

Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)

***A Thesis submitted to the
Orissa University of Agriculture and Technology
in Partial fulfilment of the Requirement for the degree of
Master of Sciences in Agriculture
(Vegetable Science)***

By

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CERTIFICATE-I

This is to certify that the thesis entitled “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE IN AGRICULTURE (VEGETABLE SCIENCE)** to the Orissa University of Agriculture and Technology is a faithful record of *bona fide* and original research work carried out by **MEERA ROJALIN** under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma.

It is further certified that the assistance and help received by her from various sources during the course of investigation has been duly acknowledged.

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CERTIFICATE-II

This is to certify that the thesis entitled “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” submitted by **MEERA ROJALIN** to the Orissa University of Agriculture and Technology, Bhubaneswar in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE (VEGETABLE SCIENCE)** has been approved by the students’ advisory committee and external examiner.

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ABSTRACT

The present investigation entitled, “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” was conducted at All India Coordinated Research Project on Vegetable Crops operating under Orissa University of Agriculture & Technology, Bhubaneswar, Odisha, India during *rabi* season of 2017-18. The objective was to study the nature and extent of genetic variability in determinate tomato for improvement of desirable genotype(s) for fruit yield and yield attributes. Eighteen genotypes were evaluated by adopting RBD replicated thrice. The genotypes were evaluated for 20 parameters including, vegetative growth, flowering, fruit yield and yield attributing as well as fruit quality parameters.

The results revealed significant variations among the genotypes for all the 20 characters with coefficient of error variations within 10% for most of the traits under study. Invariably, the GCV values were lower than PCV as expected. Comparatively lower difference of GCV and PCV was noticed in traits like plant height, primary branches plant⁻¹, internodal length, flowers cluster⁻¹, fruit weight, number of locules, total sugar and ascorbic acid. Moderate to high range of heritability along with moderate to high range of genetic advance as % of mean for traits such as internodal length (98.2 and 39.48), average fruit weight (87.70 and 32.33), number of locules (93.80 and 78.48), fruits plant⁻¹ (77.0 and 34.09), marketable fruit yield plant⁻¹ (61.30 and 37.08), ascorbic acid (95.50 and 78.87) and total sugar (82.90 and 36.36), respectively. Thus, simple selection will be very effective for improvement of these traits in determinate tomato. Correlation study indicated that at both phenotypic and genotypic level, marketable fruit yield plant⁻¹ was positive and significantly correlated with plant height (0.45 and 0.31) and primary branches plant⁻¹ (0.51 and 0.38). Similarly, traits like average fruit weight (0.334), number of locules (0.204), fruit length (0.143), % of fruit set (0.126), flowers cluster⁻¹ (0.106), days to fruit set (0.102), fruits plant⁻¹ (0.096), primary branches plant⁻¹ (0.070) and plant height at final harvest (0.009) in order of merits imposed positive direct effect on marketable fruit yield plant⁻¹. Out of five clusters, derived through Tocher's method of genetic divergence analysis, it can be concluded that, crosses involving genotypes of cluster III (2016/TODVAR-06, 2016/TODVAR-08, 2016/TODVAR-09) and cluster II (2016/TODVAR-05, 2016/TODVAR-11, 2016/TODVAR-12, Pusa 120, Pusa Rohini) can be used in hybridization programme to produce either desirable hybrids or recombinants in segregating generations due to high genetic divergence.

Hence, it may be concluded that, 2016/TODVAR-12 (414.27 qha⁻¹), Pusa Rohini (342.28 qha⁻¹), 2016/TODVAR-05 (340.05 qha⁻¹), Pusa Gaurav (319.42 qha⁻¹) and Pusa 120 (303.85 qha⁻¹) were identified as better performing determinate tomato genotypes having significantly higher vegetative growth, yield and quality attributes suitable for Bhubaneswar condition. These genotypes may be further evaluated for their yield stability in future.

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ABBREVIATIONS USED

%	:	Per cent
/	:	Per
@	:	At the rate
C.D.	:	Critical Difference
cm	:	Centimeter
DAT	:	Days after Transplanting
ESS	:	Error sum of square
<i>et al.</i>	:	And others
etc.	:	Etcetera
g	:	Gram
ha	:	Hectare
Hrs.	:	Hours
i.e.	:	(<i>Id est.</i>) that is
kg	:	Kilogram
P		Phosphorus
m	:	Meter
Max.	:	Maximum
Min.	:	Minimum
mm	:	Millimeter
No.	:	Number
R.H.	:	Relative humidity
RSS	:	Replication sum of square
TSS	:	Treatment sum of square
GCV	:	Genotypic Coefficient of Variation
PCV	:	Phenotypic Coefficient of Variation
GA	:	Genetic Advance
TSS	:	Total soluble solids
q	:	Quintal
<i>viz.</i>	:	(<i>Videlicet</i>) Namely
°C	:	Degree Celsius

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) belongs to family Solanaceae, is one of the important vegetable crops of the world next to only to potato. Tomato is cultivated in all the three major climates of temperate, sub-tropical and tropical regions of the world, under both open and protected conditions as well. Tomato is so unique in nature, which can be used both as fresh vegetable as well as a variety of processed products such as juice, ketchup, sauce, canned fruits, puree, paste, etc. Apart from contributing nutritive elements, colour and flavour to the diet, tomatoes also act as a valuable source of antioxidants or chemo-protective compounds and may thus be termed a “functional food” (Ranieri *et al.*, 2004).

Tomato is mostly considered as ‘Protective food’ based on its nutritive value and antioxidant properties due to the presence of lycopene and flavonoids (Sepat *et al.*, 2013). High antioxidant capacity in both fresh and processed tomatoes associated with the higher capacity to eliminate reactive oxygen species (ROS) and helps in lowering the incidence of certain forms of human cancer (Capanoglu *et al.*, 2010).

Quality and flavour of the processed products depends primarily on chemical components like reducing sugar, acidity, ascorbic acid, lycopene, β -carotene, T.S.S. and total sugar which has been reported to vary greatly with variety (Balasubramanian, 1984).

The market of tomato processing products around the world are expanding whereas, in the tropics, the tomato processing industry often confronted with the problem of limited supply of processing tomatoes. Low yield increases the cost and the risk of growing tomatoes. Therefore, farmer’s income is decreased. Scientists from the tropical regions have identified the reasons why tomato varieties grow in these areas are unadapted. The reasons fall into three major categories, i.e., susceptibility to diseases, low fruit setting ability and poor quality fruits. However, in the developing countries of wet and humid tropics, there are far more important steps that need to be taken. First is to improve the processing tomato varieties to adaptable varieties of the tropics, since the potential for tomatoes in tropics is great. With 11% share of global production, India produces more tomatoes than any other country,

except China. Despite this, less than 1% of India's tomato production is processed, way below the average of 26% for the world's top 10 tomato producing countries (Subramanian, 2016). Tomato quality depends on many factors such as cultivar, growing condition and ripening on and off the plant. The physical and chemical characteristics of tomato also affect the quality of processed product. Therefore, high yield coupled with good processing qualities are the pre-requisites for the general acceptance of the determinate processing varieties by the farmers.

In general, the growth of the determinate tomato varieties does not continue throughout life of plant although after sometime the growing point terminates into an inflorescence, which gives self-topping. Plant first completes its growth then starts flowering, fruiting, maturity and ripening. Branching starts emerging from top to bottom and this type of branching pattern is called basipetal movement. Determinate cultivars are usually earlier than indeterminate ones and are especially desirable where the growing season is short. With fruit ripening nearly at one time, it makes this plant type suitable for mechanical harvesting and highly suitable for processing industries.

China, India, USA, Turkey, Egypt, Iran, Italy, and Spain etc. are the major producers of tomato. India is the 2nd largest producer of tomato in terms of both area and production (FAO, 2016). Indian yield levels (24.2 t ha^{-1}) are far below the world average of 37 t ha^{-1} (NHB, 2016). In India during the year 2016-17, it was cultivated over an area of 797'000ha with production of 20708'000 MT and average productivity of 24.4 t ha^{-1} (NHB, 2016-17). Andhra Pradesh, Madhya Pradesh, Karnataka, Telangana, Gujarat, Odisha, West Bengal are the major producing states of tomato in India. In the year 2016-17 Odisha produced 1374.9'000 MT of tomato from an area of 96.6'000ha area and average productivity was 14.4 t ha^{-1} (Horticulture Statistics Division, DACFW, 2017).

There are many factors which contribute to yield in all crops including tomato, genetic constitution being one of them. Therefore, a thorough knowledge regarding the amount of genetic variability existing for various characters is essential for initiating the crop improvement programme. Diverse plants are expected to give high hybrid vigour (Harrington, 1940). Hence, it necessitates the study of genetic divergence among the existing varieties and germplasm collection for identification of

parents for hybridization programme. In order to develop desired determinate tomato cultivars, it is important to catalogue the genetic diversity within the germplasm (Islam *et al.*, 2004). Considering the potentiality of determinate tomato, there is a need to develop varieties suitable for cultivation under specific agro-ecological conditions and also for specific end use.

Yield is a quantitative character controlled by many genes. The consideration of yield components in selection is based on the assumption that a strong positive correlation exists between yield and yield components and that these component characters have higher heritability than yield (Lungu, 1978). The technique of path coefficient analysis was developed by Wright (1921) and demonstrated by Dewey and Lu (1959) as a means of separating direct and indirect contribution of various traits. Therefore, it is necessary to study the path coefficient analysis to find out the characters which directly or indirectly contributes to yield.

Hence, the present study entitled “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” has been designed with the following objectives to be carried out with a set of genotypes including varieties and advanced lines.

Objectives of the study:

1. To study the nature and extent of genetic variability present in the experimental material.
2. To examine the nature and magnitude of character association and path coefficient analysis.
3. To study the extent of genetic divergence among the test genotypes using D^2 analysis.



REVIEW OF LITERATURE

The success of any crop improvement programme mainly depends on the extent and magnitude of variability existing in the population. Therefore, a thorough and adequate knowledge of genetics of various characters is very much essential in vegetable breeding programme for improvement of both qualitative and quantitative traits. Hence, genetic variability in relation to fruit yield and its attributes is the main concern for any breeder. The literature available pertinent to the present study entitled “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” have been reviewed under the following headings.

- 2.1 Genetic variability
- 2.2 Heritability and Genetic advance
- 2.3 Correlation studies
- 2.4 Path analysis
- 2.5 Genetic diversity

2.1 Genetic variability

The basic understanding of genetic variability is a prerequisite for the planning of any crop improvement programme. Generally, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are measured to study the variability that exists in the population. Literature pertaining to genetic variability studies on tomato is presented below.

Brar *et al.* (2000) reported high magnitude of PCV for number of marketable fruits plant⁻¹ and total number of fruits plant⁻¹ whereas low GCV and PCV were observed for number of fruits cluster⁻¹ and moderate for marketable fruit yield and total fruit yield plant⁻¹. In a study on tomato by Joshi and Singh (2003) high GCV and PCV was reported for traits like plant height, number of flowers cluster⁻¹, number of branches plant⁻¹, number of flower clusters plant⁻¹, number of fruits plant⁻¹, weight of fruits plant⁻¹ and number of locules fruit⁻¹ in tomato. Similarly, Mohanty (2003) reported high GCV and PCV for average fruit weight (38.96%, 37.91%), number of branches plant⁻¹(32.35%, 30.62%), fruits plant⁻¹ (31.79%, 30.29%) and plant height (28.07, 26.81%), indicating presence of greater variability in these traits

According to Ara *et al.* (2009), fruit yield plant⁻¹ (35.34, 37.30), number of primary branches plant⁻¹ (30.33, 30.36) and number of fruits plant⁻¹ (30.08, 30.13) recorded high GCV and PCV. They also observed moderate GCV and PCV for characters like average fruit weight (22.31, 22.33), TSS (19.33, 20.88), vitamin C content (19.172, 19.173), plant height (19.61, 19.63), pericarp thickness (18.19, 19.09) and number of fruits cluster⁻¹ (12.57, 14.08).

In a study on tomato by Khan *et al.* (2012), it was found that PCV and GCV were high in tomato for fruit weight, fruits plant⁻¹, plant height and fruit yield plant⁻¹. Similarly, Manna and Paul (2012) observed that GCV and PCV, respectively were high (>30%) for locules, fruit plant⁻¹ followed by fruit weight, moderate (20-30%) for total acid %, fruits plant⁻¹, vitamin C content, fruit yield plant⁻¹, fruit length and pericarp thickness whereas low (<20%) for fruit width and TSS. Kumar *et al.* (2013) reported that GCV was high for number of fruits plant⁻¹ (45.85), fruit weight (41.28), fruit yield plant⁻¹ (36.51) and plant height (33.73). Moderate GCV was observed for number of fruits cluster⁻¹ (31.92), fruit length (29.38), fruit diameter (21.47), pericarp thickness (25.09), number of locules fruit⁻¹ (22.69). The GCV was found low for days to 1st harvest (12.98), harvest duration (11.32) and TSS (13.29).

Agarwal *et al.* (2014) observed highest GCV for number of fruits plant⁻¹. PCV values were slightly higher for all the traits as compared to GCV but the difference between GCV and PCV values were low indicating less influence of environmental condition on these traits. Similarly, Kumar *et al.* (2014) while evaluating 21 thermo tolerant tomato genotypes observed that PCV was higher than the corresponding GCV in most of the traits. High PCV was observed for fruit yield plant⁻¹, whereas high GCV was recorded for yield plant⁻¹ and total chlorophyll content. Meitei *et al.* (2014) reported high GCV for fruits plant⁻¹, single fruit weight, fruit yield plant⁻¹ and fruit yield ha⁻¹ in tomato. A study by Meena and Bahahdur (2015) also reported high estimates of PCV and GCV for plant height.

Basavraj *et al.* (2015) reported highest GCV for average fruit weight (89.28) followed by number of fruits plant⁻¹ (85.14), TSS (70.92), branches plant⁻¹ (52.75), plant height (33.80), yield plant⁻¹ (33.63), equatorial diameter (26.01), polar diameter (20.98), number of fruits cluster⁻¹ (14.73) and number of locules fruit⁻¹ (6.75). They also observed highest PCV for average fruit weight (97.36) followed by number

of fruits plant⁻¹ (92.33), equatorial diameter (69.40), yield plant⁻¹ (58.86), number of branches plant⁻¹ (57.32), TSS (47.24), polar diameter (22.08), fruits cluster⁻¹ (17.06) and number of locules fruit⁻¹ (10.13). A study carried out by Singh *et al.* (2015) observed high magnitude of PCV and GCV for fruit yield plant⁻¹ followed by average fruit weight, number of locules fruit⁻¹, number of fruits plant⁻¹, plant height and number of primary branches plant⁻¹.

Hasan *et al.* (2016) reported that PCV was higher than the GCV for plant height, primary branches plant⁻¹, days to 1st flowering, days to 50% flowering, days to 1st harvest, individual fruit weight and fruits plant⁻¹ indicating the influence of environment for the expression of these characters. A study on tomato by Kumar *et al.* (2016) reported higher GCV and PCV values for fruits plant⁻¹, polar diameter, fruit weight, number of clusters plant⁻¹, number of seed fruit⁻¹, test weight, plant height, number of primary branches plant⁻¹, number of fruits cluster⁻¹, locule number, flowers cluster⁻¹ and equatorial diameter. High estimates of heritability and GA were recorded for number of fruits plant⁻¹, average fruit weight, fruit yield plant⁻¹, locular wall thickness and lycopene content in a study carried out by Rai *et al.* (2016) on 56 genotypes of tomato.

In tomato Bhandari *et al.* (2017) reported that the maximum estimate of PCV and GCV was recorded for number of seeds fruit⁻¹ followed by plant height, average fruit weight and total number of fruits plant⁻¹. An experiment conducted by Ligade *et al.* (2017) reported high values of GCV and PCV for characters viz., number of fruits plant⁻¹, number of locules fruit⁻¹, average fruit weight, fruit yield plant⁻¹, marketable fruit yield plot⁻¹ which indicated the presence of high genetic variation in the population. A study conducted by Mamatha *et al.* (2017) to find out the genetic variability in F₂ population of Utkal Raja x Arka Sourabh indicated higher estimates of PCV and GCV for the traits like plant height, number of branches at peak harvest stage, number of clusters plant⁻¹, days to 1st flowering, number of fruits plant⁻¹, average fruit weight and yield plant⁻¹. Moderate PCV and GCV were found for TSS. Patel *et al.* (2017) carried out a study on 24 tomato genotypes and found that GCV and PCV were high for average fruit weight, number of fruits plant⁻¹, fruit yield plant⁻¹, number of primary branches plant⁻¹ and plant height at maturity. However, Savitharamma (2017) working on F₄ segregating population of the cross EC

771612 × LA 2657 observed high GCV and PCV along with narrow difference between PCV and GCV for fruits plant⁻¹, fruit diameter, plant height, number of clusters plant⁻¹ and fruit yield plant⁻¹ indicating less influence of environment on expression of these characters.

2.2 Heritability and Genetic advance

In general heritability refers to the degree to which the variability of quantitative character in a population is transmitted to the progeny. Genetic advance (GA) is a product of heritability and infers the potentiality of selection intensity. GA when considered along with heritability gives reasonable assessment of the resultant effects of selection in breeding populations (Johnson *et al.*, 1955).

Kour *et al.* (2008) observed high heritability for fruits plant⁻¹ (93.00% and 82.50%) and plant height (32.33% and 33.50%) in F₁ and F₂ generations. A study on tomato carried out by Ara *et al.* (2009) reported high values of GCV, heritability and higher value of GA for fruit yield plant⁻¹, number of primary branches plant⁻¹, number of fruits plant⁻¹ and average fruit weight.

Khan *et al.* (2012) reported high and moderate to high heritability coupled with high and moderate to high GA for number of locules fruit⁻¹, fruit weight, fruit length, number of fruits plant⁻¹, pericarp thickness and vitamin C which indicated the predominance of additive gene action and therefore, these were regarded as more reliable for effective selection. Kumar *et al.* (2013) observed high heritability estimates for characters like fruit weight (98.04%), number of fruits plant⁻¹ (97.52%), fruit length (96.74%), days to 1st harvest (94.59%), plant height (91.20%), pericarp thickness (86.21%) and fruit yield plant⁻¹ (82.13), number of fruits cluster⁻¹, fruit diameter, number of locules fruit⁻¹, harvest duration and TSS were found to be moderately heritable. High heritability with high GA was observed in traits like plant height, individual fruit weight, fruit length and fruits plant⁻¹.

High heritability, GCV and GA were observed for number of fruits plant⁻¹ and average fruit weight in a study conducted by Agarwal *et al.* (2014) on tomato. Basavraj *et al.* (2015) reported high heritability associated with high GA for number of clusters plant⁻¹, number of branches plant⁻¹, number of locules fruit⁻¹, average fruit weight, equatorial and polar diameter of fruit. Singh *et al.* (2015) reported high

heritability along with high GA (>15%) for traits like plant height, number of primary branches plant⁻¹, average fruit weight, fruit length, pericarp thickness, number of locules fruit⁻¹, number of fruits plant⁻¹, fruit yield plant⁻¹, marketable fruits plant⁻¹ and TSS.

Hamisu *et al.* (2016) working on tomato under heat stress condition reported highest broad sense heritability for days to 50% flowering, number of clusters plant⁻¹, number of flowers cluster⁻¹, number of fruits cluster⁻¹, number of fruit plant⁻¹, fruit length, fruit diameter, fruit shape index, fruit yield plant⁻¹ and moderate for plant height, number of branches plant⁻¹, number of flowers plant⁻¹, percentage of fruit set and leaf chlorophyll content. Similarly, Hasan *et al.* (2016) observed high heritability with high GA for traits like plant height, fruit weight, fruits plant⁻¹ indicating that these characters were under additive genetic effects. High heritability with low GA was observed for characters like number of primary branches plant⁻¹, days to 1st flowering, days to 50% flowering, days to 1st harvest, fruit diameter, yield plant⁻¹, days to last harvest, TSS and ascorbic acid content. However, Kumar *et al.* (2016) working on tomato reported high heritability along with high GA as % of mean for traits like fruits plant⁻¹, fruit weight and number of seeds fruit⁻¹.

Bhandari *et al.* (2017) observed that fruit yield plant⁻¹ recorded the maximum heritability (98.92%) followed by fruits cluster⁻¹ (98.69%) in tomato. Similarly, a study conducted by Mamatha *et al.* (2017) to find out the genetic variability in F₂ population of cross Utkal Raja x Arka Sourabh reported higher heritability coupled with high GA as % mean for plant height, days to 1st flowering, number of fruits plant⁻¹, average fruit weight and yield plant⁻¹ indicating predominance of additive gene component which implies much scope for improvement of these characters by simple selection in the next generations. Similarly, Savitharamma (2017) observed high heritability coupled with high GA as % mean for fruits plant⁻¹ (99.80% and 145.61), plant height (95.11% and 30.26), and flower clusters plant⁻¹ (91.66% and 84.23) and fruit yield plant⁻¹ (98.70% and 112.75) indicating the involvement of additive gene action for expression of these traits in the crosses studied.

2.3 Correlation study

Association of characters, important from economic point of view are determined statistically by correlation coefficient. This helps in selecting the component characters which are quite useful as a basis of selection. Correlation studies between fruit yield and its components provides information of relative contribution of those characters to yield which will help in planning and execution of any crop improvement programme. Thus, the review pertaining to correlation among different traits is presented below.

In tomato, fruits plant⁻¹ had positive association with average fruit weight plant⁻¹ as reported by Moya *et al.* (1996) and Das *et al.* (1998).

Hidayatullah *et al.* (2008) reported that number of pickings and fruits plant⁻¹ had positive correlation with fruit weight plant⁻¹. Fruits plant⁻¹ had negative correlation with fruit size, single fruit weight, number of locules and pericarp thickness. Fruit length had positive correlation with fruit diameter, single fruit weight and pericarp thickness. A study by Ara *et al.* (2009) reported that the fruit yield plant⁻¹ exhibited high positive significant correlation with fruit size, plant height, number of fruits plant⁻¹ and number of primary branches plant⁻¹ at both phenotypic as well as genotypic levels. Similarly, Sharma *et al.* (2009) reported positive genotypic and phenotypic association of fruit yield with fruits plant⁻¹, fruit weight with plant height and negative with locules fruit⁻¹.

A Study by Manna and Paul (2012) on tomato reported that fruit yield plant⁻¹ was positively and significantly correlated with pericarp thickness, fruit length, fruit weight and number of fruits plant⁻¹. Similarly, Kumar *et al.* (2013) reported fruit yield plant⁻¹ was significantly and positively associated with number of fruits plant⁻¹ at the phenotypic and genotypic levels and number of fruit clusters plant⁻¹ only at the genotypic level. Fruit weight was significantly and positively correlated with fruit length, fruit diameter and pericarp thickness whereas, it is significantly and negatively correlated with number of fruits plant⁻¹ at both phenotypic and genotypic level. However, Monamodi *et al.* (2013) working with determinate tomato reported positive and significant association between fruit yield and number of trusses plant⁻¹ with plant height and fruits plant⁻¹, respectively. They also reported that three components, marketable fruits, single fruit weight and fruits truss⁻¹ were potential selection criteria

for improving determinate tomato fruit yield. Reddy *et al.* (2013) reported that fruits cluster⁻¹ and ascorbic acid had significant positive association with primary branches plant⁻¹ and days to 50% flowering whereas, days to last fruit harvest had negative association with primary branches plant⁻¹. Similarly, fruits plant⁻¹ and fruit width had significant positive correlation with fruit yield plant⁻¹.

Correlation studies by Kiran (2014) revealed strong inheritant association between fruit yield plant⁻¹ with number of fruit bunches plant⁻¹, fruits plant⁻¹, average fruit weight, length of the fruit and girth of the fruit, plant height with number of primary branches plant⁻¹ and TSS, number of primary branches plant⁻¹ with number of fruits bunch⁻¹ and number of fruits plant⁻¹, number of fruits bunch⁻¹ with number of fruits plant⁻¹, average fruit weight with number of locules fruit⁻¹, number of locules fruit⁻¹ with girth of the fruit and length of the fruit with girth of the fruit. However, Shankar *et al.* (2014) reported positive and significant genotypic and phenotypic correlation of yield plant⁻¹ with pericarp thickness, average fruit weight, fruit length, number of flowers cluster⁻¹ and fruit width.

Basavraj *et al.* (2015) reported that fruit yield was significantly and positively correlated with fruit yield plant⁻¹, number of fruits plant⁻¹ and average fruit weight whereas, number of flowers cluster⁻¹ and TSS were negatively correlated with fruit yield. Rahman *et al.* (2015) reported that the genotypic correlation coefficient was higher than the respective phenotypic correlation coefficient which indicated the suppressive effect of the environment. Hasan *et al.* (2016) suggested that yield plant⁻¹ had significant positive correlations with individual fruit weight and number of fruit clusters plant⁻¹ whereas significant negative correlation was observed with number of primary branches plant⁻¹. Kumar *et al.* (2016) reported that fruit yield had significant positive correlation with fruits cluster⁻¹ and fruits plant⁻¹.

Phenotypic and genotypic correlation coefficient studies carried out by Ambresh *et al.* (2017) in recombinant inbred line population of Vaibhav x Anaga cross. They reported that fruit yield plant⁻¹ had positive correlation with plant height, average fruit weight, number of branches plant⁻¹, number of fruits plant⁻¹, TSS and number of locules fruit⁻¹ at both genotypic and phenotypic level. Similarly, average fruit weight was significantly and negatively correlated with number of fruits plant⁻¹, both at the genotypic and phenotypic level. Number of branches plant⁻¹ was

negatively correlated with TSS. A study by Rasheed *et al.* (2017) involving total of eight parents and 15 F₁s revealed that plant height, number of branches plant⁻¹, number of clusters plant⁻¹, number of flowers cluster⁻¹, number of fruits cluster⁻¹, single fruit weight and fruit set% cluster⁻¹ exhibited significant correlation with fruit yield plant⁻¹ at genotypic level and highly significant at phenotypic level and these traits could be used as selection criteria for improvement of yield plant⁻¹ in tomato.

In a study on tomato conducted by Rawat *et al.* (2017) fruit yield was significantly and positively correlated with number of fruits plant⁻¹ and average fruit weight while it was significantly and negatively correlated with days to 1st fruit ripening and days to 50% flowering. The average fruit weight and number of fruits plant⁻¹ exhibited significant positive correlation and direct effect on fruit yield and emerged as the important components that contributed to fruit yield. Similarly, Savitharamma *et al.* (2017) working on genetic parameters in F₄ segregating population of the cross EC 771612 × LA 2657 reported that characters like fruits plant⁻¹, plant height, fruits cluster⁻¹, clusters plant⁻¹ and fruit diameter exhibited positive significant association with fruit yield among F₄ segregants.

2.4 Path coefficient analysis

Path analysis was originally developed by Wright (1921), who defined the path coefficient as the ratio of standard deviation of the effect due to a given cause (independent variable) to the total standard deviation of the effect (dependent variable). As the study of simple correlation does not provide an exact picture of relative importance of direct and indirect influence of each of the component character towards the desired character. So, this can be overcome by following path coefficient analysis technique by further dividing the correlation coefficient into direct and indirect effects. The available literature on path analysis of yield with other component traits in tomato is briefly reviewed as follows:

Ara *et al.* (2009) observed that days to 1st picking had highest positive direct effect on fruit yield followed by harvest duration, number of fruits plant⁻¹, average fruit weight, plant height and number of flowers cluster⁻¹. They suggested that characters viz., minimum days to 1st fruit picking, more number of fruits plant⁻¹, average fruit weight, fruit size, plant height, number of primary branches plant⁻¹ and extended harvest duration should be given priority over other traits for selecting high yielding

genotypes. On the other hand, Mohanty (2003) reported that fruits plant⁻¹ had the maximum positive direct effect on fruit yield followed by days to 1st harvest and average fruit weight.

Manna and Paul (2012) reported that number of locules fruit⁻¹, TSS, fruit length, number of fruits plant⁻¹, fruit weight, vitamin C content and pericarp thickness had positive direct effect on fruit yield whereas, fruit width and total acid content had strong negative effect on the fruit yield. Path analysis study by Kumar *et al.* (2013) indicated that fruit weight had the most positive direct effect on yield plant⁻¹ followed by number of fruits plant⁻¹, fruit diameter and number of fruits cluster⁻¹ at the genotypic level. The most positive indirect effects of fruit diameter, fruit length, pericarp thickness were via fruit weight to affect yield plant⁻¹. Path coefficient analysis study by Monamodi *et al.* (2013) showed that marketable fruit number and single fruit weight were directly related to fruit yield with direct effect of 0.752 and 0.446, respectively. Similarly, Reddy *et al.* (2013) revealed that plant height, number of fruits plant⁻¹, fruit length, fruit width and ascorbic acid had high positive direct effects on fruit yield plant⁻¹. High negative direct effects on fruit yield plant⁻¹ had been observed for number of primary branches plant⁻¹, days to 50% flowering, clusters plant⁻¹, flowers cluster⁻¹ and days to 1st fruit set, days to 1st fruit harvest and fruit weight.

Path analysis study by Kiran (2014) showed that average fruit weight, number of fruits plant⁻¹, number of locules plant⁻¹, plant height, number of bunches plant⁻¹ and length of the fruit had direct positive effect on fruit yield. However, Shankar *et al.* (2014) working on 37 genotypes of tomato for genotypic and phenotypic path coefficient analysis revealed that positive direct effect was exerted by pericarp thickness, number of flowers cluster⁻¹, shelf life whereas days to 50% flowering showed negative direct effect.

Hasan *et al.* (2016) observed maximum positive direct contribution towards yield was through individual fruit weight whereas, plant height showed negative direct contribution towards yield. Path analysis studies by Rasheed *et al.* (2017) revealed that plant height, branches plant⁻¹, flower clusters plant⁻¹, flowers cluster⁻¹, fruit weight and fruit set % cluster⁻¹ directly contributed to yield improvement. Rawat

et al. (2017) confirmed that the number of fruits plant⁻¹ had highest positive direct effect on fruit yield followed by average fruit weight.

2.5 Genetic Diversity

The information on genetic divergence of various traits particularly of those contributing to yield and quality would be of most useful while planning any crop improvement programme. D² statistics developed by Mahalanobis (1936) provides a measure of magnitude of the extent of diversity among genotypes under comparison. Grouping of genotypes based on D² analysis will be useful while choosing suitable parental lines for heterosis breeding programme and it can further help in development of improved open pollinated varieties for commercial cultivation.

Arun *et al.* (2003) studied the nature and magnitude of genetic divergence for quantitative traits and grouped the genotypes into 15 clusters, indicating the presence of a wide range of genetic diversity among the genotypes. Reddy *et al.* (2013) conducted a study on genetic divergence analysis using 19 exotic collections of tomato following Mahalanobis D² statistics. The results revealed considerable genetic diversity among the genotypes of tomato under study with respect to 18 quantitative characters pertaining to growth, earliness, yield and quality. They also reported that fruit weight, plant height and fruits plant⁻¹ contributed 92.40% to the total divergence. Diversity within and between the clusters was observed. The characters fruit weight, fruits plant⁻¹ and plant height were the potent factors in differentiating the germplasm of tomato under study.

Chernet *et al.* (2014) used Mahalanobis D² to estimate genetic distance between pair of clusters. In the study they grouped 36 genotypes into six distinct clusters. Maximum and minimum distance was recorded between clusters IV and V and cluster II and III, respectively. This indicated that hybridization can be carried out among genotypes from any pair of clusters and subsequent selection can be made from segregating generations. However, Nalla *et al.* (2014) grouped 27 genotypes into nine clusters, indicating the presence of diversity for different traits. Cluster I had the highest number containing 16 genotypes followed by cluster III and VII containing three and two genotypes, respectively. However, cluster II, IV, V, VI, VIII and IX were solitary. The maximum intra-cluster distance was recorded within cluster III (10.88) and the maximum inter-cluster distance between cluster VI and VII (20.80), indicating the existence of wide genetic variability. Based on mean performances,

cluster VIII with single genotype ranked first and appeared to contain the potential genotype. Cluster VIII and II registered high plant height. The genotypes included in clusters V and VIII took less number of days to 50% flowering (29.67). Cluster III registered high fruit yield plant⁻¹ (1004.60), average fruit weight (38.07) and ascorbic acid (28.7). Cluster IX had high number of fruits plant⁻¹ (40.53).

As per a study carried out by Kiran (2014), 45 genotypes were grouped into nine clusters using D² statistics. Cluster VIII, the largest group included nine tomato genotypes (IIVR SEL-2, BT-428-3, BT-306-1-2, BT 224-3-1, BT-305-2-4-2, BT-3, BT-101, Arka Saurabh and BT-136), Cluster I comprised of eight tomato genotypes (BT-442-2, BT-437-1-2, BT-429-2-2, BT-413-1-2, BT-429-1-1, BT-215-3-3-1, BT-317 and BT-106), Cluster III included seven tomato genotypes (BT-12-2, BT-507-2-2, BT-506-1, BT112-1, BT-508-1-1, Megha Tomato and BT-21-2), Cluster IV comprised of six tomato genotypes (BT-433-2-1, Arka Vikash, BT-17-2, BT-433-3-2, BT-18 and Utkal Pragyan). Similarly Cluster IX comprised of five tomato genotypes such as (Utkal Pallavi ,Utkal Urbashi, Utkal Raja, BT-218 and BMZ-21) whereas Cluster II had four tomato genotypes (BT-22-4-1, BT-19-1-1-1, BT-19-1-1 and BT-207-2). Remaining three clusters *i.e.* cluster V (BT-21 and BT-17), cluster VI (BT-17-2 (5) and Utkal Deepti) and Cluster VII (BT-12-3-2 and Utkal Kumari) comprised of two tomato genotypes each. Out of which cluster III and cluster VI were more divergent consisting of seven and two genotypes. Plant height contributed maximum towards genetic divergence followed by number of fruits plant⁻¹, average fruit weight and yield plant⁻¹.

A study was carried out by Ullah *et al.* (2015) with 20 genotypes of tomato. Based on D² values of 11 yield related characters, the genotypes were grouped into five clusters. Maximum six number of genotypes were grouped in cluster II (TM 368, TM 371, TM 384, TM 388, TM 360 and TM 528) followed by five in cluster IV (TM 356, TM 382, TM 410, TM 422 and TM 423), four in cluster III (TM 390, TM 392, TM 419 and TM 409), 3 in cluster I (TM 361, TM 403 and TM 386) and 2 genotypes in cluster V (TM 377 and TM 349). Clustering pattern indicated that there was no association between geographical distribution of genotypes and genetic divergence. The mean intra and inter cluster distance revealed that cluster I had highest intra cluster distance (0.979), while the inter cluster distance was maximum between cluster III and I (13.55) followed by III and V (11.22). As per their study the characters which

contributed maximum to genetic divergence were plant height, fruit weight, fruits plant⁻¹. Dar *et al.* (2015) grouped 60 genotypes into 20 clusters in tomato. They reported 14 clusters to be monogenotypic and cluster I possessed 25 numbers of genotypes. Out of 20 clusters, cluster VII had high average fruit weight and cluster VIII had highest number of locules fruit⁻¹, fruit yield plant⁻¹ and yield ha⁻¹ and cluster XVII was superior for ascorbic acid. Similarly, cluster XX was found promising with respect to number of fruits plants⁻¹. The highest inter cluster D² values were estimated between clusters XII and XX followed by clusters XI and XX, clusters VII and XX, and clusters XV and XX which predicted enough scope for the improvement of tomato crop by hybridization and selection.

A study carried out by Bhattarai *et al.* (2016) demonstrated a high level of morphological diversity within 71 germplasm of tomato which were grouped into six distinct clusters. Genetic divergence analysis was carried out by Lekshmi *et al.* (2016) for polyhouse tomato using Mahalanobis D² statistics on 40 tomato genotypes which were grouped into eight clusters. Cluster I was the largest cluster with 24 genotypes followed by cluster II with 10 genotypes and all other clusters had one genotype each. The highest intracluster distance was noticed in cluster II followed by cluster I. The highest intercluster distance was observed between clusters VII and VIII, followed by clusters IV and VIII. Similarly, about 40 genotypes were evaluated for 19 growth, yield and quality traits which were grouped into seven clusters by Kumar *et al.* (2016). Cluster II topped in having maximum of 24 genotypes which was followed by cluster I and VII with two genotypes each while cluster III, IV and V were monotypic. The maximum intracluster distance was observed in cluster VII (2097.24) followed by clusters VI (824.01) and II (265.05) which were identified genetically divergent. The maximum intercluster distance was noticed between cluster II and VI (1647.87) and lowest between cluster III and IV (125.29). The genotypes of cluster III and VII recorded maximum mean values for number of fruits plant⁻¹, average fruit weight and fruit yield plant⁻¹ while minimum values were recorded in genotypes belonging to clusters IV and VI. Therefore, crossing between genotypes belonging to cluster III and IV as well as between cluster VII and VI were expected to give maximum heterosis.



MATERIALS AND METHODS

The present research work entitled, “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” was carried out to study the genetic variability, correlation, path analysis and D² analysis of 18 genotypes.

The experiment was carried out during *rabi*, 2017-18 at All India Co-ordinated Research Project on Vegetable Crops, Orissa University of Agriculture and Technology, Bhubaneswar, Odisha, India. The details of materials and methods adopted for conducting the experiment are described in this chapter with relevant information supported by tables, figures, photographs etc. as and when required.

3.1 Experimental site

The experiment was carried out during the *Rabi* season of 2017-18 at All India Co-ordinate Research Project on Vegetable Crops, Orissa University of Agriculture and Technology, Bhubaneswar. The farm is situated about 7 km away from the university.

3.2 Topography and climate conditions

Geographically, the experimental site falls under the eighteenth agro-climatic region of the country *i.e.* eastern coastal plain and is termed as sub-humid characterized by warm moist climate with mild winter and is located at latitude of 20°15' N and longitude of 85°52'E. It is about 60 km away from Bay of Bengal having an altitude of 25.5 m above mean sea level. The average annual rainfall of Bhubaneswar is 1552 mm (Based on average of preceding 10 years). Most of the rainfall *i.e.* 85% is received from July to September. The rainfall code of the place is D₁ E₃ (B₁A₂B₁) C₁D₁E₂. The average temperature varies from 14° C in winter to 40° C in summer and relative humidity varies between 49 and 90% from June to December.

A perusal of Fig.1 revealed the prevailing climate condition during the time of field experimentation.

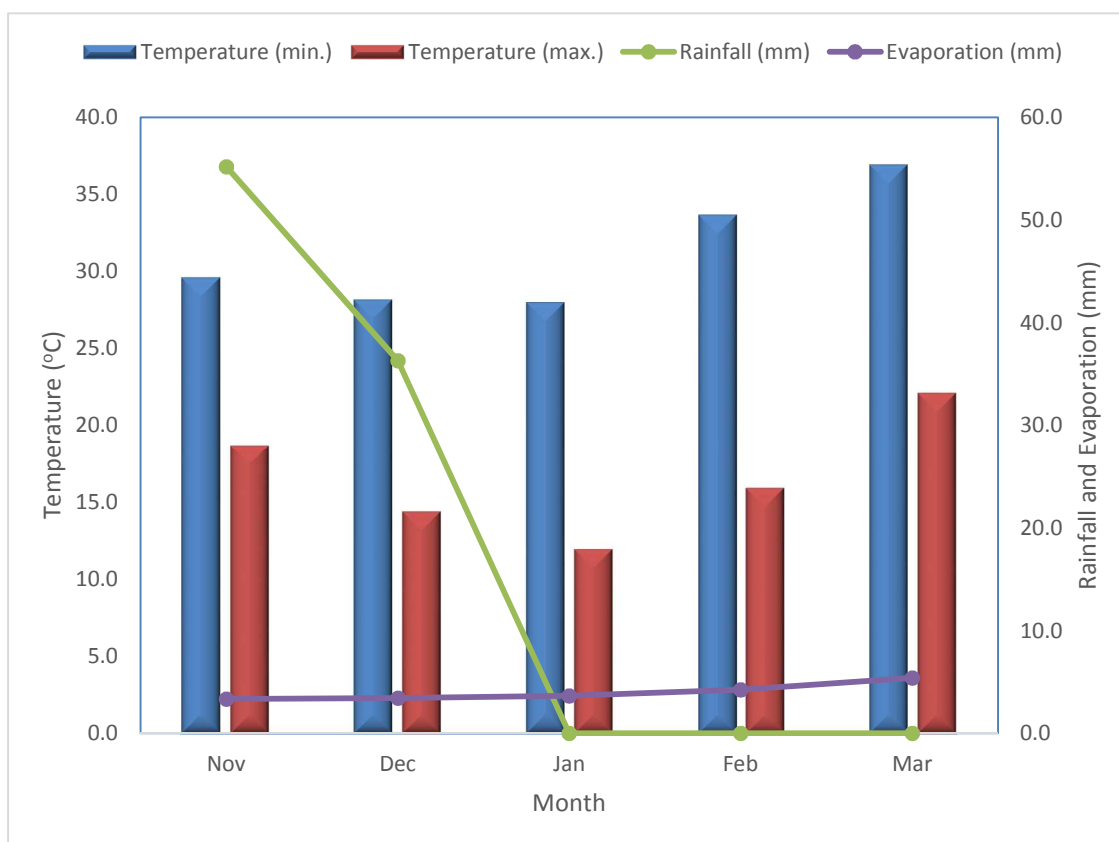
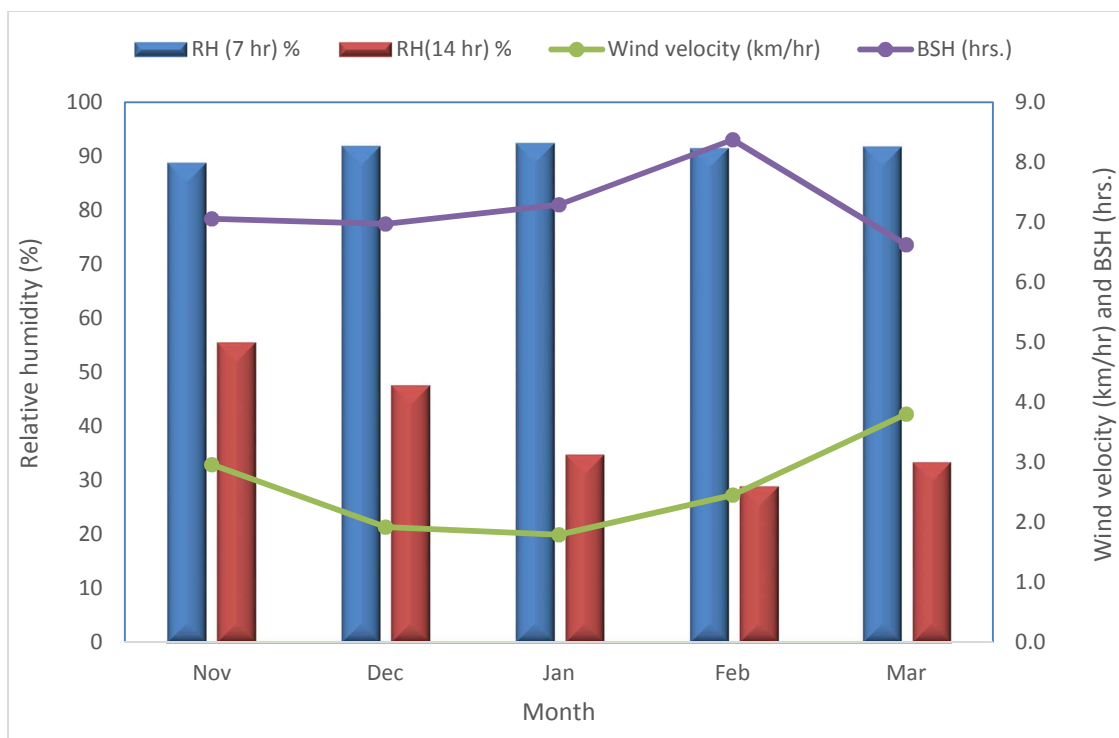


Fig. 1. Meteorological data during the cropping season

3.3 Experimental details

The experiment was laid out in Randomized Block Design (RBD) with three replications. There were eighteen genotypes and each genotype was allocated randomly in each replication in the trial. The details of field layout of the experiment are presented in table 3.1 and 3.2. Proper standard procedure was adopted to raise healthy diseased free seedlings. All the recommended package of practices was adopted uniformly to all the 18 genotypes in order to raise a good tomato crop. During the period of field experimentation all the observations were recorded from randomly selected plants (5 plants).

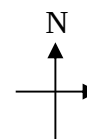
Table 3.1 Details of layout

01	Crop	Tomato
02	Date of sowing	29.11.2017
03	Design	Randomized Block Design (RBD)
04	Number of Genotypes	18
05	Number of Replications	03
06	Plot size	3.0m×2.0m
07	Spacing	60cm×45cm
08	Total number of plots	54
09	Number of rows per plot	5
10	Number of plants per row	6
11	Number of plants per plot	30

Table 3.2 Origin and source of collection of determinate tomato genotypes under study

Sl No.	Genotype	Source
1	2016/TODVAR-01	IIVR, Varanasi (U.P)
2	2016/TODVAR-02	
3	2016/TODVAR-03	
4	2016/TODVAR-04	
5	2016/TODVAR-05	
6	2016/TODVAR-06	
7	2016/TODVAR-07	
8	2016/TODVAR-08	
9	2016/TODVAR-09	
10	2016/TODVAR-10	
11	2016/TODVAR-11	
12	2016/TODVAR-12	
13	Pusa Rohini	IARI, New Delhi
14	Pusa Gaurav	
15	Pusa 120	
16	Utkal Pallavi	OUAT, Bhubaneswar, Odisha
17	Utkal Deepti	
18	Utkal Pragyan	

Fig. 3.2 LAYOUT PLAN OF EXPERIMENTAL FIELD



RIII		RII		RI	
V10	V13	V01	V18	V10	V11
V17	V06	V03	V08	V14	V06
V14	V16	V14	V10	V09	V16
V11	V03	V13	V11	V01	V13
V01	V05	V09	V15	V08	V15
V08	V07	V02	V07	V02	V05
V18	V12	V12	V05	V04	V17
V15	V04	V04	V16	V18	V07
V09	V02	V17	V06	V12	V03

V1-2016/TODVAR-01, V2-2016/TODVAR-02, V3-2016/TODVAR-03, V4- 2016/ TODVAR-04, V5-2016/TODVAR-05, V6- 2016/TODVAR-06, V7-2016/TODVAR-07, V8- 2016/TODVAR-08, V9- 2016/TODVAR-09, V10- 2016/ TODVAR-10, V11- 2016/TODVAR-11, V12- 2016/TODVAR-12, V13- Pusa Rohini , V14- Pusa Gaurav, V15- Pusa 120 , V16- Utkal Pallavi , V17- Utkal Deepti , V18- Utkal Pragyan



Fig. 3.3 Sowing seeds in nursery beds Fig. 3.4 Transplanting of seedlings to main field



Fig. 3.5 Taking field observations Fig. 3.6 During Laboratory analysis



Fig. 3.7 1st flowering observation



Fig. 3.8 Field overview at peak flowering



Fig. 3.9 Field Overview at peak fruiting stage

3.4 Biometric observations

3.4.1 Sampling technique

Observations on various biometric characters were recorded by selecting randomly five competitive plants of each genotype in a replication which were tagged properly. The border plants were excluded while selecting the sample plants. The observations of these tagged plants were taken time to time starting from initiation of 1st flowering to final harvesting of fruits.

I. Vegetative growth parameters

i. 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 time of final harvest and the average height (cm) was calculated.

ii. Number of primary branches plant⁻¹

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

iii. Internodal length (cm)

The internodal length of five randomly selected plants in each replication for each genotype was recorded with the help of a meter scale and then averaged to get the final value for each genotype.

II. Flowering parameters:

i. Days to 1st flowering

Each plot was daily observed to record the date of 1st flowering. The period from the transplanting date to the date of 1st flowering was recorded and expressed in terms of number of days, when 1st flower of the plot bloomed.

ii. Days to 50% flowering

Each plot was daily observed to record the date of 50% flowering. The period between transplanting to the date of 50% flowering was recorded and expressed in terms of number of days, when 50% plants of the plot bloomed.

iii. Number of flowers cluster⁻¹

Number of flowers cluster⁻¹ was recorded as average of full bloom clusters on five randomly tagged plants at flowering stage and the average was calculated.

iv. Percentage of Fruit set (%)

The average number of fruits cluster⁻¹ was calculated in the same manner as for flowers. Taking the average values obtained in number of flowers cluster⁻¹ and number of fruits cluster⁻¹, percentage fruit set is calculated using the formula

$$\% \text{ Fruit set} = \frac{\text{Number of fruits cluster}^{-1}}{\text{Number of flowers cluster}^{-1}} \times 100$$

vi. Days to fruit set

The period from the date of transplanting to the date to the date of fruit setting was recorded, when first fruit setting occur after daily observations. The average values per genotypes were then calculated.

III. Fruit yield attributing parameters

i. Days to 1st fruit harvest

The period from the transplanting date to the date of fruit setting was recorded, when first fruit setting occur after daily observations. The average values per genotypes were then calculated.

ii. Number of fruits plant⁻¹

During each harvesting the number of fruits harvested from the five numbers of randomly tagged plants in each plot was recorded and summed up after final harvest. The average values per genotypes were then calculated on plot basis.

iii. Average fruit weight (g)

The weight (g) of ten randomly selected ripened fruits of each genotype in each replication was recorded in each harvest and then average fruit weight was calculated.

iv. 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 then average was calculated.

v. 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 then average was calculated.

vi. Pericarp thickness (mm)

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

vii. Number of locules fruit⁻¹

Five fruits were selected randomly from each replications of each genotype and cut transversely to get the number of locules fruit⁻¹ in and then averaged to get a final value.

IV. Fruit yield

i. Marketable fruit yield plant⁻¹ (kg)

The weight of marketable fresh fruits from five numbers of tagged plants from each plot was taken and mean was calculated.

ii. Marketable yield plot⁻¹ (kg)

The weight of marketable fresh fruits from each plot was taken and mean was calculated. The mean marketable plot yield (kg plot⁻¹) was averaged over replications.

iii. Marketable fruit yield (qha⁻¹)

The marketable plot yield (kg plot⁻¹) thus obtained for each plot was converted to marketable fruit yield in qha⁻¹ for each replication of the genotypes under study.

iv. Total fruit yield plant⁻¹ (kg)

The weight of marketable fruits and unmarketable fruits from five numbers of tagged plants from each plot was added up and averaged to get the final value for total fruit yield plant⁻¹ (kg).

v. Total yield plot⁻¹ (kg)

The weight of both marketable fruits and unmarketable fruits from each plot was taken and mean was summed up. The mean of total yield plot⁻¹ was then averaged over replications.

vi. Total fruit yield (qha⁻¹)

The total fruit yield plot⁻¹ thus obtained was converted to total fruit yield in qha⁻¹ for each of the replications for each genotype under study.

V. Fruit Quality parameters:

The following procedures were adopted to estimate the quality parameter in determinate tomato.

Sl.No.	Parameters	Methods
1	TSS	Hand Refractometer (Ranganna, 1995)
2	Ascorbic Acid	Titration with dichloro phenol indophenols (Ranganna, 1995)
3	Total Sugar	Lane & Eynon's method (Ranganna, 1995)
4	Reducing sugar	Lane & Eynon's method (Ranganna, 1995)
5	Non-reducing Sugar	Lane & Eynon's method (Ranganna, 1995)

3.5 Statistical analysis

3.5.1 Analysis of variances

The analysis of variances for each of the characters stated was done to find out differences among the varieties. The analysis was carried out separately for each trait following the procedure of randomized block design analysis (Panse and Sukhatme, 1954).

Analysis of variance was done on basis of following model.

$$Y_{ij} = m + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic observation in the i^{th} genotype and the j^{th} replication

m = General mean

g_i = Effect of the i^{th} genotype/treatment

r_j = Effect of j^{th} replication

e_{ij} = random error associated with i^{th} genotype and j^{th} replication

Table 3.3 Analysis of variance and expected mean sum of square

SOURCE	df	MSS	EXPECTED MEAN SUM OF SQUARE
Replication	(r-1)	M _R	$\sigma_e^2 + g\sigma^{2r}$
Genotype	(g-1)	M _G	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1)(g-1)	M _E	σ_e^2

3.5.2 Mean, Range, Standard error and critical differences

Sample mean values were calculated for each character by dividing the total by corresponding number of observations, while the highest and lowest values for each character were taken as the range. The S.E. and C.D. values were calculated by using the following formula.

$$\text{Standard error mean (SEM)} = \sqrt{\frac{EMS}{r}}$$

Critical difference (C.D.)

$$= \sqrt{\frac{EMS}{r}} \times t \text{ value at error d.f. at 5\% and 1\% level of significance}$$

Where,

r = number of replications

EMS = Error mean sum of square

3.5.3 Phenotypic and Genotypic Coefficient of variation (PCV and GCV)

For comparing the variability of two or more than two characters, co-efficient of variation were calculated by using the formula given below:

$$\text{C.V.} = \text{S.D.} / \bar{X} \times 100 = \sqrt{EMS} / \bar{X} \times 100$$

Where,

S.D. = standard deviation which is the square root of mean square due to error (EMS)

$\bar{X}$ = Experimental mean

From the structure of the analysis of variance

$$\text{Error variance} = \sigma_e^2 = \text{ME}$$

$$\text{Genotypic variance} = \sigma_g^2 = \text{MG} - \text{Me} / r$$

$$\text{Phenotypic variance} = \sigma_p^2 = \text{MG} / r = \sigma_g^2 + \sigma_e^2 / r$$

The genotypic co-efficient of variation (GCV) and the phenotypic co-efficient of variation (PCV) were calculated by the formula given by Burton (1952).

$$\text{GCV} = \text{Genotypic standard deviation} / \text{Grand mean} \times 100$$

$$\text{PCV} = \text{Phenotypic standard deviation} / \text{Grand mean} \times 100$$

Categorization of the range of variation was effected as proposed by Sivasubramanian and Madhavamenon (1973).

- Less than 10 %: Low
- 10-20 %: Moderate
- More than 20 %: High

3.5.4 Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

$$h^2 = \text{Heritability in broad sense}$$

$$\sigma_g^2 = \text{Genotypic variance}$$

$$\sigma_p^2 = \text{Phenotypic variance} (\sigma_g^2 + \sigma_e^2)$$

$$\sigma_e^2 = \text{Environmental variance}$$

As suggested by Johnson et al. (1955) the estimates of heritability in broad sense were categorized as:

- Low: 0-30 %
- Medium: 30-60 %
- High: above 60 %

3.5.5 Expected Genetic Advance

Genetic advance was estimated as per the formula suggested by Johnson *et al.* (1955).

$$GA = K. h^2\sigma_p$$

Where,

K = Selection differential in standard units (which is 2.06 per 5% selection intensity).

h^2 = Heritability in broad sense

σ_p = Phenotypic standard deviation

GA expressed as percentage of mean = $GA / \text{Mean} \times 100$

3.5.6 Estimation of correlation co-efficient

Simple correlation co-efficient were computed at phenotypic and genotypic levels between pairs of 14 important characters that contribute to fruit yield (number of fruits per plant) using the following formula.

$$\text{Genotypic correlation } (r_g) = \sigma_g(xy) / \sigma_g(x) \times \sigma_g(y)$$

$$\text{Phenotypic correlation } (r_p) = \sigma_p(xy) / \sigma_p(x) \times \sigma_p(y)$$

Where,

$\sigma_g(xy)$ = Genotypic co-variance between the two traits x and y.

$\sigma_p(xy)$ = Phenotypic co-variance between the two traits x and y.

$\sigma_g(x)$ and $\sigma_g(y)$ = Genotypic standard deviation for x and y respectively.

$\sigma_p(x)$ and $\sigma_p(y)$ = Phenotypic standard deviation for x and y respectively.

The estimated values were compared with the table value at (n - 2) and at 5% and 1% levels of significance in order to test the significance of correlation coefficients at phenotypic and genotypic level.

3.5.7 Path co-efficient analysis

In the present study marketable fruit yield plant⁻¹ was taken as the effect with other characters like plant height, number primary branches plant⁻¹, internodal length, days to 1st flowering, number of flowers cluster⁻¹, % of fruit set, days to fruit set, average fruit weight, fruit length, fruit girth, pericarp thickness, number of locules and number of fruits plant⁻¹.

The path coefficients were obtained by solving the following simultaneous equations which give the basic relationship between correlations and path coefficients in a system of correlated causes. (Dewey and Lu, 1959)

$$r_{112} = r_{11}p_{112} + r_{12}p_{112} + r_{13}p_{112} + \dots + r_{111}p_{1112}$$

$$r_{212} = r_{21}p_{112} + r_{22}p_{112} + r_{23}p_{112} + \dots + r_{211}p_{1112}$$

$$r_{312} = r_{31}p_{112} + r_{32}p_{112} + r_{33}p_{112} + \dots + r_{311}p_{1112}$$

$$r_{1112} = r_{111}p_{112} + r_{112}p_{212} + r_{113}p_{312} + \dots + p_{1112}$$

Where, r_{ij} is the coefficient of correlation between i^{th} and j^{th} characters and p_{qi} is the path coefficient.

The solutions for path coefficients, direct and indirect effects of the casual factors were estimated as the values of the individual terms of the above equations in R.H.S. The coefficient of determination (R_2) and the residual effect ($p_{12.R}$) were calculated as follows

$$I = p_{12.R}^2 + \sum p_{iy}r_{iy}$$

$$R^2 = \sum p_i y_i y_i$$

$$= p_{112}r_{112} + p_{212}r_{212} + p_{312}r_{312} + \dots + p_{111}2r_{112}$$

$$P_{12,R} = \sqrt{1 - R^2}$$

The path analysis at the phenotypic level with the same cause and effect relationship was computed using the phenotypic correlations as stated earlier.

3.5.8 Genetic divergence

Mahalanobis (1936) generalized distance, D^2 statistics was used for computing genetic divergence as described by (Rao, 1960). The original measurements were transformed to standardized uncorrelated variables by pivotal condensation (Rao, 1960). The divergence between any two varieties was obtained as the sum of squares of the difference in the values of the corresponding transformed values (V_{ij})

$$D^2_{jk} = \sum_{i=1}^n Y_{ij} - Y_{ik}$$

Gives the D^2 between j^{th} and k^{th} germplasm for 'n' characters.

Following Tocher's method, the genotypes were grouped into clusters. The criterion of grouping was that any two genotypes belonging to the same cluster should have a smaller D^2 value than those between genotypes belong to different clusters. Inter and intra-cluster distances were determined and represented.



RESULTS

The present investigation entitled, “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” was conducted at All India Coordinated Research Project on Vegetable Crops of Orissa university of Agriculture and Technology, Bhubaneswar during *rabi* season, 2017-18. The objective was to study the nature and extent of genetic variability, character association, path analysis and clustering of 18 tested genotypes of determinate tomato.

In this chapter, brief and careful explanations have been made with respect to various observations recorded on different aspects on determinate tomato. All the recorded and analysed observations were presented with suitable tables, graphs, diagrams, photographs etc. as per the requirement.

4.1 Analysis of variance

The genetic variability study was carried out by analysis of variance (ANOVA) for 28 characters which revealed significant variations among the genotypes for all the characters under study. The details of which are presented in table 4.1.

The degree of experimental precision maintained during the study was evident from C_{Ve} values which were found within 10% for most of the characters which can be attributed to the influence of environmental factors on these characters.

4.1.1 Mean performance of the genotypes

The data presented in table 4.2 regarding the mean performance of 18 genotypes of determinate tomato revealed significant variations among tested genotypes for all the vegetative, flowering, fruit yield and yield attributing parameters as well as quality attributes.

Table 4.1 Analysis of variance for 28 characters in 18 genotypes of determinate tomato.

Sl. No.	Characters	Mean Sum of squares		
		Replication (2)	Genotypes (17)	Error (34)
1	Plant height (cm)	3.73	246.80**	15.76
2	Primary branches plant ⁻¹	0.05	1.45**	0.073
3	Internodal length (cm)	0.014	5.03**	0.03
4	Days to first flowering	0.90	24.55**	2.89
5	Days to 50% flowering	4.46	16.35**	2.29
6	No. of flowers cluster ⁻¹	0.028	2.83**	0.12
7	% of fruit set	57.44	88.10*	36.0
8	Days to fruit set	1.90	19.58**	2.75
9	Days to 1 st fruit harvest	36.24	13.13	11.83
10	Fruit weight (g)	40.35	381.41**	17.02
11	Fruit length (cm)	0.24	1.89**	0.13
12	Fruit girth (cm)	1.38	10.62**	0.67
13	Pericarp thickness (cm)	0.0008	0.014**	0.002
14	No. of locules	0.02	4.36**	0.09
15	No. of fruits plant ⁻¹	0.96	26.80**	2.35
16	Marketable fruit yield plant ⁻¹ (kg)	0.034	0.09**	0.02
17	Total fruit yield plant ⁻¹ (kg)	0.02	0.14**	0.04
18	Marketable fruit yield plot ⁻¹ (kg)	3.31	87.77**	1.05
19	Unmarketable fruit yield plot ⁻¹ (kg)	0.19	0.77**	0.24
20	Total fruit yield plot ⁻¹ (kg)	0.30	91.87**	1.33
21	Marketable fruit yield ha ⁻¹ (q)	918.24	24385.05**	290.79
22	Unmarketable fruit yield ha ⁻¹ (q)	54.10	215.07**	65.36
23	Total yield ha ⁻¹ (q)	83.25	25524.03**	370.48
24	TSS (⁰ Brix)	0.031	0.85**	0.19
25	Ascorbic acid (mg/100g)	4.9	265.05**	4.11
26	Total sugar (%)	0.11	1.30**	0.08
27	Reducing sugar (%)	0.13	0.29**	0.07
28	Non-reducing sugar (%)	0.15	1.51**	0.16

** Significant at 1% level * Significant at 5% level

Figure in parenthesis indicate degree of freedom of respective sources of variation

The results data indicated significant variations for plant height which ranged from 47.20 cm (Utkal Pallavi) to 84.55 cm (2016/TODVAR-05) with a mean value of 67.75 cm. Significantly highest plant height was recorded in genotype, 2016/TODVAR-5 (84.55 cm) than rest of the evaluated genotypes. The second tallest plant was recorded in the genotype, 2016/TODVAR-12 (77.77 cm) which was *statistically at par* with 2016/TODVAR-01 (73.86 cm), 2016/TODVAR-07 (74.60 cm), 2016/TODVAR-08 (76.49 cm), Pusa-120 (73.73 cm) and Pusa Rohini (72.48 cm).

Primary branches plant⁻¹ varied significantly among tested genotypes ranging from 3.03 (2016/TODVAR-03) to 5.40 (2016/TODVAR-12) with mean value 4.14. Significantly maximum primary branches plant⁻¹ (5.40) was recorded in 2016/TODVAR-12 than rest of the genotypes, except 2016/TODVAR-08 (5.07), Pusa 120 (5.11) and 2016/TODVAR-11 (5.16) which were *statistically at par*.

The data on internodal length indicated wide variations among tested genotypes ranging from 4.13 cm (Utkal Pallavi) to 8.66 cm (2016/TODVAR-07) with a mean value of 6.67 cm. The second highest internode length was observed in 2016/TODVAR-12 (8.14 cm) which was *statistically at par* with the genotype, Pusa 120 (7.85cm).

Regarding days to 1st flowering, the result revealed significant variations among tested genotypes which ranged from 15.33 days (2016/TODVAR-09) to 28.33 days (2016/TODVAR-04) with a mean value of 20.46 days. The genotype, 2016/TODVAR-09 showed earliness and 1st flower appeared 15.33 days after transplanting than rest of the genotypes. However, the genotypes, 2016/TODVAR-07 (17.00 days), 2016/TODVAR-06 (17.33 days) and 2016/TODVAR-02 (17.67 days) were *statistically at par* with early genotype, 2016/TODVAR-09 (15.33).

With respect to days to 50% flowering, genotype 2016/TODVAR-06 (24 days) recorded earliest to attained 50% flowering, closely followed by Utkal Deepti (25.67 days) and 2016/TODVAR-05 (26.33 days) than rest of the genotypes. On the other hand, genotype 2016/TODVAR-01 took significantly maximum days of 33.67 to attain 50% flowering.

Number of flowers cluster⁻¹ among the tested determinate tomato genotypes varied significantly ranging from 5.04 (2016/TODVAR-03) to 8.75 (2016/TODVAR-

06) with an average value of 6.34 flowers cluster⁻¹. Significantly maximum flowers cluster⁻¹ was recorded in 2016/TODVAR-06 (8.75) closely followed by Utkal Deepti (7.42), Pusa Gaurav (7.68) and Utkal Pallavi (7.71) where *statistically parity* were observed.

Regarding % of fruit set, significant variations were observed which varied significantly from 66.38% (2016/TODVAR-06) to 89.69% (2016/TODVAR-03) with mean value of 82.32% .The result data also revealed that except the genotypes, 2016/TODVAR-06, 2016/TODVAR-10, Utkal Pallavi and Utkal Deepti, all other genotypes were found *statistically at par* with 2016/TODVAR-03 (89.69%).

The research results on days to fruit set revealed significant variations among the 18 determinate tomato genotypes ranging from 25.33 days (Utkal Deepti) to 35.00 days (2016/TODVAR-10 and 2016/TODVAR-03) with a mean value of 32.19 days. The genotype, Utkal Deepti (25.33 days) was the earliest to set fruits while 2016/TODVAR-10 and 2016/TODVAR-03 (35.00 days) took maximum days for fruit set.

With respect to days to 1st fruit harvest, a narrow variation was observed from 60.33 days (2016/TODVAR-02, Pusa Rohini, Utkal Pallavi) to 69 days (2016/TODVAR-07) with a mean value of 62.96 days.

Average fruit weight observations indicated significant variations among the tested 18 genotypes of determinate tomato. Significantly heaviest fruit of 84.25 g was recorded in 2016/TODVAR-12 than other genotypes. Similarly, significantly lightest fruit was recorded in Utkal Deepti (47.63 g) .The mean value for average fruit weight was 65.98 g.

Fruit length observations among the genotypes ranged from 6.13 cm (Utkal Deepti) to 8.85 cm (2016/TODVAR-07) with a mean value of 7.63 cm. The genotype, 2016/TODVAR- 07 (8.85 cm) was *statistically at par* with genotypes, Pusa Rohini (8.37 cm), Pusa 120 (8.39 cm) and 2016/TODVAR-01 (8.45 cm).

Significantly maximum fruit girth was observed in Pusa 120 (18.35 cm) while that of lowest in Utkal Deepti (12.31 cm). However, *statistical parity* was observed with Pusa Rohini (17.14 cm), 2016/TODVAR-11 (17.91 cm) and 2016/TODVAR-07 (18.33 cm).

Result data on pericarp thickness revealed significant variations ranging from 0.49 cm (2016/TODVAR-5, 2016/TODVAR-07 and 2016/TODVAR-08) to 0.69cm (2016/TODVAR-04) with an average pericarp thickness of 0.57cm. However, genotypes like 2016/TODVAR-06 (0.64 cm), 2016/TODVAR-12 (0.64 cm), Pusa Rohini (0.65 cm), 2016/TODVAR-09 (0.66 cm), 2016/TODVAR-11(0.66 cm) recorded significantly higher pericarp thickness and were *statistically at par* with 2016/TODVAR-04 (0.69 cm).

Regarding number of locules in determinate tomato, data showed the range from 2.00 (Utkal Pallavi, Utkal Deepti, Utkal Pragyan) to 6.13 (2016/TODVAR-11) with a mean value of 3.03. Genotypes like 2016/TODVAR-01 (2.47), 2016/TODVAR-09 (2.40), Pusa Gaurav (2.27), 2016/TODVAR-06 (2.20), 2016/TODVAR-04 (2.13) and 2016/TODVAR-08 (2.07) were *statistically at par* with lowest locules count (2.00) as observed in genotypes Utkal Pallavi, Utkal Deepti, Utkal Pragyan in the present study.

The average fruits plant⁻¹ varied significantly from 10.68 (2016/TODVAR- 04) to 21.40 (Pusa Gaurav) with a mean of 15.20. Significantly maximum fruits plant⁻¹ was observed in Pusa Gaurav (21.4) and was *statistically at par* with Utkal Pragyan (19.05).

A perusal of table. 4.2 revealed significant variations among the 18 tested genotypes of determinate tomato. The marketable fruit yield plant⁻¹ varied significantly from 0.44 kg (2016/TODVAR-06) to 1.06 kg (2016/TODVAR-12) with a mean value of 0.68 kg plant⁻¹. Significantly highest marketable fruit yield plant⁻¹ was recorded in genotype 2016/TODVAR-12(1.06 kg) closely followed by 2016/TODVAR-05 (0.96) and Pusa 120 (0.88 kg) which were *statistically at par* with each other.

Total fruit yield plant⁻¹ significantly varied among the tested genotypes and ranged from 0.53 kg (2016/TODVAR-06) to 1.17 kg (2016/TODVAR-12) with a mean value of 0.86 kg. The genotype, 2016/TODVAR-12(1.17 kg) recorded significantly maximum total fruit yield plant⁻¹ closely followed by 2016/TODVAR-05 (1.16 kg), Pusa Gaurav (1.14 kg), Pusa Rohini (1.07 kg), Pusa120 (1.05 kg), 2016/TODVAR-11(1.03 kg), Utkal Pallavi (1.00 kg) and Utkal Deepti (0.99 kg) where *statistically parity* were observed than rest of the tested genotypes.

Marketable fruit yield plot⁻¹ (kg) was lowest in case of 2016/TODVAR-03(5.84) and highest was observed in 2016/TODVAR-12 (23.58) with a mean value of 13.35 kg. The next highest marketable yield plot⁻¹ was obtained by 2016/TODVAR-05 (18.97) which was *statistically at par* with genotypes 2016/TODVAR-11 (17.27) and Pusa Rohini (17.89).

The unmarketable fruit yield plot⁻¹ (kg) varied significantly ranging from 0.77 (Utkal Pragyan) to 2.65 (Pusa Rohini) with an average value of about 1.37 kg. The genotypes 2016/TODVAR-09 (0.83), Utkal Deepti (0.88), Utkal Pallavi (0.93) and 2016/TODVAR-03 (0.94) were *statistically at par* with Utkal Pragyan (0.77) which represented significant lowest range of unmarketable fruit yield plot⁻¹ among the tested genotypes.

Significant variations in total fruit yield plot⁻¹ were observed which varied from 6.06 kg (2016/TODVAR-06) to 24.85 kg (2016/TODVAR-12) with a mean value of 14.72 kg. Significantly highest total fruit yield plot⁻¹ was recorded in 2016/TODVAR-12 (24.85 kg), closely followed by Pusa Rohini (20.54 kg) and 2016/TODVAR-05 (20.40 kg).

The data on marketable fruit (qha⁻¹) indicated significant variations among the tested genotypes, which ranged from 80.29 (2016/TODVAR-06) to 393 (2016/TODVAR-12) with a mean value of 222.55 .The second maximum marketable fruit yield (qha⁻¹) was obtained in 2016/TODVAR-05 (316.21) which was *statistically at par* with the genotype, Pusa Rohini (298.17).

Significant variations were also observed for unmarketable fruit yield (qha⁻¹) which ranged from 12.83 (Utkal Pragyan) to 44.11 (Pusa Rohini) with a mean value of 22.81. Significantly lowest unmarketable fruit yield (qha⁻¹) was recorded in Utkal Pragyan (12.8) closely followed by 2016/TODVAR-03 (15.61), Utkal Pallavi (15.50), Utkal Deepti (14.72) and 2016/TODVAR-09 (13.83), where *statistical parity* were observed.

Results on total fruit yield (qha⁻¹) revealed significant variations among the tested genotypes ranging from 101.02 (2016/TODVAR-06) to 414.27 (2016/TODVAR-12) with a mean value of 245.36. The second highest yield (qha⁻¹) was obtained for Pusa Rohini (342.28) which was found to be *statistically at par* with 2016/TODVAR-05 (340.05).

The TSS (⁰Brix) of determinate tomato fruit varied significantly from 4.1 (2016/TODVAR-12) to 5.8 (2016/TODVAR-03) with a mean value of 4.8. Significantly highest TSS (⁰brix) was recorded in 2016/TODVAR-03 (5.8) closely followed by Utkal Deepti (5.67), Pusa Rohini (5.60) and 2016/TODVAR-05 (5.10).

The ascorbic acid content (mg100g⁻¹) of determinate tomato fruits among tested genotypes showed significant variations. Significantly highest ascorbic acid was recorded in 2016/TODVAR-05, (48.34) closely followed by 2016/TODVAR-10 (45.08) and lowest in Pusa Gaurav (14.35).

Variations for total sugar among the studied genotypes were in the range of 2.24% (2016/TODVAR-10) to 4.81% (2016/TODVAR-06) with a mean value of 3.29%. Significantly maximum total sugar was found in 2016/TODVAR-06 (4.81%) than rest of the genotypes. The second highest total fruit sugar content was obtained in the genotype, 2016/TODVAR-01 (4.31%) which was *statistically at par* with 2016/TODVAR-02 (4.23 %).

Reducing sugar content of determinate tomato fruits showed significant variations from 1.74% (2016/TODVAR-03) to 2.73% (Utkal Pallavi) with a mean value of 2.19%. Significantly highest reducing sugar was found in Utkal Pallavi (2.73%) and was *statistically at par* with 2016/TODVAR-12 (2.59%), 2016/TODVAR-08 (2.54%), Pusa Gaurav (2.52%), Utkal Deepti (2.45%), Utkal Pragyan (2.40%) and 2016/TODVAR-04 (2.31%).

A wide range of variations were observed with respect to non-reducing sugar content among the tested genotypes. Significantly wide variations of non-reducing sugar content from 0.24% (2016/TODVAR-10) to 2.41% (2016/TODVAR-06) to with a mean value of 1.05% were recorded. The genotypes 2016/TODVAR-01 (2.4%) and 2016/TODVAR-02 (2.35%) were found *statistically at par* with the highest recorded non-reducing sugar in the genotype 2016/TODVAR-06 (2.41%).

Table 4.2 Mean performance of 18 genotypes of determinate tomato for 28 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	26	27	28
2016/TODVAR-01	73.86	3.76	7.54	23.33	33.67	6.62	85.48	34.33	62.33	64.20	8.45	15.73	0.57	2.47	12.09	0.61	0.83	10.75	1.29	12.04	179.18	21.50	200.68	4.20	15.62	4.31	1.78	2.40
2016/TODVAR-02	57.68	3.50	6.76	17.67	26.67	5.58	82.98	30.67	60.33	69.50	7.71	15.55	0.57	3.07	12.63	0.63	0.73	13.90	1.74	15.64	231.64	29.00	260.64	4.63	22.49	4.23	1.76	2.35
2016/TODVAR-03	63.01	3.03	5.19	23.00	30.00	5.04	89.69	35.00	64.33	58.40	7.88	15.63	0.58	3.67	17.62	0.48	0.61	5.84	0.94	6.78	97.32	15.61	112.93	5.80	17.93	2.72	1.74	0.93
2016/TODVAR-04	58.38	3.85	5.37	28.33	32.33	5.92	84.80	33.00	64.33	66.70	8.13	14.69	0.69	2.13	10.68	0.52	0.79	10.67	1.15	11.82	177.84	19.11	196.95	5.03	14.95	2.64	2.31	0.32
2016/TODVAR-05	84.55	3.51	6.37	20.33	26.33	5.80	89.07	34.67	63.33	82.50	7.69	15.35	0.49	2.87	15.33	0.96	1.16	18.97	1.43	20.40	316.21	23.83	340.05	5.10	48.34	3.50	1.89	1.53
2016/TODVAR-06	61.51	3.85	7.34	17.33	24.00	8.75	66.38	31.33	62.33	80.30	6.57	13.48	0.64	2.20	12.00	0.44	0.53	4.82	1.24	6.06	80.29	20.72	111.02	4.93	17.47	4.81	2.27	2.41
2016/TODVAR-07	74.60	3.51	8.66	17.00	29.00	5.88	84.35	30.33	69.00	68.20	8.85	18.33	0.49	5.00	13.71	0.57	0.79	6.54	1.75	8.29	108.98	29.11	138.09	5.00	22.41	2.65	2.18	0.44
2016/TODVAR-08	76.49	5.07	6.78	21.67	30.00	6.22	82.36	32.67	62.33	74.80	7.94	16.14	0.49	2.07	14.30	0.54	0.64	7.48	1.47	8.95	124.62	24.50	149.12	5.00	19.66	3.32	2.54	0.74
2016/TODVAR-09	70.64	4.71	7.67	15.33	26.67	6.82	87.04	31.33	62.67	66.50	6.86	13.85	0.66	2.40	18.18	0.50	0.56	8.48	0.83	9.31	141.32	13.83	155.15	4.13	24.21	3.22	2.15	1.02
2016/TODVAR-10	65.37	3.50	7.69	21.00	29.67	6.09	75.30	35.00	62.67	74.20	7.20	14.91	0.51	3.13	12.15	0.59	0.67	9.64	1.04	10.68	160.75	17.33	178.08	4.20	45.08	2.24	1.99	0.24
2016/TODVAR-11	66.66	5.16	6.73	21.00	29.00	5.47	80.66	31.33	65.00	72.00	8.13	17.91	0.66	6.13	12.64	0.84	1.03	17.27	1.24	18.51	287.79	20.72	308.52	5.00	19.39	2.77	2.17	0.57
2016/TODVAR-12	77.77	5.40	8.14	20.67	29.00	5.65	79.82	33.00	65.00	84.25	7.29	15.18	0.64	3.60	13.98	1.06	1.17	23.58	1.28	24.85	393.00	21.28	414.27	4.10	22.62	3.18	2.59	0.56
Pusa 120	73.73	5.11	7.85	21.00	28.00	5.91	87.02	34.67	62.00	55.71	8.39	18.35	0.55	4.87	17.26	0.88	1.05	16.52	1.71	18.23	275.29	28.56	303.85	4.33	25.83	2.60	2.12	0.46
Pusa Gaurav	66.61	3.93	5.85	20.67	27.33	7.68	81.24	34.67	61.33	60.08	7.40	13.53	0.58	2.27	21.40	0.79	1.14	16.86	2.30	19.16	281.03	38.39	319.42	4.67	14.35	3.55	2.52	0.98
Pusa Rohini	72.48	4.07	6.63	19.33	28.67	5.64	82.08	32.33	60.33	65.60	8.37	17.14	0.65	2.67	15.25	0.73	1.07	17.89	2.65	20.54	298.17	44.11	342.28	5.60	32.14	3.45	1.82	1.55
Utkal Pallavi	47.20	3.98	4.13	19.00	26.67	7.71	79.43	28.33	60.33	48.76	8.19	12.90	0.50	2.00	17.55	0.73	1.00	17.00	0.93	17.93	283.27	15.50	298.76	4.73	19.25	3.39	2.73	0.63
Utkal Deepti	57.89	4.62	4.17	21.33	25.67	7.42	79.58	25.33	63.00	47.63	6.13	12.31	0.53	2.00	17.82	0.69	0.99	16.93	0.88	17.81	282.13	14.72	296.85	5.67	24.17	3.37	2.45	0.88
Utkal Pragyan	71.00	4.01	7.25	20.33	28.00	5.94	84.53	31.33	62.67	48.23	6.18	12.69	0.51	2.00	19.05	0.66	0.80	17.22	0.77	17.99	287.01	12.83	299.85	4.33	22.58	3.31	2.40	0.86
Mean	67.75	4.14	6.67	20.46	28.37	6.34	82.32	32.19	62.96	65.98	7.63	15.20	0.57	3.03	15.20	0.68	0.86	13.35	1.37	14.72	222.55	22.81	245.36	4.80	23.80	3.29	2.19	1.05
SE ($\pm$)	2.29	0.16	0.10	0.98	0.87	0.20	3.46	0.96	2.09	2.38	0.21	0.47	0.03	0.18	0.88	0.07	0.06	0.59	0.10	0.67	9.85	1.74	11.11	0.25	1.17	0.17	0.15	0.07
CD (5%)	6.59	0.45	0.29	2.82	2.51	0.57	9.96	2.75	4.09	6.85	0.59	1.35	0.08	0.51	2.54	0.21	0.12	1.70	0.20	1.92	28.30	3.41	31.94	0.72	3.36	0.48	0.44	0.14
CV	5.86	6.52	2.60	8.30	5.33	5.44	7.29	5.15	4.06	6.25	4.66	5.37	7.93	10.14	10.08	18.25	8.80	7.66	9.32	7.84	7.66	9.33	7.84	9.07	8.52	8.80	12.14	8.09

1-Plant height (cm), 2-Primary branches plant⁻¹, 3-Internodal length (cm), 4-Days to 1st flowering, 5- Days to 50% flowering, 6- Flowers cluster⁻¹, 7- % of fruit, 8- Days to fruit set, 9- Days to first fruit harvest, 10- Average fruit weight (g) , 11- Fruit length (cm), 12- Fruit girth (cm), 13-Pericarp thickness (cm), 14-Number of locules, 15- Fruits plant⁻¹, 16-Marketable fruit yield plant⁻¹ (kg), 17-Total fruit yield plant⁻¹ (Kg), 18-marketable fruit yield plot⁻¹ (kg), 19-Unmarketable fruit yield plot⁻¹ (kg), 20-Total fruit yield plot-1 (kg), 21- Marketable fruit yield ha⁻¹ (q), 22- unmarketable fruit yield ha⁻¹ (q), 23- Total fruit yield ha⁻¹ (q), 24- TSS (⁰Brix), 25-Ascorbic acid (mg100g⁻¹), 26-Total Sugar (%), 27- Reducing sugar (%), 28-Non-reducing sugar (%)

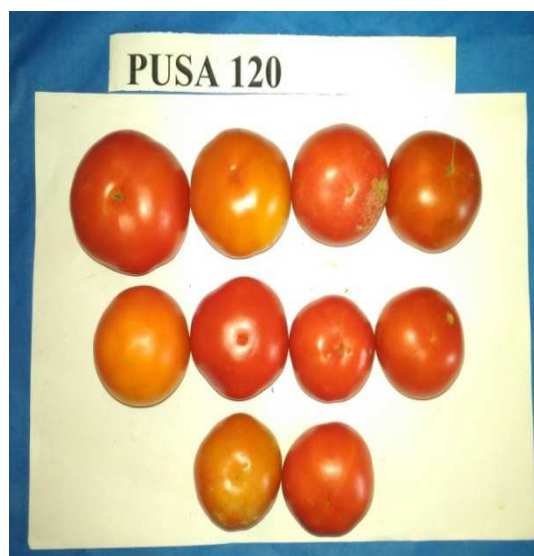
Fig. 4.1 BEST PERFORMING GENOTYPES/VARIETIES



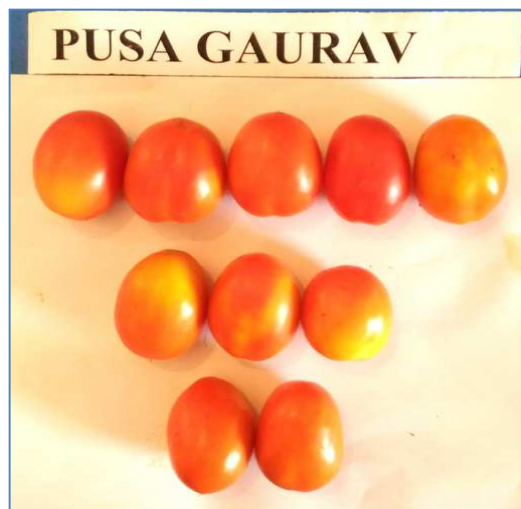
2016/TODVAR-12



Pusa Rohini



Pusa 120



Pusa Gaurav



2016/TODVAR-05



Fig. 4.2 Locule observations

4.2 Parameter of Genetic variability

The estimates of genetic variance viz. range, mean, Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability (h^2), Genetic advance (GA), GA as % of mean of determinate tomato are presented in the table 4.3.

4.2.1 Range of variation

The range of 20 characters of 18 genotypes of tomato presented in table 4.3 revealed a wide range of variations indicating wide scope for selection. The range varied for days to 1st fruit harvest (60.33 to 69.00) to ascorbic acid content of fruits (14.35 to 48.34).

4.2.2 Mean

The 20 traits under study of the 18 tested genotypes of determinate tomato also showed wide range of variations for the mean values which ranged from 0.57 (pericarp thickness) to % of fruit set (82.32). The characters like pericarp thickness (0.57), marketable fruit yield plant⁻¹ (0.68), total fruit yield plant⁻¹ (0.86), number of locules (3.03), total sugar (3.29), number of primary branches plant⁻¹ (4.14), TSS (4.80), internodal length (6.67), flowers cluster⁻¹ (6.34), fruit length (7.63), fruits plant⁻¹ (15.20), days to 1st flowering (20.46), ascorbic acid (23.80), days to 50% flowering (28.37) and days to fruit set (32.19) showed less than 50 values. However, characters like days to 1st harvest (62.96), average fruit weight (65.98), plant height (67.75), % of fruit set (82.32) showed more than 50 values in the present investigation.

4.2.3 Coefficient of variation

The estimation of coefficient of variations ranged from 2.60 (internodal length) to 18.25 (marketable fruit yield plant⁻¹). Relatively high C_{Ve} values were observed for and marketable fruit yield plant⁻¹ (18.25).

The PCV ranged from 5.56 (days to 1st harvest) to 40.63 (number of locules). The study showed that PCV estimates were low (below 10%) for days to 1st harvest (5.56), % fruit set (8.88), days to fruit set (8.98) and days to 50% flowering (9.31). Moderate PCV value (10-15%) was recorded for characters like fruit length (11.08),

fruit girth (13.30), TSS (13.33), pericarp thickness (13.66) and plant height (14.22). Relatively high PCV estimates (>15%) were observed in days to 1st flowering (15.54), flowers cluster⁻¹ (15.95), total sugar (17.37), primary branches plant⁻¹ (17.63), average fruit weight (17.84), internodal length (19.51), fruits plant⁻¹ (21.31), total sugar (21.29), marketable fruit yield plant⁻¹ (29.35), total fruit yield plant⁻¹ (30.98), ascorbic acid (40.09), number of locules (40.63).

GCV values were lower than PCV as expected with a range of 1.04 (days to 1st harvest) to 39.34 (number of locules). Larger difference in magnitude of GCV and PCV was observed for characters like days to first fruit harvest (1.04 to 5.56), % of fruit set (5.06-8.88), TSS (9.76-13.33), total fruit yield plant⁻¹ (21.14-30.98), marketable fruit yield plant⁻¹ (22.99-29.35) and pericarp thickness (11.13-13.66) and days to 50% flowering (7.63-9.31). Similarly, relatively lower difference in magnitude of GCV and PCV was observed for characters like plant height, primary branches plant⁻¹, internodal length, flowers cluster⁻¹, fruit weight, number of locules, total sugar and ascorbic acid which indicated that these traits were mostly governed by genetic factors and least influenced by environmental factors. The characters like number of locules (39.34), ascorbic acid (39.18) and marketable fruit yield plant⁻¹ (22.99) exhibited higher GCV.

4.2.4 Heritability

The heritability estimates for 20 characters under study for 18 determinate tomato genotypes revealed the range from 32.50 (% of fruit set) to 98.2% (internodal length). High heritability was estimated for ascorbic acid (95.5) and number of locules (93.80). Similarly, heritability was recorded lowest for % of fruit set (32.50) and days to fruit harvest (35.00).

4.2.5 Genetic advance

The genetic advance ranged from 0.11 (pericarp thickness) to 21.20 (average fruit weight). GA % of mean was found to be moderate (10-20) for characters like plant height (16.47) and ascorbic acid (18.78). High value (>20%) was recorded for average fruit weight (21.26). Rest other characters showed low (<10%) GA values in the present study.

Table No 4.3 Estimation of different parameters of Variability and genetic advances under selection (5%) for 20 characters in 18 genotypes.

SI No.	Characters	Range	General mean	CVe	PCV	GCV	Heritability (h ²)	GA	GA @ 5% mean
1	Plant height	47.20-84.55	67.75	5.86	14.22	12.95	83.00	16.47	24.31
2	Primary branches plant ⁻¹	3.03-5.40	4.14	6.52	17.63	16.38	86.30	1.30	31.36
3	Internodal length	4.13-8.66	6.67	2.60	19.51	19.34	98.20	2.64	39.48
4	Days to 1 st flowering	15.33-28.33	20.46	8.31	15.54	13.13	71.40	4.68	22.87
5	Days to 50% flowering	24-33.67	28.37	5.33	9.31	7.63	67.20	3.66	12.89
6	Flowers cluster ⁻¹	5.04-8.75	6.34	5.44	15.95	14.99	88.40	1.84	29.03
7	% of fruit set	66.38-89.69	82.32	7.29	8.88	5.06	32.50	4.90	5.95
8	Days to fruit set	25.33-35	32.19	5.15	8.98	7.36	67.10	4.00	12.42
9	Days to 1 st fruit harvest	60.33-69	62.96	5.46	5.56	1.04	35.00	0.26	0.41
10	Average fruit weight	47.63-84.25	65.98	6.25	17.84	16.71	87.70	21.26	32.33
11	Fruit length	6.13-8.85	7.63	4.66	11.08	10.05	82.30	1.43	18.78
12	Fruit girth	12.31-18.35	15.20	5.37	13.3	11.98	83.30	3.43	22.53
13	Pericarp thickness	0.49-0.69	0.57	7.93	13.66	11.13	66.30	0.11	18.67
14	Number of locules	2-6.13	3.03	10.14	40.63	39.34	93.80	2.38	78.48
15	Fruits plant ⁻¹	10.68-21.4	15.20	10.08	21.31	18.78	77.70	5.18	34.09
16	Marketable fruit yield plant ⁻¹	0.44-1.06	0.68	18.25	29.35	22.99	61.30	0.25	37.08
17	Total fruit yield plant ⁻¹	0.53-1.17	0.86	8.80	30.98	21.14	46.60	0.26	29.71
18	TSS	4.1-5.8	4.80	9.07	13.33	9.76	53.60	0.71	14.73
19	Ascorbic acid	14.35-48.34	23.8	8.52	40.09	39.18	95.50	18.78	78.87
20	Total Sugar	2.24-4.81	3.29	8.80	21.29	19.38	82.90	1.20	36.36

4.2.6 Heritability with Genetic advance as % of mean

In the present study, the characters like internodal length (98.2 and 39.48), average fruit weight (87.70 and 32.33), number of locules (93.80 and 78.48), fruits plant⁻¹ (77.0 and 34.09), marketable fruit yield plant⁻¹ (61.30 and 37.08), ascorbic acid (95.50 and 78.87) and total sugar (82.90 and 36.36) showed high heritability along with moderate to high GA as % of mean.

4.3 Correlation studies

A perusal to table 4.4 revealed significant variations in correlation for 14 different characters of 18 genotypes of determinate tomato at both genotypic and phenotypic levels.

Marketable fruit yield plant⁻¹ in determinate tomato exhibited positive and significant correlation at genotypic and phenotypic level with plant height (0.45 and 0.31) and primary branches plant⁻¹ (0.51 and 0.38). However, only significant positive correlation at genotypic level was observed with number of locules (0.39). The characters like internodal length, % of fruit set, days to fruit set, average fruit weight, fruit length and fruit girth were positive but non-significantly correlated with marketable fruit yield plant⁻¹ at both phenotypic and genotypic level. On the other hand, negative non-significant correlation with marketable yield was observed with flowers cluster⁻¹ and pericarp thickness in determinate tomato.

Number of fruits plant⁻¹ in determinate tomato showed significant negative correlation at both genotypic and phenotypic level with internodal length (-0.34 and -0.29), average fruit weight (-0.64 and -0.60) and fruit length (-0.33 and -0.30). Fruits plant⁻¹ also showed significant negative correlation at genotypic level only with days to 1st flowering (-0.30), fruit girth (-0.39) and pericarp thickness (-0.30). However, only positive and significant correlation at genotypic level was observed with % of fruit set (0.47). All other characters showed non-significant correlations.

Results on number of locules showed positive and significant correlation at both genotypic and phenotypic level with internodal length (0.42 and 0.41), fruit length (0.51 and 0.43) and fruit girth (0.83 and 0.73). On the other hand, significant and negative correlation at both genotypic and phenotypic level was exhibited with flowers cluster⁻¹ in determinate tomato (-0.54 and -0.50). All other characters were positively correlated but non-significant.

Similarly, pericarp thickness of determinate tomato fruits exhibited significant and positive correlation with primary branches plant⁻¹ (0.27) and average fruit weight (0.29) only at genotypic level. Characters like plant height, % of fruit set and fruit length were negatively correlated but non-significant at both genotypic and phenotypic level. All other characters showed positive non-significant correlation with pericarp thickness.

The results on correlation studies of fruit girth revealed significant positive correlation at both genotypic and phenotypic levels with plant height (0.51 and 0.41), internodal length (0.52 and 0.48), days to fruit set (0.44 and 0.28), average fruit weight (0.34 and 0.30) and fruit length (0.78 and 0.78). However, negative significant correlation at both genotypic and phenotypic level was observed with flowers cluster⁻¹ (-0.65 and -0.57). All other traits exhibited positive but non-significant correlation with fruit girth.

Fruit length of tomato was significantly and positively correlated with % of fruit set only at phenotypic level and with average fruit weight at genotypic level (0.28 and 0.38) while that of significant and negatively correlated with flowers cluster⁻¹ at both genotypic and phenotypic level (-0.43 and -0.39). All other parameter except primary branches plant⁻¹ was positively correlated but non-significant effect.

Average fruit weight showed significant positive correlation at both genotypic and phenotypic level with plant height (0.53 and 0.41), internodal length (0.53 and 0.48) and days to fruit set (0.45 and 0.34) while that of significant negative correlation with % of fruit set at only genotypic level (-0.36).

Similarly, days to fruit set in tomato was positively and significantly correlated with plant height (0.60 and 0.39), internodal length (0.43 and 0.34), days to 1st flowering (0.33 and 0.32) and % of fruit set (0.28 and 0.30) at both genotypic and phenotypic level, respectively. However, significant negative correlation was observed with flowers cluster⁻¹ (-0.40 and -0.35) at both genotypic and phenotypic level.

Percentage of fruit set in determinate tomato exhibited positive correlation with plant height (0.47 and 0.29) at both genotypic and phenotypic level, while with days to 1st flowering at genotypic level (0.33). However, significant negative correlation exist between % of fruit set with number of flowers cluster⁻¹ (-0.84 and -0.47) at both genotypic and phenotypic level.

Table 4.4 Phenotypic and genotypic correlation coefficient among 14 characters of 18 genotypes of determinate tomato

1		2	3	4	5	6	7	8	9	10	11	12	13	14
1	G	0.25	0.67**	-0.06	-0.43**	0.47**	0.60**	0.53**	0.15	0.51**	-0.16	0.26	-0.03	0.45**
	P	0.22	0.62**	-0.08	-0.35**	0.29*	0.39**	0.41**	0.15	0.41**	-0.09	0.24	0.01	0.31*
2	G		0.18	-0.03	0.02	-0.17	-0.24	0.08	-0.11	0.15	0.27*	0.23	0.11	0.51**
	P		0.17	-0.05	-0.002	0.002	-0.11	0.08	-0.09	0.14	0.22	0.22	0.04	0.38**
3	G			-0.39**	-0.26	-0.06	0.43**	0.53**	0.13	0.52**	0.05	0.42**	-0.34*	0.08
	P			-0.33*	-0.24	-0.01	0.34*	0.48**	0.13	0.48**	0.04	0.41**	-0.29*	0.05
4	G				-0.32*	0.33*	0.33*	-0.09	0.24	0.03	0.18	-0.11	-0.30*	0.07
	P				-0.20	0.16	0.32*	-0.13	0.14	0.0007	0.10	-0.07	-0.15	-0.05
5	G					-0.84**	-0.40**	-0.17	-0.43**	-0.65**	0.008	-0.54**	0.21	-0.26
	P					-0.47**	-0.35**	-0.14	-0.39**	-0.57**	-0.04	-0.5**	0.19	-0.20
6	G						0.28*	-0.36**	0.50	0.43**	-0.16	0.24	0.47**	0.14
	P						0.30*	-0.15	0.28*	0.22	-0.14	0.12	0.16	0.17
7	G							0.45**	0.38**	0.44**	0.08	0.19	-0.14	0.12
	P							0.34*	0.24	0.28*	0.11	0.16	-0.06	0.12
8	G								0.12	0.34*	0.29*	0.22	-0.64**	0.12
	P								0.12	0.30**	0.16	0.18	-0.60**	0.20
9	G									0.78**	-0.02	0.51**	-0.33*	0.11
	P									0.78**	-0.04	0.43**	-0.30*	0.09
10	G										0.07	0.83**	-0.39**	0.23
	P										0.005	0.73**	-0.34	0.14
11	G											0.10	-0.30*	-0.07
	P											0.06	-0.19	-0.03
12	G												-0.23	0.39**
	P												-0.18	0.25
13	G													0.20
	P													0.17

1-Plant height (cm), 2-Primary branches plant⁻¹, 3- Intermodal length (cm), 4-Days to first flowering., 5-Number of flowers cluster⁻¹,6- % of fruit set, 7-Days to fruit set, 8- Average fruit weight (g) , 9- Fruit length (cm),10-Fruit girth (cm), 11-Pericarp thickness (cm), 12-Number of locules 13-Number of fruits plant⁻¹ , 14-Marketable fruit yield plant⁻¹ (kg), G:Genotypic level P: Phenotypic level

Number of flowers cluster⁻¹ indicated significantly negative correlation with plant height (-0.43 and -0.35) while only genotypic level with days to 1st flowering (-0.32). Days to 1st flowering exhibited negative correlation with other parameters but was significant and negatively correlated with internodal length (-0.39 and -0.33) at both genotypic and phenotypic level. Internodal length in determinate tomato exhibited significant positive correlation with plant height (0.67 and 0.62) at both genotypic and phenotypic level. Similarly, primary branches plant⁻¹ in exhibited positive but non-significant correlation with plant height.

4.4 Path coefficient analysis

Phenotypic path coefficient analysis of 18 genotypes of determinate tomato presented in table 4.5 showed highest positive direct effect for marketable fruit yield plant⁻¹ through average fruit weight (0.334) followed by number of locules (0.204), fruit length (0.143), % of fruit set (0.126), flowers cluster⁻¹ (0.106), days to fruit set (0.102), fruits plant⁻¹ (0.096), primary branches plant⁻¹ (0.070) and plant height at final harvest (0.009). However, negative direct path was observed for marketable fruit yield plant⁻¹ with fruit girth (-0.099), days to 1st flowering (-0.085), pericarp thickness (-0.084) and internodal length (-0.070).

Positive direct effect of plant height (0.009) exhibited via indirect positive effect of characters like internodal length (0.006), days to fruit set (0.004), average fruit weight (0.004), fruit girth (0.004) and % of fruit set (0.003). Indirect negative effect was observed with respect to flowers cluster⁻¹ (-0.003). Rest other characters were indirectly associated either positively or negatively.

Primary branches plant⁻¹ (0.070) had positive direct effect on marketable fruit yield plant⁻¹ via indirect effect of characters like plant height (0.016), pericarp thickness (0.015), number of locule (0.015), internodal length (0.012) and fruit girth (0.010). All other characters had indirect positive or negative effect.

Negative direct effect was observed for internodal length (-0.070) via higher indirect negative effect with respect to plant height (-0.044), fruit girth (-0.034),

average fruit weight (-0.034), number of locules(-0.029) and days to fruit set (-0.024). Positive indirect effect was observed for characters like days to 1st flowering (0.023), fruits plant⁻¹ (0.020), and flowers cluster⁻¹ (0.017). Rest other characters exhibited indirect effect either positively or negatively.

Days to 1st flowering (-0.085) exhibited highest negative direct effect via negative indirect effect of characters like days to fruit set (-0.028), % of fruit set (-0.013) and fruit length (-0.012). Positive indirect effect was exerted by internodal length (0.028), flowers cluster⁻¹ (0.017), fruits plant⁻¹ (0.013) and average fruit weight (0.011). Rest of the characters were indirectly associated either in positive or negative direction.

Flowers cluster⁻¹ (0.106) had direct positive effect via positive indirect effect of fruits plant⁻¹ (0.021) whereas highest negative indirect effect was found in characters like fruit girth (-0.061), number of locules (-0.053), % of fruit set (-0.050), fruit length (-0.041), plant height (-0.037), days to fruit set (-0.037), internodal length (-0.025) and days to 1st flowering (-0.022). Rest other characters were indirectly associated in a negative direction.

Percentage of fruit set (0.126) showed positive direct effect via highest indirect positive effect of characters like days to fruit set (0.038), plant height (0.037), fruit length (0.036) and fruit girth (0.028). Negative indirect effect was observed for characters like of flowers cluster⁻¹ (-0.059), average fruit weight (-0.019) and pericarp thickness (-0.018). Rest other characters were non-significantly associated either positively or negatively.

Days to fruit set (0.102) exhibited positive direct effect via positive indirect effect of characters like plant height (0.040), internodal length (0.035), average fruit weight (0.035), days to 1st flowering (0.033), % of fruit set (0.031), fruit girth (0.029), fruit length (0.024), number of locules (0.016) and pericarp thickness (0.011). Negative indirect effect was observed for rest other characters.

Average fruit weight (0.334) had the highest positive direct effect on marketable fruit yield plant⁻¹. Positive indirect effect highest effect was contributed by internodal length (0.161) followed by plant height (0.137), days to fruit set (0.114), fruit girth (0.099), number of locules (0.060), pericarp thickness (0.053), fruit length

(0.040), primary branches plant⁻¹ (0.027). Indirect negative effect was contributed by fruits plant⁻¹ (-0.199), % of fruit set (-0.051), flowers cluster⁻¹ (0.048) and days to 1st flowering (0.042).

Fruit length (0.143) exhibited positive direct effect via indirect positive effect of characters like fruit girth (0.111), number of locules (0.062), % of fruit set (0.041), days to fruit set (0.034), plant height (0.021), internodal length (0.019) and average fruit weight (0.017). Rest of the characters the effect was indirect in a negative direction.

Fruit girth (-0.099) exhibited negative direct effect via highest indirect effect of negative characters like fruit length (-0.077), number of locules (-0.072), internodal length (-0.047), plant height (-0.041), average fruit weight (-0.030), days to fruit set (-0.028) and % of fruit set (-0.022) and primary branches plant⁻¹ (-0.014). Remaining characters exhibited non-significant indirect negative effect.

Pericarp thickness (-0.084) exhibited negative direct effect via positive indirect effect of characters like fruits plant⁻¹ (0.016), % of fruit set (0.012) and plant height (0.007). However, non-significant negative indirect effect was exhibited for all other characters except fruit length and flowers cluster⁻¹ which exhibited non-significant positive indirect effect.

Number of locules showed high positive direct effect (0.204) which was contributed positively but indirectly by fruit girth (0.149), fruit length (0.088), internodal length (0.083), plant height (0.049), primary branches plant⁻¹ (0.044), average fruit weight (0.037), days to fruit set (0.032) and % of fruit set (0.024). Rest all characters exhibited a negative indirect effect.

Fruits plant⁻¹ (0.096) showed positive direct effect via positive indirect effect of characters like flowers cluster⁻¹ (0.019), % of fruit set (0.015) and primary branches plant⁻¹ (0.004). The remaining characters exhibited negative indirect effect except plant height which has non-significant positive effect.

Table 4.5 Direct and indirect effects of component traits on yield on 18 genotypes of determinate tomato at phenotypic level for 13 characters.

Character	1	2	3	4	5	6	7	8	9	10	11	12	13
1	0.009	0.002	0.006	-0.001	-0.003	0.003	0.004	0.004	0.001	0.004	-0.001	0.002	0.0001
2	0.016	0.070	0.012	-0.003	-0.0001	0.0001	-0.008	0.006	-0.006	0.010	0.015	0.015	0.003
3	-0.044	-0.012	-0.070	0.023	0.017	0.001	-0.024	-0.034	-0.009	-0.034	-0.003	-0.029	0.020
4	0.007	0.004	0.028	-0.085	0.017	-0.013	-0.028	0.011	-0.012	0.0001	-0.009	0.006	0.013
5	-0.037	-0.0002	-0.025	-0.022	0.106	-0.050	-0.037	-0.015	-0.041	-0.061	-0.004	-0.053	0.021
6	0.037	0.0002	-0.001	0.020	-0.059	0.126	0.038	-0.019	0.036	0.028	-0.018	0.015	0.020
7	0.040	-0.011	0.035	0.033	-0.035	0.031	0.102	0.035	0.024	0.029	0.011	0.016	-0.006
8	0.137	0.027	0.161	-0.042	-0.048	-0.051	0.114	0.334	0.040	0.099	0.053	0.060	-0.199
9	0.021	-0.013	0.019	0.020	-0.055	0.041	0.034	0.017	0.143	0.111	-0.006	0.062	-0.043
10	-0.041	-0.014	-0.047	0.0001	0.057	-0.022	-0.028	-0.030	-0.077	-0.099	-0.0005	-0.072	0.034
11	0.007	-0.018	-0.004	-0.009	0.003	0.012	-0.009	-0.013	0.004	-0.0004	-0.084	-0.005	0.016
12	0.049	0.044	0.083	-0.015	-0.102	0.024	0.032	0.037	0.088	0.149	0.012	0.204	-0.038
13	0.001	0.004	-0.028	-0.014	0.019	0.015	-0.006	-0.057	-0.029	-0.033	-0.018	-0.018	0.096
14	0.3060	0.3800	0.052	-0.051	-0.199	0.172	0.117	0.198	0.092	0.142	-0.034	0.252	0.172
Partial R ²	0.003	0.027	-0.004	0.004	-0.021	0.022	0.012	0.066	0.013	-0.014	0.003	0.051	0.016

Residual effect: 0.448

1-Plant height (cm), 2-Primary branches plant⁻¹, 3- Intermodal length (cm), 4-Days to first flowering., 5-Number of flowers cluster⁻¹,6- % of fruit set, 7-Days to fruit set, 8- Average fruit weight (g) , 9- Fruit length (cm),10-Fruit girth (cm), 11-Pericarp thickness (cm), 12-Number of locules 13- Fruits plant⁻¹ , 14-Marketable fruit yield plant⁻¹ (kg)

4.5 Multivariate analysis of genetic divergence

In order to assess the nature and extent of genetic divergence among the 18 genotypes of determinate tomato, the Mahalanobis D^2 analysis was done and presented in table 4.6.

4.5.1 Grouping constellation using D^2 Statistics

The cluster derived using Tocher's method are presented in table 4.6. The 18 genotypes of determinate tomato used in the study were grouped on basis of genetic closeness or divergence in D^2 into five clusters. Cluster I and II were found to be the largest with five genotypes in each.

Cluster I included genotypes like 2016/TODVAR-1, 2016/TODVAR-02, 2016/TODVAR-07, 2016/TODVAR-10 and Utkal Pragyan indicating lack of significant genetic differences among them. Similarly, Cluster II consisting of five genotypes such as 2016/TODVAR-05, 2016/TODVAR-11, 2016/TODVAR-12, Pusa Rohini and Pusa-120. Cluster- III comprised of three genotypes such as 2016/TODVAR-06, 2016/TODVAR-08, 2016/TODVAR-09 whereas Cluster IV comprises of four genotypes such as 2016/TODVAR-04, Utkal Pallavi, Utkal Deepti and Pusa Gaurav. Similarly, Cluster V comprised of only single genotype (2016/TODVAR-03).

Table 4.6 Composition of D^2 based on clusters

Clusters	No. of Genotypes	Genotypes
I	5	2016/TODVAR- 01 2016/TODVAR- 02 2016/TODVAR-07 2016/TODVAR- 10 Utkal Pragyan
II	5	2016/TODVAR- 05 2016/TODVAR- 11 2016/TODVAR- 12 Pusa 120 Pusa Rohini
III	3	2016/TODVAR- 06 2016/TODVAR- 08 2016/TODVAR- 09
IV	4	2016/TODVAR- 04 Pusa Gaurav Utkal Pallavi Utkal Deepti
V	1	2016/TODVAR-03

4.5.2 Intra and inter cluster divergence

The result data presented in table 4.7 indicated four intra cluster distances, the highest average D^2 value was observed in cluster IV (103.00), which revealed maximum genetic diversity among the constituent genotypes followed in order by cluster II (83.00) and Cluster I (63.76). The least intra cluster distance was observed by cluster III (58.66) having 3 genotypes.

Similarly, inter cluster distances ranged from 133.03 (cluster III and I) to 380.39 (Cluster III and II). Other highest inter cluster distance was observed between Cluster 323.91 (Cluster V and II), 306.26 (Cluster IV and III), 239.57 (Cluster IV and II) and 223.46 (Cluster IV and I), 173.48 (Cluster V and IV), 166.56 (Cluster II and I), 161.29 (Cluster V and I) and 156.86 (Cluster V and III).

This indicated that genotypes of the clusters I, II, III, IV and V were distinctly and distantly related to each other. The minimum inter cluster distance of 133.03 (between cluster III and I) indicated relatively low divergence between the genotypes of respective clusters. The higher cluster distance of 380.39 (Cluster III and II) indicated that crosses involving genotypes from these clusters can be exploited to a maximum in further crop improvement programmes.

Table 4.7 Average intra-cluster (diagonal) and inter-cluster distance (D^2) value of 18 genotypes of determinate tomato.

	I (5)	II (5)	III (3)	IV (4)	V (1)
I (5)	63.76	166.56	133.03	223.46	161.29
II (5)		83.00	380.39	239.57	323.91
III (3)			58.66	306.26	156.86
IV (4)				103.00	173.48
V (1)					0.00

*Figures in bold letters indicate maximum and minimum (intra/inter-cluster) values.

** Figures in parenthesis indicate the number of genotypes retained in the clusters.

4.5.3 Characterization of D^2 based on cluster

The cluster means of 15 quantitative characters in 18 genotypes of determinate tomato is presented in table 4.7. The results revealed that Cluster I comprised of five genotypes was found superior with respect to internodal length (7.58). Cluster II comprising of five genotypes was found to be superior in plant

height (75.04), fruit girth (16.79), primary branches plant⁻¹ (4.65), fruit length (7.97), pericarp thickness (0.60), number of locules (4.03), marketable fruit yield plant⁻¹ (0.89). Cluster III comprising of three genotypes was found superior for characters like number of flowers cluster⁻¹ (7.26), pericarp thickness (0.60) and average fruit weight (73.87). Cluster V comprising of only one genotype (2016/TODVAR-03) was found superior for characters like % of fruit set (89.69), days to fruit set (35.00), days to 1st flowering (23.00) and fruits plant⁻¹ (17.62).

Table 4.8 Cluster means of 18 genotypes of determinate tomato for 14 quantitative characters.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
I (5)	68.50	3.65	7.58	19.87	6.02	82.53	32.33	64.87	7.68	15.44	0.53	3.13	13.93	0.61
II (5)	75.04	4.65	7.14	20.47	5.70	83.73	33.20	72.01	7.97	16.79	0.60	4.03	14.89	0.89
III (3)	69.55	4.54	7.26	18.11	7.26	78.59	31.78	73.87	7.12	14.49	0.60	2.22	14.83	0.50
IV (4)	57.52	4.09	4.88	22.33	7.18	81.26	30.33	55.79	7.46	13.36	0.57	2.10	16.86	0.68
V (1)	63.01	3.03	5.19	23.00	5.04	89.69	35.00	58.40	7.88	15.63	0.58	3.67	17.62	0.48

1-Plant height (cm), 2-Primary branches plant⁻¹, 3- Intermodal length (cm), 4-Days to first flowering., 5- Flowers cluster⁻¹,6-Fruit set%, 7-Days to fruit set, 8- Average fruit weight (g) , 9- Fruit length (cm),10-Fruit girth (cm), 11-Pericarp thickness (cm), 12-Number of locules 13- Fruits plant⁻¹ , 14-Marketable fruit yield plant⁻¹ (kg)



DISCUSSION

The present investigation entitled, “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” was conducted at All India Coordinated Research Project on Vegetable Crops of Orissa University of agriculture and Technology, Bhubaneswar, Odisha, India during *rabi*, 2017-18. The objective was to study the nature as well as extent of genetic variability for improvement of desirable genotype(s) for fruit yield and yield attributes in determinate tomato.

In the present chapter, a very brief discussion has been made on the basis of recorded observations of the investigation as well as interpretation of significant findings. The interpretation of significant findings in term of cause and effects relationship was discussed, supported by earlier established scientific views of national and international scientists.

5.1 Study of genetic variability

Analysis of variance for 28 different traits showed significantly wide genetic variation among the 18 determinate genotypes. In most of the cases, the genotypic differences were statistically significance at 5% level of significance. Further, the coefficient of variations was within 10% for most of the traits under study, indicating overall moderate precision being maintained in the present investigation.

5.2 Comparative performance of determinate tomato genotypes

The mean performance of 18 diverse genotypes of determinate tomato is presented in table 4.2. The result revealed significant variations for vegetative growth parameters (viz., plant height, primary branches plant⁻¹ and internodal length), flowering parameters (viz., days to 1st flowering, days to 50% flowering and flowers cluster⁻¹), fruit yield attributing parameters (viz., % of fruit set , days to fruit set, days to 1st harvest, average fruit weight, fruit length, fruit girth, pericarp thickness, number of locules and fruits plant⁻¹), fruit quality parameters (viz., TSS, ascorbic acid, total sugar, reducing sugar and non-reducing sugar) and fruit yield (viz., marketable fruit yield plant⁻¹, total fruit yield plant⁻¹, unmarketable fruit yield ha⁻¹, marketable fruit yield ha⁻¹ and total

fruit yield ha⁻¹) in the 18 genotypes evaluated during *rabi* 2017-18 under Bhubaneswar condition. The details of the performance of 18 genotypes are as follows.

The overall performance of the determinate tomato genotypes evaluated under Bhubaneswar condition revealed that the genotype, 2016/TODVAR-12 recorded relatively higher plant height (77.77cm), significantly highest primary branches plant⁻¹ (5.40) and higher internodal length (8.14cm) closely followed by the genotype, Pusa 120 (73.73 cm, 5.11, 7.85 cm, respectively) significantly superior than other genotypes evaluated. However, significant highest plant height was recorded in 2016/TODVAR-05 (84.55cm) while minimum in Utkal Pallavi (47.20 cm). The results also revealed that genotype, Utkal Pallavi recorded significantly lowest plant height (47.20cm) and lowest internodal length (4.13cm) with relatively lower primary branches plant⁻¹ (3.98). The overall performance on vegetative parameters of 18 diverse determinate tomato genotypes indicated superiority of 2016/TODVAR- 12 and Pusa 120 as compared to other genotypes. Similar results have been reported for Pusa 120 with respect to plant height by Basavraj *et al.* (2015) and minimum plant height for Utkal Pallavi by Mohanty and Prusty (2001) and Yende *et al.* (2018).

Regarding flowering parameters, such as days to 1st flowering, 50% flowering and number of flowers cluster⁻¹, the overall result in the present investigation revealed that the genotype, 2016/TODVAR-06 recorded significant earlier days to 1st flowering (17.33 days), significant earliest day to 50% flowering (24 days) with significantly highest number of flowers cluster⁻¹ (8.75) as compared to rest of the genotypes evaluated except Utkal Deepti which recorded significantly lower days to 50% flowering (25.67) and more flowers cluster⁻¹. The other genotypes showed moderate values for flowering characters. In general, days to 1st flowering varied widely from 15.33 days (2016/TODVAR-09) to 28.33 days (2016/TODVAR-04) while for days to 50 % flowering the range varied from 24.00 days 2016/TODVAR-06 to 33.67 days (2016/TODVAR-01). Similarly, the flowers cluster⁻¹ varied significantly among genotypes ranging from 5.04 (2016/TODVAR-03) to 8.75 (2016/TODVAR-06) with average value of 6.34 flowers cluster⁻¹. The present study also revealed significantly maximum flowers cluster⁻¹ in 2016/TODVAR-06 (8.75), followed by Utkal Pallavi (7.71), Pusa Gaurav (7.68),

Utkal Deepti (7.42) which were *statistically at par*. Similar reports on maximum flowers cluster⁻¹ in determinate tomato, Utkal Pallavi and Utkal Deepti was reported by Yende *et al.* (2018)

In determinate tomato usually the fruit yield plant⁻¹ depends not only on flowers cluster⁻¹ but also on % of flower that set fruits. The present study indicated wide range of variability among tested genotypes, varying from 66.38% (2016/TODVAR- 06) to 89.69 (2016/TODVAR-03) with a mean value of 83.2%. The genotypes such as 2016/TODVAR- 05, 2016/TODVAR-07, Pusa 120, 2016/TODVAR- 01, 2016/TODVAR-04, and 2016/TODVAR- 02 (82.98-89.07) also recorded significantly higher % of fruit set as compared to other genotypes and were *statistically at par* with 2016/TODVAR-03 (89.69). So, the result clearly indicated better performance of Pusa 120 along with genotypes 2016/TODVAR- 05, 2016/TODVAR-07, 2016/TODVAR- 01, 2016/TODVAR-04, and 2016/TODVAR-02 for better % of fruit set. Regarding days to 1st fruit set, important yield attributing parameter indicating maturity duration of determinate tomato significant variation was observed which varied from 25.33 days in Utkal Deepti to maximum of 35 days in 2016/TODVAR-10 with an average value of 32.19 days. Thus, the result indicated that Utkal Deepti was the earliest variety to set fruits and was *statistically at par* with Utkal Pallavi (28.33), 2016/TODVAR-07 (30.33) and 2016/TODVAR-02 (30.67) under Bhubaneswar condition.

Similarly, regarding fruit characters of determinate tomato significant variations were observed for average fruit weight from 47.63 g (Utkal Deepti) to 84.25 g (2016/TODVAR-12), fruit length from 6.13 cm (Utkal Deepti) to 8.85 cm (2016/TODVAR-07), fruit girth from 12.31 cm (Utkal Deepti) to 18.35 cm (Pusa 120) and number of fruits plant⁻¹ from 10.68 (2016/TODVAR-04) to 21.40 (Pusa Gaurav) among 18 genotypes evaluated under Bhubaneswar condition. Significantly heaviest fruit was recorded in 2016/TODVAR-12 (84.25 g) followed by 2016/TODVAR-05 (82.50 g) and 2016/TODVAR-06 (80.30 g). However, average fruit weight of tested genotypes was 69.98 g. Similar, variations for average fruit weight and number of fruits plant⁻¹ have also been reported by Ara *et al.* (2009), Singh *et al.* (2015) and Spaldon *et al.* (2017) in tomato under different agroclimatic conditions of India. Significantly 2016/TODVAR-07 recorded longest fruit of 8.85 cm with higher fruit

girth of 18.33 cm closely followed by Pusa 120 (8.39 cm and 18.35cm), Pusa Rohini (8.37 cm and 17.14 cm) which were *statistically at par* with each other. The present investigation also indicated that the genotype, Utkal Deepti recorded significantly lowest fruit weight (47.63 g), fruit length (6.13 cm) and fruit girth (12.31cm) than rest of the genotypes. Similar trend with respect to fruit length in tomato was also reported by Singh *et al.* (2015). Significant variations were also observed for fruits plant⁻¹ which varied from 10.68 (2016/TODVAR-04) to 21.40 (Pusa Gaurav) with mean of 15.2. Significantly maximum fruits plant⁻¹ was observed in Pusa Gaurav (21.40) and Utkal Pragyan (19.05) than rest of the genotypes. Similarly, significantly lowest fruits plant⁻¹ was recorded in 2016/TODVAR-04 (10.68). Similar reports of higher fruits plant⁻¹ in determinate tomato, Pusa Gaurav was reported by Basavraj *et al.* (2015).

Regarding fruit yield plant⁻¹, overall result of the present investigation revealed that the genotype 2016/TODAVR-12 recorded significantly higher yields both in terms of marketable fruit yield plant⁻¹ (1.06 kg) and total fruit yield plant⁻¹ (1.17 kg). In terms of marketable fruit yield plant⁻¹ (kg), a wide variation was observed ranging from 0.44 (2016/TODVAR-06) to 1.06 (2016/TODVAR-12) with an average value of 0.68 while total yield plant⁻¹ ranged from 0.53 (2016/TODVAR-06) to 1.17 (2016/TODVAR-12) with an average value of 0.86. Significantly lower yield (both marketable fruit yield plant⁻¹ and total yield plant⁻¹) was recorded in the genotype, 2016/TODVAR-06. Significantly maximum total yield plant⁻¹ (kg) was recorded in the genotypes 2016/TODVAR-05 (1.16), Pusa Gaurav (1.14), Pusa Rohini (1.07), Pusa 120 (1.05), Utkal Pallavi (1.00) and Utkal Deepti (0.99). Similar results have been reported by Basavraj *et al.* (2015) for Pusa Gaurav, Pusa 120 and Pusa Rohini. Singh *et al.* (2015) also reported such observations with respect to fruit yield plant⁻¹ (0.43 kg to 1.44kg) in tomato. Significantly highest yield in terms of marketable fruit yield (qha⁻¹) and total fruit yield (qha⁻¹) was recorded in the genotype, 2016/TODVAR-12 (393 and 414.27) whereas the genotype, 2016/TODVAR-06 (80.29 and 101.02) recorded significantly lowest, with a mean value of 222.25 qha⁻¹ for marketable fruit yield and 245.36 qha⁻¹ for total fruit yield, respectively. Similar trend was also observed with respect to marketable fruit yield plot⁻¹ (kg) and total fruit yield plot⁻¹ (kg) among the genotypes under study.

Wide range of variability from 0.24 (non-reducing sugar) to 48.34 (ascorbic acid) was observed for quality parameters. The TSS content of tomato in the present study varied from 4.10 (2016/TODVAR-12) to 5.82 (2016/TODVAR-03) with a mean value of 4.80. Significantly highest TSS was recorded in the genotype, 2016/TODVAR-03 (5.82) closely followed by Utkal Deepti (5.67) and Pusa Rohini (5.6) which were *statistically at par*. Similar findings with respect to TSS in tomato have been reported by Basavraj *et al.* (2015), Singh *et al.* (2015) and Spaldon *et al.* (2017). Regarding ascorbic acid (mg100g⁻¹), the range varied from 14.35 (Pusa Gaurav) to 48.34 (2016/TODVAR-05) with a mean value of 23.80. Significantly highest ascorbic acid (mg100g⁻¹) content of 48.34 was recorded in genotype, 2016/TODVAR-05 closely followed followed by 2016/TODVAR-10 (45.08) than other genotypes. Such wide variations in ascorbic acid content were also reported by Kumar *et al.* (2017) in tomato. Total sugar content ranged from 2.24 (2016/TODVAR-10) to 4.81 (2016/TODVAR- 06) with a mean value of 3.29. Significantly highest amount of total sugar was also reported in genotypes 2016/TODVAR-01 and 2016/TODVAR-02.

From the overall performance of 18 diverse genotypes of determinate tomato studied in present investigation, it may be concluded that genotype, 2016/TODVAR-12 was identified as best genotype under Bhubaneswar condition due to relatively better growth (plant height of 77.77 cm, 5.40 primary branches plant⁻¹ and 8.14cm of internodal length), fruit yield attributing parameters (79.82% of fruit set, 65 days to 1st fruit harvest, average fruit weight of 84.25 g and 0.64 cm pericarp thickness) , fruit yield (marketable fruit yield plant⁻¹ of 1.06 kg , total fruit yield plant⁻¹ of 1.17 kg, marketable fruit yield of 393 qha⁻¹ and total fruit yield of 414.27 qha⁻¹).

Pusa 120 was identified as better performing genotype next to 2016/TODVAR-12 under Bhubaneswar condition due to relatively better growth (plant height of 73.73cm, 5.11 primary branches plant⁻¹ and 7.85cm of internodal length), flowering parameters (28 days to 50% flowering and 5.91 flowers cluster⁻¹), fruit yield attributing parameters. (8.39 cm fruit length, 18.35 cm fruit girth) and yield (marketable fruit yield plant⁻¹ of 0.88 kg , total fruit yield plant⁻¹ of 1.05 kg and total fruit yield of 303.85 qha⁻¹).

Pusa Rohini also performed well under Bhubaneswar condition due to relatively better growth (plant height of 72.48cm), fruit yield attributing parameters (% fruit set of 82.08, fruit length of 8.37 cm and fruit girth of 17.14cm), yield (marketable fruit yield plant⁻¹ of 0.73 kg, total fruit yield plant⁻¹ of 1.07 kg, marketable fruit yield ¹ of 298.17 qha⁻¹ and total fruit yield of 342.28 qha⁻¹) and fruit quality parameters (TSS of 5.60⁰ Brix).

The genotype, 2016/TODVAR-05 was found better in performance with respect to better vegetative growth (plant height of 84.55 cm), fruit yield attributing parameters (89.07 % of fruit set, 26.33 days to 50% flowering), fruit yield attributing parameters (average fruit weight of 82.50g), yield (marketable fruit yield plant⁻¹ of 0.96 kg and total fruit yield plant⁻¹ of 1.16kg) and fruit quality parameters (TSS of 5.10⁰ Brix and ascorbic acid of 48.34 mg 100g⁻¹) than other genotypes.

Utkal Deepti was also found to perform well with respect to flowering parameters (25.67 days to 50% flowering, 7.42 flowers cluster⁻¹, 25.33 days to fruit set), yield parameter (total yield plant⁻¹ of 1.17 kg,) and fruit quality parameters (TSS of 5.67⁰ Brix).

5.3 Coefficient of variability

The result data presented in table 4.1 for ANOVA of 20 quantitative traits of 18 genotypes of tested determinate tomato clearly demonstrated the nature and magnitude of variability. Hence, there is scope for improvement of determinate tomato through crop improvement programme.

The generalized range of genetic variability of 20 studied traits revealed that most of the characters under study showed variation between lower to higher value of 14.37% in days to 1st fruit harvest (60.33 to 69.00) to maximum value of 236.86% in ascorbic acid (14.35 to 48.34). Characters like internodal length, number of locules, fruits plant⁻¹, marketable fruit yield plant⁻¹, ascorbic acid content and total sugar content showed a difference of more than 100% indicating existence of wide variability for these characters. These wide variations between minimum and maximum value of a trait in the present study indicated a wide scope for improvement of such traits as variability is treated as a basic step for selection in a crop improvement programme.

Similar reports of wide variations in range of different traits has been reported by Kumar *et al.* (2016) for fruits plant⁻¹, plant height and fruit weight.

The data on general mean values indicated wide variations among the genotypes which varied from 0.57 (pericarp thickness) to 82.32 (% of fruit set). The quantitative traits like primary branches plant⁻¹, internodal length, days to 1st flowering, days to 50% flowering, number of flowers cluster⁻¹, days to fruit set, fruit length, fruit girth, pericarp thickness, number of locules, fruits plant⁻¹, marketable fruit yield plant⁻¹, total fruit yield plant⁻¹, TSS, ascorbic acid and total sugar having the general mean value less than 50. On the other hand, traits like plant height, % of fruit set, days to 1st fruit harvest, fruit weight possess general mean value more than 50. Those generalized results of present investigation indicated wide scope for improvement in determinate tomato.

The result also stated that, invariably, PCV values were higher than corresponding GCV values for all the traits under study. This result simply implies the impact of environmental factors for expression of the traits. However, the closeness or divergence between the traits in the present study varied widely. The traits like plant height, primary branches plant⁻¹, internodal length, days to 1st flowering, flowers cluster⁻¹, fruit weight, fruit length, fruit girth, number of locules, fruits plant⁻¹, ascorbic acid and total sugar showed closeness between PCV with corresponding GCV which clearly indicated that these traits on selection is less influenced by environmental factors. Hence, simple selection method can be adopted to develop a desirable genotype. Similar reports were also reported by Agarwal *et al.* (2014) for plant height, TSS, average fruit weight and pericarp thickness and by Savitharamma (2017) for fruits plant⁻¹, fruit diameter, plant height, clusters plant⁻¹ and fruit yield plant⁻¹.

On the other hand, characters like days to 50% flowering, % of fruit set, days to fruit set, days to first fruit harvest, pericarp thickness, marketable fruit yield plant⁻¹, total fruit yield plant⁻¹ and TSS showed wide variations between PCV and corresponding GCV. The wide variation between PCV with corresponding GCV simply indicated that these traits were highly influenced by different environmental factors; hence simple selection on the basis of phenotypic performance would not be effective. Similar findings have been reported by workers like Kumar *et al.* (2014), Basavraj *et al.* (2015) and Hasan *et al.* (2016).

In crop improvement programme, it is always essential to estimate the heritable and non-heritable component of a particular trait. Actually, the heritable component, being governed by genes will be the basis for selection which can be inherited from parents to progeny. In this regard, estimation of heritability of a particular trait seems to be highly essential for further selection programme. In the present investigation, the heritability in broad sense varied widely from 32.50 (% of fruit set) to 98.20 (internodal length). The characters showing high heritability (>60%) were marketable fruit yield plant⁻¹ (61.30), pericarp thickness (66.30), days to fruit set (67.10), days to 50% flowering (67.20), days to 1st flowering (71.40), fruits plant⁻¹ (77.70), fruit length (82.30), total sugar (82.90), plant height (83.00), fruit girth (83.30), primary branches plant⁻¹ (86.30), fruit weight (87.70), flowers cluster⁻¹ (88.40), number of locules (93.80), ascorbic acid (95.50) and internodal length (98.20). Rest of the characters showed low heritability of less than 60% in the present study. Similar results of high heritability was reported by Kumar *et al.* (2013) for plant height, number of fruits plant⁻¹, yield plant⁻¹, fruit length, fruit weight and pericarp thickness in tomato.

According to Johnson *et al.* (1955) selection of characters on the basis of heritability may not be always very effective approach. It is suggested to select the characters that have high heritability coupled with moderate to high rate of GA as % of mean. In the present study, the characters like internodal length (98.2 and 39.48), average fruit weight (87.70 and 32.33), number of locules (93.80 and 78.48), fruits plant⁻¹ (77.0 and 34.09), marketable fruit yield plant⁻¹ (61.30 and 37.08), ascorbic acid (95.50 and 78.87) and total sugar (82.90 and 36.36) showed high heritability along with moderate to high GA as % of mean. Therefore, simple selection of such characters will be very effective in determinate tomato breeding programme. Similar results were also reported by Manna and Paul (2012) and Kumar *et al.* (2013).

5.4 Character association of fruit yield and component characters

In general, yield of any crop including tomato is a complex character governed by several other quantitative traits and expression of which depends on several environmental factors including both biotic and abiotic stresses. Therefore, phenotypic selection of a particular genotype may not be a sound proposition for development of a desired genotype in crop improvement programme. In general, correlation studies are highly beneficial in selecting superior genotypes for any population

improvement programme (Robinson, 1966). It is highly essential to study the interrelationship of the quantitative characters through correlation study both at genotypic and phenotypic level for an effective selection in developing a new genotype. The results obtained in the present study of 18 genotypes of determinate tomato for 14 characters are presented in table 4.4. The result indicated that significant variations for both genotypic and phenotypic correlations among the character pairs.

Invariably, the results of the present investigation indicated closeness between genotypic and phenotypic correlation between character pairs and relatively better values at genotypic level for all characters under study. These results indicated that there was least influence of environmental factors for expression of character association with fruit yield plant⁻¹ in tomato which might be due to strong genetic makeup of the limits. Similar results of closeness between genotypic and phenotypic correlation has also been reported by Ambresh *et al.* (2017).

The result showed significant phenotypic correlation ranged from 0.28 to 0.80. Out of 105 estimates of phenotypic correlation with marketable fruit yield plant⁻¹ only 30 estimates showed significance out of which 20 were positive while that of 10 were negative. Similarly, at genotypic level 41 estimates were found significant out of which 26 were positive while 15 were negative.

At genotypic level, it was found that for plant height out of six significant estimates five were positive and only one was negative whereas primary branches plant⁻¹ was positively and significantly associated with only one estimate. Similarly, internodal length was significantly associated with six estimates out of which four were positive and two were negative. However, days to 1st flowering were significantly associated positively with two estimates and negatively with two estimates. Flowers cluster⁻¹ was associated with five significant negative estimates whereas percentage of fruit set showed association with four estimates out of which three were positive and one was negative. Days to fruit set exhibited positive and significant association with only three estimates. Similarly, average fruit weight was significantly associated with two estimates out of which one was positive while the other was negative at the genotypic level. Fruit length exhibited significant association with three estimates out of which two were positive and one was negative whereas, fruit girth showed two significant associations where one was positive other

was negative. Pericarp thickness was significantly associated in a negative direction with only one estimate at the genotypic level.

At the phenotypic level, plant height showed significant association with six estimates out of which five were positive and one was negative. Similarly, internodal length exhibited six significant associations, out of which four were positive and two were negative whereas days to flowering showed significant positive association with only one estimate. Number of flowers cluster⁻¹ was significantly associated with five significant negative estimates whereas both % of fruit set and days to fruit set were positively and significantly associated with only two estimates. Average fruit weight showed two significant associations out of which one was positive and other was negative. Fruit length exhibited significant association with three estimates out of which two were positive and one was negative whereas fruit girth had significant association with only one positive estimate.

The results indicated that marketable fruit yield plant⁻¹ was significantly and positively correlated with plant height (0.45 and 0.31) and primary branches plant⁻¹ (0.51 and 0.38) at both genotypic and phenotypic level whereas, number of locules showed significant positive correlation with marketable fruit yield plant⁻¹ at genotypic level. Similar observations of significant and positive correlation in tomato have been reported by Ara *et al.* (2009) and Monamodi *et al.* (2013) for fruit yield plant⁻¹ with plant height at both phenotypic and genotypic level.

Plant height showed positive and significant correlation with internodal length (0.67 and 0.62), % of fruit set (0.47 and 0.29), days to fruit set (0.60 and 0.39), average fruit weight (0.53 and 0.41) and fruit girth (0.51 and 0.41) at both phenotypic and genotypic level. Similarly, internodal length was positively and significantly correlated with days to fruit set (0.43 and 0.34), average fruit weight (0.53 and 0.48), fruit girth (0.52 and 0.48) and number of locules (0.42 and 0.41) at both phenotypic and genotypic level. Days to 1st flowering exhibited positive and significant correlation with days to fruit set (0.33 and 0.32). Percentage of fruit set was positively and significantly correlated with days to fruit set (0.28 and 0.30). Days to fruit set was positively and significantly correlated with average fruit weight (0.45 and 0.34) and fruit girth (0.44 and 0.28) both at genotypic and phenotypic level, average fruit weight

with fruit girth (0.34 and 0.30), fruit length with fruit girth (0.78 and 0.78) and number of locules (0.51 and 0.43).

Characters which were negative and significantly correlated at both genotypic and phenotypic level were plant height with number of flowers cluster⁻¹ (-0.43 and -0.35), internodal length with days to 1st flowering (-0.39 and -0.33) and fruits plant⁻¹ (-0.34 and -0.29), flowers cluster⁻¹ with % of fruit set (-0.84 and -0.47), days to fruit set (-0.40 and -0.35), fruit length (-0.43 and -0.39), fruit girth (-0.65 and -0.57) and number of locules (-0.54 and -0.50), average fruit weight with fruits plant⁻¹ (-0.64 and -0.60), as well as fruit length with fruits plant⁻¹ (-0.33 and -0.30).

At the genotypic level, branches plant⁻¹ was positively and significantly correlated with pericarp thickness (0.27), days to 1st flowering with % of fruit set (0.33). However, percentage of fruit set was positively and significantly correlated with fruit girth (0.43), and number of fruits plant⁻¹ (0.47), days to fruit set with fruit length (0.38) and average fruit weight with pericarp thickness (0.29) at genotypic level. Similarly, negative and significant correlation was observed for days to 1st flowering with number of flowers cluster⁻¹ (-0.32), pericarp thickness with fruits plant⁻¹ (-0.30), fruit girth with number fruits plant⁻¹ (-0.30). At phenotypic level positive and significant correlation was observed for days to 1st flowering with fruit set (0.32) and % of fruit set with fruit length (0.28).

From the above discussion regarding correlation study, both at phenotypic and genotypic level in determinate tomato, it may be concluded that characters like plant height, primary branches plant⁻¹ and number of locules were important correlated characters contributing towards yield in determinate tomato. Therefore, simultaneous improvement in these characters will be highly beneficial for development of desirable genotypes in tomato. Similar observations of significant correlation in tomato have been reported by Kumar *et al.* (2016) and Ambresh *et al.* (2017), Rawat *et al.* (2017) also reported such findings for primary branches plant⁻¹.

5.5 Path analysis

Fruit yield of tomato is a complex character governed by many genes which are influenced by several environmental factors. Several factors including both direct and indirect factors are involved for expression of complex characters *i.e.* yield. In

order to obtain a desirable genotype with higher yield potential in determinate tomato, it is highly essential to study direct and indirect effects.

In general, studies on path analysis of characters showed direct and indirect effects contributing towards yield of the crop. The results presented in table 4.5 showed both direct and indirect effects of component traits on marketable fruit yield plant⁻¹ through average fruit weight (0.334) closely followed by number of locules (0.204), fruit length (0.143), % of fruit set (0.126), flowers cluster⁻¹ (0.106), days to fruit set (0.102), fruits plant⁻¹ (0.096), primary branches plant⁻¹ (0.070) and plant height at final harvest (0.009). However, the study also showed negative direct path for marketable fruit yield plant⁻¹ with fruit girth (-0.099), days to 1st flowering (-0.085), pericarp thickness (-0.084) and internodal length (-0.070). Similar results of positive association have been reported by Kumar *et al.* (2016) for average fruit weight, number of locules and plant height at final harvest by Reddy *et al.* (2013) also reported similar observations for other traits like plant height, fruits plant⁻¹, fruit length, and fruit width. The findings confirmed the findings of Ara *et al.* (2009) and Monamodi *et al.* (2013) with respect to the direct and highest direct effect of average fruit weight on fruit yield.

The present study also showed that a very low residual effect of 0.448 indicating that most of the important characters contributing towards yield through both direct and indirect path has been included in the present study. The characters which were not influenced seemed to have very negligible contribution towards yield. Similar reports of lower residual effect in determinate tomato have been reported by Kumar *et al.* (2016). They reported a residual effect of 0.6239 which showed that the characters under study contributed 99.5% variation to fruit yield. Ara *et al.* (2009) too reported a residual value of 0.2268 in tomato.

5.6 Multivariate analysis of genetic divergence

In order to assess genetic divergence among tested genotypes for heterosis breeding or selection in segregating generations after hybridization, it is highly essential to study closeness or divergence of genotypes present in the population by adopting Mahalanobis D² statistics. It is possible to assess divergence of genotypes into different cluster for further hybridization programme in crop improvement. The results presented in table 4.6, 4.7 and 4.8 revealed that, the whole 18 diverse

genotypes of determinate tomato were grouped into five clusters. Both cluster I and II included five genotypes each while cluster III included three genotypes, cluster IV had four genotypes and cluster V comprised of only one genotype indicating wide diversity among tested 18 genotypes of determinate tomato. Cluster I included genotypes like 2016/TODVAR-1, 2016/TODVAR-02, 2016/TODVAR-07, 2016/TODVAR-10 and Utkal Pragyan indicating lack of significant genetic differences among them. Similarly, Cluster II consisting of five genotypes such as 2016/TODVAR-05, 2016/TODVAR-11, 2016/TODVAR-12, Pusa Rohini, and Pusa-120. Cluster-III comprised of three genotypes such as 2016/TODVAR-06, 2016/TODVAR-08, 2016/TODVAR-09 whereas Cluster IV comprises of four genotypes such as 2016/TODVAR-04, Utkal Pallavi, Utkal Deepti and Pusa Gaurav. Cluster V comprised of only single genotype *i.e.* 2016/TODVAR-03. The results clearly indicated that genotype of different geographical origin were grouped into a single cluster, indicating closeness genetically. The study also showed that selection of superior genotypes through hybridization programme should be based on their genetic diversity rather on the basis of geographical diversity. Similar results were also reported by Basavraj *et al.* (2010) and Kumar *et al.* (2016) in tomato.

5.6.1 Intra and Intercluster distances

Maximum intracluster distance was observed in cluster IV (103.00) while minimum in cluster III (58.66). Similarly, intercluster distance ranged from 133.03 (cluster III and I) to 380.39 (cluster III and II). The results also showed wide variation for both inter and intracluster distance among 18 genotypes. The results clearly indicated that the genotypes included in clusters were distinctly and distantly related to each other due to the presence of high intercluster distance between cluster III and II (380.39). The findings are in agreement with Nalla *et al.* (2014) and Dar *et al.* (2015) in tomato. In general, the magnitude of heterosis primarily depends on the degree of genetic diversity between the parental lines. The greater the genetic divergence between two clusters, the higher is the difference between the genotypes. Therefore, hybridization between two diverse genotypes which differs distantly and distinctly produced more variability in F_1 and subsequent segregating generations. It has also been suggested that at the time of considering genetic diversity among the parents to be included in the hybridization programme their yield potential also should be considered.

It can be concluded that crosses involving cluster III (2016/TODVAR-06, 2016/TODVAR-08, 2016/TODVAR-09) with cluster II (2016/TODVAR-05, 2016/TODVAR-11, 2016/TODVAR-12, Pusa 120, Pusa Rohini) can produce desirable recombinants with maximum hybrid vigour in future and further selection in segregating generations in determinate tomato. Similarly, closeness between clusters of the present study indicated presence of maximum common genes among the genotypes.

Regarding characterisation of D^2 based on clusters, the results indicated that Cluster I comprised of five genotypes was found superior with respect to internodal length (7.58). Cluster II comprising of five genotypes was found to be superior in plant height (75.04), fruit girth (16.79), primary branches plant⁻¹ (4.65), fruit length (7.97), pericarp thickness (0.60), number of locules (4.03) and marketable fruit yield plant⁻¹ (0.89). Cluster III comprising of three genotypes was found superior for characters like number of flowers cluster⁻¹ (7.26), pericarp thickness (0.60) and average fruit weight (73.87). Cluster V comprising of only one genotype (2016/TODVAR-03) was found superior for characters like % of fruit set (89.69), days to fruit set (35.00), days to 1st flowering (23.00) and fruits plant⁻¹ (17.62).

From the present study, it can be concluded that for future breeding programme in determinate tomato, genotypes of Cluster-II (2016/TODVAR-05, 2016/TODVAR-11, 2016/TODVAR-12, Pusa 120, Pusa Rohini) should be selected for better vegetative growth and fruit yield. Similarly, cluster III should be considered for development of determinate variety with heavy fruits while that of Cluster V for earliness, higher % of fruit set and fruits plant⁻¹.



SUMMARY AND CONCLUSION

The present investigation entitled, “**Character association and diversity analysis in determinate tomato (*Solanum lycopersicum* L.)**” was conducted at All India Coordinated Research Project on Vegetable Crops operating under Orissa University of Agriculture & Technology, Bhubaneswar, Odisha, India during *rabi* season of 2017-18. The objective was to study the nature and extent of genetic variability in determinate tomato for improvement of desirable genotype(s) for fruit yield and yield attributes. Eighteen genotypes were evaluated by adopting RBD replicated thrice. The genotypes were evaluated for 20 parameters including, vegetative growth, flowering, fruit yield and yield attributing as well as fruit quality parameters. The salient findings of the investigation have been summarized below.

- The genetic variability study revealed significant variations among the genotypes. The C_{Ve} values were found within 10% for most of the characters under study.
- Significant variations for plant height were observed which ranged from 47.20 cm (Utkal Pallavi) to 84.55 cm (2016/TODVAR-05) with a mean value of 67.75 cm. Significantly highest plant height was recorded in genotype, 2016/TODVAR-5(84.55 cm).
- Significantly maximum primary branches plant⁻¹ (5.40) was recorded in 2016/TODVAR-12 than rest of the genotypes except 2016/TODVAR-08 (5.07), Pusa 120 (5.11) and 2016/TODVAR-11 (5.16) which were *statistically at par*.
- The data on internodal length indicated wide variations among tested genotypes ranging from 4.13 cm (Utkal Pallavi) to 8.66 cm (2016/TODVAR-07) with a mean value of 6.67 cm.
- The genotype, 2016/TODVAR-09 showed significantly earliness to 1st flower appearance at 15.33 days after transplanting than rest of the genotypes. However, the genotypes, 2016/TODVAR-07 (17.00 days), 2016/TODVAR-06 (17.33 days) and 2016/TODVAR-02 (17.67 days) were *statistically at par* with early genotype, 2016/TODVAR-09.

- Similarly, the genotype 2016/TODVAR-06 (24 days) recorded earliest to attained 50% flowering, closely followed by Utkal Deepti (25.67 days) and 2016/TODVAR-05 (26.33 days) than rest of the genotypes.
- Significantly maximum flowers cluster⁻¹ was recorded in 2016/TODVAR-06 (8.75) closely followed by Utkal Deepti (7.42), Pusa Gaurav (7.68) and Utkal Pallavi (7.71) where *statistically parity* were observed.
- Regarding the % of fruit set, significant variations were observed which varied significantly from 66.38% (2016/TODVAR-06) to 89.69% (2016/TODVAR-03) with mean value of 82.32%. Except the genotypes, 2016/TODVAR-06, 2016/TODVAR-10, Utkal Pallavi and Utkal Deepti, all other genotypes were found *statistically at par* with 2016/TODVAR-03 (89.69%).
- The variety, Utkal Deepti (25.33 days) was the earliest to set fruits while 2016/TODVAR-10 (35.00 days) and 2016/TODVAR-03 (35.00 days) took maximum days for fruit set.
- Days to 1st fruit harvest was found to be minimum for 2016/TODVAR-02, Utkal Pallavi and Pusa Rohini (60.33 days) whereas the genotype, 2016/TODVAR-07 (69 .00 days) took maximum days.
- Significantly heaviest fruit of 84.25 g was recorded in 2016/TODVAR-12 closely followed by 2016/TODVAR-05 (82.50) and 2016/TODVAR-06 (80.30). Similarly, significantly lightest fruit was recorded in Utkal Deepti (47.63 g). The mean value for average fruit weight was 65.98 g.
- The genotype, 2016/TODVAR- 07 (8.85 cm) recorded the longest fruit which was *statistically at par* with genotypes, Pusa Rohini (8.37 cm), Pusa 120 (8.39 cm) and 2016/TODVAR-01 (8.45 cm).
- Significantly maximum fruit girth was observed in Pusa 120 (18.35 cm) while that of lowest in Utkal Deepti (12.31 cm).
- Genotypes like 2016/TODVAR-06 (0.64 cm), 2016/TODVAR-12 (0.64 cm), Pusa Rohini (0.65 cm), 2016/TODVAR-09 (0.66 cm), 2016/TODVAR-11(0.66 cm) recorded significantly higher pericarp thickness and were *statistically at par* with 2016/TODVAR-04 (0.69 cm).

- Number of locules was lowest in the varieties, Utkal Pallavi, Utkal Deepti, Utkal Pragyan (2.00) whereas the genotype, 2016/TODVAR-11 (6.13) recorded highest local count. The genotypes 2016/TODVAR-01 (2.47), 2016/TODVAR-09 (2.40), Pusa Gaurav (2.27), 2016/TODVAR-06 (2.20), 2016/TODVAR-04 (2.13) and 2016/TODVAR-08 (2.07) were statistically at par with lowest locule count.
- The average fruits plant⁻¹ varied significantly from 10.68 (2016/TODVAR-04) to 21.40 (Pusa Gaurav) with a mean of 15.20. Significantly maximum fruits plant⁻¹ was observed in Pusa Gaurav (21.4) and was *statistically at par* with Utkal Pragyan (19.05).
- The genotype 2016/TODVAR-12 recorded significantly highest marketable fruit yield (plant⁻¹, plot⁻¹, ha⁻¹) of 1.06 kg, 23.58kg and 393.00 q whereas total fruit yield (plant⁻¹, plot⁻¹, ha⁻¹) of 1.17 kg, 24.85 kg and 414.27 q, respectively.
- Significantly highest fruit yield plant⁻¹ was recorded in the genotypes 2016/TODVAR-05 (1.16 kg), Pusa Gaurav (1.14 kg), Pusa Rohini (1.07 kg), Pusa120 (1.05 kg), 2016/TODVAR-11(1.03 kg), Utkal Pallavi (1.00 kg) and Utkal Deepti (0.99 kg) which were *statistically at par* with the genotype, 2016/TODVAR-12 (1.17 kg).
- Significantly highest TSS (⁰Brix) was recorded in 2016/TODVAR-03(5.8) closely followed by Utkal Deepti (5.67) and Pusa Rohini (5.60).
- Significantly highest ascorbic acid was recorded in 2016/TODVAR-05 (48.34) which were *statistically at par* with the genotype, 2016/TODVAR-10 (45.08).
- Significantly maximum total sugar and non-reducing sugar was found in the fruits of the genotype 2016/TODVAR-06 (4.81% and 2.41%) closely followed by 2016/TODVAR-01 (4.31% and 2.4%) and 2016/TODVAR-02 (4.23 % and 2.35%).
- Significantly highest reducing sugar content of tomato fruits was found in Utkal Pallavi (2.73%) and was *statistically at par* with 2016/TODVAR-12 (2.59%), 2016/TODVAR-08 (2.54%), Pusa Gaurav (2.52%), Utkal Deepti (2.45%), Utkal Pragyan (2.40%) and 2016/TODVAR-04 (2.31%).

- The range of the parameters under study varied from 14.37% in days to 1st fruit harvest to maximum value of 236.86% in ascorbic acid
- The general mean values ranged from 0.57 (pericarp thickness) to % of fruit set (82.32).
- The estimation of coefficient of variations ranged from 2.60 (internodal length) to 18.25 (marketable fruit yield plant⁻¹). The C_{Ve} values were observed around 10 % for all characters under study except for and marketable fruit yield plant⁻¹ (18.25).
- The PCV and corresponding GCV values ranged from 5.56 and 1.04 (days to 1st harvest) to 40.63 and 39.4 (number of locules fruit⁻¹).
- The study showed that PCV estimates were low (below 10%) for days to 1st harvest (5.56), % of fruit set (8.88), days to fruit set (8.98) and days to 50% flowering (9.31).
- Larger difference in magnitude of GCV and PCV was observed for characters like days to first fruit harvest (1.04 to 5.56), % of fruit set (5.06-8.88), TSS (9.76-13.33), total fruit yield plant⁻¹ (21.14-30.98), marketable fruit yield plant⁻¹ (22.99-29.35) pericarp thickness (11.13-13.66) and days to 50% flowering (7.63-9.31).
- Relatively lower difference in magnitude of GCV and PCV was observed for characters like total sugar (9.86%), plant height (9.81%), primary branches plant⁻¹ (7.63%), fruit weight (6.76%), flowers cluster⁻¹ (6.40%), number of locules (3.28%), and ascorbic acid (2.32%) and internodal length (0.88%) which indicated that these traits were mostly governed by genetic factors and least influenced by environmental factors.
- Heritability in broad sense varied widely from 32.50 (% of fruit set) to 98.20 (internodal length).
- The characters showing high heritability (>60%) were marketable fruit yield plant⁻¹ (61.30), pericarp thickness (66.30), days to fruit set (67.10), days to 50% flowering (67.20), days to 1st flowering (71.40), fruits plant⁻¹ (77.70), fruit length (82.30), total

sugar (82.90), plant height (83.00), fruit girth (83.30), primary branches plant⁻¹ (86.30), fruit weight (87.70), flowers cluster⁻¹ (88.40), number of locules (93.80), ascorbic acid (95.50) and internodal length (98.20).

- The genetic advance ranged from 0.11 (pericarp thickness) to 21.20 (average fruit weight). GA % of mean was found to be moderate (10-20) for characters like plant height (16.47) and ascorbic acid (18.78). High value (>20%) was recorded for average fruit weight (21.26).
- Marketable fruit yield plant⁻¹ in determinate tomato exhibited positive and significant correlation at genotypic and phenotypic level with plant height (0.45 and 0.31) and primary branches plant⁻¹ (0.51 and 0.38).
- Highest positive direct effect for marketable fruit yield plant⁻¹ was exhibited through average fruit weight (0.334) followed by number of locules (0.204), fruit length (0.143), % of fruit set (0.126), flowers cluster⁻¹ (0.106), days to fruit set (0.102), fruits plant⁻¹ (0.096), primary branches plant⁻¹ (0.070) and plant height at final harvest (0.009).
- Characters like fruit girth (-0.099), days to 1st flowering (-0.085), pericarp thickness (-0.084) and internodal length (-0.070) showed negative direct effect on marketable fruit yield plant⁻¹.
- On the basis of D² analysis 18 genotypes of determinate tomato were grouped into five clusters where Cluster I and II were found to be the largest with five genotypes in each.
- Cluster I included genotypes like 2016/TODVAR-1, 2016/TODVAR-02, 2016/TODVAR-07, 2016/TODVAR-10 and Utkal Pragyan.
- Cluster II included five genotypes such as 2016/TODVAR-05, 2016/TODVAR-11, 2016/TODVAR-12, Pusa Rohini and Pusa-120.
- Cluster- III comprised of three genotypes such as 2016/TODVAR-06, 2016/TODVAR-08, 2016/TODVAR-09 whereas Cluster IV comprises of four genotypes such as 2016/TODVAR-04, Utkal Pallavi, Utkal Deepti and Pusa Gaurav.

- Cluster V comprised of only single genotype (2016/TODVAR-03).
- The highest average D^2 value was observed in cluster IV (103.00) while least intra-cluster distance was observed by cluster III (58.66) having three genotypes.
- Highest inter-cluster distances were observed Cluster III and Cluster II (380.39) while the minimum inter cluster distance were observed between cluster III and I (133.03).
- Cluster I was found superior with respect to internodal length (7.58).
- Cluster II was found to be superior in plant height (75.04), fruit girth (16.79), primary branches plant⁻¹ (4.65), fruit length (7.97), pericarp thickness (0.60), number of locules (4.03), marketable fruit yield plant⁻¹ (0.89).
- Cluster III was superior in performance for characters like number of flowers cluster⁻¹ (7.26), pericarp thickness (0.60) and average fruit weight (73.87).
- Cluster V comprising of only one genotype (2016/TODVAR-03) was found superior for characters like % of fruit set (89.69), days to fruit set (35.00), days to 1st flowering (23.00) and fruits plant⁻¹ (17.62).

CONCLUSION

1. Analysis of variance for 20 different traits showed significantly wide genetic variations among 18 determinate genotypes. The traits like plant height, primary branches plant⁻¹, internodal length, days to 1st flowering, flowers cluster⁻¹, fruit weight, fruit length, fruit girth, number of locules, fruits plant⁻¹, ascorbic acid and total sugar showed closeness between PCV with corresponding GCV which clearly indicated that these traits on selection is less influenced by environmental factors. Hence, simple selection method can be adopted to develop a desirable genotype. Moreover, the characters like internodal length, average fruit weight, number of locules, fruits plant⁻¹, marketable fruit yield plant⁻¹, ascorbic acid and total sugar showed high heritability along with moderate to high GA as % of mean. Therefore, simple selection of such characters will be very effective in determinate tomato breeding programme as these are controlled by additive gene action.

2. Characters like plant height, primary branches plant⁻¹, number of locules were important correlated characters contributing towards marketable fruit yield plant⁻¹ in determinate tomato. Therefore, simultaneous improvement in these characters will be highly beneficial for development of desirable genotypes of determinate tomato. Highest positive direct effect for marketable fruit yield plant⁻¹ was exhibited through average fruit weight followed by number of locules, fruit length, % of fruit set, flowers cluster⁻¹, days to fruit set, fruits plant⁻¹, primary branches plant⁻¹ and plant height at final harvest. Hence, direct selection of the above mentioned traits would be effective to enhance yield of determinate tomato. A very low residual effect of 0.448 indicated that most of the important characters contributed towards yield through both direct and indirect path in the present study.
3. The highest average D² value was observed in cluster IV (103.00) while least intra-cluster distance was observed by cluster III (58.66) having three genotypes. Highest inter-cluster distances were observed for Cluster III and Cluster II (380.39) which implies that crosses involving genotypes from cluster III (2016/TODVAR-06, 2016/TODVAR-08, 2016/TODVAR-09) and cluster II (2016/TODVAR-05, 2016/TODVAR-11, 2016/TODVAR-12, Pusa 120, Pusa Rohini) can produce desirable recombinants with maximum hybrid vigour in future or further selection in segregating generations in determinate tomato.
4. The genotypes 2016/TODVAR-12 (414.27 qha⁻¹) was identified as best determinate tomato genotype having significantly higher vegetative growth, yield and quality attributes suitable for Bhubaneswar condition. However, the other better performing genotypes under Bhubaneswar conditions identified were Pusa Rohini (342.28 qha⁻¹), 2016/TODVAR-05 (340.05 qha⁻¹), Pusa Gaurav (319.42 qha⁻¹) and Pusa 120 (303.85 qha⁻¹) in order of preference. These genotypes may be further evaluated for their fruit yield stability in future.



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