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Dissertation-I (GPB-596) report

on

**ASSESSMENT OF GENETIC AND PHENOTYPIC VARIABILITY IN
TOMATO (*Solanum lycopersicum L.*)**

submitted by

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in partial fulfilment for the award of the degree

Master of Science (Agriculture)

in

Genetics and Plant Breeding

Under the guidance of

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CERTIFICATE

This is to certify that the Dissertation entitled **Assessment of genetic and phenotypic variability in tomato (*Solanum lycopersicum L.*)** is a bonafide record of independent research work to be done by **Sumant Bindal** (Reg. No.: 11700693) under my supervision in partial fulfillment for the award of the Degree of Master of Science (Agriculture) in Genetics & Plant Breeding.

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1. Introduction

Tomato (*Solanum lycopersicum L.*) is an important crop cultivated across the world due to its vast adaptability, appropriateness for use as fresh as well as a major component of almost all processed foods. It contains lycopene, a red pigment regarded as natural antioxidant. Vitamin A, C and minerals are richly found in tomato due to which it is sometimes considered as protective foods. Since it is attractive in appearance and has high nutrient value, it is regarded as poor man's orange in many countries.

India ranks second after China in tomato production with an overall production of 19696.92 thousand MT from an area of 808.54 thousand ha (Horticultural Statistics at a Glance, 2016-17). India's share in global tomato production is 11.1% with an average productivity of 21.24 t/ha while the global average productivity is 33.99 t/ha. In Punjab, tomato is grown over an area of 8.06 thousand ha with a production and average productivity of 200.15 thousand MT and 24.84 t/ha respectively which is higher than the overall average India's productivity of 24.36 t/ha but lesser than the average productivity of Himachal Pradesh followed by Uttar Pradesh and Andhra Pradesh with an average productivity of 44.21 t/ha, 39.57 t/ha and 37.86 t/ha. (Horticultural Statistics at a Glance, 2016-17).

A plant breeder works for the identification of elite genotypes and apply appropriate selection procedure for screening the existing breeding material to achieve success in a crop improvement programme (Meena and Bahadur, 2013). Diverse agricultural systems need distinct cultivars, which are suited to niche environmental conditions. A plant breeder attempts to create gene combinations through hybridization between divergent parents which are novel and can only be possible through thorough knowledge of genetic resources (glaszmann et al., 2010). Amount of genetic variability, rate of transmissibility of desired traits are the parameters for success of any breeding programme. For a plant breeder to initiate a crop improvement programme, it is of prime importance to have a deep knowledge of available variability and heritability for desirable traits. Keeping in view of this, programme of work has been planned to know the magnitude and nature of genetic variability for fruit, agronomic and quality traits with in available tomato genotypes.

For a judicious crop improvement programme, a major prerequisite is efficient selection of parents. Identification of the crosses exhibiting higher heterosis will be possible only after having an information from varying cross combinations. In order to identify good combiners to be used in a breeding programme, genetic stock can be evaluated at preliminary level using partial diallel. So, an attempt is planned by making crosses among different tomato genotypes in an appropriate design with the following objectives:

2. Objectives

1. Identification of high yielding single cross experimental hybrids.
2. Estimation of various components of variation and heterosis level.
3. Estimation of combining ability effects for determining the additive and non-additive components.
4. Study of variation in f_2 population of selected hybrids.

3. A brief resume of work done

Saleem *et al.* (2009) evaluated the performance of thirteen parents along with thirty hybrids in a line x tester experiment in tomato and found significant variance due to crosses, line x testers and treatments for different traits which were days to fruiting, number of fruit per plant, fruit length, fruit width, fruit weight and yield per plant. Degree of dominance, variance of sca, gca and their ratio showed importance of non-additive gene action in all the characters.

Ara *et al.* (2009) studied genetic variability, path coefficient analysis and correlation among 35 tomato genotypes for estimation of yield, growth and quality parameters and concluded that the traits per plant number of branches, average fruit weight, per plant number of fruits, titratable acidity, per plant fruit yield and juice-pulp ratio showed the high magnitude for genetic gain, heritability and GCV. Per cluster number of flowers, average fruit weight, fruit

yield, per plant number of fruits, plant height and harvest duration were directly highly positively effected by days to first picking as unveiled by path coefficient analysis.

Sanchez *et al.* (2010) studied genetic effects with quality analysis and yield as variables for evaluation using four parents and direct possible six breeds in field as well as in greenhouse conditions. Highly significant differences were found between environments for yield as well as average fruit weight. Also, for days to first harvest significant differences were observed, where for genotypes including hybrids and parents, environmental state differs for all the respective places proving that genotypes performed differently and also stating genetic diversity of parents as the reason for differed performance of the hybrids.

Ghosh *et al.* (2010) studied variability, association among characters and path coefficient analysis using exotic tomato hybrids of F₂ segregating generations and observed that traits, days to first flowering, fruit length and fruit diameter showed very less differences between PCV and GCV. All the traits contributing to yield except per cluster number of flowers showed high heritability. Per plant fruit yield, per cluster number of fruits, individual fruit weight, per plant number of branches, fruit clusters per plant, fruits per plant showed high heritability associated with high genetic advance. Positive significant GCV and PCV was noted between plant height at first flowering, per plant number of flowers, per cluster number of fruits, per plant number of fruit clusters, per plant number of fruits with per plant fruit yield.

Dar *et al.* (2011) evaluated sixty genotypes in a RBD design to know the extent of genetic advance, genetic variability and heritability for the investigation of quality and yield characters in tomato. They concluded that overall GCV was lower than that of PCV for all the considered traits. Per plant number of fruits, fruit average weight and per hectare yield in quintals showed the high magnitude for PCV whereas for β -carotene, the GCV was found to be on a higher side. Also the traits lycopene content, ascorbic acid and β -carotene showed high heritability.

Mohamed *et al.* (2012) studied genetic variability, heritability and genetic advance among thirty genotypes of tomato for traits of plant and fruit at Hudeiba Research Station and observed that the phenotypic and genotypic variance was highest for the fruit weight and lowest for the yield of fruit per plant. Also, the plant height showed the highest heritability i.e. 97%

while yield of fruit per plant was the lowest. Additive genes action were found to be controlling all the traits under observation as estimated through high heritability of these.

Chernet *et al.* (2013) used thirty six genotypes of tomato in a 6 x 6 simple lattice design for estimation of genetic variability and traits association among themselves. Per plant number of matured fruits and fruit set percentage were the traits which gave highest GCV and PCV. Per plant number of matured fruits showed the highest heritability while lowest was observed for number of primary branches. Fruits per plant, fruit set percentage and per plant weight of fruits were found to be highly significant phenotypically and positively correlated to yield per hectare.

Meena *et al.* (2013) conducted a RBD experiment using thirty genotypes of tomato for estimation of genetic variability, genetic advance and heritability. They observed that the GCV values were lower than that of the PCV. TSS, plant height, ascorbic acid and leaf curl incidence percent were the traits for which values of GCV and PCV were higher. It was observed that improvement of the traits having high genetic variability as indicated by the higher values of GCV can be carried out by simple selection. High heritability for these traits ranging from 92-100% indicated the preponderance of additive gene action.

Kumar *et al.* (2013) made an attempt to find out path coefficient analysis, variability and correlation among 26 tomato genotypes for yield and yield attributing traits which revealed that for EC-357838 mean value was observed to be highest for per plant yield, TSS and per plant number of fruits. Fruit weight, per plant number of fruits, plant height and per plant yield were under the effect of additive gene action as indicated by high GCV, PCV, genetic gain and heritability. Per plant yield followed by per cluster number of fruits, per plant number of fruits and fruit diameter were positively directly effected by fruit weight as indicated by path analysis.

Saeed *et al.* (2014) used four testers and three lines for a line x tester analysis for the identification of parents that are potential along with their hybrids, making a set of twelve crosses that resulted in significant distinction in SCA and GCA effects. Excluding per plant fruit yield, genetic determination all the traits resulted in additive and non-additive gene action with preponderance of non-additive gene action for the values of SCA and GCA.

Sidhva *et al.* (2014) evaluated six cultivars of tomato for variability studies and found that moderate values of GCV and PCV were shown by polar fruit diameter, per plant number of

fruits, equatorial fruit diameter, per plant fruit yield, plant height and fruit weight whereas higher values were obtained for seeds per fruit. Per plant fruit yield, per plant number of fruits, plant height, fruit weight, equatorial fruit diameter and seeds per fruit gave the higher values of heritability along with high value of genetic advance as percent of mean.

Kumar *et al.* (2015) considered thirteen genotypes and thirty crosses derived from them accompanying with two check cultivar of tomato tomato for genetic variability and character association for quality, yield and yield attributing traits. For titrable acidity minimum and for plant height maximum PCV and GCV was recorded, respectively. For all the quality and yield traits, GCV was found to be lower than that of PCV. For pericarp thickness, PCV, GCV and heritability gave higher values and simultaneously for plant height genetic advance was found to be on a higher side.

Prajapati *et al.* (2015) studied thirty nine genotypes of tomato for genetic variability and found that per plant number of fruits showed highest phenotypic and genotypic variance whereas found it to be lower for test weight. Genetic components can be indicated to contribute more towards total variation as genotypic variance was observed to be high for majority of the traits. Days to 50% fruit setting showed the lowest GCV and PCV while per fruit number of seeds and average fruit weight gave higher magnitude of PCV and GCV. Heritability (broad senses) was found to be on a lowest side for test weight whereas it was on a higher side for number of secondary branches and average fruit weight. Results for days to 50% fruit setting shown lowest genetic advance while the average fruit weight showed the highest.

Kumar *et al.* (2015) did line x tester analysis using 4 testers and 10 lines of tomato along with their hybrids for estimation of SCA and GCA. It was depicted by the results that for equally efficient evaluation of all the traits, we cannot go for a particular cultivar or hybrid. Line LBR-12 and LBR-13 were regarded as good general combiner for dry matter, lycopene content, pericarp thickness with LBR-12 for total fruit yield, TSS and LBR-13 for titrable acidity and carotenoids. Similarly line LBR-19 and testers 8-2-1-2-5 and EC-119197 were also found suitable for many traits.

Kathayat *et al.* (2015) studied genetic variability among seventeen quantitative traits of 29 genotypes of tomato and concluded that for the trait per plant number of fruit clusters highest

GCV and PCV was observed while it was lowest for days to first fruit picking. Per plant number of fruit cluster showed the highest heritability while it was lowest for days to first fruit picking. Genetic advance found to be higher for 1000 seed weight and lowest for diameter of fruit. Phenotypic correlation coefficient was observed to be lower than genotypic correlation coefficient in general.

Rai *et al.* (2016) evaluated 56 genotypes of tomato in a RCBD design for quality and yield characters to know about the genetic gain, genetic variability and heritability. GCV was found to be on a slightly lower side as compared to PCV for all the considered characters. Lycopene content, pericarp thickness, per plant fruit yield, per plant number of fruits and average fruit weight gave high magnitude of genetic gain and heritability.

Kherwa *et al.* (2018) considered 29 genotypes of tomato to record data on thirteen traits for the evaluation of genetic variability, heritability and genetic advance. Average weight of fruit followed by thickness of pericarp, total fruit yield, equatorial fruit diameter and per fruit number of locules were the traits for which high values of GCV and PCV recorded. *S. pimpinellifolium*, the species of tomato was found to be noted to be a potential donor for improvement of cultivated genotypes in terms of yield and quality.

Tamta *et al.* (2018) considered 10 parents with 3 testers and thirty hybrids for evaluation of standard heterosis by identifying cross-combinations which are unique in order to increase quality, growth and yield. It was found that the traits, per plant fruit yield, average fruit weight and per plant number of fruits gave positive heterosis whereas per plant number of branches, fruit width, plant height, days to first harvest showed negative heterosis.

4. Technical programme of work

The brief outline will be as follows:

Number of genotypes	:	25
Local Checks	:	2

Location	:	Research farm, Department of Genetics & Plant Breeding, School of Agriculture, Lovely Professional University, Jalandhar, Punjab
Season	:	Spring-Kharif, 2018
Design	:	Randomized Complete Block Design (RCBD)
Replication	:	Three
Plot size/ plant population	:	8 Plants per treatment per replication

Observations to be recorded

The data will be recorded on five random competitive plants for each cultivar across replications on the following traits:

A. Fruit characters

1. Fruit yield (ha)
2. Pericarp thickness (mm)
3. Average fruit weight (g)
4. Number of locules/fruit
5. Fruit shape index
6. Total number of fruits/plant
7. Marketable fruits/plant
8. Marketable yield/plant (kg)
9. Fruit length (cm)
10. Fruit diameter (cm)
11. Fruit volume (cc)
12. Number of fruit cluster/plant
13. Gross yield/plant (kg)

B. Agronomic characters

1. Days to 50% flowering
2. Days to first harvest
3. Plant height (cm)
4. Days to last harvest
5. Number of flowers/cluster

C. Quality parameters

1. Total Soluble Solids (degrees Brix)
2. Lycopene content
3. Titrable acidity
4. Ascorbic acid (mg/100g)

Statistical Analysis

For each character, mean value will be calculated using the data collected on different characters and the statistical data will be applied for the replicated mean data. Description of various statistical methods to be used is given below:

Randomized Complete Block design (RCBD) using ANOVA among genotypes.

Diallel analysis following Griffing's numerical approach (1956) to estimate combining ability, gene effects, heritability, Phenotypic and genotypic coefficient of variation, relative advance, etc.

5. References

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6. Facilities available

All the required facilities are available in the Department of Genetics & Plant Breeding, School of Agriculture, Lovely Professional University, Jalandhar.

7. Collaboration with other Departments/Institutes/University

Nil