Experimental site

The research work relating to determine the genetic diversity of tomato was conducted at the Sher-e-Bangla Agricultural University Farm, Dhaka-1207 during November 2010 to March 2011.

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 in Appendix II.

3.4 Characteristics of soil

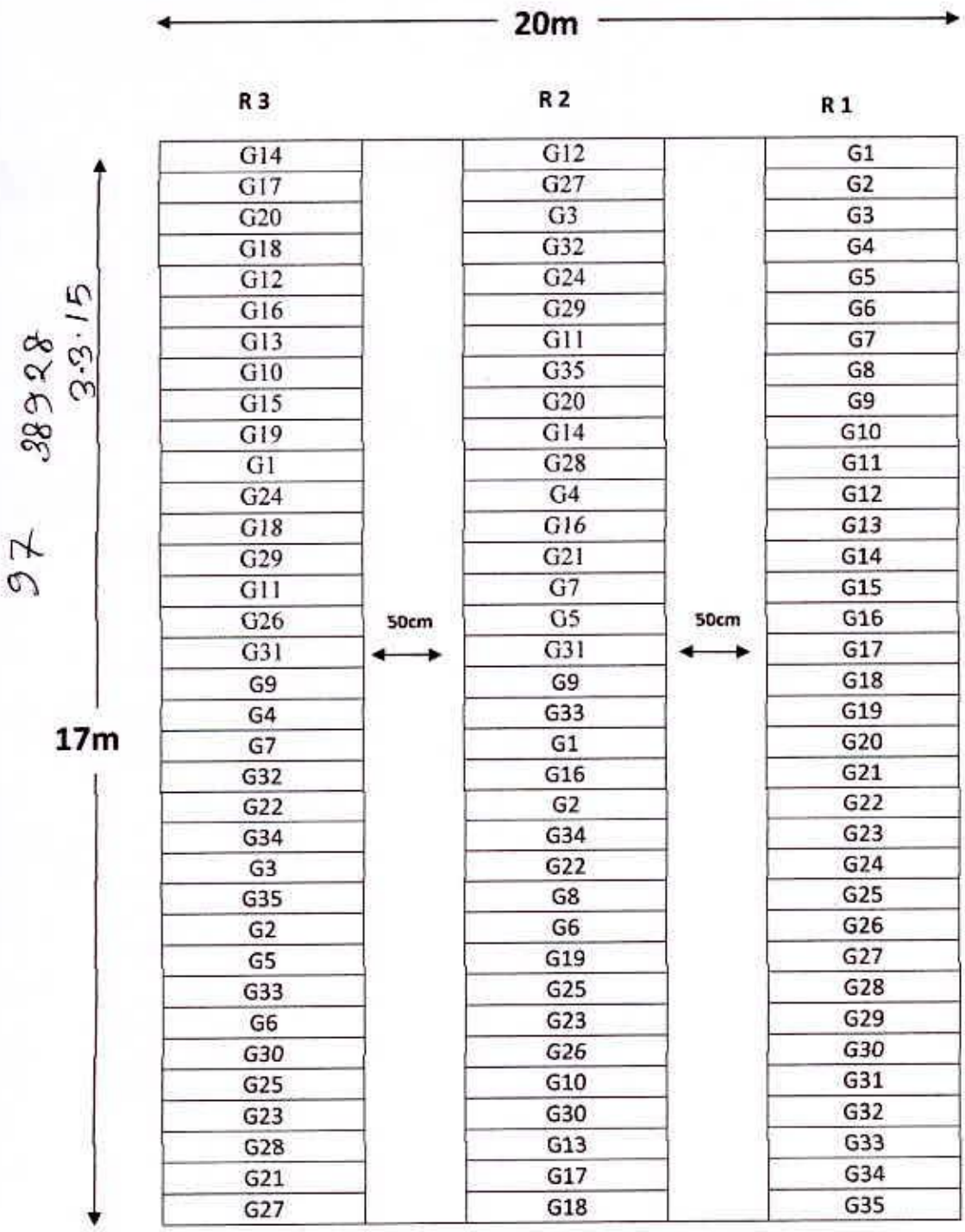
Soil of the experimental site belongs to the general soil type, Shallow Red Brown Terrace Soils under Tejgaon Series. Top soils were clay loam in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental 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. Physicochemical properties of the soil are presented in (Appendix III).

3.5 Planting materials

Thirty five (35) genotypes of tomato were used for the present research work. The purity and germination percentage were leveled as around 100 and 80 respectively. 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. The name and origin of these genotypes are presented in Table 1.

3.6 Design and layout of the experiment

The study was laid out in Randomized Complete Block Design (RCBD) with three (3) replications. The plot size was 340 m^2. A distance of 50 cm from block to block, 45 cm from



R 3		R 2		R 1
G14		G12		G1
G17		G27		G2
G20		G3		G3
G18		G32		G4
G12		G24		G5
G16		G29		G6
G13		G11		G7
G10		G35		G8
G15		G20		G9
G19		G14		G10
G1		G28		G11
G24		G4		G12
G18		G16		G13
G29		G21		G14
G11		G7		G15
G26	50cm	G5	50cm	G16
G31		G31		G17
G9		G9		G18
G4		G33		G19
G7		G1		G20
G32		G16		G21
G22		G2		G22
G34		G34		G23
G3		G22		G24
G35		G8		G25
G2		G6		G26
G5		G19		G27
G33		G25		G28
G6		G23		G29
G30		G26		G30
G25		G10		G31
G23		G30		G32
G28		G13		G33
G21		G17		G34
G27		G18		G35

Figure 1. Showing the layout of the experimental plot

Table 1. Name and origin of thirty five tomato genotypes used in the present study

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Origin
1	G_1	BD-7257	PGRC, BARI
2	G_2	BD-7258	PGRC, BARI
3	G_3	BD-7259	PGRC, BARI
4	G_4	BD-7260	PGRC, BARI
5	G_5	BD-7269	PGRC, BARI
6	G_6	BD-7270	PGRC, BARI
7	G_7	BD-7276	PGRC, BARI
8	G_8	BD-7278	PGRC, BARI
9	G_9	BD-7279	PGRC, BARI
10	G_{10}	BD-7281	PGRC, BARI
11	G_{11}	BD-7285	PGRC, BARI
12	G_{12}	BD-7286	PGRC, BARI
13	G_{13}	BD-7287	PGRC, BARI
14	G_{14}	BD-7289	PGRC, BARI
15	G_{15}	BD-7290	PGRC, BARI
16	G_{16}	BD-7291	PGRC, BARI
17	G_{17}	BD-7292	PGRC, BARI
18	G_{18}	BD-7295	PGRC, BARI
19	G_{19}	BD-7301	PGRC, BARI
20	G_{20}	BD-7302	PGRC, BARI
21	G_{21}	BD-7306	PGRC, BARI
22	G_{22}	BD-7759	PGRC, BARI
23	G_{23}	BD-7760	PGRC, BARI
24	G_{24}	BD-7761	PGRC, BARI
25	G_{25}	BD-7762	PGRC BARI
26	G_{26}	BARI Tomato- 2	PGRC, BARI
27	G_{27}	BARI Tomato- 3	PGRC, BARI
28	G_{28}	BARI Tomato- 4	PGRC, BARI
29	G_{29}	BARI Tomato- 6	PGRC, BARI
30	G_{30}	BARI Tomato- 7	PGRC, BARI
31	G_{31}	BARI Tomato- 8	PGRC, BARI
32	G_{32}	BARI Tomato- 9	PGRC, BARI
33	G_{33}	BARI Tomato- 11	PGRC, BARI
34	G_{34}	BARI Tomato- 14	PGRC, BARI
35	G_{35}	BARI Tomato- 15	PGRC, BARI

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

row to row and 40 cm from plant to plant was maintained. The genotypes were randomly distributed to each row within each line.

3.7 Seedbed preparation and raising seedling

The sowing was carried out on 11 November 2010 in the seedbed; before sowing seeds were treated with Bavistin for 5 minutes. Seedlings of all genotypes were raised in seedbeds in the Sher-e-Bangla Agricultural University, Dhaka-1207 farm Unit. Recommended cultural practices were taken up before and after sowing the seeds. When the seedlings become 25 days old; those were transplanted in the main field.

3.8 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 to good tilth in the first week of December 2010. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

3.9 Manure and fertilizers application

Total cowdung and triple super phosphate (TSP) were applied in the field during final land preparation. Half Urea and half murate of potash (MOP) were applied in the plot after three weeks of transplanting. Remaining urea and murate of potash (MOP) were applied after five weeks of transplanting. Doses of manure and fertilizers used in the study are showing in Table 2.

3.10 Transplanting of seedlings

The seedlings were raised in the seedbed in usual way and 25 days old seedlings were transplanted in the main field on 05 December, 2012. The transplanted seedlings were watered regularly to make a firm relation with roots and soil to stand along.

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

Sl. No.	Fertilizers/ Manures	Dose	
		Applied in the plot	Quantity/ha
1.	Urea	20 kg	550 kg
2.	TSP	17 kg	450 kg
3.	MOP	10 kg	250 kg
4.	Cow dung	400 kg	10 ton

3.11 Intercultural operations

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

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 gap filling was done by 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 plants erect.

3.11.3 Weeding and mulching

Several 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 4 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, since there was no significant pest infestation in the field, hence no control measure was undertaken. In order to prevent disease infestation ' Ripcord' was used for 6 times at an interval of 7 days from 06 January to 11 February 2011. There were different types of weeds which were controlled effectively by hand weeding.

3.12 Harvesting:

Harvesting continued for about one month because fruits of different lines matured progressively at different dates and over long time. Fruits were picked on the basis of horticultural 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 09 March and completed by 29 March. 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 Plate 4.

Plate 1: Field view of the experimental plot

Plate 2: A single tomato plant in the experimental plot

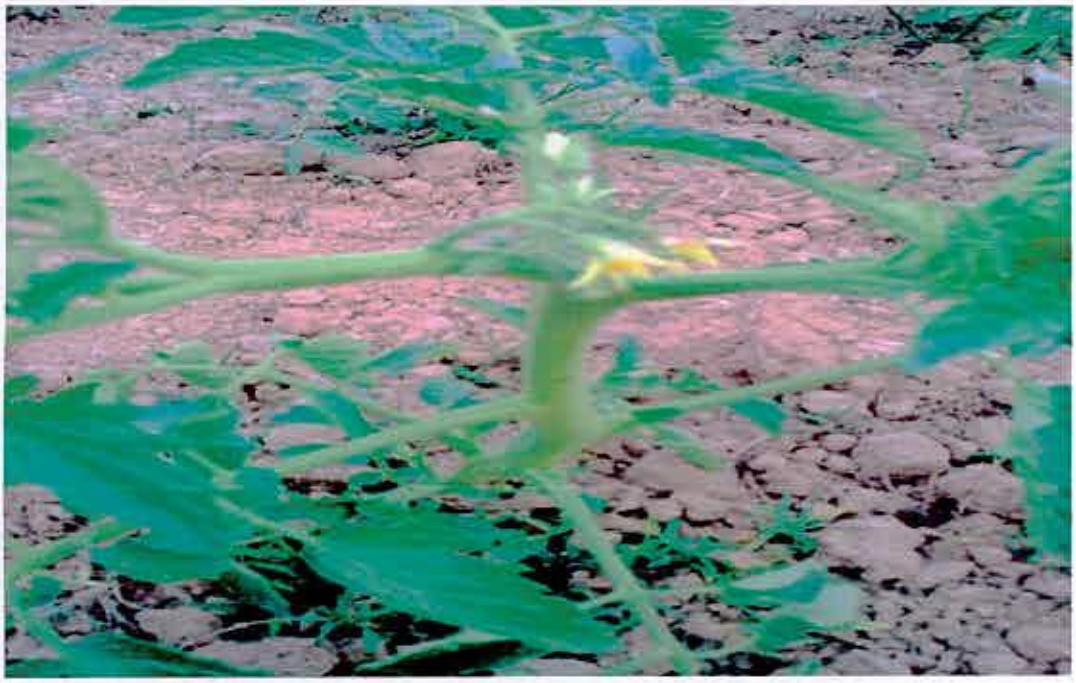


Plate 3: A tomato plant with flower

Plate 4: A tomato plant with a cluster of tomatoes

3.13. Data recording

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

3.13.1 Days to first flowering

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

3.13.2. Days to 50 per cent flowering

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

3.13.3. Days to maturity

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

3.13.4. Plant height (cm)

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

3.13.5. Number of branches per plant

The number of branches arising from the main stem above the ground was recorded at 60 days after transplanting.

3.13.6. Number of clusters per plant

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

3.13.7. Number of fruits per cluster

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

3.13.8. Number of fruits per plant

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

3.13.9. Fruit weight (g)

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

3.13.10. Fruit Length (cm)

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

3.13.11. Fruit Diameter (cm)

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

3.13.12. Fruit yield per plant (kg)

The weight of fruits from each picking was recorded from the five labeled plants of each experimental plots. 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 Chaudhury, 1985) and was estimated using MSTAT-C computer programme. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C. Multivariate analysis was done by computer using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA).

3.14.1.1 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 squares

EMS = Error mean sum of square

r = number of replications

Phenotypic variance (σ^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 co-efficient of variation

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

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

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly,

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

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

Where,

σ^2_{ph}= Phenotypic variance

$\bar{x}$ = Population mean

3.14.1.3 Estimation of heritability

Broad sense heritability was estimated 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

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_{ph}$ = 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 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 Johnson *et al* (1955).

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

3.14.2 Multivariate analysis

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

3.14.2.1 Principal Component analysis (PCA)

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

3.14.2.2 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).

3.14.2.3 Cluster analysis (CA)

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

switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

3.14.2.4 Canonical Vector analysis (CVA)

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

3.14.2.5 Calculation of D^2 values

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

3.14.2.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested Rao (1952).

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

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.

3.14.2.7 Computation of average inter-cluster distances

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

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

Where,

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

n_i = Number of populations in cluster i.

n_j = Number of populations in cluster j.

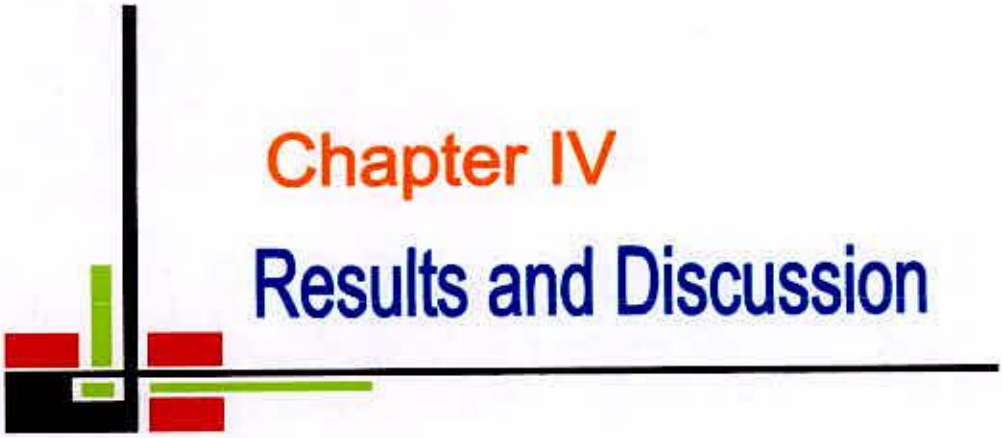
3.14.2.8 Cluster diagram

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

3.14.2.9 Selection of varieties for future hybridization programme

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

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



Chapter IV

Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

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 pre-requisite 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 days to first flowering, days to 50% flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of fruits per cluster, number of fruits per plant, fruit weight (g), fruit Length (cm), fruit Diameter (cm), fruit yield per plant (Kg) etc. were recorded, Genetic diversity was analyzed using GENSTAT software programme. Genetic diversity analysis involves several steps. Therefore, Genetic parameters and more than one multivariate techniques were required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001; Juned *et at.*, 1988 and Ario, 1987). In the analysis of genetic diversity in tomato (*Solanum lycopersicon*) multivariate techniques were used.

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, coefficients of genotypic and phenotypic variations, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in Table 3.

The results are discussed character wise as follows:

4.1.1 Days to first flowering

The mean number of days to first flowering was 62.55 DAS. It had a range of 58 to 69 DAS (Table 3). The accession G-20 (BD-7302) and G-24 (BD-7761) was the earliest to flower at 57.66 days while G-30 'BARI Tomato-7' were late to flower (69.33 days) (Appendix IV). The PCV and GCV were 8.25 and 4.43 percent, respectively. There was a very little differences between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. Such values of GCV with least difference were also observed by Singh *et al.* (1973) and Korla *et al.* (1998).The heritability (30.68%) estimates for this trait was very low, genotypic advance (4.91) and genetic advance over percentage of mean (3.02) were found also low (Table 3), indicated that this trait was controlled by non-additive gene. Heritability and genetic advance over mean in tomato are showing in Figure 3. Patil (1996) also found similar result in tomato. Genetic advances as percent of mean was low which is in accordance with the findings Singh *et al.* (1973). Genotypic and phenotypic variability in tomato are showing in Figure 2.

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

Parameters	Range	Mean	MS	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV	h^2_b	GA (5%)	GAPM	CV (%)
DFF	58.00-69.00	62.55	24.86**	26.64	7.69	1.78	8.25	4.43	2.13	28.86	3.07	4.91	2.13
D50%F	68.00-74.00	70.79	12.63**	14.93	3.44	2.30	5.45	2.62	2.14	66.86	1.84	2.59	2.14
DM	120.0-133.00	122.63	14.27**	15.23	4.44	0.96	3.18	1.71	0.80	29.15	2.34	1.91	0.80
PH	55.33-106.70	83.05	748.76**	843.84	217.89	95.08	34.97	17.77	11.74	25.82	15.45	18.60	11.74
NBPP	5.00-11.00	8.23	5.29**	6.54	1.35	1.25	31.03	14.10	13.57	20.64	1.08	13.16	13.57
NCPP	9.00-16.33	12.49	11.48**	13.22	3.25	1.74	29.08	14.42	10.55	24.58	1.84	14.72	10.55
FPC	2.66-17.33	4.09	16.93**	5.72	5.49	0.45	58.33	57.14	16.36	95.97	2.71	66.29	16.37
FPP	31.00-224.00	50.32	2931.68**	984.78	960.19	51.10	62.36	61.57	14.20	97.50	36.22	71.97	14.21
FW	5.00-62.67	29.15	633.54**	634.45	210.87	0.91	86.40	49.81	3.28	33.24	17.25	59.16	3.28
FL	1.75-5.16	3.45	52.87**	1.87	1.62	0.02	39.63	36.89	4.09	86.63	4.99	144.63	4.36
FD	1.16-4.75	3.11	1.26**	1.34	0.40	0.07	37.22	20.33	8.50	29.86	0.71	22.82	8.54
FYP	0.46-3.97	1.35	1.63**	0.65	0.53	0.03	59.28	53.53	12.33	81.53	0.85	62.50	12.31

Here, ** Mean square is significant at the 0.01 level, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Branches per plant, NCP = Number of clusters per plant, FPC = Fruits per cluster, FPP = Fruits per plant, FW = Fruit weight (g), FL = Fruit length (cm), FD = Fruit diameter (cm), FYP = Fruit yield per plant (kg), MS = Mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation, h^2b= Heritability, GA= Genetic advance, GAPM= Genetic advance in percent of mean and CV% = Coefficient of variation.

4.1.2 Days to 50 percent flowering

Significant differences were recorded among the entries with respect to days to 50 per cent flowering (Appendix IV). The value ranged from 68.00 to 74.00 DAS, The accession G-24 (BD-7761) showed minimum (68 DAS) and the accession G-12 (7286), G-16 (BD-7291), G-22 (BD-7759), G-23 (BD-7760), G-29 (BARI Tomato-6), G-31 (BARI Tomato-8) were showed maximum (74 DAS) days to 50 percent flowering (Appendix IV). The PCV and GCV were 5.45 and 2.62 percent with a overall mean of 70.79 days (Table 3). There was a very little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. Low genotypic and phenotypic coefficient of variability were observed for days to 50 per cent flowering which are in line with the earlier observation of Singh *et al.* (1973) and Prasad and Prasad (1976) . The heritability (h^2b) estimates were moderate (66.86 %) with an expected genetic advance over mean of 1.84 percent (Table 3). High heritability coupled with low genetic advance was observed for days to 50 per cent by Singh *et al.* (1973) and Kumar *et al.* (1980).

4.1.3 Days to maturity

Significant differences were recorded among the entries with respect to days to maturity. The value ranged from 120 to 133 DAS, The accession G-22 (BD-7759) showed minimum (120 DAS) and the accession G-1 (BD-7257)' showed maximum (133 DAS) days to maturity, respectively (Appendix IV). The PCV and GCV were 3.18 and 1.71 percent with a overall mean of 122.63 days. The heritability (bs1) estimates were low (29.15%) with an expected genetic advance over mean of 2.34 percent. low heritability and low genetic advance for days to maturity was also found by Kumari *et al.* (2007).

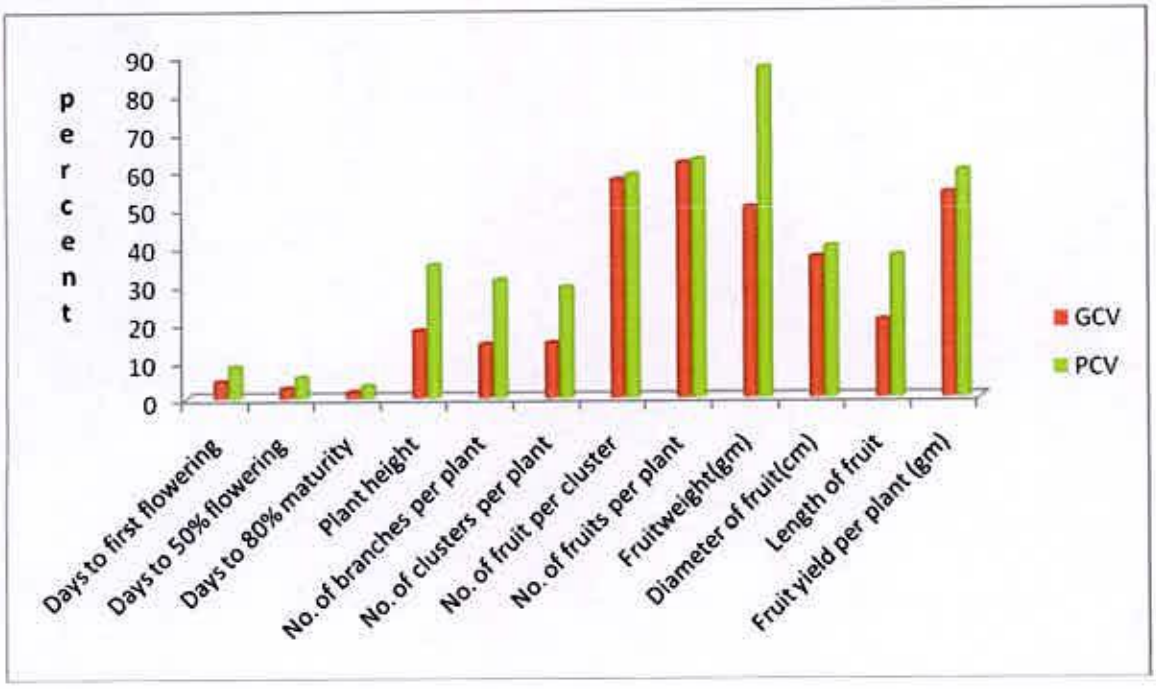


Figure 2. Genotypic and phenotypic variability in tomato

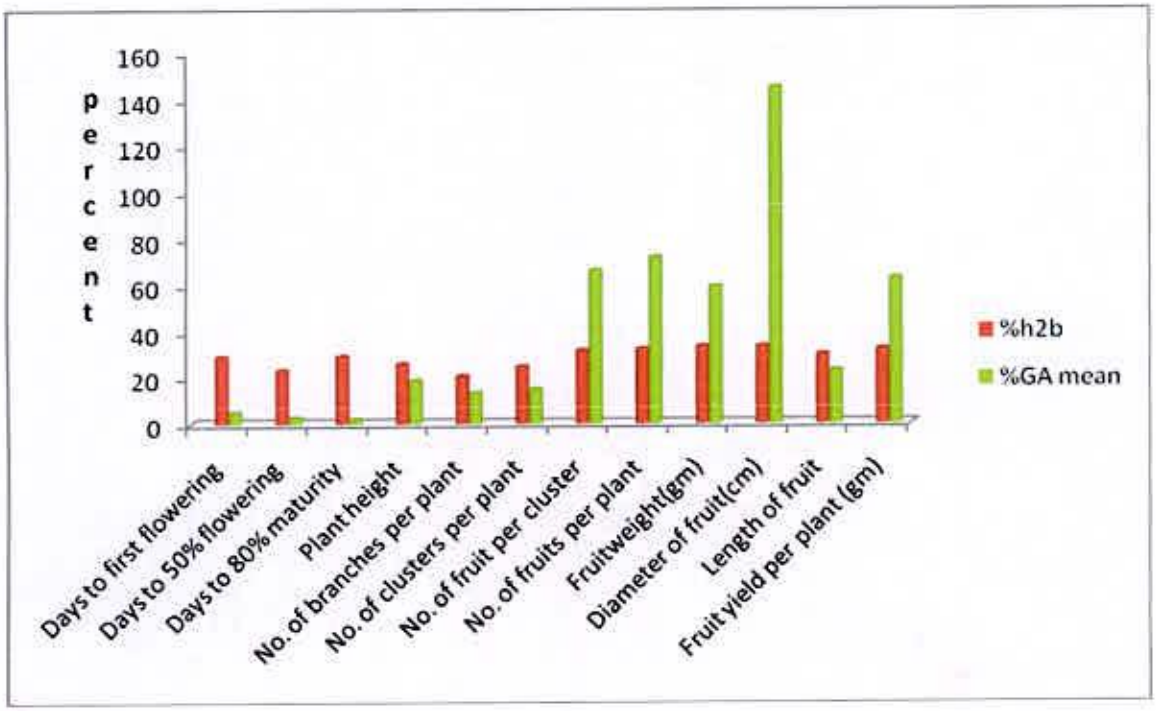


Figure 3. Heritability and genetic advance over mean in

4.1.4 Plant height (cm)

The grand mean plant height recorded was 83.05 cm. It ranged from 55.33 cm to 106.70 cm (Table 3). The analysis of variance revealed highly significant differences among the genotypes with respect to plant height. The maximum plant height (106.70 cm) was recorded by the G-13(BD-7287) and the lowest plant height (55.33 cm) was recorded by 'BD-7301' (Appendix IV). The PCV and GCV were 34.97 and 17.77 percent respectively, (Table 3). There was little difference between phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. In the present study, the genotypic and phenotypic co-efficient of variability were moderate for plant height. Similar observations were made by Mariane *et al.* (2003). Singh *et al.* (2002) showed that the phenotypic coefficient of variation was greatest for this character. The estimates of heritability was high at 25.82 per cent with an expected genetic advance (18.60%) (Table 3). Plant height exhibited low heritability and genetic advance as per cent mean which is similar to the earlier findings by Kumari *et al.* (2007), Singh *et al.* (2006) and Joshi *et al.* (2003). Low heritability and low genetic advance for this charecter was observed by Joshi *et al.* (2004).

4.1.5 Number of branches per plant

It ranged from 6.00 to 11.00 with a mean value of 8.23. Maximum number of branches was recorded in 'BD-7287' and 'BARI Tomato-15' genotype showed the minimum number of branches (Appendix IV). The PCV and GCV observed were 31,03 and 14.10 percent, respectively (Table 3). There was little difference between phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. Genotypic and phenotypic coefficient of variability for number of branches per plant were high. Mohanty (2002) recorded moderate to high variability for this character.

Singh *et al.* (2002) also showed that the phenotypic coefficient of variation was greatest for number of primary branches per plant. Heritability (h^2b) of 20.64 percent coupled with low genetic advance over percentage of mean 13.16 percent were noticed (Table 3). Low genetic advance as per cent mean was similar to the results obtained by Prabhushankar (1990) and Anandagowda (1997). This character also showed high heritability estimates. The results are in agreement with the results obtained by Ara *et al.* (2009), Kumari *et al.* (2007) and Singh (2005).

4.1.6 Number of clusters per plant

Wide variation of 9.00 to 16.33 cluster per plant with a mean of 12,49 cluster was observed per plant. The differences between the values of PCV and GCV were 29.08 and 14.42 respectively (Table 3). The difference between GCV and PCV indicated less influence of environment on this trait. The genotypes 'BD-7291'and BARI Tomato-15 recorded the minimum number of clusters per plant. Whereas, accession 'BD-7759' showed the highest number of clusters per plant (Appendix IV). A moderate value of genotypic coefficient of variation and phenotypic coefficient of variation were noticed for number of clusters per plant (Table 3). The phenotypic coefficient of variation was greatest for this character was observed by Singh *et al.* (2002). Moderate heritability estimate of 24.58 percent with low genetic advance as percent mean (14.72) were recorded for this trait (Table 3). This character showed low heritability coupled with genetic advance. Similar findings were also obtained by Singh *et al.* (2002) and Kumar *et al.* (1980).

4.1.7 Number of fruits per cluster

It was ranged from 2.66 to17.33 with a mean of 4.09. The coefficient of variability for phenotypic and genotypic were 58.33 and 57.14, respectively (Table 3). The difference between GCV and PCV indicated less influence of environment on this trait. The maximum

fruits per cluster of 16.33 was observed in the genotype 'BD-7759' and the minimum of 2.66 with the genotype 'BD-7291'and BARI Tomato-14 (Appendix IV). In the present study, the genotypic and phenotypic coefficients of variability were high for number of fruits per cluster. These observations are in accordance with the findings of Singh *et al.* (2002). Moderate PCV and GCV were found by Aradhana and Singh (2003). High heritability of 95.97 percent was noticed with a genetic gain of 66.29 percent (Table 3). High heritability and moderate genetic gain for this character were also observed by Joshi *et al.* (2004).

4.1.8 Number of fruits per plant

A wide variation was found among the germplasm accessions for the number of fruits per plant. It varied 31.00 to 224.00 significantly among the genotypes with a overall mean of 50.32 (Table 3). The accession G-1 (BD-7257) and G-4 (BD-7260) showed lowest number of fruits per plant and the highest number of fruits per plant was recorded by the entry 'BARI Tomato-11' (Appendix IV). The PCV and GCV were 62.36 and 61.57 respectively, (Table 3). Coefficient of variation observed at genotypic and phenotypic level was high for number of fruits per plant. Highest phenotypic coefficient of variation was observed by Singh *et al.* (2002) and highest phenotypic and genotypic coefficient of variation was observed by Joshi *and* Choudhury (2003). The high heritability estimates of 97.51 percent with an expected genetic advance over mean of 71.97 percent were noticed for number of fruits per plant (Table 3). This character showed high heritability coupled with high genetic gain and the findings are in agreement with the observations of Ara *et al.* (2009), and Singh *et al.* (2001). High heritability and moderate genetic advance as per cent of mean was found by Naidu (1993) and Patil (1996). Similar observations were made by Mohanty *et al.* (2003) and Singh *et al.* (2001).

4.1.9 Fruit weight (g)

It ranged from 5.00 to 62.67 g with a mean of 29.15 g. The minimum fruit weight was recorded by the variety 'BARI Tomato-11' and variety 'BARI Tomato-3' showed the maximum fruit weight (Appendix IV). The PCV and GCV obtained were 86.40 and 49.81 percent, respectively demonstrated that environment has little influence of the expression of this character (Table 3). Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. High genotypic and phenotypic coefficient of variation for average fruit weight were noticed. Similar values have been reported by Singh *et al.* (2002). The values of high heritability (33.24%) along with high genetic advance as per cent mean (59.16%) were observed for this trait (Table 3). High heritability coupled with high genetic advance as percentage of mean for average fruit weight was observed by Ara *et al.* (2009) and Singh *et al.* (2002). High estimates of heritability coupled with moderate genetic advance observed for this character is in accordance with earlier findings of Mohanty *et al.* (2003).

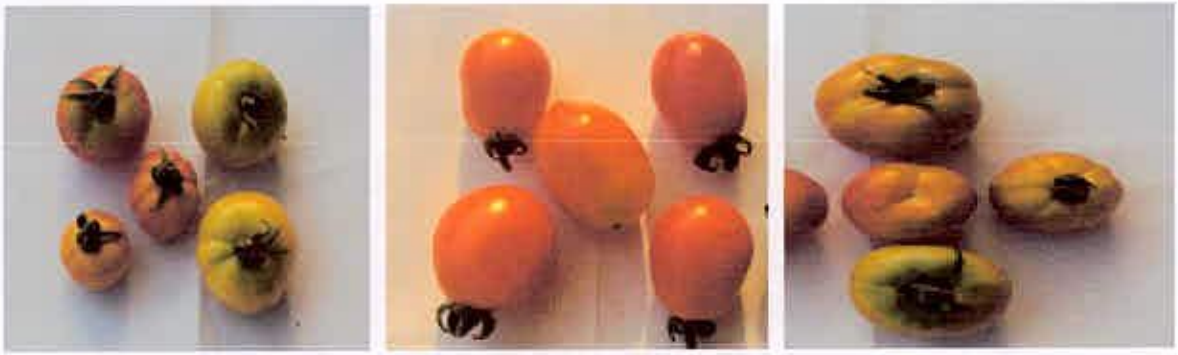
4.1.10 Fruit Length (cm)

The mean fruit length was 3.45 cm with a range of 1.75 cm to 5.16 cm. The accession 'BD-7295' showed the minimum fruit length and the maximum fruit length was recorded in the 'BARI Tomato-8'and 'BARI Tomato-15' (Appendix IV). The values of 39.63 and 36.89 are noticed for PCV and GCV, respectively (Table 3). There was a little difference between phenotypic and genotypic co-efficient of variation, indicating minor environmental influence on this character. Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Singh *et al.* (2002) showed that the phenotypic coefficient of variation was greatest for this character. The heritability estimate was 86.63 percent with high genetic advance over mean of 144.63 percent could be noted

(Table 3). High heritability and High genetic gain for this character was observed by Joshi *et al.* (2004). Phtographs are showing variation of fruit length and fruit diameter among different genotypes of tomato in plate 5a, 5b and 5c.

4.1.11 Fruit Diameter (cm)

The mean fruit diameter was 3.11 cm with a range of 1.16 cm to 4.75 cm. The line 'BARI Tomato-11' showed the minimum fruit diameter and the maximum fruit diameter was recorded in the accession 'BARI Tomato-8' (Appendix IV). The values of 37.22 and 20.33 are noticed for PCV and GCV, respectively (Table 3). There was a little difference between GCV and PCV, indicating minor environmental influence on this character. Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. Singh *et al.* (2002) also observed that the PCV was greatest for this character. The heritability estimate was 29.86 percent with moderate genetic advance over mean of 22.82 percent could be noted (Table 3). Moderate heritability and moderate genetic gain for this character were also observed by Joshi *et al.* (2004).



G1 G2 G3

G4 G5 G6

G7 G8 G9

Plate 5a. Showing phenotypic variation in fruits among different genotypes of tomato (G_1-G_9)

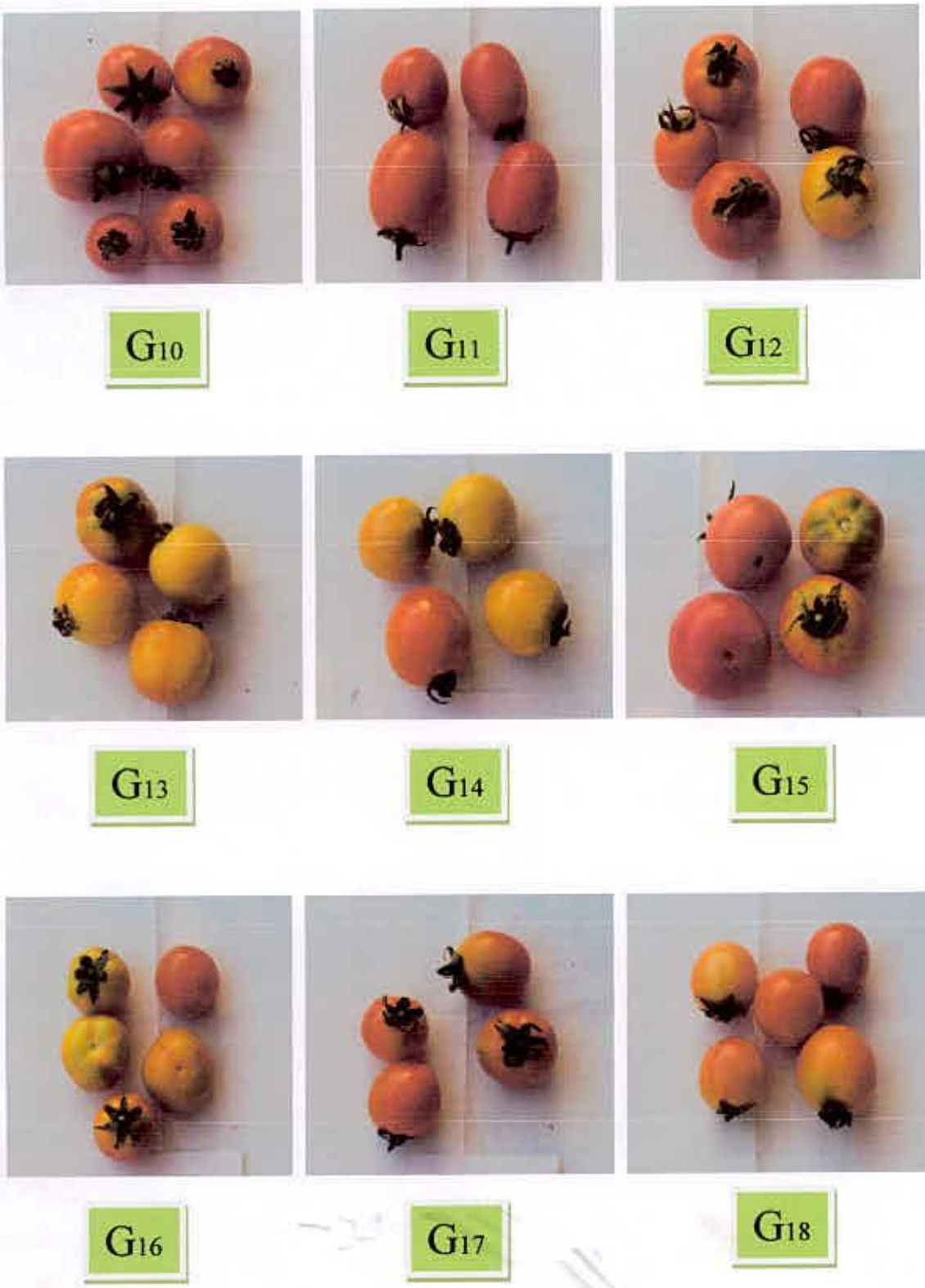


Plate 5b. Showing phenotypic variation in fruits among different genotypes of tomato (G_{10}-G_{18})

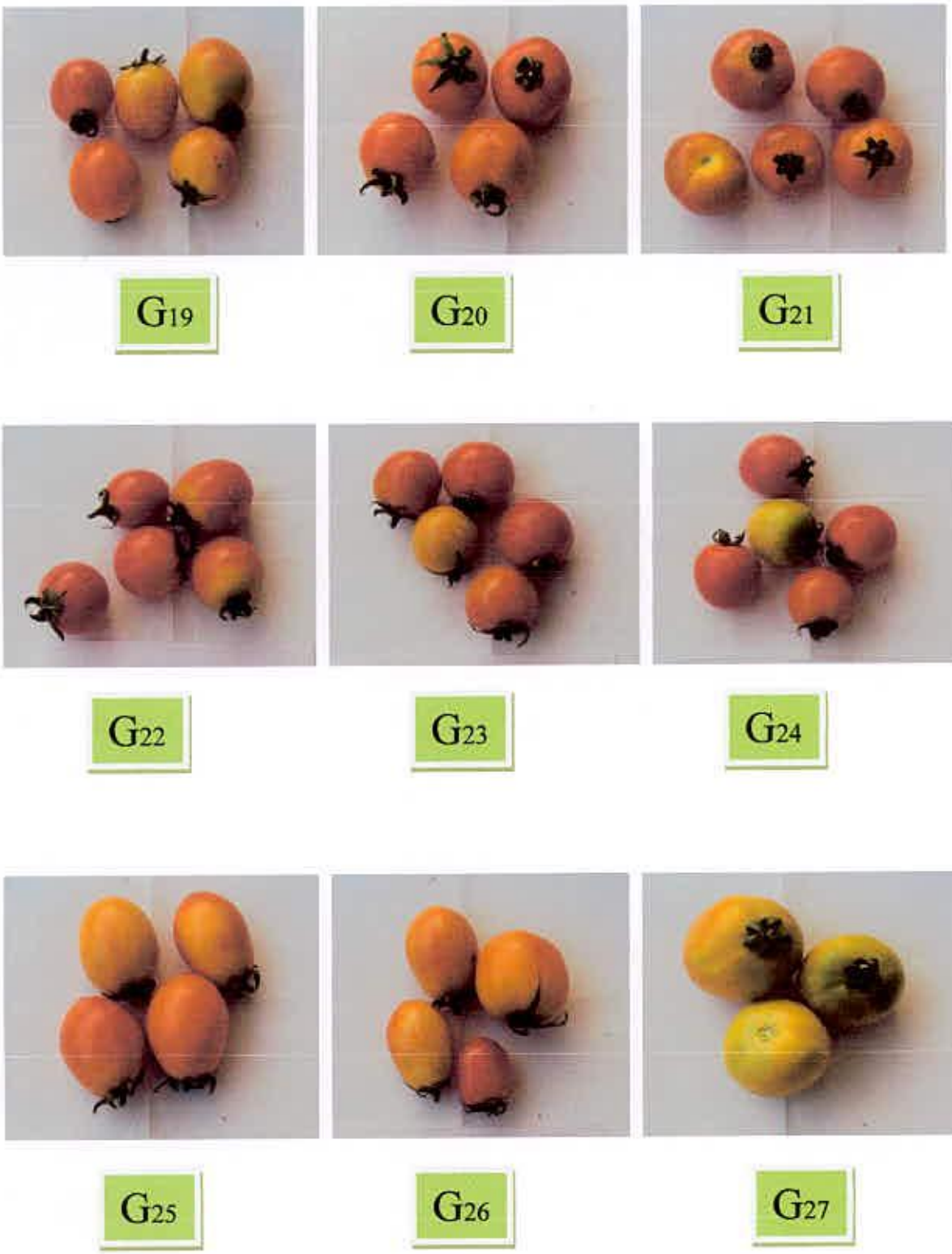
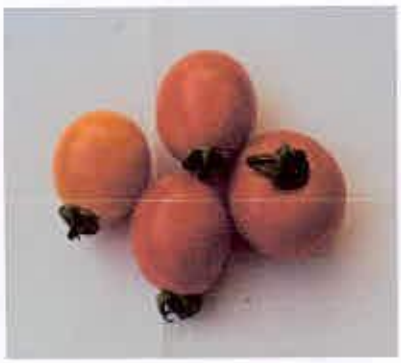
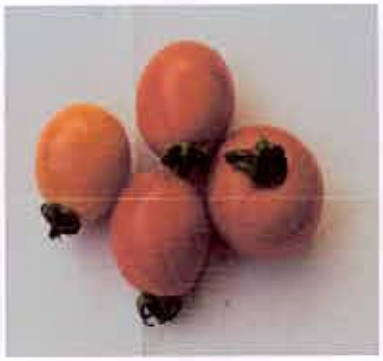


Plate 5c. Showing phenotypic variation in fruits among different genotypes of tomato (G_{19}-G_{27})



G28



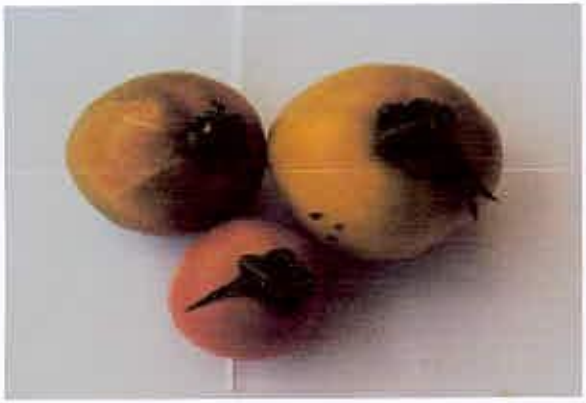
G29

G30

G31

G32

G33



G34

G35

Plate 5d. Showing phenotypic variation in fruits among different genotypes of tomato (G_{28}-G_{35})

4.1.12 Fruit yield per plant (Kg)

The mean fruit yield per plant was 1.35 kg with a range of 0.46 kg to 3.97 kg in the genotype 'BD-7302' and 'BARI Tomato-3' respectively (Appendix IV). High phenotypic coefficient of variability (59.28%) and genotype coefficient of variability (53.53%) were recorded for this character (Table 3). The high genotypic and phenotypic coefficient of variability were exhibited by fruit yield per plant, these findings are similar with earlier reports of Singh *et al.* (2002). High heritability (81.53%) and genetic advance as percent mean (62.50) were recorded for this character (Table 3). High heritability and high genetic advance was also observed by Ara *et al.* (2009) and Anupam *et al.* (2002). The heritability estimate was high and genetic advance as per cent of mean was also found to be moderate. Similar values was also reported by Mariane *et al.* (2003).

4.2 MULTIVARIATE ANALYSIS

4.2.1 Principal component analysis (PCA)

Principal component analysis was carried out with 35 genotypes of tomato. First three Eigen values for three principal coordination axes of genotypes accounted for 69.69% variation (Table 4). A two dimensional scattered diagram (Fig. 4 & Fig. 5) was developed on the basis of the principal component score, Z_1 and Z_2 score (Appendices VI).

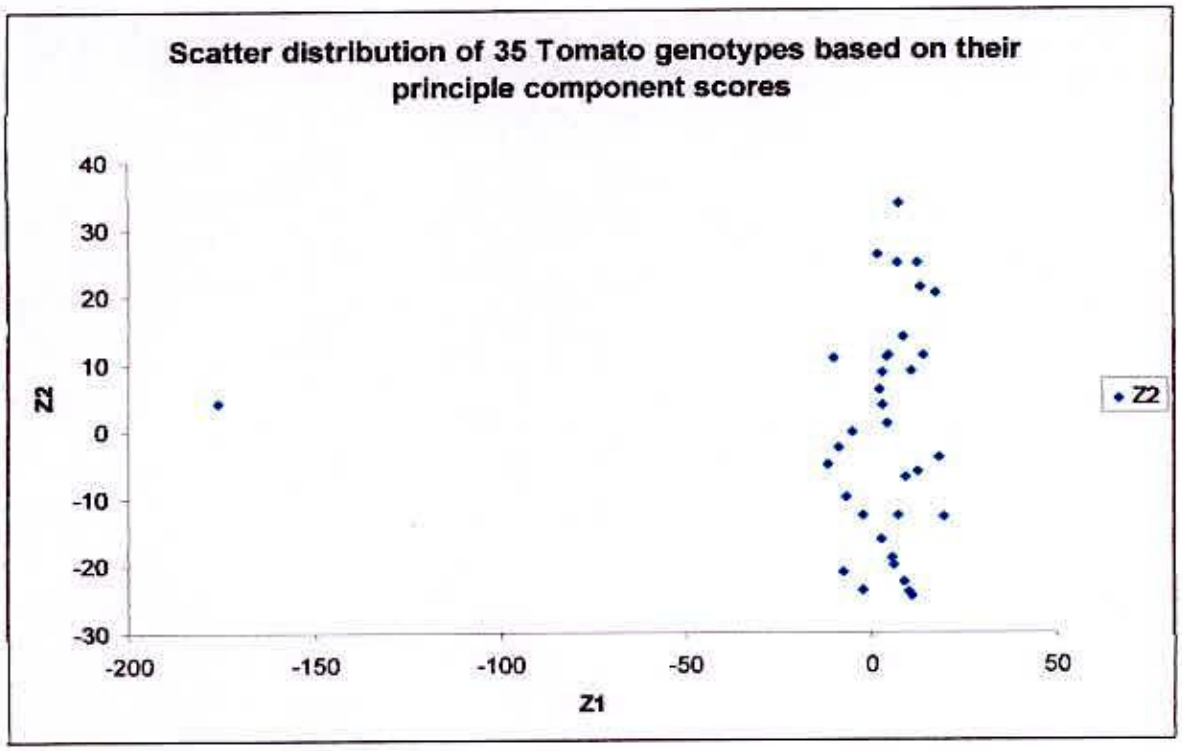


Figure 4. Scatter diagram of 35 tomato genotypes of based on their principal component scores.

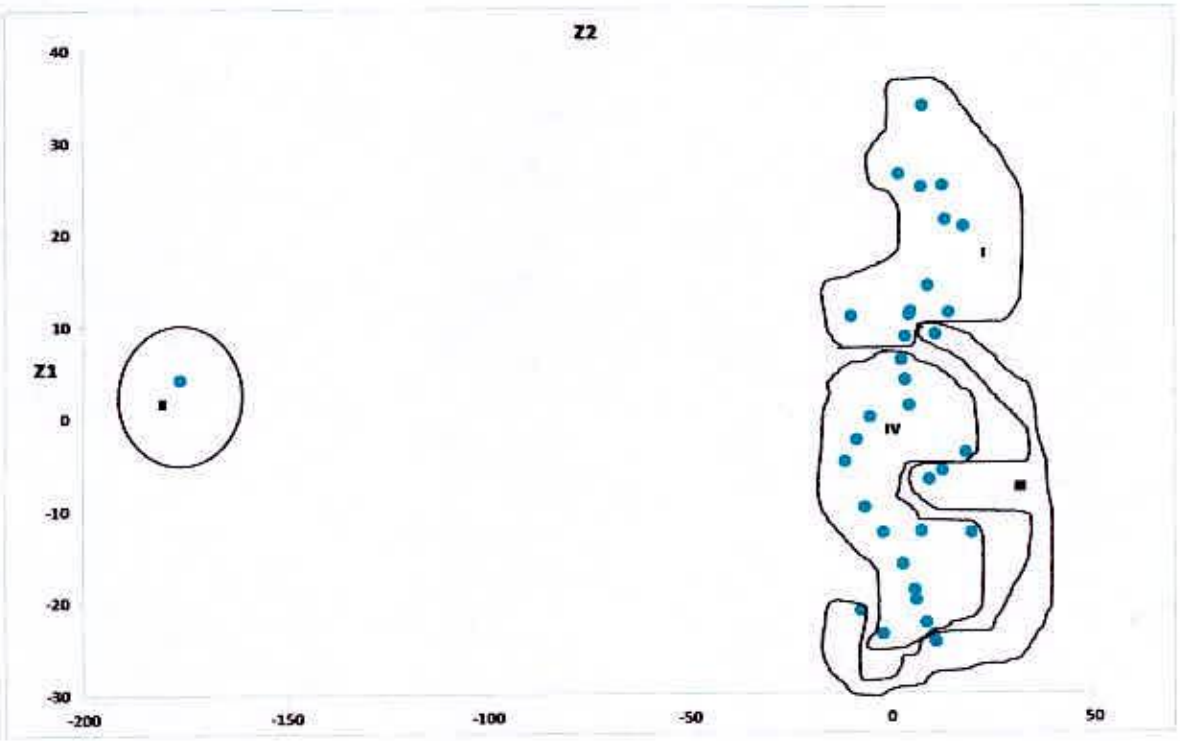


Figure 5: Scatter distribution of 35 Tomato genotypes based on their principle component scores superimposed with clustering.

Table 4. Eigen values and yield percent contribution of twelve characters of thirty five tomato germplasm

Characters	Eigen values	% contribution	Cumulative variation (%)
Days to first flowering	4.2474	35.4	35.4
Days to 50% flowering	2.3387	19.49	54.89
Days to maturity	1.774	14.78	69.69
Plant height (cm)	1.1147	9.29	78.96
No. of branches per plant	0.9771	8.14	87.1
No. of cluster per plant	0.7189	5.99	93.09
No. of fruits per cluster	0.468	3.9	96.99
No. of fruits per plant	0.2606	2.17	99.16
Fruit weight (g)	0.0811	0.68	99.84
Fruit length (cm)	0.051	0.46	99.87
Fruit diameter (cm)	0.0167	0.14	99.98
Fruit yield per plant (kg)	0.0026	0.02	100.00

4.2.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes G20 and G27 (3512.4) followed by G10 and G27 (3449.5) and the lowest distance was observed (9.2) between genotypes G14 and G18 followed by the distance (14.5) between genotypes G6 and G18 (Table 5). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 35 genotypes of tomato. The highest intra-cluster distance was recorded in cluster III (15.916) containing six genotypes viz. BARI Tomato-3, BARI Tomato -6, BARI Tomato -7, BARI Tomato -8, BARI Tomato-14, BARI Tomato-15 (Table 6).The lowest intra-cluster distance was observed in cluster II (00) having one genotypes viz. BARI Tomato-11. In cluster I the intra-cluster distance was (12.147) having twelve genotypes viz. BD-725, BD-7276, BD-7278, BD-7279, BD-7281, BD-7287, BD-7289, BD-7292, BD-7295, BD-7302, BD-7306, BD-7760 (Table 6). It favored to decide that intra-group diversity was the highest in cluster III and the lowest in cluster I. Cluster II having one genotypes viz. BARI Tomato-11and had no intra-cluster distance. Cluster IV having sixteen genotypes viz. BD-7258, BD-7259, BD-7260, BD-7269, BD-7270, BD-7285,BD-7286, BD-7290, BD-7291, BD-7301, BD-7759, BD-7761, BD-7762, BARI Tomato-2, BARI Tomato-4, BARI Tomato-9 and had an intra-cluster distance 13.88. (Table 6 and 8).

4.2.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among 35 genotypes of tomato and grouped them into four clusters (Table 6). The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. Table 6 represents the clusters

Table 5. Twelve highest and tweve lowest inter genotypic distance among the thirty five tomato genotypes

Sl No.	Genotypeic combination	Distances
	A. Twelve highest inter genotypic distance	
01	$G_{20} - G_{27}$	3512.4
02	$G_{10} - G_{27}$	3449.5
03	$G_{1} - G_{27}$	3431.5
04	$G_{9} - G_{27}$	3350.5
05	$G_{17} - G_{27}$	3193.6
06	$G_{3} - G_{27}$	3179.4
07	$G_{23} - G_{27}$	3164.4
08	$G_{19} - G_{27}$	3157.5
09	$G_{21} - G_{27}$	3074.5
10	$G_{13} - G_{27}$	3041.5
11	$G_{33} - G_{27}$	2841.2
12	$G_{29} - G_{1}$	2376.5
	B. Twelve lowest inter genotypic distance	
01	$G_{14} - G_{18}$	9.2
02	$G_{6} - G_{18}$	14.5
03	$G_{11} - G_{22}$	15.5
04	$G_{15} - G_{26}$	16.7
05	$G_{11} - G_{24}$	17.9
06	$G_{4} - G_{24}$	20.6
07	$G_{3} - G_{23}$	20.6
08	$G_{1} - G_{10}$	21.8
09	$G_{22} - G_{24}$	22.6
10	$G_{6} - G_{14}$	22.6
11	$G_{11} - G_{4}$	23.5
12	$G_{16} - G_{12}$	29.3

Table 6. Distribution of thirty five tomato genotypes in four clusters

Cluster no.	No. of Genotypes	Designation
I	12	BD-7257,BD-7276,BD-7278,BD-7279,BD-7281,BD-7287,BD-7289,BD-7292,BD-7295,BD-7302,BD-7306,BD-7760.
II	1	BARI Tomato-11.
III	6	BARI Tomato-3, BARI Tomato -6, BARI Tomato -7, BARI Tomato -8, BARI Tomato-14, BARI Tomato-15 .
IV	16	BD-7258,BD-7259,BD-7260,BD-7269,BD-7270,BD-7285,BD-7286,BD-7290,BD-7291,BD-7301,BD-7759,BD-7761,BD-7762,BARI Tomato-2, BARI Tomato-4, BARI Tomato-9.

occupied by 35 genotypes of tomato. It explains that cluster IV contained the highest number of sixteen genotypes, cluster I constitute by twelve genotypes, cluster II constitute by single genotype, and cluster III constitute by six genotypes. Cluster I was composed of BD-7257, BD-7276, BD-7278, BD-7279, BD-7281, BD-7287, BD-7289, BD-7292, BD-7295, BD-7302, BD-7306, BD-7760. All the genotypes of cluster I were collected from Plant Genetic Resource Centre, BARI, Gazipur.

Intra cluster mean for 12 traits are presented in Table 7. The highest cluster mean value was achieved for three characters viz. days to maturity (123.17), plant height (98.62) and number of branches per plant (9.17). Cluster II was formed by single genotype viz. BARI Tomato-11 was collected from Plant Genetic Resource Centre, BARI, Gazipur. The highest cluster mean value was achieved for three character viz. number of cluster per plant (13.00), number of fruits per cluster (17.00) and number of fruits per plant (224.00). Cluster III was formed by six genotypes viz. BARI Tomato-3, BARI Tomato-6, BARI Tomato-7, BARI Tomato-8, BARI Tomato-14, and BARI Tomato-15 were collected from Plant Genetic Resource Centre, BARI, Gazipur (Table 6). These clusters were able to lead in respect of the highest cluster mean value for maximum characters. Among 12 characters, the highest cluster mean value was achieved for six character viz. Days to first flowering (64.67), days to 50% flowering (87.67), fruit weight (57.00), fruit length (4.15), fruit diameter (3.69) and fruit yield per plant (2.70). Cluster IV was formed by sixten genotypes viz. BD-7258, BD-7259, BD-7260, BD-7269, BD-7270, BD-7285, BD-7286, BD-7290, BD-7291, BD-7301, BD-7759, BD-7761, BD-7762, BARI Tomato-2, BARI Tomato-4, BARI Tomato-9,which were collected from Plant Genetic Resource Centre, BARI, Gazipur (Table 6), were unable to lead in respect of the highest cluster mean value for maximum characters.

Table 7. Cluster mean of twelve different characters of thirty five tomato genotypes

Characters	I	II	III	IV
Days to first flowering	61.50	62.00	64.67	62.50
Days to 50% flowering	84.50	85.00	87.67	85.50
Days to maturity	123.17	123.00	122.50	122.31
Plant height (cm)	98.62	88.33	84.06	70.69
No. of branches per plant	9.17	7.00	6.33	7.75
No. of clusters per plant	12.67	13.00	10.00	12.62
No. of fruits per cluster	2.83	17.00	4.00	3.25
No. of fruits per plant	41.92	224.00	46.67	47.19
Fruit weight(gm)	21.03	5.00	57.00	26.31
Fruit length (cm)	3.04	2.16	4.15	3.58
Fruit diameter (cm)	2.88	1.17	3.69	3.19
Fruit yield per plant (kg)	0.86	1.14	2.70	1.22

4.2.4 Canonical variate analysis

The highest inter-cluster distance was observed (Table 8 or Figure 6) between cluster II and III (185.41). The lowest inter-cluster distance was observed between cluster I and IV (29.0) followed by cluster III and IV (33.8). Moderate or intermediate distance was found between cluster II and IV (179.51). On the other hand, the highest intra cluster distance was found in cluster III (15.916) followed by cluster IV (13.88). The lowest intra cluster distance was observed in cluster II (00). The inter cluster distances were found much higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups. Results of different multivariate analysis were superimposed in figure 5 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

As per scatter diagram the genotypes were apparently distributed into four clusters. It was also revealed that the genotypes of cluster II were more diverse from the genotypes of cluster III. Rai *et al.* (1998) also observed the similar result. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeding, the objective

Table 8. Average Intra (bold) and inter-cluster distances (D^2) of thirty five tomato Genotypes

Cluster	I	II	III	IV
I	**12.147**	183.65	39.632	29.00
II		**00**	185.41	179.51
III			**15.916**	33.8
IV				**13.88**

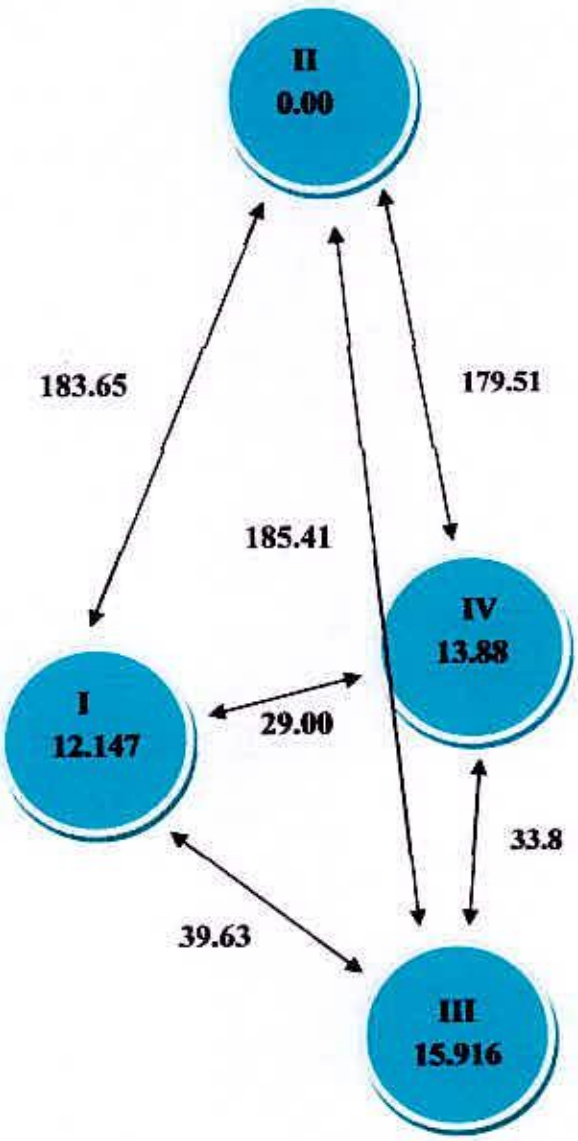


Figure 6. Diagram showing intra and inter -cluster distances (D^2) of thirty five genotypes in tomato

is not only high heterosis but also to achieved high-level production. In the present study the maximum distance existence between cluster III and III. But considering the yield and duration crossing involving cluster V and VI may be exhibit high heterosis for yield. Mohanty and Prusti (2001) reported that genetic diversity was not associated with geographic distribution. Shashikanth *et al.* (2010) also observed that there was no parallelism between genetic diversity and geographical divergence in tomato and suggested that high diversity among the genotypes can be selected in hybridization programmes to obtain good seggregants.

4.2.5 Contribution of characters towards divergence of the genotypes

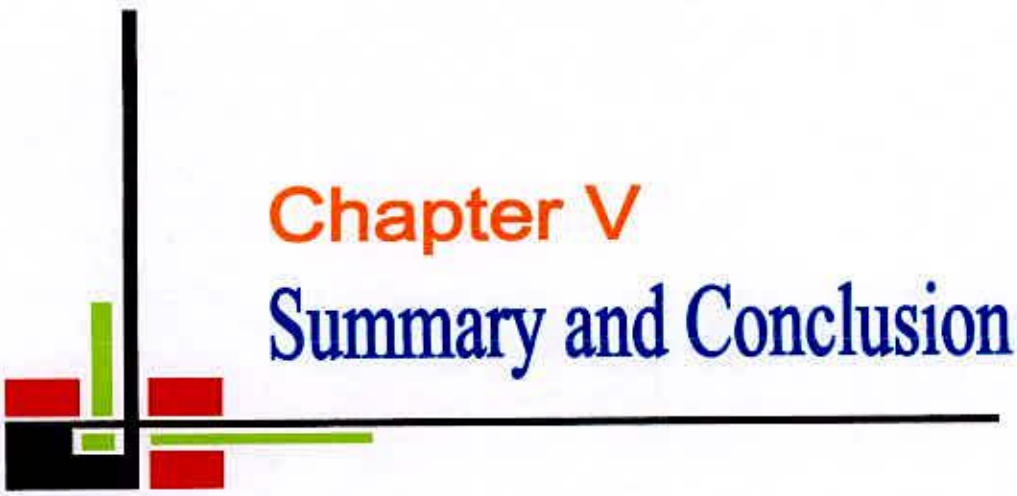
The values of Vector I and Vector II are presented in Table 9. Vector I obtained from PCA expressed that days to maturity (0.021), plant height (0.193), No of branches per plant (0.302), No of cluster per plant (0.323), No. of fruits per cluster (0.111), and no of fruits per plant (0.181) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to first flowering (0.197), days to 50% flowering (0.197), days to maturity (0.080), no. of fruits per cluster (0.591), No of fruits per plant (0.565), fruit weight (0.083) and fruit yield per plant (0.247) showed their important role toward genetic divergence. The value of Vector I and Vector II revealed that both Vectors had positive values for no. of fruits per cluster (0.591), no of fruits per plant indicating the highest contribution of these traits towards the divergence among 35 genotypes of tomato. Negative values in both vectors for fruit length and fruit diameter had lower contribution towards the divergence.

Table 9. Latent vectors for twelve principal component characters of thirty five tomato genotypes

Characters	Vector-1	Vector-2
Days to first flowering	-0.263	0.197
Days to 50% flowering	-0.263	0.197
Days to maturity	0.021	-0.080
Plant height (cm)	0.193	-0.026
No. of branches per plant	0.302	-0.288
No. of bunches per plant	0.323	-0.026
No. of fruits per bunch	0.110	0.591
No. of fruits per plant	0.181	0.565
Fruit weight(gm)	-0.432	0.083
Fruit length (cm)	-0.346	-0.198
Fruit diameter (cm)	-0.393	-0.232
Fruit yield per plant (g)	-0.347	0.247

4.2.6 Selection of genotypes as parent for hybridization programme.

Selectoion of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distance parents (Falconer, 1960; Moll *et al.*, 1962; Ramanujan and Tirumalachar 1974; and Ghaderi *et al.*, 1984). Cosidering the magnitude of cluster mean and agronomic performance the genotype G24 (BD-7761) for minimum days to first flowering from cluster IV; G33 (BARI Tomato-11) for maximum number of fruits per cluster and number of fruits per plant from cluster II; G29 (BARI Tomato-6) for maximum fruit weight from cluster III; G27 (BARI Tomato-3) for maximum fruit yield per plant from cluster III; G31 (BARI Tomato-8) for maximum fruit length and fruit diameter from cluster III were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G24 (BD-7761) and G33 (BARI Tomato-11); G24 (BD-7761) and G29 (BARI Tomato-6); G24 (BD-7761) and G27 (BARI Tomato-3); G24 (BD-7761) and G31 (BARI Tomato-8); G33 (BARI Tomato-11) and G29 (BARI Tomato-6); G33 (BARI Tomato-11) and G27 (BARI Tomato-3); G33 (BARI Tomato-11) and G31 (BARI Tomato-8);G29 (BARI Tomato-6) and G27 (BARI Tomato-3); G29 (BARI Tomato-6) and G31 (BARI Tomato-8); G27 (BARI Tomato-3) and G31 (BARI Tomato-8) may be suggested for future hybridization program.



Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted with a view to identify divergent parents for hybridization programme, identify the characters contributing to genetic diversity, asses the magnitude of genetic divergence in genotypes and determine the variability in respect of yield and some yield contributing characters, the degrees of association among the characters and their direct and indirect effects of thirty five genotypes of *Solanum lycopersicon* at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2010 to March 2011. Seeds are grown in seed bed and transplanted in the main field after 25 DAS in Randomized Complete Block Design (RCBD) with three (3) replications. Data on different characters were recorded and analyzed statistically. The analysis of variance of all the traits was computed and significant variations were found for different characters among the genotypes. The highest mean value was observed for days to maturity. This character exhibited the highest range of variation (120.0-133.0) indicated that all the genotypes showed wide range of variation in respect of this character. This character showed moderate heritability (29.15%) accompanied with low genetic advance in percentage of mean and the phenotypic variance (3.18) was higher than the genotypic variance (1.71). However, these differences were in case of days to first flowering and days to 50% flowering indicating greater influence on environment for the expression of these characters. Among these characters, days to 50% flowering, fruit weight, fruit length and fruit diameter showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of this characters. All these characters showed moderate to high phenotypic

and genotypic co-efficient of variation except days to first flowering, days to 50% flowering and days to maturity. Among the characters the highest genotypic co-efficient of variation was recorded no. of fruits per plant (61.57), fruit per cluster (57.14) followed by fruits yield per plant (53.53), fruit weight (49.81), fruit length (36.89), fruit diameter (20.33), plant height (17.77), number of clusters per plant (14.42), number of branches per plant (14.10). Heritability in broad sense was low to high for all the characters studied and it ranged from 20.64 % to 97.50 % which indicated that selection based on phenotypic expression of any character for breeding could be effective.The genetic advance was very low to moderate. These findings revealed that it was indicative of non-additive gene action. The high heritability was being exhibited due to favorable influence of environment rather than genotypes.

Multivariate analysis was carried out through principal component analysis (PCA), principal coordinate analysis (PCO), cluster analysis, and canonical vector analysis (CVA) using Genstat software programme. The first four principal characters with Eigen values were greater than unity contributed 78.96% variation toward divergence. As per as PCA, D^2 and cluster analysis using the genotypes were grouped into four different clusters. Cluster I, II, III and IV comprised twelve, one, six, and sixteen genotypes, respectively.

The maximum cluster distance was observed between cluster II and III (185.41) followed by the distance between clusters I and II (183.65), II and IV (179.51), I and III (39.632). The lowest inter-cluster distance was observed between cluster I and IV (29.00) followed by III and IV (33.8).

The highest intra-cluster distance was identified in cluster III (15.916) and the lowest intra-cluster distance was observed in cluster II (00). Genotypes included in cluster I were suitable for days to maturity (123.17 days), plant height (98.62) and number of branches per plant (9.17). Cluster II had the highest mean for number of clusters per plant (13.00), number of fruits per cluster (17.00) and number of fruits per plant (224.00). Cluster III had the highest cluster mean value was achieved for six character viz. days to first flowering (64.67), days to 50% flowering (87.67), fruit weight (57.00), fruit length (4.15), fruit diameter (3.69) and fruit yield per plant (2.70).

Findings of the present study indicated significant variation among the genotypes for all the character studied. Considering diversity pattern and other field performances, the genotype G24 (BD-7761) for minimum days to first flowering from cluster IV; G33 (BARI Tomato-11) for maximum number of fruits per cluster and number of fruits per plant from cluster II; G29 (BARI Tomato-6) for maximum fruit weight from cluster III; G27 (BARI Tomato-3) for maximum fruit yield per plant from cluster III; G31 (BARI Tomato-8) for the maximum fruit length and fruit diameter from cluster III could be the best choice as suitable parents for efficient hybridization programme. The inter genotypic crosses between G24 (BD-7761) and G33 (BARI Tomato-11); G24 (BD-7761) and G29 (BARI Tomato-6); G24 (BD-7761) and G27 (BARI Tomato-3); G24 (BD-7761) and G31 (BARI Tomato-8); G33 (BARI Tomato-11) and G29 (BARI Tomato-6); G33 (BARI Tomato-11) and G27 (BARI Tomato-3); G33 (BARI Tomato-11) and G31 (BARI Tomato-8);G29 (BARI Tomato-6) and G27 (BARI Tomato-3); G29 (BARI Tomato-6) and G31 (BARI Tomato-8); G27 (BARI Tomato-3) and G31 (BARI Tomato-8) might be suitable choice for future hybridization programme.

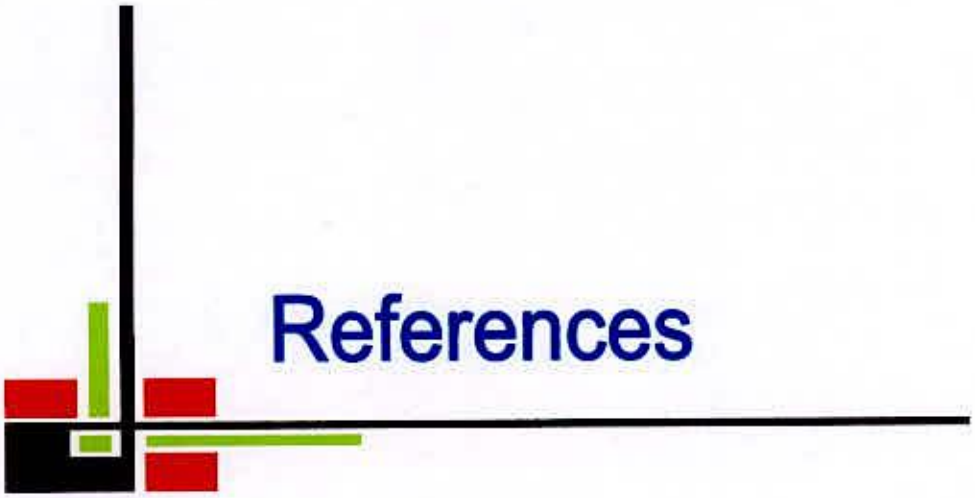
The result of the present study revealed that a wide variability exists among the collected tomato genotypes. In addition, there was also genotypic variability of different yield contributing characters with yield of tomato. From the findings of the present study, the following conclusions could be drawn:

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

ii. Selection procedure would be applied for desired characters such as the lowest days to first flowering and increase number of clusters per plant, number of fruits per cluster, number of fruits per plant, fruit weight, fruit length, fruit diameter to develop high yielding varieties.

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

iv. Further collection of tomato germplasms would be continued for getting more variability and desired traits in tomato.



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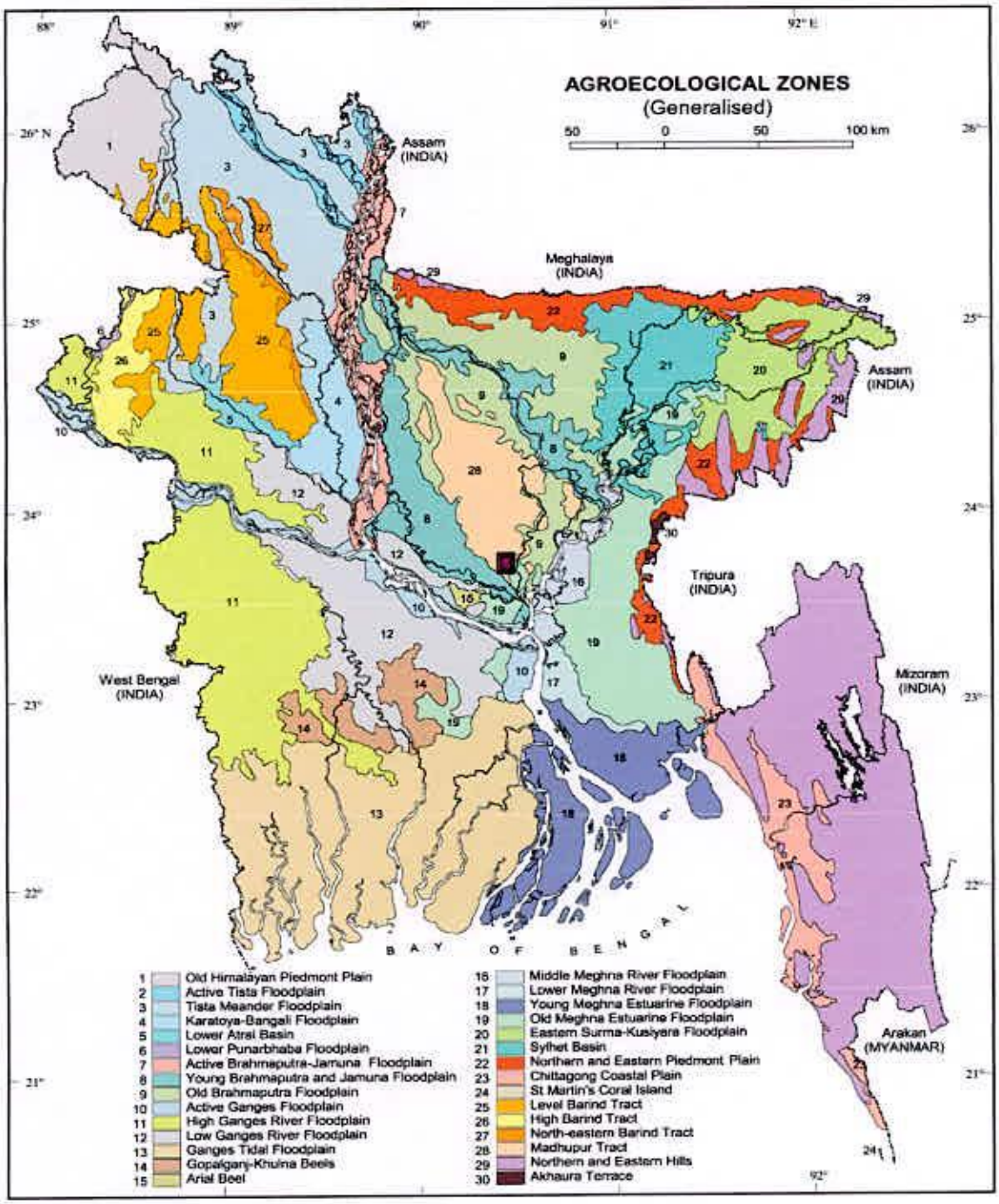
Appendices

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 to March, 2011

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
October, 2010	34.8	18.0	77	227	5.8
November, 2010	32.3	16.3	69	0	7.9
December, 2010	29.0	13.0	79	0	3.9
January, 2011	28.1	11.1	72	1	5.7
February, 2011	33.9	12.2	55	1	8.7
March, 2011	34.6	16.5	67	45	7.3

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

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

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

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

Appendix IV. Mean performance of twelve characters for thirty five varieties of tomato

VARIETY	DFF	D50%F	DM	PH	BPP	NCPP	FPC	FPP	FW	FL	FD	FYP
BD-7257	65.33	69.00	133.00	98.67	10.00	11.67	2.66	31.00	17.67	3.25	3.25	0.54
BD-7258	60.33	71.00	122.00	66.33	7.66	13.00	3.66	48.00	32.67	3.43	2.83	1.56
BD-7259	60.33	69.00	121.00	83.33	6.66	14.00	3.33	46.00	17.33	3.25	3.25	0.79
BD-7260	63.00	70.33	123.00	69.00	7.00	10.33	3.00	31.00	32.33	4.58	3.58	1.00
BD-7269	63.66	68.33	121.00	77.00	10.00	16.00	3.66	58.00	22.33	3.25	3.25	1.30
BD-7270	61.66	68.66	121.00	83.67	8.33	14.00	3.33	46.00	22.67	3.35	3.25	1.05
BD-7276	61.66	68.66	121.00	97.33	9.00	11.33	3.66	41.00	27.33	3.25	3.16	1.13
BD-7278	61.00	69.00	121.00	97.33	8.00	14.00	3.33	46.00	32.67	3.82	3.58	1.50
BD-7279	64.33	69.00	121.00	104.3	7.33	11.00	3.33	36.00	17.33	3.15	2.25	0.62
BD-7281	64.66	71.00	122.00	98.67	9.66	13.00	2.66	35.00	15.00	3.55	3.32	0.52
BD-7285	63.66	71.00	122.00	80.33	8.00	13.67	3.33	45.00	22.33	3.53	3.25	0.99
BD-7286	61.66	74.00	124.00	59.00	9.00	12.33	3.66	44.00	27.67	3.51	3.25	1.22
BD-7287	61.00	68.66	125.00	106.7	11.00	14.00	3.00	42.00	22.33	3.16	3.17	0.93
BD-7289	62.33	70.00	122.00	91.67	10.67	13.67	3.33	45.00	23.00	3.16	3.25	1.03
BD-7290	66.33	74.00	125.00	59.00	8.66	11.33	3.66	42.00	32.67	4.16	3.75	1.37
BD-7291	66.33	74.00	122.00	81.67	8.33	9.00	3.66	33.00	37.00	3.16	3.33	1.21
BD-7292	60.33	70.00	124.00	115.00	8.33	12.67	3.33	41.00	19.00	2.15	2.25	0.78
BD-7295	59.66	69.00	122.00	88.67	10.00	14.33	3.33	46.00	22.67	1.75	2.25	1.04

Here, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Number of branches per plant, NCPP = Number of clusters per plant, FPC = Number of fruits per cluster, FPP = Number of fruits per plant, FW = Fruit weight (g), FL = Fruit length (cm), FD = Fruit diameter (cm) and FYP = Fruit yield per plant (kg)

Appendix IV. Mean performance of twelve characters for thirty five varieties of tomato (Cont'd)

VARIETY	DFF	D50%F	DM	PH	BPP	NCPP	FPC	FPP	FW	FL	FD	FYP
BD-7301	58.33	69.66	122	55.33	7.00	13,00	3.33	43.00	19.00	3.66	3.16	0.82
BD-7302	57.66	70.00	122	90.67	9.00	10.67	3.33	35.00	22.33	3.58	3.25	0.46
BD-7306	58.33	70.00	123	106.7	10.33	13.33	3.66	47.00	19.00	2.55	2.16	0.90
BD-7759	64.33	74.00	120	77.33	9.00	16.33	3.33	54.00	18.33	3.15	2.33	0.98
BD-7760	62.33	74.00	122	87.67	9.00	16.00	3.66	58.00	14.00	3.15	2.66	0.81
BD-7761	57.66	68.00	123	65.00	7.00	11.67	3.66	42.00	23.67	3.75	3.16	0.99
BD-7762	59.66	69.33	124	78.00	8.00	13.33	4.66	62.00	29.00	3.85	3.25	1.79
BARI Tomato-2	63.00	71.66	121	68.00	7.66	11.67	4.33	50.00	27.33	3.66	3.33	1.36
BARI Tomato-3	62.33	69.00	123	78.00	7.66	13.67	4.66	63.00	62.67	3.88	3.25	3.97
BARI Tomato-4	63.66	73.00	122	69.00	8.33	14.33	4.00	56.00	23,00	2.78	2.25	1.28
BARI Tomato-6	65.66	74.00	124	93.33	5.66	10.00	4.66	46.00	63,00	3.36	3.16	2.92
BARI Tomato-7	69.33	73.00	121	91.33	6.66	10.33	4.33	42.00	57.33	3.16	3.16	2.43
BARI Tomato-8	67.00	74.00	121	68.67	6.66	9.333	4.66	43.00	54.33	5.16	4.75	2.34
BARI Tomato-9	66.33	71.00	123	59.00	7.66	12.67	4.33	53.00	33.67	4.16	3.83	1.81
BARI Tomato-11	62.33	73.00	123	88.33	7.00	13.00	17.33	224.00	5.00	2.16	1.16	1.14
BARI Tomato-14	65.00	70.00	124	102.7	8.00	9.00	4.66	42.00	47.67	4.16	3.66	1.98
BARI Tomato-15	59.00	69.33	122	70.33	6.00	9.667	4.66	44.00	57.00	5.16	4.16	2.51
Mean	62.55	70.79	122.63	83.05	8.23	12.49	4.09	50.32	29.15	3.45	3.11	1.35
CV (%)	2.13	2.14	0.80	11.74	13.57	10.55	16.37	14.21	3.28	4.36	8.54	12.31

Here, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Number of branches per plant, NCPP = Number of clusters per plant, FPC = Number of fruits per cluster, FPP = Number of fruits per plant, FW = Fruit weight (g), FL = Fruit length (cm), FD = Fruit diameter (cm) , FYP = Fruit yield per plant (kg) and CV (%) = Coefficient of variation in per cent

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

Source of variation	df	Mean sum of squares											
		DFF	D50%F	DM	PH	BPP	NCPP	FPC	FPP	FW	FL	FD	FYP
Replication	2	9.781	4.72	8.94	510.20	9.15	52.92	7.38	131.55	171.66	0.01	0.28	0.68
Genotype	34	24.86**	12.62**	14.27**	748.75**	5.28**	11.47**	16.93**	2931.67**	633.53**	1.23**	1.26**	1.62**
Error	68	1.78	2.30	0.96	95.02	1.25	1.73	0.45	51.10	0.91	0.02	0.07	0.02

Here, ** indicates significant at the 0.01 level, df =Degrees of freedom, DFF = Days to first flowering, D50%F = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), BPP = Number of branches per plant, NCPP = Number of cluster per plant, FPC = Number of fruits per cluster, FPP = Number of fruits per plant, FW = Fruit weight (g), FL = Fruit length (cm), FD = Fruit diameter (cm), FYP = Fruit yield per plant (kg).

Appendix VI. Principal component score thirty five genotypes of Tomato

SL. NO.	Z1	Z2
G1	17.65	20.54
G 2	2.77	-16.04
G3	2.53	6.14
G4	19.61	-12.68
G5	-8.55	-2.56
G6	3.35	3.92
G7	9.04	14.03
G8	4.83	11.27
G9	12.54	24.96
G10	13.26	21.28
G11	4.33	1.08
G12	6.04	-19.89
G13	7.3	24.86
G14	4.42	10.95
G15	8.82	-22.42
G16	18.39	-4.02
G17	7.8	33.65
G18	3.31	8.61
G19	5.67	-18.86
G20	14.18	11.16
G21	1.83	26.18
G22	-5.2	-0.15
G23	-9.78	10.82
G24	7.39	-12.53
G25	-11.6	-4.97
G26	-1.94	-12.64
G27	-7.66	-20.99
G28	-6.56	-9.87
G29	9.28	-6.91
G30	12.44	-5.94
G31	10.99	-24.49
G32	-1.98	-23.71
G33	-175.82	4.17
G34	11.04	8.9
G35	10.27	-23.82

Appendix VII . Mean performance of different parameters of thirty five genotypes in tomato

Parameters	Minimum	Mean	Maximum
Days to first flowering	58.00	62.55	69.00
Days to 50% flowering	68.33	70.79	74.00
Days to 80% maturity	120.00	122.63	133.00
Plant height	55.33	83.06	106.70
No. of branches per plant	5.00	8.24	11.00
No. of clusters per plant	9.00	12.50	16.33
No. of fruit per cluster	2.66	4.10	17.33
No. of fruits per plant	31.00	50.32	224.00
Fruit weight(gm)	5.00	29.15	62.67
Diameter of fruit(cm)	1.75	3.45	5.16
Length of fruit	1.16	3.11	4.75
Fruit yield per plant (gm)	0.46	1.36	3.97