INTERRELATIONSHIP AND GENETIC DIVERGENCE IN TOMATO (*Lycopersicon esculentum* Mill.)

THESIS SUBMITTED IN PARTIAL FULFILMENT OF
THE REQUIREMENTS FOR THE DEGREE OF

Master of Science (Agriculture)

In

Horticulture

Supervisor
Dr. Anand Kumar Singh

Submitted by
Abhilash Swaroop Mahapatra

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The Registrar (Academic)
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Dear Sir,

I feel great pleasure in forwarding the thesis entitled **"GENETIC DIVERGENCE STUDY IN TOMATO (*Solanum lycopersicum* L.)"** of **Sri *Abhilash Swaroop Mahapatra,* I.D No. H-0993**, submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **HORTICULTURE** from Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi.

I certify that the work has been carried out solely by **Sri Abhilash Swaroop Mahapatra** under my supervision and guidance and his findings and data presented herein are to the best of my knowledge and belief genuine and original and no part of the work has been submitted for any other degree or distinction.

Yours faithfully

(Dr. Anand Kumar Singh)
Supervisor

FORWARDED

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ACKNOWLEDGEMENT

*It is by the unfathomable grace and blessings of **Maa Bhubaneswari** that I have been able to bring out this humble piece of work.*

*I bow my head with great reverence in the pious feet of **Late Mahamana Pandit Madan Mohan Malviya Ji**, a man of great vision and founder of the Banaras Hindu University, Varanasi, India, whose everlasting euphoria and desired was to serve the mankind.*

*I feel a great pleasure in expressing my whole hearted sense of gratitude to the Chairman of Advisory committee **Dr. Anand Kumar Singh** Asso. Professor, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi for his Scholastic guidance, incisive and articulate criticism, cordial discussion, valuable suggestions, everlasting zeal, never stop attitude and constant encouragement which assisted me to overcome every problem that came in my way during the period of the investigation and preparation of the manuscript. I am very fortunate to have been blessed with the privilege of working under his guidance.*

*I feel immense gratefulness to express my heartfelt gratitude to the members of my advisory committee, **Prof. J. N. Singh, Head,** Department of Horticulture and, **Dr. J. K. Singh** Department of Agronomy, Institute of Agriculture Sciences, Banaras Hindu University, Varanasi for their benevolent guidance and valuable suggestions during the course of the investigation.*

*It gives me immense pleasure in extending my sincere feelings of gratitude to **Prof. B. K. Singh**, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, for his support and guidance which went a long way in shaping this humble piece of work.*

*I express my sincere thanks to **Prof. B.P. Singh, Prof. S.P. Singh, Prof. M.M, Syamal, Prof. A.K, Singh, Dr. A.K, Pal** and the staff members Shri Ram*

Nath, Shri Sukant Ghosh, Shri Shiv Dhani and Lalji for extending their help to me during the strenuous period of my research work.

I am greatly beholden and accolade my highest respects with deep sense of honour and to whom I am extending indebted my heart beats to my beloved grandmother (Late) Smt. ***Khirodri Mahapatra****. I am over whelmed with rejoice to avail this rare opportunity to evince my profound sense of veneration and gratitude to the ideal of my life ;my beloved father* ***Shri Chintamani Mahapatra****, mother* ***Smt. Puspanjali Mahapatra*** *and my lovely brother* ***Mr. Ashirwad Swaroop Mahapatra*** *for their consistent inspiration, unyielding love, support, and encouragement throughout my educational career.*

I feel great contentment to express my gratitude and affection to my friends ***Ramanand, Amit, Anil, Anshuman, Dilip, Jnyana, Pawan, Ramakant, Brijesh, Kuldeep, Raju, Gaurav, Tarun, Sanjaya, Devendra, Shyam, Shiva*** *and all my juniors for their vital support and sparing their valuable time to compile and complete my research document.*

I am getting short of words to express my regards to my seniors ***Vartika Mam, Prashant Sir, Madhur Sir, Anuj Sir, Vinod Sir, Sunil Sir and Durgesh Sir*** *for their co-operation and help.*

Last but not the least my heartfelt love to ***Punyatoya,*** *whose everlasting love, support, understanding and encouragement walked with me like my soul during my entire research work.*

Place*: Varanasi*
Date: *May, 2011*

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Contents

LIST OF TABLES

Glossary of Principal Symbols and Abbreviations

- % Per cent
- ^{0}C Degree Celsius
- ^{0}F Degree Fahrenheit
- / Per
- ≥ More than or equal
- < Less than
- P Phenotypic correlation
- G Genotypic correlation
- D^2 Genetic distance
- m meter
- Sq m Square meter
- cm centimeter
- kg Kilo gram
- g gram
- P M Post Meridian
- ml milliliter
- L liter
- mm millimeter
- q/ha quintal per hectare
- ANOVA Analysis of Variance
- C. D. Critical Difference
- cm^2 Square centimeter
- D. F. Degree of Freedom
- M. S. S. Mean Sum of Square
- ha hectare
- Fig. Figure
- No. Number
- RBD Randomized Block Design
- B. H. U. Banaras Hindu University.

Introduction

CHAPTER-I

INTRODUCTION

All nations have been anxious to improve the standard of living; those that are backward are moving fast and advanced are still trying to perfect their standards. But a high standard of living necessarily means improvement not only in having enough amount of nourishing food, but also to assure a balance diet to the people and to get maximum out of the soil in the minimum of time. Here comes the vegetables , which are not only the important source of balance dietary items like proteins, unsaturated fat, carbohydrate, minerals and vitamins but also gives maximum returns per unit area then the normal growing cereals in the minimum of time. Hence, we can expect a parallel increase in the demand for vegetables with our standard of living.

Vegetables have high value in terms of their comparatively high fiber content which stimulate peristaltic movement of the intestine and thus increases the efficiency of digestion. They are also known to help in neutralizing the acid substances produced in the process of digestion.

It is really fortunate that the excellent attributes of vegetables in term of their role in the metabolism of human system is being appreciated and the area is expanding day by day. In India, if we will take a look in the national scenario; the area (million ha.), production (million tonnes), and productivity (MT/ha) of vegetable crops has increased from **3.9, 23.45 and 6** in **1960-65** to **5.5, 58.53 and 10.5** in **1991** to **7.9, 129.08 and 16.2** in **2008-09** respectively (NHB, 2008-2009). As a result of concerted efforts made in the research and development of vegetable crops in the post- independent era, India has immerged as second largest producer of vegetables after China, contributing about 15% of the world vegetable production. India also ranks first in the production of peas and okra; second in egg fruit, cabbage,

cauliflower and onion; third in potato and tomato. The credit for this significant achievement goes to extensive research and development network.
No doubt, we are in the second position in area and production of vegetables but still we have not achieved the target to supply the recommended vegetable consumption which is 300g/capita/day to the common people. This signifies that, there are some areas of vegetable production which have to be explored for the better excess to the vegetables.

Vegetables yield more per unit area, give larger profit to the growers and improve the health of the nation. It is therefore high time that we pull all our resources and technical knowhow to boost the production of vegetables in our country. During recent years, the interest in vegetable production has increased rapidly as a result of greater appreciation of the food value of the vegetables and of the place of vegetables in the nation's food requirements. The finding of scientific study and their wide application in the field have enhanced this interest to a great extent among growers and consumers alike.

Among vegetables, Tomato is one of the most important warm season vegetable crops grown throughout the world under field and green house conditions. In India this crop has 3rd rank in terms of area and production and 5th rank in productivity. The **total area** and **production** of tomato in India comes to about **6 lakh hectares** and **111.1 lakh tones** respectively and the **national average yield** is **18.61 tones per hectare** (NHB, 2008-2009). In India the major tomato growing states are Bihar, Karnataka, Uttar Pradesh, Orissa, Andhra Pradesh, Maharashtra, Madhya Pradesh and Assam. This is a widely grown vegetable in the world ranking third in importance to potato and Sweet Potato in many countries.

Tomato belongs to the family Solanaceae and old name of this crop was *Lycopersicon esculentum* Mill., having two distinct species *L. esculentum* and *L. pimpinellifolium*. The immediate ancestor of cultivated tomato was probably

L. esculentum var. *cerasiformae* found throughout tropical and sub-tropical America **(Jenkins, 1948)**.

Scientific information indicates that the cultivated tomato has originated in a wild form in the Peru-Ecuador-Bolivia area of the Andes. The distribution of the alleles studied on genetic basis also gives evidence of origin of cultivated tomato in the Peru- Ecuador region **(Rick, 1969)**.

Usually tomato is an herbaceous, annual to perennial, prostrate and sexually propagated plant which typically reaches up to a height of 1-3 meters. The stem is soft, brittle, and hairy when young and hard, woody, and copiously branched when mature. Tomato has a strong tap root system but very often it is damaged at the time of transplanting **(Stoffela, 1983)**. The leaf is alternate, petiolate, 2”-15” in wide; the leaflets are unequal odd pinnate; the apex is narrowed or acuminate, acute, irregularly serrate and the number of leaflets varies from four to several where as the length of the leaf from 6” to 12” **(Colemon and Greyson, 1976)**. Tomato has an inflorescence of extra-auxiliary cymes with dichotomous or polycotomous branching and it may be terminal or may continue with vegetative shoot **(Muller, 1940)**. The flowers are bright yellow in colour, pentamerous, bisexual, regular, complete, ebracteate and hypogynous **(Cooper, 1927)**. The fruit is soft berry having glandular hairs and glands in young stage which degenerate in advanced stage. This character varies from cultivar to cultivar. Tomato seeds are oval, flattened, buff to pale brown and 3-5 mm in length.

Tomato is one of the most important protective foods as because of its richness of minerals and vitamins. There are various types of flavoring compounds found in the fruit which enrich their taste. The attractive red colour of the fruit is due to *lycopene,* and the yellow colour is due to *carotenes* which are great source of vitamin A **(Cole and Kapur, 1957)**. Tomato fruit mainly comprises of pericarp, radial wall, and locular tissues. The chemical composition is influenced by the variety, age and some external or internal

factors. Tomato is one of the most nutritive vegetable which is very rich in Vitamin A and Vitamin C, proteins, fats and carbohydrates, food energy calories as well as other essential minerals and food elements.

Tomato is also rich in medicinal value. The pulp and juice are digestible, a promoter of gastric secretion and blood purifier. It is considered to be intestinal antiseptic. It is said to be useful in mouth cancer. Dried tomato juice retains vitamin C. It stimulates torpid liver and is good in chronic dyspepsia. It is one of the richest vegetable which keeps stomach and intestine in good condition.

It is one of the popular salad vegetables in the raw state and is also popular as soup. Perhaps no other vegetable may take a lead upon the use of tomato as it is used in cannery, pickles, ketchup, sauces, juice, tomato pastes, and puree. It is served raw, backed, stewed, fried, and as a sauce with various other foods. Tomato juice has become an excellent delicacy as appetizer and beverage. The processed product regulates the market price of tomato and reaches the consumers in a variety of forms or as ingredients in a wide array of processed commodities.

Long ago tomato was included in the genus *Solanum* by some taxonomist while most of the taxonomists included this in *Lycopersicon*. **Linnaeus (1753)** has applied the name *Solanum peruvianum* L. as the first nomenclatorial history has indicated. Later **Miller (1754)** has recognized tomato as a separate genus from solanum and later in 1788 has named it *Lycopersicon esculentum* as the cultivated type and *Lycopersicon pimpinellifolium* as the wild form. The genus *Lycopersicon* was further divided in to two sub-genera:

1. **Eulycopersicon**: - Annual fruit edible and red coloured with carotinoid pigmentation. It includes two species, i.e.
   (a) *L. esculentum* Mill.-Cultivated tomato
   (b) *L. pimpinellifolium* (Juslen) Mill.-Resistant to wilt, leaf curl virus and low temperature.

2. **Ericopersicon**:- This sub-genera has nine species as follows

(a) *L. pissisi* Phil. - Perennial plants, green fruits, no bitterness.

(b) *L. peruvianum* L. Mill - Perennial plants, resistant to TMV, leaf curl virus.

(c) *L. hirsutum* Humb & Bonpl - Perennial in nature, bitter and green fruits. New name:-*Solanum habrochaites*.

(d) *L. glandulosum* C.H. Mull - Resistant to curly top disease.

(e) *L. cheesmanii* Riley - perennial plants, tolerant to salinity.

(f) *L. chilensis* Dun - Presence of gametophytic self-incompatibility.

(g) *L. pennellii* Corr- Drought tolerant, gametophytic self-incompatible.

(h) *L. parviflorum* - Fruits are small (1.0-1.4 cm diameter)

(i) *L. chmielewskii* - Plants similar to *L.parviflorum* with large flowers.

Mainly tomato plant is characterized by two types of growth habits **(Hartman and Woldhor, 1975)**

A. **Determinate type**:

a. Inflorescence almost at every internode.

b. Main axis terminates with a flower cluster.

B. **Indeterminate type**:

a. Inflorescence at every third internode.

b. Main axis continues growing indefinitely.

Tomato is a self pollinating crop. But a wide range of Natural Cross Pollination (NCP) also takes place which is largely influenced by the environmental factors. The degree of NCP has been extensively studied and it varied from 0 to 42 per cent **(Rick, 1947)**. The factors affecting the NCP are genetical factors, cross incompatibility and floral structure etc. This crop is highly influenced by environmental factors, particularly temperature, light, and Carbon dioxide. When the temperature goes beyond 30º C or goes below 14º C, the growth habit is adversely affected. Studies indicate that tomato is a day

neutral plant, however it is not completely day neutral in its reproductive responses to photoperiod **(Withrow and Withrow, 1949).**

What is the purpose of this research?

When we are talking about food and nutritional security everywhere, it is necessary to develop high yielding and better quality hybrid varieties of vegetables which will be able to provide us bags of vegetables from a small piece of land within a minimum period of time. The task can only be achieved by improvement in breeding programs of vegetables. Breeding programs are done for the improvement in the qualitative and quantitative traits of the prescribed crops and its success depends up on a high degree of availability of desired parents to the breeder.

A breeding program can only be called as a successful one, when it will be associated with diversity of parents with better chance of improving its economic characters. This genetic divergence existing in the population helps in selecting the suitable parents for hybridization program resulting in superior hybrids and desirable recombinants. From a large population selection of a number of desired germplasm is a task with a minimum probability of success. So divergence study is a valuable tool for obtaining divergence with respect to various traits between biological populations. It has been recognized that the use of diverse parents in a breeding program results in superior hybrids and desirable recombinants and the genetic divergence existing in the population helps in selecting suitable parents for hybridization program.

Before 1970 genetic diversity in crop plant was generally determined from pedigree data **(Lubberstedt *et al.*, 2000)** and morphological traits **(Yee *et al.*, 1999)**. Today, some of the genetic diversity study methods applied in crop includes Malecot's (1948) Coefficient of co-ancestory. This method however, is not commonly used because of several assumptions that are not fulfilled (**Messmer *et al.*, 1993)**. Information regarding the intraspecies genetic relationship is used to identify the heterotic difference with in them which

further helps the breeders for the better selection of parents for the breeding program.

Multivariate analysis is a powerful tool in quantifying degree of divergence of genotype level. Multivariate analysis based on Mahalanobis's D^2 statistics considered to be a good index of genetic diversity **(Rao, 1952).** As tomato is an important vegetable grown in India and more then thousands of varieties have been developed but still we don't have the **"expect to be the best variety"** with us, the present study was planned to generate information on genetic diversity present in 68 diverse genotypes of tomato with keen desire to help the breeders for the selection of best genetically diverse parents for bringing the desired improvement in the breeding result.

The genetic gain is the product of the heritability and selection differential expressed in terms of phenotypic standard deviation of that character. Heritability and genetic advance, both are the components of selection process so. It is necessary to utilize heritability estimates for estimating the diversity in the crop which will be able to bring the expected genetic gain in the future developed cultivars.

Keeping all the above points under consideration, the present investigation was carried out with the following objectives:

1. To estimate the genotypic and phenotypic coefficient of variability in the genotypes under evaluation.

2. To study the estimate of heritability and genetic advance for various important traits.

3. To find out the nature and magnitude of association between important traits through correlation and path coefficient analysis.

4. To estimate the genetic divergence using Mahalanobis's D^2 statistics.

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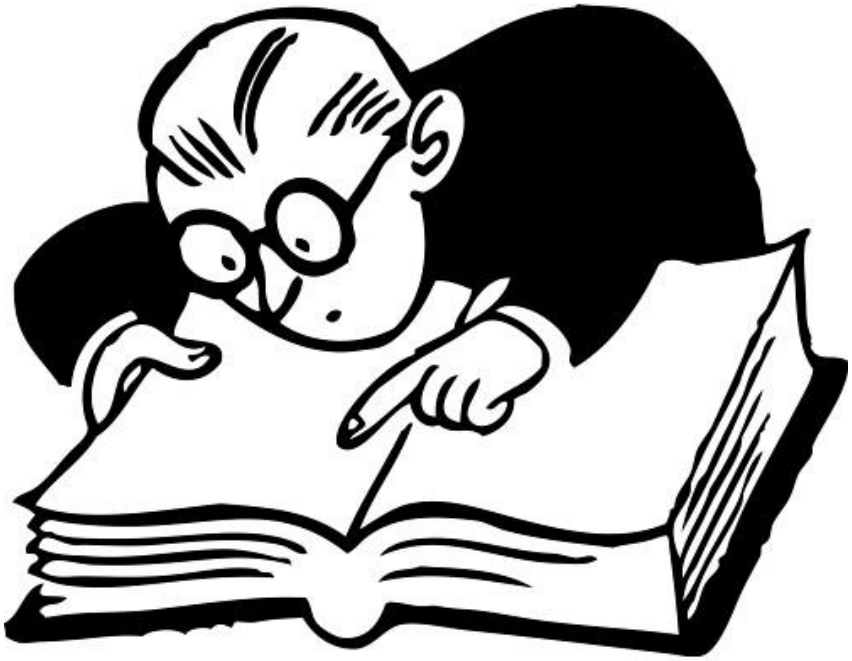

Review of Literature

CHAPTER-II

REVIEW OF LITERATURE

Differentiation of elite genotypes, based on reliable traits will not only help in preserving identity but also reflect genetic variation valuable in analyzing genetic diversity, monitoring and promoting efficient conservation of genetic resources and effective utilization of germplasm. The success of any breeding program depends on the quantum of genetic variability available for exploitation. The information on the type of variation in the available genetic material and the factors exclusively affecting those traits has significant importance for the possible improvement of a crop. Parameters like genetic variability, heritability and genetic gain have direct or indirect influence on the fate of the breeding program of a crop. To make selection of genotypes more efficient, knowledge of association of character is very much important. Several investigators have screened tomato genotypes from different resources, which exhibited immense range of variation in morphological and physiological traits that govern the performance. The literature related to the present investigation has been collected and is reviewed under the following headings.

2.1 Genetic variability

2.2 Heritability and Genetic Advance

2.3 Correlation coefficient

2.4 Path coefficient analysis

2.5 Genetic divergence

2.1 Genetic variability:

It is an important aspect of crop breeding program that there should be a wide range of genetic variability for yield and yield components in the base population. The success of phenotypic selection depends upon variability.

Sindhu and Singh (1989) reported high GCV (25.92%) and PCV (27.16%) for average fruit weight. **Lal *et al.* (1991)** reported significant differences in the plant height during summer season. Genotype Pant-4 produced the tallest one where as Kirti produced the shortest plant due to environment as well as genotype- environment interaction. **Singh *et al.* (1992)** evaluated twelve cultivars of tomato during summer season and the maximum plant height was observed in HS-101(87.2cm) which might be due to vigorous growth and better genetic makeup of the plant towards the environment. **Reddy and Reddy (1992)** studied 139 genotypes of tomato and reported that the maximum range of variation for fruit number per plant, yield per plant and average fruit weight, while lowest variation for days to 50% flowering.

Bhangu and Singh (1993) reported a wide range (24.66 to 66.69g) of variability for average fruit weight in 7 tomato varieties. **Jasmine and Ramdas (1993)** recorded the highest yield per plant (1.06) in hybrid ARTH-4 and lowest yield per plant (0.40) in FM-2. **Matiar *et al.* (1994)** reported maximum (2.67kg) and minimum (1.32kg) yield per plant in Manik and TMO 290 respectively among the 12 lines compared for yield potentiality.

Bharadwaj and Thakur (1994) reported that fruit yield of tomato depends upon factors like number of fruits per plant and size of fruits. Both these attributes were directly influenced by high temperature during summer which caused reduction in fruit yield of some genotypes. **Kumari and Subramanian (1994)** reported wide range of variability (1.94-5.68) for number of locules per fruit in 87 cultivar of tomato.

Nair and Thamburaj (1995a) estimated high variability at genotypic and phenotypic levels as indicated by highest estimates of GCV and PCV for

number of fruits per plant (40.79% and 41.93%), which is an important yield component.

Mittal *et al.* (1996) conducted the variability studies in tomato under sub-humid condition of Himachal Pradesh and showed highly significant difference among the cultivars, indicating substantial amount of genetic variability for marketable fruit yield per plant, average fruit weight, plant height and number of fruits per plant. These characters are under the control of additive genes which holds a good chance of improvement through selection.

Kumar and Tiwari (1999) conducted study on genetic variability in processing character of tomato and observed moderate GCV and PCV for number of locules per fruit on 67 genotypes of the crop.

Mohanty (2002) reported that high GCV for number of fruits per plant (27.87%) which could be improved by single selection. **Singh and Narayan (2004)** conducted experiment on 10 diverse genotypes of tomato in Kargil, J&K during the summer season and found a wide range of variability along with high estimates of GCV and PCV for plant height, fruit length, number of fruits per plant and number of branches per plant.

Mahesha *et al.* (2006) studied on 30 genotypes of tomato and revealed a wide range of variation for plant height, number of branches for plant, fruit length, fruit diameter, number of locules per fruit and fruit yield per plant. Likewise high GCV and PCV (47.23% and 52.74% respectively) were observed for number of fruits per plant by **Prasanth *et al.* (2006)**. **Kumar *et al.* (2006)** and **Golani *et al.* (2007)** reported high GCV and PCV (29.64%, 32.37% respectively) for number of locules per fruit.

Jagdish *et al.* (2007) studied the genotypic variation and hierarchical clustering of tomato and reported that highest variability was observed in plant height followed by average fruit weight and number of fruits per plant.

Marim *et al.* (2009) studied the variability and importance of characters by evaluating 70 genotypes of tomato along with the control varieties *viz.*,

Santa clara and Debora plus. In the first experiment (January to July 2002), 30 accessions were evaluated; in the second (August to December 2002) and the third (January to July 2003) experiments, 20 accessions were evaluated. The variability for 16 characters was verified by the Scott-Knott test, and the accessions were separated in ten groups according to Tocher's method. There is great genetic diversity between tomato accessions of BGH-UFV, with high variation in morphologic, agronomic and quality characteristics.

2.2 Heritability and Genetic Advance:

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. The success of any breeding programme is achieved by the efficient utilization of heritability and variability available in the population.

The ratio of genotypic variance to phenotypic variance is known as heritability which is generally expressed in percent. Thus heritability is the heritable portion of phenotypic variance. High Heritability with high genetic advance as percentage of mean was reported by many workers.

Singh *et al.* (1973) recorded a high heritability and genetic advance (39.53) for days to 50% flowering. Similar trend was also noticed by **Nair and Thamburaj (1995)** and **Mittal *et al.* (1996)**.

Singh and Singh (1993) reported high heritability with high genetic gain (43.70%) as a percentage of mean for number of primary branches per plant. **Supe and Kale (1991)** reported high heritability (62.46%) with low genetic gain as a percentage of mean (19.91%) for number of primary branches per plant in 12 indigenous varieties of tomato.

Kumari and Subramanian (1994) reported high heritability with low genetic gain for number of flowers per cluster. Further, **Mehta and Asati**

(2008) recorded high heritability (96%) coupled with high genetic advance (49.61%) for number of clusters per plant.

High heritability with low genetic gain for days to 50% flowering and moderate heritability (57%) with low genetic advance as percentage of mean (17.56%) in 64 genotypes of tomato for TSS was also reported by **Kurien and Peter (1995).**

High heritability (91.27%) and genetic advance was recorded for number of fruits per plant in tomato by **Nair and Thamburaj (1995a)**. On the other hand high heritability with genetic advance was reported for number of fruits per plant (**Das *et al.*, 1998**) which was earlier confirmed by many workers (**Singh *et al.*, 1990; Natrajan, 1990; Bora *et al.*, 1993 and Kurien and peter, 1995)**

Kumar and Tiwari (1999) recorded high value of genetic advance with high estimates of heritability for number of locules per fruit, high heritability coupled with moderately high genetic advance for fruit yield.

2.3 Correlation coefficient:

Simple correlation can be identified as three types *viz*. Phenotypic, Genotypic and Environmental. Phenotypic correlation is the observable correlation between two variables, measures the environmental deviation together with non additive gene action. Genotypic correlation in the other hand is the inherent association between two variables which can be estimated through estimated data only. It is important to study correlation analysis as because it measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for the improvement in yield. For the ease of evaluation, it is very much necessary for a plant breeder to have the knowledge of the association between characters. The magnitude and direction of association of characters is measured by correlation coefficients.

Singh *et al.* (1990) reported significant positive correlation between number of branches and fruit yield in two consecutive years in 19 genotypes of tomato. **Dundi and Madalagiri (1991)** reported that shelf life was positively correlated with pericarp thickness and fruit shape and negatively correlated with locules number per fruit. **Kadam *et al.* (1992)** reported that yield was positively correlated with total dry matter, number of fruits and size of fruit in variety Pusa Ruby.

Patil and Bojappa (1993) found that number of branches per plant showed significant and positive association with number of fruits per cluster. They also found the positive and significant correlation of days to 50 percent flowering with average fruit weight, number of seeds per fruit, and pericarp thickness. Fruit yield was strongly associated with plant height, number of branches per plant and number of leaves per plant and also has positive but moderate association with number of fruits per plant, average fruit weight, number of fruits per cluster, number of locules per fruit, number of seeds per fruit and pericarp thickness.

Soorinatha *et al.* (1994) in their study with 18 double cross hybrids of tomato found that number of flowers per cluster was the important yield contributing character in tomato. Yield in general was positively influenced by number of flowers per cluster. They also recorded positive correlation between fruit yield and number of fruits per plant.

Nair and Thamburaj (1995b) studied correlation between different plant characters of tomato and found that fruit yield had a positive and significant correlation with number of fruits per plant. **Maheshwary *et al.* (1997)** in a study with 40 F_1 hybrids reported that days to flowering were negatively associated with fruit yield. **Prasad and Rai (1999)** reported highly significant positive correlation coefficient between fruit yield and fruit weight, fruit length, and fruit breadth, number of locules and pulp thickness.

Kumar and Tiwari (1999) found that locule number was found to be negatively correlated with pericarp thickness and viscosity of fruit. **De *et al.* (2002)** observed a significantly positive correlation between yield and shelf life of tomato. **Mohanty and Prusty (2002)** observed that higher yield of hybrid tomato was to a greater extent due to higher number of fruits and branches per plant and to a lesser extent due to increased sized of the fruit.

Mohanty (2003) conducted a field experiment on 18 genotypes of tomato during rabi season and found that yield was significantly and positively correlated with number of fruits per plant and number of days to harvest, and significantly but negatively correlated with plant height, number of branches per plant and average fruit weight. The number of fruits per plant was inversely related to average fruit weight.

Singh *et al.* (2004) by conducting an experiment on 92 tomato genotypes revealed that number of fruits per plant and number of fruits per cluster showed highly significant positive correlation with yield. Similarly there was a negative correlation between the number of fruits per cluster and average fruit weight. Plant height was positively correlated with days to 50% flowering, days to first fruit set, number of fruits per plant and total soluble solids. The number of primary branches per plant was negatively and none significantly correlated with days taken to first fruit set, number of fruits per cluster, number of fruits per plant, average fruit weight, fruit length and fruit diameter. Days to 50% flowering showed a highly significant and negative correlation with number of fruits per cluster and fruit length. The number of fruits per cluster showed a highly significant and positive correlation with number of fruits per plant and fruit length.

Jagdish *et al.* (2007) reported that yield was positively correlated with number of fruits per plant, average fruit weight, fruit diameter and number of locules. Significant correlation was also observed between plant height and number of branches. On other hand **Golani *et al.* (2007)** reported that plant

height has significant and negative correlation with fruit weight, fruit girth, TSS and number of locules per fruit while conducting a study on 10 genotypes of tomato.

Sriharsa (2008) reported that the number of fruit per plant was positive and significantly correlated with yield of fruits. On the other hand **Meheta and Asati (2008)** reveled that fruit yield was positively associated with days to 50 percent flowering (0.683).

Anjum *et al.* (2009) experimented on 35 genotypes of tomato where the correlation study revealed that economically important traits like fruit yield per plant exhibit high positive significant correlation with fruit size, plant height, number of fruits per plant and number of primary branches per plant at both genotypic as well as phenotypic levels.

Rana *et al.* (2010) conducted experiment on 33 genotypes of tomato to study the correlation between characters and found that, number of primary branches, leaf area and number of fruits per plant were positively associated with fruit yield per plant.

2.4 Path Coefficient Analysis:

Knowledge of Interrelation ship between yield and its component is obvious for efficient selection of desirable plant type. Unlike the correlation coefficient values, which measure the extent of relationship, path coefficient **(Wright, 1921; Dewey and Lu, 1959)** measure the magnitude of direct and indirect effects of characters on complex dependent characters like yield and thus enable the breeder to judge best about the important characters during selection. In other words it measures direct and indirect contribution of various independent characters on a dependent character.

Srivastav and Sachan (1973) reported that fruit weight had negative direct effect on yield where as number of fruits per plant had the maximum positive effect on yield followed by fruit diameter. **Singh and Mittal (1976)**

reported that number of branches and fruit weight had a high positive effect on yield.

Prasad and Rai (1999) concluded from the path analysis that the attributes like plant height, fruit length, fruit breadth, fruit firmness and number of locules were the major yield components.

Kumar *et al.* (2003) studied 30 diverse tomato genotypes through path coefficient analysis and reported that the fruit number per plant had the highest positive direct effect on yield per plant followed by average fruit weight.

Mohanty (2003) evaluated 18 genotypes of tomato through path analysis and found that the number of fruits per plant and average fruit weight registered positive direct effect on yield and negative direct effect through each other on yield.

Joshi *et al.* (2004) by taking 37 genotypes of tomato revealed that the number of fruits per plant is the most important yield contributing character followed by fruit length, fruit width and plant height.

Singh *et al.* (2004) analyzed the path coefficient by taking 92 genotypes of tomato and found that the number of fruits per plant has positive direct effect on yield followed by fruit diameter, average weight per fruit, fruit length, days to 50 percent flowering, number of fruits per cluster and days to first harvest of fruit. However days to first fruit set, number of primary branches per plant, plant height, number of fruit cluster per plant and total soluble solids had negative direct effects on yield. **Manivanan *et al.* (2004)** carried out path analysis in cherry tomato and reported that fruit weight had the highest direct effect on fruit yield.

Golani *et al.* (2007) reported that plant height manifested significant and negative relationship with fruit yield and its direct effect was negative but its indirect effect via fruit girth was high and positive. **Prashanth *et al.* (2007)** conducted experiment on 67 genotypes and reported that early yield and average fruit weight had high direct positive effects on total yield.

Mehta and Asati (2008) reported that plant height had the highest positive direct effect on fruit yield at genotypic level which was followed by weight of fruit per plant, days to first fruiting, days to 50 percent fruiting where as number of branches per plant had highest negative direct effect on fruit yield which was followed by total soluble solids, yield per plot, days to 50 percent flowering, number of fruits per plant, number of fruits per cluster, average fruit weight, days to first flowering, number of cluster per plant and number of locules per fruit.

2.5 Genetic divergence:

The multivariate analysis using Mahalanobis D^2 statistics is a valuable tool to quantify the degree of divergence at genetic level. While formulating the tomato crop improvement program, understanding about the nature and degree of genetic divergence available in the germplasm plays a pivotal role. It is well recognized that the use of diverse parents results in superior hybrids and desirable recombinants. Thus genetic divergence existing in the population helps in selecting suitable parents for hybridization program.

Genetic divergence was assessed by **Rai *et al.* (1998)** in 37 genotypes of tomato which were grouped into four clusters. The clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The number of primary branches contributed maximum (25.60%) to the total divergence in yield with in average ranging from 3.65 for cluster IV to 5.50 of cluster I. It was observed that major divergence contribution traits in tomato were number of primary branches, longitudinal fruit length, days to flowering, pericarp thickness, plant height and average fruit weight.

Sharma and Verma (2001) studied 18 genotypes of tomato, which were grouped in to five clusters irrespective of geographic divergence,

indicating that there was no parallelism between genetic divergence and geographical divergence.

Dharmatti *et al.* (2001) conducted experiment to study the diversity in 402 genotypes of tomato where Observations were recorded for plant height, number of branches, number of clusters per plant, fruits per cluster, number of fruits per plant, yield per plant, incidence of tomato leaf curl virus (TLCV), and number of whiteflies per plant. The 402 lines were grouped into 4 clusters based on the similarities of D^2 values. Cluster II was the most divergent consisting of 51 genotypes/hybrids with potato leaf types and pink fruits, which exhibited field tolerance to TLCV. Cluster I was the biggest, having 217 genotypes/hybrids, which also consisted of commercial TLCV susceptible genotypes, namely Rupali, DWD-1, DWD-2, Cross B, Marikrit, L-15, UC-204B and LE-79. Cluster III and IV had 99 and 35 genotypes, respectively. Considerable diversity within and between the clusters was noted, and it was observed that the characters TLCV resistance, fruit yield per plant and number of whiteflies per plant contributed maximum to the divergence. Therefore, selection of divergent parents based on these characters may be useful for heterosis breeding in summer tomato.

Parthasarathy and Aswath (2002) reported considerable diversity among tomato genotypes for different morphological characters (plant height, fruit number and fruit size). It was further reported that *L. pimpinellifollium* is the most divergent genotype.

Joshi *et al.* (2003) studied on 73 tomato genotypes and found maximum value of coefficient of variability (53.20%) was recorded for shelf-life of fruits while it was minimum (9.20%) for days to first picking. The grouping of the genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes. The clustering pattern of tomato genotypes indicated non-parallelism between geographic and genetic diversity. Genotypes belonging to cluster 5 and 6 were highly diverse from each other. The mean

fruit yield per plant (1034.64 g/plant) and average fruit weight (102.76 g) were highest in Cluster 5 and 3, respectively. The plant height (135.91 cm) and harvest duration (37.77 days) were highest in Cluster 15. **Karasawa *et al.* (2005)** evaluated the genetic divergence among 70 tomato accessions and observed significant genetic variation among the accessions for many fruit characters.

Mahesh *et al.* (2006) studied 30 genetically diverse group of tomato and grouped them in to nine clusters irrespective of geographic divergence, indicating no parallelism between genetic diversity and geographical divergence. There were maximum numbers of genotypes in cluster II. The maximum genetic distance was observed between clusters VI and IX (8132.17), whereas it was minimum between clusters I and IV (405.05).

Sharma *et al.* (2006) conducted non-hierarchical analysis on 60 genotypes of tomato (*Lycopersicon esculentum* Mill.). The genotypes were grouped into 10 clusters. Maximum divergence within a cluster was exhibited by the cluster VIII (1.531), closely followed by cluster III (1.528) and cluster V (1.460), whereas, cluster VIII and cluster II were the most divergent from each other followed by cluster VII and cluster VIII. Promising genotypes selected were FT-5, LBR-10-2, THS-1-1, THS-2-2, T-99-1-2 and T-99-2-3 for yield per plant, fruit size index, pericarp thickness and plant height, whereas, W 55, Campbell and EC-123018 were found to be the best for average fruit weight. However, genotypes EC-170785 and Red Cherry may be used to improve the number of fruits per plant and earliness.

Prashanth *et al.* (2007) evaluated the genetic divergence among 67 genotypes of tomato to determine the value and magnitude of genetic divergence using Mahalanobis D^2 statistics. He groped all the genotypes in to seven clusters. The maximum inter cluster distance was observed between cluster V and VI closely followed by cluster III and V, cluster IV and V,

cluster IV and VII, cluster VI and VII and cluster V and VII. Cluster II showed the least distance relationship with cluster III.

Sekhar *et al.* (2008) assessed genetic divergence in tomato hybrids and opined that the average fruit weight and total soluble solids contributed towards genetic divergence followed by number of flowers per cluster, plant height and number of locules per fruit.

Mehta and Asati (2008) conducted genetic divergence study of tomato by taking 22 determinate genotypes and groped them in to six clusters. The cluster I was the largest containing seven genotypes followed by cluster III with six genotypes. In the experiment the higher order of divergence was recorded between cluster II and V.

Singh *et al.* (2008) studied 48 genotypes of tomato for their genetic divergence and based on D^2 values of eight yield related characters genotypes were grouped in to eight clusters. Clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The characters like number of fruits per plant, average fruit weight, plant height and fruit yield contributed maximum to genetic divergence.

Genetic divergence was studied by **Jogi *et al.* (2008)** using 28 tomato genotypes, which were grouped into five clusters irrespective of geographical diversity indicating no parallelism between geographic and genetic diversity. Cluster V. topped having maximum eight genotypes, while cluster II having minimum number of genotypes. The maximum inter-cluster distance was noticed between cluster II and V.

Rana *et al.* (2010) carried out experiment with 33 genotypes of tomato in a randomized block design with three replications. All thirty three genotypes were grouped into eight clusters. cluster I was the largest with 22 genotypes followed by clusters II & III with three genotypes in each whereas clusters IV to VIII had single genotype in each. Highest value of genetic distance was observed between cluster IV with single genotype ARTH-210 and cluster VIII

with NTH-242 (5.63). Cluster III had highest values for number of primary branches, leaf area, number of fruits per plant, number of seeds per fruit and fruit yield per plant.

Shashikanth *et al.* (2010) conducted experiment by taking 30 genotypes of tomato to determine inter and intra cluster distances and parental tomato groups likely to yield superior segregates in hybridization. Observations were recorded for days to first flowering, days to 50% flowering, plant height, number of branches per plant, number of flowers per cluster, days to first fruit set, number of fruit clusters per plant, number of fruits per cluster, number of fruits per plant, fruit shape index, number of locules per fruit, pericarp thickness, total soluble solids, fruit weight, fruit yield per plant and fruit yield per plot. Mahalanobis generalized distance was used to determine to degree of divergence. Analysis of variance of the genotypes showed significant differences for all the characters studied indicating the existence of genotypic variation. Mahalanobis's D^2 statistics helped in grouping the 30 genotypes into 10 diverse clusters. The composition of clusters of heterogeneous geographic origin indicated that the strains were distributed among the different clusters randomly irrespective of their geographical origin. This indicated that there was no parallelism between genetic diversity and geographical divergence in tomato. A high diversity among the genotypes suggested that those belonging to cluster VII (genotype NDTTNR-76) and X (genotype ATL-02-39) can be selected in hybridization programs to obtain good seggregants.

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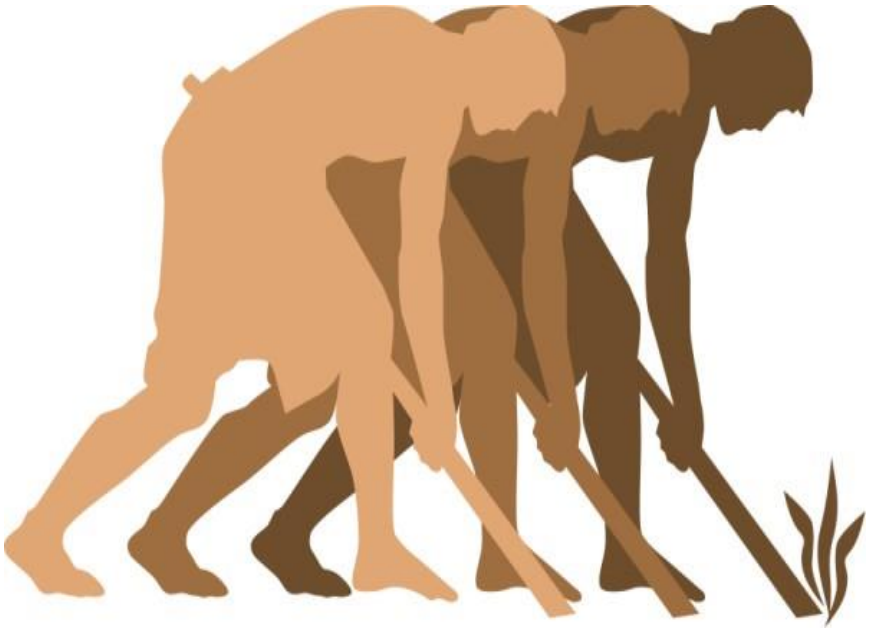

Materials & Methods

CHAPTER-III

MATERIALS AND METHODS

The present investigation entitled "Interrelationship and Genetic divergence in tomato (*Lycopersicon esculentum* Mill.)" was carried out at the Vegetable Research Farm, Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (UP) during the year 2009-2010. The details of the materials used and the methods adopted in the experimentation are given below:

3.1 CLIMATE:

Geographically Varanasi is situated 25.282^0 North latitude and 82.9563^0 East latitude. It has an elevation of about 120.23 meters above mean sea level. Varanasi experiences a humid subtropical climate with large variation between summer and winter temperatures. Summers are long, from early April to October, with intervening monsoon seasons and are also extremely hot, even by South Asian standards. The temperature ranges from 32°C – 46°C (90°F – 115°F) in the summers. Winters in Varanasi sees very large diurnal variations, with warm days and downright cold nights. Cold waves from the Himalayan region cause temperatures to dip across the city in the winter from December to February and temperatures below 5°C are not uncommon. The average annual rainfall is 1110 mm. Fog is common in the winters, while hot dry winds, called Loo, blows in the summers.

3.2 EXPERIMENTAL SITE:

A homogeneous piece of land was selected from the composite block of the experimental farm, keeping the view of irrigation facilities and gradient of the soil. Composite soil samples from the experimental plot were taken to assess the initial physical and chemical status of the soil. The results of the analysis are presented in the following tables.

Table-3.1 Mechanical Analysis (Physical status of the soil)

SL. No.	PARAMETERS	VALUES (%)
1	Coarse Sand	5.36
2	Fine Sand	42.75
3	Silt	28.73
4	Clay	17.42

Table-3.2 Chemical Analysis

SL. No	PARAMETERS	VALUES (%)
1	Available Nitrogen	0.084
2	Available Phosphorus	0.120
3	Available Potash	0.645

3.3 EXPERIMENTAL MATERIAL:

Seeds of 68 genotypes of tomato (*Lycopersicon esculentum* Mill.) were grown under field conditions which were obtained from the Department of Horticulture, Institute of Agricultural Sciences, B.H.U., Varanasi. The cultivars have been demarcated by particular symbols as bellow:

S.No	Genotype	Symbol
1	Sel-7-2	L_1
2	Sikkim Local	L_2
3	RCMT-2-2	L_3
4	CTS-05-05	L_4
5	LCT-9-4	L_5
6	Amrita	L_6
7	Punjab Upma	L_7
8	Swarna Samridhi	L_8
9	Floradade	L_9
10	CO-3-1	L_{10}
11	FLA-7171	L_{11}
12	KS-229	L_{12}
13	NDTVR-60	L_{13}
14	Potato leaf	L_{14}
15	NDT-5	L_{15}
16	LCT-10-3	L_{16}
17	VR-20	L_{17}

S.No	Genotype	Symbol
18	AZAD-T-5	L_{18}
19	Angoorlata	L_{19}
20	NUN-4	L_{20}
21	IC-177371	L_{21}
22	RCMT-1-3	L_{22}
23	VTG-88	L_{23}
24	NUN-2	L_{24}
25	PANT-T-7	L_{25}
26	LCT-6	L_{26}
27	Avinav	L_{27}
28	DVRT-2	L_{28}
29	LCT-10	L_{29}
30	LCT-7	L_{30}
31	DT-10	L_{31}
32	Navodaya	L_{32}
33	NUN-3	L_{33}
34	TLC-1	L_{34}

S.No	Genotype	Symbol
35	TO-1389	L_{35}
36	DVRT-1-3	L_{36}
37	HS-102	L_{37}
38	LCT-10-5	L_{38}
39	RCMT-1	L_{39}
40	CTS-05-25	L_{40}
41	S-12	L_{41}
42	PANT T-1-5	L_{42}
43	BT-12	L_{43}
44	CO-3	L_{44}
45	Pusa Gaurav	L_{45}
46	NUN-1	L_{46}
47	DT-2-1	L_{47}
48	Shalimar-1	L_{48}
49	Kashi Amrit	L_{49}
50	LCT-9-3	L_{50}
51	RCMT-2-4	L_{51}

S.No	Genotype	Symbol
52	Sel-7	L_{52}
53	CTS-05-05-2	L_{53}
54	LCT-1	L_{54}
55	NUN-5	L_{55}
56	VRT-2	L_{56}
57	Punjab Keshri	L_{57}
58	RCMT-1-2	L_{58}
59	H-24	L_{59}
60	LCT-9	L_{60}
61	KS-229-1	L_{61}
62	ATL-02-39	L_{62}
63	PANT-T-3	L_{63}
64	LCT-9-1	L_{64}
65	RCMT-2-1	L_{65}
66	RCMT-2	L_{66}
67	CTS-05-25-1	L_{67}
68	NDT-108	L_{68}

3.4 LAYOUT PLAN:

The details of layout plan for this study are mentioned below:

1	**Design**	Randomized Block Design
2	**Number of Replications**	3
3	**Number of genotypes**	68
4	**Number of plots**	204
5	**Size of plot**	3×3 sqm.
6	**Field border**	1m
7	**Block border**	1m
8	**Main channel**	1m
9	**Sub- channel**	60cm
10	**Spacing**	60×45cm
11	**Date of Sowing**	15.10.2009
12	**Date of transplanting**	16.11.2009
13	**Fertilizers**	100N-60P_2O_5-60K_2O(kg/ha)
14	**Number of Irrigations**	7 (Irrigation Interval-8-10days)
15	**Date of harvesting**	15.03.2010 to 30.03.2010

3.5 CULTIVATION DETAIL:

3.5.1 Raising of the Seedlings

The seeds were sown in a well prepared seed bed having sufficient farm yard manure and compost. The sowing was done on 15.10.2009. The seeds were lightly pressed in to the soil and were covered with a fine mixture of soil and leaf mould at the time of sowing. Frequent irrigation by means of a rose cane was given to maintain optimum moisture condition in the bed.

3.5.2 Preparation of Experimental plot:

The ideal field preparation is basically essential constituent for good yield of tomato. These factors have good effect through their influence upon physical properties particularly air circulation and soil moisture, availibility of plant nutrients and absorption etc. The experimental plot was given repeated ploughing and planking for 3 times to obtain a suitable tilth for Tomato cultivation. The required area was then marked and the plots were prepared according to the plan of lay out. Entire dose of phosphorus, potash and half dose of nitrogen were applied as basal dose at the time of transplanting. Remaining half dose of nitrogen was applied in two splits viz., 30^{th} day and 45^{th} day after transplanting.

3.5.3 Transplanting

Thirty three days old seedlings were transplanted in the main field in the afternoon between 3 PM to 6 PM. During transplanting proper care was taken to record the sequence of genotypes which was in a random manner. After transplanting a light irrigation was provided with a rose-cane. All intercultural operation such as weeding and hoeing were followed at their respective times frequently.

3.5.4 After Care

Gap filling was done within a week after transplanting. Irrigation was given at 7-10 days intervals depending on the requirement during crop period uniformly. Weeding was done at 15 days interval six times after transplanting to maturity. Application of granular insecticides like Furadon 3G (30kg/ha) was applied 12 days after transplanting followed by 2-3 foliar sprayings with 0.05% Dimethoate (2.5ml/L) at 10

days interval. Two sprays of 0.2% carbaryl (Sevin 3ml/L) was given to control fruit borer (*Helicoverpa armigera*) at 10 days interval after fruit initiation and Copper Oxychloride (Blitox 50, 3gm/L) to control wilting of tomato crop.

3.6 OBSERVATIONS RECORDED:

In the present investigation, observations were recorded on 5 randomly selected plants leaving the border plants on 14 characters as follows. The characters were categorized in to 3 parts viz. (1) Study of plant growth (2) Study of flowering and fruiting (3) Study of yield and post-harvest character.

3.6.1 Study of plant growth

3.6.1.1 Plant height (cm)

The final height of the main stem of the observational plants were measured from ground level to the tip of main axis, with the help of meter scale and recorded in cm.

3.6.1.2 Number of primary branches per plant

The total number of primary branches developed from the main axis of tagged plant were counted and recorded at maturity.

3.6.2 Study of Flowering and fruiting

3.6.2.1 Days to 50% flowering

The days to 50% flowering were taken for all the genotypes and average time taken from the date of transplanting was calculated.

3.6.2.2 Number of flower clusters per plant

Total numbers of flower clusters in the tagged plants were recorded and averaged at maturity.

3.6.2.3 Number of fruits per plant

Numbers of fruits per plant were recorded in tagged plants and their average value was calculated.

3.6.2.4 Fruit length (cm)

Five fruits from each replication were selected randomly and fruit length was measured in cm.

3.6.2.5 Fruit width (cm)

The diameters of five fruits from each replication of the observational plants were taken in cm with the help of Vernier Calipers.

3.6.2.6 Pericarp thickness (mm)

Five fruits were taken for the recording of pericarp thickness (mm). The fruits were cut transversely and thickness of pericarp was measured with the help of Vernier Calipers.

3.6.2.7 Number of locules per fruit.

Taking the above mentioned cut fruits locules were counted and average number of locules were calculated.

3.6.2.8 Average fruit weight (g)

The weights of the randomly selected 5 fruits were taken in each genotype per replication and average value was calculated to obtain the average fruit weight in gram.

3.6.2.9 Number of seeds per fruit

Selected number of ripen tomato fruits from each genotype in each replication were extracted and counted manually. Finally average was worked out.

3.6.3 Study of yield & Post-Harvest Character

3.6.3.1 Fruit yield per plant (kg/ha)

Average fruit yield per plant was calculated after last picking and average was taken by multiplying average fruit weight with number of fruits per plant.

3.6.3.2 Fruit yield per hectare (q/ha)

As per the spacing, number of plants per hectare was calculated and it was got multiplied with fruit yield per plant in each genotype from the three replications.

3.6.3.3 Shelf life of the fruit (days)

Healthy and uniform fruits were taken for this purpose. Shelf life was recorded for each genotype an in each replication and mean was calculated.

3.7 ANALYSIS OF VARIANCE:

The table for analysis of variance (ANOVA) was set as explained by **Gomez and Gomez (1983)**. The calculated F values were compared with tabulated F value where ever F value was found significant.

The analysis of variance in a single environment is based on the mathematical model

$$\mathbf{Y_{ij} = \mu + g_i + b_j + e_{ij}}$$

Where,

Y_{ij} = Mean performance of the i^{th} genotype in j^{th} block

μ = General mean

g_i = The effect of i^{th} genotype

b_j = The effect of j^{th} block

e_{ij} = The environmental effect specific to the i^{th} genotype in the j^{th} block

On the basis of the above model, analysis of variance was set up as follows

$$\text{Grand Mean} = \frac{\text{Grand Total}}{N}$$

Where,

N= Number of treatments (g) × Replications (r)

Correction Factor = $(\text{Grand Total})^2 / N$

Total Sum of Square (T.S.S.) = Double Sum of observations corresponding to i^{th} row and j^{th} column

Treatment Sum of Square (S.S.G.) and Replication Sum of Square (S.S.R.) were calculated by subtracting Correction Factor from the division of Sum of Square of respective totals.

Error Sum of Square (S.S.E.) = T.S.S. - (S.S.T. + S.S.R.)

Source of Variation	Degree of freedom	Sum of square	Mean sum of square	Expected M.S.S	'F' Variance Ratio
Replication	r-1	S.S.R.	$\frac{\text{S.S.R.}}{\text{r-1}} = M_R$	$\sigma^2_e + g\sigma^2_r$	$\frac{M_R}{M_E}$
Genotypes (Treatments)	g-1	S.S.G.	$\frac{\text{S.S.G.}}{\text{g-1}} = M_G$	$\sigma^2_e + r\sigma^2_g$	$\frac{M_G}{M_E}$
Error	(r-1)(g-1)	S.S.E.	$\frac{\text{S.S.E.}}{\text{(r-1)(g-1)}} = M_E$	σ^2_e	
Total	(rg-1)	T.S.S.			

Where,

r = number of replications

g = number of genotypes/treatment

σ^2_g = Genotypic Variance

σ^2_e = Error Variance (or) Environmental Variance

Phenotypic and Genotypic variance were calculated by using the formula given by **Cochran and Cox (1957)**.

$$\text{Genotypic Variance } (\sigma^2_g) = \frac{\text{M.S.S. due to genotypes} - \text{M.S.S. due to error}}{r}$$

Phenotypic variance (σ^2_p) = Genotypic variance (σ^2_g) + Error variance (σ^2_e)

The characters which showed significant differences among genotypes were further subjected to analysis for the following parameters.

3.7.1 Parameters of Variability

3.7.2 Heritability

3.7.3 Genetic Advance

3.7.4 Genetic Gain (as percentage of grand mean)

3.7.5 Correlation Coefficient

3.7.6 Path Coefficient Analysis

3.7.7 Genetic Divergence

3.7.1 PARAMETERS OF VARIABILITY:

The parameters of Variability were estimated by the formula given by **Burton and Devane (1953)**

3.7.1.1 Mean

The mean value of each character was determined by dividing the total number by the corresponding number of observations

$$\text{Mean} = \frac{\text{Sum of All observations}}{\text{Number of observations}}$$

3.7.1.2 Range

The lowest and highest value for each character was taken as the range.

3.7.1.3 Standard Error of Difference between two Means

S.E.d. (M) was calculated with the help of error mean square from ANOVA

$$\text{S.E.d. (M)} = \frac{\sqrt{2MSE}}{r}$$

CD 0.05 = SE (d) × table value of‘t’ 0.05 at error degree of freedom

Where

M.S.E. = Mean sum of Square due to error

r = Number of replications

CD 0.05 = Critical difference at 5% level of significance

3.7.1.4 Phenotypic coefficient of Variation (Burton, 1952)

$$PCV\ (\%) = \frac{\sqrt{\text{Phenotypic Variance}}}{\text{General mean of population}} \times 100$$

3.7.1.5 Genotypic Coefficient of Variation (Burton, 1952)

$$GCV\ (\%) = \frac{\sqrt{\text{Genotypic Variance}}}{\text{General Mean of population}} \times 100$$

PCV and GCV were categorized as per **Sivasbramanian and Madhavamenon (1973)** and shown below:

<10% (low), 10-20% (Moderate), >20% (High)

3.7.2 HERITABILITY IN BROAD SENSE (h^2):

Heritability in the concerned genotypes were calculated by the formula given by **Burton and Devene (1953)** and **Allard (1960)**

$$\text{Heritability } (h^2\ \%) = \frac{\text{Genotypic Variance } (\sigma^2_g)}{\text{Phenotypic Variance } (\sigma^2_p)} \times 100$$

According to **Robinson *et al*. (1966)** heritability estimates in cultivated plants can be placed in the following category:

0-30% (low), 30-60% (Moderate), >60% (high)

3.7.3 GENETIC ADVANCE (GA):

The genetic advance i.e., expected genetic gain resulting from selection of five per cent superior plants were worked out as formula given by **Johnson *et al.* (1955)**

Genetic Advance (Expected) = $\mathbf{h^2 \times \sigma^2_p \times K}$

Where

h^2 = Heritability in broad sense

$\sqrt{\sigma^2_p}$ = Phenotypic Standard deviation

K =Selection differential in standard units which is 2.06 for 5% selection intensity (Allard, 1960)

Genetic Advance was classified as:

>20% (high), 10-20% (Moderate), <10% (low)

3.7.4 GENETIC GAIN:

Genetic gain which is the expression of genetic advance as per cent of population mean was calculated by the formula given by **Johnson *et al.* (1955)**

$$\text{Genetic Gain (\%)} = \frac{\text{Expected Genetic Advance}}{\text{General mean of population}} \times 100$$

Genetic Advance as percent of population mean was categorized as given below as suggested by **Johnson *et al*. (1955)**

<10% (low), 10-20% (Moderate), >20% (High)

3.7.5 CORRELATION COEFFICIENT:

Genotype and phenotypic correlations were calculated by employing the technique of statistical analysis in variance – co-variance matrix in which total variability had been split into replications, genotypes and errors. All the components of variance were

estimated from analysis of variance table (ANOVA) and those of covariance from the ANOVA table given below:

3.7.5.1 Analysis of Variance and Covariance

Source of variation	DF	MSS		Mean sum of product	Variance
		X	Y		
Replication (r)	r-1				
Genotypes (g)	g-1	M_{gx}	M_{gy}	M_{gxy}	$\frac{M_{P1}}{M_{P2}}$
Error	(r-1) × (g-1)	M_{ex}	M_{ey}	$M_{exy} = M_{p2}$	

Genotypic, phenotypic and environmental covariance between characters X and Y were calculated as follows

Phenotypic covariance (σ^2_{pxy}) = $\sigma^2_{gxy} + \sigma^2_{exy}$

Where,

$$\sigma^2_{gxy} \text{ (Genotypic Covariance)} = \frac{M_{P1} - M_{P2}}{r}$$

σ^2_{exy} (Environmental covariance) = M_{P2}

The phenotypic and genotypic coefficients of correlation were computed following **Al-Jibouri *et al.* (1958)**

3.7.5.2 Phenotypic coefficient of correlation

$$r_p = \frac{\sigma^2_{pxy}}{\sqrt{\sigma^2_{px}\ \sigma^2_{py}}}$$

Where

$\sigma^2_{p\,x\,y}$ = Phenotypic covariance between x and y

σ^2_{px} = Phenotypic variance of x

σ^2_{py} = Phenotypic variance of y

3.7.5.3 Genotypic coefficients of correlation

$$r_g = \frac{\sigma^2_{gxy}}{\sqrt{\sigma^2_{gx}\,\sigma^2_{gy}}}$$

Where

σ^2_{gxy} = Genotypic covariance between x and y

σ^2_{gx} = Genotypic variance of x

σ^2_{gy} =Genotypic variance of y

The significance of phenotypic and genotypic correlation coefficients were compared with tabulated 'r' value, as given by Fisher and Yates (1963) at n-2 degree of freedom where 'n' denotes the number of genotypes.

3.7.6 PATH COEFFICIENT ANALYSIS:

The path coefficient analysis was carried out using phenotypic correlation values of yield components on fruit yield as suggested by **Wright (1921)** and illustrated by **Dewey and Lu (1959)**. Standard path coefficients which are the standardized partial regression coefficient were obtained by solving the simultaneous equations.

$Py_1 + Py_2\, r_{12} + Py_3\, r_{13} + \ldots\ldots\ldots\ldots + Py_n\, r_{1n} = ry_1$

$Py_1\, r_{12} + Py_2 + Py_3\, r_{23} + \ldots\ldots\ldots\ldots + Py_n\, r_{2n} = ry_2$

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$Py_1\, r_{1n} + Py_2\, r_{2n} + Py_3\, r_{3n} + \ldots\ldots\ldots\ldots + Py_n = ry_n.$

Where,

Py_1, Py_2, Py_3 …… Py_n are the direct path effects of 1, 2, 3 … n variables on dependent variable 'y'.

r_{12}, r_{13} …….. r_{1n} are the genotypic coefficients of correlation between various independent variables.

ry_1, ry_2 …… ry_n are the genotypic correlation coefficients of independent variables with dependent variable 'y'.

$Py_1\, r_{12}$, $Py_3\, r_{23}$ ……. $Py_n\, r_{2n}$ are the indirect effects

The variation in the independent variable which remained undetermined by including all variables was assumed to be due to variable (s) not included in the present investigation. The degree of determination (P^2_{yx}) of such variable (s) on dependent variable was calculated as follows:

$P^2_{yx} = 1- (P^2y_1 + 2Py_1\, Py_2\, r_{12} + 2Py_1\, Py_3\, r_{13} \ldots. + P^2y_2 + 2Py_2\, Py_3\, r_{23} + \ldots\ldots + P^2\, y_n)$

And Residual effect (factor) = $\sqrt{P^2_{yx}}$

The values of path coefficient analysis were categorized as below:

0.00 to 0.09 (Negligible); 0.10 to 0.19 (Low);

0.20 to 0.29 (Moderate); 0.30 to 1.0 (High); >1.0 (Very high)

3.7.7 GENETIC DIVERGENCE ANALYSIS:

Genetic divergence was computed by using Mahalanobis's generalized distance as described by **Rao (1952)**. Transformation of original means of various characters X_1's, to uncorrelated variable Y_1's was carried out by pivotal condensation method of inversion matrix. The divergence (D^2) values between any two cultivars were obtained as the sum of square of differences in the value of corresponding transformed variables

The generalized distance between any two populations is defined as:

$$\mathbf{D^2p = b_1d_1 + b_2d_2 + \ldots\ldots\ldots\ldots\ldots\ldots + bpdp}$$

Where

X_1, X_2, X_3……. Xp as a multiple measurements available on each individual d_1, d_2 ……d_2 as X_1^{-1}, $X_2^{-1} - X_2^{-2}$ …… $Xp^{-1} - Xp^{-2}$, respectively, is being the difference in the means of two populations.

In term of variance and covariance, the D^2 value is obtained as follows:

$$D^2P = Wij\ (Xi^{-1} - Xj^{-1})\ (Xj^{-1} - Xj^{-2})$$

Where,

Wij is the inverse estimated variance covariance matrix.

3.7.7.1 Clustering of genotypes using D^2 values

All the genotypes used were clustered in to different groups by following Tocher's method (**Rao, 1952**). The intra and inter cluster distance were also computed. The criterion used in clustering by this method was that any two varieties belonging to the same cluster at least on an average show a smaller D^2 values then those belonging to two different clusters.

The device suggested by Tocher **(Rao, 1952)** was strated with two closely associated populations and find a third population which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average of D^2 value from the first three and so on. If at any stage increase in average D^2 value exceeded the average of already included, because of addition of new genotypes, then the genotype was deleted. The genotypes those are included already in that group were considered as the first cluster. This procedure was repeated till D^2 values of the other genotypes were exhausted omitting those, that were already included in former cluster and grouping them in to different clusters.

3.7.7.2 Intra and Inter cluster distance

Based on D^2 values, average intra and inter cluster distances were calculated as per Euclidean method

3.7.7.2.1 Intra cluster distance:

The average intra cluster distances were calculated by the formula given by **Singh and Chaudhary (1985):**

$$\textbf{Intra cluster distance} = \frac{\Sigma Di^2}{n}$$

Where,

ΣDi^2 = Sum of distance between all possible combinations.

n = number of all possible combinations

3.7.7.2.2 Inter cluster distance:

The average inter distances were calculated by the formula given by **Singh and chaudhary (1985)**.

$$\textbf{Inter cluster distance} = \frac{\Sigma Di^2}{n_i\, n_j}$$

Where,

ΣDi^2 = Sum of distance between all possible combinations (n_i n_j) of the entries included in the cluster study

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j

3.7.7.3 Contribution of Individual characters

The character contribution towards genetic divergence was computed by using the method given by **Singh and Chaudhary (1985)**. In all the combination, each character is ranked on the basis of

$$\mathbf{di = y_i^j - y_i^k}$$

Where,

di = mean deviation

y_i^j = mean value of j^{th} genotype for the i^{th} character

y_i^k = mean value of k^{th} genotype for the i^{th} character

Rank 'I' is given to the highest mean difference and rank 'p' is given to the lowest mean difference

Where,P is the total number of characters.

Finally, number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

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Experimental Findings

CHAPTER-IV

EXPERIMENTAL FINDINGS

In tomato genetic divergence studies were conducted on 68 genotypes. During the course of experiment, information obtained regarding the extent of variability, association among different traits, magnitude of association among different traits and divergence have been submitted under following sub heads.

4.1 Analysis of variance

4.2 Mean performance of genotypes

4.3 Parameters of variability

4.5 Correlation coefficient

4.6 Path coefficient analysis

4.7 Genetic divergence (D^2 statistics)

4.1 ANALYSIS OF VARIANCE:

The analysis of variance for experimental design revealed significant differences among the genotypes for all the traits studied (table 4.1). The significant differences indicated existence of good deal of variability with respect to various quantitative traits. The analysis of variance for experimental design in respect of 14 characters exhibited highly significant results for characters namely days to 50% flowering, plant height, number of branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, pericarp thickness, average fruit weight, number of locules per fruit, number of seeds per fruit, fruit yield per plant, fruit yield per hector and shelf life of fruit.

4.2 MEAN PERFORMANCE OF GENOTYPES:

The mean values of 14 characters for 68 genotypes of tomato have been given in table 4.2.

4.2.1 Days to 50% flowering:

Always earliness in flowering is considered to be a favorable character with respect to yield and also to avoid different biotic and abiotic stresses during the crop period. The genotype FLA-7171 was the earliest in producing flowers. The genotype took an average 23 days to produce flowers, where as the genotypes CTS-05-05 and RCMT-1-2 took longest time (38 days) for flowering. The other genotypes took values in between 23-38 days. The population mean was 31.24 days. The results are given in 4.2.

4.2.2 Plant height (cm):

Highest mean value of plant height was recorded by genotype Pant T-7 (129.40 cm) which was found significantly higher and statistically at par with VTG-88 (125.45). The lowest value (46.90 cm) was found in CTS-05-05-2 and the mean value of population for this trait was observed to be 83.06 cm.

4.2.3 Number of primary branches per plant:

The maximum number of primary branches was recorded in genotype RCMT-2-1 (15.03) which is statistically at par with RCMT-2, VTG-88 and PANT T-7. The minimum number of branches was recorded in genotype LCT-6 (4.60) and the mean value of population for this trait was observed to be 8.64 branches.

4.2.4 Number of flower clusters per plant:

Fruit yield is also affected by the number of flower clusters per plant as it helps to increase number of fruits if proper condition is maintained. The highest number of flower cluster per plant was recorded for the genotype RCMT-2-1 (17.73) followed by KS-229-1 (13.55), NUN-4 (12.86) and PANT-T-7 (12.76). Minimum number of flower clusters per plant was recorded for the genotype LCT-6(3.43) and the mean value of population for this trait was about 8.86.

4.2.5 Number of fruits per plant:

A perusal of data (table 4.2) indicated that genotype IC-177371 had maximum number of fruits (47.11) followed by NUN-4 (43.31). The lowest value for this trait

was recorded for the genotype LCT-6 (11.57). The population mean was 27.59 for this trait. The other genotypes took values in between 11.57-47.11.

4.2.6 Fruit length (cm):

The fruit of different cultivars ranged between 2.70 cm (TLC-1) to 5.77 cm (LCT-9-4). The highest value 5.77 cm LCT-9-4 was followed by 5.47 cm (Punjab Upma) and 5.45 cm (NUN-4). The population mean was recorded as 4.01 cm (table 4.2) for this trait.

4.2.7 Fruit width (cm):

As shown in the table 4.2, considerable variability was observed in fruit width. Genotype RCMT-2-1 exhibited maximum fruit width (6.08 cm) followed by Punjab Keshri (5.64 cm) which was statically at par and showed no significant difference. The lowest value i.e. 2.35 cm was recorded in TLC-1. The population mean was found to be 4.05 cm.

4.2.8 Pericarp thickness (mm):

As presented in table considerable variabilities were observed in pericarp thickness. The highest value for this parameter was recorded for the genotype KS-229-1 (0.86 mm) followed by RCMT-2-1 (0.83 mm) and these values were statistically at par. The least value for pericarp thickness was obtained in genotype RCMT-2-2 (0.31 mm). The population mean for this trait was estimated 0.50 mm.

4.2.9 Number of locules per fruit:

The maximum number of locules per fruit was recorded for the genotype RCMT-2-1 (7.61) which was statistically at par with the genotype DVRT-2 (5.81) and LCT-10 (5.66). Minimum number of locules per fruit was obtained in the genotype LCT-7 (1.92). The mean value of population for this trait was recorded as 3.78.

4.2.10 Average fruit weight (g):

As it is obvious from the table**,** the range of fruits weight varies between 21 g to 78 g. The highest fruit weight 78 g was recorded in genotype RCMT-2-1 followed by KS-229-1 (73g). The lowest value (23.40g) was found in Angoorlata. The population mean was found to be 42.21 g.

4.2.11 Number of seeds per fruit:

Among the tested entries, the number of seeds per fruit ranged from 54.77 to 234.29. The highest number of seeds (234.29) found in the genotype VRT-2 followed by LCT-1 (218.84), NOTVR-60 (211.97), and Sel-7-2 (208.00) where as lowest number seeds (54.77) were obtained from the genotype Angoorlata. The population mean was found to be 141.93.

4.2.12 Fruit yield per plant (kg):

From the data recorded, it was found that fruit yield from a single plant varied from 0.35 kg to 2.67 kg. The highest fruit yield per plant was recorded in genotype KS-229-1 (2.67 kg) followed by RCMT-2-1 (2.63 kg), NUN-4 (2.11 kg), and LCT-9-3 (1.99 kg) which was statistically at par and showed no significant difference. The least value for this trait was observed in LCT-6 (0.35 kg). The mean performance of population was found to be 1.16 kg.

4.2.13 Fruit yield per hectare (q/ha):

The variation in fruit yield (q/ha) was in accordance with the variation at yield per plant. The maximum yield per hectare was recorded for KS-229-1 (987.49 q/ha) followed by RCMT-2-1 (973.17 q/ha), NUN-4 (780.01 q/ha) and LCT-9-3 (736.11 q/ha) which were statistically at par. Least value for this trait (131.40) was exhibited by LCT-6. The population mean was estimated to be 429.48 q/ha.

4.2.14 Shelf life:

The shelf life period of the genotypes ranged from 4.00 days to 12.85 days. The highest value for this trait (12.85 days) was recorded for the genotype CTS-05-05-2 followed by Sel-7 (11.34 days), DVRT-2 (10.45 days) and CTS-05-25 (10.30 days). The least value (4.00 days) was recorded for the genotype Sikkim Local. Mean of the population was found to be 7.68 days.

4.3 PARAMETERS OF VARIABILITY:

The parameters of variability viz. mean, range, phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in broad sense (h^2), genetic

advance and genetic gain were statistically worked out to facilitate selection for various traits and have been presented in table 4.3**.**

4.3.1 Coefficient of Variation:

It is evident from the table 4.3, that in general coefficient of variation at phenotypic level was higher in magnitude than corresponding genotypic level though the differences were not much in all the cases. Maximum PCV (49.55) and GCV (47.30) were registered for Shelf life while days to 50 per cent flowering had the lowest PCV (8.66) and GCV (7.40). High PCV and GCV (>30%) were also exhibited by number of locules per fruit (34.00; 32.95), number of seeds per fruit (31.45; 31.37) and fruit yield per hector (39.63; 39.54). Moderate PCV and GCV (15-30%) was recorded for plant height (27.04; 26.91), number of primary branches per plant (24.45; 21.14), number of flower clusters per plant (29.60; 26.68), number of fruits per plant (24.50; 23.74), fruit length (17.19; 16.71), fruit width (19.27; 18.83), and pericarp thickness (22.75; 22.60).

4.3.2 Heritability and Genetic Advance / Genetic Gain

The estimates made with regard to heritability (broad sense), genetic advance and genetic gain are presented in table 4.3. The range of heritability was observed between 73.10 to 99.60 per cent. Highest value of heritability 99.60 was observed for fruit yield per plant and fruit yield per hectare, while it was lowest for days to 50% flowering (73.10). Heritability estimate was also high for number of seeds per fruit (99.50), plant height (99.00), pericarp thickness (98.70), average fruit weight (97.00), fruit width (95.50), fruit length (94.50), number of fruits per plant (93.90) and number of locules per fruit (93.90)

Genetic gain presented in table 4.3 reflect that highest genetic gain (83.20%) was recorded for shelf life followed by fruit yield per plant (81.57%), fruit yield per hectare (81.27%), number of locules per fruit (65.87%), number of seeds per fruit (61.41%), average fruit weight (60.34%), plant height (54.97%), number of flower clusters per plant (49.54%), number of fruits per plant (47.37%), pericarp thickness (46.00%), fruit width (38.02%), number of primary branches per plant (37.61%) and fruit length (33.41%) whereas days to 50% flowering exhibited moderate genetic gain (13.02%).

4.4 CORRELATION COEFFICIENT:

Correlation coefficients among 14 characters for 68 genotypes were worked out in all possible combinations at phenotypic and genotypic levels (table 4.4). The results revealed that genotypic correlation coefficient values were mostly higher than their corresponding phenotypic values.

Phenotypic and Genotypic Correlation Coefficient

The phenotypic and genotypic correlation coefficient table revealed that plant height had positive significant correlation with number of primary branches per plant (0.758 P, 0.842 G), number of flower clusters per plant (0.693 P, 0.738 G), number of fruits per plant (0.540 P, 0.544 G), and fruit yield per plant (0.452 P, 0.455 G). Number of primary branches per plant recorded positive significant correlation with number of flower clusters per plant (0.834 P, 0.858 G), number of fruits per plant (0.564 P, 0.595 G), fruit width (0.319 P, 0.382 G) and fruit yield per plant (0.499 P, 0.575 G). Number of flower clusters per plant exhibited positive and significant correlation with number of fruits per plant (0.700 P, 0.712 G), fruit width (0.309 P, 0.353 G) and fruit yield per plant (0.599 P, 0.660 G). Number of fruits per plant recorded positively and significantly correlation with fruit yield per plant (0.591 P, 0.605 G). Fruit length was found positively significantly correlated with fruit width (0.626 P, 0.646 G), pericarp thickness (0.548 P, 0.568 G) average fruit weight (0.600 P, 0.626 G) and fruit yield per plant (0.522 P, 0.537 G). Fruit width exhibited positive significant phenotypic and genotypic correlation with pericarp thickness (0.729 P, 0.747 G), number of locules per fruit (0.566 P, 0.599 G), average fruit weight (0.725 P, 0.753 G), number of seeds per fruit (0.256 P, 0.264 G) and fruit yield per plant (0.675 P, .692 G). Pericarp thickness had positive and significant correlation with number of locules per fruit (0.567 P, 0.589 G), average fruit weight (0.931 P, 0.953 G) and fruit yield per plant (0.725 P, 0.731 G). Number of locules per fruit showed positive and significant correlation with average fruit weight (0.602 P, 0.635 G) and fruit yield per plant (0.404 P, 0.415 G). Average fruit weight had positive significant correlation with fruit yield per plant (0.748 P, 0.768 G).

4.5 PATH COEFFICIENT ANALYSIS:

Path analysis was carried out at phenotypic and genotypic level considering fruit yield per plant and fruit yield per hectare as dependent characters and its attributes as independent characters viz. Days to 50% flowering, plant height, number of branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, pericarp thickness, number of locules per fruit, number of seeds per fruit, average fruit weight and average shelf life. Each component has two path actions viz. direct effect on yield and indirect effect through components which are not revealed by correlation studies.

4.5.1 Days to 50% flowering:

Days to 50% flowering had negligible negative direct effect on fruit yield per plant and fruit yield per hectare at both phenotypic and genotypic level (-0.025 P and -0.039 G).

4.5.2 Plant height:

Plant height had negligible positive direct effect (0.005) at phenotypic level and negligible negative direct effect (-0.050) at genotypic level on fruit yield per hectare.

4.5.3 Number of primary branches per plant:

At both phenotypic and genotypic level number of primary branches per plant had negligible positive direct effect (0.006 P and 0.061 G) on per plant fruit yield.

4.5.4 Number of flower clusters per plant:

Number of flower clusters per plant showed negligible positive direct effect (0.073) on fruit yield per plant and per hectare where as at genotypic level it showed low positive direct effect (0.092) on the fruit yield per plant and fruit yield per hectare.

4.5.5 Number of fruits per plant:

At both genotypic and phenotypic level, number of fruits per plant recorded high positive direct effect (0.559 and 0.525) on fruit yield per hectare.

4.5.6 Fruit length (cm):

Fruit length showed negligible positive direct effect (0.019) and high positive indirect effect (0.431) through average fruit weight on fruit yield per hectare both at phenotypic and genotypic level.

4.5.7 Fruit Width (cm):

At both phenotypic and genotypic level, fruit width showed negligible positive direct effects (0.028 and 0.015) and high indirect positive effects (0.520 and 0.489) on fruit yield per hectare.

4.5.8 Pericarp thickness (mm):

This character showed negligible positive direct effect (0.052) on fruit yield phenotypically where as low positive direct effect (0.100) genotypically. It also exhibited high positive indirect effects (0.668 and 0.620) via. Average fruit yield at both phenotypic and genotypic level respectively.

4.5.9 Number of locules per fruit:

Number of locules per fruit showed negligible negative direct effects (-0.045, -0.052) both at phenotypic and genotypic level respectively where as high positive direct effect through average fruit weight (0.432, 0.413) on fruit yield at both phenotypic and genotypic level respectively.

4.5.10 Average fruit weight (g):

The character showed high positive direct effect on fruit yield per hectare at both phenotypic and genotypic level (0.718, 0.650 respectively).

4.5.11 Number of seeds per fruit:

Number of seeds per fruit exhibited negligible positive direct effect (0.003, 0.005) and low positive indirect effect (0.143, 0.132) through average fruit weight on fruit yield per hectare at both phenotypic and genotypic level.

4.5.12 Shelf life:

Both at phenotypic and genotypic level shelf life showed negligible negative direct effect (-0.034, -0.034) on fruit yield where as low positive indirect effects (0.155, 0.153) on fruit yield through average fruit weight.

4.6 GENETIC DIVERGENCE (D^2 STATISTICS):

The quantitative assessment of genetic diversity was made by adopting Mahalanobis's D^2 statistic for yield and its contributing characters.

4.6.1 Grouping of genotypes in to different clusters

Based on D^2 values, the 68 genotypes were grouped in to nine highly divergent clusters (table 4.6)**.** Some of genotypes were so divergent in all the characters; hence each single genotype formed a separate cluster. Thus eight clusters viz., VI, VII and IX were solitary with one genotype in each cluster.

The remaining six clusters were having maximum number of genotypes. Cluster I was biggest with 27 genotypes followed by cluster II, cluster IV, cluster III, cluster V and cluster VIII with 21, 6, 5, 4and 2 genotypes respectively.

4.6.2 Average intra and inter cluster distances

The mean intra and inter cluster D^2 values among the twelve clusters are given in (table 4.7). The intra cluster D^2 value ranged from 0.00 (cluster VI, VII and IX) to 1161.76 (cluster VIII). The cluster VIII had the maximum D^2 value (1161.76) followed by cluster V (948.19), cluster IV (863.80), cluster I (849.37), and cluster II (712.35) while it was least in cluster III (699.52).

The inter cluster D^2 values of the fourteen clusters revealed that highest inter cluster generalized distance (9573.80) was between cluster III and cluster VIII, while the lowest (1246.57) was between cluster I and cluster VI.

The nearest and distant clusters from each of the cluster based on D^2 values are present in (table 4.8)**.** Cluster I was nearest to cluster VI (1246.57) and distant from cluster VIII (5584.32). Cluster II exhibited close proximity with cluster I (1342.31) and maximum divergence with cluster VIII (7792.22).

Cluster III was nearest to cluster VI (1340.75), while it was farthest from cluster VIII (9573.80). Cluster IV showed close proximity with cluster VII (1451.75) and maximum divergence with cluster VIII (3552.55). Cluster V exhibited intimate relation with cluster I (1663.17) and wide diversity with cluster III (3835.15). Nearest and farthest clusters for cluster VI are I (1246.57) and VIII (5590.27).

Cluster VII was nearest to cluster IX (1308.71) and distant from cluster III (3528.53). Cluster VIII exhibited close proximity with cluster V (2413.45) and maximum divergence with cluster III (9573.80). Cluster IX exhibited intimate relation with cluster VII (1308.71) and wide diversity with cluster VIII (6234.40).

4.6.3 Cluster means of characters:

The cluster mean of 14 characters studied in tomato genotypes revealed that considerable differences among all the clusters (tables 4.9)**.** The cluster VII had the early days to 50% flowering (28.00 days) followed by cluster VIII (29.16 days) and cluster V (29.41 days) whereas; cluster III had the late days to 50% flowering (32.07 days). From the data it is evident that plant height was highest in cluster IV (116.30 cm) and lowest in cluster VI (46.92 cm). Maximum number of primary branches was recorded in cluster VIII (13.22) whereas minimum was recorded in cluster VI (6.07).

With regards to number of clusters per plant, cluster VIII (15.64) had the maximum mean value while cluster VI (5.40) showed the minimum. The number of fruits per plant was recorded maximum in cluster IV (49.31) and minimum in cluster IX (14.53). Fruit length was highest in cluster V (5.13 cm) and lowest in cluster II (3.44 cm) likewise Fruit width was found to be highest in cluster VII (5.64 cm) and lowest in cluster II (3.48 cm). For the character like pericarp thickness, highest value was obtained from cluster VIII (0.75 mm) and the lowest value was obtained from cluster II (0.42 mm). Locules per fruit were highest in cluster IX (7.55) and lowest in cluster II (3.00).

The cluster VIII had the highest value for average fruit weight (75.55 gm) whereas, cluster II had the lowest average fruit weight (33.29 gm). Number of seeds per fruit was highest in cluster III (177.33) and lowest in cluster VII (66.02).

Fruit yield per plant was highest in cluster VIII (2.65 kg) and lowest in cluster III (0.73 kg). The highest yield per hectare was obtained from cluster VIII (980.33 q)

and lowest yield was recorded for cluster III (271.16 q). Maximum shelf life (12.85 days) was recorded in cluster VI while minimum (5.68 days) in cluster VII.

4.6.4 Per cent contribution toward total divergence

The percent contribution of each character toward divergence is presented in the table 4.9**.** It was observed that number of fruits per plant contributed maximum (16.72) towards total divergence followed by average fruit weight (15.51), plant height (12.66), number of primary branches per plant (7.81), fruit length (7.45), yield per hectare (7.02), fruit yield per plant (6.58), fruit width (5.91), number of flower clusters per plant (5.51), number of seeds per fruit (5.33), shelf life (4.60), number of locules per fruit (1.73), pericarp thickness (1.64), and days to 50% flowering (1.53).

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Table-4.1 Analysis of Variance (ANOVA) of 68 genotypes of tomato for 14 characters:

Source of Variation	df	Days to 50 per cent flowering	Plant height (cm)	No. of primary branches Per plant	No. of flower clusters per plant	No. of fruits per plant	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (mm)	No. of locules per fruit	Fruit weight (g)	No. of seeds per fruit	Fruit yield per plant (kg)	Fruit yield per hector (q/ha)	Shelf life (days)
Replication	2	9.79	13.06	6.00	14.92	7.52	0.07	0.00	0.00	1.13	14.47	18.50	0.00	174.00	3.32
Treatment (Genotypes)	**67**	**18.00****	**1493.16****	**11.14****	**18.07****	**131.44****	**1.38****	**1.77****	**0.03****	**4.77****	**465.76****	**5957.12****	**0.61****	**84528.84****	**56.37****
Error	134	1.97	4.90	1.13	1.29	2.80	0.02	0.02	0.00	0.10	4.74	10.70	0.00	123.04	1.78

Table-4.2 Average performance of 68 genotypes of tomato for 14 characters:

SL. No.	Genotypes	Days to 50 per cent flowering	Plant height (cm)	No. of primary branches Per plant	No. of flower clusters per plant	No. of fruits per plant	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (mm)	No. of locules per fruit	Fruit weight (g)	No. of seeds per fruit	Fruit yield per plant (kg)	Fruit yield per hector (q/ha)	Shelf life (days)
1	Sel-7-2	30.33	90.63	10.50	10.13	36.57	2.90	3.30	0.34	4.43	34.30	208.00	1.25	462.96	9.85
2	Sikkim Local	33.00	80.63	8.77	8.43	22.47	3.13	4.80	0.57	5.17	37.60	182.93	0.84	312.71	4.00
3	RCMT-2-2	34.33	66.00	8.20	7.40	26.17	4.77	3.40	0.31	3.63	56.55	112.10	1.48	548.17	5.97
4	CTS-05-05	38.00	56.30	6.67	6.53	14.40	3.97	3.77	0.57	5.53	44.70	162.50	0.64	238.01	9.25
5	LCT-9-4	30.67	110.97	10.70	11.53	31.17	5.77	5.10	0.64	4.40	62.60	172.57	1.95	722.56	6.15
6	Amrita	35.67	90.73	11.23	10.57	20.67	3.83	3.47	0.33	3.03	24.60	91.57	0.51	187.98	5.37
7	Punjab Upma	33.33	91.22	9.63	8.41	29.00	5.47	5.10	0.59	4.81	61.47	177.39	1.78	659.70	6.58
8	Swarna Samridhi	30.67	59.20	9.42	9.50	30.78	3.90	4.04	0.59	3.58	51.17	126.24	1.57	582.43	4.61
9	Floradade	31.00	62.73	7.59	9.12	23.53	4.94	4.74	0.58	5.75	53.70	196.24	1.26	467.50	5.33
10	CO-3-1	30.00	69.60	7.36	7.64	30.42	3.91	3.93	0.48	2.98	30.00	115.05	0.91	337.26	5.26
11	FLA-7171	**23.00**	59.13	6.83	7.58	29.48	3.00	3.02	0.33	3.71	28.59	140.13	0.84	311.77	5.00
12	KS-229	30.33	71.50	6.34	6.66	26.33	4.95	3.34	0.58	3.42	47.28	173.56	1.24	460.18	6.20
13	NDTVR-60	35.00	58.10	7.33	7.22	24.65	3.75	4.32	0.54	5.19	45.60	211.97	1.12	414.91	4.17

14	Potato Leaf	33.00	96.22	8.65	8.64	33.66	3.42	3.57	0.32	3.68	27.70	103.62	0.93	343.22	4.27
15	NDT-5	29.67	57.21	8.55	7.66	30.42	3.50	3.41	0.32	3.17	25.57	176.89	0.78	287.45	5.03
16	LCT-10-3	33.67	71.67	7.33	7.33	29.74	4.32	4.18	0.47	2.68	37.15	71.86	1.10	408.64	5.37
17	VR-20	32.00	60.28	6.44	8.54	29.60	4.15	4.13	0.46	3.31	36.90	165.89	1.09	404.00	5.53
18	AZAD-T-5	36.00	51.57	6.66	6.98	29.32	3.09	3.04	0.35	3.20	26.13	149.44	0.76	282.19	4.03
19	Angoorlata	33.00	61.25	7.66	9.11	33.31	2.85	2.80	0.42	2.13	23.40	54.77	0.78	288.9	5.17
20	NUN-4	32.00	103.15	9.66	12.86	43.31	5.45	4.81	0.58	2.09	48.64	88.66	2.11	780.01	6.22
21	IC-177371	29.67	120.07	11.38	13.39	47.11	4.05	3.83	0.46	3.03	33.02	74.08	1.55	575.40	5.76
22	RCMT-1-3	31.67	90.62	7.50	9.33	27.05	3.49	3.14	0.49	3.27	41.30	111.67	1.11	412.31	5.02
23	VTG-88	34.67	125.45	11.88	10.33	35.04	3.50	4.45	0.51	5.29	43.63	79.08	1.53	565.28	9.10
24	NUN-2	31.33	88.09	5.77	6.39	19.33	4.50	4.35	0.60	2.98	49.10	87.77	0.95	350.76	7.33
25	Pant T-7	30.00	129.40	11.88	12.76	39.31	3.71	3.83	0.39	2.10	33.61	112.66	1.32	488.76	7.80
26	LCT-6	27.67	51.23	4.60	3.43	11.57	3.22	3.02	0.35	3.03	30.77	134.55	0.35	131.40	8.60
27	Avinav	30.00	59.79	6.66	7.66	27.99	3.00	3.01	0.46	2.51	34.07	96.04	0.95	352.28	7.17
28	DVRT-2	31.33	80.78	8.53	6.79	26.66	5.34	5.15	0.62	5.81	67.50	213.20	1.80	665.75	10.45
29	LCT-10	29.67	87.82	9.44	8.33	28.77	3.42	4.71	0.53	5.66	47.60	171.89	1.37	506.74	6.32
30	LCT-7	30.00	68.93	8.33	6.00	22.38	4.11	3.83	0.45	1.92	36.63	201.33	0.82	303.00	5.85

31	DT-10	30.00	101.16	9.75	10.44	31.93	5.00	4.62	0.61	4.77	56.60	133.82	1.81	668.88	9.24
32	Navodaya	34.00	108.80	9.89	8.78	23.49	3.64	3.54	0.52	4.66	42.93	190.00	1.01	373.02	8.83
33	NUN-3	31.00	78.69	7.33	6.00	21.66	4.20	3.50	0.39	2.66	32.87	98.19	0.71	262.95	6.60
34	TLC-1	34.33	81.44	9.11	8.00	30.43	2.70	2.35	0.35	2.55	26.38	97.00	0.80	297.00	9.63
35	TO-1389	33.00	72.31	6.55	7.98	22.22	3.19	2.53	0.45	2.61	35.30	104.33	0.78	288.81	9.60
36	DVRT-1-3	30.00	52.07	6.40	5.55	14.53	4.62	4.64	0.68	7.55	71.61	86.33	1.04	385.02	10.13
37	HS-102	32.33	70.13	7.92	8.19	24.12	4.02	3.78	0.56	5.74	45.35	171.22	1.09	404.47	9.27
38	LCT-10-5	33.67	68.67	8.33	7.28	18.34	4.24	3.97	0.69	3.72	59.77	188.00	1.09	405.20	7.33
39	RCMT-1	30.67	103.02	11.64	12.50	32.22	4.38	4.27	0.55	3.54	43.69	192.83	1.40	519.84	9.15
40	CTS-05-25	29.33	87.27	9.00	9.56	31.18	3.54	3.79	0.43	2.71	34.33	155.43	1.06	394.64	10.30
41	S-12	30.33	72.71	8.33	6.64	20.49	3.93	4.62	0.63	4.72	53.90	200.05	1.10	408.02	9.55
42	Pant T-1-5	30.00	118.54	10.00	11.33	33.16	3.80	3.70	0.42	2.67	32.57	110.39	1.08	398.98	7.81
43	BT-12	32.00	70.11	8.53	7.50	26.75	3.94	4.20	0.48	2.54	39.67	187.89	1.06	391.91	9.37
44	CO-3	31.00	57.26	7.19	6.33	22.48	3.99	4.18	0.54	3.28	44.03	140.50	0.99	366.28	8.56
45	Pusa Gaurav	32.67	71.59	9.11	8.50	29.53	3.94	3.87	0.47	2.33	41.63	130.22	1.23	454.90	9.21
46	NUN-1	30.33	94.18	7.00	5.55	21.00	3.87	3.81	0.58	3.33	47.50	191.66	1.00	369.63	9.10
47	DT-2-1	30.33	108.10	9.12	11.00	31.33	4.04	3.85	0.47	5.00	36.85	132.94	1.15	426.79	9.60

48	Shalimar-1	29.33	78.08	8.33	7.94	30.63	3.41	3.60	0.43	2.66	32.96	104.44	1.01	373.36	8.56
49	Kashi Amrit	26.00	70.83	7.33	9.29	32.29	4.99	5.24	0.58	3.33	51.65	148.44	1.67	618.33	9.54
50	LCT-9-3	29.67	125.00	11.44	12.63	38.77	4.43	4.65	0.60	4.33	51.29	163.00	1.99	736.11	7.63
51	RCMT-2-4	29.67	121.95	9.40	10.33	33.62	3.77	4.09	0.47	3.33	38.48	155.09	1.29	477.27	8.55
52	Sel-7	31.67	65.22	6.66	8.55	31.66	3.84	3.61	0.42	3.33	32.69	89.33	1.03	382.93	11.34
53	CTS-05-05-2	31.67	46.90	6.07	5.40	21.43	3.94	5.15	0.65	3.33	57.92	156.78	1.24	459.27	12.85
54	LCT-1	32.33	89.17	8.09	6.60	23.49	4.48	4.83	0.52	4.55	42.63	218.84	1.00	370.51	8.33
55	NUN-5	30.00	60.91	7.11	6.66	24.64	3.77	4.18	0.42	4.41	31.24	200.75	0.77	284.02	8.72
56	VRT-2	29.67	87.30	10.00	11.50	32.75	4.31	5.55	0.51	4.72	41.34	234.29	1.35	500.35	7.86
57	Punjab Kesari	28.00	69.18	8.44	9.53	30.69	4.22	5.64	0.63	5.69	54.82	66.02	1.68	620.51	5.68
58	RCMT-1-2	**38.00**	98.13	9.98	11.84	23.87	4.61	4.38	0.52	3.33	45.43	124.81	1.08	400.35	6.30
59	H-24	32.00	60.79	6.67	8.20	23.09	3.08	2.55	0.37	2.70	27.82	101.66	0.64	237.24	7.42
60	LCT-9	30.00	97.20	8.89	11.13	23.03	3.85	4.09	0.49	2.74	32.42	102.37	0.75	275.76	8.85
61	KS-229-1	29.00	110.44	11.42	13.55	36.50	5.11	5.18	0.86	5.31	73.10	177.44	2.67	987.49	9.55
62	ATL-02-39	29.00	104.31	8.77	7.67	19.50	5.09	4.18	0.45	3.07	35.30	163.39	0.69	254.40	9.77
63	Pant T-3	30.00	112.83	11.52	12.57	29.23	3.80	4.10	0.41	3.83	33.43	132.31	0.97	360.82	8.45
64	LCT-9-1	32.33	51.80	5.67	6.04	16.39	3.92	3.88	0.46	2.95	34.00	101.53	0.55	205.54	8.27

65	RCMT-2-1	29.33	115.15	15.03	17.73	33.70	4.19	6.08	0.83	7.61	78.00	93.29	2.63	973.17	7.93
66	RCMT-2	31.00	118.60	12.14	9.98	27.13	3.53	4.34	0.50	4.82	36.27	98.75	0.98	361.13	9.37
67	CTS-05-25-1	29.33	102.97	10.42	9.31	25.01	4.17	3.31	0.42	2.43	32.37	166.11	0.81	298.50	10.15
68	NDT-108	31.00	76.14	7.66	8.86	23.62	4.34	4.02	0.54	3.08	41.13	178.42	0.97	359.46	7.55
*****	**Grand Mean**	**31.24**	**83.06**	**8.64**	**8.86**	**27.59**	**4.01**	**4.05**	**0.50**	**3.78**	**42.21**	**141.93**	**1.16**	**429.48**	**7.68**
*	**SEM ±**	**1.14**	**1.80**	**0.86**	**0.93**	**1.36**	**0.13**	**0.13**	**0.01**	**0.26**	**0.18**	**2.67**	**0.02**	**9.05**	**1.08**
*	**CD at 5%**	**2.23**	**3.52**	**1.68**	**1.82**	**2.66**	**0.25**	**0.25**	**0.02**	**0.50**	**0.35**	**5.23**	**0.04**	**17.73**	**2.12**
*	**CD at 1%**	**2.94**	**4.64**	**2.21**	**2.40**	**3.50**	**0.33**	**0.33**	**0.025**	**0.67**	**0.46**	**6.89**	**0.06**	**23.34**	**2.79**

Table 4.3: Range, mean, genotypic and phenotypic coefficient of variation (GCV and PCV), heritability and genetic advance for 14 characters in 68 genotypes of tomato

SL. No.	Character	Mean Sum of Squares	Range	Grand mean	GCV	PCV	HA (%)	GA	Genetic Gain (%)
1	Days to 50% Flowering	18.00**	23.00-38.00	31.24	7.40	8.66	73.10	4.07	13.02
2	Plant Height (cm)	1493.16**	51.23-129.40	83.06	26.91	27.04	99.00	45.66	54.97
3	No. of primary Branches per plant	11.14**	4.60-15.03	8.64	21.14	24.45	74.70	3.25	37.61
4	No. of flower Clusters per plant	18.07**	5.40-17.73	8.86	26.68	29.60	81.30	4.39	49.54
5	No. of fruits Per plant	131.44**	11.57-47.11	27.59	23.74	24.50	93.90	13.07	47.37
6	Fruit length (cm)	1.38**	2.70-5.77	4.01	16.71	17.19	94.50	1.34	33.41
7	Fruit width (cm)	1.77**	2.35-6.08	4.05	18.83	19.27	95.50	1.54	38.02
8	Pericarp Thickness (mm)	0.03**	0.31-0.86	0.50	22.60	22.75	98.70	0.23	46.00
9	No. of locules Per fruit	4.77**	2.09-7.61	3.78	32.95	34.00	93.90	2.49	65.87
10	Avg. fruit Weight (g)	465.76**	21.00-78.00	41.68	29.74	30.19	97.00	25.15	60.34
11	No. of seeds Per fruit	5957.12**	54.77-234.29	148.93	31.37	31.45	99.50	91.47	61.41
12	Fruit yield Per plant (kg)	0.61**	0.35-2.67	1.14	39.54	39.62	99.60	0.93	81.57
13	Fruit yield Per hector (q/ha)	84528.84**	187.98-987.49	424.22	39.54	39.63	99.60	344.78	81.27
14	Shelf Life(days)	56.37**	4.00-12.85	7.68	47.30	49.55	91.10	6.39	83.20

Table 4.4: Phenotypic (P) and Genotypic (G) correlation coefficient among yield and yield attributes in 68 genotypes for 14 characters in tomato.

Characters	P/G	Days to 50% flowering	Plant Height (cm)	No. of Primary Branches Per plant	No. of Flower Clusters per plant	No. of fruits per plant	Fruit length(cm)	Fruit width(cm)	Pericarp thickness (mm)	No. of locules per fruit	Avg. fruit Weight(g)	No. of seeds per fruit	Fruit yield Per plant	Fruit yield Per hector	Shelf Life (days)
Days to 50% Flowering	P	--	-0.078	-0.026	-0.091	-0.194	-0.035	-0.140	-0.056	0.005	-0.080	-0.053	-0.196	-0.196	-0.271
	G	--	-0.094	-0.037	-0.118	-0.236	-0.059	-0.0181	-0.072	-0.007	-0.088	-0.064	-0.229	-0.229	-0.316*
Plant height (cm)	P		--	0.758**	0.693**	0.540**	0.203	0.240	0.131	0.089	0.108	-0.057	0.452**	0.452**	0.060
	G		--	0.842**	0.738**	0.544**	0.211	0.247	0.133	0.090	0.121	-0.060	0.455**	0.455**	0.064
No. of primary branches per plant	P			--	0.834**	0.564**	0.132	0.319*	0.184	0.220	0.143	-0.005	0.499**	0.499**	0.013
	G			--	0.858**	0.595**	0.157	0.382**	0.214	0.261	0.224	-0.015	0.575**	0.576**	0.017
No. of flower Cluster per plant	P				--	0.700**	0.159	0.309*	0.227	0.152	0.148	-0.160	0.599**	0.599**	-0.062
	G				--	0.712**	0.190	0.353**	0.248	0.166	0.223	-0.181	0.660**	0.660**	-0.066
Number of Fruits per plant	P					--	0.041	0.142	-0.025	-0.078	-0.055	-0.178	0.591**	0.592**	-0.120
	G					--	0.045	0.147	-0.028	-0.092	-0.019	-0.186	0.605**	0.606**	-0.127
Fruit length(cm)	P						--	0.626**	0.548**	0.235	0.600**	0.222	0.522**	0.522**	0.045
	G						--	0.643**	0.568**	0.252*	0.626**	0.230	0.537**	0.537**	0.051
Fruit width (cm)	P							--	0.729**	0.566**	0.725**	0.256*	0.675**	0.675**	0.210
	G							--	0.747**	0.599**	0.753**	0.264*	0.692**	0.692**	0.223
Pericarp thickness(mm)	P								--	0.567**	0.931**	0.204	0.725**	0.725**	0.210
	G								--	0.589**	0.953**	0.206	0.731**	0.731**	0.226
No of locules per fruit	P									--	0.602**	0.244	0.404**	0.403**	0.109
	G									--	0.635**	0.253*	0.415**	0.414**	0.109
Av. Fruit weight(gm)	P										--	0.199	0.748**	0.748**	0.217
	G										--	0.203	0.761**	0.760**	0.234
No of seeds per fruit	P											--	0.041	0.041	0.149
	G											--	0.041	0.041	0.158
Fruit yield per plant	P												--	0.999**	0.070
	G												--	0.999**	0.075
Fruit yield per hectare	P													--	0.071
	G													--	0.079

***, ** Significant at 5% and 1% probability level respectively.**

Table 4.5: Phenotypic and Genotypic path of 68 genotypes of tomato for 14 characters.

Characters	P/G	Days to 50% flowering	Plant Height (cm)	No. of Primary Branches Per plant	No. of Flower Clusters per plant	No. of fruits per plant	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (mm)	No. of locules per plant	Avg. fruit Weight (g)	No. of seeds per fruit	Shelf Life (days)	Correlation coefficient
Days to 50% Flowering	P	**-0.025**	0.000	0.000	-0.007	-0.018	-0.001	-0.004	-0.003	0.000	-0.057	0.000	0.009	-0.196**
	G	**-0.039**	0.005	-0.002	-0.011	-0.124	-0.002	-0.003	-0.007	0.000	-0.057	0.000	0.011	-0.229**
Plant height (cm)	P	0.002	**0.005**	0.004	0.050	0.302	0.004	0.007	0.007	-0.004	0.078	0.000	-0.002	0.452**
	G	0.004	**-0.050**	0.052	0.068	0.286	0.007	0.004	0.013	-0.005	0.079	0.000	-0.002	0.455**
No. of primary branches per plant	P	0.001	0.004	**0.006**	0.061	0.315	0.003	0.009	0.010	-0.010	0.103	0.000	0.000	0.499**
	G	0.001	-0.042	**0.061**	0.079	0.312	0.005	0.006	0.021	-0.014	0.145	0.000	-0.001	0.576**
No. of flower Cluster per plant	P	0.002	0.003	0.005	**0.073**	0.391	0.003	0.009	0.012	-0.007	0.106	0.000	0.002	0.599**
	G	0.005	-0.037	0.053	**0.092**	0.374	0.007	0.005	0.025	-0.009	0.145	-0.001	0.002	0.660**
Number of Fruits per plant	P	0.005	0.003	0.003	0.051	**0.559**	0.001	0.004	-0.001	0.003	-0.039	-0.001	0.004	0.592**
	G	0.009	-0.027	0.036	0.065	**0.525**	0.002	0.002	-0.003	0.005	-0.012	-0.001	0.004	0.606**
Fruit length(cm)	P	0.001	0.001	0.001	0.012	0.023	**0.019**	0.017	0.029	-0.011	0.431	0.001	-0.002	0.522**
	G	0.002	-0.011	0.010	0.017	0.023	**0.035**	0.010	0.057	-0.013	0.407	0.001	-0.002	0.537**
Fruit width (cm)	P	0.004	0.001	0.002	0.022	0.079	0.012	**0.028**	0.038	-0.025	0.520	0.001	-0.007	0.675**
	G	0.007	-0.012	0.023	0.032	0.077	0.022	**0.015**	0.075	-0.031	0.489	0.001	-0.008	0.692**
Pericarp thickness(mm)	P	0.001	0.001	0.001	0.016	-0.014	0.010	0.020	**0.052**	-0.025	0.668	0.001	-0.007	0.725**
	G	0.003	-0.007	0.013	0.023	-0.015	0.020	0.011	**0.100**	-0.031	0.620	0.001	-0.008	0.731**
No of locules per plant	P	0.000	0.000	0.001	0.011	-0.044	0.005	0.016	0.030	**-0.045**	0.432	0.001	-0.004	0.403**
	G	0.000	-0.005	0.016	0.015	-0.048	0.009	0.009	0.059	**-0.052**	0.413	0.001	-0.004	0.414**
Av. Fruit weight(g)	P	0.002	0.001	0.001	0.011	-0.031	0.011	0.020	0.049	-0.027	**0.718**	0.001	-0.007	0.748**
	G	0.003	-0.006	0.014	0.020	-0.010	0.022	0.011	0.095	-0.033	**0.650**	0.001	-0.008	0.760**
No of seeds per fruit	P	0.001	0.000	0.000	-0.012	-0.100	0.004	0.007	0.011	-0.011	0.143	**0.003**	-0.005	0.041**
	G	0.002	0.003	-0.001	-0.017	-0.098	0.008	0.004	0.021	-0.013	0.132	**0.005**	-0.005	0.041**
Shelf life (days)	P	0.007	0.000	0.000	-0.004	-0.067	0.001	0.006	0.011	-0.005	0.155	0.000	**-0.034**	1.000**
	G	0.012	-0.003	0.001	-0.006	-0.067	0.002	0.003	0.023	-0.006	0.153	0.001	**-0.034**	1.000**

Table 4.7: Average Intra and Inter-cluster D^2 and D values (In bold) for 14 characters in 68 genotypes of Tomato.

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	849.37 **(29.14)**	1342.31 **(36.64)**	1601.36 **(40.02)**	2151.78 **(46.39)**	1663.17 **(40.78)**	1246.57 **(35.31)**	2147.34 **(46.34)**	5584.32 **(74.73)**	2322.43 **(48.19)**
II		712.35 **(26.69)**	1378.91 **(37.13)**	2580.11 **(50.79)**	3267.81 **(57.16)**	1453.11 **(38.12)**	1875.91 **(43.31)**	7792.22 **(88.27)**	1982.84 **(44.53)**
III			699.52 **(26.45)**	4602.37 **(67.84)**	3835.15 **(61.92)**	1340.75 **(36.61)**	3528.53 **(59.40)**	9573.80 **(97.84)**	2933.10 **(54.16)**
IV				863.80 **(29.39)**	1869.32 **(43.23)**	3198.63 **(56.55)**	1451.75 **(38.10)**	3552.55 **(59.60)**	2929.74 **(54.13)**
V					948.19 **(30.79)**	1934.67 **(43.98)**	1860.03 **(43.13)**	2413.45 **(49.13)**	3185.11 **(56.44)**
VI						0.00 **(0.00)**	1475.86 **(38.41)**	5590.27 **(74.77)**	1362.53 **(36.91)**
VII							0.00 **(0.00)**	3335.85 **(57.75)**	1308.71 **(36.17)**
VIII								1061.76 **(32.58)**	6233.40 **(78.95)**
IX									0.00 **(0.00)**

Table 4.8: The nearest and farthest clusters from each cluster based on D^2 values in tomato genotypes

Cluster No.	Nearest cluster with D^2 value	Farthest cluster with D^2 value
I	**VI** (1246.57)	**VIII** (5584.32)
II	**I** (1342.31)	**VIII** (7792.22)
III	**VI** (1340.75)	**VIII** (9573.80)
IV	**VII** (1451.75)	**VIII** (3552.55)
V	**I** (1663.17)	**III** (3835.15)
VI	**I** (1246.57)	**VIII** (5590.27)
VII	**IX** (1308.71)	**III** (3528.53)
VIII	**V** (2413.45)	**III** (9573.80)
IX	**VII** (1308.71)	**VIII** (6234.40)

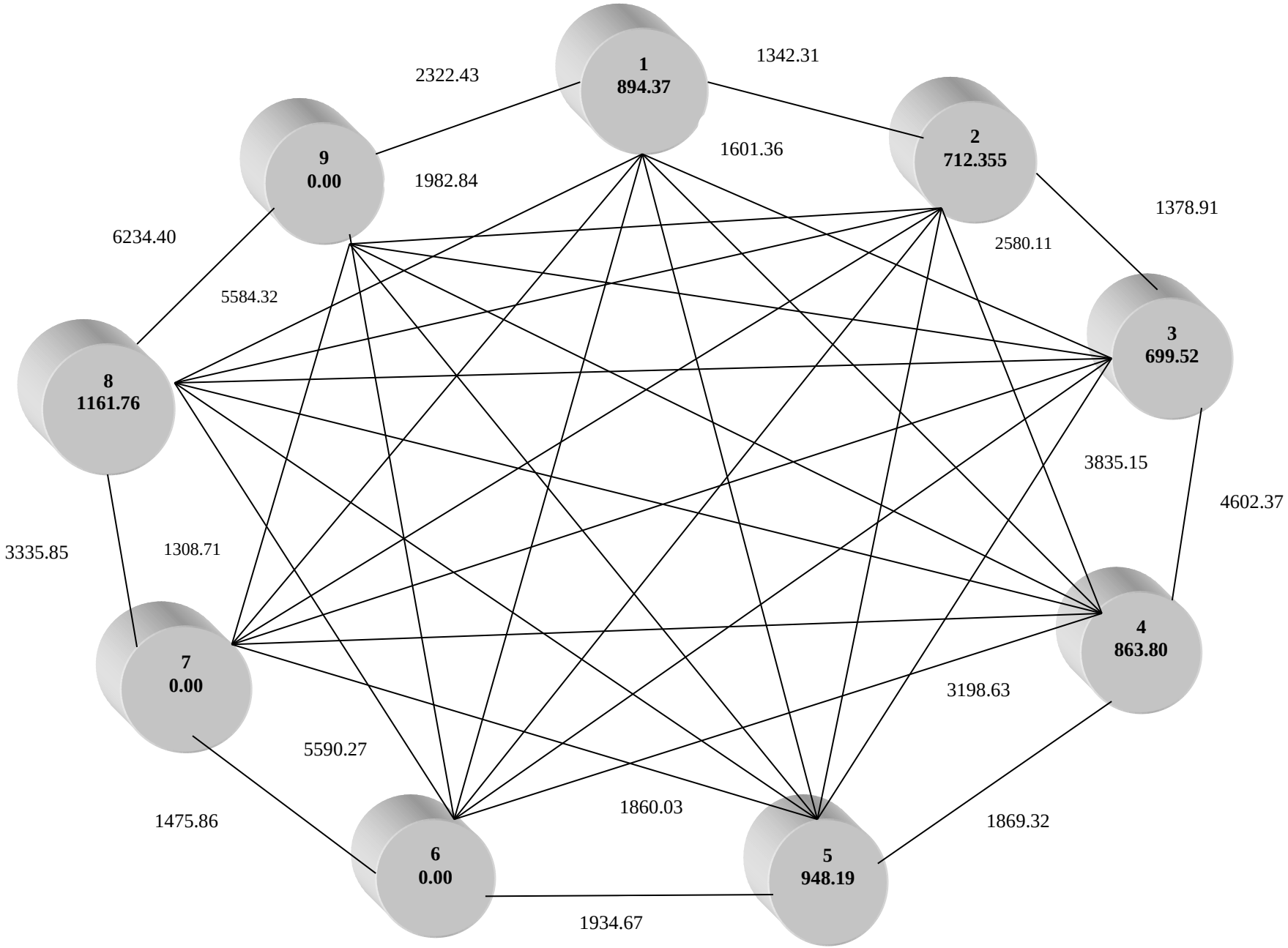
1
894.37
2
712.355
3
699.52
4
863.80
5
948.19
6
0.00
7
0.00
8
1161.76
9
0.00
2322.43
1342.31
1601.36
1982.84
6234.40
1378.91
2580.11
5584.32
3835.15
4602.37
3335.85
1308.71
3198.63
5590.27
1860.03
1475.86
1869.32
1934.67

Table 4.9: Cluster means and percent contribution of yield contributing characters towards divergence in 68 genotypes of tomato.

SL. No.	Characters	Clusters									% Contribution
		I	II	III	IV	V	VI	VII	VIII	IX	
1	Days to 50% Flowering	31.25	31.77	32.07	31.22	29.41	31.67	28.00	29.16	30.00	1.53
2	Plant Height (cm)	89.22	69.39	56.75	116.30	96.89	46.90	69.18	81.12	52.07	12.66
3	No. of primary Branches per Plant	8.99	8.42	6.85	11.11	9.50	6.07	8.44	13.22	6.40	7.81
4	No. of flower Clusters per Plant	8.96	7.97	6.30	11.62	10.06	5.40	9.53	15.64	5.55	5.51
5	No. of fruits Per Plant	26.62	26.76	21.14	49.31	32.22	21.43	30.69	35.10	14.53	16.72
6	Fruit length (cm)	4.08	3.44	3.64	4.25	5.13	3.94	4.22	4.65	4.62	7.45
7	Fruit width (cm)	4.10	3.48	3.74	4.31	5.03	5.15	5.64	5.63	4.64	5.91
8	Pericarp Thickness (mm)	0.51	0.42	0.44	0.50	0.59	0.65	0.63	0.75	0.68	1.64
9	No. of locules Per fruit	3.85	3.00	4.26	3.68	4.46	3.33	5.69	6.46	7.55	1.73
10	Avg. fruit Weight (g)	42.12	33.29	35.57	41.96	58.26	57.92	54.82	75.55	71.61	15.51
11	No. of seeds Per fruit	172.12	107.32	177.33	97.84	174.30	156.78	66.02	95.29	86.33	5.33
12	Fruit yield Per Plant (kg)	1.10	0.88	0.73	1.55	1.85	1.29	1.68	2.65	1.04	6.58
13	Fruit yield Per hectare (q/ha)	407.68	327.44	271.16	573.24	685.68	459.27	620.51	980.33	385.02	7.02
14	Shelf Life(days)	7.97	6.71	7.15	7.91	8.44	12.85	5.68	8.74	10.13	4.60

DVRT 2

Kashi Amrit

NUN-4

RCMT 2-1

KS 229-1

LCT 9-3

Discussion

CHAPTER-V

DISCUSSION

The knowledge in the amount of variability and its heritable portion present in the source population is a pre requisite for attempting any successful breeding program aimed at improving the yield and other characters. It is therefore important to generate information on the extent of variability, heritability and genetic advance for different characters under consideration.

The phenotypic variance measures the magnitude of variation arising out of difference in phenotypic values, while the genotypic variation measures the magnitude of variation due to differences in genotypic values. The absolute value of phenotypic and genotypic variances cannot be used for comparing the magnitude of variability for different characters since the mean and units of measurement of the characters may be different. Hence the coefficient of variation expressed at phenotypic and genotypic levels have been used to compare the variability observed among different characters. While genotypic coefficient of variation indicates the amount of genetic variability present in the character, the heritability estimates aid in determining the relative amount of heritable portion of variation. However, heritability values alone itself provide no indication of the amount of genetic progress that would result from selecting the best individuals. **Ramanujam and Tirumalachar (1967)** while studying the genetic variability in red-pepper discuss the limitation of estimating the heritability in broad sense as it included both additive and non-additive genetic effects. According to them heritability estimates in broad sense would be reliable if high genetic advance will be accompanied. Yield being an important and complex character is function of several component characters and their interaction with the environment. In the integrated structure of a plant, most of the characters are inter related and often change in one character will influence the other. Hence direct selection based on yield alone will not be very effective.

Grafius (1964) pointed out that it would be more meaningful if the structure of yield is probed through its components rather than *per se* yield. For improving yield through breeding, it is necessary to study these components, their inter relationships with yield and their direct and indirect contribution. The phenotypic and genotypic correlation reveals the extent of association between different characters. Thus, it helps to base selection procedure to a required balance, when two opposite desirable characters affecting the principal characters are being selected. It also helps to improve different characters simultaneously **(Falconer, 1981)**. The other genetic parameter commonly used in the path analysis given by **Dewey and Lu (1959)**. Path analysis gives a cause and effect relationship. It critically breaks up different direct and indirect effects which finally make up correlation coefficient.

In the recent years, the cognizance of genetic diversity and evolutionary history of crop plants yielded major advances in crop improvement. Measure of genetic divergence reveals the difference in gene frequencies. Mahalanobis's generalized distance estimated by D^2 statistic **(Rao, 1952)** is a unique tool for discriminating population by considering a set of parameter together. In addition to estimation of variability, cognizance of the gentic diversity of the germplasm is necessary for effective choice of parents in hybridization.

5.1 GENETIC VARIABILITY:

The success of any breeding program depends on the availability of genetic variability present in the population, which is however not directly measurable by itself, but has to be inferred with phenotypic expression. The phenotype may therefore be defined as a linear function of genotype (G), environment (E) and genotype × environment (G × E) interaction effect. A wide spectrum of variability will provide an insight to all local conditions. The extent of genetic variation observed in the present studies for most of the attributes in tomato was quite high and the same can be exploited by the breeders for increasing productivity.

In the present study, sixty eight genotypes from diverse sources were evaluated. The genotypes exhibited significant differences for all the fourteen characters studied and a wide range of variability was observed for days to 50%

flowering, plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, pericarp thickness, number of locules per fruit, average fruit weight, number of seeds per fruit, fruit yield per plant, fruit yield per hector and average shelf life indicating the scope for selection of suitable in breeding material for further improvement.

The PCV values were slightly higher than the respective GCV for all the characters denoting little environmental factors influencing their expressions to some degree or others. The difference between values of PCV and GCV were less for all traits in present investigation. It means these traits were less influenced by environment and they could be improved by following different phenotypic selections like directional, disruptive and stabilized selections. The PCV and GCV values were very high particularly for number of locules per fruit, average fruit weight, number of seeds per fruit, fruit yield per plant, fruit yield per hector, and shelf life due to very high variability available in these traits. The PCV and GCV values were also high for plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, and pericarp thickness suggesting that these characters can be improved through simple selection.

Moderate PCV and GCV (10%-20%) values for fruit length, fruit width, indicated the presence of moderate genetic variability for these traits whereas the component, days to 50% flowering showed low (<10%) PCV and GCV values indicating the existence of less variability in the material studied. Similar kinds of observations were also reported by **Pujari *et al*. (1995), Mittal *et al*. (1996), Singh and Narayan (2004), Singh (2005), Singh *et al*. (2007) and Singh (2009).**

5.2 HERITABILITY AND GENETIC ADVANCE:

Heritability estimates were high for all the characters studied. This suggested the greater effectiveness of selection due to less influence of environment and improvement to be expected for these characters in future breeding program. High estimates of heritability for these traits were also observed by **Singh and Singh (1993), Kumari and Subramanian (1994), Kurien and Peter (1995), Nair and Thamburaj (1995), Pujari *et al.* (1995), Mittal *et al.* (1996), Das *et al.* (1998),**

Prasad and Rai (1999), Sharma *et al.* (2006), Mehta and Asati (2008), Singh *et al.* (2008) and Singh (2009).

Johnson *et al.* (1955) suggested that high heritability coupled with high genetic advance as percentage of mean were more useful than h^2 alone in predicting the resultant effect during selection of best individual genotype. Genetic advance is the measure of genetic gain under selection and expression in percentage of mean.

In the present experiment genetic advance as percent of mean was high for plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, pericarp thickness, number of locules per fruit, average fruit weight, number of seeds per fruit, shelf life, fruit yield per plant, and fruit yield per hector. Interestingly, high h^2 in broad sense was also observed for these traits indicating that these traits were under strong influence of additive gene action as such, simple selection based on phenotypic performance of these traits would be more effective. Similar kind of results were observed in tomato for the traits like plant height and fruit yield per plant by **Supe and Kale (1991), Singh and Singh (1993), Pujari *et al.* (1995) Mittal *et al.* (1996), Das *et al.* (1998), Prasanth *et al*. (2006), Mehta and Asati (2008) and Singh *et al.* (2008).**

High heritability and moderate genetic gain values were also observed for the character, days to 50% flowering. This indicates that influence of non additive gene action and considerable influence of environment in the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis **(Padmini and Vadivel, 1997)**. Therefore, the breeder should adopt suitable breeding methodology to utilize both additive and non additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programs especially in case of tomato.

5.3 CORRELATION COEFFICIENT:

There is ample evidence to show that direct selection for fruit yield is not sufficiently effective, as yield is polygenically controlled and associated with number of related traits. Therefore indirect selection is desirable for improvement of yield. A knowledge of association between yield and its component traits and inter relationship

among themselves may provide information fruitful for planning an effective and successful breeding program.

In present study the phenotypic and genotypic correlation coefficients were worked out in respect of fourteen quantitative characters in all possible combinations (Table 4.4). In general, it was found that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic values. High genotypic correlation coefficients suggested that there was inherent relationship between the traits under study and environment had not played much role in reducing their actual association. The statistics which measures the relationship between two or more variable is known as correlation coefficient.

Basically yield is the main character with which all other characters are positively or negatively correlated. Fruit yield per hectare has positive and significant correlation with plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, pericarp thickness, number of locules per fruit, average fruit weight, and fruit yield per plant.

The phenotypic and genotypic correlation coefficient table revealed that plant height had positive significant correlation with number of primary branches per plant, number of flower clusters per plant and number of fruits per plant. Number of primary branches per plant had positive significant correlation with number of flower clusters per plant, number of fruits per plant and fruit width. Similar reports were reported for tomato for different components viz., association of fruit yield with number of branches **(Singh *et al.*, 1990)**, and plant height and number of branches per plant **(Patil and Bojappa, 1993)**. Number of flower clusters per plant had positive and significant correlation with number of fruits per plant and fruit width. Similar results were obtained in tomato for association between number of flower clusters per plant and fruits yield per plant by **Soorinath *et al.* (1994), Singh *et al.* (2004), Singh (2005), Sharma *et al.* (2006), Singh *et al.* (2007), and Singh (2007).**

In present experiment, it was observed that as the plant height increased, there was corresponding increase in number of primary branches per plant, days to 50% flowering and number of flower clusters per plant. The association recorded significant improvement in yield. Similar results were obtained in tomato by **Nair and**

Thamburaj (1995). Fruit length was found positively significantly correlated with fruit width, pericarp thickness and average fruit weight. Fruit width exhibited positive significant phenotypic and genotypic correlation with pericarp thickness, number of locules per fruit, average fruit weight and number of seeds per fruit. Pericarp thickness had positive and significant correlation with number of locules per fruit and average fruit weight. Number of locules per fruit showed positive and significant correlation with average fruit weight. Such reports were earlier reported in tomato by **Das *et al.* (1998) and Prasad and Rai (1999)**. Similar reports were also reported by **Joshi *et al.* (2004), Singh (2005), Sharma *et al.* (2007), and Singh (2007).**

5.4 PATH COEFFICIENT ANALYSIS:

The estimation of correlation indicates only the extent and nature of association between yield and its components, but does not show the direct and indirect effects of different yield attributes on yield. Fruit yield is dependent on several characters which are mutually associated; these will in turn impair the true association existing between a component and fruit yield. A change in any one component is likely to disturb the whole network of cause and effect. Thus each component has two paths of action viz., the direct influence on fruit yield, indirect effect through components which are not revealed from the correlation studies. Direct or indirect effects are categorized as follows, negligible **(0.00-0.09), low (0.10-0.19), moderate (0.20-0.29), high (0.30-0.99) and very high (>1.00)** by **Lenka and Mishra (1973).**

The traits like number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, pericarp thickness, average fruit weight and number of seeds per fruit exhibited positive direct effects on fruit yield and these traits also recorded positive correlation with yield. This suggested that direct selection based on these traits will be rewarding for crop yield improvement and similar results were also reported in tomato by **Prasad and Rai (1999), Singh *et al.* (2003), Prasanth *et al.* (2007), Singh *et al.* (2007), Singh (2007), and Singh *et al.* (2008).**

At both phenotypic and genotypic level number of primary branches per plant had negligible positive direct effect on per plant fruit yield. Number of flower clusters

per plant showed negligible positive direct effect at phenotypic level where as at genotypic level it showed low positive direct effect on the fruit yield. At both genotypic and phenotypic level, number of fruits per plant recorded high positive direct effect on fruit yield. Average fruit weight showed high positive direct effect on fruit yield per plant at both phenotypic and genotypic level.

Number of fruits per plant showed positive indirect effect through the characters like plant height, number of primary branches per plant, number of flower clusters per plant and fruit width. Similarly, number of flower clusters per plant exhibited positive indirect effect towards yield through number of primary branches per plant and number of fruits per plant. Again fruit length showed high positive indirect effect through average fruit weight on fruit yield. Fruit width also exhibited high indirect positive effects on fruit yield. Pericarp thickness showed high positive indirect effects via. Average fruit yield at both phenotypic and genotypic level respectively for fruit yield. This suggests that indirect selection based on fruit length, fruit width, pericarp thickness and average weight of fruit will be effective on yield improvement.

The residual effect in phenotypic and genotypic paths was 0.0329 and 0.0272 respectively. It predicted that 67.10 and 72.80 per cent variation in yield at phenotypic and genotypic level respectively had been determined. It further imparted the occurrence of some more factors, not considered here, contributing to fruit yield of tomato.

5.5 GENETIC DIVERGENCE STUDIES:

Assessment of divergence in the germplasm is essential to know the spectrum of diversity so that improvement in fruit yield can be normally attained through involvement of the genetically diverse parents in breeding programs. Mahalanobis's D^2 statistics, a powerful tool has been used to quantify the genetic divergence between the genotypes and to identify diverse parents for crossing. This also helps to relate clustering pattern with the geographical origin. This technique has been employed widely to resolve divergence at inter varietal, species and sub species levels in classifying problems in crop plants.

In the present investigation 68 genotypes of tomato were classified into groups based on days to 50% flowering, plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, pericarp thickness, number of locules per fruit, average fruit weight, number of seeds per fruit, fruit yield per plant, fruit yield per hector and shelf life. The presence of considerable variation in the introduced and indigenous lines and their grouping into different clusters would aid in breeding program involving hybridization and selection as hybrid between lines of diverse parents generally display greater heterosis then those between closely related strains **(Singh and Singh, 1993)**. The great deal of germplasm indicates better chances for future development.

Analysis of variance between cluster means indicated significant difference in respect of all characters. On the basis of D^2 values, 68 genotypes were grouped into 9 clusters. Cluster I had the largest number of twenty seven genotypes followed by twenty one genotypes in II, six in cluster IV, five in cluster III, four genotype in cluster V, two in cluster VIII and one each in cluster VI, VII and IX.

The data of the cluster means for different characters (table) indicated the wide difference between cluster means. Highest mean values for number of primary branches per plant, number of clusters per plant, average fruit weight, yield per plant and yield per hector, were observed in cluster VIII. A highest mean value for number of seeds per fruit was observed in cluster V. The lowest mean value for days to 50 per cent flowering was observed in cluster VII. Highest mean values for plant height and number of fruits per plant were obtained in cluster IV.

Inter and intra cluster distance (D) were computed for nine clusters and presented in table 4.7. The maximum and minimum intra cluster distances were observed in cluster VIII and cluster VI, VII and IX respectively. Inter cluster distance was obtained minimum between cluster I and VI, while it was maximum between cluster III and VIII. The larger inter cluster distance were observed between III and VIII followed by II and VIII, VIII and IX and VI and VIII.

Contribution of different plant character for genetic divergence is important for the purpose of further selection and choice of parents for hybridization. The maximum contribution was by number of fruits per plant followed by average fruit weight, plant

height, number of primary branches per plant, fruit length, yield per hectare, fruit yield per plant, fruit width, number of flower clusters per plant, number of seeds per fruit, shelf life, number of locules per fruit, pericarp thickness, and days to 50% flowering.

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Summary & Conclusion

CHAPTER-VI

SUMMARY & CONCLUSION

The present investigation entitled “Interrelationship and Genetic divergence in tomato (*Lycopersicon esculentum* Mill.)” was carried at Vegetable Research Farm of Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh during *rabi*, 2009-2010.

The experimental material comprised of 68 tomato genotypes, maintained at Department of Horticulture, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The crops of different genotypes were raised in randomized block design with three replications. Observations were recorded on fourteen characters *viz*, days to 50% flowering, plant height (cm), number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length (cm), fruit width (cm), pericarp thickness (mm), number of locules per fruit, average fruit weight (g), number of seeds per fruit, fruit yield per plant (kg), fruit yield per hectare (q/ha) and shelf life. The data obtained during the course of study were analyzed statistically to work out mean performance of the genotypes, range for various traits, phenotypic and genotypic coefficient of variation, heritability, genetic advance/genetic gain, correlation coefficient, path coefficient analysis and genetic divergence.

A wide range of variability along with estimates of genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) recorded for plant height, number of branches per plant, number of flower clusters per plant, number of fruits per plant, pericarp thickness, number of locules per fruit, average fruit weight, number of seeds per fruit, fruit yield per plant, fruit yield per hectare and shelf life indicating the scope for selection of suitable initial breeding material for further improvement. High value of heritability coupled with high GCV and genetic gain were observed for shelf life, plant height, number of branches per plant, number of flower clusters per plant, number of fruits per plant, pericarp thickness, number of

locules per fruit, average fruit weight, number of seeds per fruit, fruit yield per plant and fruit yield per hectare which might be assigned to additive gene action conditioning their expression and phenotypic selection for their amelioration could be brought about by simple methods. The difference between PCV and GCV values were low, indicating that the traits under study were less influenced by environment and these characters could be improved by following phenotypic selection.

Correlation analysis showed that yield per plant was positively and significantly correlated with plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, pericarp thickness, number of locules per fruit and average fruit weight. The average fruit weight was positively correlated with fruit length, fruit width, pericarp thickness and number of locules per fruit whereas average shelf life is significantly negatively correlated with days to 50% flowering. Direct selection based on these traits could result in simultaneous improvement for aforesaid traits and fruit yield in tomato.

Path coefficient analysis showed that the average fruit weight was the most important yield contributing trait followed by the number of fruits per plant pericarp thickness and number of flower clusters per plant. Average fruits per plant and number of fruits per plant exhibited positive direct effects on fruit yield and these traits also recorded positive correlation with yield. This suggested that direct selection based on these traits will be rewarding for crop yield improvement. Pericarp thickness, fruit length and fruit width showed high positive indirect effect through average fruit weight on fruit yield. Number of primary branches per plant and number of flower clusters per plant exhibited low indirect positive effect through average fruit weight on yield. This suggested that indirect selection based on the characters like pericarp thickness, fruit length, fruit width, number of primary branches per plant and number of flower clusters per plant will be effective in yield improvement.

All the 68 tomato genotypes were classified into 9 clusters. The presence of considerable variation in the lines and their grouping into different clusters would aid in breeding program, involving hybridization and selection as hybrid between lines of diverse origin which generally displays greater heterosis than those between closely

related strains **(Singh, 1983)**. Analysis of variance between clusters means indicated significant difference in respect of all characters. Cluster I had the largest number of twenty seven genotypes followed by twenty one genotypes in II ,six in cluster IV, five in cluster III, four genotypes in cluster V, two in cluster VIII and one each in Cluster VI, VII and IX. Maximum and minimum intra cluster distance was observed in cluster VIII and cluster VI, VII and IX respectively. Inter cluster distance was obtained minimum between cluster I and VI (1246.57), while it was maximum (9573.80) between cluster III and VIII. Highest mean values for yield per plant and yield per hectare were observed in cluster VIII. Highest mean values for fruit weight, number of branches per plant and number of flower clusters per plant were observed in cluster VIII. Cluster VII was earliest in flowering.

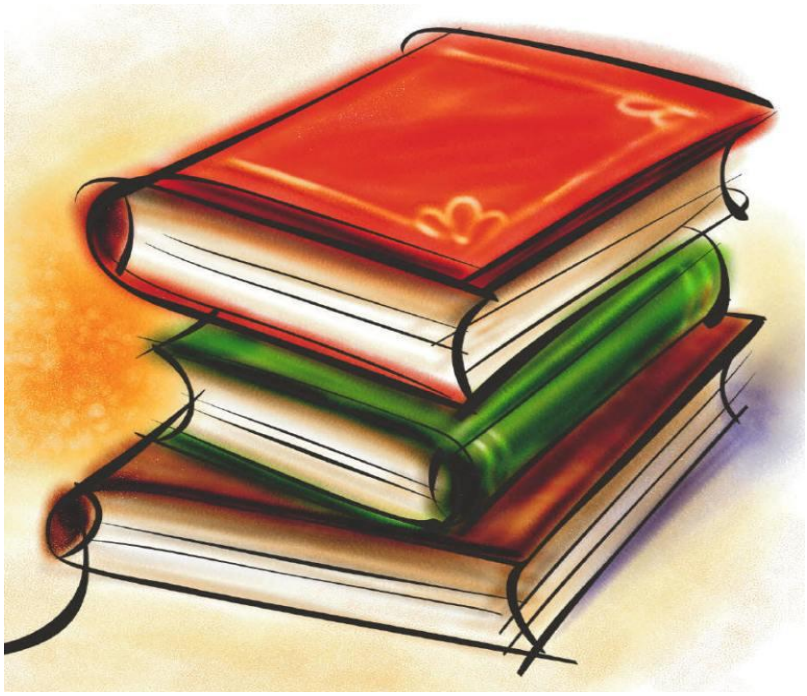
Based on results obtained in the present study, following are the main attributes for yield improvement in tomato:

1. Correlation and path coefficient analysis showed that the average fruit weight, number of fruits per plant, pericarp thickness and number of flower clusters per plant were the most important yield contributing traits in tomato.
2. On the basis of mean performance of the genotypes among the different traits studied, the following were identified as promising lines *viz*., KS-229-1, RCMT-2-1, Pant T-7, IC-177371, DVRT-2, FLA-7171, LCT-9-4, CTS-05-05-2 and Sel-7.
3. Genetic divergence among 68 genotypes revealed that the genotypes *viz*., Pant T-7, IC-177371, VTG-88, NUN-4, DT-10 and RCMT-2 were identified as genetically divergent for plant height and hence, these genotypes can be utilized as donor parents for improving plant height. Punjab Kesari can be utilized as a donor for earliness in flowering. LCT-9-4, DVRT-2, Kashi Amrit (DVRT-1), and LCT-9-4 are the genotypes which can be taken as donor parents for producing tomatoes mainly for seed purpose.
4. The genotypes *viz*., KS-229-1 and RCMT-2-1 can be taken as the most preferable donor for number of primary branches per plant, number of flower

clusters per plant, average fruit weight and fruit yield. CTS-05-05-2 can be used for improving shelf life.

5. LCT-9-4, DVRT-2, Kashi Amrit (DVRT-1), and LCT-9-4the genotypes which can be used as better parent for increasing fruit length while the genotypes KS-229-1 and RCMT-2-1 are good donor to increase fruit width. Varieties belonging to cluster II can be used as donor parents for producing a variety having less number of locules per fruit.

It is concluded that the yield improvement in tomato can be achieved, by considering all the above said genotypes through selection and hybridization program.



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CHAPTER-VII

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