"EVALUATION OF CHERRY TOMATO *(Solanum lycopersicum* L. var. *cerasiforme)* IN CHHATTISGARH PLAINS"

M.Sc. (Ag.) THESIS

by

KIRAN KUMAR

DEPARTMENT OF HORTICULTURE

COLLEGE OF AGRICULTURE

INDIRA GANDHI KRISHI VISHWAVIDYALAYA

RAIPUR (C.G.)

2014

"EVALUATION OF CHERRY TOMATO (*Solanum lycopersicum* L. var. *cerasiforme*) IN CHHATTISGARH PLAINS"

Thesis

Submitted to the

Indira Gandhi Krishi Vishwavidyalaya, Raipur

by

KIRAN KUMAR

IN PARTIAL FULFILLMENT OF THE
REQUIREMENTS FOR THE
DEGREE OF

Master of Science
in
Agriculture
(HORTICULTURE)

ROLL NO. 15501 **ID NO. 112508020**

JULY, 2014

CERTIFICATE – I

This is to certify that the thesis entitled **"EVALUATION OF CHERRY TOMATO *(Solanum lycopersicum* L. var. *cerasiforme)* IN CHHATTISGARH PLAINS"** submitted in partial fulfillment of the requirements for the degree of **"Master of Science in Agriculture" (Horticulture)** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **KIRAN KUMAR** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma (certificate awarded etc.) or has been published/published part has been fully acknowledged. All the assistance and help received during the course of the investigation has been duly acknowledged by him.

Date: 22/7/14

Dr. Jitendra Trivedi 22/7/14
Chairman
Advisory Committee

THESIS APPROVED BY THE STUDENTS ADVISORY COMMITTEE

Chairman : (Dr. Jitendra Trivedi) 22/7/14

Member : (Dr. Dhananjay Sharma) .....

Member : (Dr. Girish Chandel) 22/7/14

Member : (Dr. R.R. Saxena) .....

CERTIFICATE – II

This is to certify that the thesis entitled **"EVALUATION OF CHERRY TOMATO *(Solanum lycopersicum* L. var. *cerasiforme)* IN CHHATTISGARH PLAINS"** submitted by **KIRAN KUMAR** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur, in partial fulfillment of the requirements for the degree of **"Master of Science in Agriculture"** in the **Department of Horticulture** has been approved by external examiner and student's Advisory Committee after oral examination.

Date : 30.8.14

EXTERNAL EXAMINER

Major Advisor .....

Head of the Department .....

Dean/Dean Faculty .....

Director of Instructions .....

ACKNOWLEDGEMENT

No work can be turned as a one-man show. It needs the close co-operation of friends and colleagues and the guidance of experts in the yield to achieve something work while and substantial. This is not just to follow the custom of writing acknowledgement but also to express and record my heart full feeling of gratefulness to all and those who directly or indirectly helped me in this work.

My first and foremost gratitude to the ALMIGHTY GOD with soulful respect, I bow down my head to Him, who gave me strength and courage to carry out my work.

"Education plays vital role in personal and social development and teacher plays a fundamental role in imparting education. Teachers have crucial role in shaping young people not only to face the further with confidence but also to build up it with aim and responsibility. There is no substitute for teacher pupil relationship".

I am glad to express my deep sense of heart gratitude to my Hon'ble guide and Chairman of my Advisory Committee Dr. Jitendra Trivedi, Astt. Prof., Department of Horticulture, IGKV, Raipur (C.G.). whose help and support, complete involvement, invaluable guidance and encouragement and critical analysis of my results to complete this project and gain preliminary knowledge of research and management of time and resources. I am sincerely thankful to him for his meticulous efforts devoted towards my research work even in the midst of his busy schedule.

I am highly indebted to member of my advisory committee Dr. Dhananjay Sharma, Scientist, Department of Horticulture for his inspiring guidance, constructive criticism and timely advisement during the entre course of investigation and preparation of manuscript and providing necessary infrastructure and resources to accomplish my research work. I am very much thankful to him for picking me up as a student at the critical stage of my M.Sc. and Dr. Girish Chandel , Professor, Department of Plant Molecular Biology and Biotechnology, for his able guidance, encouragement, valuable suggestions, generosity and affection in my research investigation .

I am greatly thankful to Dr. R.R. Saxena, Professor Department of Agricultural Statistics and Social Science (L.), for their critical suggestion and regular encouragement during tenure of my investigation.

I have immense pleasure in expressing my whole heart thanks to Dr. S. N. Dikshit, Professor and Head, Department of Horticulture, for providing all the facilities and help as well as of his valuable suggestions.

I am highly obliged to Hon'ble Vice Chancellor, Dr. S. K. Patil, Shri K. C. Painkra, Ragistrar, Dr., S. S. Shaw Director of Instructions, IGKV, Raipur, Dr. J.S. Urkurkar Director Research Services and Dr. S. R. Patel, Dean, College of Agriculture, IGKV Raipur and for providing necessary facilities to conduct the present investigation.

I feel honored to express my sincere thanks to all my teachers Dr. H.G. Sharma, Dr. Neeraj Shukla, Dr. Jitendra Singh, Dr. Pravin Kumar Sharma, Dr. Guarav Sharma, Shri G.L. Sharma, Shri T. Tirkey, Dr. Amit Dixit, Dr. G.D. Sahu and other technical and non-technical staff members Shri T.S.Harinkhere, Vijay,

Gautam, and Purshottam of the Department of Horticulture, IGKV, Raipur for their help, affectionate encouragement and useful suggestions during the tenure of this investigation.

I am greatly thankful to Dr. Suinl Nair Scientist, Department of Genetics and Plant Breeding for his help

I would like to express my sincere gratitude to Dr. M. Pandey (Librarian, Nehru Llibrary, Raipur) and Shri U.K, Watti for giving me their kind help during my present study.

It is my honour and privilege to express my gratitude to my senior Shri Vikrant Kumar Sahu, Ph.D Scholar, Deppt. Of Plant Molecular Biology and Biotechnology, for their help and guidance.

I am also thankful to my senior Dr. Jitendra Tiwari, Mayank baghel, Shiv vijay singh, Kanhaiya patel , Hitendra Meshram,Fanindra Patel, Deepika Candravansi, Bavesh Patel, Kavach Bhagat, Ajay Srivash, Sandip Painkra, Chandres Dhurwe, Kamlesh Diwan.

There are many friend and well wishers who helped me in various ways towards the present Study and they deserve my sincere thanks. Among them my special thanks to my batch mates and friends Mithalesh,Varsha, Diklesh, Ishu, Pawan, Naveen, Vandana, Disha, Abhi, Indra, Deepak, Narayan, Sadhna, Hariom, Okesh, Naresh, Savita, Padmakshi, Patram, Purnendra, Nanak, kousal, Srinkhala, Omesh, Ruchi, Sasmita, Nutan, Prathyusha, Nithish, Dikesh for their true help and Support and I am also thankful to my Juniors Lokesh, Suman, Sekhar, Akash, Bhujendra, Laxmi, Puja, Lekhraj, Pundas.

Words can hardly express the heartfelt gratitude to my beloved father Sri A.R. Nagraj, mother Smt.Usha Bai Nagraj my beloved grandmother Bisahin Bai Nagraj, my elder brother Arun Nagraj, and My younger brother Pankaj Nagraj, Sweet Sister-Jija ji Smt. Babita Sinha - Sri Sudama Sinha, my brother's son Gourav, my sister's children Mahi and Devashish and other beloved family members whose selfless love, filial and silent blessing were the source of my inspiration, encouragement and appreciation that opened the gate and pave that way to my higher studies and made my path easier.

These words are small acknowledgment but never fully recompensed for their great help and co - operation to convert my dreams in practical in this manuscript. Finally I would like to convey my cordial thanks to all those unmentioned persons who have directly and indirectly helped me to reach up to this level in my life.

(KIRAN KUMAR)

Department of Horticulture

College of Agriculture, I.G.K.V. Raipur (C.G.)

Date:

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

LIST OF ABBREVIATIONS

Abbreviations	Description
%	Per cent
@	At the rate
^{0}C	Degree Celsius
CD	Critical difference
Cm	Centimeter
CV	Coefficient of variation
Df	Degree of freedom
et al.	And others/ Co- workers
Fig.	Figure
FYM	Farm yard manure
G	Gram
GA	Genetic Advance
GCV	Genotypic coefficient of variation
Ha	Hectare
Hrs	Hours
h^2	Heritability
i.e.	That is
Kg	Kilogram
m^2	Square meter
MT	Million tonne
NPK	Nitrogen, Phosphorus and Potassium
PCV	Phenotypic coefficient of variation
Q	Quintal
RBD	Rendomized block design
var.	variety
via.	Through
viz.	For example
µl	Micro liter
bp	Base pair
L	Ladder

INTRODUCTION

CHAPTER-I

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most widely grown and economically important vegetables in the world. It belongs to the large and diverse *Solanaceae* family, also called Nightshades which includes more than three thousand species. It is a very versatile vegetable for culinary purposes. Ripe fresh tomato fruit is consumed fresh as salads and consumed after cooking and utilized in the preparation of range of processed products such as puree, paste, powder, ketchup, sauce, soup and canned whole fruits. Unripe green fruits are used for preparation of pickles and chutney. The crop is rightly known as an industrial crop because of its outstanding processing quality. There are several species of tomato but the fruits are edible only of two species namely, *S. lycopersicum and S. pimpinellifolium*. All the species of tomato are native of Western South America (Rick *et al*., 1976).

Tomato is grown worldwide with annual production of 159 million tonnes (Anon, 2011). China is the leading producer which accounted for 30 % of the global tomato production with 50 million tonnes production and it is about one quarter of the global output, followed by India. In India it was introduced in the 17th century by Europeans and today it has become part and parcel of Indian food besides becoming one of the leading vegetables with lot of research work and outcomes. India stands second position in tomato producing countries of the world accounted 10 % production (17.5 million tonnes) with an area of 8.79 million hectares and 18.22 million tonnes production, average productivity 20.7 tonnes per hectare (Anon, 2012-13). In India, Andhra Pradesh state occupies 1st position with 6.0 million tonnes production whereas Chhattisgarh state occupies 9th position with an area of 0.047

million ha having production of 0.76 million tones, average productivity 15.9 tonnes per hectare (Anon, 2013).

Cherry tomato is regarded as a botanical variety of the cultivated tomato, *Solanum lycopersicum* L.var.*cerasiforme* with small fruits (1.5 - 3.5 cm in diameter) on long panicles and the demand for cherry tomato has increased in the market, chiefly due to the recognition of their high quality and good taste (Kobryn and Hallmann, 2005). Cherry tomatoes are good source for providing disease resistance and adaptability to cool and hot seasons. They has become more popular all over the world because of its favorable characteristics such as good source of vitamin A and C, sugars, taste and low calories and fruit set even at high temperature (Prema *et al*., 2011) and are also beneficial to human health because of its high content of antioxidant and phytochemical compound, including lycopin, ß carotene, flavonoids, vitamin C and many essential nutrients (Rosales *et al*., 2011). In general with ever increasing demand it has become imperative to develop high yielding varieties with resistance to biotic and abiotic stresses and suitable to fresh market and processing. Therefore, potential value of cherry tomatoes has to be improved by evaluating the cultivated species for its desirable characters under various agro climatic regions.

The cherry tomatoes are widely used in salads, as an appetizer or as garnishing. In order to incorporate desirable characters to maximize marketable yield, the information on the nature and extent of genetic variability in a population of cherry tomato for desirable characters must improve.

Considering the potentiality of this crop, there is a need for improvement and to develop varieties suited to specific agro-ecological conditions and also for specific end use. A thorough knowledge regarding the amount of genetic variability existing for various characters is essential for initiating the crop improvement programme.

Breeding to enhance tomato with higher yield, tolerance to biotic and abiotic stresses, and better nutritional quality is a continuous process that aims to meet the demands of producers and consumers. Breeding efficiency in tomato has been improved by using molecular markers to tag and transfer useful alleles from germplasm to elite cultivars (Foolad, 2007). However, there is a lack of sufficient polymorphic markers between closely related tomato species and within cultivars of the same species because the majority of molecular markers were developed based on polymorphisms between domesticated tomato and its wild relatives (Tanksley *et al*., 1992; Fulton *et al*., 2002; Frary *et al*., 2005).

The scope of improvement is more in tomato which is based on the extent of genotype and phenotype variability present in the population. Greater the diversity in the material and greater are the chances for selection to the get desired types.

The estimates of different genetic parameters and the association of different characters are important for better understanding of the nature and the magnitude of genetic variability present in the breeding material. As we know that, the yield is a complex character being influenced by various component factors. Knowledge of inter-relationship among these factors is necessary for indirect selection of higher fruit yielding genotypes by giving appropriate emphasis for each of these characters.

Genetic diversity in the wild tomato species has been studied using various marker techniques. Simple sequence repeat (SSR) markers are often the preferred molecular markers for the purpose of marker-assisted plant breeding when they are available, because the SSR markers possess properties suitable for high-throughput genotyping, such as high reproducibility, co-dominance nature, multi-allelic variation, simplistic assay, low distributing cost and easy automation (Edwards and McCouch, 2007).

The genetic improvement of cherry tomato mainly depends upon the amount of genetic variability present in the population for yield and yield contributing characters. The best diverse genotypes having desirable characters with maximum variability identified could be included in hybridization programme for crop improvement.

In Chhattisgarh, good amount of variability is present for fruit size, fruit weight, colour, flowering behavior, plant habit, stem length, no. of branches, no. of fruits per cluster, and other morphological traits, which provides a greater opportunity in cherry tomato crops to select high yielder and better quality attributes. Greater the diversity in the genotype and greater are the chances for selection to the get desired types. The information on the nature and degree of genetic divergence for fruit characters would help in choosing the right parent for the development of variety with improved desirable genotype of cherry tomato.

Looking to the above facts, the present investigation "Evaluation of cherry tomato (*Solanum lycopersicum* L.var. *cerasiforme*) in Chhattisgarh plains" was undertaken with the following objectives –

1. To evaluate suitable cherry tomato genotype for Chhattisgarh plains.
2. To workout genetic divergence in cherry tomato genotype.
3. To assess genetic variability, heritability and genetic advance for various quantitative character.
4. To estimate association in between fruit yield and yield contributing characters in cherry tomato.
5. Characterization of cherry tomato genotype using DNA markers.

REVIEW OF LITERATURE

CHAPTER -II

REVIEW OF LITERATURE

"Evaluation of cherry tomato *(Solanum lycopersicum* L. var. *cerasiforme)* in Chhattisgarh plains" the review of literature concerning to the studies conducted for this study is outlined under the following headings:

2.1 Genetic divergence and molecular diversity analysis

2.2 Genetic variability

2.3 Heritability

2.4 Genetic advance

2.5 Correlation studies

2.6 Path coefficient analysis

2.1 Genetic divergence and molecular diversity analysis

2.1.1 Genetic divergence

The assessment of genetic diversity using quantitative traits has been of prime importance in many contexts particularly in differentiating well defined populations. The concept of D^2 statistics was originally developed by P.C. Mahalonobis (1936). Then C.R. Rao (1952) suggested the application of this technique for the arrangement of genetic diversity in plant breeding. This method is widely used in self and often cross pollinated crops to establish relationship between genetic divergence of parental types and other populations. Now, this technique is extensively used in vegetable breeding for the study of genetic divergence in the various breeding material

including germplasm. This analysis also helps in the selection of diverse parents for the development of hybrids.

Sachan and Sharma (1971) evaluated 7 varieties from U.S.A, 5 from India, 3 from Australia, 2 from Holland and 1 each from England, Switzerland and Russia by using D^2 analysis and grouped into 4 clusters. The observations demonstrated substantial divergence of an indigenous material 'Jaipuri' from both exotic and indigenous stocks and established its utility for hybridization. Genetic divergence was not found to be related with geographic diversity in this crop. The traits like stem length, number of branches, number of inflorescence and number of fruits per plant accounted for total divergence.

Gadekar *et al*. (1992) evaluated 38 strains of tomato for genetic diversity and grouped them into 8 clusters irrespective of geographical divergence, indicating no parallelism between geographical and genetic diversity. The characters like plant height, number of branches per plant, single fruit weight, and number of fruits per plant, number of seeds per fruit and fruit yield per plant played an important role in divergence between the populations.

Alice-Kurian and Peter (1994) reported that genetic diversity in a population of 64 tomato lines assessed using D^2 value indicated considerable diversity and were grouped into eight clusters with a maximum contribution to total genetic divergence made by locules per fruit.

Sharma and Verma (2001) used 18 genotypes of tomato for genetic divergence studies. The genotypes were grouped into 9 clusters irrespective of genetic diversity and geographical divergence. The character of fruit yield per plant played an important role in divergence between the populations.

Parthasarathy and Aswath (2002) evaluated 23 genotypes of tomato during summer and rainy season. There was considerable diversity among genotypes for morphological characters and plant height, number of fruits and fruit size contributed to the divergence. *L. pimplinellifolium* was the most divergent among genotypes. Crosses involving IIHR-1872, Pant Bahar, L-964 and L-154 with Arka Alok, Arka Abha, Floradude and LE- 79 were recommended for improvement of yield and better size.

Arun *et al*. (2003) studied the nature and magnitude of genetic divergence in 73 tomato genotypes of different origin for quantitative characters and grouped genotypes into 15 clusters indicating the presence of wide range of genetic diversity among the genotypes. The mean fruit yield per plant (1034 g/plant) and average fruit weight (102.76 g) were highest in cluster V and III respectively. The plant height (135.91 cm) was maximum in cluster XV, while cluster VI consisted of highest number of fruits per cluster (4.90).

Shashikanth (2008) grouped 30 genotypes into 10 clusters using Mahalanobis D^2 statistics method. Cluster I had 17 genotypes, cluster II had 3 genotypes, cluster IV and V had 2 genotypes each, while remaining were solitary. The D^2 value ranged from 18.56 between Cluster III and VI to 67.68 between cluster VIII and X, indicating the existence of wide genetic variability. It is desirable to select accessions from the clusters having high intercluster distance. Intra cluster distances were highest (16.47) in the cluster I and lowest (9.97) in cluster IV.

Mehta and Asati (2008) studied genetic divergence analysis using Mahalonabis D^2 statistic in twenty two tomato determinate genotypes. These genotypes were grouped into six clusters based on sixteen important fruit characteristics. The cluster-I was the largest containing seven genotypes followed by

cluster-III with six genotypes. The diversity among the cultivars was measured by inter-cluster distance. The higher order of divergence was recorded between cluster II and V which was adequate for improvement of tomato by hybridization and selection.

Singh *et al.* (2008) reported forty eight genotypes of tomato for their genetic divergence using Mahalanobis D^2 statistics in eight clusters. Maximum genotypes were grouped in cluster I and II (10 in each), the remaining 28 genotypes were distributed in six clusters, six each in cluster III, IV and V, five in cluster VI, four in cluster VII and one genotype in cluster VIII indicated that there was no association between geographical distribution of genotypes and genetic divergence. The mean intra and inter cluster distance (D) revealed that cluster V had highest intra cluster distance (2.12), while the inter cluster distance was maximum between cluster VIII and III (6.79). The characters like number of fruits per plant, average fruit weight, plant height and fruit yield (q/ha) contributed maximum to genetic divergence.

Yashvant kumar (2008) grouped 70 genotypes into seven different clusters using Mahalanobis D^2 statistics method. Cluster I had 37 genotypes, cluster II had 23 genotypes, cluster III and IV had five and two genotypes respectively, while remaining clusters were solitary. The D^2 value ranged from 189.935 between cluster V and VI to 1484.249 between cluster I and V, indicating the existence of wide genetic variability.

Emami and Eivazi (2013) studied cluster analysis classified genotypes in two groups. Flower inflorescence had the most significant regression coefficient (0.63) with fruit yield. Two first components explained 97% of total variations in principal components analysis.

Reddy *et al*. (2013a) studied nineteen exotic collections of tomato for genetic divergence analysis by following Mahalanobis D^2 statistics test for eighteen quantitative characters. Appreciable diversity within and between the clusters was observed. The characters fruit weight, number of fruits per plant and plant height were the potent factors in differentiating the germplasm of tomato.

2.1.2 Molecular diversity analysis

The analysis of genetic variation or diversity in plants has been conventionally assessed by analysis of morphological or biochemical traits. The evaluation of phenotype may not be a trustworthy measure of genetic difference because of the influence of environment on gene expression. The analysis of plant DNA allows the direct assessment of diversity in genotypes at molecular level. The reviews pertaining to molecular diversity are presented below.

2.1.2.1 Assessment of molecular diversity using RAPD

Archak *et al*. (2002) analyzed genetic diversity of 27 tomato cultivars grown in India with RAPD markers, generated by 42 random primers. The overall high levels of pair wise similarity and low levels of marker diversity implied the existence of limited genetic variation in the investigated material. Interestingly, old introductions and locally developed cultivars of the 1970s exhibited significantly greater genetic variation than the ones released during the 1990s indicating the reduction in the genetic diversity among modern tomato cultivars which may be attributed to the recent trend towards breeding for similar plant and fruit characteristics.

Kochieva *et al*. (2002) used RAPD genetic analysis for 53 species and cultivars of the genus Lycopersicon which revealed high genetic polymorphism in

population. The study revealed that the intraspecific polymorphism was maximum (79%) in *L. peruvianum* and minimum (9%) in *L. parviflorum*. In general, genetic divergence among cross pollinating tomato species was substantially higher than in self-pollinating species.

Goncalves (2008) studied the genetic divergence among 78 tomato accessions, based on 74 RAPD markers. Correlation between the molecular profile and 27 morphological and agronomic data was performed. Cluster analysis resulted in 13 groups that were correlated with five descriptors (growth habit, leaf type, fruit color, locule number, and fruit shape). Some groups had particularities, such as group IV that assembled accessions with pear shape fruits; group IX, which gathered accessions with potato leaf type, which suggests that for a wise use of the germplasm bank accessions, both characterization, molecular and morphoagronomic, should be carried out.

Salunke *et al.* (2012) conducted an experiment in tomato for diversity analysis using RAPD markers, genetic diversity in thirty tomato genotypes was analyzed by RAPD markers generated by 23 random primers. The amplification profile consisted of 202 fragments of size ranging from 174 bp to 3650 bp of which 39 were monomorphic and 163 were polymorphic with 80.69 % polymorphism. The number of bands generated by each primer varied from 4 (OPM-18) to 13 (OPK-04) with an average of 8.78 fragments per primer. The percentage of polymorphic bands with different primers ranged from 40 to 100 %. The efficiency of RAPD marker for cultivar identification was found 2.97 % as only six fragments are cultivar specific. Orange fruited genotype NBC showed three unique fragments, OPK 03-968 bp, OPL 17-322 bp and OPM 12-2349 bp. The similarity coefficients detected by RAPD ranged from 0.63 to 0.96 which revealed existence of limited genetic variation among

tomato genotypes. The consensus tree constructed showed three major clusters. First cluster comprise of 16 genotypes, second cluster of 13 genotypes and the red fruited tomato genotype M-1-2B formed third independent cluster. The RAPD technology proved useful in describing genetic diversity among tomato genotypes.

Naz *et al.* (2013) conducted an experiment in tomato for assessment of genetic diversity of tomato using RAPD markers, all tomato accessions were analyzed by molecular parameters. A total 25 RAPD decamer primers were selected for the genetic analysis of all tomato accessions. Only 15 polymorphic RAPD primers were accessed for the genetic distance calculation to find out the phylogenetic relationship among 25 tomato accessions under study. A total of 130 loci were generated out of which 98 were polymorphic by 15 primers with 05-14 loci/primer having fragment's size range from 400 to 2500 bp maximum. The Nie and Lie's Coefficients was used to calculate the genetic similarity. The extent of genetic diversity and construction of phylogenetic tree was done by DNAMANN software. The average genetic similarity observed across all the genotypes was 75.6% with 24.4% polymorphismin 25 tomato accessions. Although RAPD study supports the morphological characters but not upto 100%.

Sharifova *et al.* (2013) conducted an experiment in tomato using Random Amplified Polymorphic DNA (RAPD) analysis on 19 Azerbaijan tomato genotypes including both cultivars and local populations. A total of 26 amplified products were revealed by 6 primers. The genetic similarity among evaluated genotypes ranged from 0.188 to 1.000. The lowest similarity was observed between cultivars 'Azerbaijan' and 'Shakar' (0.188), while the highest between 'El-nur' and 'Garatag' (1.000). The Unweighted pair group method with arithmetic mean (UPGMA) cluster analysis based on Jaccard's similarity coefficient divided genotypes into four main groups.

The first group was the largest and consisted of 12 genotypes, while the fourth group was the smallest consisted of 1 genotype only. The most polymorphic primer was OPB-18 that presented a genetic diversity index of 0.823, while the least informative was primer OPG-17 with an index of 0.349. The average genetic diver-sity calculated from RAPD data was 0.665.

2.1.2.2 Assessment of genetic diversity using SSR (Simple sequence repeats) markers

Rajput *et al*. (2005) conducted an experiment in tomato for reproducibility testing using RAPD and SSR markers in which the reproducibility of two popular molecular marker techniques was examine. Random-amplified fragment length polymorphism (RAPD) and sequence-tagged micro satellites (SSR). For each technique, an optimal system was chosen, which had been standardized and routinely used by one individual. The results obtained were compared with those of the original generator or sender. Different experiences were gained in the exchange experiment with the different techniques. RAPDs proved difficult to reproduce. Whilst SSR alleles were amplified, but small differences in their sizing were obtained.

Grushetskaya *et al.* (2007) conducted an experiment in tomato for mapping of *Cf-6* Tomato leaf mould resistance locus using SSR markers, the *Cf-6* locus of tomato conferring resistance to the Belarus population of the leaf mould causative agent was mapped to the chromosomal region, located 2.2 and 3.4 cM apart from the microsatellite markers, SSR128 and SSR48, respectively. It was demonstrated that the *Cf-6* gene, like the *Cf-2/Cf-5* cluster, was located on the short arm of tomato chromosome 6. However, *Cf-6* differed from these genes concerning phytopathology and molecular characteristics. Based on the *Cf-2* gene sequence, a molecular marker, 2-2C, capable of identification of the *Cf-6*, *Cf-2* , and *Cf-5* loci, was constructed.

Kwon *et al*. (2009) clustered group of varieties, based on the results of SSR analysis, were categorized into cherry and classic fruit type varieties. Almost all of the varieties were discriminated by SSR marker genotypes. The relationship between morphological and molecular data for 33 varieties out of 63 varieties was analyzed using Mantel matrix correspondence test. 'The correlation value between two methods was 0.644. However, SSR based dendrogram topology showed some similar form with morphological traits at the two main groups. Therefore, these markers may be used. wide range of practical application in variety identification and pre-screening for distinctiveness test of tomato varieties.

Subramaniam *et al*. (2010) studied for development of SSR markers pertaining to chromosome 6 from bacterial artificial chromosome (BAC) sequences available at Solanaceae Genomics Network. A total of 54 SSR primer pairs from 17 BAC clones on chromosome 6 were designed and validated. Polymorphism of these loci was evaluated in a panel of 16 genotypes comprising of Solanum *lycopersicum* and its wild relatives. Genetic diversity analysis based on these markers could distinguish genotypes at species level. 21 SSR markers derived from 13 BAC clones were polymorphic between two closely related tomato accessions. A major QTL associated with resistance to bacterial wilt was mapped on chromosome 6 at similar location of the reported Bwr-6 locus. These chromosome 6-specific SSR markers developed in this study are useful tools for cultivar identification, genetic diversity analysis and genetic mapping in tomato.

Mohamed *et al.* (2012a) conducted an experiment in tomato for genetic diversity and DNA fingerprint study using SSR markers, 20 simple sequence repeat (SSR) primers in order to determine genetic identities, genetic diversity and genetic relationships among these cultivars. On an average, 38 alleles were amplified using

SSR primers with scorable fragment sizes ranging from approximately 75 to 275 bp. 23 alleles were polymorphic thus revealing 60.5% of polymorphism. The genetic similarity estimated according to SSR data was scaled between 17.6 and 93.2%, suggesting the potential of SSR markers in discriminating among plants of close or distant genetic backgrounds. Unweighted pair group method with arithmetic mean (UPGMA) clustering grouped the cultivars into two groups where the two Egyptian cultivars Edkawy and Giza 80 were clustered in different group. In addition, clustering was found consistent with the known information regarding growth habit. The genetic distance information obtained in this study might be useful to breeder for planning crosses among these cultivars.

Xiaorong *et al.* (2012) studied that twenty six morphological traits as well as 47 single nucleotide polymorphism and simple sequence repeat markers were used to investigate genetic variation in 67 tomato (*Solanum lycopersicum* L.) varieties collected from Argentina between 1932 and 1974. Approximately 65.0% of the morphological traits and 55.3% of the molecular markers showed polymorphisms in the 67 varieties. Average taxonomic distance between any two varieties ranged from 0.6643 to 1.1776, while Nei's genetic distance varied from 0 to 0.2022. Cluster analysis indicated that 67 varieties could be grouped into three clusters at both morphological and molecular levels. The varieties collected before 1960 had larger genetic variation than those collected after 1960.

Parmar *et al.* (2013) introduce a new SSR marker (TOM-144) which was deduced after evaluation of eight microsatellite loci amongst the twenty-one different tomato cultivars. The marker selected was inherited and segregated in Mendelian fashion as demonstrated in successive generation of a cross between parent cvs. H-24 x GT-2.

2.2 Genetic variability

Variability is the foundation stone for initiating vegetable improvement programme. Study of existing variability amongst available germplasm is foremost step in any crop improvement programme. So, a knowledge of the genetic variability and is components being very useful in designing selection procedure to any variable population.

Rattan *et al.* (1983) reported that the genotypic coefficient of variation was higher for fruit weight, seed percentage, number of fruits per plant, ascorbic acid content, fruit length, fruit breadth, fruit yield per plant, mesocarp thickness, acidity and lowest for juice percentage in tomato.

Trivedi (1996) conducted an experiment on 22 F_1 hybrids/varieties of tomato and reported that the Avinash-2 recorded the highest fruit yield (946 q. per hectare) with yield per plot, number of locules per fruit, fruit diameter and plant height. The maximum average fruit weight and volume of fruit was obtained in Gid Ron. Chunky had showed maximum acidity and juice percent whereas, Red Star was the minimum acidity.

Verma (1996) reported high magnitude of genotypic coefficient of variation for number of locules per fruit, plant height, average fruit weight, fruit length, number of primary branches per plant and pericarp thickness in tomato.

Singh *et al.* (1997) reported that the phenotypic and genotypic coefficient of variation indicated that selection may be made for fruit weight, number of fruit per plant, number of locules per fruit and fruit yield per hectare.

Das *et al.* (1998) reported wide range of variation for almost all the characters. Fruit yield per plant ranged from 1.10 to 2.45 kg with all over mean of 1.83 kg. Fruit

yield per plant, number of fruits per plant, fruit weight, fruit diameter, fruit length and locules per fruit had high estimates of genotypic coefficient of variation.

Prasad and Rai (1999) conducted an experiment on seventyfive exotic genotypes of tomato at Namkum, Ranchi and found considerably high amount of phenotypic and genotypic coefficient of variation for plot yield, plant height, fruit firmness, total soluble solids (TSS) and number of locules.

Brar *et al.* (2000) observed high magnitude of phenotypic coefficient of variation in number of marketable fruit per plant and total number of fruit per plant. The genotypic and phenotypic coefficients of variation were moderate for marketable and total yield per plant. Comparatively low genotypic and phenotypic coefficients of variation were observed for number of fruits per cluster.

Singh *et al.* (2002b) at Ludhiana, conducted an experiment on fifteen heat-tolerant tomato genotypes and reported high phenotypic (PCV) and genotypic (GCV) coefficient of variation for average fruit weight, shelf life of ripe red fruits, total and marketable fruit yield, but were moderate for days from fruit setting to mature green stage and shelf life of mature green fruits. In all the traits, GCV was lower than PCV, indicating the role of the environment in the expression of these characters.

Joshi and Kohli (2003) conducted an experiment in seventy three genotypes at Nauni, Solan, H. P. and recorded maximum value of coefficient of variability for shelf life of fruit, while it was minimum for days to first picking.

Joshi *et al*. (2004) conducted an experiment at Solan, H. P. on thirty-seven tomato genotypes and observed highest coefficient of variation (genotypic and phenotypic) for shelf life.

Kumar *et al.* (2004) conducted an experiment in Uttar Pradesh on thirty tomato genotypes and observed highest genotypic and phenotypic coefficient of variation along with high genetic advance which indicated that it was less affected by the environment and these characters may be improved directly through simple selection.

Karasawa *et al.* (2005) studied genetic divergence among seventy tomato accession at Brazil. A significant variation among the accession was recorded for total number of fruits, total fruit weight, mean number of fruits, mean fruit weight, fruit length, fruit diameter, number of days to germination, number of days to fruit set, number of flower per inflorescence, total soluble solid content, number of locules and number of days to flowering, indicating significant genetic variation among the accessions.

Dhankhar *et al.* (2006) observed the maximum variation for fruit yield followed by number of fruit weight and fruits per plant and were minimum for branches per plant.

Singh *et al.* (2006) at Dholi, Bihar, India evaluated nineteen genotypes of tomato and observed considerable range of genetic variability for fruit yield, quality components along with biochemical characters in the materials under study. Maximum genotypic coefficient of variation was recorded for number of leaves per plant followed by number of fruit clusters per plant.

Hydar *et al.* (2007) at Bangladesh observed maximum genotypic variation was found for fruit weight followed by number of flowers in three clusters per plant and number of fruits in three clusters per plant while the same was minimum for number

of leaves at flowering. Phenotypic variation was also maximum for fruit weight and minimum for number of leaves at flowering.

Mehta and Asati (2008a) conducted an experiment on fourteen genotypes of diverse origin of tomato were analyzed for their yield and various yield contributing characters and estimates of genetic parameters revealed that phenotypic and genotypic coefficient of variation was high for weight of fruit per plant, average fruit weight, number of locules per fruit, number of branches per plant, plant height, number of fruits per cluster, fruit yield per plot and fruit yield per hectare.

Shashikanth (2008) reported that significant variability (GCV & PCV) was seen among 30 tomato genotypes evaluated for 19 quantitative traits. The mean fruit yield per plant noticed was 1.26 kg with a range of 0.67 kg to 2.33 kg.

Ghosh *et al.* (2010) conducted an experiment on F_2 segregating generations of exotic tomato hybrids and observed very little differences were observed between phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) for the traits days to first flowering, fruit length and fruit diameter. They observed that fruit yield per hectare ranged from 347.10 to 625.60 q. with all over mean of 485.56 q.

Hosamani (2010) reported that genotypes had highly significant variation amongst themselves for all the 19 characters in all seasons. High GCV and PCV were observed for plant height, fruits per cluster, fruits per plant, locules per fruit, TSS, fruit length and width; The highest yield in Pant-T-10 followed by H-24, DVRT-2 and VR-35 with fruit yield per plant. Number of fruits per plant was maximum in Arka Vikas followed by PAU-2372 and Dwd-T-11.

Dar and Sharma (2011) conducted an experiment on sixty genotypes of tomato and revealed that magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters under study. The higher values of Phenotypic Coefficient of Variation (PCV) were recorded for yield quintals per hectare, average fruit weight, number of fruits per plant whereas high genotypic coefficients of variation (GCV) was recorded with β-carotene. The maximum fruit yield in EC-521086 followed by EC-538151 and EC-538151/3. The maximum average weight of fruit in VR-415 followed by EC-538151 and maximum number of fruit per plant observed in EC-521067 followed by EC-538151/3 and EC-521041.

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

Mohamed *et al.* (2012b) studied heritability, genetic advance, genetic advanced as percentage over mean and genetic variability among different plant and fruit characters of thirty tomato genotypes showed significant variation among the genotypes for all tested characters.

Prema *et al.* (2011a) studied six cherry tomato genotypes for genetic components such as variability, heritability and genetic advance for growth, yield and quality traits. The analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes from all the characters were studied except the plant height at 60 and 90 DAT. The high PCV and GCV were observed for average fruit weight (g), pericarp thickness of fruit (cm), fruit firmness (kg/cm2), shelf life of fruit

(days), fruit yield per plant (kg), lycopene content (µg/100g), fruit length (cm), TSS of fruit (°Brix) and fruit width (cm).

Tiwari and Upadhyay (2011) conducted an experiment on nineteen genotypes along with two checks of tomato and reported that Arka Vikash recorded the highest fruit yield of 369.99 q. per hectare followed by NDT-9 (365.92 q. per hectare), Pant T-10 and DVRT-2. The maximum plant height observed that the VTG-86 followed by PAU-2374 and VTG-90. The maximum average fruit weight was obtained in Pant T-10; H-24 had showed maximum number of locules per fruit followed by Pant T-11, DVRT-2 and VTG-93.

Buckseth *et al.* (2012) conducted an experiment with 40 genotypes of tomato. The statistical analysis was done according to the methods for genetic coefficients of variation for heritability. The analysis of variance revealed highly significant differences among the genotypes for all the characters studied. However, a close correspondence between GCV and PCV in respect of all the characters indicated that environment has very little influence on the expression of the characters under study.

Manna and Paul (2012) studied genetic variability and characters association of different fruit quality parameters in 15 tomato genotypes grown in a two year field experiments. High and moderate to high GCV and PCV were recorded for number of locules per fruit, fruit weight, total acid (%), number of fruits per plant, vitamin C (mg per 100g), fruit yield per plant, fruit length and pericarp thickness and they observed that fruit yield per hectare ranged from 437.10 to 1285.00 q. with all over mean of 825.30q.

Rahaman *et al.* (2012) evaluated thirty four genotypes of tomato during *Rabi* season of 2006 - 2007 for genetic parameters *viz.,* variability, heritability and genetic

advance. The estimates of PCV and GCV were high for fruit weight followed by fruit length and lowest for number of flowers per cluster and total acid (%). Moderate value (20-30%) of PCV and GCV were recorded for fruits per plant, while, other characters displayed less than 20 per cent. Moderate to low estimates of PCV was recorded against plant height, primary branches per plant, fruits per plant and yield per plant.

Islam *et al.* (2012) observed nine traits of cherry tomato (*Solanum lycopersicum* L.) var. *cerasiforme* (Dunal) A. Gray) inbred lines exhibited a wide range of genetic variability. High genotypic and phenotypic coefficients of variation were obtained for individual fruit weight (68.16 and 74.23%, respectively) followed by number of fruits/plant (58.8 and 68.34%, respectively).

Emami and Eivazi (2013) carried out an experiment in order to evaluate genetic variations of tomato genotypes. Combined analysis of variance showed that for agronomic and quality related traits were significant differences. Selb-Jino, TO2, Early-Urbana, Carmina, Cal-J-N and Falat-Shof with more than 10.5 kg/m2 had the highest fruit yield. With increasing fruit number per plant decreased fruit weight. Carmina had 170cm plant height and indeterminate growth. TO4, Chase, Selb-Jino and Carmina with more than 5.2% had the most total soluble solid.

Kumar *et al.* (2013) carried out an experiment to evaluate the diverse genotypes of tomato. A wide range of variability present in any crop always provides the better chances of selecting desired types. Analysis of variance indicated highly significant differences among the genotypes for all the characters. The highest GCV and PCV were observed with the character fruit yield per plant followed by number of seeds per fruit. Whereas, the lowest GCV and PCV were recorded by the character days to 50% fruiting followed by days to 50% flowering.

Reddy *et al.* (2013b) studied the genetic parameters to elucidate the genetic variability, heritability and genetic advance in tomato (*Solanum lycopersicum* L.) by evaluation of nineteen genotypes of tomato. The genotypes exhibited a wide range of variability for all the characters. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters.

Saleem *et al.* (2013) generated twenty-five F1 hybrids from 5×5 diallel crosses and were evaluated to study the quantitative genetics of yield and some yield related traits during 2009 10. Worth of room was realized for improvement due to highly significant genetic variations among all traits studied. The highest estimates of genotypic and phenotypic coefficients of variability were recorded for number of fruits per plant while fruit width was the most heritable trait.

Shankar *et al.* (2013) computed the genetic variability of twenty four hybrids along with their 11 parents (8 lines and 3 testers) to indicate that genetic material possessed variability which provides sufficient basis for selection by breeder. High estimates of PCV and GCV were obtained for plant height, number of fruits per cluster, average fruit weight, yield per plant, titrable acidity, ascorbic acid and lycopene indicated a good deal of variability in those characters signifying the effectiveness of selection of desirable types for improvement.

Ramzan *et al.* (2014) carried out genetic analysis for yield and its contributing traits in parents and their F1 hybrids in determinate tomato. The study was comprised 15 new crosses (determinate), their parental lines along with international hybrids for primary evaluation. Significant differences were observed for the characters viz; number of fruits per plant, number of clusters per plant, number of fruits per cluster, number of flowers per plant, fruit length (cm), fruit width (cm), plant height (cm) and fruit yield (t/ha). Data was analyzed for genotypic variance, phenotypic variance,

genetic advance, broad sense heritability *(h2bs)*, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV).

2.3 Heritability

The term heritability in broad sense was defined as the ratio of genetic variance to the total phenotypic variance (Lush, 1940; Johnson *et al*., 1955). The estimate of heritability gives indication of the amount of progress expected from selection, as they are most meaningful when accompanied by estimate of genetic advance. Genetic advance is the measure of improvement that can be achieved by practicing selection in a population.

Prasad and Rai (1999) conducted an experiment on seventy five exotic genotypes of tomato at IIVR, Varanasi and observed very high heritability estimates along with high genetic advance for fruit weight, fruit length, fruit breadth and pulp thickness due to additive gene effect.

Brar *et al.* (2000) reported that the heritability estimates were high for number of marketable per fruit, number of fruits per cluster, and number of fruits per plant. The total fruit yield and marketable fruit per plant showed moderate values of heritability.

Naidu (2001) conducted an experiment in 22 genotypes and recorded the fruit volume, fruit weight, acidity, pericarp thickness, juice percent, fruit per cluster, fruit length and number of locules per fruit showed high heritability associated with high genetic advance.

Singh *et al*. (2002b) evaluated fifteen heat- tolerant tomato cultivars in Ludhiana, Punjab and reported high heritability for days to anthesis, days from fruit setting to mature green stage, average fruit weight, total fruit yield, shelf life of

mature green fruits and shelf life of ripe red fruits except days from fruit setting to red ripe stage. The high genetic advance was predicted for average fruit weight, followed by shelf life of ripe fruits.

Mohanty (2002) reported that the evaluation of 18 genotypes of tomato revealed high heritability with genetic advance for average fruit weight, number of branches per plant number of fruit per plant, plant height and days to first harvest which could be improved by simple selection.

Mariame *et al*. (2003) conducted an experiment on twenty one fresh market tomato genotypes and recorded high heritability estimates coupled with high genetic advance as per cent of mean for plant height, number of nodes on main stem, number of flowers per cluster, number of fruits per plant and number of seeds per fruit, which revealed that simple selection may improve these traits.

Joshi *et al*. (2004) evaluated fifteen heat- tolerant tomato cultivars at Ludhiana, Punjab and reported moderate heritability and moderate genetic gain for number of fruits per cluster, fruit length, fruit breadth, number of locules per fruit, whole fruit firmness, ascorbic acid content and plant height indicating additive gene effects. Low heritability and low genetic gain was observed for pericarp thickness.

Kumar *et al*. (2004) conducted an experiment in Uttar Pradesh on thirty tomato genotypes and reported that the average fruit weight showed high heritabilities that ranged from 89.10 to 96.50%.

Singh and Cheema (2005) conducted an experiment on fifteen advance generation breeding lines of tomato including four control cultivars at Lucknow, India and estimated high heritability for total soluble solids (TSS), pericarp thickness, fruit firmness, acidity and dry matter content except lycopene content.

Mahesha *et al*. (2006) conducted an experiment on thirty genotypes of tomato and observed that fruit weight, number of fruits per plant and plant height exhibited very high heritability values along with high genetic gain.

Saeed *et al.* (2007) observed that broadsense heritability was highest for number of fruits per plant (96.56%) followed by number of flowers per plant (93.45%) reflecting the effectiveness of selection in the present germplasm of tomato improvement.

Ghosh *et al.* (2010) conducted an experiment on F_2 segregating generations of exotic tomato hybrids and reported high heritability (>50%) for all the yield contributing characters except flowers per cluster (47.83%). High heritability associated with high genetic advance was observed for fruit clusters per plant (105.11), fruits per plant (103.43), branches per plant (34.49), fruits per cluster (47.43), individual fruit weight (77.73) and fruit yield per plant (108.25).

Kaushik *et al.* (2011) reported that high values of heritability coupled with high genetic advance were observed for number of leaves at 60 days after transplanting (99.4 and 64.9) and fruit yield (99.9 and 24.7).

Prema *et al.* (2011) reported high heritability coupled with high genetic advance were observed for average fruit weight (g), days to 50 % flowering and high heritability coupled with moderate genetic advance were observed for plant height at 90 DAT (cm), days to first flowering, shelf life of fruit (days) and ascorbic acid content (mg/100g) indicating these characters are governed by additive gene action.

Islam *et al.* (2012) reported fruit yield/plant showed low heritability along with low genetic advance and did not show significant and positive correlation with

the remaining characters. It indicates that improvement of high yield through selection is difficult; rather hybridization can be effective for improving the fruit yield/plant.

Manna and Paul (2012) reported high and moderate to high heritability coupled with moderate to high genetic gain in number of locules per fruit, fruit weight, fruit length, number of fruits per plant, pericarp thickness, vitamin C (mg/100g) and total acid (%) indicated the pre dominance of additive gene action and therefore, these are more reliable for effective selection.

Rahaman *et al.* (2012) reported high heritability coupled with high genetic advance expressed in percentage of mean was observed for selection of primary and secondary branches, plant height, fruits per plant, fruit length, fruit diameter, and fruit weight indicating that these traits were mainly governed by additive gene action and responsive for further improvement of these traits.

Kumar *et al.* (2013) reported that the heritability estimates were high for all the characters except number of branches per plant which showed moderate heritability.

Reddy *et al.* (2013b) studied the genetic parameters to elucidate the genetic variability, heritability and genetic advance in tomato (*Solanum lycopersicum* L.) by evaluation of nineteen genotypes of tomato. High heritability combined with high genetic advance was observed for the characters plant height, number of clusters per plant, number of flowers per cluster, number of fruits per cluster, number of fruits per plant, fruit length, fruit weight and fruit yield per plant, ascorbic acid, acidity, shelf life and TSS. High heritability combined with high genetic advance indicates that additive gene action plays a major role in governing these traits and these traits can be improved by simple selection.

Osekita and Ademiluyi (2014) conducted an experiment with five genotypes of tomato to study the interrelationship among quantitative traits; days to 50% flowering, plant height (cm), number of branches per plant, days to first fruit set, number of fruit per plant, number of cluster per plant, number of fruit per cluster, average fruit weight (g), pericarp thickness (cm), number of locules per fruit and fruit shape index. Phenotypic and genotypic coefficients of variation PCV and GCV were determined to show the degree of inherent traits or heritable variation on the component traits. The traits showed wide variability hence, they can be exploited by direct selection for improving yield in tomato.

2.4 Genetic advance

Singh *et al.* (1997) reported that heritability and genetic advance values of effective selection may be made for fruit weight and number of fruits plants-1.

Prasad *et al.* (1999) reported that very high heritability estimates along with high genetic advance were observed for fruit weight, fruit length, fruit width and pulp thickness due to additive genetic effect.

Brar *et al.* (2000) reported that the high estimates of genetic advance for number of marketable fruits per plant and total number of fruits per plant whereas, total yield per plant and marketable fruit yield and number of fruits per cluster showed low genetic advance.

Mohanty (2002) reported that the evaluation of 18 genotypes of tomato revealed high heritability with moderate to high genotypic coefficient of variation and genetic advance for average fruit weight (93.0, 34.94, 68.59%, respectively), number of branches per plant (92.3, 32.52, 64.40%, respectively) and fruits per plant (87.4, 27.87, 53.69%, respectively), plant height (87.1, 22.35 43.57% respectively) and days

to first harvest (91.4, 15.29, 28.53%, respectively) which could be improved by simple selection at Bhawanipatna Orissa.

Singh *et al*. (2002b) reported that the highest genetic advance for average fruit weight, followed by, shelf life of red ripe fruits.

2.5 Correlation studies

Correlation studies provide information that the selection for one character will result in progress for all correlated characters. Genotypic and phenotypic correlation coefficient was calculated by standard procedures (Johnson *et al*., 1955). Correlation coefficient was further partitioned into components of direct and indirect effects by path analysis (Wright, 1921; Dewey and Lu, 1959).

The necessity of coefficient of correlation to describe the degree of association between independent and dependent variables which was first suggested by Galton (1888) and its theory was developed by Pearson (1904). Mathematical utilization at phenotypic, genotypic and environmental levels was described by Searle (1961).

Parsanna *et al*. (2005) reported yield per plant the most important economic trait, exhibited positive association with average fruit weight (0.53) and number of fruits per plant (0.38). The negative correlation was observed for number of fruits per plant with average fruit weight (-0.54), number of locules (-0.45) and flesh thickness (-0.34). Therefore simultaneous improvement for all the traits associated with yield would be difficult in the population.

Ghosh *et al*. (2010) reported that the number of fruits per cluster, fruit clusters per plant and fruits per plant had positive and highly significant association with fruit yield. Number of branches per plant had positive correlation with number of flowers per plant and demonstrated positive association of number of fruits per cluster with

number of fruit clusters per plant, number of fruits per plant and fruit yields per plant and number of fruit per plant.

Islam *et al.* (2010) conducted an experiment on thirty nine exotic tomato genotypes for nine yield contributing characters and studied that the correlation coefficients were determined to find out the inter relationship among the characters studied. Yield per plant was found highly significant and positively correlated with flowers per plant, fruits per plant, fruit length, fruit diameter and individual fruit weight which indicated that yield could be increased by improving a traits.

Dar *et al.* (2011) observed that yield q/ha was positively correrlated with lycopene content, fruit pH, total soluble solid, pericarp thickness, number of locules per fruit, number of fruits per plant, fruit yield per plant and average fruit weight at genotypic as well as phenotypic level. Negative correlation was observed with ascorbic acid and polygalacturonase activity at genotypic as well as phenotypic level.

Kaushik *et al.* (2011) evaluated the positive association of yield per hectare observed with number of leaves at 60 days after transplanting (0.78) followed by number of leaves at 30 days after transplanting (0.68), fruit length (0.66) and plant height (0.51).

Tiwari and Upadhyay (2011) conducted an experiment on nineteen genotypes along with two checks of tomato and reported that significant positive correlation therefore, fruit weight as an important character which may be included in selection criteria for improvement in fruit yield per plant

Manna and Paul (2012) worked out correlation coefficient and result revealed that fruit yield per plant was positively and significantly correlated with pericarp thickness, fruit length, fruit weight and number of fruits per plant indicating relative

importance of these characters for yield improvement. Significantly positive and negative associations among different fruit quality parameters were also observed in the present study.

Mahapatra *et al*. (2013) reported that fruit yield had positive and significant correlation with plant height, number of primary branches per plant, number of flower clusters per plant, number of fruits per plant, fruit length, fruit width, pericarp thickness, number of locules per fruit, average fruit weight and fruit yield per plant. It was observed that with increase in plant height, there was corresponding increase in number of primary branches per plant, days to 50 % flowering and number of flower clusters per plant.

Saleem *et al.* (2013) reported that the plant height, number of fruits per plant and fruit weight revealed significant positive genotypic and phenotypic association along with direct positive effect on fruit yield per plant. It is therefore, recommended that fruit weight, number of fruits per plant and plant height should be given due importance in selection of promising crosses to develop commercial hybrid variety in tomato.

Srivastava *et al*. (2013) reported that the yield per plant was found highly significant and positively correlated with days to 50% flowering, days to 50% fruiting, plant height (cm), number of primary branches per plant, number of fruits per cluster, number of fruits per plant and average fruit weight (gm), which indicated that yield could be increased by improving a traits.

2.6 Path coefficient analysis

The concept of path coefficient analysis was originally developed by Wright in 1921, but the technique was first used for plant selection by Dewey and Lu (1959).

Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects. In other hands, it measures the direct and indirect contribution of various independent characters on a dependent character.

Verma and sarnaik (2000) computed path coefficient analysis using thirty genotypes for eighteen characters at Raipur and observed that number of fruits per plant, average weight of fruit, thousand seed weight and number of branches per plant exhibited positive as well high direct effects. Therefore, these traits may be considered, while selecting the genotype for high fruit yield potential.

Mohanty (2002) conducted an experiment on eighteen indigenous and exotic genotypes of tomato at Hisar, India and observed that number of branches per plant and average fruit weight exerted high positive direct effect on fruit yield and high positive indirect effect with each other.

Joshi *et al.* (2004) evaluated thirty-seven tomato genotypes at Solan, H.P. and reported that path coefficient analysis showed that the number of fruits per plant is the most important fruit- yield contributing traits followed by fruit length, fruit breadth and plant height.

Lakshmi-Kant and Mani (2004) at Hawalbagh, U. P. studied nineteen genotypes of tomato and indicated the importance of number of fruits per plant, fruit width, days to 50% flowering and fruits per bunch as these characters showed the highest direct effect on fruit yield per plant.

Singh *et al.* (2006) conducted an experiment at Ludhiana on fifteen advanced breeding lines of tomato along with four checks and observed that total fruit yield per plant, number of fruit per plant and fruit weight had exerted positive and direct effect

on marketable fruit yield per plant. Days for transplanting to first fruit maturity was involved indirectly in the improvement of marketable yield per plant.

Anitha, *et al.* (2007) path analysis revealed that oxalates, acidity, ascorbic acid and TSS had positive and direct effects on lycopene.

Mehta and Asati (2008a) found 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% fruiting.

Ara *et al*. (2009) path analysis revealed that days to first picking had highest positive direct effect on fruit yield followed by harvest duration, number of fruits per plant, average fruit weight, plant height and number of flowers per cluster. Direct positive effect of days to first picking followed by harvest duration, number of fruits per plant, average fruit weight and plant height on fruit yield per plant.

Islam *et al.* (2010) conducted an experiment on thirty nine exotic tomato genotypes for yield contributing characters and reported that fruits per plant showed the highest positive direct effect (0.980) on yield per plant followed by individual fruit weight (0.958). On the other hand, the highest negative direct effect on yield per plant showed by days to first flowering (-0.277) followed by fruit length (-0.141). The characters showed high direct effect on yield per plant indicated that direct selection for these traits might be effective and there is a possibility of improving yield per plant through selection based on these characters.

Dar *et al.* (2011) at Srinagar, J & K, reported that path coefficient analysis indicated that fruit yield per plant had highest positive direct effect on yield q/ha.

Manna and Paul (2012) found that significantly positive and negative associations among different fruit quality parameters were also observed in the

present study. The path coefficient analysis revealed that number of locules /fruit, TSS, fruit length, number of fruits/plant, fruit weight, vitamin C content and pericarp thickness had positive direct effect on fruit yield, while, fruit width and total acid content had strong negative effects on the fruit yield.

Tasisa *et al.* (2012) conducted an experiment on twenty three tomato genotypes and reported that positive direct effects were exerted by days to flowering, fruit clusters per plant and plant height on yield per plant, suggesting their importance in yield improvement and that these traits would be considered in selection programme.

Ahirwar *et al*. (2013) found that number of fruits per plant exhibited the highest positive direct effect followed by days to flower per cent, ascorbic acid content, plant height 120 DAT and fruit diameter at genotypic level.

Mahapatra *et al*. (2013) observed that the association recorded significant improvement in yield. 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 towards yield and these traits also recorded positive significant correlation with yield.

Reddy *et al*. (2013c) found that path analysis studies done to study the cause and effect relationship revealed that plant height, number of fruits per plant, fruit length, fruit width and ascorbic acid had high positive direct effects on fruit yield per plant. Hence, direct selection for these traits is done for improving fruit yield per plant.

Srivastava *et al.* (2013) studied path coefficient analysis in 52 exotic tomato (*Solanum lycopersicum* L.) genotypes for eight yield contributing characters to find out the inter relationship among the characters studied. The data revealed that average fruit weight (1.0218) showed the highest positive direct effect on yield/plant followed by number of fruits/plant (0.7286), day to 50% flowering, number of primary branches/plant (0.1101) and number of fruits/cluster (-0.3707) and plant height (-0.0617) showed negative direct effects.

MATERIALS AND METHODS

CHAPTER-III

MATERIALS AND METHODS

An experiment was carried out to study **"**Evaluation of cherry tomato *(Solanum lycopersicum* L. var. *cerasiforme)* in Chhattisgarh plains **"** was conducted during *rabi* season 2013-14 under All India Co-ordinated Research Project on Vegetable Crops at Horticultural Instructional cum Research Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.). The details of the material used for the study, experimental designs adapted, statistical procedures followed and methodology adopted are presented in this chapter.

3.1 Geographical situation

Raipur is situated in mid eastern part of Chhattisgarh at latitude $21^{o}11'$N, longitude $81^{o}36'$E and at an altitude of 289.56 meters above the mean sea level.

3.2 Agro-climatic condition

The general climate prevailing in the district Raipur of Chhattisgarh region is dry sub-humid type with annual rainfall varying from 1200 to 1400 mm. The temperature reaches upto maximum of 42.8^{o}C and minimum temperature during winter may go down to 9^{o}C in Raipur. May is the hottest and December is the coolest month of the year.

3.3 Weather conditions during crop period

Weekly average weather data recorded during the period of investigation from sowing to harvesting are presented in fig. 3.1 and Appendix-1.

The crop received 92 mm rainfall during its growing period. There was no rainfall in the month of December, January and April. Maximum relative humidity throughout the crop season varied between 59 to 91 per cent and minimum relative

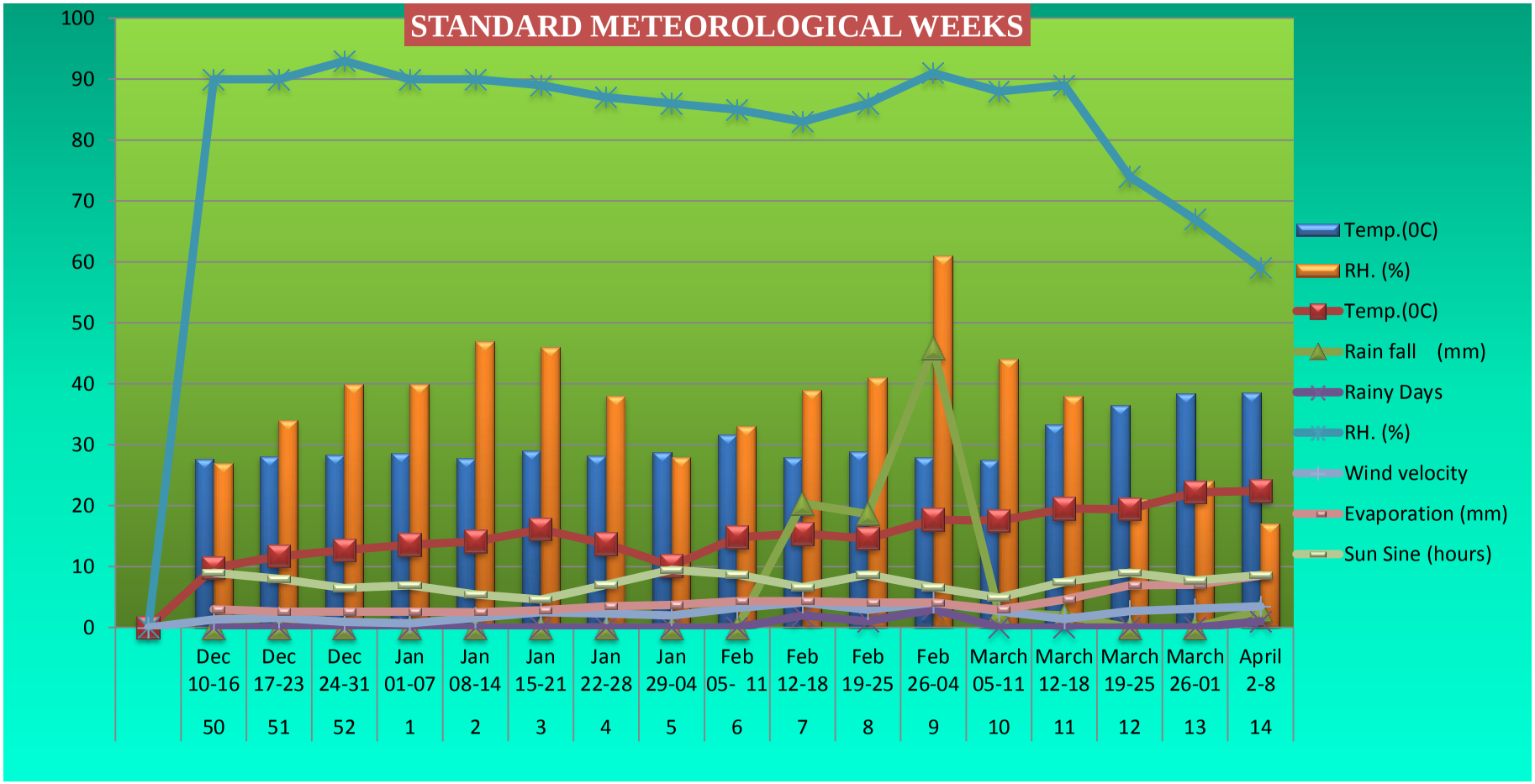

Fig.3.1 weekly meteorological observation during the crop growth period.

humidity throughout the crop season varied between 17 to 61 per cent. The values for open pan evaporation ranged from 2.5 to 8.5 mm per day, whereas, sunshine values varied from 4.6 to 9.5 hours per day. The maximum temperature during the growth period varied between 27.5 to 38.5 ^{o}C, whereas, minimum temperature varied between 9.8 to 22.4^{o}C.

3.4 Soil of the experimental field

The soil of the experimental field was clay loam in texture which is locally known as "*dorsa*" and is neutral in reaction with the pH 7.1. The Physico-chemical analysis of soil sample has been summarized in Table 3.1.

Table 3.1: Physico-chemical properties of the soil

Particulars	Values	Rating	Method used
A. Physical properties			
1. Mechanical composition			
Sand (%)	25.67	-	International Pipette method (Black, 1965)
Silt (%)	32.54	-	
Clay (%)	41.79	-	
Texture class		clay loam	
B. Chemical composition			
1. Organic carbon (%)	0.46	Medium	Walkley and Black's rapid titration method (Jackson, 1967)
2. Available N (kg ha^{-1})	330.0	Medium	Alkaline permanganate method (Subbiah and Asija, 1956)
3. Available P (kg ha^{-1})	20.0	High	Olsen's method (Olsen, 1954)
4. Available K (kg ha^{-1})	400.0	High	Flame photometric method (Jackson, 1967)
5. pH (1:2.5 soil:water)	7.1	Neutral	Glass electrode pH meter (Piper, 1967)

3.5 Experimental materials and design

The experiment consists of fifteen genotypes of cherry tomato, which was laid out in Randomized Block Design (RBD) with three replications. Details of treatment are given below:

Experimental details:

Design : Randomized Block Design (RBD)
Number of Replications : 3
Number of Genotype : 15
Plot size : 4 m × 5 m
Spacing : 100cm × 45 cm (R-R × P-P)

Table 3.2: Details of the genotypes

S.No.	Genotypes	Source/Place of collection
1	Cherry Tomato 1	AICRP Vegetable Raipur
2	Cherry Tomato 2	AICRP Vegetable Raipur
3	Cherry Tomato 3	AICRP Vegetable Raipur
4	Cherry Tomato 4	AICRP Vegetable Raipur
5	Cherry Tomato 5	AICRP Vegetable Raipur
6	Cherry Tomato 7	AICRP Vegetable Raipur
7	Cherry Tomato 8	AICRP Vegetable Raipur
8	Cherry Tomato 9	AICRP Vegetable Raipur
9	Cherry type - 1	I.A.R.I New Delhi
10	Cherry T.4 × Pant T. -3	AICRP Vegetable Raipur
11	Cherry T.1 × Co - 3 - 1	AICRP Vegetable Raipur
12	Cherry T.1 × Co - 3 - 2	AICRP Vegetable Raipur
13	Cherry T.1 × Co - 3 - 3	AICRP Vegetable Raipur
14	Cherry T.3 × Cherry T.4	AICRP Vegetable Raipur
15	Pusa Ruby	AICRP Vegetable Raipur

3.6 Nursery raising

The sowing was carried out on 12th November 2013 in the nursery bed of 10 m x 1m x 0.15 m, were prepared on well-ploughed and levelled field at 30 cm distance between two beds. A well-rotten cow dung manure @ 30 kg per 5.0 m long and 1.0 m wide nursery bed was well mixed in the soil with the help of spade. The seeds of each genotype were treated with Diathane M-45 @ 2.5 g per kg of seeds before sowing and then sown in lines 10 cm apart @ 500 g seeds per ha. A gap of 10 cm was kept in between two genotypes sown in the nursery bed. After sowing, the seeds were covered by sieved well-rotten FYM. The bed was covered with the dry grass and it was irrigated with the help of water can. The grass covered on the nursery bed was removed immediately after germination. To protect the seedling from damping off disease drenching was done with 2.5 g Diathane M-45 per liter of water at ten days interval after germination.

3.7 Field preparation

The preparation of field was done by tractor drawn cultivator followed by two cross-harrowing to pulverize the soil. To enrich the soil, well-rotten FYM @ 25 t/ha was applied before harrowing and well-mixed with the soil by planking. Finally, the field was levelled with leveler and then experiment was laid out.

3.8 Transplanting

The healthy 28 days old seedling were transplanted in the experimental field at the spacing of 100 cm between rows to row and 45 cm between plant to plant. A plot size of 4 m × 5 m was kept for each genotype.

3.9 Fertilizer application

The recommended doses of fertilizer *viz*., 100 kg N, 80 kg P_2O_5 and 60 kg K_2O per ha was applied through urea, single super phosphate and muriate of potash,

respectively. A half dose of nitrogen and full dose of phosphorus and potash were applied at the time of planting and the remaining quantity of nitrogen was applied in two equal splits at 30 and 60 days after transplanting (DAT).

3.10 Irrigation

The nursery bed was irrigated one day before transplanting to uproot the seedlings conveniently. Later on, one irrigation was applied just after the transplanting of seedlings in the experimental plots. Subsequent six irrigations were applied as per the need of the crop.

3.11 Intercultural operations

The weeds were completely removed at the time of field preparation. At later growth stages, two hand weeding at 15 and 45 DAT (days after transplanting) were done to keep the plot free from weeds.

3.12 Plant protection measures

Suitable plant protection measures were adopted to control the major insect pests during crop period. To control the infestation of early blight disease spraying of 0.25% Dithane M-45 was done at 15 days interval till flowering.

3.13 Harvesting

The picking of fruits was done at the turning stage of the fruits. Picking of fruits was done at an interval of 05 to 08 days. Fruits of 5 randomly selected plants were picked up separately for studying the various yields and quality attributes. The net plot yield was also recorded in kg/plot. Fruits of five plants were taken from net plot area for observation of yield attributing characters.

3.14 Observations recorded

Five randomly selected competitive plants from each genotype in all plot, and were tagged. These tagged plants were used for recording observations for the following characters.

3.14.1 Growth characters

3.14.1.1 Plant height (cm)

The plant height of five randomly selected plants was recorded with the help of a meter scale from the base of the plant to the shoot tip at the final picking and the average height (cm) per plant was calculated.

3.14.1.2 Number of primary branches per plant

The total number of primary branches of five randomly selected plants were counted and averaged at the time of final picking.

3.14.1.3 Number of secondary branches per plant

The total number of secondary branches of five randomly selected plants were counted and averaged at the time of final picking.

3.14.2 Flowering and physical characters of fruits

3.14.2.1 Days to first flowering

Each plot was daily observed to record the date of first flowering. The period from the transplanting date to the date of first flowering was recorded and expressed in term of number of days, when first flower of the plot bloomed. The average values per genotypes were calculated on plot basis.

3.14.2.2 Days to 50% flowering

Each plot was daily observed to record the date of 50% flowering. 50 % of the total number of plants flowered in each plot was recorded and expressed in term of number of days. The average values per genotypes were calculated on plot basis.

3.14.2.3 Number of flowers per cluster

Number of flowers per cluster was recorded as average of five random clusters at flowering stage and the average was calculated.

3.14.2.4 Days to first fruit set

Each plot was daily observed to record the date of first fruit setting. The numbers of days were counted from the date of transplanting to first fruit set and expressed in term of number of days, when first fruit setting occur. The average values per genotypes were calculated on plot basis.

3.14.2.5 Number of fruits per cluster

Number of fruits per cluster counted before first picking, three fruit bunches were chosen at random in each of labeled plant to calculate the average number of fruits per cluster.

3.14.2.6 Days to fruit ripening

Each plot was daily observed to record the date of fruit ripening after fruit setting. The period from the fruit setting to the date of fruit ripening was recorded and expressed in term of number of days, when first red ripen fruit occur. The average values per genotypes were calculated on plot basis.

3.14.2.7 Days to first fruit harvest

The first picking of fruits was done at the turning stage of the fruits. The period from the transplanting date to the date of first harvesting was recorded and expressed in term of number of days. The average values per genotypes were calculated on plot basis.

3.14.2.8 Number of picking

Picking of fruits was started at ripening stage and done at an interval of 05 to 08 days. number of pickings is different for different genotypes

3.14.2.9 Crop duration (days)

Crop duration of each genotype determines the no of days taken by the crop from transplanting to harvesting. It is expressed in days.

3.14.2.10 Fruit length (cm)

Five randomly selected fruits of each genotype were measured for fruit length (cm) at peak fruiting with the help of vernier calipers and the average was calculated.

3.14.2.11 Fruit Girth (cm)

Five randomly selected fruits of each genotype were measured for fruit Girth (cm) at peak fruiting with the help of vernier calipers and the average was calculated.

3.14.2.12 Average fruit weight (g)

The weight (g) of twenty randomly selected ripened fruits of each genotype at peak fruiting in each replication was recorded and then average fruit weight was calculated.

3.14.2.13 Number of locules per fruit

Five ripe fruits were randomly selected from each genotype and fruits were cut transversely and locules were counted in each fruit, then average number of locules per fruit was calculated and averaged over replication.

3.14.2.14 Pericarp thickness (cm)

Five fruit were selected randomly from each genotype and cut transversely. Then pericarp thickness (cm) was measured with the help of vernier calipers and the average was calculated.

3.14.2.15 100 seed weight (g)

100 well-developed seed were collected from the bulk of five selected plant and weight was recorded with the help of electronic balance and expressed in gram (g).

3.14.3 Studies on quality characters of tomato fruit

3.14.3.1 Total soluble solid (T.S.S.) %

Five fruits from each genotype were randomly taken from the harvested lot and thoroughly washed under tap water. The fruits were cut into small pieces and squeezed to obtain the juice and with the help of Erga hand refractometer, juice was

used to determine T.S.S. (%) of fruit. Then average was calculated and was expressed as per cent soluble solids in juice.

3.14.3.2 Acidity

Acid content of the extracted juice of five fruits was determined by titrating 10 ml of tomato juice against 0.1 N NaOH using phenolphthalein as an indicator. Acidity was expressed in terms of percentage of anhydrous citric acid per 100 ml of tomato juice by using following formula:

$$\text{Acidity As anhydrous citric acid} = \frac{\text{Titre} \times \text{Normality of alkali} \times \text{Equivalent weight of acid} \times \text{Volume made up}}{\text{Volume of sample taken for estimation} \times \text{Wt. of volume of sample taken} \times 1000} \times 100$$

3.14.4 Fruit yield

3.14.4.1 Number of fruits per plant

Number of fruits counted from five randomly selected tagged plants from each plot at each harvest and total number of fruits per plant was calculated by dividing the total fruits harvested in all the pickings with five and value was averaged over replications.

3.14.4.2 Fruit weight per plant (kg)

The weight of fruits of five selected plants was recorded at each picking and the total weight of fruits was calculated by cumulative harvest in kilograms, which was averaged over replications.

3.14.4.3 Marketable yield per plot (kg)

The weight of fresh fruit from each plot was taken and mean was expressed. The mean plot yield (kg/plot) was averaged over replications.

3.14.4.4 Marketable fruit yield (q/ha)

The weight of fresh fruit from each plot was taken and mean was expressed. The mean thus obtained was calculated by the following formula for getting marketable fruit yield in quintal per hectare.

$$\text{Fruit yield (q/ha)} = \frac{\text{Weight of fresh fruit (kg per plot)}}{\text{Net plot area (sq.m.)}} \times \frac{10000}{100}$$

3.14.4.5 Total fruit yield (q/ha)

The fruit yield in q/ha was worked out with the help of the following formula

$$\text{Total fruit yield (q/ha)} = \frac{\text{Weight of total fruits in kg per plot (fresh+damaged)}}{\text{Net plot area (sq.m.)}} \times \frac{10000}{100}$$

3.15 Statistical analysis

Statistical analysis was done by taking the mean value of five plants from each genotype in each replication.

3.15.1 Analysis of variance

The data collected from different characters were processed and analyzed by the method of analysis of variance as derived by Panse and Sukhatme (1967).

Source of variation	Degree of freedom	Sum of squares	Mean sum of squares	F value	
				Calculated	Tabulated at 5% and 1%
Replication	(r-1)	SS_r	MS_r	MSr / MS_e *Significant at 5%	
Treatment	(t-1)	SS_t	MS_t	$M S_t / MS_e$**Significant at 1%	
Error	(r-1)(t-1)	SS_e	MS_e		
Total	(rt-1)				

Where,

r = Replication
t = Treatments
SS_r = Replication sum of squares
SS_t = Treatment sum of squares
SS_e = Error sum of squares
MS_r = Replication mean sum of squares
MS_t = Treatment mean sum of squares
MS_e = Error mean sum of squares

The significance of treatment differences was determined by comparing the calculated value of F with the tabulated value at five per cent and or one per cent level of significance. If calculated value of 'F' ratio was greater than the tabulated value of 'F' than the 'F' value was significant otherwise non-significant.

3.15.2 Biometrical parameter of variation

Mean, Rang, Components of variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance.

3.15.2.1 Mean

This mean was calculated by summing up all the observations and dividing the sum by the number of observations.

$$\overline{X} = \frac{\sum_{i=1}^{n} Xi}{N}$$

$\overline{X}$ = Mean of the respondents

Where,

$\sum X$ = Sum of total number of respondents

3.15.2.2 Range

The limit of smallest and the largest value of each observation expressed the range of variation.

3.15.2.3 Genotypic and phenotypic coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated using formula as suggested by Burton (1952).

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2 g}}{\overline{X}} \times 100$$

$$\text{PCV (\%)} = \frac{\sqrt{\sigma^2 p}}{\overline{X}} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

$\overline{X}$ = Mean of the character

3.15.2.4 Heritability

Heritability in broad sense was estimated from the method as given by Hanson *et al.* (1956).

$$h^2_{bs}(\%) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2_{bs} = Heritability in broad sense.

Broad sense heritability (h^2) estimates were classified as low, moderate and high as below (as per) given by Robinson (1966).

0-30% - Low

31-60% - Moderate

>60% - High

3.15.2.5 Genetic advance

3.15.2.5.1 Expected genetic advance

It was obtained by the method given by Johanson *et al.* (1955)

$$GA = K\ \sigma p\ h^2$$

Where,

K = Constant 2.06 at 5% selection intensity (Lush, 1940)

σp = Phenotypic standard deviation.

h^2 = Heritability estimate.

GA = Genetic advance.

Genetic advance can be categorized as given below (as per) given by Johnson *et al.* (1955)

>20% = High

10-20% = Moderate

<10% = Low

3.15.2.5.2 Genetic advance as percentage of mean

It was obtained by the formula

$$\overline{GA}\% = \frac{GA}{\overline{X}} \times 100$$

Where,

$\overline{X}$ = mean of the character

3.15.3 Character association (Correlation coefficient)

Coefficient correlation was calculated for all possible combination among the characters at genotypic, phenotypic and environmental levels were estimated as given by Searle (1961).

i. Phenotypic correlation between characters x and y.

$$R_{xy}\,(p) = \frac{Cov\ xy(p)}{\sqrt{(var\ x(p) \times var\ y(p)}}$$

ii. Genotypic correlation between characters x and y.

$$R_{xy}\,(g) = \frac{Cov\ xy(g)}{\sqrt{(var\ x(g) \times var\ y(g)}}$$

iii. Environmental correlation between characters x and y.

$$R_{xy}\,(e) = \frac{Cov\ xy(e)}{\sqrt{(var\ x(e) \times var\ y(e)}}$$

Where,

Cov xy (p), cov xy (g) and cov xy (e) = Phenotypic, Genotypic and Environmental variances between character x and y, respectively.

Var x (p), var x (g) and var x (e) = Phenotypic, Genotypic and Environmental variances between character x, respectively.

Var y (p), var y (g) and var y (e) = Phenotypic, Genotypic and Environmental variances between character y, respectively.

The significance of correlation coefficients was tested, against Fisher's table value (1936) for (g-2) degree of freedom at 5 % and 1 % level of significance, where g is the number of genotypes.

3.15.4 Test of significance

Phenotypic and genotypic correlation coefficients were tested for their significance

't' test as follows

$$t_c = r\sqrt{\left(\frac{n-2}{1-r^2}\right)}$$

at (n-2) degree of freedom

Where, n = Number of genotype

If 't' calculated (t_c) is greater than 't' tabulated (t_t) at (n -2) degree of freedom at given probability level the phenotypic correlation is taken as significant.

The calculated (r) is then compared with table value of 'r' at 5% and 1% level of significance (Snedecor and Cochran, 1967).

3.15.5 Path-coefficient analysis

The genotypic correlation coefficients were further partitioned into direct and indirect effects with the help of path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Path coefficient was calculated separately for all important characters considering fruit yield as dependable variable.

Path-coefficient was estimated using simultaneous equations and the equations showed a basic relationship between correlation coefficient and path-coefficient. These equations were solved by presenting them in matrix notations.

$$A = B.C$$

The solution for the vector 'C' may be obtained by multiplying both sides by inverts of 'B' matrix i.e. $B^{-1}.A = C$. After calculation of values of path-coefficient i.e.

'C' vector, it is possible to obtain path values for residual (R). Residual effect was calculated using formula from Singh and Chaudhary (1985).

$$R = \sqrt{1 - \sum di \times rij}$$

Where,

di = direct effect of i^{th} character

rij = correlation coefficient of i^{th} character with j^{th} character

Direct and indirect effects of different characters on fruit yield were calculated at genotypic level.

3.15.6 Genetic divergence analysis

The genetic divergence among the genotypes was carried out using Mahalanobis' D^2 statistic (Rao, 1952). The difference in the means of two populations, Mahalanobis, D^2- statistics is defined as follows:

$pD^2 = b_1d_1+b_2d_2+\ldots\ldots+b_pd_p$

In term of variances and co variances, the D^2 value is obtained as follows:

$pD^2 = W^{ij} (X^1_i - X^2_i) (X^1_j - X^2_j)$

3.15.7 Molecular studies

3.15.7.1 Genetic divergence analysis

Molecular marker based diversity analysis of fifteen genotypes including Pusa Ruby had done by Simple Sequence Repeats (SSR) marker.

The genetic divergence among the genotypes was carried out using Simple Sequence Repeats (SSR) DNA markers. Seeds of each genotype were grown in small plastic trays and leaves were collected for DNA extraction.

3.15.7.2 Genomic DNA Isolation

The search for a more efficient means of extracting DNA of both higher quality and yield has lead to the development of a variety of protocols, however the fundamentals of DNA extraction remains the same. DNA must be purified from

cellular material in a manner that prevents degradation. Because of this, even crude extraction procedures can still be adopted to prepare a sufficient amount of DNA to allow for multiple end uses. DNA extraction from plant tissue can vary depending on the material used. Essentially any mechanical means of breaking down the cell wall and membranes to allow access to nuclear material, without its degradation is required. In the current study Genomic DNA of Cherry tomato had been isolated from the 15 genotypes including Pusa Ruby by CTAB method (Murry and Thompson, 1980) with little modification as reported by Ginwal and Mittal, 2010 for removing the phenolics and RNA.

Tomato genomic DNA was extracted from 30 days old plants of the Cherry tomato genotypes followed the CTAB protocol as follows. Before starting, add B-merceptaethanol (20 µl/20 ml Buffer), 8M Lithium chloride (300 µl/ 1000 µl) and 4% poly vinyl pyrollidone (PVP) to CTAB extraction buffer then follow the stepwise protocol given below:

1. About 100mg of young leaf was grinded in 1000 µl 2X CTAB extraction buffer with the help of tissue homogenizer.
2. Then 700 µl of solution transferred into 1.5 ml eppendorf tube.
3. Incubated at 65°c on water bath for 15-20 min and then cooled briefly and 700 µl of Chloroform: Isoamylalcohol (24:1) was added.
4. The content were shaken by hands intermittently and kept at room temperature for 15 min. tubes were centrifuged at 13000 rpm for 3 min.
5. 600 µl of upper aqueous phase was transferred into a new 1.5 ml eppendorf tube. 900 µl of absolute ethanol was added and mixed gently and the tubes were kept for 2 hrs at -20°c.

6. The sample was centrifuged for 3 min at 10,000 rpm, the supernatant was decanted. The pellet was washed with wash buffer (998 µl of 76% ethanol and 2 µl of 5M ammonium acetate) and air-dried.
7. DNA pellet was air dried and then dissolved in 50 µl of TE buffer.

3.15.7.3 Quantification and quality test of genomic DNA

For quantification, 4 µl of DNA of all Cherry tomato genotypes, was loaded on 0.8% agarose gel and electrophoresis was done for about 1 hour at 50 volts. The DNA was stained with ethidium bromide and visualized in UV under gel documentation system of Biorad where amount of fluorescence is directly proportional to the total mass of DNA. Another method used to quantify the DNA sample by nanodrop methods. The NanoDrop ND-1000 is a full-spectrum spectrophotomer that can require only 1-2uL samples and measure up to 2500ng/µl for DNA absorbance spectral analysis, providing a calculated DNA concentration and purity ratios. The ratio of absorbance at 260 nm and 280 nm is used to assess the purity of DNA and RNA. A ratio of ~1.8 is generally accepted as "pure" for DNA; a ratio of ~2.0 is generally accepted as "pure" for RNA. If the ratio is appreciably lower in either case, it may indicate the presence of protein, phenol or other contaminants that absorb strongly at or near 280 nm (ND-1000 Spectrophotometer V3.5 User's Manual, 2007). After the quantification, the DNA was diluted with sterile water to get a final concentration 50ng DNA/µl.

3.15.7.4 PCR analysis to detect polymorphism among Cherry tomato genotypes

PCR analysis was done using the 50 Simple Sequence Repeat (SSR) markers (27 EST based SSR, 8 Tom SSR and 15 BAC clone based SLM marker) reported by (Kwon *et al.*, 2009, Ei- Awady *et al*., 2012 and Subramaniam *et al*., 2010

respectively) used in this study to identify the polymorphic loci between the 15 Cherry tomato genotypes including Pusa Ruby.

Table 3.3: PCR components with their quantity for microsatellite analysis

S. n.	Components	Concentration	Quantity
1	PCR buffer with $MgCl_2$	10X	2.0 µl
2	dNTPS	2 mM	2.0 µl
3	Primer (Forward)	10 µM	1 µl
4	Primer (Reverse)	10 µM	1 µl
5	Taq DNA Polymerase	2U	0.5 µl
6	Sterile water	-	11.5 µl
7	Template DNA	50 ηg/µl	2.0 µl
	Total		**20.0 µl**

Table 3.4: Temperature profile used for PCR amplification

Steps	Temperature (°C)	Duration (min.)	Cycles	Activity
1	95	4 min	1	Initial denaturation
2	95	1min		Denaturation
3	45-55	1min	35	Annealing
4	72	2min		Extension
5	72	7 min	1	Final Extension
6	4	∞	1	Storage

3.15.7.5 Agarose Gel Electrophoresis

The 20 µl products from the PCR amplification were prepared for analysis by 2.5% agarose gel electrophoresis and detection was performed with the Bio RAD system of gel electrophoresis at 120 volts for 1.5 hr.

3.15.7.6 Detection of polymorphism using simple sequence repeats (SSR) primers

The polymorphism was detected by using SSR primers. The primers used for this purpose are presented in the table 3.5.

Table 3.5 List of primers used for polymorphism analysis

S.N.	Primer	Sequence 5' ⟶ 3'		Product size (bp)	Annealing temp.
1.	SSR9	Forward	CCCTTTGCAAGTTCTTCTTCA	168	55
		Reverse	TTCATGAGCCAACATAGGAGG		
2.	SSR13	Forward	GGGTCACATACACTCATACTAAGGA	104	55
		Reverse	CAAATCGCGACATGTGTAAGA		
3.	SSR19	Forward	CCGTTACCTTGGTCCATCAC	188	55
		Reverse	GGGAGATGCCACATCACATA		
4.	SSR20	Forward	GAGGACGACAACAACAACGA	157	55
		Reverse	GACATGCCACTTAGATCCACAA		
5.	SSR22	Forward	GATCGGCAGTAGGTGCTCTC	217	55
		Reverse	CAAGAAACACCCATATCCGC		
6.	SSR26	Forward	CGCCTATCGATACCACCACT	178	55
		Reverse	ATTGATCCGTTTGGTTCTGC		
7.	SSR28	Forward	ACCAAATGGAAATGGGTCAA	164	55
		Reverse	CCCTAAGACTAACGACAACCAA		
8.	SSR32	Forward	TGGAAAGAAGCAGTAGCATTG	186	55
		Reverse	CAACGAACATCCTCCGTTCT		
9.	SSR47	Forward	TCCTCAAGAAATGAAGCTCTGA	191	55
		Reverse	CCTTGGAGATAACAACCACAA		
10.	SSR50	Forward	CCGTGACCCTCTTTACAAGC	205	55
		Reverse	TTGCTTTCTTCTTCGCCATT		
11.	SSR63	Forward	CCACAAACAATTCCATCTCA	250	
		Reverse	GCTTCCGCCATACTGATACG		
12.	SSR65	Forward	GGCAGGAGATTGGTTGCTTA	230	55
		Reverse	TTCCTCCTGTTTCATGCATTC		
13.	SSR76	Forward	ACGGGTCGTCTTTGAAACAA	199	55
		Reverse	CCACCGGATTCTTCTTCGTA		
14.	SSR86	Forward	AGGGCAACAAATCCCTCTTT	210	55
		Reverse	GGAGACGAGGCTGCTTACAC		
15.	SSR92	Forward	AAGAAGAAGGATCGATCGAAGA	172	55
		Reverse	TCATGACCACGATACTACATGTTTC		
16.	SSR94	Forward	AATCAGATCCTTGCCCTTGA	187	55
		Reverse	AGCTGAGAAAGAGCAGCCAT		
17.	SSR99	Forward	GCCTCGGATTCAATAGCATTA	176	55
		Reverse	CACAAAGAAGCAAACAACTCCA		
18.	SSR110	Forward	TGTAACGTCAAACTTCAGGTG	170	55
		Reverse	CTCCGCAATGTGTTGTATGG		
19.	SSR111	Forward	TTCTTCCCTTCCATCAGTTCT	188	55
		Reverse	TTTGCTGCTATACTGCTGACA		
20.	SSR115	Forward	CACCCTTTATTCAGATTCCTCT	211	55
		Reverse	ATTGAGGGTATGCAACAGCC		
21.	SSR214	Forward	AAATTCCCAACACTTGCCAC	221	55
		Reverse	CCCACCACTATCCAAACCC		
22.	SSR248	Forward	GCATTCGCTGTAGCTCGTTT	249	55
		Reverse	GGGAGCTTCATCATAGTAACG		
23.	SSR253	Forward	CCACAAACAATTCCATCTCA	250	55
		Reverse	GCTTCCGCCATACTGATACG		
24.	SSR255	Forward	TGTGAATACAATTTGCACCC	243	55
		Reverse	GGGTTACTAATGCACAAGCGA		
25.	SSR268	Forward	CTGAAGCTGAGAAAGGCGAC	218	55
		Reverse	CTGGCATTTAAGGCAAAGAA		
26.	SSR288	Forward	TCGTGGGAATTTGTTAACCC	275	55
		Reverse	TCTTCATCGTCCTCCTCCTG		

27.	SSR450	Forward	AATGAAGAACCATTCCGCAC		55
		Reverse	ACATGAGCCCAATGAACCTC		
28.	Tom 39A-40A	Forward	TAACACATTCATCAAAGTACC	160-220	45
		Reverse	TTGCGTGATAATCCAGTAAT		
29.	Tom 8-9	Forward	GCATTGATTGAACTTCATTCTCGTCC	175-246	48
		Reverse	ATTTTTGTCCACCAACTAACCG		
30.	Tom11-28	Forward	ATTGTA ATGGTGATGCTCTTCC	207-254	48
		Reverse	CAGTTACTACCAAAAATAGTCAAACAC		
31.	Tom41-42	Forward	GAAATCTGTTGAAGCCCTCTC	164-196	48
		Reverse	GAC TGT GAT AGT AAG AAT GAG		
32.	Tom31A-32A	Forward	AATGTC CTTCGTATCCTTTCGT	182-210	45
		Reverse	CTC GGTTTTAAT TTTTGTGTCT		
33.	Tom43-44	Forward	GCAGGAGATAATAACAGAATAAT	205-232	40
		Reverse	GGTAGAAGCCCGAATATCATT		
34.	Tom47-48	Forward	CAAGTTGATTGCATTACCTATTG	75-95	48
		Reverse	TACAACAACATTTCTTCTTCCTT		
35.	Tom49-50	Forward	AAGAAACTTTTTGAATGTTGC	232-285	48
		Reverse	ATTACAATTTAGAGGTCAAGG		
36.	SLM6-3	Forward	GAAGGGGTTTGGAGCTTTCT	130	55
		Reverse	GACAGAACCCGAATTTGGAC		
37.	SLM6-4	Forward	GGGATCATTTGTTGCTGGTT	172	55
		Reverse	ACACCAAAGGCTCACAACCT		
38.	SLM6-5	Forward	ATGCACGCAAAGGTTATTCC	160	55
		Reverse	AGTCGAAGTTGGCTTGACCA		
39.	SLM6-6	Forward	CCCGTGTCGAATTCTCCTAA	241	55
		Reverse	TCTGCTTCTGCTTCCTCACC		
40.	SLM6-7	Forward	CAATTGAAGATTGGGGCTTT	236	55
		Reverse	AGCAGCTCACCTCACGTTTT		
41.	SLM6-8	Forward	AGTCCACGCAGCATCATTTT	235	55
		Reverse	GTCGTGGTGGATGGTAGTCA		
42.	SLM6-9	Forward	GCCTTGAGGGGAGTCTTAGG	287	55
		Reverse	ACAAGTGCAATGACCAAGCA		
43.	SLM6-10	Forward	ACAGCGTGAGCGAGACAATA	299	50
		Reverse	GCATGTAAGGGGAACCTTGA		
44.	SLM6-11	Forward	CTGATGGGGAAGGACTCTTG	219	55
		Reverse	TCGTCCTTGACACAGGGTAA		
45.	SLM6-12	Forward	GAGATCACGTTTTTCCTTCCA	214	55
		Reverse	GATGGACTATGAAGGAGACTTCG		
46.	SLM6-14	Forward	TCCGTAATAAGTTGAGGAACCA	262	55
		Reverse	TCACAAGAATATTTGCCGTCAT		
47.	SLM6-15	Forward	GGATTTCAGCTGCCTACTGAG	240	55
		Reverse	TTCGGAGAACATAATAGGGGTTT		
48.	SLM6-17	Forward	TCCTTCAAATCTCCCATCAA	186	55
		Reverse	ACGAGCAATTGCAAGGAAAA		
49.	SLM6-18	Forward	TCAAATGGTGCTCCTTATATTTCA	137	55
		Reverse	AGGAGTATGCAAGCTGATCTGA		
50.	SLM6-44	Forward	ATATACCTCATCGCCGTGGA	152	55
		Reverse	GGATCGATTTAACGCACACA		

3.15.7.6 Data analysis/Scoring of data.

Each sample was scored as "1" for each band if a fragment of that size was present, and as "0" if not. A table containing this binary information was used to calculate Similarity matrices using NTSYS (Numerical Taxonomy System Biostatistics) computer program on binary data of selected groups of primers detailed elsewhere. The 0/1 matrix was used to calculate Similarity as coefficient using SIMQUAL subroutine in SIMILARITY routine. Cluster analysis was done within the SAHN program by using UPGMA (unweighted pair-group method with arithmetic averages) method and the results were presented as dendrograms (Rohlf, 1997). Data from all primer combinations were analyzed separately and combined. The dendrograms were visualized and edited using coral draw version 13.

3.15.7.7 Cluster analysis

PCR amplification product of SSR analysis using 10 polymorphic SSR primers were scored as present (1) or absent (0) depending on decreasing order of their molecular weights of each DNA sample. To determine the genetic relationship among isolates, the presence or absence of bands was converted into binary data (1 for presence and 0 for absence of each band). Similarity matrices were calculated using NTSYS (Numerical Taxonomy System Biostatistics) computer program on binary data of selected groups of primers detailed. Cluster analysis was done within the SAHN program by using UPGMA (unweighted pair-group method with arithmetic averages) method.

3.15.7.8 Buffer, Reagents and solutions

3.15.7.8.1 Reagents for PCR

a. Primers: Microsatellite markers from Imperial Life Sciences (p) Ltd. were used.

b. dNTPS: (dATP/dCTP/dGTP/dTTP)

100 mM stock of each dNTPS was diluted to 10 mM of dNTPS (i.e., 10 µl of each dNTPS + 460 µl of sterile water).

c. PCR buffer (10X) (Stored at -20^{0}c)

Table 3.6: Components of PCR buffer

Components	**Stock Concentration**	**Final Concentration**	**For 10 ml**
Tris (pH 8.3)	1 mM	200 mM	2.0 ml
KCl	1 mM	500 mM	2.0 ml
$MgCl_2$	150 mM	15 mM	1.0 ml
Gelatin	-	0.01%	1.0 mg
H_2O	-		2.0 ml

d. Taq polymerase

3.15.7.8.2 Stock solutions

a. DNA extraction buffer

Trizma base	12.11 gm
EDTA disodium salt	18.07 gm
NaCl	29.22 gm
SDS (10%)	12.05 gm

SDS was added after autoclaving when the solution was hot. The pH was adjusted to 8.0 and final volume was adjusted to one liter.

b. 5M Potassium Acetate

490.7 gm Potassium Acetate was dissolved in 350 ml of distilled water and the final volume was made up to one liter and autoclaved.

c. 3M Sodium Acetate

204.12 gm of Sodium Acetate was dissolved in 350 ml of distilled water and pH was adjusted to 5.2 and final volume was made upto 500 ml and autoclaved.

d. 8M Lithium chloride

33.6 gm of Lithium chloride was dissolved in final volume was made upto 100 ml and autoclaved.

e. 4 % PVP

4 gm PVP dissolved in 100 ml CTAB buffer

f. 5M Ammonium Acetate

38.54 gm ammonium acetate dissolve in 100 ml of distill water.

g. TE buffer

Trizma base	1.21 gm
EDTA disodium salt	0.372 gm

pH was adjusted to 8.0, final volume was adjusted to one liter and autoclaved.

h. RNase A

Stock solutions

1. 10 mM Tris HCl (pH 7.5)

2. 15 mM NaCl

10 mg of RNase A was added per ml of above solution, mixed, boiled and allowed to cool at room temperature and stored in freezer.

i. 1M Tris (pH 8.3 at 25° C)

30.28 gm of Trizma base was dissolved in 200 ml of distilled water. The pH was set to 8.3 using concentrated HCl. The final volume was adjusted to 250 ml with distilled water and sterilized by autoclaving.

k. 1M KCl

18.64 gm of Potassium Chloride was dissolved in 200 ml of distilled water and the final volume was made to 250 ml with distilled water and sterilized by autoclaving.

l. 15 mM $MgCl_2$

1.43 gm of Magnesium Chloride was dissolved in 80 ml of distilled water. Final volume was adjusted to 100 ml with distilled water and sterilized by autoclaving.

m. Iso propanol (pre chilled)

n. Absolute alcohol (pre chilled)

o. 76% Ethanol (pre chilled)

p. Tank buffer (1X TAE)

20 ml 50X TAE + 980 ml of distilled water.

q. Orange loading dye

RESULTS AND DISCUSSION

CHAPTER –IV

RESULTS AND DISCUSSION

The results obtained from the present study with respect to mean performance, genetic variability, heritability, genetic advance, correlation, path analysis, genetic and molecular diversity analysis are presented here under:

4.1 Analysis of variance

4.2 Mean performance

4.3 Variability

4.4 Heritability and genetic advance

4.5 Phenotypic and genotypic correlation coefficient analysis

4.6 Path coefficient analysis

4.7 Genetic and molecular diversity analysis

4.1 Analysis of variance

The analysis of variance for the different traits (Table 4.1) indicated that the mean sum of squares due to genotypes were highly significant for all the characters, this is an indication of presence of good amount of genetic variability among the genotypes.

4.2 Mean performance

The observation for each genotype in three replications for fruit yield and its components characters were used for calculating the mean performance. The observations were recorded on five randomly selected tagged competitive plants from each replication and averaged. The mean performance of different genotype and its components characters are presented in table 4.2 and described below.

4.2.1 Days to first flowering

The mean days to first flowering ranged from 21.33 days (Cherry type -1) to 33.67 days (Cherry Tomato-4) with overall mean of 28.88 days. The earliest flowering was noted in Cherry type-1 (21.33 days) which was followed by Pusa Ruby (24.33 days) Cherry Tomato-4×Pant Tomato-3 (25.67 days), Cherry Tomato-3×Cherry Tomato-4 (26.67 days), Cherry Tomato-1×Co-3-1 (27.33 days) and Cherry Tomato-2 (28.00 days) whereas, the delayed flowering was noted in Cherry Tomato -4 (33.67 days).

The results are in accordance with Singh *et al.* (1974) observed days to first flowering ranged from 18.00 to 33.00 days with overall mean of 25.08 days; Prashanth (2003) who reported that days to first flowering ranged from 18.33 to 33.67 days an average 28.02 days and Prema *et al.* (2011) also reported similar range for days to first flowering in Cherry tomato.

4.2.2 Days to 50% flowering

Days to 50% flowering ranged from 25.67 days (Cherry type-1) to 39.67 days (Cherry Tomato-4) with overall mean of 34.96 days. The earliest days to 50% flowering was noted in Cherry type-1 (25.67 days) which was followed by Pusa Ruby (31.33 days), Cherry Tomato-4×Pant Tomato-3 (32.33 days), Cherry Tomato-3×Cherry Tomato-4 (33.33 days), Cherry Tomato-2 (33.67 days) whereas, the delayed days to 50% flowering was noted in Cherry Tomato-4 (39.67 days).

Similar results have been reported by Veershety (2004) reported that the days to 50% flowering ranged from 23.00 to 33.00 days with all over mean of 28.18 days and Prashanth (2003) studied 67 genotypes of tomato and reported that days to 50% flowering ranged from 20.00 to 35.67 days with all over mean of 30.47 days.

4.2.3 Days to fruit set

The days to fruit set ranged from 30.67 days (Pusa Ruby) to 40.33 days (Cherry Tomato-4) with overall mean of 35.22 days. The earliest days to fruit set was noted in Pusa Ruby (30.67 days) which was followed by Cherry Tomato4×Pant Tomato-3 (31.67 days), Cherry type-1, Cherry Tomato-1×Co-3-1 and Cherry Tomato-3×Cherry Tomato-4 (32.67 days), Cherry Tomato-2 (33.33 days) and Cherry Tomato -3 (35.33 days) whereas, the delayed days to fruit set was noted in Cherry Tomato-4 (40.33 days).

Veershety (2004) reported that days to first fruit set ranged from 22.33 to 31.67 days with an average 27.79 days to first fruit set. Prashanth (2003) reported that days to first fruit set ranged from 25.00 to 41.00 days an average 34.78 days.

4.2.4 Days to fruit ripening

Days to fruit ripening ranged from 72.00 days (Cherry type -1) to 79.67 days (Cherry Tomato-9) with overall mean of 76.69 days. The earliest days to fruit ripening was noted in Cherry type-1 (72.00 days) which was followed by Cherry Tomato-4×Pant Tomato-3 (74.67 days), Cherry Tomato-1×Co-3-2 (75.00 days), Cherry Tomato-1 (75.33 days), Cherry Tomato-3×Cherry Tomato-4 (75.67 days), Cherry Tomato-1×Co-3-1 (76.33 days) whereas, the delayed days to fruit ripening was noted in Cherry Tomato-9 (79.67 days).

4.2.5 Average fruit weight (g)

Average fruit (single fruit) weight ranged from 2.90 g (Cherry Tomato-1) to 57.15 g (Cherry Tomato-8) with overall genotypes mean of 17.05g. The maximum average fruit (twenty fruits) weight was recorded in Cherry Tomato-8 (1143.00 g) whereas, the minimum average fruit weight was noted in Cherry Tomato -1 (58.00 g).

Similar result are accordance with Sahu (2005) reported that fruit weight ranged from 42.50 to 95.8 g and over all mean from 65.59 g; Mehta and Asati (2008) reported that fruit weight ranged from 42.50 to 95.83 g average fruit weight was recorded 65.59 g and Trivedi (1996) reported fruit weight range from 80.48 to 126.46 g.

4.2.6 Fruit length (cm)

The fruit length ranged from 1.63cm (Cherry Tomato-1) to 4.17 cm (Cherry Tomato-8) with overall mean of 2.62 cm. The maximum fruit length was recorded in Cherry Tomato-8 (4.17 cm) whereas; the minimum fruit length was recorded in Cherry Tomato-1 (1.63 cm). Shorter fruit length in genotype cherry tomato 1 may due to character of cerasiforme species.

Similar finding have been reported by Prema *et al.* (2011), Naidu (2001), Manna and Paul (2012), Trivedi (1996), Ghosh *et al.* (2010) and Kaushik *et al.* (2011).

4.2.7 Fruit girth (cm)

Fruit girth ranged from 1.76 cm (Cherry Tomato-1) to 5.16 cm (Cherry Tomato-8) with over all mean of 3.10 cm. The maximum fruit girth was observed in Cherry Tomato-8 (5.16 cm) and Cherry Tomato-7(4.79 cm). Whereas the minimum fruit girth was observed in Cherry Tomato-1 (1.76 cm).

4.2.8 Pericarp thickness (mm)

The pericarp thickness ranged from 0.10 mm (Cherry Tomato-1, Cherry Tomato-3, Cherry Tomato-5, Cherry Tomato-3×Cherry Tomato-4) to 0.47 mm (Pusa Ruby) with overall mean of 0.25 mm. The maximum pericarp thickness was observed in Pusa Ruby (0.47 mm) which was found to be statistically similar with Cherry Tomato-8 (0.44 mm) whereas, minimum pericarp thickness was observed in Cherry

Tomato-1, Cherry Tomato-3, Cherry Tomato-5, Cherry Tomato-3×Cherry Tomato-4 (0.10 mm). However, the very thin pericarp thickness of some genotype may be due to genetic character of particular genotype of small fruited tomato.

The findings are in accordance with Naidu (2001) reported found pericarp thickness ranged from 0.24 cm to 0.78 cm; Manna and Paul (2012) reported that pericarp thickness ranged from 0.37 to 0.70 cm with over all mean of 0.51 cm Shashikanth (2008) also reported similar results.

4.2.9 Numbers of locules per fruit

Numbers of locules per fruit ranged from 2.00 (Cherry Tomato-3) to 3.80 (Cherry Tomato-7) with overall mean of 2.78. The maximum numbers of locules per fruit was observed in Cherry Tomato-7 (3.80) which was found to be statistically similar with Cherry Tomato-1×Co-3-2 (3.67) whereas, minimum numbers of locules per fruit was observed in Cherry Tomato-3 (2.00).

The results are in accordance with Kumar *et al.* (2006), Shashikanth (2008) and Tiwari and Upadhyay (2011).

4.2.10 Plant height (cm)

The plant height ranged from 40.13 cm (Pusa Ruby) to 168.47 cm (Cherry Tomato-5) with overall genotypes mean of 112.26 cm. The maximum plant height was observed in Cherry Tomato-5 (168.47 cm) which was found to be statistically similar with Cherry Tomato-2 (158.00 cm) whereas, the minimum plant height was observed in Pusa Ruby (40.13 cm).

Similar results were also reported by Singh *et al.* (2000), Mohanty (2003), Aradhana Joshi and Singh (2003) and Arun *et al.* (2004) for plant height in tomato.

4.2.11 Number of primary branches per plant

Number of primary branches per plant ranged from 7.07 (Cherry Tomato-8) to 16.60 (Cherry Tomato-2) with overall genotypes mean of 12.95. The maximum number of primary branches per plant was observed in Cherry Tomato-2 (16.60) whereas, the minimum number of primary branches per plant was observed in Cherry Tomato-8 (7.07).

Similar results were also reported by Naidu (2001), Golani *et al.* (2007), Mehta and Asati (2008a) and Sahu (2005) for numbers of primary branches per plant in tomato.

4.2.12 Number of secondary branches per plant

Number of secondary branches per plant ranged from 9.20 (Cherry Tomato-8) to 45.87 (Cherry Tomato-4) with overall genotypes mean of 25.99. The maximum number of secondary branches per plant was observed in Cherry Tomato-4 (45.87) which was followed by Cherry Tomato-2 (39.73) and Cherry Tomato-1 (37.40) whereas, the minimum number of secondary branches per plant was observed in Cherry Tomato-8 (9.20).

4.2.13 Number of flowers per cluster

Number of flowers per cluster ranged from 4.47 (Pusa Ruby) to 8.93 (Cherry type -1) with overall mean of 5.82. The highest number of flowers per cluster was noted in Cherry type-1 (8.93), Cherry Tomato-2, Cherry Tomato-4×Pant Tomato-3 (6.00) whereas, the lowest number of flowers per cluster was noted in Pusa Ruby (4.47).

The result was accordance with Prashanth (2003) reported number of flowers per cluster ranged from 4.13 to 7.53 with over all mean of 5.76 while Joshi and Singh (2005), Prema *et al.* (2011a) also reported similar results in tomato.

4.2.14 Number of fruits per cluster

Number of fruits per cluster ranged from 3.93 (Pusa Ruby) to 7.40 (Cherry type-1) with overall mean of 5.05. The highest number of fruits per cluster was noted in Cherry type-1 (7.40) which was found to be statistically similar with Cherry Tomato-3 (5.80) and Cherry Tomato-2 (5.47) whereas, the lowest number of fruits per cluster was noted in Pusa Ruby (3.93).

The results was similar with Singh *et al.* (2000) reported number of fruits per cluster ranged from 4.30 to 8.70 with over all mean of 5.90 and Mohanty (2003), Prashanth (2003) Mehta and Asati (2008) Prema *et al.* (2011a) also reported similar results.

4.2.15 100 seed weight (g)

100 seed weight ranged from 0.14 g (Cherry Tomato-3 and Cherry Tomato-5) to 0.34 g (Pusa Ruby) with over all mean of 0.21 g. The highest 100 seed weight was noted in Pusa Ruby (0.34 g) which was followed by Cherry Tomato-8 (0.32 g) whereas; the lowest 100 seed weight was noted in Cherry Tomato-3 and Cherry Tomato-5 (0.14 g). Light weight of Cherry tomato seeds may be due to genetic character of the cerasiforme species.

4.2.16 Days to first fruit harvest

Days to first fruit harvest ranged from 83.67 days (Cherry Tomato-1, Cherry Tomato-3 and Cherry Tomato-1×Co-3-1) to 87.67 days (Cherry Tomato-9) with over all mean of 85.08 days. The earliest days to first fruit harvest was noted in Cherry Tomato-1, Cherry Tomato-3 and Cherry Tomato-1×Co-3-1 (83.67 days) which was followed by Cherry Tomato-7, Cherry type-1, Cherry Tomato-3×Cherry Tomato-4, Cherry Tomato-4×Pant Tomato-3, Pusa Ruby (84.33 days) and Cherry Tomato-2,

Fig: 4.1a Variation in fruit morphology of Cherry tomato genotypes

Cherry Tomato-5, Cherry Tomato-8, Cherry Tomato-1×Co-3-2 (85.67 days) whereas, the delayed days to first fruit harvest was noted in Cherry Tomato-9 (87.67 days).

4.2.17 Number of fruits per plant

Number of fruits per plant ranged from 42.60 (Pusa Ruby) to 238.27 (Cherry Tomato-2) with overall mean of 132.46. The highest number of fruits per plant was noted in Cherry Tomato-2 (238.27) which was found to be statistically similar with Cherry Tomato-9 (221.80) and Cherry Tomato-1 (208.87) whereas, the lowest number of fruits per plant was noted in Pusa Ruby (42.60).

Similar results were also reported by Nandapuri *et al.* (1977), Anupam *et al.* (2002), Mehta and Asati (2008) and Sahu (2005) for number of fruits per plant in tomato.

4.2.18 Fruit weight per plant (kg)

Fruit weight per plant ranged from 0.46 kg (Cherry Tomato-5) to 2.56 kg (Cherry Tomato-8) with overall mean of 1.26 kg. The highest fruit weight per plant was noted in Cherry Tomato-8 (2.56 kg) which was found to be *statistically at par* with Cherry Tomato-7 (1.89 kg), Pusa Ruby (1.73 kg), Cherry Tomato-1×Co-3-2 (1.58 kg), Cherry Tomato-4 (1.51 kg), Cherry Tomato-1×Co-3-1 (1.49 kg) and Cherry Tomato-4×Pant Tomato-3 (1.35 kg) whereas, the lowest fruit weight per plant was noted in Cherry Tomato-5 (0.46 kg).

The result was similar with Tiwari and Upadhyay (2011) reported an average of 0.826 kg per plant and ranged from 0.76 kg to 0.89 kg and Naidu (2001) reported fruit yield per plant ranged from 0.79 kg to 1.58 kg per plant and overall mean from 1.068 kg.

Fig: 4.1b Variation in fruit morphology of Cherry tomato genotypes

4.2.19 Total soluble solid (%)

Total soluble solid percent ranged from 3.52% (Cherry Tomato-1×Co-3-1) to 6.44% (Cherry type-1) with overall mean of 5.04%. The highest total soluble solid percent was noted in Cherry type-1 (6.44%) which was followed by Cherry Tomato-2 (6.32%), Cherry Tomato-5 (6.28%) Cherry Tomato-3×Cherry Tomato-4 (5.71%), Cherry Tomato-4×Pant Tomato-3 (5.47%) and Cherry Tomato-1×Co-3-3 (5.44%) whereas, the lowest total soluble solid percent was noted in Cherry Tomato-1×Co-3-1 (3.52%) Similar result are also reported by Akhilesh and Gulshanlal (2005) 4.04 % to 6.34% Sahu (2005) observed that total soluble solid percent ranges from 3.28% to 4.85% and Mehta and Asati (2008) reported an average 3.87% total soluble solid and ranged from 3.28% to 4.85%. Prema *et al.* (2011a) also reported similar results.

4.2.20 Acidity %

Acidity ranged from 0.91 (Cherry Tomato-1×Co-3-1) to 1.44 (Cherry Tomato-2) with over all mean of 1.08. The maximum acidity was observed in Cherry Tomato-2 (1.44) which was found to be *statistically at par* with Cherry Tomato-5 (1.35) whereas, the minimum acidity was observed in Cherry Tomato-1×Co-3-1 (0.91).

The results are in accordance with Manna and Paul (2012) reported that acidity ranged from 0.30 to 0.73 and overall mean from 0.48; Naidu (2001) reported that acidity ranged from 0.23 to 0.54 percent and Trivedi (1969) that acidity ranged from 0.22 to 0.41 percent and Prema *et al.* (2011a) also reported similar results.

4.2.21 Number of picking

Mean Number of picking ranged from 5.33 (Cherry Tomato-7) to 9.33 (Cherry Type-1) with over all mean of 7.22. The maximum number of picking was noted in Cherry Type-1(9.33) which was found to be *statistically at par* with Cherry Tomato-5 (9.00) whereas; the lowest number of picking was noted in Cherry Tomato-7 (5.33).

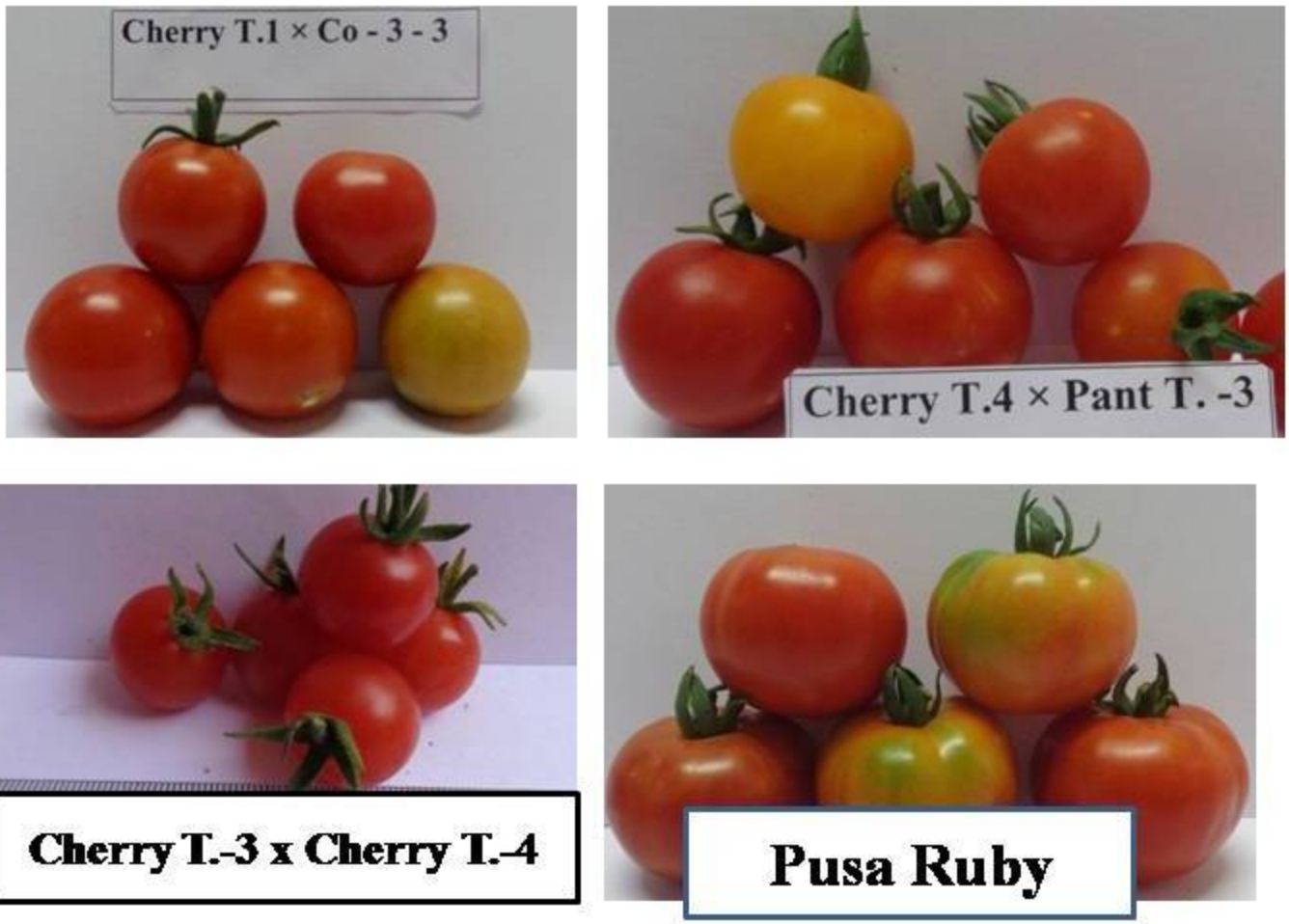

Fig: 4.1c Variation in fruit morphology of Cherry tomato genotypes

4.2.22 Crop duration

The crop duration ranged from 110.00 days (Cherry Tomato-1×Co-3-1) to 124.33 days (Cherry Tomato-9) with over all mean of 115.64 days. The maximum days of crop duration was noted in Cherry Tomato-9 (124.33 days) which was found to be *statistically at par* with Cherry Tomato-3 (120.33 days) whereas, the minimum days of crop duration was noted in Cherry Tomato-1×Co-3-1 (110.00).

4.2.23 Marketable yield per plot (kg)

Mean marketable yield per plot ranged from 15.71 kg (Cherry Tomato-5) to 32.62 kg (Cherry Tomato-8) with over all mean of 24.76 kg. The highest marketable yield per plot was noted in Cherry Tomato-8 (32.62 kg) which was found to be *statistically at par* with Pusa Ruby (32.46 kg) whereas; the lowest marketable yield per plot was noted in Cherry Tomato-5 (15.71kg). Lower marketable yield of cherry tomato genotype may be due to their yield potential.

4.2.24 Marketable Fruit yield (q/ha)

The marketable fruit yield ranged from 78.53q (Cherry Tomato-5) to 163.12 q (Cherry Tomato-8) with over all mean of 123.79 q. The highest marketable fruit yield was noted in Cherry Tomato-8 (163.12 q) which was found to be *statistically at par* with Pusa Ruby (162.28 q), Cherry Tomato-1×Co-3-2 (153.03 q), Cherry Tomato-1×Co-3-1 (140.57 q) and Cherry Tomato-1×Co-3-3 (132.68 q.) whereas, the lowest marketable fruit yield was noted in Cherry Tomato-5 (78.53q). Lower marketable yield of cherry tomato genotype may be due to their yield potential.

Tiwari and Upadhyay (2011) studied 19 genotypes of tomato and reported that fruit yield per hectare ranged from 318.98q to 369.99 q per hectare and Mehta and Asati (2008) who reported fruit yield per hectare ranged from 354.00q to 506.00 q with overall mean of 453.59 q per hectare.

Cherry Tomato- 1

Cherry Tomato-2

Cherry Tomato - 3

Cherry Tomato- 4

Cherry Tomato- 5

Cherry Tomato- 7

Cherry Tomato- 8

Cherry Tomato- 9

Fig:4.2a variation in leaf structure of Cherry tomato

Cherry Type - 1

Cherry T. 1 x Co- 3-1

Cherry T. 1x Co-3-2

Cherry T.1 x Co-3-3

Cherry T.3x Cherry T.4

Cherry T.4x Cherry T. 3

Pusa Ruby

Fig:4.2b variation in leaf structure of Cherry tomato

4.2.25 Total Fruit yield (q/ha)

The total fruit yield ranged from 85.50q (Cherry Tomato-5) to 183.38 q (Pusa Ruby) with over all mean of 135.44 q. The highest total fruit yield was noted in Pusa Ruby (183.38 q) which was found to be *statistically at par* with Cherry Tomato-8 (178.02 q). Among all the Cherry tomato genotypes Cherry tomato 8 (178.02 q) was found superior for total fruit yield (q/ha) which is followed by Cherry Tomato-1×Co-3-2 (175.17 q), Cherry Tomato-1×Co-3-1 (157.10 q) and Cherry Tomato-1×Co-3-3 (144.04 q) whereas, the lowest total fruit yield was noted in Cherry Tomato-5 (85.50 q).

4.3 Variability

The information on the nature of extent of genetic variability present in the population for desirable characters is very important for crop improvement programme. The knowledge of genotypic and phenotypic coefficient of variation is being useful in designing selection criteria from variable population.

Genotypic and phenotypic coefficients of variation of different characters are presented in Table 4.3. High phenotypic and genotypic coefficients of variation were observed for average fruit weight (97.45 and 97.25%), pericarp thickness (55.10 and 54.84%), number of fruits per plant (50.05 and 49.94%), fruit weight per plant (44.37 and 44.07%), plant height (39.32 and 39.19%), fruit girth (35.67 and 35.65%), fruit length (31.39 and 31.35%), 100 seed weight (29.63 and 29.15%), number of primary branches per plant (26.20 and 25.35%), numbers of locules per fruit (23.75 and 22.90%), total fruit yield (22.47 and 21.98%), number of flowers per cluster (17.38 and 16.76%), number of fruits per cluster (16.14 and 15.16%) whereas, moderate phenotypic and genotypic coefficient of variation were observed for days to first flowering (12.41 and 11.14%), days to 50% flowering (10.78 and 9.74%), days to

Table 4.1: Analysis of variance for fruit yield and its component characters in cherry tomato

S. No.	Character	Mean sums of square		
		Replication	Treatment	Error
	(df)	2	14	28
01	Days to first flowering	0.35	33.55**	2.49
02	Days to 50% flowering	0.20	37.37**	2.59
03	Days to fruit set	0.28	24.12**	2.12
04	Days to fruit ripening	2.50	12.07**	2.41
05	Average fruit weight (g)	0.39	331.2**	4.46
06	Fruit length (cm.)	3.46	2030.7**	1.70
07	Fruit girth (cm.)	0.25	3.70**	1.02
08	Pericarp thickness	8.08	560.69**	1.80
09	Numbers of locules per fruit	0.24	12.48**	3.06
10	Plant height (cm.)	0.97	581.9**	1.36
11	Number of primary branches per plant	0.21	33.06**	7.36
12	Number of flowers per cluster	9.86	29.32**	7.10
13	Number of fruits per cluster	0.70	18.41**	7.87
14	100 seed weight	7.26	12.32**	1.33
15	Days to first fruit harvest	0.70	4.68**	1.44
16	Number of fruits per plant	1.09	131.4**	2.05
17	Fruit weight per plant (Kg.)	1.23	940.82**	4.21
18	Total fruit yield (q/ha)	5.85	26.99**	3.94

***Significant at 0.05, ** significant at 0.01**

Cherry Tomato- 1

Cherry Tomato-2

Cherry Tomato - 3

Cherry Tomato- 4

Cherry Tomato- 5

Cherry Tomato- 7

Cherry Tomato- 8

Cherry Tomato- 9

Fig: 4.3a variation in number of locules in Cherry tomato

Cherry Type - 1

Cherry T. 1 x Co- 3-1

Cherry T. 1x Co-3-2

Cherry T.1 x Co-3-3

Cherry T.3x Cherry T.4

Cherry T.4x Cherry T. 3

Pusa Ruby

Fig: 4.3b variation in number of locules in Cherry tomato

fruit set (8.73 and 7.69%), days to fruit ripening (3.10 and 2.34%) and days to first fruit harvest (1.87 and 1.22%)

These results are in accordance with the findings of Mohanty (2003), Manivannan *et al.* (2005), Mahesha *et al.* (2006), Ahmed *et al.* (2006), Mehta and Asati (2008), Tiwari and Upadhyay (2011), Dar and Sharma (2011), Manna and Paul (2012) Verma (1996), Das *et al.* (1998), Prasad and Rai (1999), Naidu (2001), Singh *et al.* (2002b), Joshi *et al*. (2004), Kumar *et al.* (2004), Golani *et al.* (2007), Shashikanth (2008), Ghosh *et al.* (2010) and Kaushik *et al.* (2011).

4.4 Heritability and genetic advance

Heritability estimate provides the information regarding the amount of transmissible genetic variation to total variation and determines genetic improvement and response to selection. The term heritability in broad sense was defined as the ratio of genetic variance to the total phenotypic variance (Lush, 1940; Jonson *et al*., 1955).

The estimates of genetic advance as percentage of mean provide more reliable information regarding the effectiveness of selection in improving a trait. Genetic advance denotes the improvement in the genotypic value of the new population compared to the original population. Thus, the estimates of heritability and genetic advance are of great significance to the vegetable breeders for developing suitable selection strategy.

Broad sense heritability estimates and genetic advance expressed as percentage of mean have been presented in Table 4.3. Most of the characters showed high broad sense heritability. Among the characters studied, highest heritability estimate was recorded for fruit girth (99.8%), fruit length (99.7%), average fruit weight (99.6%), number of fruits per plant (99.5%), plant height (99.3%), pericarp thickness (99.0%), fruit weight per plant (98.7%), 100 seed weight (96.8%), total fruit

Table – 4.2 Mean performances for fruit yield and its components along with quality traits in cherry tomato

Characters / Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
Cherry Tomato 1	29.67	36.33	36.00	75.33	58.00	1.63	1.76	0.10	2.20	147.67	14.07	37.40	5.93	5.07	0.15	83.67	208.87	0.59	5.36	1.18	7.00	119.33	25.53	127.67	139.68
Cherry Tomato 2	28.00	33.67	33.33	76.67	116.67	1.96	2.32	0.14	2.40	158.00	16.60	39.73	6.00	5.47	0.17	85.67	238.27	1.06	6.32	1.44	8.33	120.00	21.21	106.05	112.95
Cherry Tomato 3	29.33	35.67	35.33	76.67	95.33	1.97	2.13	0.10	2.00	151.20	16.53	37.47	6.60	5.80	0.14	83.67	204.87	0.81	4.68	0.94	7.33	120.33	19.22	96.10	102.12
Cherry Tomato 4	33.67	39.67	40.33	79.00	232.00	2.55	2.93	0.23	2.20	78.07	15.67	45.87	5.53	4.93	0.24	86.67	155.00	1.51	4.64	0.97	6.33	111.67	19.95	99.77	107.13
Cherry Tomato 5	31.00	37.33	37.00	77.33	65.67	1.65	1.82	0.10	2.27	168.47	14.60	31.07	5.47	4.93	0.14	85.67	143.80	0.46	6.28	1.35	9.00	118.33	15.71	78.53	85.50
Cherry Tomato 7	32.33	38.67	38.33	77.00	715.00	3.97	4.79	0.43	3.80	44.33	8.07	10.07	5.53	4.80	0.24	84.33	52.07	1.89	4.13	0.98	5.33	112.67	25.73	128.63	137.72
Cherry Tomato 8	30.67	35.67	36.33	77.33	1143.00	4.17	5.16	0.44	3.40	45.73	7.07	9.20	5.13	4.27	0.32	85.67	47.93	2.56	4.23	0.94	6.67	114.00	32.62	163.12	178.02
Cherry Tomato 9	32.33	38.33	38.67	79.67	97.67	1.83	2.20	0.12	3.27	120.40	14.60	19.80	5.80	5.07	0.16	87.67	221.80	1.04	4.55	0.93	8.00	124.33	19.02	95.08	102.03
Cherry type – 1	21.33	25.67	32.67	72.00	134.67	2.40	2.47	0.20	2.13	73.60	9.20	10.13	8.93	7.40	0.18	84.33	78.73	0.59	6.44	1.28	9.33	114.67	21.88	109.38	121.22
C. T.1 × Co -3 -1	27.33	33.33	32.67	76.33	353.67	2.91	3.28	0.33	2.93	131.60	13.00	28.47	5.47	4.73	0.26	83.67	131.87	1.49	3.52	0.91	7.33	110.00	28.11	140.57	157.10
C. T.1 × Co -3 -2	30.33	36.00	35.67	75.00	651.33	3.51	4.19	0.31	3.67	115.00	12.73	18.13	5.80	5.00	0.25	85.67	114.33	1.58	4.35	1.01	6.33	114.67	30.61	153.03	175.17
C. T.1 × Co -3 -3	30.67	37.00	37.00	79.00	245.33	2.59	2.95	0.33	2.13	135.00	11.13	26.27	5.07	4.53	0.26	86.67	79.27	1.07	5.44	1.20	6.67	115.33	26.54	132.68	144.40
C. T.3 × C. T.4	26.67	33.33	32.67	75.67	135.33	2.05	2.52	0.10	3.40	135.73	16.40	31.87	5.67	4.93	0.17	84.33	170.67	1.29	5.71	0.93	7.67	114.33	26.28	131.42	141.85
C.T.4 × Pant T.-3	25.67	32.33	31.67	74.67	259.67	2.81	3.37	0.33	2.53	139.00	15.87	21.47	6.00	5.00	0.25	84.33	96.87	1.35	5.47	1.08	6.67	110.67	26.51	132.53	143.42
Pusa Ruby	24.33	31.33	30.67	78.67	818.67	3.35	4.63	0.47	3.40	40.13	8.73	22.93	4.47	3.93	0.34	84.33	42.60	1.73	4.50	1.09	6.33	114.33	32.46	162.28	183.38
Mean (x)	28.88	34.96	35.22	76.69	341.47	2.62	3.10	0.25	2.78	112.26	12.95	25.99	5.82	5.05	0.21	85.08	132.46	1.26	5.04	1.08	7.22	115.64	24.76	123.79	135.44
SEm±	0.53	0.54	0.49	0.52	7.05	0.01	0.01	0.00	0.06	1.23	0.29	0.90	0.09	0.09	0.00	0.40	1.51	0.02	0.05	0.02	0.38	0.51	0.41	2.04	2.09
CD (p=0.05)	1.53	1.56	1.41	1.50	20.41	0.04	0.04	0.01	0.17	3.57	0.83	2.60	0.26	0.27	0.01	1.16	4.38	0.06	0.15	0.05	1.11	1.49	1.18	5.92	6.06
CV (%)	5.47	4.60	4.14	2.03	6.19	1.57	0.10	5.40	6.29	3.29	6.62	10.36	4.57	5.54	5.29	1.41	3.42	5.12	3.02	4.55	1.07	1.33	4.95	4.95	4.63

(1) Days to first flowering
(2)Days to 50% flowering
(3) Days to fruit set
(4) Days to fruit ripening
(5) Average (twenty) fruit weight (g)
(6) Fruit length (cm.)
(7) Fruit girth (cm.)
(8.) Pericarp thickness
(9) Numbers of locules per fruit
(10) Plant height (cm.)
(11)No. of primary branches/plant
(12) No. of secondary branches/plant
(13)Number of flowers per cluster
(14) Number of fruits per cluster
(15) 100 seed weight
(16) Days to first fruit harvest
(17) Number of fruits per plant
(18) Fruit weight per plant (Kg.)
(19) TSS%
(20.) Acidity %
(21.)Number of picking
(22.) Crop duration
(23.) Marketable yield per plot (Kg.)
(24.)Marketable fruit yield (q/ha)
(25.)Total fruit yield (q/ha)

yield (95.7%), number of primary branches per plant (93.6%), number of flowers per cluster (93.1%), numbers of locules per fruit (93.0%), number of fruits per cluster (88.2%), days to 50% flowering (81.7%), days to first flowering (80.6%) and days to fruit set (77.6%). Whereas, moderate heritability estimates was observed for days to fruit ripening (57.1%) and days to first fruit harvest (42.7%).

Present findings are in accordance with Naidu (2001), Kumar *et al*. (2004), Ahmed *et al*. (2006). These results are conformity with the findings of Mariame *et al*. (2003) for plant height and number of seeds per fruit while Joshi *et al*. (2004) reported moderate heritability for fruit length, fruit width, number of locules per fruit and plant height; Singh *et al*. (2005) for total soluble solids (TSS), pericarp thickness, fruit length and acidity; Mahesha *et al*. (2006) for fruit weight and plant height; Singh *et al*. (2006) for average weight of fruits, number of leaves per plant, number of locules per fruit; Tiwari and Upadhyay (2011) for fruit weight, days to 50% flowering, fruit width and plant height and Manna and Paul (2012) for number of locules and fruit, fruit weight and fruit length.

Genetic advance was worked out as percent mean for all the characters and presented in Table 4.3. The highest estimate of genetic advance as percent of mean was recorded for average fruit weight (99.30%) followed by pericarp thickness (98.66%), number of fruits per plant (98.62%), fruit weight per plant (90.47%), plant height (80.44%), fruit girth (73.70%), fruit length (64.50%), 100 seed weight (61.90%), number of primary branches per plant (50.50%), numbers of locules per fruit (45.68%), total fruit yield (44.31%), number of flowers per cluster (33.33%), number of fruits per cluster (29.30%), days to first flowering (20.60%) whereas, moderate genetic advance was obtain for days to 50% flowering (18.14%), days to

Table – 4.3 Genetic parameters of variation for fruit yield and its component characters in cherry tomato

S.No.	Characters	Mean	Range		Coefficient of variation (%)		Heritability (h^2 %)	Genetic advance as % of mean
			Minimum	Maximum	Phenotypic	Genotypic		
1	Days to first flowering	28.88	21 .33	33.67	12.41	11.14	80.6	20.60
2	Days to 50% flowering	34.95	25.67	39.67	10.78	9.74	81.7	18.14
3	Days to fruit set	35.22	30.67	40.33	8.73	7.69	77.6	13.94
4	Days to fruit ripening	76.68	72.00	79.67	3.10	2.34	57.1	3.63
5	Average fruit weight (g)	341.46	58.00	1143.00	97.45	97.25	99.6	99.30
6	Fruit length (cm.)	2.62	1.63	4.17	31.39	31.35	99.7	64.50
7	Fruit girth (cm.)	3.10	1.76	5.16	35.84	35.80	99.83	73.70
8	Pericarp thickness	0.24	0.10	0.47	55.10	54.84	99.0	98.66
9	Numbers of locules per fruit	2.78	2.13	3.80	23.75	22.90	93.0	45.68
10	Plant height (cm.)	112.26	40.13	168.47	39.32	39.19	99.3	80.44
11	Number of primary branches per plant	12.95	7.07	12..73	26.20	25.35	93.6	50.50
12	Number of flowers per cluster	5.82	4.47	8.93	17.38	16.76	93.1	33.33
13	Number of fruits per cluster	5.05	3.93	7.40	16.14	15.16	88.2	29.30
14	100 seed weight	0.21	0.14	0.34	29.63	29.15	96.8	61.90
15	Days to first fruit harvest	85.08	83.67	87.67	1.87	1.22	42.7	1.64
16	Number of fruits per plant	132.46	42.60	238.27	50.05	49.94	99.5	98.62
17	Fruit weight per plant (Kg.)	1.26	0.46	2.56	44.37	44.07	98.7	90.47
18	Total fruit yield (q/ha)	135.44	85.50	183.39	22.47	21.98	95.7	44.31

fruit set (13.94%), days to fruit ripening(3.63%) and days to first fruit harvest (1.64%) had lower genetic advance.

These results are in agreement with the finding of Sahu (2005) for weight of fruit per plant, number of locules per fruit, average fruit weight, plant height, number of branches per plant, number of fruits per plant; Naidu (2001) for fruit weight, acidity and pericarp thickness; Sahu and Mishra (1995) for fruit yield per plant and number of fruit per plant; Das *et al*. (1998) for number of fruits per plant, fruit weight, fruit diameter, fruit length and number of locules per fruit; and Mohanty (2002) for average fruit weight, number of branches per plant, number of fruits per plant, plant height and days to first harvest. The present findings are similar to the results of Joshi *et al*. (2004), Singh *et al*. (2006), Mehta and Asati (2008), Tiwari and Upadhyay (2011) and Ghosh *et al.* (2010).

On the other hand, high estimates of heritability coupled with high genetic advance as percentage of mean were observed for fruit girth (99.83 and 73.70%), fruit length (99.7 and 64.50%), average fruit weight (99.6 and 99.30%), number of fruits per plant (99.5 and 98.62%), plant height (99.3 and 80.44%), pericarp thickness (99.0 and 98.66%), fruit weight per plant (98.7 and 90.47%), 100 seed weight (96.8 and 61.90%), total fruit yield (95.7 and 44.31%), number of primary branches per plant (93.6 and 50.50) and number of flowers per cluster (93.1 and 33.33) These results are in accordance with the findings of Brar *et al.* (2000) for number of fruit per plant and total yield per plant; Joshi *et al.* (2004) for fruit width and pericarp thickness; Singh *et al*. (2006) for average weight of fruits, number of fruits per plant and plant height; Mehta and Asati (2008) for fruit yield per hectare, plant height, number of cluster per plant, number of locules per fruit, number of branches per plant and weight of fruit per plant; Kaushik *et al.* (2011) for fruit yield and Manna and Paul (2012) for number

of locules per fruit, fruit weight, fruit weight, number of fruit per plant and pericarp thickness.

4.5 Phenotypic and genotypic correlation coefficient analysis

Association analysis is an important approach in a breeding programme. It gives an idea about relationship among the various characters and determines the component characters, on which selection can be used for genetic improvement in the fruit yield. The degree of association also affects the effectiveness of selection process. The degree of association between independent and dependent variables was first suggested by Galton in (1888), its theory was developed by Pearson (1904) and their mathematical utilization at phenotypic, genotypic and environmental levels was described by Searle (1961).

The genotypic and phenotypic correlation coefficient for fruit yield and its component character in Cherry tomato are presented in Table 4.5 and only significant correlations are discussed here.

The total fruit yield showed positive correlation with average fruit weight (0.777 and 0.760), fruit length (0.745 and 0.728), fruit girth (0.781 and 0.765), pericarp thickness (0.770 and 0.744) , numbers of locules per fruit (0.605 and 0.566) and fruit weight per plant (0.697 and 0.678) at genotypic and phenotypic levels and 100 seed weight (0.829) at genotypic level only. Whereas, number of primary branches per plant (-0.581 and -0.560) and number of fruits per plant (-0.625 and 0.610) expressed significant negative correlation at genotypic and phenotypic levels.

Days to first flowering expressed significant positive correlation with days to 50% flowering (0.992 and 0.964) and days to fruit set (0.901 and 0.909) at genotypic and phenotypic levels and days to fruit ripening (0.762), days to first fruit harvest (0.687) at genotypic level only . Whereas, number of flowers per cluster (-0.517)

expressed significant negative correlation at genotypic level only.

Days to 50% flowering expressed significant positive correlation with days to fruit set (0.838 and 0.846) and days to fruit ripening (0.814 and 0.544) at genotypic and phenotypic levels and days to first fruit harvest (0.595) at genotypic level only. Whereas number of flowers per cluster (-0.619 and -0.524) expressed significant negative correlation at both genotypic and phenotypic levels and number of fruits per cluster (-0.565) at genotypic level.

Days to fruit set had significant positive correlation with days to fruit ripening (0.595) and days to first fruit harvest (0.763) at genotypic level only.

Days to fruit ripening had significant positive correlation with days to first fruit harvest (0.675 and 0.543) at genotypic and phenotypic levels. Whereas number of flowers per cluster (-0.833), number of fruits per cluster (-0.763) expressed significant negative correlation at genotypic level only.

Average fruit weight had significant positive correlation with fruit length (0.938 and 0.934), fruit girth (0.964 and 0.961), pericarp thickness (0.870 and 0.864), numbers of locules per fruit (0.696 and 0.674), 100 seed weight (0.847 and 0.832) and fruit weight per plant (0.898 and 0.893) at both genotypic and phenotypic levels. Whereas plant height (-0.767 and -0.764), number of primary branches per plant (-0.773 and -0.746), number of fruits per plant (-0.734 and -0.731) expressed significant negative correlation at genotypic and phenotypic level and number of fruits per cluster (-0.540) at genotypic level only.

Fruit length showed significant positive correlation with fruit girth (0.983 and 0.981), pericarp thickness (0.927and 0.920), numbers of locules per fruit (0.666 and 0.637), 100 seed weight (0.849 and 0.834) and fruit weight per plant (0.892 and 0.884) at genotypic and phenotypic levels. Whereas plant height (-0.769 and -0.766),

number of primary branches per plant (-0.755 and -0.727) and number of fruits per plant (-0.804 and -0.802) expressed significant negative correlation at genotypic and phenotypic levels.

Fruit girth showed significant positive correlation with pericarp thickness (0.936 and 0.931), numbers of locules per fruit (0.721 and 0.698), 100 seed weight (0.883 and 0.867) and fruit weight per plant (0.917 and 0.908) at genotypic and phenotypic levels. Whereas plant height (-0.783 and -0.778), number of primary branches per plant (-0.733 and -0.714) and number of fruits per plant (-0.787 and -0.785) expressed significant negative correlation at genotypic and phenotypic levels and number of fruits per cluster (-0.515) at genotypic level only.

Pericarp thickness showed significant positive correlation with 100 seed weight (0.953 and 0.933) and fruit weight per plant (0.803 and 0.792) at genotypic and phenotypic levels. Whereas plant height (-0.736 and -0.729), number of primary branches per plant (-0.763 and -0.736) and number of fruits per plant (-0.863 and -0.856) expressed significant negative correlation at genotypic and phenotypic level and number of fruits per cluster (-0.519) at genotypic level only.

Numbers of locules per fruit showed significant positive correlation with fruit weight per plant (0.712 and 0.693) at genotypic and phenotypic levels. Whereas plant height (-0.525) expressed significant negative correlation at genotypic level only.

Plant height showed significant positive correlation with number of primary branches per plant (0.817and 0.784) and number of fruits per plant (0.718 and 0.715) at genotypic and phenotypic levels. Whereas 100 seed weight (-0.686and -0.673) and fruit weight per plant (-0.692 and -0.685) expressed significant negative correlation at genotypic and phenotypic levels.

Number of primary branches per plant had expressed significant positive

correlation with number of fruits per plant (0.842 and 0.811) at genotypic and phenotypic levels. Whereas 100 seed weight (-0.667 and -0.615) expressed significant negative correlation at both genotypic and phenotypic levels and fruit weight per plant (-0.530) at genotypic level only.

Number of flower per cluster expressed significant positive correlation with number of fruits per cluster (0.992 and 0.973) at genotypic and phenotypic levels. Whereas fruit weight per plant (-0.520) expressed significant negative correlation at genotypic level only.

Number of fruits per cluster expressed significant negative correlation with 100 seed weight (-0.603 and -0.546) and fruit weight per plant (-0.608 and -0.568) at genotypic and phenotypic levels.

100 seed weight had expressed significant positive correlation with fruit weight per plant (0.816) at genotypic level whereas number of fruits per plant (-0.791) expressed significant negative correlation at genotypic level only.

Number of fruits per plant expressed significant negative correlation with fruit weight per plant (-0.566 and -0.557) at genotypic and phenotypic levels.

The present findings are in conformity with the result of Blay *et al.* (1999), Prasad and Rai (1999), Sharma and Varma (2000), Naidu, (2001), Harer *et al.* (2002), Singh *et al*.(2002), Kumar *et al*. (2003), Mohanty (2003), Joshi *et al*. (2004), Lakshmi Kant and Mani (2004), Singh *et al*. (2005), Sahu (2005), Kulkarni (2006), Singh *et al.* (2006), Golani *et al.* (2007), Jogi (2007), Mehta and Asati (2008), Prashanth *et al.* (2008), Shashikant (2008), Ghosh *et al.* (2010), Rani *et al.* (2010), Tiwari and Upadhyay (2011), Manna and Paul (2012) and Tasisa *et al.* (2012).

Table – 4.4 Genotypic and phenotypic correlation coefficient between fruit yield and its components in cherry tomato

S.NO.	Characters		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	Days to first flowering	G	1.000	0.992**	0.901**	0.762**	0.075	0.044	0.028	-0.074	0.126	0.063	0.141	-0.517*	-0.464	-0.101	0.687**	0.249	0.210	-0.273
		P	1.000	0.964**	0.909**	0.509	0.046	0.043	0.026	-0.059	0.085	0.065	0.124	-0.436	-0.373	-0.098	0.432	0.217	0.163	-0.256
2	Days to 50% flowering	G		1.000	0.838**	0.814**	0.040	0.001	0.008	-0.075	0.135	0.117	0.212	-0.619*	-0.565*	-0.095	0.595*	0.264	0.185	-0.249
		P		1.000	0.846**	0.544*	0.020	0.005	0.011	-0.060	0.093	0.109	0.168	-0.524*	-0.456	-0.095	0.388	0.233	0.139	-0.239
3	Days to fruit set	G			1.000	0.595*	-0.036	-0.027	-0.081	-0.156	-0.040	-0.076	0.011	-0.178	-0.129	-0.209	0.763**	0.178	0.045	-0.434
		P			1.000	0.410	-0.052	-0.020	-0.070	-0.128	-0.057	-0.059	0.008	-0.142	-0.098	-0.186	0.462	0.152	0.011	-0.399
4	Days to fruit ripening	G				1.000	0.170	0.033	0.130	0.177	0.153	-0.114	0.014	-0.833**	-0.763**	0.248	0.675**	0.093	0.295	-0.118
		P				1.000	0.127	0.026	0.096	0.115	0.103	-0.096	0.013	-0.633	-0.568	0.192	0.543*	0.069	0.223	-0.088
5	Average fruit weight (g)	G					1.000	0.938**	0.964**	0.870**	0.696**	-0.767**	-0.773**	-0.440	-0.540*	0.847**	-0.029	-0.734**	0.898**	0.777**
		P					1.000	0.934**	0.961**	0.864**	0.674**	-0.764**	-0.746**	-0.424	-0.505	0.832**	-0.016	-0.731**	0.893**	0.760**
6	Fruit length (cm.)	G						1.000	0.983**	0.927**	0.666**	-0.769**	-0.755**	-0.308	-0.411	0.849**	-0.083	-0.804**	0.892**	0.745**
		P						1.000	0.981**	0.920**	0.637*	-0.766**	-0.727**	-0.297	-0.385	0.834**	-0.039	-0.802**	0.884**	0.728**
7	Fruit girth (cm.)	G							1.000	0.936**	0.721**	-0.783**	-0.733**	-0.415	-0.515*	0.883**	-0.060	-0.787**	0.917**	0.781**
		P							1.000	0.931**	0.698**	-0.778**	-0.714**	-0.403	-0.485	0.867**	-0.031	-0.785**	0.908**	0.765**
8	Pericarp thickness	G								1.000	0.533*	-0.736**	-0.763**	-0.421	-0.519*	0.953**	-0.062	-0.863**	0.803**	0.770**
		P								1.000	0.504	-0.729**	-0.736**	-0.401	-0.482	0.933**	-0.062	-0.856**	0.792**	0.744**
9	Numbers of locules per fruit	G									1.000	-0.525*	-0.439	-0.419	-0.490	0.461	0.053	-0.375	0.712**	0.605*
		P									1.000	-0.497	-0.410	-0.406	-0.459	0.446	0.005	-0.359	0.693**	0.566*
10	Plant height (cm.)	G										1.000	0.817**	0.088	0.177	-0.686**	-0.009	0.718**	-0.692**	-0.497
		P										1.000	0.784**	0.079	0.163	-0.673**	-0.022	0.715**	-0.685**	-0.481
11	Number of primary branches per plant	G											1.000	0.064	0.165	-0.667**	0.066	0.842**	-0.530*	-0.581*
		P											1.000	0.069	0.153	-0.615*	0.049	0.811**	-0.502	-0.560*

12	Number of flowers per cluster	G												1.000	0.992**	-0.507	-0.290	0.149	-0.520*	-0.380
		P												1.000	0.973**	-0.463	-0.181	0.146	-0.500	-0.373
13	Number of fruits per cluster	G													1.000	-0.603*	-0.243	0.257	-0.608*	-0.498
		P													1.000	-0.546*	-0.119	0.245	-0.568*	-0.475
14	100 seed weight	G														1.000	0.029	-0.791**	0.816**	0.829**
		P														1.000	0.026	-0.776	0.798	0.790
15	Days to first fruit harvest	G															1.000	0.156	0.094	-0.306
		P															1.000	0.095	0.052	-0.222
16	Number of fruits per plant	G																1.000	-0.566*	-0.625*
		P																1.000	-0.557*	-0.610*
17	Fruit weight per plant (Kg.)	G																	1.000	0.697**
		P																	1.000	0.678**
18	Total fruit yield (q/ha)	G																		1.000
		P																		1.000

***Significant at 0.05, ** significant at 0.01**

4.6 Path coefficient analysis

Direct and indirect effect of deferent character on total fruit yield is presented in Table 4.5. The genotypic correlation coefficient of total fruit yield and along with its components was partitioned into direct and indirect effect taking total fruit yield as depended variable.

Fruit length (7.833) expressed highest positive direct effect on total fruit yield followed by average fruit weight (6.703), number of primary branches per plant (3.387), pericarp thickness (3.325), numbers of locules per fruit (2.208), 100 seed weight (1.129), number of fruits per plant (0.880), number of fruits per cluster (0.798), days to first flowering (0.717), days to fruit ripening (0.133) whereas, negative direct effect on total fruit yield was observed for fruit girth (-17.356), plant height (-1.924), fruit weight per plant (-1.581), days to fruit set (-0.975), number of flowers per cluster (-0.707), days to 50% flowering (-0.189) and days to first fruit harvest (-0.149).

Days to of first flowering had positive indirect effect through average fruit weight (0.501), number of primary branches per plant (0.479), number of flowers per cluster (0.365), fruit length (0.341), numbers of locules per fruit (0.278) and days to fruit ripening (0.101) while rest of characters exhibited indirect negative values.

Days to 50% flowering had positive indirect effect through number of primary branches per plant (0.720), days to first flowering (0.711), number of flowers per cluster (0.438), numbers of locules per fruit (0.298), average fruit weight (0.265), days to fruit ripening (0.108) and fruit length (0.011). While rest of characters exhibited indirect negative values.

Days to fruit set had positive indirect effect through fruit girth (1.408), days to first flowering (0.646), plant height (0.146), number of flowers per cluster (0.126),

days to fruit ripening (0.079) and number of primary branches per plant (0.037) whereas, other characters exhibited indirect negative values.

The positive indirect effect of days to fruit ripening recorded on total fruit yield was highest via average fruit weight (1.138), number of flowers per cluster (0.589), pericarp thickness (0.588), days to first flowering (0.546), 100 seed weight (0.280), fruit length (0.259), plant height (0.220) and number of primary branches per plant (0.047) whereas, other characters exhibited indirect negative values.

Average fruit weight had positive indirect effect through fruit length (7.344), pericarp thickness (2.893), numbers of locules per fruit (1.537), plant height (1.475), 100 seed weight (0.956), number of fruits per plant (0.645), number of flowers per cluster (0.311), days to first flowering (0.054), days to fruit set (0.035), days to fruit ripening (0.023) and days to first fruit harvest (0.004) whereas, rest of the characters indirect negative values.

Fruit length had positive indirect effect through average fruit weight (6.285), pericarp thickness (3.081), plant height (1.480), numbers of locules per fruit (1.470) 100 seed weight (0.958), number of fruits per plant (0.708), number of flowers per cluster (0.218), days to first flowering (0.031), days to fruit set (0.026), days to first fruit harvest (0.012) and days to fruit ripening (0.004). Whereas, rest of the characters indirect negative values.

Fruit girth had positive indirect effect through fruit length (7.703), average fruit weight (6.641), pericarp thickness (3.112), numbers of locules per fruit (1.593), plant height (1.505), 100 seed weight (0.997), number of fruits per plant (0.692), number of flowers per cluster (0.294), days to fruit set (0.079), days to first flowering (0.017) and days to first fruit harvest (0.009) while, rest of the characters indirect negative values.

Pericarp thickness had positive indirect effect through fruit length (7.257), average fruit weight (5.833), plant height (1.416), numbers of locules per fruit (1.176), 100 seed weight (1.076), number of fruits per plant (0.759), number of flowers per cluster (0.298), days to fruit set (0.152), days to fruit ripening (0.023), days to 50% flowering (0.014) and days to first fruit harvest (0.009) while, rest of the characters indirect negative values.

Numbers of locules per fruit had positive indirect effect through fruit length (5.217), average fruit weight (4.667), pericarp thickness (1.771), plant height (1.009), 100 seed weight (0.520), number of fruits per plant (0.330), number of flowers per cluster (0.296), days to first flowering (0.090) and days to fruit ripening (0.020) While, rest of the characters indirect negative values.

Plant height had positive indirect effect through fruit girth (13.582), number of primary branches per plant (2.767), fruit weight per plant (1.094), number of fruits per cluster (0.141), days to fruit set (0.074), days to first flowering (0.045) and days to first fruit harvest (0.001) while, rest of the characters indirect negative values.

Number of primary branches per plant had positive indirect effect through fruit girth (12.728), fruit weight per plant (0.838), number of fruits per cluster (0.132), days to first flowering (0.101) and days to fruit ripening (0.002) while, rest of the characters exhibited indirect negative values.

The positive indirect effect of number of flowers per cluster recorded on total fruit yield was highest via fruit girth (7.208), fruit weight per plant (0.822), number of fruits per cluster (0.792), number of primary branches per plant (0.215),days to fruit set (0.174),days to 50% flowering (0.117) and days to first fruit harvest (0.043) whereas, rest of the characters indirect negative values.

Number of fruits per cluster had positive indirect effect through fruit girth (8.944), fruit weight per plant (0.962), number of primary branches per plant (0.559), days to fruit set (0.126), days to 50% flowering (0.107) and days to first fruit harvest (0.036) While, rest of the characters indirect negative values.

100 seed weight had positive indirect effect through fruit length (6.674), average fruit weight (5.675), pericarp thickness (3.167), plant height (1.320), numbers of locules per fruit (1.018), number of fruits per plant (0.696), number of flowers per cluster (0.359), days to fruit set (0.204), days to fruit ripening (0.033) and days to 50% flowering (0.018). Whereas, rest of the characters indirect negative values.

Days to first fruit harvest had positive indirect effect through fruit girth (1.047), days to first flowering (0.492), number of primary branches per plant (0.225), number of flowers per cluster (0.205), numbers of locules per fruit (0.118), days to fruit ripening (0.089),100 seed weight (0.033) and plant height (0.018) While, rest of the characters exhibited indirect negative values.

Number of fruits per plant had positive indirect effect through fruit girth (13.657), number of primary branches per plant (2.851), fruit weight per plant (0.894), number of fruits per cluster (0.205), days to first flowering (0.179) and days to fruit ripening (0.012) whereas, rest of the characters indirect negative values.

Fruit weight per plant had positive indirect effect through fruit length (6.984), average fruit weight (6.018), pericarp thickness (2.669), numbers of locules per fruit (1.579), plant height (1.332), 100 seed weight (0.922), number of flowers per cluster (0.368), number of fruits per plant (0.497), days to first flowering (0.150) and days to fruit ripening (0.039) whereas, rest of the characters indirect negative values.

Overall the path analysis confined that direct effect on total fruit yield of fruit length, average fruit weight, number of primary branches per plant, pericarp

Table – 4.5 Genotypic path coefficient analysis for fruit yield and its component character in cherry tomato

Characters	Days to first flowering	Days to 50% flowering	Days to fruit set	Days to fruit ripening	Average fruit weight (g)	Fruit length (cm.)	Fruit girth (cm.)	Pericarp thickness	Numbers of locules per fruit	Plant height (cm.)	Number of primary branches per plant	Number of flowers per cluster	Number of fruits per cluster	100 seed weight	Days to first fruit harvest	Number of fruits per plant	Fruit weight per plant (Kg.)	Total fruit yield (q/ha)
1	**0.717**	-0.188	-0.878	0.101	0.501	0.341	-0.485	-0.246	0.278	-0.122	0.479	0.365	-0.370	-0.114	-0.102	-0.219	-0.332	-0.273
2	0.711	**-0.189**	-0.817	0.108	0.265	0.011	-0.147	-0.249	0.298	-0.226	0.720	0.438	-0.451	-0.108	-0.088	-0.232	-0.293	-0.249
3	0.646	-0.159	**-0.975**	0.079	-0.243	-0.211	1.408	-0.520	-0.088	0.146	0.037	0.126	-0.103	-0.236	-0.113	-0.156	-0.072	-0.434
4	0.546	-0.154	-0.580	**0.133**	1.138	0.259	-2.262	0.588	0.337	0.220	0.047	0.589	-0.609	0.280	-0.100	-0.082	-0.467	-0.118
5	0.054	-0.007	0.035	0.023	**6.703**	7.344	-16.730	2.893	1.537	1.475	-2.616	0.311	-0.432	0.956	0.004	0.645	-1.419	0.777**
6	0.031	0.000	0.026	0.004	6.285	**7.833**	-17.068	3.081	1.470	1.480	-2.556	0.218	-0.328	0.958	0.012	0.708	-1.410	0.745**
7	0.020	-0.002	0.079	0.017	6.461	7.703	**-17.356**	3.112	1.593	1.505	-2.484	0.294	-0.411	0.997	0.009	0.692	-1.449	0.781**
8	-0.053	0.014	0.152	0.023	5.833	7.257	-16.247	**3.325**	1.176	1.416	-2.585	0.298	-0.415	1.076	0.009	0.759	-1.269	0.770**
9	0.090	-0.026	0.039	0.020	4.667	5.217	-12.522	1.771	**2.208**	1.009	-1.486	0.296	-0.391	0.520	-0.008	0.330	-1.131	0.605*
10	0.045	-0.022	0.074	-0.015	-5.139	-6.027	13.582	-2.447	-1.158	**-1.924**	2.767	-0.062	0.141	-0.775	0.001	-0.632	1.094	-0.497
11	0.101	-0.040	-0.011	0.002	-5.178	-5.912	12.728	-2.538	-0.969	-1.572	**3.387**	-0.045	0.132	-0.753	-0.010	-0.740	0.838	-0.581*
12	-0.370	0.117	0.174	-0.110	-2.951	-2.415	7.208	-1.400	-0.924	-0.170	0.215	**-0.707**	0.792	-0.573	0.043	-0.131	0.822	-0.380
13	-0.333	0.107	0.126	-0.101	-3.623	-3.216	8.944	-1.727	-1.082	-0.340	0.559	-0.701	**0.798**	-0.680	0.036	-0.226	0.962	-0.498
14	-0.072	0.018	0.204	0.033	5.675	6.647	-15.327	3.167	1.018	1.320	-2.260	0.359	-0.481	**1.129**	-0.004	0.696	-1.291	0.829**
15	0.492	-0.113	-0.744	0.089	-0.196	-0.647	1.047	-0.206	0.118	0.018	0.225	0.205	-0.194	0.033	**-0.149**	-0.137	-0.149	-0.306
16	0.179	-0.050	-0.173	0.012	-4.918	-6.301	13.657	-2.868	-0.829	-1.382	2.851	-0.105	0.205	-0.893	-0.023	**0.880**	0.894	-0.625*
17	0.150	-0.035	-0.044	0.039	6.018	6.984	-15.908	2.669	1.579	1.332	-1.795	0.368	-0.486	0.922	-0.014	0.497	**-1.581**	0.697**

Residual effect = 0.0712, **Significant at 0.01, *Significant at 0.05
Bold value show direct effect

thickness, numbers of locules per fruit, 100 seed weight, number of fruits per plant, number of fruits per cluster, days to first flowering and days to fruit ripening should be considered simultaneously for amenability in total fruit yield of cherry tomato.

Similarly positive direct effect of various characters on fruit yield per plant was observed by Barman *et al.* (1996), Patil (1998), Sharma and Varma (2000), Dhankhar *et al.* (2001), Padma *et al*. (2002), Kumar *et al.* (2003), Joshi *et al.* (2004), Lakshmi Kant and Mani (2004), Singh *et al.* (2004), Manivannan *et al.* (2005), Singh (2005), Singh *et al*. (2006), Golani *et al.* (2007), Prashanth *et al.* (2008), Revanasidappa (2008), Sivaprasad (2008), Islam *et al.* (2010), Rani *et al.* (2010), Tiwari and Upadhyay (2011), Atugwu and Uguru (2012) and Tasisa *et al.* (2012).

4.7 Genetic and molecular diversity analysis

4.7.1 Genetic divergence analysis

The concept of D^2 statistics was originally developed by P.C. Mahalonobis (1936). Then C.R. Rao (1952) suggested the application of this technique for the arrangement of genetic diversity in plant breeding. Now, this technique is being extensively used in vegetable breeding also to study the selection of different parents. Genetic variability and selection of parents from diverse breeding material including germplasm and there diverse parents, can be used for the development of hybrids in cherry tomato.

On the basis of D^2 analysis, fifteen genotypes were grouped into three clusters Table (4.6). Maximum number of genotypes were grouped into cluster III (Cherry Tomato-1, Cherry Tomato-2, Cherry Tomato-3, Cherry Tomato-4, Cherry Tomato-5, Cherry Tomato-9, Cherry Tomato-1 × Co -3 -3) included seven genotypes, whereas, cluster I (Cherry type -1, Cherry Tomato-1 × Co -3 -1, Cherry Tomato-3 × Cherry

Tomato-4, Cherry Tomato-4 × Pant Tomato-3), and cluster II (Cherry Tomato-7, Cherry Tomato-8, Cherry Tomato-1 × Co -3 -2, Pusa Ruby).

It is vivid from the Table 4.7 that maximum inter cluster distance was observed between cluster III and II (6.365) followed by cluster II and I (5.359). The minimum inter-cluster D^2 values were recorded in case of cluster III and I (4.001). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other.

The intra-cluster distance varied from 2.625 to 3.132. The maximum intra-cluster distance was shown by cluster I (3.132) followed by cluster III (2.648) and cluster II (2.625), which indicate distance within the cluster.

Table 4.6: Composition of clusters

Cluster Number	Number of genotypes included	Name of genotypes
I	**4**	Cherry type -1, Cherry Tomato-1 × Co -3 -1, Cherry Tomato-3 × Cherry Tomato-4, Cherry Tomato-4 × Pant Tomato-3
II	**4**	Cherry Tomato-7, Cherry Tomato-8, Cherry Tomato-1 × Co -3 -2, Pusa Ruby
III	**7**	Cherry Tomato-1, Cherry Tomato-2, Cherry Tomato-3, Cherry Tomato-4, Cherry Tomato-5, Cherry Tomato-9, Cherry Tomato-1 × Co -3 -3

Table 4.7: Intra (bold) and Inter cluster distance values in Cherry tomato

Cluster Number	I	II	III
I	**3.132**		
II	5.359	**2.625**	
III	4.001	6.365	**2.648**

4.7.1.1 Mean performance of clusters

The mean performance for different clusters of genotypes for fruit yield and its components are presented in Table 4.8. The data of cluster means for all the characters showed appreciable differences.

Days to first flowering showed the lowest mean performance for cluster I (25.25days), which was followed by cluster II (29.42days), and highest in cluster III (30.67days). Days to 50% flowering showed the lowest mean performance for cluster I (31.17 days), which was followed by cluster II (35.42 days), and cluster III (36.86 days).

Days to fruit set exhibited the lowest mean performance for cluster I (32.42 days) followed by cluster II (35.25 days), and most delayed days to fruit set by cluster III (36.81 days). Days to fruit ripening, the earliest mean performance was recorded in cluster I (74.67 days), which was followed by cluster II (77.00 days) and cluster III (77.67 days). Average fruit weight showed minimum cluster mean performance in cluster III (130.10g), which was followed by cluster I (220.83g) and cluster II (832.00g).

Fruit length exhibited the maximum mean performance for cluster II (3.75cm) followed by cluster I (2.54cm) and cluster III (2.03cm). Fruit girth showed maximum cluster mean performance in cluster II (14.74 cm), which was followed by cluster I (9.15 cm) and cluster III (7.26 cm). Pericarp thickness showed maximum cluster mean performance in cluster II (0.41 cm), which was followed by cluster I (0.24 cm) and cluster III (0.16 cm). Numbers of locules per fruit the highest average performance was recorded in cluster II (3.57), which was followed by cluster I (2.75) and cluster III (2.35).

Table 4.8 Mean performance of different clusters of Cherry total for fruit yield and its component traits

Characters / Clusters	Days to first flowering	Days to 50% flowering	Days to fruit set	Days to fruit ripening	Average fruit weight (g)	Fruit length (cm.)	Fruit girth (cm.)	Pericarp thickness	Numbers of locules per fruit	Plant height (cm.)	Number of primary branches per plant	Number of flowers per cluster	Number of fruits per cluster	100 seed weight	Days to first fruit harvest	Number of fruits per plant	Fruit weight per plant (Kg.)	Total fruit yield (q/ha)
I	25.25	31.17	32.42	74.67	220.83	2.54	9.15	0.24	2.75	119.98	13.62	6.52	5.52	0.22	84.17	119.53	1.18	140.90
II	29.42	35.42	35.25	77.00	832.00	3.75	14.74	0.41	3.57	61.30	9.15	5.23	4.50	0.29	85.00	64.23	1.94	168.57
III	30.67	36.86	36.81	77.67	130.10	2.03	7.26	0.16	2.35	136.97	14.74	5.77	5.11	0.18	85.67	178.84	0.93	113.40

Plant height exhibited the highest mean performance for cluster III (136.97cm) followed by cluster I (119.98cm) and cluster II (61.30). Number of primary branches per plant showed maximum cluster mean performance in cluster III (14.74), which was followed by cluster I (13.62) and cluster II (9.15).

Number of flowers per cluster showed maximum cluster mean performance in cluster I (6.52), which was followed by cluster III (5.77) and cluster II (5.23). Number of fruits per cluster showed maximum cluster mean performance in cluster I (5.52), which was followed by cluster III (5.11) and cluster II (4.50). 100 seed weight showed maximum cluster mean performance in cluster II (0.29), which was followed by cluster I (0.22) and cluster III (0.18). Days to first fruit harvest showed minimum cluster mean performance in cluster I (84.17), which was followed by cluster II (85.00) and cluster III (85.67).

Number of fruits per plant showed maximum cluster mean performance in cluster III (178.84), which was followed by cluster I (119.53) and cluster II (64.23). Fruit weight per plant showed maximum cluster mean performance in cluster II (1.94 kg), which was followed by cluster I (1.18kg) and cluster III (0.93kg). Total fruit yield showed maximum cluster mean performance in cluster II (168.57 q), which was followed by cluster I (140.90 q) and cluster III (113.40 q).

Thus, while planning hybridization programme for the development of better transgressive segregants one should select genotypes Cherry type -1, Cherry Tomato-1 × Co -3 -1, Cherry Tomato-3 × Cherry Tomato-4, Cherry Tomato-4 × Pant Tomato-3 for Days to first flowering, days to 50% flowering, days to fruit set, days to fruit ripening, number of flowers per cluster, number of fruits per cluster. Whereas, genotypes Cherry Tomato-7, Cherry Tomato-8, Cherry Tomato-1 × Co -3 -2, Pusa Ruby for maximum average fruit weight, fruit length, fruit girth, Pericarp thickness,

numbers of locules per fruit, 100 seed weight, fruit weight per plant, and total fruit yield from cluster II. Maximum Plant height, number of primary branches per plant and number of fruits per plant from cluster III.

These results are in general agreement with the findings of Mahapatra *et al***.** (2013), Kaushik *et al.* (2011), Reddy *et al.* (2013a).

4.7.1.2 Contribution of characters towards divergence

In the contribution of each character to divergence presented in table 4.9 which showed days to first fruit harvest contributes highest (52.38%) to divergence followed by fruit weight per plant (19.05%), number of fruits per plant (15.24%) and total fruit yield (7.62%) Whereas, average fruit weight, plant height (1.90%) and pericarp thickness, 100 seed weight (0.95%).

The results of the present study was close agreement with findings of Mehta and Asati (2008) who reported that primary branches per plant, fruit length and weight, number of fruits and yield per plant contributed the most of the total genetic divergence.

The inter-cluster distances in present investigation were higher than the intra-cluster distance reflecting the wider diversity among the breeding lines of the distant group. Hence, it is suggested that intercrossing of genotypes from diverse clusters showing high mean performance will be helpful in obtaining better recombinants with higher genetic variability

Genetic divergence is one of the useful tools for selection and efficient use of parents for hybridization to develop high yielding potential cultivars/hybrids. Inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining stronger heterosis and gives broad spectrum of variability in segregating generations. The better genotypes can be selected for most of characters on the basis

Table 4.9: Contribution of each character to divergence

Characters	Days to first flowering	Days to 50% flowering	Days to fruit set	Days to fruit ripening	Average fruit weight (g)	Fruit length (cm.)	Fruit girth (cm.)	Pericarp thickness	Numbers of locules per fruit	Plant height (cm.)	Number of primary branches per plant	Number of flowers per cluster	Number of fruits per cluster	100 seed weight	Days to first fruit harvest	Number of fruits per plant	Fruit weight per plant (Kg.)	Total fruit yield (q/ha)	Total
Number times appearing first time	0	0	0	0	2	0	0	1	0	2	0	0	0	1	55	16	20	8	**105**
Per cent contribution	0	0	0	0	1.90	0	0	0.95	0	1.90	0	0	0	0.95	52.38	15.24	19.05	7.62	**100**

of mean performance in the cluster. In this study, group constellation showed that cluster I (Cherry type -1, Cherry Tomato-1 × Co -3 -1, Cherry Tomato-3 × Cherry Tomato-4, Cherry Tomato-4 × Pant Tomato-3) were highly divergent from all other genotypes and may be used as parents in breeding programme and may directly be used as a pure line variety for total fruit yield and quality characters in Cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme* L.) for Chhattisgarh plains.

4.7.2 Molecular diversity analysis

Creation of genetic variation and then selection of suitable genotypes is one of the common ways that can assist in crop improvement. It is becoming easier to enhance the exploitation of the germplasm of crop species with the advent of molecular markers like Amplified Fragment Length Polymorphism (AFLP), Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), and Sequence Tagged Site (STS) and so on.

A variety is traditionally identified by a set of morphological characteristics (UFOV, 2002). Morphological descriptors do not always allow the quantification of genotypic difference because quantitative character can be altered by environmental factors (Cooke, 1995). In contrast, molecular markers such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAFD). amplified fragment length polymorphism (AFLP), and simple sequence repeats (SSR can provide an effective tool for variety identification since they are independent of environmental variation (Lee and Henry, 2001), Among the different available marker systems, SSR markers have become an important marker system for variety identification because of their property of genetic co-dominance, High reproducibility and multiallelic variation (Powell *et al*., 1996).

4.7.2.1 Similarly coefficient analysis

NTSYS (Numeric Taxonomy System Biostatistics) computer program was used to calculate the similarly matrices. Cluster analysis was done using UPGMA (unweighed pair group method with arithmetic averages) method based upon both genotypic and phenotypic data.

4.7.2.2 Clustering based on genotypic data

The polymorphic SSR (Figur 4.4) were scored for the presence (1) or absence (0) of all polymorphic bands generated in a 12 x 156 binary data matrix for 10 SSR markers. Pair wise genetic similarities based on Jaccard's (1912) coefficient were applied to the SSR data-sets. The similarity matrices were subjected to sequential agglomerative hierarchical nested (SAHN) clustering using UPGMA in NTSYS-pc software version 2.0 (Rohlf, 1997). The SSR data was used for similarly matrix using NTSYS (Numerical Taxonomy System Biostatistics) computer program. PCR based amplification requires two primers which are able to amplify specific fragment in the genome and produce bands that could exhibit polymorphism. 10 SSR primers were used to screen the polymorphism. A total of 142 reliable polymorphic bands were observed in the 10 polymorphic primers. This polymorphic band demonstrates that SSR analysis is a robust and efficient method for detecting differences between 15 cherry tomato genotypes. The clustering pattern indicated the existence of low similarity among the cherry tomato genotypes.

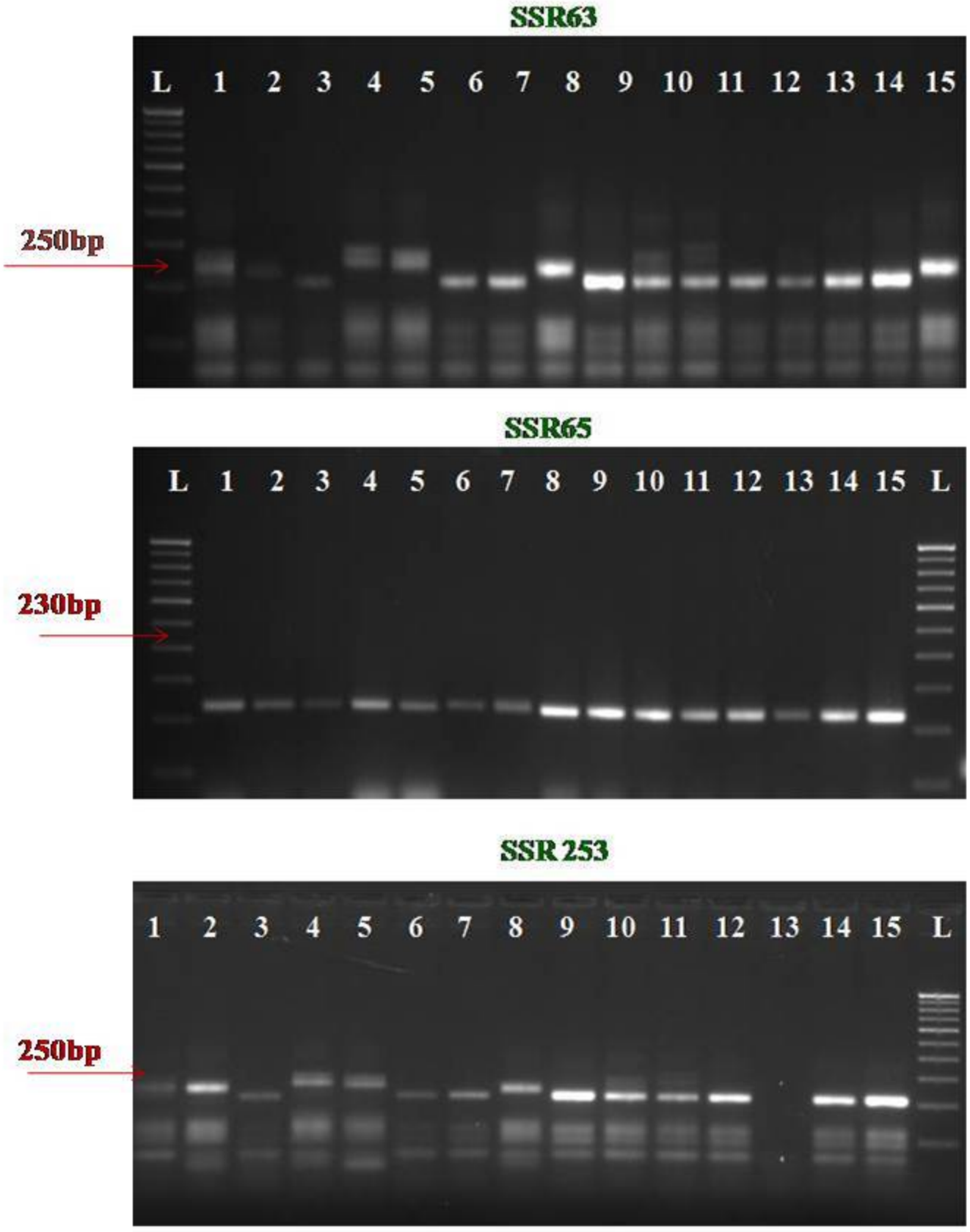

Fig: 4.4a **Banding pattern of Cherry tomato genotypes based on different SSR markers**

Table 4.10: Banding pattern of Cherry tomato genotypes based on different SSR markers

(1) Cherry Tomato 1 (2) Cherry Tomato 2 (3) Cherry Tomato3 (4) Cherry Tomato4
(5) Cherry Tomato 5 (6) Cherry Tomato 7 (7) Cherry Tomato 8 (8) Cherry Tomato 9
(9) Cherry Type – 1 (10) Cherry T1×Co-3-1(11) CherryT1×Co -3-2 (12) CherryT1×Co-3- 3
(13) Cherry T.3 × Cherry T.4 (14) Cherry T.4 × Pant T.-3 (15) Pusa Ruby

Marker\Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
SSR26-1	1	0	0	0	0	0	0	0	1	0	1	0	0	1	1
SSR26-2	0	1	1	1	0	1	1	1	0	1	0	1	1	0	0
SSR32-1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
SSR32-2	0	0	0	0	0	1	1	1	1	1	1	0	1	1	0
SSR32-3	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1
SSR50-1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0
SSR50-2	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0
SSR50-3	0	0	0	0	0	0	1	1	1	1	1	0	1	1	0
SSR50-4	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
SSR47-1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1
SSR47-2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
SSR47-3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
SSR47-4	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1
SSR65-1	1	1	1	1	1	1	1	0	0	0	0	0	1	0	0
SSR65-2	0	0	0	0	0	0	0	1	1	1	1	1	0	1	1
SSR63-1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0
SSR63-2	0	1	0	0	0	0	0	1	0	0	0	0	0	0	1
SSR63-3	0	0	1	0	0	1	1	0	1	1	1	1	1	1	0
SSR253-1	1	1	0	0	0	0	0	0	1	1	1	1	0	1	1
SSR253-2	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0
SSR253-3	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0
SLM6-14-1	0	0	0	1	0	0	1	0	1	0	0	0	0	0	1
SLM6-14-2	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
SLM6-14-3	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
SLM6-17-1	1	0	0	0	0	1	1	1	0	1	0	0	0	0	1
SLM6-17-2	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0
SLM6-17-3	0	0	0	0	0	1	1	1	0	1	0	0	0	0	0
SLM6-18-1	1	0	0	0	0	1	1	1	0	1	1	0	0	0	1
SLM6-18-2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0

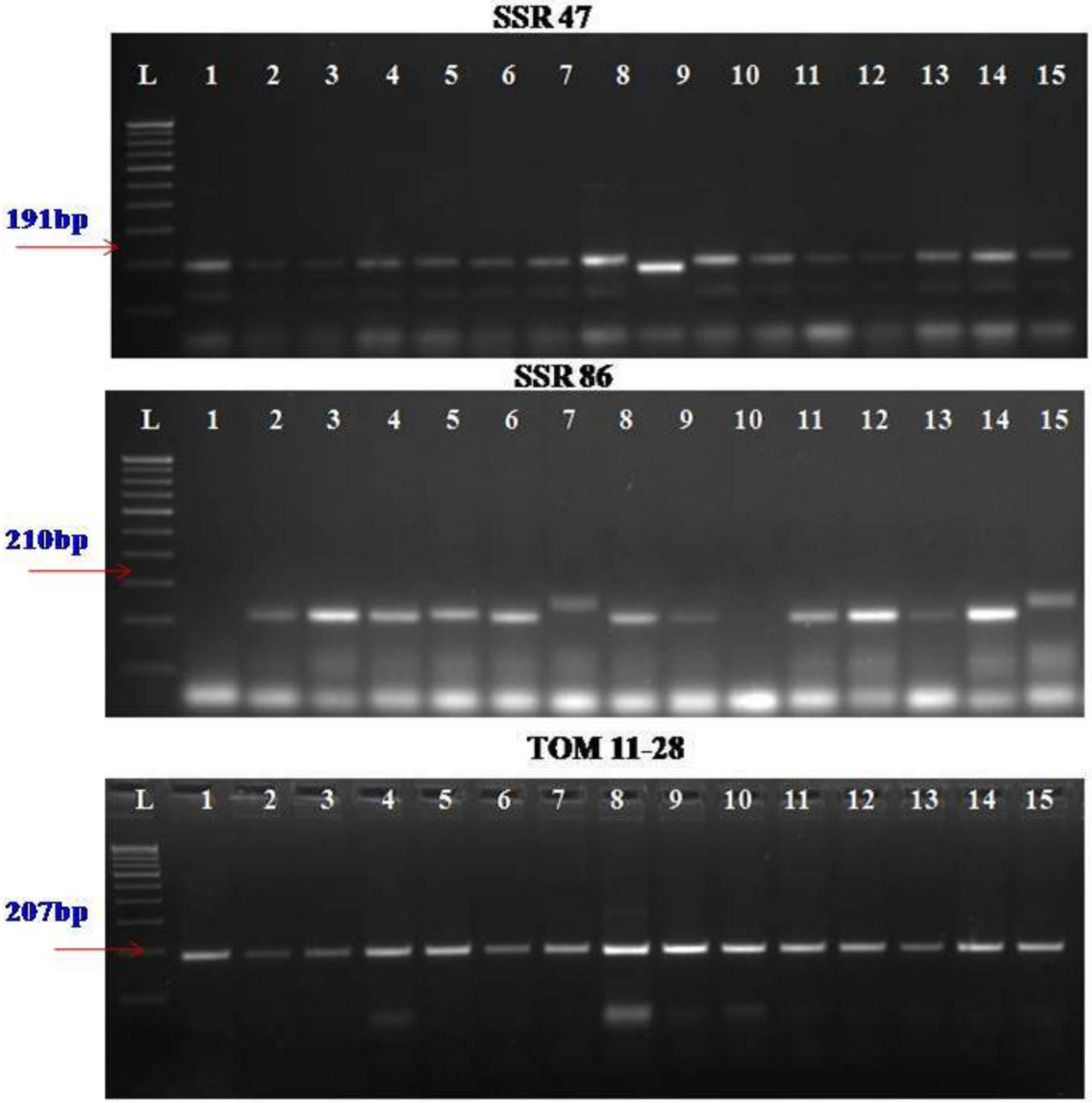

Fig: 4.4 **Genotypes use**

(1) Cherry Tomato 1 (2) Cherry Tomato 2 (3) Cherry Tomato3 (4) Cherry Tomato4 (5) Cherry Tomato 5 (6) Cherry Tomato 7 (7) Cherry Tomato 8 (8) Cherry Tomato 9 (9) Cherry Type –1 (10) Cherry T1×Co-3-1 (11) CherryT1×Co -3-2 (12) CherryT1×Co-3- 3 (13) Cherry T3 × Cherry T4 (14) Cherry T4 × Pant T-3 (15) Pusa Ruby

Bp = base pair

L = Ladder

A perusal dendrogram (fig.4.5) indicates there were two major clusters ‘A’ and ‘B’ at 23 % similarly level. Major cluster ‘A’ consists of five genotypes (Cherry Tomato1, Cherry Tomato 2, Cherry Tomato 3, Cherry Tomato 4, Cherry Tomato 5) rest of other genotypes present in major cluster B. Five genotypes present in major cluster A similar at 29.6% similarity level. Major cluster A divided in to two sub-clusters A1 and A2 at 44% similarity level.

Table- 4.11: Clustering of Cherry tomato genotypes based on molecular (SSR) marker

Clusters			Genotypes
A (5)	A1(3)	A1a (1)	Cherry tomato-1
		A1b (2)	Cherry tomato-2 and Cherry tomato-3
	A2(2)	A2a (1)	Cherry tomato-4
		A2b (1)	Cherry tomato-5
B (10)	B1(4)	B1a (3)	Cherry tomato-7, Cherry tomato-8 and C.T.3 x C.T.4
		B1b (1)	Cherry tomato-9
	B2(6)	B2a (1)	Cherry type-1
		B2b (5)	C.T.1 x CO-3-1, C.T.1 x CO-3-2, C.T.4 x P.T.3, C.T.1 x CO-3-3, Pusa Ruby

Ten genotypes present in major cluster B similar at 32.2% similarity level. Major cluster B divided in to two sub-clusters B1 and B2 at 37% similarity level. The cluster B1 again divided in to two sub-cluster B1a and B1b at 37% similarity level. The cluster B1a consists of Cherry Tomato 7, Cherry Tomato 8, Cherry T.3 × Cherry T.4 has 50.6% level of similarity, rest of the other genotypes are present in cluster B1b and so on. The maximum level of similarity was found between Cherry T.1×Co -3-2 and Cherry T.4 × Pant T. -3 showing 89% similarity (Figure 4.5)

The detection of minor and nonspecific products that could be shadow, heteroduplex or faint bands may affect the allele scoring process and increases the difficulty of legitimate allele identification. We also considered these minor bands during allele scoring however, Wang *et al*. (2003) and Rodriguez *et al.* (2001) reported that the minor bands can be useful during gel scoring for genotype verification, because they are generally consistent.

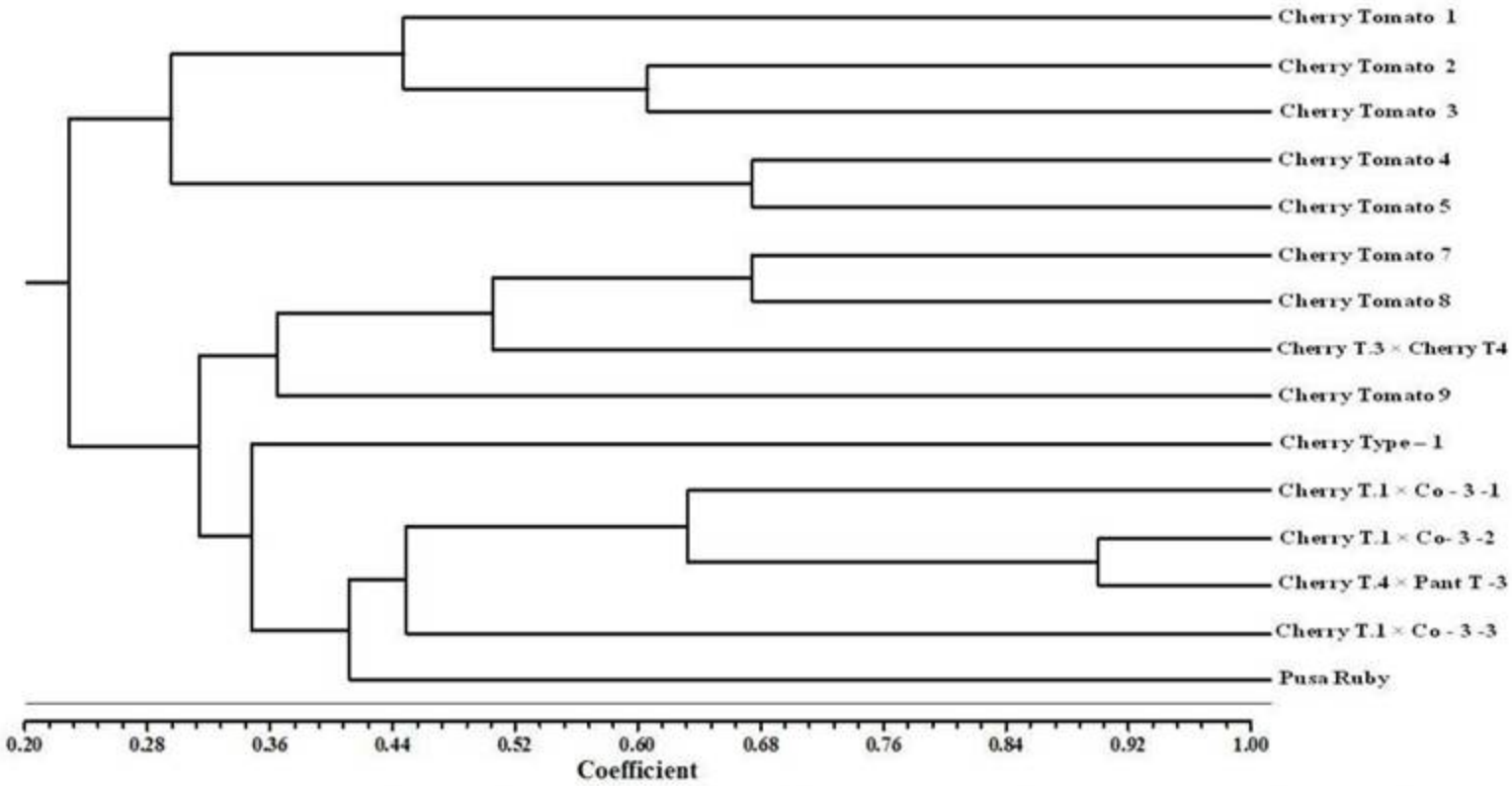

Figure 4.5 Genetic relationship inferred through un weighted pairgroup method analysis (UPGMA) clustering of SSR primer generated binary matrics (of pooled primer for different genotypes of Cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme)* analysised using Jaccard (1912) similarility coefficient.

Similarly A set of SSR markers used to tomato varieties identification by Bredemeijer *et al.* (2002). He differentiated 468 out of 521 European tomato varieties using 20 SSR markers. The researches of He et *al.* (2003) and Garcla-Martinez *et a1*. (2006) confirmed the utility of SSR markers for the genetic diversity and variability for tomato variety. Unfortunately, these markers were shown to low level of polymorphism for marketing tomato varieties in Korea (Kwon *et al.*, 2006). Recently, expressed sequence tag (EST) SSR or genic SSRs are useful as molecular markers because their development is inexpensive, and they are useful for functional diversity in natural diversity or germplasm collections (Varshney *et a1*., 2005) , To date , EST derived SSR markers have been created for several crops such as rice Cho *et al*., 2000), rye (Hackauf and Wehling, 2002), and wheat (Peng and Lapitan 2005), In tomato, more than 600 EST-derived SSR markers have been identified and made available for genome research through solanaceae genome network (SGN) http/www.sgn.comell.edul (Frary *et al* 2005). In our current study we also used SSR marker for diversity analysis and get 10 polymorphic out of 50 used. Moreover, 76 SSRs have been mapped to specific location in tomato genome. A set of mapped SSR markers providing genome wide coverage should facilitate an unbiased assay of genetic diversity and thus giving a robust, unambiguous molecular description of variety (Singh *et al*., 2004).

In the present study, SSR gave definite identification of cherry tomato genotypes. These unique bands could have a number of potential applications including the determination of cultivar purity, efficient use and management of genetic resources collection and the establishment of property rights. The obtained data confirmed the efficacy of the SSR markers as a highly variable markers that detect the co dominant single locus and suitable to distinguish between the genetically related genotypes.

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FUTURE RESEARCH WORK

CHAPTER-V

SUMMARY, CONCLUSION AND SUGGESTIONS FOR FUTURE RESEARCH WORK

The present investigation entitled **"Evaluation of cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) in Chhattisgarh plains"** was conducted during *rabi* season 2013-2014 under All India Co-ordinated Research Project on Vegetable crops at Horticultural Research cum Instructional Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.). The experiment was comprised of 15 genotypes of cherry tomato including Pusa Ruby. The experiment was laid out in Randomized block design (RBD) with three replications to estimate the genetic variability, heritability, genetic advance, correlation coefficient, path analysis, genetic and molecular diversity analysis

SUMMARY

Five randomly selected plants were considered for observations of different characters *viz*., days to first flowering, days to 50% flowering, days to fruit set, days to fruit ripening, average fruit weight (g), fruit length (cm.), fruit girth (cm.), pericarp thickness, numbers of locules per fruit, plant height (cm.), number of primary branches per plant, number of secondary branches per plant, number of flowers per cluster, number of fruits per cluster, 100 seed weight, days to first fruit harvest , number of fruits per plant, fruit weight per plant (kg.), TSS% , acidity %, number of picking, crop duration, marketable yield per plot (kg.), marketable fruit yield (q/ha), total fruit yield (q/ha).

The analysis of variance indicated that the mean sum of square due to genotypes were significant for all the characters i.e. days to first flowering, days to 50 % flowering, days to fruit set, days to fruit ripening, plant height, number of primary

branches per plant, average fruit weight, fruit length, fruit girth, number of locules per fruit, pericarp thickness, number of fruits per plant, 100 seed weight, number of flowers per cluster, number of fruits per cluster, fruit weight per plant, days to first fruit harvest and total fruit yield quintal per hectare.

The highest total fruit yield was recorded in genotype Pusa Ruby. Among all the small fruited tomato maximum fruit yield was recorded in Cherry Tomato-8 which was followed by, Cherry Tomato1×Co-3-2, Cherry Tomato1×Co-3-1 and Cherry Tomato1×Co-3-3. Whereas, the lowest total fruit yield was recorded in genotype Cherry Tomato-5. The maximum number of fruits per plant was recorded under genotype Cherry Tomato-2 which was followed by Cherry Tomato-9 and Cherry Tomato-1. The highest average fruit weight was recorded under genotype Cherry Tomato-8 whereas, the lowest average fruit weight was recorded in genotype Cherry Tomato-1.

The highest total soluble solid percent was noted in Cherry type-1 which was followed by Cherry Tomato-2, Cherry Tomato-5, Cherry Tomato 3×Cherry Tomato4, Cherry Tomato4×Pant Tomato3 and Cherry Tomato1×Co-3-3. On other hand, the lowest total soluble solid percent was noted in Cherry Tomato1×Co-3-1. The highest 100 seed weight was noted in Pusa Ruby which was followed by Cherry Tomato-8, while, the lowest 100 seed weight was noted in Cherry Tomato-3. The maximum numbers of locules per fruit was observed in Cherry Tomato-7 which was followed by Cherry Tomato1×Co-3-2 whereas, minimum numbers of locules per fruit was observed in Cherry Tomato-3. The genotypes Pusa Ruby and Cherry Tomato-8 were observed the maximum pericarp thickness, whereas, the minimum pericarp thickness was noted in genotype Cherry Tomato-1.

Genotype Cherry Tomato-8 had the maximum fruit girth which was followed by Cherry Tomato-7 and genotype Cherry Tomato-1 had the minimum fruit girth. Genotypes Cherry Tomato-8 and Cherry Tomato -1 were identified for maximum and minimum fruit length respectively. The maximum fruit weight per plant was recorded in Cherry Tomato-8, whereas, the minimum fruit weight per plant was noted in Cherry Tomato-5. The maximum number of flowers per cluster was noted in Cherry type-1 which was followed by Cherry Tomato-3, Cherry Tomato-2, Cherry Tomato-4 × Pant Tomato-3 whereas, the lowest number of flowers per cluster was noted in Pusa Ruby.

The maximum number of secondary branches per plant was recorded in genotype Cherry Tomato-4 which was followed by Cherry Tomato-2 and Cherry Tomato-1. The genotype Cherry Tomato-2 observed the maximum number of primary branches per plant, whereas, the minimum in genotype Cherry Tomato-8. The highest plant height was recorded under Cherry Tomato-5 which was followed by Cherry Tomato-2 and lowest plant height was recorded in genotype Pusa Ruby. The earliest days to first fruit harvest was noted in Cherry Tomato-1, Cherry Tomato-3 and Cherry Tomato1×Co-3-1 which was followed by Cherry Tomato-7, Cherry type-1, Cherry Tomato-3 × Cherry Tomato-4, Cherry Tomato-4 × Pant Tomato-3, Pusa Ruby Whereas, the delayed days to first fruit harvest was noted in Cherry Tomato -9.

The highest acidity recorded in genotype Cherry Tomato-2 which was followed by Cherry Tomato-5 the minimum in genotype Cherry Tomato1×Co-3-1. The days to first flowering was noted in Cherry type-1 which was followed by Pusa Ruby, Cherry Tomato-4×Pant Tomato-3, Cherry Tomato-3×Cherry Tomato-4, Cherry Tomat-1×Co-3-1and Cherry Tomato-2 whereas, the delayed days to first flowering was noted in Cherry Tomato-4. The earliest days to 50% flowering was noted in

Cherry type-1 which was followed by Pusa Ruby, Cherry Tomato-4×Pant Tomato-3, Cherry Tomato-3×Cherry Tomato-4 and Cherry Tomato-2 whereas, the delayed days to 50% flowering was noted in Cherry Tomato-4. The earliest days to fruit set was noted in Pusa Ruby, Cherry Tomato-4×Pant Tomato-3, Cherry type-1, Cherry Tomato-1×Co-3-1 and Cherry Tomato-3×Cherry Tomato-4 and the delayed days to fruit set was noted in Cherry Tomato-4. Genotype Cherry type -1 had the earliest days to fruit ripening which was followed by Cherry Tomato-4×Pant Tomato-3, Cherry Tomato-1×Co-3-2, Cherry Tomato-1, Cherry Tomato-3×Cherry Tomato-4, Cherry Tomato-1×Co-3-1 and genotype Cherry Tomato-9 had the delayed days to fruit ripening.

A wide range of phenotypic variability was observed for all the character, among genotypes studied. The analysis of variance for eighteen characters indicated highly significant of PCV were greater than the GCV for all the traits which this suggested the role of environmental in the expression of the characters. High phenotypic and genotypic coefficient of variation were observed for average fruit weight, pericarp thickness, number of fruits per plant, fruit weight per plant, plant height, fruit girth, fruit length, 100 seed weight, number of primary branches per plant, numbers of locules per fruit, total fruit yield, number of flowers per cluster and number of fruits per cluster . Whereas, moderate phenotypic and genotypic coefficient of variation were observed for days to first flowering, days to 50% flowering, days to fruit set, days to fruit ripening and days to first fruit harvest.

Among the characters studied, highest heritability estimate was recorded for fruit girth followed by fruit length, average fruit weight, number of fruits per plant, plant height, pericarp thickness, fruit weight per plant, 100 seed weight, total fruit yield, number of primary branches per plant, number of flowers per cluster, numbers

of locules per fruit, number of fruits per cluster, days to 50% flowering, days to first flowering, days to fruit set. On other hand, moderate heritability estimates was observed for days to fruit ripening, and days to first fruit harvest

Expected genetic advance as percent of mean and its estimated percent mean for various character revealed that the average fruit weight showed highest genetic advance percentage of mean followed by pericarp thickness, number of fruits per plant, fruit weight per plant, plant height, fruit girth, fruit length, 100 seed weight, number of primary branches per plant, numbers of locules per fruit, total fruit yield, number of flowers per cluster, number of fruits per cluster, days to first flowering. In general genetic advance was higher for most of the characters studied. The traits days to 50% flowering, days to fruit set, days to fruit ripening and days to first fruit harvest had lower genetic advance values.

The highest heritability coupled with highest genetic advance were observed for characters *viz.*, Fruit girth, Fruit length, average fruit weight, number of fruits per plant, plant height, pericarp thickness, fruit weight per plant, 100 seed weight and total fruit yield.

The association analysis revealed that the total fruit yield exhibited significant positive correlation with average fruit weight, fruit length, fruit girth, pericarp thickness, numbers of locules per fruit, and fruit weight per plant at genotypic and phenotypic levels and 100 seed weight at genotypic levels whereas, number of primary branches per plant and number of fruits per plant expressed significant negative correlation at genotypic and phenotypic level.

Significant positive correlation of average fruit weight was recorded with fruit length fruit girth, pericarp thickness, numbers of locules per fruit, 100 seed weight, and fruit weight per plant at genotypic and phenotypic levels. Whereas plant height,

number of primary branches per plant and number of fruits per plant expressed significant negative correlation at genotypic and phenotypic level and number of fruits per cluster at genotypic level only. number of fruits per plant expressed significant negative correlation with fruit weight per plant at genotypic and phenotypic levels. significant positive correlation of days to first flowering was recorded with days to 50% flowering and days to fruit set at genotypic and phenotypic levels and days to fruit ripening, days to first fruit harvest at genotypic levels. Whereas, number of flowers per cluster expressed significant negative correlation at genotypic level only. Days to 50% flowering expressed significant positive correlation with days to fruit set and days to fruit ripening at genotypic and phenotypic level and days to first fruit harvest at genotypic level. Whereas number of flowers per cluster expressed significant negative correlation at genotypic and phenotypic level and number of fruits per cluster at genotypic level.

Pericarp thickness showed significant positive correlation with 100 seed weight and fruit weight per plant at genotypic and phenotypic levels. Whereas plant height number of primary branches per plant and number of fruits per plant expressed significant negative correlation at genotypic and phenotypic level and number of fruits per cluster at genotypic level only. Days to fruit set had significant positive correlation with days to fruit ripening and days to first fruit harvest at genotypic levels only. Days to fruit ripening had significant positive correlation with days to first fruit harvest at genotypic and phenotypic levels. Whereas number of flowers per cluster number of fruits per cluster expressed significant negative correlation at genotypic levels.

Fruit length showed significant positive correlation with fruit girth, pericarp thickness, numbers of locules per fruit, 100 seed weight and fruit weight per plant at

genotypic and phenotypic levels. Whereas plant height, number of primary branches per plant and number of fruits per plant expressed significant negative correlation at genotypic and phenotypic level. Fruit girth showed significant positive correlation with pericarp thickness numbers of locules per fruit, 100 seed weight and fruit weight per plant at genotypic and phenotypic levels. Whereas plant height, number of primary branches per plant and number of fruits per plant expressed significant negative correlation at genotypic and phenotypic level and number of fruits per cluster at genotypic level only.

Numbers of locules per fruit showed significant positive correlation with Fruit weight per plant at genotypic and phenotypic levels. Whereas plant height expressed significant negative correlation at genotypic levels. Plant height showed significant positive correlation with number of primary branches per plant and number of fruits per plant at genotypic and phenotypic levels. Whereas 100 seed weight and fruit weight per plant expressed significant negative correlation at genotypic and phenotypic levels. Number of primary branches per plant had expressed significant positive correlation with number of fruits per plant at genotypic and phenotypic levels. Whereas 100 seed weight expressed significant negative correlation at genotypic and phenotypic levels and fruit weight per plant at genotypic levels.

Number of flower per cluster expressed significant positive correlation with number of fruits per cluster at genotypic and phenotypic levels. Whereas fruit weight per plant expressed significant negative correlation at genotypic levels only. Number of fruits per cluster expressed significant negative correlation with100 seed weight and fruit weight per plant at genotypic and phenotypic levels. 100 seed weight had expressed significant positive correlation with fruit weight per plant at genotypic levels whereas number of fruits per plant expressed significant negative correlation at

genotypic levels only.

Path coefficient analysis revealed that fruit length, average fruit weight, number of primary branches per plant, pericarp thickness, numbers of locules per fruit, 100 seed weight, number of fruits per plant, number of fruits per cluster, days to first flowering and days to fruit ripening had positive direct effect on total fruit yield. Whereas, negative direct effect on total fruit yield was observed for fruit girth, plant height, fruit weight per plant, days to fruit set, number of flower per cluster, days to 50% flowering, days to first fruit harvest.

D^2 values recorded on total fruit yield and its components for fifteen genotypes, indicated the presence of appreciable amount of genetic diversity among the genotypes, which were grouped into three clusters based on relative magnitude of D^2 values.

Thus, while planning hybridization programme for the development of better transgressive segregants one should select genotypes Cherry type -1, Cherry Tomato-1 × Co -3 -1, Cherry Tomato-3 × Cherry Tomato-4, Cherry Tomato-4 × Pant Tomato-3 for Days to first flowering, days to 50% flowering, days to fruit set, days to fruit ripening, number of flowers per cluster, number of fruits per cluster. Whereas, genotypes Cherry Tomato-7, Cherry Tomato-8, Cherry Tomato-1 × Co -3 -2, Pusa Ruby for maximum average fruit weight, fruit length, fruit girth, Pericarp thickness, numbers of locules per fruit, 100 seed weight, fruit weight per plant, and total fruit yield from cluster II. Maximum Plant height, number of primary branches per plant and number of fruits per plant from cluster III.

Molecular marker based diversity analysis by SSR was done by using 50 SSR markers. Out of these 10 markers found to be polymorphic. A total of 142 alleles generated by 10 polymorphic SSR were used for generation of dendrogram using

NTSYS programme. The generated dendrogram of 15 Cherry tomato genotypes including Pusa Ruby shows low level of similarity among these genotypes. Two major clusters were generated at 23 % level of similarity. The cluster A consists of five genotypes whereas cluster B consist of rest 10 genotypes. The result also shows that the genotypes CherryT1×Co -3-2 and Cherry T-4 × Pant T-3 showing 89% similar.

CONCLUSION

It can be concluded from the result of the present investigation that:

1. The analysis of variance indicated that mean sum of square due to genotypes were significant for all the characters.
2. Genotype Pusa Ruby is superior performed in Chhattisgarh plains Pusa Ruby gave maximum yield but among all Cherry tomato genotypes highest total fruit yield was recorded in Cherry Tomato-8 and also found promising for pericarp thickness, days to fruit set, plant height, days to first fruit harvest, 100 seed weight, fruit length, fruit girth, fruit weight per plant and total fruit yield quintal per hectare.
3. The phenotypic coefficient of variation was in general higher than the genotypic coefficient of variation for all the characters except fruit length, which may be due to environmental effect.
4. The high magnitude of phenotypic and genotypic coefficient of variation was recorded for average fruit weight, pericarp thickness, number of fruits per plant, fruit weight per plant, plant height, fruit girth, fruit length, 100 seed weight, number of primary branches per plant, numbers of locules per fruit, total fruit yield, number of flowers per cluster, number of fruits per cluster

revealed the presence of high genetic variability in the population under the study.

5. The fruit girth, fruit length, average fruit weight, number of fruits per plant height, pericarp thickness, fruit weight per plant, 100 seed weight, and total fruit yield, showed high heritability coupled with high genetic advance.

6. The correlation coefficient of total fruit yield was found to positive and significant with average fruit weight, fruit length, fruit girth, pericarp thickness, numbers of locules per fruit, fruit weight per plant, 100 seed weight.

7. The path coefficient analysis revealed that direct selection for fruit length, average fruit weight, number of primary branches per plant, pericarp thickness, numbers of locules per fruit, 100 seed weight, number of fruits per plant, number of fruits per cluster, days to first flowering and days to fruit ripening had positive direct effect on total fruit yield will be effective and would help to select the genotypes having highest total fruit yield.

8. The D^2 values recorded for fifteen genotypes indicated the presence of appreciable amount of genetic diversity among the genotypes. In this study, group constellation showed that cluster I (Cherry type -1, Cherry Tomato-1 × Co -3 -1, Cherry Tomato-3 × Cherry Tomato-4, Cherry Tomato-4 × Pant Tomato-3) were highly divergent from all other genotypes and may be used as parents in hybrid breeding programme and may directly be used as a pure line variety for total fruit yield and quality characters in Cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*)

9. Molecular Marker based diversity analysis by SSR was done by using 50 SSR markers. Out of these 10 markers found to be polymorphic. A total of 142

alleles generated by 10 polymorphic SSR were used for generation of dendrogram using NTSYS programme.

10. The generated dendrogram of 15 Cherry tomato genotypes shows low level of similarity among these genotypes. The result also shows that the genotypes CherryT1×Co -3-2 and Cherry T-4 × Pant T-3 were 89% similar.

SUGGESTIONS FOR FUTURE RESEARCH WORK

Since the results of present investigation belong to only one year of experiment, for reaching to any definite conclusion and recommendation, it needs further confirmation of the same for at least two successive years. However, following studies are also suggested to be undertaken in future.

1. The experiment should be conducted during different seasons also to find out whether the genotypes give same effect over seasons.
2. There is need of in depth study on qualitative aspect and post harvest preservation technology of the cherry tomato which has not been adequately covered under the present study.
3. There is need to compare the yield potential of different genotypes with number of hybrids available in the market and research station.
4. More number of genotypes may be collected from different untouched places of the Chhattishgarh state.
5. In the present investigation the best diverse genotypes having desirable characters with maximum variability identified could be included in hybridization programme for crop improvement.

6. There are large numbers of local genotypes available in Chhattisgarh which may have valuable genes for different characters, should be collected and evaluated for different quality and quantity parameters.
7. There is need to screen the genotypes against biotic (disease and insect pests) and abiotic stresses (drought tolerant/resistant).
8. Molecular techniques should be applied in Cherry tomato for future breeding work.
9. These selected SSR markers will be very useful for Screening of Large number of germplasm and varietal idenfication.
10. A more number of polymorphic markers will be required for the further precise analysis of genotypes.

ABSTRACT

"EVALUATION OF CHERRY TOMATO *(Solanum lycopersicum* L. var. *cerasiforme)* IN CHHATTISGARH PLAINS"

By

Kiran Kumar

ABSTRACT

The present investigation was conducted during *rabi* season 2013-14 under All India Co-ordinated Research Project on Vegetable Crops at Horticultural Instructional cum Research Farm, Department of Horticulture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.).The experiment was laid out in Randomized Block Design with three replications and comprised of 15 genotypes of Cherry tomato including Pusa Ruby. The analysis of variance was significant for all the characters indicating genetic variability in the genotypes under the study. Genotype Cherry tomato-8 gave highest fruit yield, average fruit weight, fruit length, fruit girth, pericarp thickness, 100 seed weight and fruit weight per plant among the Cherry tomato.

Expected genetic advance as percent of mean and its estimated percent mean for various character revealed that the average fruit weight showed highest genetic advance percentage of mean followed by pericarp thickness, number of fruits per plant, fruit weight per plant and plant height.The high magnitude of phenotypic and genotypic coefficient of variation was recorded for average fruit weight, pericarp thickness, number of fruits per plant, fruit weight per plant, plant height, fruit girth, fruit length, 100 seed weight, number of primary branches per plant, numbers of locules per fruit, total fruit yield, number of flowers per cluster and number of fruits per cluster.

High heritability coupled with high genetic advance as percentage of mean was recorded for the traits, fruit girth, fruit length, average fruit weight, numbers of fruits per plant, plant height, pericarp thickness, fruit weight per plant, 100 seed weight and total fruit yield.

The correlation coefficient of total fruit yield was found to positive and significant with average fruit weight, fruit length, fruit girth, pericarp thickness, numbers of locules per fruit, fruit weight per plant, 100 seed weight. The path coefficient analysis revealed that direct selection for fruit length, average fruit weight, number of primary branches per plant, pericarp thickness, numbers of locules per fruit, 100 seed weight, number of fruits per plant and number of fruits per cluster.

The D^2 values recorded for fifteen genotypes indicated the presence of appreciable amount of genetic diversity among the genotypes. Molecular marker based characterization of Cherry tomato genotypes reveals that low level of similarity among Cherry tomato genotypes, whereas CherryT1×Co -3-2 and Cherry T-4 × Pant T-3 shows 89 % similarity.

Department of Horticulture
College of Agriculture,
IGKV, Raipur (C.G.)

Dr. Jitendra Trivedi 22/7/14
Chairman
Advisory Committee

REFERENCES

REFERENCE

Ahirwar, C. S., Bahadur, V. and Prakash, V. 2013. Genetic variability, heritability and correlation studies in tomato genotypes (*Lycopersicon esculentum* Mill.). *Intl. J. Agril. Sciences*., **9** (1): 172-176.

Ahmed, N., Khan, M. I. and Gupta, A. J. 2006. Variability and heritability in tomato. *Environment and Ecology*, **24S** (2): 386-388.

Akhilesh Tiwari and Gulshan Lal. 2005. Variability and genetic parameters of yield components and processing characters in tomato ((*Lycopersicon esculentum* Mill.). *Progr. Hort.*, **37** (2): 372-376.

Alice Kurian and Peter, K.V. 1994. Genetic divergence in processing characteristics of tomato. *South Indian Hort*., **42**: 85-88.

Anitha, P., Sharma, R. R., Tiwari, R. N. and Sureja, A. K. 2007. Correlation and path analysis for some horticultural traits in tomato. *Indian J. Hort*., **64** (1): 90-93.

Anonymous, 2011, *FAOSTAT database.*

Anonymous, 2012, *FAOSTAT database.*

Anonymous, 2013. National Horticulture Board, Ministry of Agriculture, Government of India 85, Institutional Area, Sector - 18, Gurgaon - 122 015 (Website: www.nhb.gov.in).

Anupam Bharti, Jain, B. P. and Verma, A. K. 2002. Genetic variability heritability and genetic advance in tomato (*Lycopersicon esculentum* (L.) Karst.). *J. Res. Birsa Agril.Uni.*, **14** (2): 249-252.

Ara, A., Narayen, R., Ahmed, N. and Khan, S. H. 2009. Genetic variability and selection paramerters for yield and quality attributes in tomato. *Indian J. Hort.*, **66** (1): 73-78.

Archak, S., Karihaloo J. L. and Jain A. 2002. RAPD markers reveal narrowing genetic base of Indian tomato cultivars. *Curr. Sci.*, **82**: 1139-1143.

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

Atugwu, A. I. and Uguru, M. I. 2012. Generation by generation Correlation and Path analysis for yield and yield components in advanced generations of tomato (*Solanum lycopersicom* Mill.) hybrids. *J. of Environ. Issues and Agric. in Dev. Countries,* **6**: 18-23.

Baraman, D., De, L. C., Sharma, L. K. and Singh, I. P. 1996. Correlation and path coefficient analysis of some quantitative characters in tomato. *J. Hill Res.,* **9** (2): 414-418.

Black, C. K. 1965. Method of soil analysis. *American Agronomy Inc*., Madison, Wisconsin, USA. pp. 131-137.

Blay, E.T., Danquah, E.Y., KoffeI, S. and Kudadjie, C. 1999. Morphological and agronomic characterization of some tomato *(Lycopersicon esculentum* L.*)* germplasm in Ghana. *Ghana J. Agric. Sci.,* **2**: 169-175.

Bredemeijer GMM. Cooke R. J., Ganal Mr. N., Peeters R. Isaac P. Noordijk Y. Rendell, S., Jackson, J., Rt'lder M. S., Wendehake, K., Dijcks, M., Amelaine, M., WICkaert, V., Bertrand L. and Vosman B. 2002. Construction and testing of a microsatellite database containing more than 500 tomato varieties. *Theor. Appl. Genet*. **105**: 1019-1026.

Brar, G.S., Singh, S., Cheema, D.S. and Dhaliwal, M.S. 2000. Studies on variability, heritability and genetic advance for yield and components characters in tomato. *Res. J. Punjab Agric. Uni.,* **37** (3-4): 190-193.

Buckseth, T., Sharma M. K. and Thakur K.S. 2012. Genetic diversity and path analysis in tomato (*Solanum lycopersicum* L.) *Veg. Science* **39** (2): 221-223.

Burton, G.M. 1952. Quantitative inheritance in grasses. *Grass Land Cong*., **1**: 277-285.

Cho Y.G. 1sN; T. Temny H. S. Chen X. Upovich L. McCouch S.R. Park W.O. Ayres N. and Cartinhour S. 2000. Diversity of microsatellites derived from genomic libraries and Gen Bank sequences in rice *Oryza sativa* L. *Theor. Appl. Genet*. **100**: 713-722.

Cooke, R.J. 1995. Varietal identification of crop plants. In *New Diagnostics in Crop Sciences.* J. H. Skerritt and R. *Appels, eds. CABI Int. Wallingford*. 33-63.

Dar, R. A. and Sharma, J. P. 2011. Genetic variability studies of yield and quality traits in tomato (*Solanum lycopersicum* L.). *Int. J. of Plant Breeding and Genetics,* **5**: 168-174.

Dar, R. A., Sharma, J. P., Gupta, R. K. and Chopra, S. 2011. Studies on correlation and path analysis for yield and physico chemical traits in tomato (*Lycopersicon esculentu m* Mill.). *Indian J. Hort.,* **24** (2): 136-141.

Das, B., Hajarika, M. H. and Das, P. K. 1998. Genetic variability and correlations in fruit cha racters of tomato. *Ann. Agric. Res.,* **19** (1): 77-80.

Dewey, D. R. and Lu, K. H.1959. A correlation and path coefficient analysis of components of crested wheat grass and seed production. *Agron. J.,* **5**: 515-518.

Dhankhar, S. K., Dhankhar, B. S. and Dudi, B. S. 2006. Inheritance of number of flowers per cluster at high temperature in tomato. *Haryana J. Hort. Sci*., **31**(1-2): 97-99.

Dhankhar, S. K., Dhankar, B. S. and Sharma, N. K., 2001. Correlation and path analysis in tomato under normal and high temperature conditions. *Haryana J. Hort. Sci.,* **30**: 89-92.

Edwards J.D., McCouch S.R. 2007. Molecular markers for use in plant molecular breeding and germplasm evaluation. In: Guimaraes EP, Ruane J, Scherf BD, Sonnino A, Dargie JD (eds) Marker-assisted selection. Current status and future perspectives in crops, livestock, forestry, and fish. Food and Agriculture Organization of the United Nations, Rome, pp 29–49.

El-Awady, M. A. M., El-Tarras, A. A. E. and Hassan, M. M. 2012. Genetic diversity and DNA fingerprint study in tomato (*Solanum lycopersicum* L.) cultivars grown in Egypt using simple sequence repeats (SSR) markers. *Afri J. Biot*. **11**(96): 16233-16240.

Emami, A. and Eivazi, A. R. 2013. Evaluation of genetic variations of tomato genotypes (*Solanum lycopersicum* L.) with multivariate analysis. *Int. J. Scientific Res. in Envi. Sci.,* **1**(10): 273-284.

Foolad, M. R. 2007. Genome mapping and molecular breeding of tomato. *Int. J. Plant Genomics*. doi:**10**.1155-64358.

Frary A., Xu Y, Liu J, Mitchell S, Tedeschi. E., Tanksley S.D. 2005. Development of a set of PCR based anchor markers encompassing the tomato genome and evaluation of their usefulness for genetics and breeding experiments. *Theor Appl. Genet*. **111**(2):291–312.

Fulton T. M., Van der Hoeven R., Eannetta N.T., Tanksley S. D. 2002. Identification, analysis, and utilization of conserved ortholog set markers for comparative genomics in higher plants. Plant Cell **14**:1457–1467.

Gadekar, D.A., Dhonushke, B.L., and Patil, F, B. 1992. Genetic divergence in tomato. *Veg. Sci*., **19** (1): 30-35.

Galton, F. 1888. Correlations and their measurement chiefly from arthropometric data. *Proc. Royal. Soc*., **45**: 135-145.

Garcla-Martlnez S. Andreani L, Garcla-Gusano M. Geuna F and Ruiz J.J 2006. Evaluation of amplified fragment length polymorphism and simple sequence repeats for tomato germplasm finger" printing: utility for grouping closely related traditional cultivars. *Genome* **49**: 648-656.

Ghosh, K.P., Islsm, A.K.M.A., Mian, M.A.K. and Hossain, M. M. 2010. Variability and character association in F_2 segregating population of different commercial hybrids of tomato (*Solanum lycopersicum* L.). *J. Appl. Sci. Environ. Manage.* **14** (2): 91-95.

Ginwal, H. S., and Mittal, N. 2010. An efficient genomic DNA isolation protocol for RAPD and SSR analysis in (Acorus calamus L.) Indian, *J. Biote*., **9**: 213- 216.

Golani, I. J., Mehta, D. R., Purohit, V. L., Pandya, H. M. and Kanzariya, M.V. 2007. Genetic variability, correlation and path coefficient studies in tomato. *Indian J. Agric. Res.,* **4 (**2): 146-149.

Goncalves, Leandro, S. A. 2008. Genetic divergence among tomato accessions using RAPD markers and its comparison with multicategoric descriptors. *Hortic. Bras,* **26** (3): 364-370.

Grushetskaya Z. E., Lemesh V. A., Poliksenova V. D. and Khotyleva L. V. 2007. Mapping of the *Cf-6* tomato leaf mould resistance locus using ssr markers. *Russian J. Genet.* **43** (11):1266–1270.

Hackauf, B. and Wehling, P. 2002. Ident ification of microsatellite polymorphisms in an expressed portion of the ryegenome. *Plant Breed.*, ***12t***: 17- 25.

Hanson, C. M., Robinsen, R. R. and Comstock, R. R., 1956. Biometrical studies on yield in segregating population of Kotean, Lespedeza. *Agron. J.,* **48** : 268-272.

Harer, P. N., Lad, D. B. and Bhor, T. J. 2002. Correlation and path analysis studies in tomato. *J. Maharashtra Agric. Uni.,* **27** (3): 302-303.

Haydar, A. Mandal, M. A., Ahmed, M. B., Hannan, M. M. and Karim, R. 2007. Studies on genetic variability and interrelationship among different traits in tomato (*Lycopesicon esculantum* Mill.). *Middle East J. Scientific Res.,* **2** (3-4): 139-142.

He, C. Poysa V. and Yu K., 2003. Development and characterization of simple sequence repeat SSR markers and their use in determining relationship among (*Lycopercicon esculentum)* cultivars. *Theor. Appl. Genet*. **lQ6**: 363-373.

Hosamani, R. M. 2010. Biometrical and transformation studies in tomato (*Solanum lycopersicum* L.). Ph.D. Thesis submitted to University of Agricultural Sciences, Dharwad (India).

Islam M. S., Mohanta H. C., Ismail M. R., Rafiim Y. And Malek M. A. 2012. Genetic variability and trait relationship in cherry tomato (*Solanum lycopersicum* L. Var. *Cerasiforme* (dunnal) a. Gray) Bangladesh J. Bot. **41**(2): 163-167.

Islam, B. M. R., Ivy, N. A., Rasul, M. G. and Zakaria, M. 2010. Character association and path analysis of exotic tomato (*Solanum lycopersicum* L.) genotypes. *Bangladesh J. Pl. Breed. Genet*., **23** (1): 13-18.

Jackson, M. L. 1967. Soil chemical analysis. *Prentice-hall of India Private Limited*, New Delhi.

Jogi, P. 2007. Genetic divergence for fruit traits in tomato (*Lycopersicon esculentum* Mill). *M.Sc. (Ag.) Thesis*, submitted to I.G.K.V., Raipur (C.G.).

Johnson, H.W., Robinson, H. F. and Comstock, R. E., 1955. Estimation of genetic and enviro nmental variability in soybean. *Agron. J.,* **47**: 477-483.

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

Joshi, Arun., Amit, Vikram and Thakur, M. C. 2004. Studies on genetic variability, correlation and path analysis for yield and physico-chemical traits in tomato (*Lycopersicon esculentum* Mill.). *Prog. Hort.*, **36** (1): 51-58.

Karasawa, M., Rodrigues, R., Sudre, C. P., Silva, M. P., da, Riva, E. M. and Amaral Junior, A.T. 2005. Cluster analysis for the evaluation of genetic divergence among tomato accessions. *Horticultura Brasileri.,* **23** (4): 1000-1005.

Kaushik, S. K., Tomar, D. S. and Dixit, A. K. 2011. Genetics of fruit yield and it's contributing characters in tomato (*Solanum lycopersicom*). *J. of Agric. Biotech. and Sustainable Dev.,* **3** (10): 209-213.

Kobryn, J. and Hallmann, E. 2005. The effect of nitrogen fertilization on the quality of three tomato types cultivated on Rockwool. Acta Horticult., **691**: 341 – 348.

Kochieva, E.Z., Rhyzova, N. N., Khrapalova, I.A. and Pukhalskyi, V.A. 2002. Using RAPD for

Kulkarni, P. G. 2006. Genetic and breeding investigations in tomato (*Lycopersicon esculentum* Mill.). *M.Sc. (Ag.) Thesis*, submitted to University of Agricultural Sciences, Dharwad (India).

Kumar M. S., Pal A. K., Singh A. K., Sati K. and Kumar D. 2013. Studies on genetic parameters to improve the genetic architecture of Tomato (*Solanum* lycopersicum L.) *Int. J. Applied Bio. and Pharm. Tech.*,**4 (**4):234-237.

Kumar, R., Kumar, N., Singh J. and Rai, G. K., 2006, Studies on yield and quality traits in tomato. *Veg. Sci.,* 33 (2): 126-132.

Kumar, S. Singh, T., Singh, B. and Singh, J. P. 2004. Studies on heretability and genetic advance in tomato (*Lycopersicon esculentum* Mill.). *Prog. Hort.,* **4** (1): 76-77.

Kumar, V. R., Thakur, M. C. and Hedau, N. K. 2003. Correlation and path coefficient analysis in tomato (*Lycopersicon esculentum* Mill.) *Ann. Agric. Res.,* **24** (1): 175-177.

Kwon Y. S. Park E. K. Bae K. M. YI S. I. Park S. G and Cho I. H. 2006. Use of simple sequence repeat SSR markers for variety identification of tomato (*Lyropersiron escu1entum*) *W.* Korean *J. Plant Biotechnol*. **33**: 289-295.

Kwon Y. S. Park S. G. and YI S. I. 2009. Assessment of genetic variation among commercial tomato *(Solanum lycopersicum* l.) varieties using SSR markers and morphological characteristics. Genes & genomics **31**(1): 1-10.

Lakshmi Kant and Mani, V. P. 2004. Association and contribution of different characters towards fruit yield in tomato (*Lycopersicon esculentum* Mill.). *Indian J. Hort.*, **61**(4): 327-330.

Lee, L. S. and Henry R. J. 2001. Commercial applications of plant genotyping. In *Plant GenotypirwThe DNA Jilngeqrinting Plants,* R. J. Henry, ed, *CABI Publ.Oxen*. 265-273.

Lush, J. L. 1940. Intensive correlation and regression of offspring on dam as a method of estimating heritability of characters. *Prod. Amer. Soc. An. Prod*., 293-301.

Mahalonobis, P. C. (1936). A statistical study at Chinese head measurement. *J. Asiatic Soc. Bengal*, **25**: 301-377.

Mahapatra, A. S., Singh, A. K., Vani, V. M., Mishra, R., Kumar, H. and Rajkumar, B. V. 2013. Inter relationship for various components and path coefficient analysis in tomat o (*Lycopersicon esculentum* Mill.). *Int. J. Curr. Microbiol. App. Sci.* **2** (9): 147-152.

Mahesh, D. K., Apte, Y. B. and Jadhav, B. B. 2006. Studies on genetic divergence in tomato (*Lycopersicon esculentum* Mill.).*Crop Res.,* **32** (2): 401-402.

Mahesha, D. K., Apte, U. B. and Jadhav, B. B. 2006. Genetic variability in tomato (*Lycopersicon esculentum* Mill.). *Research on Crops.*, **7** (3): 771-773.

Manivannan, M. I., Prasad, D. and Mir, M. 2005. Correlation and path coefficient analysis in cherry tomato (*Lycopersicon esculentum* var. cerasiforme). *New Agriculturist*, **16** (1-2): 151-154.

Manna, M. and Paul, A. 2012. Studies on Genetic Variability and characters association of fruit quality parameters in tomato. *Hort. Flora Research Spectrum,* **1** (2): 110-116.

Mariame, F., Ravishankar, H. and Dessalegne, L. 2003. Study on variability in tomato germpl asm under condition of Central Ethiopia. *Vegetable Crop Research Bulletin,* **58**:41-50.

Mehta, N. and Asati, B. S. 2008a. Genetic relationship of growth and development traits with fruit yield in tomato (*Lycopersicon esculentum* Mill). *Karnataka J. Agric. Sci.,* **21** (1): 92-96.

Mehta, N. and Asati, B. S. 2008. Genetic divergence for fruit characters in tomato (*Lycopersicon esculentum* Mill.) *Agric. Sci. Digest*, **28** (2): 141-142.

Mohamed A. M., El-Awady, Adel A. E., El-Tarras and Mohamed M. Hassan 2012a. Genetic diversity and DNA fingerprint study in tomato (*Solanum lycopersicum* L) cultivars grown in Egypt using simple sequence repeats (SSR) markers. *Afr. J. Biotechnol* **11**(96):16233-16240.

Mohamed, S. M., Ali E. E., Mohamed, T. Y. 2012b. Study of heritability and genetic variability among different plant and fruit characters of tomato (*Solanum lycopersicon* L.). *Int. J. Scientific & Tech. Res.* **1**(2):55-58.

Mohanty, B. K. 2003. Genetic variability, correlation and path coefficient studies in tomato. *Indian J. Agril. Res.,* **37** (1): 68-71.

Mohanty, B. K. 2002. Variability, heritability, correlation and path coefficient studies in tomato. *Haryana J. Hort. Sci.*, **31** (3/4): 230-233.

Murry, M. G. and Thompson, W. F. 1980. Rapid isolation of high molecular weight plant DNA. *Nucleic Acid Res.,* **8**: 4321 -4325.

Naidu, K. N. 2001. Study of growth, yield and quality attributes of promising genotype of tomato (*Lycopersicon esculentum* Mill) in Chhattisgarh plains. *M.Sc. (Ag.) Thesis*, submitted to I.G.K.V. Raipur (C.G.).

Nandpuri, K. S., Kanwar, J. S. and Roshanlal. 1977. Variability path analysis and discriminate function selection in tamato (*Lycopersicon esculentum* Mil1.). *Haryana J. Hort. Sci.,* **6**: 73-78.

Naz S., Zafrullah A., Shahzadhi K. and Munir, N. 2013. Assessment of genetic diversity within germplasm accessions in tomato using morphological and molecular markers. *J. Anim. Plant Sci.* **23** (4): 1099 -1106.

Olsen, S. R., Cole, C.V., Watanable, E. S. and Dean, L. A. 1954. Estimation of available phosphorus in soils by extraction with sodium bicarbonate. United State Department of Agriculture, Circ. 939 and Washington, D.C.

Osekita O. S. and Ademiluyi A. T. 2014. Genetic advance, heritability and character association of component of yield in some genotypes of tomato (*Lycopersicon esculentum* Mill.) Wettsd. *Academia J. Bio*.**2** (1): 06 -10.

Padma, E., Ravishankar, C. and Srinivasulu, R. 2002. Correlation and path coefficient studies in tomato (*Lycopersicon esculentum Mill*.). *Journal of Research,* ANGRAU, **30** (4): 68-71.

Pang J.H. and Lapitan N.L.V 2005. Characterization of EST-derived microsatellite in the wheat genome and development of SSR markers. Funct . *Int rgr. Genomics* **5**: 80-96.

Panse, V. G. and Sukhatme, P. V. 1967. Statistical methods for agricultural workers. ICAR, New Delhi, pp 97-151.

Parmar P, Sudhir A., Preethi R., Dave B., Panchal K. K., Subramanian R. B., Patel A., and Kathiria K. B. 2013. Identification of a SSR marker (TOM-144) linked to Fusarium wilt resistance in (*Solanum lycopersicum). American J. Mole.Bio*. **3**: 241-247.

Parsanna, H. C., Verma , A., Rai, M. and Singh, A. K. 2005. Genetic variability and association analysis in exotic cherry tomato. *Indian J. Plant Genet Reso.,* **18** (1):90-91.

Parthasarathy, V. A. and Aswath, E. 2002. Genetic diversity among tomato genotype. *South Indian J. Hort*., **59** (2): 162-166.

Patil, S. S., 1998. Studies on association of characters, heterosis and combining ability in processing tomato (*Lycopersicon esculentum* Mill.). *M.Sc. (Agri.) Thesis*, submitted to University of Agricultural Sciences, Dharwad (India).

Pearson, A. K. 1904. On the generalized theory of alternative inheritance with special reference to mendal's law. *Phil.Trass. Roy. A.,* **203**: 53-86.

Piper, C. S. 1967. Soil and plant analysis. Bombay/New Delhi Asia Publishign Honse. pp. 30-38.

Powell, W., Morgante M. Andre C. Hanafey M. Vogel J. Tingey S. and Rafalski A. 1996. A comparison of RFLP, RAPD, AFLP and SSR markers for germplasm analysis. *Mol. Breed*. **2**: 225-238.

Prasad, V. S. R. K. and Rai, M. 1999. Genetic variation component association and direct and indirect selection in some exotic tomato germplasm. *Indian J. Hort.,* **56** (3): 262-266.

Prashanth, S. J. 2003. Genetic variability and divergence study in tomato (*Lycopersicon esculentum* Mill). *M. Sc. (Agri.) Thesis*, Uni. Agric. Sci., Dharwad (India).

Prashanth, S. J., Jaiprakashnarayan, R. P., Mulge, R. and Madalageri, M. B. 2008. Correlation and path analysis in tomato (*Lycopersicon esculentum* Mill.). *Asian J. of Hort.* **3** (2): 403-408.

Prema, G., Indiresh, K. M. and Santosha, H. M. 2011a. Studies on genetic variability in cherry tomato (*Solanum lycopersicum* var.*Cerasiforme*). *Asian J. Hort.*, **6** (1): 207-209.

Prema, G., Indiresh, K. M. and Santosha, H. M. 2011. Evaluation of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*). genotypes for growth, yield and quality traits. *Asian J. Hort.*, **6**(1): 181-184.

Rahaman, Sahanur, Lakshman, S. S. and Maitra, N. J. 2012. Genetic variability and heritability studies in tomato (*Lycopersicon esculentum* Mill.). *Internat. J. Plant Sci.*, **7** (1): 58-62.

Rajput S. G., Wable K. J., Sharma K. M., Kubde P. D. and Mulay S. A. 2005. Reproducibility testing of RAPD and SSR markers in tomato. *Afri. J. Bio.* **5** (2): 108-112.

Ramzan, A., Khan T. N., Nousherwan Nobel Nawab N. N., Noor A. H. T. and Jillani, G. 2014. Estimation of genetic components in f1 hybrids and their parents in determinate tomato (*Solanum lycopersicum* L.) *J. Agric. Res.,* **52** (1):65-75.

Rani, C. I., Muthuvel, I. and Veeraragavathatham, D. 2010. Correlation and path coefficient for yield components and quality traits in tomato (*Lycopersicon Esculentum* Mill.). *Agril. Sci. Digest.,* **30** (1): 11-14.

Rao, C. R. 1952. Advanced statistical methods in biometric research. John Wiley and Sons Inc., Newyork. *Indian J. Gen. Pl. Breed*., **31**(1): 86-93.

Rattan, R. S., Kanwar, H. S. and Saini, S. S. 1983. Variability, path coefficient and discriminant function analysis in tomato. *Vegetable Sci*., **10**: 22-29.

Reddy B. R., Reddy M. P., Begum H. and Sunil N. 2013a. Genetic diversity studies in tomato (*Solanum lycopersicum* L.) *IOSR J.Agri. Vet. Science.,* **4** (4):53-55.

Reddy, B. R., Reddy, D. S., Reddaiah, K. and Sunil, N. 2013b. Studies on genetic variability, heritability and genetic advance for yield and quality traits in Tomato (*Solanum lycopersicum* L.) *Int. J. Curr. Microbiol. App. Sci* **2** (9): 238-244.

Reddy, B. R., Reddy, M. P., Reddy, D. S., Begum, H. 2013c. Correlation and path analysis studies for yield and quality traits in tomato (*Solanum lycopersicum* L.). *IOSR J. of Agri. and Vete. Sci.,* **4** (4): 56-59.

Revanasiddappa, K.V., 2008. Breeding investigations involving biparental mating and selection approaches in tomato (*Solanum lycopersicum* (Mill.) Wettsd.). *M.Sc.(Agri.) Thesis,* submitted to University of Agricultural Sciences, Dharwad (India).

Rick, C. M., Kesicki, E., Faber, J. F. and Holle, M. 1976. Genetic and biosystematic studies on two new sibling species of *Lycopersicon* from interandean Peru. *Theoret. Appl. Genet*., **47**: 55-68.

Robinson, H. F. 1966. Quantitative genetics in relation to breeding on the central mendalism. *Indian J. Genet.,* **26A**:171-187.

Rodriguez, S, Visedo G, Zapata C. 2001. Detection of errors in dinucleotide repeats typing by non-denaturating electrophoresis. Electrophoresis **22**:2656-2664.

Rohlf, F. J**.** 1997. "NTSYS-pc: Numerical Taxonomy and Multivariate Analysis System, Version 2.0". *Exeter Software, Setauket*, New York.

Rosales, M. A., L. Cervilla, E. Sanchez-Rodriguez, M. Rubio-Wilhelmi and B. Blasco. 2011. The effect of environmental conditions on nutritional quality of cherry tomato fruits: Evaluation of two experimental Mediterranean greenhouses. *J. Sci. Food Agric*., **9:** 152 -162.

Sahu, A. R. 2005. Performance of tomato genotypes for Chhattisgarh plains. *M.Sc. (Ag.) Thesis*, submitted to I.G.K.V. Raipur (C.G.).

Sahu, G. S. and Mishra, R. S. 1995. Genetic divergence in tomato. *Mysore. J. Agric. Sci.* **29**: 5-8.

Saeed, A., Hayat, K., Khan, A. A., Iqbal, S. And Abbas, G. 2007. Assessment of genetic variability and heritability in *Lycopersicon esculentum* Mill. *International J. of Agric. & Bio.*, **9** (2): 375–377.

Saleem M.Y., Iqbal Q. and Asghar, M. 2013. Genetic variability, heritability, character associ ate on and path analysis in F1 hybrids of tomato. *Pak. J. Agri. Sci.,* **50** (4): 649-653.

Salunke D. S., Jadhav A. S., Pawar B. D., Kale A. A. and Chimote V. P. 2012. Diversity analysis of tomato genotypes using RAPD markers and high performance liquid chromatography in relation to β - carotene content. *Society for plant research Vegetos.,* **25** (2): 95-101.

Searle, S.R. 1961. Phenotypic, genotypic and environmental correlations. *Biometrics*. **17**: 474 -480.

Shankar A., Reddy R. V. S. K., Sujatha M. and Pratap M. 2013. Genetic variability studies in F1 generation of tomato (*Solanum lycopersicon* L.) *IOSR J. Agri. Vet. Sci.* **4** *(5): 31-34.*

Sharifova S., Mehdiyeva S., Theodorikas K., Roubos K. 2013. Assessment of genetic diversity in cultivated tomato (*Solanum Lycopersicum* L.) genotypes using RAPD primers. *J.of Hort. Research.,* **21**(1): 83-89.

Sharma, K.C. and Varma, S. 2000. Path coefficient analysis in tomato (*Lycopersicum esculentum* Mill.). *Indian J. Agric. Sci.,* **70** (10): 700-702.

Sharma, K. C. and Verma, S. 2001. Analysis of genetic divergence in tomato. *Ann. Agric. Res*., **22** (1): 71-73.

Shashikanth, 2008. Genetic variability studies in tomato (*Solanum lycopersicon* Mill.). M.Sc. (Ag.) Thesis, submitted to University of Agricultural Sciences, Dharwad (India).

Singh, A. K. 2009. Genetic variability, heritability and genetic advance studies in tomato under cold arid region of Ladakh. *Indian J. Hort.,* **66** (3): 400-403.

Singh, A. K., Sharma, J. P., Satesh Kumar and Chopra, S. 2008. Genetic divergence in tomato (*Lycopersicon esculentum* Mill.) *J. Res., SKUAST-J.,* **7** (1): 1-8.

Singh, D. N., Sahu, A. and Parida, A. K. 1997. Genetic variability and correlation studies in tomato. *Environment and Ecology*, **15** (1): 117-121.

Singh, H. and Cheema, D. S. (2005). Studies on genetic variability and heritability for quality traits of tomato (*Lycopersicon esculentum* Mill.) under heat stress conditions. *Journal of Applied Horticulture, Lucknow*. **7**(1): 55-57.

Singh, H. N., Singh, R. R. and Mital, R. K. 1974. Genotypic and phenotypic variability in tomato. *Indian J. Agril. Sci.,* **44** (2): 807-811.

Singh, J. K., Singh, J. P., Jain, S. K. and Joshi, Aradhana 2004. Correlation and path-coefficient analysis in tomato. *Progressive Hort.*, **36** (1): 82-86.

Singh, K. P., Mandal, G. and Saha, B. C. (2006). Genetic variability of yield components and bio-chemical characters in spring season tomato (*Lycopersicon esculentum* Mill.). *Journal of Interacademicia*. **10** (3): 314-318.

Singh, P., Singh, S., Cheema, D. S. and Dhaliwal, M. S. 2002b. Genetic variability and correlation study of some heat tolerant tomato genotypes. *Veg. Sci.*, **29** (1): 68-70.

Singh, P. K. and Gopalkrishnan, T. R., (2000). Variability and heritability estimates in brinjal (*Solanum melongena* L.). *South Indian Hort*. **47** (1-6): 174-178.

Singh, R. K. and Chaudhary B. D. 1985. Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi.

Singh R. K., Singh A. K., Singh V. P., Singh N. K., Tiwari S. P. and Mohapatra T. 2004. Suitability of mapped sequence tagged microsatellite site markers for establishing distinctness, uniformity and stability in aromatic rice. *Euphytica* **135**: 135-143.

Sivaprasad, K. 2008. Genetic variability and correlation studies in biparental mating populations of tomato (*Solanum lycopersicon* (Mill) Wettsd.). *M.Sc. (Agri.) Thesis*, submitted to University of Agricultural Sciences, Dharwad (India).

Snedecor, G.W. and Cochran, W. G. 1967. Statistical methods (VI ed.). Oxford and IBH Publ. Co., New Delhi, pp. 534.

Srivastava, K., Kumari, K., Singh, S. P. and Kumar R. 2013. Association studies for yield and its component traits in tomato (*Solanum lycopersicum* L.). *Plant Archives* **13** (1): 105-112.

Subbiah, B.V. and Asija, G. L. 1956. A rapid proceducer for the determination of available nitrogen in soils. *Current Science*., **25**: 259-260.

Subramaniam G., Chen K .Y., Davidson V. Pastrana. and Wang J. F. 2010. Development and characterization of tomato SSR markers from genomic sequences of anchored BAC clones on chromosome 6. *Euphytica.,* **173**: 85–97.

Tanksley S. D., Ganal M.W., Prince J, P., De Vicente M. C., Bonierbale M. W., Broun P, Fulton TM., Giovannoni J. J., Grandillo S., Martin G.B., Messeguer, R., Miller J.C., Miller, L., Paterson A. H., Pineda, O., Roder M. S., Wing R. A., Wu W, Young ND. 1992 High density molecular linkage maps of the tomato and potato genomes. *Genetics.,* **132**:1141– 1160.

Tasisa, J., Belew, D. and Bantte, K. 2012. Genetic associations analysis among some traits of tomato (*Lycopersicon esculentum* Mill.) genotypes in West Showa, Ethiopia. *Int. J. Pl. Breed. and Genet.,* **6** (3): 129-139.

Tiwari, J. K. and Upadhyay, D. 2011. Correlation and path-coefficient studies in tomato (*Lycopersicon esculentum* Mill.). *Res. J. of Agric. Sci.,* **2** (1): 63-68.

Trivedi, J. 1996. Evaluation of F_1 hybrids/varieties of tomato (*Lycopersicon esculentum* Mill.). *M.Sc. (Ag.) Thesis*, submitted to I.G.K.V. Raipur (C.G.).

UPOV-BMT. 2002. BMT/36f1O Progress report of the 36th session of the technical committee, the technical working parties and working group on biochemical and molecular techniques and DNA profiling in particular, Geneva.

Varshney R.V., Graner A. and Sorells M. E. 2005. Genic microsatellite markers in plants: features and applications. *Trend in Biotechnology* **23**: 48-55.

Veershety, 2004. Studies on variability, character association and genetic diversity in tomato (*Lycopersicon esculentum* Mill.). *M. Sc. (Agri.) Thesis*, Uni. Agric. Sci., Dharwad (India).

Verma, S. 1996. Study of genetic variability and diversity in tomato (*Lycopersicum esculentum* Mill.) *M.Sc. (Ag.) Thesis*, submitted to I.G.K.V, Raipur, (C.G.).

Verma, S. K. and Sarnaik, D. A. 2000. Path analysis of yield component in tomato (*Lycopersicon esculentum* Mill.). *J. Appld. Bio.*, **10** (2): 136-138.

Wang, D. Shi J., Carlson, S. R., Cregan, P. B., Ward R.W. and Diers B.W. 2003. A low-cost high-through full polyacrylamide gel electrophoresis system for genotyping with microsatellite DNA markers. *Crop Sci*. **43**:1828-1832.

Wright, S. 1921. Correlation and Causation. *J. Agric. Res*., **20**: 557-585.

Xiaorong H., Wang H., Chen J. And Yang W., 2012 Genetic diversity of argentina tomato varieties revealed by morphological traits, simple sequence repeat, and single nucleotide polymorphism markers. *Pak. J. Bot*., **44** (2): 485-492.

Yashvantakumar, K. H. 2008. Heterosis and combining ability for resistance against tospo virus in tomato (*Solanum lycopersicum* Mill.) Wettsd. *M.Sc. (Agri.) Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).

Yong S. k., Sun G. P. and Seung I. Y. 2009. Assessment of genetic variation among commercial tomato *(Solanum lycopersicum* L.) varieties using SSR mariters and morphological characteristics. *Genes & Genomics* **31** (1): 1-10.

APPENDICES

APPENDIX-I

Weekly meteorological data during crop growth period (Dec. 2013 to April, 2014)

Week. No.	Date	Temp.(^{0}C)		Rain fall (mm)	Rainy Days	RH. (%)		Wind velocity (Km/h)	Evaporation (mm)	Sun Sine (hours)
		max.	min.			I	II			
50	Dec 10-16	27.7	9.8	0	0	90	27	1.3	3	9
51	Dec 17-23	28.1	11.7	0	0	90	34	1.6	2.6	8
52	Dec 24-31	28.3	12.7	0	0	93	40	0.9	2.6	6.5
1	Jan 01-07	28.6	13.6	0	0	90	40	0.7	2.6	6.9
2	Jan 08-14	27.8	14.1	0	0	90	47	1.6	2.5	5.4
3	Jan 15-21	29	16.1	0	0	89	46	2.5	2.8	4.6
4	Jan 22-28	28.2	13.7	0	0	87	38	2.3	3.5	7
5	Jan 29-04	28.8	10.1	0	0	86	28	2	3.7	9.5
6	Feb 05- 11	31.7	14.8	0	0	85	33	3.2	4.3	8.7
7	Feb 12-18	27.9	15.4	20.4	2	83	39	4.1	4.3	6.6
8	Feb 19-25	28.9	14.6	18.6	1	86	41	2.9	4.1	8.7
9	Feb 26-04	27.9	17.7	45.8	3	91	61	4.1	4.1	6.6
10	March 05-11	27.5	17.5	2.4	0	88	44	2.7	2.9	4.9
11	March 12-18	33.3	19.5	2	0	89	38	1.4	4.6	7.5
12	March 19-25	36.4	19.4	0	0	74	21	2.7	6.9	9
13	March 26-01	38.4	22.2	0	0	67	24	3.1	7	7.7
14	April 2-8	38.5	22.4	2.8	1	59	17	3.5	8.5	8.6