

**GENETIC STUDIES ON NEUTRACEUTICALS, INDUSTRIAL
QUALITY TRAITS AND YIELD COMPONENTS OF TOMATO
(*Solanum lycopersicum* L.)**

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DHARWAD – 580 005**

JULY, 2016

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QUALITY TRAITS AND YIELD COMPONENTS OF TOMATO
(*Solanum lycopersicum* L.)**

*Thesis submitted to the
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IN

GENETICS AND PLANT BREEDING

BY

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CERTIFICATE

This is to certify that the thesis entitled "GENETIC STUDIES ON NEUTRACEUTICALS, INDUSTRIAL QUALITY TRAITS AND YIELD COMPONENTS OF TOMATO (*Solanum lycopersicum* L.)" submitted by Mr. ANJAN GOWDA. S for the degree of MASTER OF SCIENCE (AGRICULTURE) in GENETICS AND PLANT BREEDING, to the University of Agricultural Sciences, Dharwad is a record of research work done by his during the period of her study in this university under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

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**DHARWAD
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(ANJAN GOWDA S.)

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1. INTRODUCTION

Tomato (*Solanum lycopersicum* L.) ($2n = 2x = 24$) is a self-pollinated vegetable crop grown widely all over the world and it belongs to solanaceae family. It is native of Peru-Ecuador region (Rick, 1969). Tomato is a typical day neutral plant and self-pollinated, but certain percentage of cross-pollination also occurs (Hewilt and Ho, 1988).

India is the second largest tomato producer in the world after China, which contributes to 11 % of the world tomato production. The area and production of tomato in India was about 0.77 million hectare and 16.38 million tones, respectively with an average productivity of 21.4 tonnes/ ha. Karnataka ranks second to Andhra Pradesh with an area of 64.3 thousand hectare, with the production and productivity of 2.034 million tonnes and 31.7 tonnes/ ha respectively (Anon., 2015).

Tomato is used directly as raw vegetable in the sandwiches, preparation of juice, soup, salad etc. (Joshi and Kohli, 2006). It is a very good appetizer and its soup is said to be a good remedy for patients suffering from constipation. Tomato is a moderate nutritional crop and is considered as an important source of vitamin A, vitamin C and several minerals. Under Indian condition, the fruits are mainly consumed either as raw or in the preparation of sambar, chatni, pickles etc.

Lycopene is the most abundant carotenoid in tomatoes with concentrations ranging from 0.9–4.2 mg/100 g depending upon the variety. Tomato sauce and ketchup are concentrated sources of lycopene compared to unprocessed tomatoes. Lycopene is acyclic and lacks a bionone ring, and has no pro-vitamin A activity. The extended conjugated polyene chain of lycopene is an electron-rich system, susceptible to attack by electrophilic reagents. Therefore, carotenoids like lycopene are unstable and highly reactive towards oxygen and free radicals. This reactivity of lycopene is the basis for its anti-oxidant activity in biological systems (Paola *et al.*, 2011).

It is reported by many researchers that lycopene has potential human health benefits. It reduces the risks of nervous system problems, heart disease, cancer and obesity. Similarly, it is indicated that lycopene, prevents from skin disease induced by UV-light. Lycopene protects human skin from various cancers and cardiovascular disease. High tomato or lycopene consumption reduces the risk of prostate gland cancer (Jiregna, 2013). While, high β -carotene reduces risk of night blindness. Soluble solids, acidity and pH play important role in deciding the flavor and quality of tomato. Tomatoes with high TSS and low pH are preferred in processing industry thus favoring higher price for farmers particularly at the time of glut in the market. In order to exploit the potential human health benefits of lycopene, it is very important to enhance its concentration through genetic manipulation.

Creation and utilization of variability using proper breeding procedures is a prerequisite for the genetic improvement of any crop. Assessment of genetic variation and degree of transmission of desirable characters is helpful for planning a sound breeding programme. In this regard it is necessary to evaluate variability and nature of association among the various plant characters, while partitioning the total variability into heritable and non-heritable components which enables to know whether the superiority of genetic advance could expected after selection (Robinson *et al.*, 1949). Generally the amount of variability generated is more in the early segregating generations as compared to later generations. The nature and magnitude of variability released in F_2 population helps in identifying the segregants which can be tested for their combining ability in advanced generation by crossing them with suitable testers to form heterotic pools. This helps in identifying good hybrids or to isolate best parental lines for hybridization.

Selection based on multiple traits is always better than selection based on yield alone. Since yield is a quantitative character controlled by many genes, an adequate knowledge about the magnitude and degree of association of yield with its attributing characters is of great significance to the breeders, through which they can clearly understand the strength of correlated traits, when they have to exercise selection for simultaneous improvement of more than one character. However, correlation alone does not provide information on the contribution of related characters, which necessitates the study of cause and effect relationship of different characters among themselves. Therefore, the path analysis depicts the exact relationship of characters there by providing more information than correlation.

Keeping these things in the view present study is planned to estimate the extent of genetic variability in the segregating populations of tomato and to find variability and diversity for nutraceuticals and industrial quality trait in popular hybrids, varieties and germplasm with the following objectives.

1. To assess the genetic variability and diversity for lycopene, ascorbic acid, β -carotene (nutraceuticals) total soluble solids, pH (industrial quality traits) and yield components in popular hybrids, varieties and selected germplasm.
2. To assess the variability, character association and direct and indirect effects among the yield and yield components in the F_2 of double cross hybrids.

2. REVIEW OF LITERATURE

The main requirement of plant breeder is genetic variability for starting breeding programme and to increase the yielding ability of the crop plants, after thorough understanding of diversity. The literature pertaining to the various features of present investigation has been thoroughly reviewed and has been presented under the following headings.

- 2.1 Genetic diversity analysis
- 2.2 Genetic variability studies
- 2.3 Correlation studies for yield and yield attributing traits
- 2.4 Path analysis for yield and yield attributing traits

2.1 Genetic diversity analysis

For getting high heterosis or for recovering transgressive segregants, parents chosen for hybridization need to be genetically diverse or distant. The cultivars from widely separated localities have been usually included in the hybridization programme, presuming the presence of genetic divergence and maximum likelihood of recovering promising segregants. As per expectations this has not yielded very satisfactory results. Though eco-geographical diversity has been regarded as a reasonable index of genetic diversity (Vavilov, 1926; Moll *et al.*, 1962 and Ram and Panwar, 1970) it was reported later that, there may not exist any parallelism between geographic distribution and genetic diversity (Sachan and Sharma, 1971 and Peter and Rai, 1976) in tomato.

Assessment of genetic diversity using quantitative traits has been of prime importance in many cases particularly in differentiating well defined populations. Several methods of divergence analysis based on quantitative traits have been proposed to suit various objectives, of which Mahalanobis generalised distance (Mahalanobis, 1936) is a good method widely used in self and often-cross pollinated crops to establish the genetic divergence among genotypes.

It is a very sensitive and potent biometrical tool in quantifying the degree of divergence between biological populations and also to assess the relative contribution of different components to the total divergence both at inter and intra cluster levels (Nair and Mukherjee, 1960; Khanna and Misra, 1977 and Singh and Singh, 1980). The concept of Mahalanobis's D^2 statistic as a measure of genetic divergence was used for the first time in the field of plant breeding by Nair and Mukherjee (1960) in the classification of natural and plantation teak.

Sachan and Sharma (1971) while studying genetic divergence in 20 varieties of tomato from diverse geographical sources reported substantial divergence of an indigenous material 'Jaipuri' from both exotic and other indigenous stocks and established its utility for hybridization programmes. Tomato genotypes were grouped into four clusters and it was also concluded that, genetic divergence was not found to be related with geographic diversity in this crop. In the relative ranking of different components of D^2 , the authors found that, the maximum contribution to the total divergence was by stem length, followed by number of branches, number of inflorescence and number of fruits per plant.

Chaurasia and Major Singh (1998) evaluated 71 genotypes during 1993-94 and 1994-95. Based on Mahalanobis's D^2 values, genotypes were grouped into 9 clusters in 1993-94 and 10 clusters in 1994-95. Fruit weight showed maximum contribution to the genetic diversity in both years followed by plant height.

Dharmatti *et al.* (2001) studied genetic divergence for 402 summer tomato lines using multivariate analysis method. The 402 lines were grouped into 4 clusters based on similarities of D^2 values. Considerable diversity within and between the clusters was observed and the characters like tomato leaf curl virus resistance, fruit yield per plant and number of white flies per plant contributed maximum to the divergence.

Parthasarathy and Aswath (2002) studied genetic divergence among 23 tomato genotypes. These genotypes were grouped into 5 clusters based on the characters like average yield, medium fruits with average yield, medium fruits with average fruit number (cluster 1), more fruit number of cherry type with tall plants (cluster 2), plants which were high yielders with medium fruit weight (cluster 3), vigorous plants with very small fruits of *Lycopersicon pimpinellifolium* (cluster 4) and high yielders distance with all the groups. For high yield with good fruit size and maximum number of fruits, crosses involving cluster 3 and 5 were recommended. Peter and Rai (1976) reported that, plant height and locule number greatly contributed to diversity. Sachan and Sharma (1971) found that, plant height, number of branches and number of fruits contributed for divergence.

Prashanth (2003) studied 67 genotypes of tomato which were grouped into seven clusters. The cluster IV showed maximum intracluster distance and the maximum intercluster distance was observed between cluster V and VI. Among 12 characters included in D^2 analysis, number of seeds per fruit contributed maximum to genetic diversity followed by average fruit weight, number of fruits per plant and fruit volume.

Mahesh *et al.* (2006) studied 30 genetically diverse genotypes of tomato for genetic diversity. The genotypes were grouped into a cluster irrespective of geographical divergence with the maximum number of genotypes included in cluster II was 11. The cluster mean indicated that day to 50 % flowering, plant height, number of branches per plant, number of clusters per plant, number of fruits per cluster, fruit weight, fruit length, fruit diameter, number of locules per fruit, number of seeds per fruit, fruit set percentage, fruits per plant and yield per plant were important characters contributed towards the maximum genetic divergence. The maximum genetic distance was observed between clusters V1 and IX (8132.17), whereas it was minimum between clusters I and IV (405.05). However, no close correspondence was evident between geographical distribution and genetic divergence as estimated by D^2 statistics.

Tomato germplasm collected from different sources and lines developed through pedigree method of breeding were assessed by Ravindra *et al.* (2012) based on Mahalanobis D^2 analysis. Totally 67 genotypes were grouped into 7 clusters where, maximum of 44 genotypes entered in cluster I, followed by 11 genotypes in cluster II, 7 genotypes in cluster IV, two genotypes in cluster III and the clusters V, VI and VII had solitary genotype each.

Khapte and Jansirani (2014b) conducted genetic diversity study in twenty four tomato (*Solanum lycopersicum* L.) genotypes. The genotypes were grouped into eight clusters based on yield contributing traits. Cluster VI contained maximum number of genotypes (8) followed by cluster V and VII having three genotypes each and remaining clusters were having two genotypes each. Maximum intra cluster distance was recorded by cluster VIII (219.73) followed by cluster VII (169.84), cluster V (162.80) and Cluster VI (157.31) which revealed the existence of considerable genetic divergence

among the genotypes of the respective clusters. The highest inter cluster distance of (375.75) was observed between cluster V and VIII, followed by cluster V and VII (304.85) and cluster III and V (304.81), revealing enormous diversity between genotypes belonging to respective pairs of the clusters.

Using Mahalanobis D^2 statistics method, the 27 genotypes were grouped into nine clusters by Manoj *et al.* (2014), indicating the presence of diversity for different traits. The cluster I had the highest number containing 16 genotypes followed by cluster III and VII containing three and two genotypes respectively. However, the 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, the cluster VIII with single genotype ranked first and appeared to contain the potential genotype. The cluster VIII and II registered higher plant height. The genotypes included in clusters V and VIII took less number of days to 50 % flowering (29.67). The cluster III registered high fruit yield per plant (1004.60), average fruit weight (38.07), and ascorbic acid (28.7) can be utilised in breeding programme for enhancing their respective characters. The cluster IX had maximum number of fruits per plant (40.53).

The genetic diversity among 50 genotypes in tomato studied by Anita *et al.* (2014) showed highly significant differences among the genotypes for all the characters indicating presence of sufficient amount of variability in all the traits. Mahalanobis D^2 statistics revealed that considerable genetic diversity within and among nine clusters. The characters viz., fruit weight, number of fruits per plant, root length and plant height were the potent factors in differentiating the germplasm of tomato under this study. In addition to the genetic divergence, considering the mean performance, eleven genotypes for fruit yield from I, II, III and IX clusters, eight genotypes for earliness from II, III, IV, VI, VIII and IX clusters, nine genotypes for root length from I, II, III IV and VII clusters and seven genotypes for RDW/SDW from I, III and VIII clusters were superior and they can be used for future breeding programmes.

2.2 Genetic variability studies

2.2.1 Genetic variability studies for Neutraceuticals, Industrial quality traits and yield components

The success of breeding programme depends upon the extent and magnitude of variability existing in the germplasm. Variability may be defined as the amount of variation present among the members of a population or species for one or more characters at genotypic or phenotypic levels. Phenotypic variability is observable, and it includes both genotypic and environmental variation and therefore, it is also called as total variation. Genotypic variation refers to genetic or inherent variability which remains unaltered by environmental conditions. It is measured in terms of genotypic variance and consists of additive, dominance and epistatic components. Environmental variance is measured in terms of error mean variance.

Generally, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are used to assess the extent of variation between two different contrasting characters.

Table 1: Review of literature on mean, range, components of variance, heritability and GAM for different characters in tomato

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
1. Plant height (cm)									
21 genotypes	<i>rabi</i>	99.34	-	-	31.23	30.44	94.70	60.97	Taiana <i>et al.</i> (2015)
43 genotypes	-	101.16	-	-	13.05	12.76	96.00	25.98	Ravindra <i>et al.</i> 2015)
45 genotypes	<i>rabi</i>	87.04	70.37	120.00	13.19	12.14	84.81	23.03	Khaidem <i>et al.</i> (2014)
24 genotypes	-	76.28	62.70	90.67	11.74	10.03	72.90	22.61	Khapte and Jansirani (2014a)
5 genotypes	-	56.13	-	-	22.40	18.56	68.69	-	Osekita and Ademiluyi (2014)
25 genotypes	summer	-	-	-	27.00	25.59	89.00	49.20	Muhammad <i>et al.</i> (2013)
37 genotypes	<i>kharif</i>	99.86	48.33	153.63	25.00	23.17	86.00	44.23	Adhishankar <i>et al.</i> (2013)
19 genotypes		95.89	-	-	19.84	17.41	77.00	31.48	Rajashekar <i>et al.</i> (2013)
21 genotypes	<i>rabi</i>	84.05	-	-	32.45	32.01	-	-	Jiregna (2013)
11 Inbred lines	<i>rabi</i>	114.45	71.40	153.6	22.66	18.62	68.00	34.40	Islam <i>et al.</i> (2012)
30 genotypes	winter	105.22	-	-	34.83	34.36	97.00	69.60	Mohamed <i>et al.</i> (2012)
14 genotypes	-	64.05	40.67	80.63	21.09	18.89	74.40	33.50	Kumar <i>et al.</i> (2011)
10 genotypes	<i>rabi</i>	023.2	20.20	26.00	6.40	5.50	74.20	2.30	Kaushik <i>et al.</i> (2011)
40 exotic hybrids	winter	41.28	22.74	68.50	17.35	12.40	51.08	44.22	Ghosh <i>et al.</i> (2010)
12 genotypes	winter	51.77	-	-	140.16	125.20	89.20	30.23	Haydar <i>et al.</i> (2007)
20 genotypes	<i>kharif</i>	94.31	69.89	122.11	21.72	18.27	70.80	31.56	Golani <i>et al.</i> (2007)
52 genotypes	-	88.14	42.00	150.00	31.72	31.03	95.69	62.54	Pradeep <i>et al.</i> (2001)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
2. Number of primary branches per plant									
21 genotypes	<i>rabi</i>	9.39	-	-	20.98	15.61	55.37	23.93	Taiana <i>et al.</i> (2015)
43 genotypes	-	9.63	-	-	17.62	13.13	56.00	20.16	Ravindra <i>et al.</i> (2015)
45 genotypes	<i>rabi</i>	4.11	3.03	5.70	14.96	13.15	77.33	23.84	Khaidem <i>et al.</i> (2014)
24 genotypes	-	5.22	3.26	8.47	26.05	19.81	57.80	39.77	Khapte and Jansirani (2014a).
37 genotypes	<i>kharif</i>	8.11	58.33	10.60	16.32	15.11	86.00	28.83	Adhishankar <i>et al.</i> (2013)
19 genotypes	-	16.58	-	-	24.68	18.71	57.50	29.21	Rajashekar <i>et al.</i> (2013)
14 landraces	summer	4.83	3.27	6.63	22.69	22.20	95.83	38.30	Firas <i>et al.</i> (2012)
30 genotypes	winter	10.15	-	-	24.33	20.39	70.00	35.07	Mohamed <i>et al.</i> (2012)
40 exotic hybrids	winter	11.27	5.00	22.00	28.06	21.68	59.68	306.20	Ghosh <i>et al.</i> (2010)
20 genotypes	<i>kharif</i>	4.86	3.47	6.27	18.40	13.04	50.20	19.14	Golani <i>et al.</i> (2007)
30 genotypes	winter	7.10	5.30	10.50	37.61	35.80	90.60	71.83	Dhankhar and Dhankhar (2006)
14 cultivars (1 adopted cultivar)	autumn	7.75	5.30	9.40	15.58	15.51	99.10	31.80	Samadia <i>et al.</i> (2006)
6 include pure lines	<i>kharif</i>	9.40	7.67	12.33	16.12	10.68	43.90	14.57	Kumar <i>et al.</i> (2006)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
3. Number of clusters per plant									
45 genotypes	rabi	19.46	11.93	38.43	33.04	31.29	89.07	61.04	Khaidem <i>et al.</i> (2014)
5 genotypes	-	7.61	-	-	44.08	7.08	2.60	-	Osekita and Ademiluyi (2014)
19 genotypes	-	12.97	-	-	42.51	45.32	88.00	82.15	Rajashekar <i>et al.</i> (2013)
11cherry tomato genotypes	rabi	25.44	13.90	42.40	50.01	45.33	82.00	22.60	Islam <i>et al.</i> (2012)
32 genotypes	kharif	17.25	6.20	31.33	37.77	33.38	78.10	60.75	Veerashetty (2004)
42 genotypes	summer	-	-	-	34.60	27.35	65.52	44.56	Arun and Veraragavathatham (2005)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
4. Number of fruits per plant									
21 genotypes	rabi	121.10	-	-	71.43	69.73	95.30	140.23	Taiana <i>et al.</i> (2015)
43 genotypes	-	41.47	-	-	10.28	8.86	74.00	15.74	Ravindra <i>et al.</i> (2015)
45 genotypes	rabi	34.70	20.01	112.41	65.16	64.69	98.55	132.33	Khaidem <i>et al.</i> (2014)
24 genotypes	-	36.74	26.32	54.64	17.76	17.30	95.00	44.52	Khapte and Jansirani (2014a)
5 genotypes	-	39.25	-	-	52.04	19.11	13.32	-	Osekita and Ademiluyi (2014)
25 genotypes	summer	-	-	-	31.85	26.60	70.00	45.52	Muhammad <i>et al.</i> (2013)
59 genotypes	rabi	-	19.02	171.00	16.42	11.52	49.22	16.65	Reddy <i>et al.</i> (2013)
11 Inbred lines	rabi	153.00	44.00	291.00	68.34	58.08	72.00	109.60	Islam <i>et al.</i> (2012)
19 genotypes	-	44.92	-	-	31.93	27.51	74.20	48.82	Rajshekar <i>et al.</i> (2013)
21 genotypes	rabi	23.64	-	-	57.24	54.33	-	-	Jiregna (2013)
14 landraces	summer	62.45	20.13	184.97	92.67	89.11	92.47	150.81	Firas <i>et al.</i> (2012)
14 genotypes	-	43.09	27.33	64.67	254.06	20.10	64.40	33.23	Kumar <i>et al.</i> (2011)
60 genotypes	kharif	15.45	10.67	28.60	29.15	24.52	70.00	42.65	Dar <i>et al.</i> (2011)
40 exotic hybrids	winter	38.42	11.86	114.00	65.38	57.30	76.79	269.23	Ghosh <i>et al.</i> (2010)
60 genotypes	-	15.45	-	-	29.15	24.52	70.00	42.60	Ruskar and Jag (2010)
12 genotypes	winter	19.04	-	-	1810.15	1796.58	99.25	199.36	Haydar <i>et al.</i> (2007)
30 genotypes	winter	40.10	19.50	65.00	32.23	31.30	95.00	61.18	Dhankhar and Dhankhar (2006)
52 genotypes	-	30.86	7.00	136.00	68.21	58.07	72.50	101.86	Pradeep <i>et al.</i> (2001)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
5. Number of fruits per cluster									
43 genotypes	-	4.58	-	-	15.61	14.20	83.00	26.30	Ravindra <i>et al.</i> (2015)
5 genotypes	-	27.01	-	-	76.06	31.18	16.57	-	Osekita and Ademiluyi (2014)
19 genotypes	-	4.39	-	-	17.54	17.52	99.70	36.03	Rajashekar <i>et al.</i> (2013)
30 genotypes	<i>rabi</i>	4.70	-	-	22.10	15.29	68.00	30.80	Mohamed <i>et al.</i> (2012)
35 genotypes	summer	5.02	3.92	6.53	14.08	12.57	79.00	1.16	Anjum <i>et al.</i> (2009)
14 cultivrars(1 adapted cultivar)	utumn	2.45	1.48	4.51	41.86	41.83	99.80	86.10	Samadia <i>et al.</i> (2006)
29 hybrids	<i>kharif</i>	-	-	-	20.15	19.74	95.90	39.84	Mayavel <i>et al.</i> (2005)
32 genotypes	<i>kharif</i>	4.33	3.23	5.97	15.25	13.53	78.80	24.71	Veerashetty (2004)
40 genotypes	summer	3.39	2.67	4.47	19.98	10.54	27.82	11.47	Aradhana and Singh (2003)
67 genotypes	<i>rabi</i>	4.47	3.07	6.00	13.67	11.53	71.10	20.10	Prashanth (2003)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
6. Average fruit weight (g)									
43 genotypes	-	92.17	-	-	7.020	6.23	79.00	11.39	Ravindra <i>et al.</i> (2015)
21 genotypes	<i>rabi</i>	34.02	-	-	55.63	52.18	87.98	100.82	Taiana <i>et al.</i> (2015)
45 genotypes	<i>rabi</i>	53.70	21.35	71.33	22.68	21.55	90.28	42.19	Khaidem <i>et al.</i> (2014)
5 genotypes	-	0.66	-	-	104.97	90.91	75.00	-	Osekita and Ademiluyi (2014)
24 genotypes	-	61.00	44.50	86.33	16.97	15.55	84.00	37.63	Khapte and Jansirani (2014a)
25 genotypes	summer	-	-	-	28.38	26.14	85.00	49.25	Muhammad <i>et al.</i> (2013)
37 genotypes	<i>kharif</i>	73.04	40.20	105.53	22.88	22.76	99.00	46.66	Adhishankar <i>et al.</i> (2013)
59 genotypes	<i>rabi</i>	-	15.17	119.20	23.32	21.45	84.65	40.66	Reddy <i>et al.</i> (2013)
19 genotypes	-	62.26	-	-	26.91	25.66	90.90	50.40	Rajshekar <i>et al.</i> (2013)
30 genotypes	winter	55.96	-	-	49.05	48.55	92.00	92.90	Mohamed <i>et al.</i> (2012)
11 Inbred lines	<i>rabi</i>	16.28	5.60	36.50	74.23	68.16	84.00	134.30	Islam <i>et al.</i> (2012)
14 landraces	summer	79.71	11.02	130.26	52.62	47.80	83.16	77.02	Firas <i>et al.</i> (2012)
60 genotypes	<i>kharif</i>	57.04	21.58	87.85	28.01	24.96	80.00	45.93	Dar <i>et al.</i> (2011)
52 genotypes	-	58.12	1.40	115.00	42.29	39.74	88.32	76.95	Pradeep <i>et al.</i> (2001)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
7. Fruit yield per plant (kg)									
43 genotypes	-	3.53	-	-	16.25	15.08	95.00	31.65	Ravindra <i>et al.</i> (2015)
21 genotypes	<i>rabi</i>	1.76	-	-	37.36	33.95	82.58	63.55	Taiana <i>et al.</i> (2015)
45 genotypes	<i>rabi</i>	0.80	0.54	1.30	23.55	21.88	86.33	41.87	Khaidem <i>et al.</i> (2014)
24 genotypes	-	1.91	0.96	3.07	29.44	27.85	89.50	69.53	Khapte and Jansirani (2014a)
25 genotypes	summer	-	-	-	28.73	24.92	75.00	43.76	Muhammad <i>et al.</i> (2013)
37 genotypes	<i>kharif</i>	2.44	1.00	3.90	31.65	31.29	89.00	63.70	Adhishankar <i>et al.</i> (2013)
59 genotypes	<i>rabi</i>	-	0.18	5.63	30.57	21.05	47.41	29.85	Reddy <i>et al.</i> (2013)
19 genotypes	-	1.21	-	-	46.13	40.04	75.40	71.61	Rajshekar <i>et al.</i> (2013)
21 genotypes	<i>rabi</i>	0.88	-	-	50.74	43.94	-	-	Jiregna (2013)
11 Inbred lines	<i>rabi</i>	1.59	1.24	1.89	18.49	12.40	31.40	7.50	Islam <i>et al.</i> (2012)
14 landraces	summer	2.52	1.57	3.68	23.25	16.95	53.06	21.83	Firas <i>et al.</i> (2012)
30 genotypes	winter	1.59	-	-	39.24	25.91	43.00	33.90	Mohamed <i>et al.</i> (2012)
40 exotic hybrids	winter	2.70	0.64	9.11	69.40	60.39	75.71	4016.15	Ghosh <i>et al.</i> (2010)
52 genotypes	-	1.20	0.08	2.37	40.20	31.28	60.54	50.14	Pradeep <i>et al.</i> (2001)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
8. Number of locules/ fruit									
5 genotypes	-	3.44	-	-	27.27	9.64	12.50	-	Osekita and Ademiluyi (2014)
24 genotypes		2.54	2.00	4.00	22.65	15.26	45.40	27.13	Khapte and Jansirani (2014a)
37 genotypes	<i>kharif</i>	4.40	2.33	6.50	19.65	17.13	76.00	30.77	Adhishankar <i>et al.</i> (2013)
20 genotypes	late <i>kharif</i>	4.04	2.33	6.44	32.37	29.64	83.80	55.94	Golani <i>et al.</i> (2007)
6 include pure Lines	<i>kharif</i>	5.21	3.33	8.33	30.17	20.45	46.00	28.60	Kumar <i>et al.</i> (2011)
34 genotypes	summer	3.11	2.00	5.66	33.30	26.28	62.28	13.32	Upadhyay <i>et al.</i> (2005)
67 genotypes	<i>rabi</i>	3.46	2.20	5.87	24.22	25.75	88.40	46.98	Prashanth (2003)
40 genotypes	summer	3.35	2.33	5.42	22.83	17.58	59.28	27.88	Aradhana and Singh (2003)
32 genotypes	<i>kharif</i>	4.14	2.73	5.73	16.97	11.07	42.60	14.97	Veershetty (2004)
52 genotypes	-	2.94	2.00	7.00	39.93	38.45	92.76	76.29	Pradeep <i>et al.</i> (2001)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
9. Polar length (cm)									
21 genotypes	<i>rabi</i>	3.50	-	-	25.57	23.13	81.78	43.088	Taiana <i>et al.</i> (2015)
24 genotypes		2.54	2.00	4.00	22.65	15.26	45.40	27.13	Khapte and Jansirani (2014a)
25 genotypes	summer	-	-	-	12.81	12.25	91.00	23.94	Muhammad <i>et al.</i> (2013)
37 genotypes	<i>kharif</i>	4.33	3.00	6.10	15.47	13.97	82.00	25.98	Adhishankar <i>et al.</i> (2013)
19 genotypes	-	4.71	-	-	12.99	11.48	78.10	20.91	Rajshekar <i>et al.</i> (2013)
21 genotypes	<i>rabi</i>	-	-	-	19.62	17.92	-	-	Jiregna (2013)
11 Inbred lines	<i>rabi</i>	3.85	3.04	5.00	27.30	12.04	19.45	14.20	Islam <i>et al.</i> (2012)
14 genotypes	-	4.03	3.46	4.90	13.05	8.89	43.40	12.16	Kumar <i>et al.</i> (2011)
20 genotypes	late <i>kharif</i>	4.04	2.33	6.44	32.37	29.64	83.80	55.94	Golani <i>et al.</i> (2007)
6 include pure Lines	<i>kharif</i>	5.21	3.33	8.33	30.17	20.45	46.00	28.60	Kumar <i>et al.</i> (2006)
34 genotypes	summer	3.11	2.00	5.66	33.30	26.28	62.28	13.32	Upadhyay <i>et al.</i> (2005)
32 genotypes	<i>kharif</i>	4.14	2.73	5.73	16.97	11.07	42.60	14.97	Veershetty (2004)
40 genotypes	summer	3.35	2.33	5.42	22.83	17.58	59.28	27.88	Aradhana and Singh (2003)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
10. Equatorial length (cm)									
43 genotypes	-	5.40	-	-	13.60	13.29	95.00	26.74	Ravindra <i>et al.</i> (2015)
21 genotypes	<i>rabi</i>	3.70	-	-	24.78	22.08	84.66	43.22	Taiana <i>et al.</i> (2015)
45 genotypes	<i>rabi</i>	5.23	2.78	6.47	15.18	14.14	86.78	27.15	Khaidem <i>et al.</i> (2014)
24 genotypes		2.54	2.00	4.00	22.65	15.26	45.40	27.13	Khapte and Jansirani (2014a)
25 genotypes	summer	-	-	-	16.64	16.03	93.00	32.13	Muhammad <i>et al.</i> (2013)
37 genotypes	<i>kharif</i>	5.28	3.43	6.97	13.95	13.56	95.00	27.18	Adhishankar <i>et al.</i> (2013)
19 genotypes	-	3.47	-	-	15.18	9.96	43.10	13.47	Rajshekar <i>et al.</i> (2013)
21 genotypes	<i>rabi</i>	-	-	-	19.02	17.76	-	-	Jiregna (2013)
11 Inbred lines	<i>rabi</i>	3.00	2.05	4.50	29.03	27.07	86.84	53.80	Islam <i>et al.</i> (2012)
14 genotypes	-	4.84	3.92	5.83	15.31	10.40	46.10	14.46	Kumar <i>et al.</i> (2011)
6 include pure Lines	<i>kharif</i>	5.21	3.33	8.33	30.17	20.45	46.00	28.60	Kumar <i>et al.</i> (2006)
20 genotypes	late <i>kharif</i>	4.04	2.33	6.44	32.37	29.64	83.80	55.94	Golani <i>et al.</i> (2007)
34 genotypes	summer	3.11	2.00	5.66	33.30	26.28	62.28	13.32	Upadhyay <i>et al.</i> (2005)
32 genotypes	<i>kharif</i>	4.14	2.73	5.73	16.97	11.07	42.60	14.97	Veershetty (2004)
40 genotypes	summer	3.35	2.33	5.42	22.83	17.58	59.28	27.88	Aradhana and Singh (2003)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
11. Lycopene (mg/100 g of fruit)									
43 genotypes	-	5.86	-	-	23.16	19.62	72.00	34.24	Ravindra <i>et al.</i> (2015)
37 genotypes	<i>kharif</i>	5.65	2.07	11.73	41.73	41.11	97.00	83.41	Adhishankar <i>et al.</i> (2013)
21 genotypes	<i>rabi</i>	1.94	-	-	46.21	43.22	-	-	Jiregna (2013)
14 genotypes	-	4.19	2.07	5.83	31.09	29.87	87.70	2.42	Kumar <i>et al.</i> (2011)
60 genotypes	-	3.08	-	-	20.99	20.19	92.00	39.90	Ruskar and jag (2010)
12. β-carotene (mg/100 g of fruit)									
60 genotypes	-	1.64	-	-	25.22	25.02	98.00	50.90	Ruskar and jag (2010)
13. Ascorbic acid (mg/100 g of fruit)									
43 genotypes	-	0.56	-	-	12.66	9.97	62.00	16.17	Ravindra <i>et al.</i> (2015)
37 genotypes	<i>kharif</i>	24.42	14.67	40.67	27.50	27.49	1.00	56.61	Adhishankar <i>et al.</i> (2013)
59 genotypes	<i>rabi</i>	-	8.67	38.53	12.90	8.45	42.99	11.42	Reddy <i>et al.</i> (2013)
19 genotypes	-	24.38	-	-	21.04	18.96	81.20	35.19	Rajasekhar <i>et al.</i> (2013)
14 genotypes	-	28.40	14.13	39.00	26.03	24.14	86.00	46.13	Kumar <i>et al.</i> (2011)
60 genotypes	-	27.04	-	-	15.72	15.21	94.00	30.9	Ruskar and jag (2010)

Material used for the study	Season of evaluation	Mean	Range		Phenotypic coefficient of variance (PCV %)	Genotypic coefficient of Variance (GCV %)	Heritability (h ² _{bs} %)	Genetic advance as per cent mean (GAM)	References
			Min.	Max.					
14. TSS (Brix°)									
43 genotypes	-	5.86	-	-	23.16	19.62	72.00	34.24	Ravindra <i>et al.</i> (2015)
37 genotypes	<i>kharif</i>	5.65	2.07	11.73	41.73	41.11	97.00	83.41	Adhishankar <i>et al.</i> (2013)
21 genotypes	<i>rabi</i>	1.94	-	-	46.21	43.22	-	-	Jiregna (2013)
14 genotypes	-	4.19	2.07	5.83	31.09	29.87	87.70	2.42	Kumar <i>et al.</i> (2011)
60 genotypes	-	3.08	-	-	20.99	20.19	92.00	39.90	Ruskar and jag (2010)
15. Total acidity (%)									
43 genotypes	-	0.56	-	-	12.66	9.97	62.00	16.70	Ravindra <i>et al.</i> (2015)
37 genotypes	<i>kharif</i>	5.65	2.07	11.73	41.73	41.11	97.00	83.41	Adhishankar <i>et al.</i> (2013)
21 genotypes	<i>rabi</i>	1.94	-	-	46.21	43.22	-	-	Jiregna (2013)
15 genotypes	-	0.48	0.30	0.73	29.09	28.82	-	58.33	Madhurina <i>et al.</i> (2012)
14 genotypes	-	0.20	0.09	0.52	62.02	58.70	89.60	115.00	Kumar <i>et al.</i> (2011)
60 genotypes	-	3.08	-	-	20.99	20.19	92.00	39.90	Ruskar and jag (2010)

Heritability is the transmission of characters from parents to offspring. Heritability in a broad sense is the ratio of genotypic variance to total phenotypic variance in percentage. Effectiveness of selection of genotype depends on heritability. Genetic advance (GA) is the improvement over the base population that can be potentially achieved from selection. It is a function of the heritability of the trait, the amount of phenotypic variation and the selection differential (s) that the breeder uses. When high heritability is accompanied with high genetic advance, it indicates additive gene effects and selection may be effective. When low heritability accompanied with low genetic advance, it indicates predominance of environmental effects and selection would be ineffective. High heritability with low genetic advance indicates the importance of non-additive gene effects while low heritability with high genetic advance indicates the importance of additive gene effects. Reviews on variability for yield and yield contributing characters are presented in Table 1.

2.2.2 Genetic variability studies for yield and yield attributing traits in double cross F_2 population

Shobha *et al.* (2004) advanced the F_2 populations of black gram of two three way and one double cross population to F_3 generation through different selection method i.e. bulk, individual plant selection (IPS) and single pod descent (SPD) method. They were compared for relative efficiency in generating desirable variability. SPD method exhibited high variability for plant height, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight and seed yield per plant. High PCV and GCV in the double cross population i.e., (TAU-1 x 169) x (Manikya x 216) was observed for plant height, number of clusters per plant, number of pods per plant and seed yield per plant.

In soybean, Bizeti *et al.* (2002) evaluated in early generations of self-fertilization the potential of single, double and multiple crosses as producers of base population for breeding programme for the traits like number of days to flowering, days to maturity and plant height at flowering and at maturity. The means obtained with the F_3 populations of single crosses, the F_3 populations of double crosses and the F_2 populations of multiple crosses were similar. The best results for grain yield per plant were obtained with the F_3 populations of double crosses. In general, there was no change in the values of genetic variance of the segregating populations, due to the number of parents used in the crosses.

Reddy (2003) carried out an investigation in groundnut segregating population of three single crosses with their corresponding three way crosses and two multiple crosses in order to know the magnitude of genetic variability for shelling percentage, number of kernels per plant, 100 seed weight and days to first flowering. In general, the three-way crosses had higher magnitude of genetic variability as measured by GCV and PCV over single crosses for shelling percentage, number of kernels per plant, 100 seed weight and days to first flowering.

Loganathan and Gopalan (2006) estimated genetic variability in three F_2 generations of cross combination, PI 307942 X GP 270, CO 3 X GP 270 and CO 3 X TNPH 2 of sunflower. High estimates of phenotypic and genotypic coefficients of variation were obtained for 100 seed weight in PI 307942 X GP 270.

Seven F_2 populations of inter sub-specific crosses of rice were evaluated by Vaithiyalingan and Nandarajan (2006) to estimate the variability. The differences between F_2 populations were highly significant for all the characters studied. Among them, grain yield showed high genotypic coefficient of variation followed by spikelet fertility per cent, productive tillers per plant and number of grains per panicle.

Analysis for superior segregants in F_2 for important metric traits in okra by Ajjappa *et al.* (2009) revealed that more number of segregants were released from double cross population BH-16 followed by single cross population BH-13.

Analysis of variance by Gosh *et al.* 2010, revealed significant differences among the populations for plant height, number of fruits per plant, number of flowers per plant, average fruit weight, number of inflorescence per plant, fruit yield per plant and TSS, indicating that considerable variability existed among the populations of tomato.

A study to assess the genetic variability in four single cross and three double cross F_4 and F_5 populations of bhendi by Prakash *et al.* (2013) indicated higher magnitude of variability in double cross populations compared to single cross populations for number of fruits per plant, plant height, internodal length, fruit weight and fruit yield per plant. Moderate variability for fruit length and fruit diameter and low variability for days to first flowering, days to 50 % flowering, number of seeds per fruit and 100-seed weight was also reported

Sharanappa and Mogali 2014, showed that the genotypic coefficient of variation was the highest for number of fruits per plant, followed by number of flowers per plant, average fruit weight, number of inflorescence per plant, and fruit yield per plant, whereas the lowest GCV was found for days to 50 per cent flowering, followed by plant height, number of primary branches per plant, The highest phenotypic coefficient of variation was recorded for number of fruits per plant, followed by number of flowers per plant, number of inflorescence per plant, average fruit weight, number of primary branches per plant, and fruit yield per plant, whereas the lowest PCV was recorded for days to 50 per cent flowering and plant height.

2.3 Correlation studies for fruit yield and its attributing traits

Association of economically important quantitative characters which is statistically determined by correlation coefficient has been quite useful as a basis of selection. Correlation studies provide information that the selection for one character will result in progress for all correlated characters. Thus, the review pertaining to the correlation among the different traits is presented in Table 2 to 11.

2.4 Path analysis for fruit yield and its attributing traits

The studies of simple correlation do not provide an exact picture of relative importance of direct and indirect influence of each of the component character towards the desired character. This can be overcome by following path coefficient analysis technique by further partitioning the correlation coefficient into direct and indirect effects.

Mayavel *et al.* (2005) reported that number of branches per plant had the highest positive direct effect on fruit yield. Whereas plant height, number of fruits per cluster, number of fruits per plants and number of locules per fruit had negative direct effects on fruit yield.

Path analysis by Haydar *et al.* (2007) showed highest direct contribution towards yield was evident through plant height at flowering followed by number of flowers in three cluster/plant and days to flowering. Number of fruits in three cluster/plant had shown high negative direct effect followed by number of leaves at flowering. Path analysis revealed that number of branches/plant was the first component of yield. On the other hand the indirect effect of plant height at flowering via days to flowering is high. High direct effects by fruits per plant and average fruit weight towards yield were reported that obtained highest positive direct effect was found for fruit shape index followed by size of stem end scar on yield/plant.

Golani *et al.* (2007) reported that plant height manifested significant direct negative relationship with fruit yield but its indirect effect via fruit girth was high and positive.

Among the traits studied by Indu *et al.* (2008), the fruit weight exerted very high direct effect upon yield per plant. The direct effect of number of fruits per plant was also appreciably high towards yield per plant.

Path coefficient analysis studies by Gosh *et al.* (2010) found that fruits per plant showed the highest positive direct effect on fruit yield per plant. Flowers per plant also showed positive direct effect on fruit yield per plant. On the other hand, negative direct effect on yield per plant was showed by number of flowers per cluster, fruit clusters per plant and fruit diameter. Where in fruits per cluster and individual fruit weight showed positive direct effect. Days to first flowering, plant height at first flowering, branches per plant and fruit length showed negative direct effect on yield per plant. Plant height at first flowering, fruits per cluster, fruit clusters per plant, flowers per plant and fruits per plant showed significant positive genotypic correlation with yield per plant. The highest indirect effect of fruits per plant was observed with fruit clusters per plant.

Tiwari and Upadhyay (2011) revealed that days to 50 % flowering showed the highest positive direct effect on fruit yield followed by number of locules per fruit, fruit weight. Number of locules per plant showed positive indirect effect on fruit yield through number of branches per plant. Plant height exhibited positive indirect effect on fruit yield via number of locules, fruit weight, days to 50 % flowering and number of branches per plant.

According to Kumar and Dudi (2011), number of fruits per plant, total soluble solids and acidity had positive and direct influence on yield, while number of locules per plant, number of fruits per cluster and flesh thickness had negative direct effects on yield.

Firas *et al.* (2012) revealed that number of fruits per plant had the positive and maximum direct effect on fruit yield per plant and negative indirect effects via number of primary branches per plant and harvest index.

Maximum positive direct effect towards fruit yield per plant as found by Santosh *et al.* (2013) was contributed by average fruit weight followed by number of fruits per plant, pericarp thickness and number of fruits per cluster. The other characters which showed positive direct effects but in small magnitude were ascorbic acid content, number of locules per fruit, days to first flowering, Total soluble solids, days from anthesis to turning stage, plant height, harvest duration and number of seeds per fruit.

Table 2: Correlation of plant height with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Number of primary branches per plant	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
2.	Number of cluster per plant	Positive	Islam <i>et al.</i> (2012)
		Negative	Osekita and Ademiluyi (2013)
3.	Number of fruits per plant	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
		Negative	Osekita and Ademiluyi (2013), Islam <i>et al.</i> (2012)
4.	Number of fruits per cluster	Positive	Santosh <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)
		Negative	Osekita and Ademiluyi (2013)
5.	Average fruits weight	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
		Negative	Osekita and Ademiluyi (2013)
6.	Polar length	Negative	Muhammad <i>et al.</i> (2013)
7.	Equatorial length	Positive	Ravindra <i>et al.</i> (2015), Muhammad <i>et al.</i> (2013)
8.	Fruits yield per plant	Positive	Ravindra <i>et al.</i> (2015), Muhammad <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)

Table 3: Correlation of number of primary branches per plant with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
2.	Number of fruits per plant	Positive	Ravindra <i>et al.</i> (2015), Khaidem <i>et al.</i> (2014), Rajesh <i>et al.</i> (2006), Vinod <i>et al.</i> (2013)
3.	Number of fruits per cluster	Positive	Vinod <i>et al.</i> (2013)
4.	Average fruits weight	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
5.	Equatorial length	Positive	Ravindra <i>et al.</i> (2015)
6.	Fruits yield per plant	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)

Table 4: Correlation of number of cluster per plant with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height	Positive	Islam <i>et al.</i> (2012)
		Negative	Osekita and Ademiluyi (2013)
2.	Number of fruits per plant	Positive	Islam <i>et al.</i> (2012)
		Negative	Osekita and Ademiluyi (2013)
3.	Number of fruits per cluster	Positive	Osekita and Ademiluyi (2013)
4.	Polar length	Negative	Islam <i>et al.</i> (2012)
5.	Equatorial length	Negative	Islam <i>et al.</i> (2012)

Table 5: Correlation of number of fruits per plant with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height (cm)	Positive	Ravindra <i>et al.</i> (2015), Khaidem <i>et al.</i> (2014), Vinod <i>et al.</i> (2013)
		Negative	Osekita and Ademiluyi (2013), Islam <i>et al.</i> (2012)
2.	Number of primary branches per plant	Positive	Ravindra <i>et al.</i> (2015), Khaidem <i>et al.</i> (2014), Rajesh <i>et al.</i> (2006)
3.	Number of cluster per plant	Positive	Islam <i>et al.</i> (2012), Kashif <i>et al.</i> (2013), Santosh <i>et al.</i> (2013)
		Negative	Osekita and Ademiluyi (2013)
4.	Number of fruits per cluster	Positive	Ravindra <i>et al.</i> (2015), Khaidem <i>et al.</i> (2014), Vinod <i>et al.</i> (2013)
		Negative	Osekita and Ademiluyi (2013)
5.	Average fruits weight	Positive	Ravindra <i>et al.</i> (2015), Santosh <i>et al.</i> (2013)
		Negative	Vinod <i>et al.</i> (2013)
6.	Polar length	Negative	Muhammad <i>et al.</i> (2013), Madhurina <i>et al.</i> (2012)
7.	Equatorial length	Positive	Ravindra <i>et al.</i> (2015)
		Negative	Khaidem <i>et al.</i> (2014), Muhammad <i>et al.</i> (2013), Madhurina <i>et al.</i> (2012)
8.	Number of locules	Negative	Madhurina <i>et al.</i> (2012)
9.	Fruits yield per plant	Positive	Ravindra <i>et al.</i> (2015), Monamodi <i>et al.</i> (2013), Muhammad <i>et al.</i> (2013), Kashif <i>et al.</i> (2013), Santosh <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)
		Negative	Rajesh <i>et al.</i> (2006)

Table 6: Correlation of number of fruits per cluster with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height	Positive	Ravindra <i>et al.</i> (2015), Santosh <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)
		Negative	Osekita and Ademiluyi (2013)
2.	Number of primary branches per plant	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
3.	Number of fruits per plant	Positive	Ravindra <i>et al.</i> (2015), Khaidem <i>et al.</i> (2014), Osekita and Ademiluyi (2013), Kashif <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)
4.	Average fruits weight	Positive	Ravindra <i>et al.</i> (2015)
5.	Equatorial length	Positive	Ravindra <i>et al.</i> (2015), Khaidem <i>et al.</i> (2014)
6.	Fruits yield per plant	Positive	Kashif <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)

Table 7: Correlation of average fruit weight with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
2.	Number of primary branches per plant	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
3.	Number of fruits per plant	Positive	Ravindra <i>et al.</i> (2015)
		Negative	Santosh <i>et al.</i> (2013)
4.	Number of fruits per cluster	Positive	Ravindra <i>et al.</i> (2015)
5.	Equatorial length	Positive	Ravindra <i>et al.</i> (2015)
6.	Number of locules	Positive	Osekita and Ademiluyi (2013)
7.	Fruits yield per plant	Positive	Ravindra <i>et al.</i> (2015), Santosh <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)
8.	Tss	Negative	Vinod <i>et al.</i> (2013)

Table 8: Correlation of polar length with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height	Negative	Muhammad <i>et al.</i> (2013)
2.	Number of cluster per plant	Negative	Islam <i>et al.</i> (2012)
3.	Number of fruits per plant	Negative	Muhammad <i>et al.</i> (2013), Patel <i>et al.</i> (2013), Madhurina <i>et al.</i> (2012)
4.	Average fruits weight	Negative	Patel <i>et al.</i> (2013)
5.	Equatorial length	Positive	Islam <i>et al.</i> (2012)
		Negative	Muhammad <i>et al.</i> (2013), Patel <i>et al.</i> (2013)
6.	Number of locules	Negative	Madhurina <i>et al.</i> (2012)
7.	Fruits yield per plant	Positive	Madhurina <i>et al.</i> (2012)
		Negative	Muhammad <i>et al.</i> (2013)
8.	Tss	Negative	Madhurina <i>et al.</i> (2012)

Table 9: Correlation of equatorial length with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height	Positive	Ravindra <i>et al.</i> (2015), Muhammad <i>et al.</i> (2013)
2.	Number of primary branches per plant	Positive	Ravindra <i>et al.</i> (2015)
3.	Number of cluster per plant	Negative	Islam <i>et al.</i> (2012)
4.	Number of fruits per plant	Positive	Ravindra <i>et al.</i> (2015), Patel <i>et al.</i> (2013)
		Negative	Muhammad <i>et al.</i> (2013), Madhurina <i>et al.</i> (2012)
5.	Number of fruits per cluster	Positive	Ravindra <i>et al.</i> (2015)
		Negative	Khaidem <i>et al.</i> (2014)
6.	Average fruits weight	Positive	Ravindra <i>et al.</i> (2015), Patel <i>et al.</i> (2013)
7.	Polar length	Positive	Islam <i>et al.</i> (2012)
		Negative	Muhammad <i>et al.</i> (2013)
8.	Number of locules	Positive	Madhurina <i>et al.</i> (2012)
9.	Fruits yield per plant	Positive	Muhammad <i>et al.</i> (2013)

Table 10: Correlation of number of locules with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Number of fruits per plant	Negative	Madhurina <i>et al.</i> (2012)
2.	Average fruits weight	Positive	Osekita and Ademiluyi (2013)
3.	Polar length	Negative	Madhurina <i>et al.</i> (2012)
4.	Equatorial length	Positive	Madhurina <i>et al.</i> (2012)
5.	Fruits yield per plant	Positive	Rajesh <i>et al.</i> (2006)
		Negative	Madhurina <i>et al.</i> (2012)

Table 11: Correlation of fruit yield per plant with other component characters

Sl. No.	Characters	Nature of correlation	References
1.	Plant height	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
2.	Number of primary branches per plant	Positive	Ravindra <i>et al.</i> (2015), Vinod <i>et al.</i> (2013)
3.	Number of cluster per plant	Positive	Kashif <i>et al.</i> (2013)
4.	Number of fruits per plant	Positive	Ravindra <i>et al.</i> (2015), Rajesh <i>et al.</i> (2006), Kashif <i>et al.</i> (2013), Santosh <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)
5.	Number of fruits per cluster	Positive	Vinod <i>et al.</i> (2013)
6.	Average fruits weight	Positive	Santosh <i>et al.</i> (2013), Vinod <i>et al.</i> (2013)
7.	Polar length	Positive	Islam <i>et al.</i> (2012), Madhurina <i>et al.</i> (2012)
8.	Equatorial length	Positive	Islam <i>et al.</i> (2012)
9.	Number of locules	Positive	Rajesh <i>et al.</i> (2006)
		Negative	Madhurina <i>et al.</i> (2012)
		Negative	Rajesh <i>et al.</i> (2006)

Manamodi *et al.* (2013) reported that the direct effects of marketable fruit number and fruit weight on fruit yield were positive and large. Fruit number per truss also showed positive direct effect on fruit yield.

Muhammad *et al.* (2013) revealed that Plant height employed direct positive effect on fruit yield per plant as well as indirect positive effects via days to maturity, number of fruits per plant, fruit weight and fruit length. Number of fruits per plant applied positive direct effect and positive indirect effects by means of plant height, fruit length and fruit width on fruit yield per plant. However, negative indirect effect of days to maturity and fruit weight curtailed it. Fruit weight revealed positive direct effect and positive indirect effect through days to maturity, plant height and fruit length on fruit yield per plant however, it was lessened via number of fruits per plant and fruit width. Because of significant genotypic associations and direct positive effects of fruit weight, number of fruits per plant and plant height on fruit yield per plant, direct selection of these traits would be effective to enhance yield. Days to maturity had negative direct effect on yield per plant. This trait also exhibited negative indirect effects on plant height, fruit weight and fruit length. Fruit length had negative direct and indirect effects on fruit yield per plant through all the characters except fruit width. Similarly fruit width had also negative direct and indirect effects through number of fruits per plant on fruit yield per plant.

Kashif *et al.* (2013) showed that lycopene contents, which is an important fruit quality character, showed no direct correlation with any morphological fruit character, hence indirect selection for high lycopene contents is challenging. Number of fruit clusters per plant had maximum direct effect on fresh fruit yield followed by fruit weight, number of fruits per plant and days to 50 % flowering. Total soluble salts had high negative direct effect on yield per plant. However total soluble salts had positive indirect effect on yield through number of fruits per plant and number of fruit clusters per plant. Positive effect of pericarp thickness on fruit yield was diluted due to negative effects through number of fruit clusters per plant and number of fruits per plant.

Patil *et al.* (2013) reported that days to first harvest had maximum positive direct effect on average fruit weight followed by pericarp thickness.

The path coefficient analysis study done by Khapte and Jhansirani (2014a) indicated that the high positive direct effect was noted for average fruit weight, followed by number of fruits per plant. It was also observed that the high negative direct effect was exerted by fruit diameter and by fruit shape index. The indirect effect was medium to high for most of the characters via average fruit weight, fruit weight, fruit shape index, fruit diameter and number of fruits per plant.

Study on path analysis made by Meena and Bahadur (2014) revealed that fruit weight had a very high positive direct genotypic and phenotypic effect on fruit yield per plant followed by fruit set per cent, number of fruits per plant and number of clusters per plant, while plant height exhibited positive indirect effect on fruit yield via days to 50 % flowering, number of flower clusters per plant, number of flowers per plant, number of fruits per plant, fruit weight, radial diameter of fruit and polar diameter of fruits. TSS exhibited positive indirect effect on fruit yield via number of leaves per plant, number of flower clusters per plant, number of flowers per plant, fruit weight, radial diameter of fruit, polar diameter of fruit and leaf curl incidence per cent, whereas fruit weight recorded high positive direct effect and had significant positive correlation with fruit yield per plant.

3. MATERIAL AND METHODS

The present investigation on diversity and variability for lycopene, ascorbic acid, β -carotene, (neutraceuticals) total soluble solids, pH (Industrial quality traits) and yield components in popular hybrids, varieties and selected germplasm, was conducted in summer 2016. The other experiment was to assess the variability, character association and direct and indirect effects among the yield and yield components in the F_2 of double cross hybrids in tomato and this experiment was conducted during summer 2015. Both investigations were carried at Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad. The details of the material and methods used and the experimental techniques employed for the study are outlined in this chapter.

Experimental location

Geographically, Dharwad is in the Agro-climatic Zone-8 (Northern Transitional Zone) and located at 15° 28' North latitude, 76° 27' East longitude and at an altitude of 678 m above mean sea level (MSL).

3.1 Experiment 1: Study on genetic diversity for neutraceuticals, industrial quality traits and yield components in popular hybrids, varieties and germplasm of tomato

3.1.1 Genotypes used for diversity studies in tomato

Thirteen popular hybrids (Mahyco anagha, Mahyco 303, S-85, Soubhagya, Laxmi, NS962, Arka rakshak, Arka samrat, Sagar, Shivum, Abhilash, Abhishek and Holi), eight varieties (Arka abha, Arka alok, Arka vikas, DMT-1, DMT-4, DMT-5, PKM-1 and S-21) and seven germplasm (Line-1, Line-2, Line-3, Line-4, Line-6, Line-9 and Line-10) of tomato were sown during summer 2015 and evaluated for lycopene, TSS, pH and yield related characters.

3.1.2 Experimental description

Experiment had two replication laid out in randomized block design. Each genotype had single row of ten plants in each replication, with the spacing between row of 60 cm and spacing between rows of 60 cm. Standard package of practices for raising good crop was followed. Observation was recorded in five plants in each replication, which were tagged randomly at the time of crop maturity. General view of experimental plot, color variation and locule variation in tomato is depicted in Plate 1, 2 and 3 respectively.

3.1.3 Observations recorded

The following observations were recorded on five plants per row in each replication and mean was worked out.

1. Plant height (cm): Plant height was measured in centimeters from the ground level to the tip of the plant at the time of last harvest.
2. Number of primary branches: Number of branches per plant was counted at the time of harvest.
3. Number of clusters per plant: Number of clusters per plant was counted.
4. Number of fruits per plant: Total number of fruits harvested from all the pickings was pooled and average number of fruits per plant was calculated.

5. Average fruit weight per plant (g): Average fruit weight in grams was computed by dividing total weight of all the fruits by number of fruits per plant.
6. Polar length of fruit (cm): Polar length of fruit was taken using vernier caliper and expressed in centimeter.
7. Equatorial length of the fruit (cm): Equatorial length was taken using vernier caliper and expressed in centimeter.
8. Fruit yield per plant (kg): Fruit yield was determined by weighing all the fruits from all the pickings from each reference plant and expressed in kilograms.
9. Number of locules per fruit: Fruits are cut in horizontal axis and number of locules per plant was counted.
10. Total soluble solids (%): The juice was prepared by crushing the fruits in mortar and pestel and used to measure total soluble solids by using Abbe hand refractometer.
11. Lycopene (mg/100 g fresh weight): Spectrophotometric determination of lycopene from tomatoes by extraction with acetone and absorbance measurement at 503 nm.
12. Ascorbic acid (mg/100 g of fresh weight): Total ascorbic acid content was found by titration using 2, 6-Dichlorophenol indophenol sodium salt dye.
13. β -carotene (mg/100 g fresh weight): Analysis of β -Carotene by UV-Spectrophotometry at 461nm.
14. Determination of pH values: The juice is prepared by crushing the fruits in mortar and pestel and used to measure pH using pH meter.

3.1.4 Lycopene estimation (Ranganna, 1976)

Three to four tomato fruits were taken, were grinded to a smooth consistency in a pestle and mortar. Five to ten gram of this pulp was taken and the pulp was extracted repeatedly with acetone using pestle and mortar until the residue is colorless. Then acetone extract was pooled and then transferred to a separating funnel containing about 20 ml petroleum ether and mixed gently. About 20 ml of 5 % sodium sulphate solution was added and the separating funnel was shaken gently. Volume of petroleum ether gets reduced during the processes because of its evaporation, so we added 20 ml more of petroleum ether to the separating funnel for clear separation of the phases. Most of the color was noticed in the upper petroleum ether layer. Two phases were separated and the lower aqueous phases was re-extracted with additional 20 ml petroleum ether until the aqueous phases is colorless. Petroleum ether extracts was pooled and washed once with a little distilled water. Petroleum ether extracts containing carotenoids was poured into brown bottle containing about 10 g anhydrous sodium sulphate and kept it aside for 30 min. Petroleum ether extract was decanted into 100 ml volumetric flask through a funnel containing cotton wool. Sodium sulphate slurry was washed with petroleum ether until it is colorless and was transferred to the volumetric flask. Volume was made up and absorbance was measured in spectrophotometer at 503 nm using petroleum ether as blank.

Calculation

mg Lycopene in 100g tomato

$$= (31.206 \times \text{Absorbance}) / \text{weight of sample (g)}$$



Plate 1: General view of experimental plot



Plate 2: Colour variation in popular hybrids, varieties and selected germplasm



Plate 3: Locule variation in popular hybrids, varieties and selected germplasm

3.1.5 β -carotene estimation (Mishra and Gupta, 1995)

Preparation of extract

Fresh tomato pulp of 10 g was weighed and was dispersed it into 50 ml of water saturated n-butanol to give a homogeneous suspension. It was then shaken gently and was allowed it to stand overnight (16 hrs) at room temperature under dark. This mixture was then shaken and filtered completely through the filter paper (Whatman no.1) into a 100 ml volumetric flask.

Determination

Optical density of the clear filtrate was measured at 440nm as absorbance, using spectrophotometer. Unfiltered water- saturated n-butanol was used as blank, evaluation of the contents is based on β -carotene calibration curve (related to the β -carotene content in 10 ml solution)

Preparation of Standard Solution of β -carotene

In 100 ml volumetric flask, 0.025 g of β -carotene was weighed and was dissolved in diethyl ether and volume was made up to the mark with diethyl ether. The 20 ml of this homogenous solution (=5 mg β -carotene) was pipetted into a 250 ml volumetric flask and volume was made up to the mark with water saturated n-butanol. The 25 ml of this solution was poured into 100 ml volumetric flask and volume was made up with water saturated n-butanol.

This standard solution has the following concentration

$$1 \text{ ml} = 0.005 \text{ mg} = 5 \text{ micro grams } \beta\text{-carotene}$$

Preparation of Calibration Curve

Suitable dilutions of the standard solution was prepared with water saturated n-butanol in the calibrated 10 ml volumetric flask (e.g. from 0.5 ml to 3 ml of the standard in 10 ml). Absorbance of each dilution was measured and calibration curve was established (β -carotene in 10 ml of solution as a function of absorbance).

Calculation

The yellow pigment content, W_p , expressed as milligrams of β -carotene in 100g dry matter, is equal to

$$W_p = a \cdot s / 100 \cdot H$$

Whereas, a = the β -carotene content of 10 ml extract

(Equivalent to 2 g of the test sample) in mgs

H = the moisture content of the test samples, expressed as percentage by mass

3.1.6 Ascorbic acid estimation (Sadasivam and Theymoli, 1987)

Five ml of the working standard solution was pipetted into a 100 ml conical flask. 10 ml of 4 % oxalic acid was added and was titrate against the dye (2, 6-dichloro phenol indophenol) (V_1 ml). End point is the appearance of pink color which persist for a few minutes. The amount of the dye consumed is equivalent to the amount of ascorbic acid. Sample (0.5-5 g depending on the sample) was extracted in 4 % oxalic acid and volume was made up to a known volume (100 ml) and centrifuged. Five ml of this supernatant was pipetted out, 10 ml of 4 % oxalic acid was added and titrated against the dye (V_2 ml).

Calculation

Amount of Ascorbic acid (mg/100 g tomato)

$$= (0.5 \text{ mg}/V_1 \text{ ml}) * (V_2 \text{ ml}/5 \text{ ml}) * (100 \text{ ml}/\text{wt. of the sample}) * 100$$

Experiment 2: To assess the genetic variability for Nutraceuticals, Industrial quality traits and yield components in tomato

Thirteen popular hybrids (Mahyco anagha, Mahyco 303, S-85, Soubhagya, Laxmi, NS962, Arka rakshak, Arka samrat, Sagar, Shivum, Abhilash, Abhishek and Holi), eight varieties (Arka abha, Arka alok, Arka vikas, DMT-1, DMT-4, DMT-5, PKM-1 and S-21) and seven germplasm (Line-1, Line-2, Line-3, Line-4, Line-6, Line-9 and Line-10) of tomato were sown during summer 2015 and evaluated for lycopene, TSS, pH and yield related characters. Observations were recorded as explained in the section 3.1.3.

3.2 Experiment 1: Assessment of variability in double cross F_2 populations of tomato

To study character association and direct and indirect effects among the yield and yield components in the F_2 of double cross hybrids (TSH-2 x TSH-3 and TSH-8 x TSH-7). These double cross F_2 population were evaluated during summer 2015. Observation was recorded for, 270 plants in F_2 population of double cross hybrids TSH-2 x TSH-3 and 390 plants in F_2 population of double cross hybrids TSH-8 x TSH-7.

3.2.1 Observations recorded

1. Plant height (cm)
2. Number of primary branches
3. Number of clusters per plant
4. Number of fruits per plant
5. Average fruit weight (g)
6. Polar length of fruit (cm)
7. Equatorial length of fruit (cm)
8. Fruit yield per plant (kg)
9. Number of locules per fruit

3.3 Statistical analysis

Data collected on individual plants of each genotype were used to calculate mean, range, genetic parameters, correlation and path analysis were done.

3.3.1 Analysis of variance

The mean values of the genotypes were used for analysis of variance. Replication wise mean values were subjected to RBD analysis (Snedecor and Cochran, 1967). The significant differences among the genotypes were tested using 'F' test.

Sources of variation	d.f.	MSS	Expectations	Variance ratio or 'F'
Replication	r-1	RMSS		
Genotypes	v-1	VMSS	$\sigma^2_e + r \sigma^2_g$	VMSS/ EMSS
Error	(r-1) (v-1)	EMSS	σ^2_e	
Total	(rv-1)			

Where,

r = number of replications

v = number of genotypes

σ^2_g = genotypic variance

σ^2_e = environmental variance

3.3.2 Mean and range

- General mean ($\bar{X}$) = Sum of observations of all the genotypes / number of genotypes
- Range = the maximum and minimum values for each trait among the genotypes.

3.3.3 Estimation of genetic parameters

In order to assess and quantify the genetic variation among the genotypes for quantitative characters under study, the following parameters were estimated.

a) Estimation of variance components

Phenotypic and genotypic variance were estimated using the following formula

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{MSS (genotype)} - \text{MSS (error)}}{\text{Number of replications}} = \frac{M2 - M3}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \text{Genotypic variance } (\sigma^2_g) + \text{Environmental variance } (\sigma^2_e)$$

b) Coefficients of variation

Both genotypic and phenotypic coefficients of variability were computed as per the method suggested by Burton and De vane (1953).

$$\text{a. Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{b. Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{X}$ = General mean of the character.

GCV and PCV values were categorized as low, moderate and high by Shivasubramanian and Menon (1973) as given below.

0-10 %	: Low
10-20 %	: Moderate
20 % and above	: High

c) Heritability (h^2)

Heritability in broad sense was estimated as the ratio of genotypic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$\text{Heritability } (h^2) = (\sigma_g^2 / \sigma_p^2) \times 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance.

The heritability percentage was categorized as low, moderate and high as given by Robinson *et al.* (1949).

0-30 %	: Low
30-60 %	: Moderate
60 % and above	: High

d) Genetic advance (GA)

Genetic advance was estimated by using the formula given by Johanson *et al.* (1955).

$$GA = h^2 k \sigma_p$$

Where,

h^2 = Heritability in broad sense

k = Selection differential which is equal to 2.06 at 5 % intensity of selection

σ_p = Phenotypic standard deviation.

e) Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = General mean of the character.

Genetic advance as per cent mean was categorized as low, moderate and high by Johnson *et al.* (1955).

0-10 %	: Low
10-20 %	: Moderate
20 % and above	: High

3.3.4 Correlation studies

The correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components.

Genotypic and phenotypic correlations were computed by using the formula given by Weber and Moorthy (1952).

$$r_p = \text{Cov}(X, Y)_p / \sqrt{X_p^2 \times Y_p^2}$$

Where,

r_p = Phenotypic correlation

$\text{Cov}(X, Y)_p$ = Phenotypic covariance between the characters 'X' and 'Y',

X_p^2 and Y_p^2 = Phenotypic variance of the characters 'X' and 'Y' respectively.

$$r_g = \text{Cov}(X, Y)_g / \sqrt{X_g^2 \times Y_g^2}$$

Where,

r_g = Genotypic correlation

$\text{Cov}(X, Y)_g$ = Genotypic covariance between the characters 'X' and 'Y',.

X_g^2 and Y_g^2 = Genotypic variance of the characters 'X' and 'Y' respectively.

Estimated correlation coefficients were compared against r values given in Fisher and Yates (1963) table at (n – 2) degrees of freedom at the probability levels of 0.05 to test their significance.

3.3.5 Path coefficient analysis

Path coefficient analysis was carried out for all the traits to know the direct and indirect effects on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

Path coefficients were obtained by solving the simultaneous equations, which express the basic relationship between correlations and path coefficients. The equations are as follows.

$$r_{1.y} = P_{1y} + r_{1.2} P_{2y} + r_{1.3} P_{3y} + \dots + R_{1.k} + P_{ky}$$

$$r_{2.y} = r_{2.1} P_{1y} + r_{2.2} P_{2y} + r_{2.3} P_{3y} \dots r_{2.k} P_{ky}.$$

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$$r_{k-1.y} = r_{k-1.1} P_{1y} + r_{k-1.2} P_{2y} + r_{k-1.3} P_{3y} + \dots P_{k-1y}$$

Where,

$r_{1.y}$ to $r_{k-1.y}$ denote the correlation coefficients between independent characters, 1 to k-1 and dependent characters 'y', $r_{1.2}$ to $r_{k-2, k-1}$ denote the correlation coefficient between all possible combinations of independent characters. P_{1y} to P_{k-1y} denote the direct effects of characters 1 to k-1 on character Y.

3.3.6 Genetic diversity analysis

Mahalanobis (1936) D^2 -statistic was used for assessing the genetic divergence among the promising genotypes. The generalized distance between any two genotypes is defined as,

$$D^2 = Y_{ij} \beta_i \beta_j$$

where,

Y_{ij} = The reciprocal matrix to the common dispersion matrix

β_i = The difference between the two mean values of the two populations for i^{th} character ($\mu_i - \mu_i$
2)

β_j = The difference between the mean values of the two populations for the j^{th} character ($\mu_{j1} - \mu_{j2}$)

μ = Vector mean values for all the characters

The formula for the estimation of distance, D^2 from samples

$$D^2 p = d_1 (S-1) d$$

where,

$D^2 p$ = Square of the distance considering P values.

$$d_1 = (X_{i1} - X_{i2})$$

X = Vector for mean values of all the characters

S - 1 = Inverse of variance covariance matrix.

Formula for computation of D values, which requires inversion of the matrix, becomes complicated especially when the number of variables under consideration are large. Therefore, the original correlated un-standardized variables (X_i) were transformed to standardized uncorrelated variables (Y_i) so that the computation of D^2 values reduce to simple summation of squares of the differences between values of transformed variables of the two accessions *i.e.*, D^2_i .

From the newly transformed uncorrelated variables, the square of the distance was computed using the following formula,

$$D^2 = (Y_{i1} - Y_{i2})^2$$

where,

Y_{i1} = Vector of transformed mean values, for first accession

Y_{i2} = Vector of transformed mean values, for second accession

The square root of the D^2 values gives the generalized distance (D) between the two entries. The D^2 values were arranged in a matrix form. The significance of D^2 values between any two genotypes was tested using the following formula.

$$F = \frac{(n_1 + n_2 - p - 1)}{(n_1 + n_2 - 2) P} \times \frac{(n_1 n_2) D^2}{(n_1 + n_2)}$$

The computed F value was compared with table F value at 5 per cent and 1 per cent levels of significance with P (number of characters) and $(n_1 + n_2 - p - 1)$ degrees of freedom.

4. EXPERIMENTAL RESULTS

The results of the investigation are presented under the following headings.

- 4.1 Genetic diversity for nutraceuticals (Lycopene, β -carotene and Ascorbic acid), industrial quality traits (pH and total soluble solids) and yield components in popular hybrids, varieties and selected germplasm
- 4.2 Variability for nutraceuticals (Lycopene, β -carotene and Ascorbic acid), industrial quality traits (pH and total soluble solids) and yield components in popular hybrids, varieties and selected germplasm
- 4.3 Variability in F_2 populations of double cross hybrids of tomato
- 4.4 Phenotypic correlation coefficients for yield and yield contributing traits in F_2 populations of double cross hybrids of tomato
- 4.5 Path coefficient analysis for various yield and yield attributing traits in F_2 populations of double cross hybrids of tomato

4.1 Genetic diversity for nutraceuticals and industrial quality traits

4.1.1 Genetic diversity of twenty eight genotypes of tomato

The relative ranking of different character components of D^2 recorded that out of 14 characters studied, the maximum contribution to the total divergence was made by β -carotene (22.75 %) followed by TSS(22.22 %), Ascorbic acid (18.78 %), pH(14.81) and yield (9.79 %) (Table 12).

By employing D^2 statistics, the genetic diversity among 28 genotypes were measured and were grouped into 12 clusters based on the D^2 values by (Fig. 1) using Tocher's method as given by Rao (1952). Of the 12 clusters, cluster I was comprised of 3 hybrids (Mahyco 303, Shivum and Holi), 6 varieties (Arka abha, Arka vikas, S-21, DMT-4, DMT-5 and Arka alok) and 5 germplasm (Line-9, Line-10, Line-6, Line-3 and Line-1). The cluster II with 1 hybrids (Abhilash), 2 varieties (Arka rakshak and DMT-1) and 1 germplasm (Line-2). While III cluster (line-4), IV cluster (Mahyco anagha), V cluster (NS962), VI cluster (S-85), VII cluster (Sagar), VIII cluster (Soubhagya), IX cluster (Laxmi), X cluster (Abhishek), XI cluster (Arka samrat) and XII cluster (PKM-1) were solitary (Table 13).

The intra cluster distance (Table 14) was observed in two clusters which was highest in cluster II (626.72) followed by cluster I (475.31). The inter cluster D^2 values were maximum between VIII and IX (3890.41). The minimum distance was observed between cluster V and VI (412.22), indicating close relationship among the genotypes included.

The cluster means for 14 characters (Table 15) indicated, considerable difference between clusters for all the characters. The maximum plant height (75.5 cm) was observed in cluster IX, while minimum (28 cm) was observed in cluster III. Maximum number of primary branches (7.5) was observed in cluster IX, while minimum (3) was observed in cluster III. Minimum and maximum number of clusters of 3.05 and 11.37 were observed in cluster III and cluster XI, respectively. The cluster X recorded minimum (5.74) and cluster XI recorded maximum (24.67) number of fruits respectively. Highest number of locules (4.42) and lowest number of locules (2.6) observed in cluster II and cluster IV, respectively. Minimum yield per plant (0.15 kg) was observed in cluster VIII, while maximum (0.65) was observed in cluster XI.

Table 12: Per cent contribution of fourteen characters towards divergence in thirteen hybrids, eight varieties and seven germplasm of Tomato (*Solanum lycopersicum* L.)

Sl. No.	Characters	Contribution percentage
1	Plant height	0.00
2	Primary branches	0.00
3	Number of clusters	1.59
4	Number of fruits	0.00
5	Number of locules	5.56
6	Yield	9.79
7	Polar length	3.70
8	Equatorial length	0.26
9	Average fruit weight	0.26
10	Lycopene	0.26
11	Ascorbic acid	18.78
12	β -carotene	22.75
13	pH	14.81
14	TSS	22.22

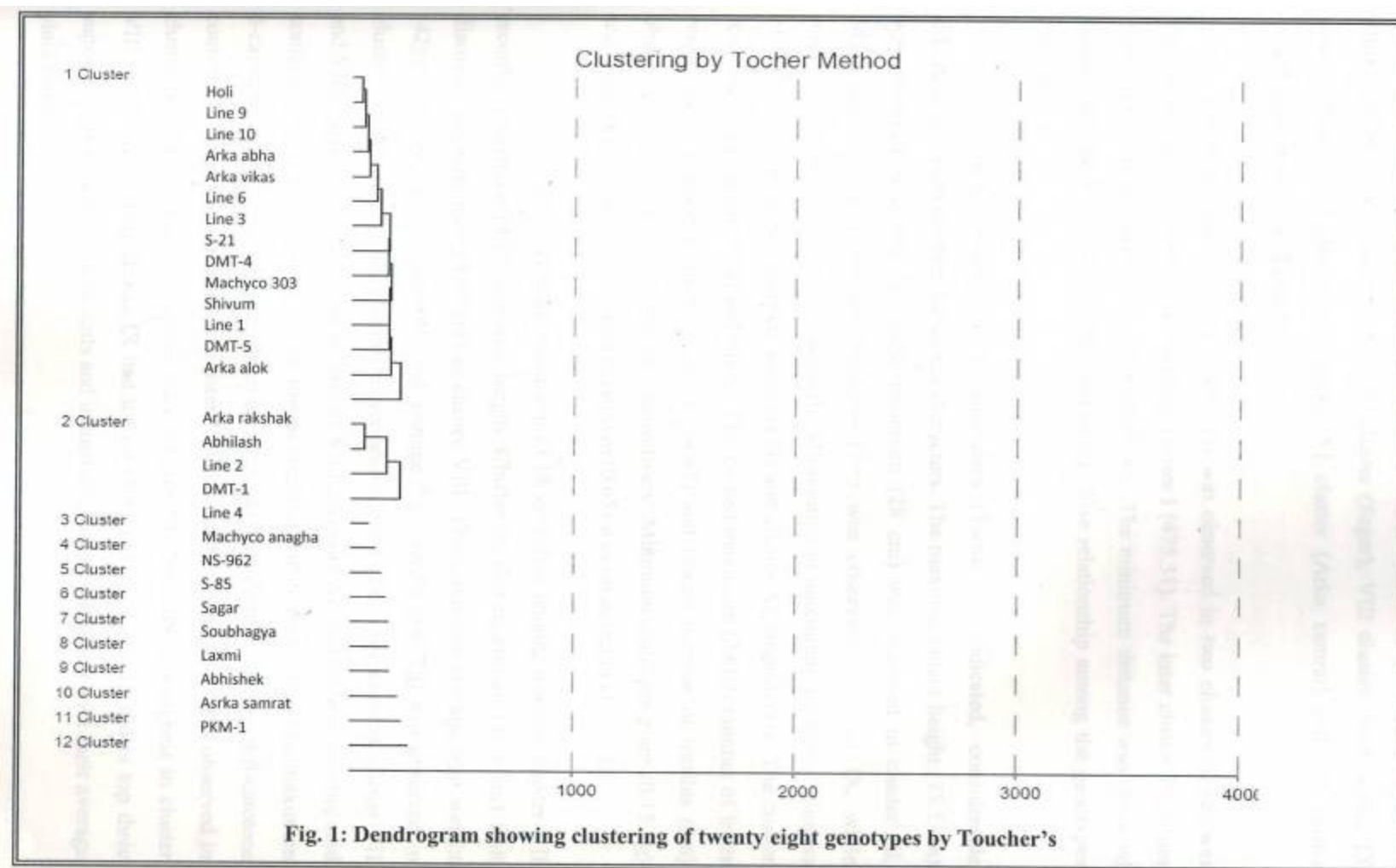


Fig. 1: Dendrogram showing clustering of twenty eight genotypes by Tocher's

Table 13: Clustering pattern of twenty eight genotypes based on D² analysis

Cluster	No of genotypes	Genotypes
I	14	Holi, Line-9, Line-10, Arka abha, Arka vikas, Line-6, Line-3, S-21, DMT-4, Mahyco 303, Shivum, Line-1, DMT-5, Arka alok
II	2	Arka rakshak, Abhilash, Line-2, DMT-1
III	1	Line-4
IV	1	Mahyco anagha
V	1	NS962
VI	1	S-85
VII	1	Sagar
VIII	1	Soubhagya
IX	1	Laxmi
X	1	Abhishek
XI	1	Arka samrat
XII	1	PKM-1

Table 14: Average intra-cluster and inter-cluster D^2 values of twenty eight genotypes observed in Tomato

[illegible]

Table 15: Cluster means for twelve characters in twenty eight genotypes of Tomato

Sl. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII
1	Plant height (cm)	43.27	55.35	28.00	72.84	65.84	59.50	61.00	41.00	75.50	37.84	65.84	45.00
2	Primary branches	3.94	4.52	3.00	3.47	5.54	5.52	4.37	5.74	7.50	5.27	5.95	4.74
3	Number of clusters	4.16	6.16	3.05	6.72	7.54	9.37	5.74	3.59	9.95	3.10	11.37	3.15
4	Number of fruits	6.04	10.23	8.90	9.15	11.67	13.54	14.25	10.50	18.00	5.74	24.67	10.37
5	Number of locules	3.29	4.42	3.55	2.60	3.00	3.54	3.32	3.37	3.05	2.74	4.05	2.47
6	Yield (kg)	0.19	0.19	0.20	0.35	0.43	0.38	0.38	0.15	0.62	0.20	0.65	0.18
7	Polar length (cm)	3.43	3.54	3.43	3.18	3.84	3.58	4.77	4.27	3.63	3.27	4.22	3.34
8	Equatorial Length (cm)	3.81	3.67	3.70	4.07	4.25	4.25	3.99	3.69	4.35	3.70	3.84	3.85
9	Average fruit weight (g)	23.97	18.36	22.84	42.00	31.50	37.06	25.30	16.77	32.50	36.50	27.22	18.00
10	Lycopene (mg/100 g of fruit)	2.17	1.83	2.23	2.27	2.23	1.57	1.80	1.80	1.99	2.77	2.87	2.36
11	Ascorbic acid (mg/100 g of fruit)	25.79	18.50	16.00	32.50	35.50	28.50	20.50	31.50	40.5	21.50	44.50	56.00
12	β -carotene (mg/100 g of fruit)	1.74	1.33	1.35	1.75	1.35	3.30	1.20	3.20	0.70	1.05	1.45	2.40
13	pH	5.05	4.49	6.40	5.05	6.10	5.45	6.10	5.40	6.05	6.15	4.55	4.70
14	TSS (%)	5.33	5.06	4.35	7.53	5.75	7.20	4.60	8.65	3.80	6.50	6.75	4.35

Table 16. Superior clusters for nutraceuticals, industrial quality traits and their average yield levels

Cluster number	Lycopene (mg/100 g)	Yield/plant (kg)	Cluster number	Ascorbic acid (mg/100 g)	Yield/plant (kg)	Cluster number	β -carotene (mg/100 g)	Yield/plant (kg)	Cluster number	pH	Yield/plant (kg)	Cluster number	TSS (%)	Yield/plant (kg)
Cluster XI	2.87	0.65	Cluster XII	56.00	0.18	Cluster VI	3.30	0.38	Cluster II	4.49	0.19	Cluster VIII	8.65	0.15
Cluster X	2.77	0.20	Cluster XI	44.50	0.65	Cluster VIII	3.20	0.15	Cluster XI	4.55	0.65	Cluster IV	7.53	0.35
Cluster XII	2.36	0.18	Cluster IX	40.50	0.62	Cluster XII	2.40	0.18	Cluster XII	4.70	0.18	Cluster VI	7.20	0.38

The cluster IV recorded minimum (3.18 cm) fruit length, whereas cluster VII recorded maximum (4.77 cm) fruit length. Cluster IX had maximum (4.35 cm) fruit diameter and minimum (3.69 cm) in cluster VIII. The maximum average fruit weight (42g) was observed in cluster IV and average fruit weight (16.77g) was observed in cluster VIII. Cluster XI had maximum lycopene content (2.87 mg) whereas, cluster VII and VIII had minimum lycopene content (1.8 mg). Cluster XII had highest ascorbic acid content (56 mg) while, cluster III had lowest ascorbic acid content (16g). The maximum β -carotene content (3.3 mg) was observed in cluster VI, whereas the lowest β -carotene content (0.7 mg) was observed in cluster IX. The maximum pH (6.4) was observed in cluster III and pH (4.55) was observed in cluster XI. The TSS was highest in cluster VIII (8.65 %), whereas cluster IX had lowest (3.8 %) TSS. Table 16 shows top three superior clusters for nutraceuticals and industrial quality traits along with their average yield levels.

4.2 Variability for nutraceuticals (Lycopene, β -carotene and Ascorbic acid), industrial quality traits (pH, Total soluble solids) and yield components in popular hybrids, varieties and germplasm

To compare the extent of genetic variability present in the available germplasm, the data on mean, range, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability (h^2) and genetic advance as per cent over mean (GAM) character wise is presented in Table 18. The analysis of variance in Table 17 and best performing five genotypes for lycopene, ascorbic acid, β -carotene, pH and TSS are mentioned in Table 19. Graph showing variation in PCV and GCV (%) are depicted in Fig. 2.

4.2.1 Plant height (cm)

Plant height ranged from 28 cm to 75.50 cm with an average mean of 49.04 cm. High PCV (26.31 %) and GCV (23.38) was recorded for this trait.

4.2.2 Number of Primary branches

Number of primary branches ranged from 7.50 to 2.55 branches with an average of 4.44 branches. This character exhibited high PCV (25.16 %) and GCV (24.49 %).

4.2.3 Number of clusters

The number of clusters ranged from 11.37 to 2.75 clusters with mean value of 5.02 clusters, high GCV (43.93 %) and high PCV (44.17) were found in existing genotype was found for this trait.

4.2.4 Number of fruits per plant

Number of fruits had mean value of 9.01 fruits, where as it ranged between 2.78 to 24.67 fruits. However higher PCV (56.25 %) and GCV (54.82 %) was exhibited.

4.2.5 Polar length (cm)

Fruit length ranged from 4.77 cm to 2.95 cm with an average mean of 3.56 cm. experiment recorded moderate PCV (10.43 %) and GCV (10.71 %).

4.2.6 Equatorial length (cm)

Fruit breadth ranged from 4.45 cm to 3.17 cm with showing an average mean of 3.84 cm. For this trait low coefficients of variation like low PCV (8.61 %) and GCV (8.91 %) were recorded.

Table 17: Analysis of variance in commercial hybrids, varieties and germplasm

SV	df	Plant height (cm)	Primary branches	Number of Clusters	Number of fruits	Number of locules	Yield per plant (kg)	Polar length (cm)
Replicate	1	84.94	0.088	0.55	0.004	0.058	0.0025	0.0274
Treatments	27	8120.01**	2.42**	10.39**	50.05**	1.15**	0.056**	0.282**
Error	27	956.62	0.065	0.0847	1.29	0.011	0.002	0.0075

SV	df	Equatorial length (cm)	Average fruit weight (g)	Lycopene (mg/100 g of fruit)	Ascorbic acid (mg/100 g of fruit)	β-carotene (mg/100 g of fruit)	pH	TSS (%)
Replicate	1	0.0301	63.75	0.008	8.64	0.664	0.348	0.117
Treatments	27	0.226**	98.76**	0.35**	184.64**	0.991**	1.01**	3.37**
Error	27	0.0079	1.52	0.355	0.939	0.182	0.043	0.024

*, ** Significant at 5 per cent and 1 per cent level of significance

Table 18: Mean, range and genetic parameter values for fourteen characters of tomato in commercial hybrids, varieties and selected germplasm

Characters	Mean	Range		PCV (%)	GCV (%)
		Min	Max		
Plant height (cm)	49.27	28.00	75.5	26.31	23.38
Primary branches	4.44	2.55	7.50	25.16	24.49
Number of clusters	5.20	2.75	11.37	44.17	43.93
Number of fruits	9.01	2.78	24.67	56.25	54.82
Number of locules	3.41	2.37	5.50	22.44	22.23
Polar length (cm)	3.56	2.95	4.77	10.71	10.43
Equatorial Length (cm)	3.84	3.17	4.45	8.91	8.61
Lycopene (mg/100 g of fruit)	2.13	1.53	3.16	20.39	19.17
Ascorbic acid (mg/100 g of fruit)	27.21	16.00	56.00	35.40	35.22
β-carotene (mg/100 g of fruit)	1.69	0.70	3.30	45.32	37.61
pH	5.16	3.55	6.40	14.11	13.52
TSS (%)	5.51	3.40	8.65	23.64	23.47
Average fruit weight (g)	24.96	16.00	42.00	28.38	27.94
Yield/plant (kg)	0.24	0.05	0.65	70.25	67.88

Table 19. Superior genotypes for nutraceuticals, industrial quality traits and their average yield levels

Genotype	Lycopene (mg/100 g)	Yield/plant (kg)	Genotype	Ascorbic acid (mg/100 g)	Yield/plant (kg)	Genotype	β - carotene (mg/100 g)	Yield/plant (kg)	Genotype	pH	Yield/ plant (kg)	Genotype	TSS (%)	Yield/ plant (kg)
Mahyico 303	3.15	0.12	PKM	56.00	0.17	S85	3.30	0.37	DMT1	3.55	0.34	Soubhagy	8.65	0.15
Arka samrat	2.86	0.64	Samrat	44.50	0.64	Soubhagy	3.20	0.15	Line10	4.15	0.25	Mahyco anagha	7.53	0.35
Abhishek	2.77	0.19	Laxmi	40.50	0.61	Mahyico 303	3.00	0.12	Line1	4.15	0.45	S85	7.2	0.37
Alok	2.65	0.11	DMT4	40.50	0.13	DMT4	2.50	0.13	Line2	4.25	0.09	DMT4	7.1	0.13
DMT 4	2.58	0.13	NS962	35.50	0.42	Line6	2.45	0.14	S21	4.55	0.55	DMT5	6.85	0.18
CD (@ 5%)	0.21	0.06	CD (@ 5%)	1.38	0.06	CD (@ 5%)	0.60	0.06	CD (@ 5%)	0.29	0.06	CD (@ 5%)	0.22	0.06

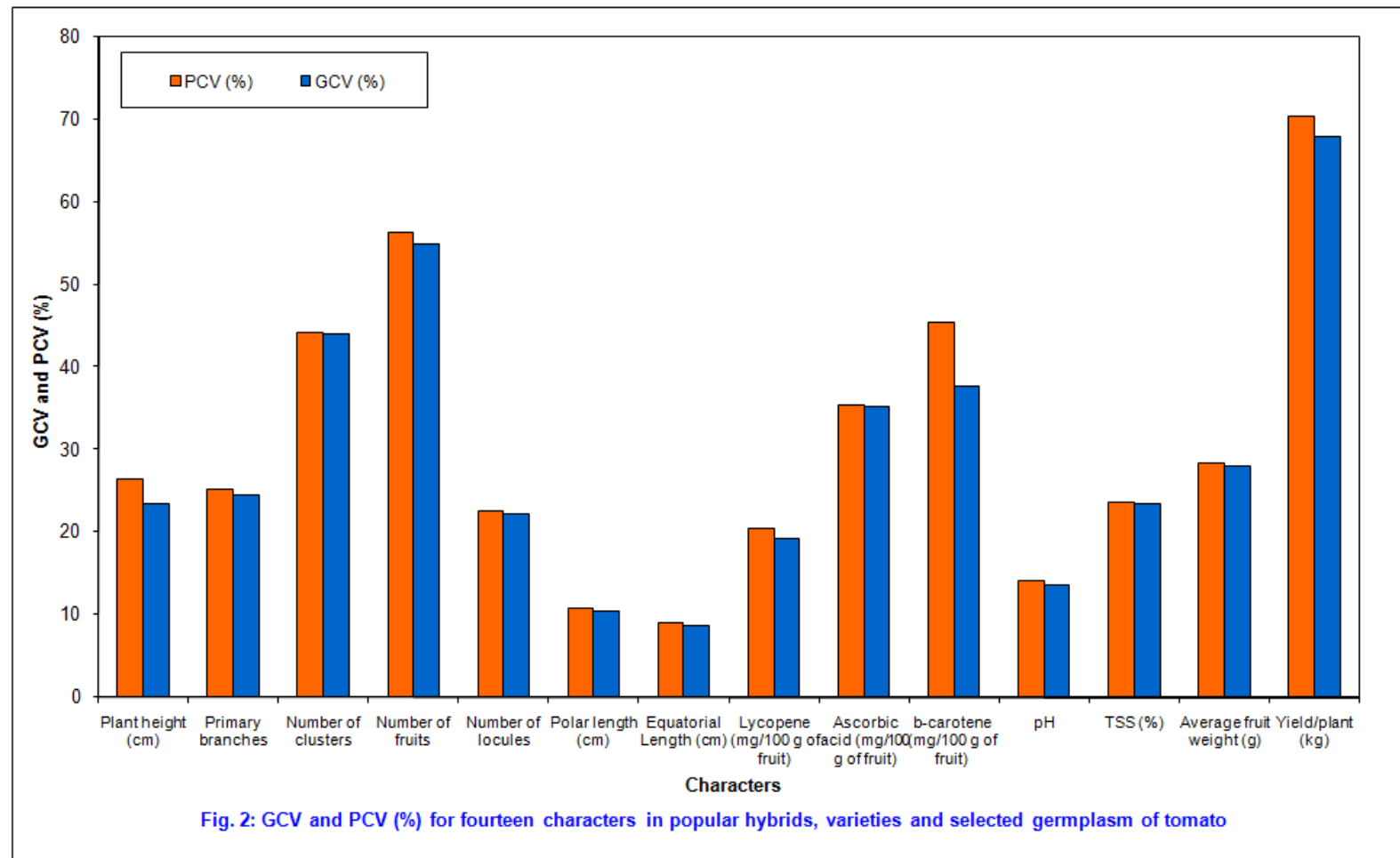


Fig. 2: GCV and PCV (%) for fourteen characters in popular hybrids, varieties and selected germplasm of tomato

4.2.7 Number of locules

In present investigation, a minimum of 2.37 locule and maximum of 5.5 locule with an average of 3.41 locules were observed. The high PCV (22.44 %) and GCV (22.23 %) were observed for this trait.

4.2.8 Lycopene (mg/100 g of fruit)

The lycopene content ranged from 1.53 mg to 3.16 mg with mean value of 2.13 mg, it was found moderate GCV (19.17 %) and high PCV (20.39 %) in existing genotype for this trait.

4.2.9 Ascorbic acid (mg/100 g of fruit)

This trait had a mean value of 27.21 mg where as it ranged between 16 mg to 56 mg. However higher PCV (35.22 %) and GCV (35.40 %) was exhibited.

4.2.10 β -carotene (mg/100 g of fruit)

β -carotene showed a range between 0.7 mg to 3.3 mg with an average mean of 1.69 mg. This trait recorded high PCV (45.32 %) and GCV (37.61 %).

4.2.11 pH

This trait ranged from 6.4 units to 3.55 units with an average mean of 5.16 unit. For this trait moderate PCV (14.11 %) and GCV (13.52 %) were recorded.

4.2.12 Total soluble solids (%)

In present investigation a minimum of 3.40 % TSS and maximum of 8.65 % TSS was found with an average of 5.51 % TSS were observed. High PCV (28.38 %) and GCV (27.94 %) were observed for this trait.

4.2.13 Average fruit weight (g)

The fruit weight ranged from 16 g to 42 g with an average mean of 24.96 g. This trait exhibited high PCV (28.38 %) and GCV (27.94 %).

4.2.14 Fruit yield per plant (kg)

Yield per plant ranged from 0.05 kg to 0.65 kg with an average mean of 0.24 kg. High PCV (70.25 %) and GCV (67.88 %) were recorded.

4.3 Variability studies in F_2 populations of two double cross hybrids of tomato

To compare the extent of genetic variability present in the double cross F_2 populations, the data on mean, range, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability (h^2) and genetic advance as per cent over mean (GAM) character wise is presented in Table 20. Graph showing variation in PCV and GCV are depicted in Fig. 3. Graph showing variation in heritability and GAM (%) are depicted in Fig. 4.

4.3.1 Plant height (cm)

In double cross F_2 populations, the plant height ranged from 25 cm (TSH-8 x TSH-7) to 125 cm (TSH-8 x TSH-7) with an average mean of 67.17 cm from both the population. High PCV and GCV, high heritability accompanied with high GAM was recorded for this trait. The double cross TSH-2 x TSH-3 recorded lower PCV (24.05 %), GCV (22.4 %), lower heritability (87.04 %) and lower GAM (43.12 %) in comparison with TSH-8 x TSH-7 double F_2 population.

Table 20: Mean, range and components of variance for nine characters in two double cross F₂ populations of tomato

Sl. No.	Character	Genotype	Mean	Range		Variance		PCV (%)	GCV (%)	Heritability (%)	GA	GAM (%)
				Minimum	Maximum	Phenotypic	Genotypic					
1	Plant height (cm)	TSH-8 x TSH-7	71.07	25.00	125.00	351.18	341.81	26.37	24.92	89.32	34.48	48.52
		TSH-2 x TSH-3	63.27	35.00	120.00	231.48	223.88	24.05	22.44	87.04	27.28	43.12
2	Number of primary branches	TSH-8 x TSH-7	4.33	1.00	10.00	2.39	1.61	35.69	33.77	89.52	2.85	65.81
		TSH-2 x TSH-3	5.29	2.00	14.00	3.66	2.70	36.19	35.19	94.54	3.73	70.49
3	Number of cluster per plant	TSH-8 x TSH-7	6.69	1.00	19.00	10.99	9.34	49.58	44.97	82.26	5.62	84.02
		TSH-2 x TSH-3	6.88	1.00	18.00	12.33	10.58	51.07	47.86	87.84	6.35	92.41
4	Number of fruits per plant	TSH-8 x TSH-7	6.03	1.00	32.00	23.28	20.87	80.06	53.59	44.80	4.45	73.89
		TSH-2 x TSH-3	6.02	1.00	24.00	19.23	17.04	72.84	26.15	12.89	1.16	19.34

5	Polar length (cm)	TSH-8 x TSH-7	3.77	2.00	7.00	255.63	247.63	14.49	13.64	88.61	1.00	26.45
		TSH-2 x TSH-3	4.00	2.20	6.00	289.99	281.47	13.63	13.33	95.62	1.07	26.86
6	Equatorial length (cm)	TSH-8 x TSH-7	4.18	2.00	5.70	0.30	0.03	12.28	11.51	87.85	0.93	22.22
		TSH-2 x TSH-3	4.26	2.20	5.80	0.30	0.02	12.75	12.12	90.34	1.01	23.73
7	Number of locules	TSH-8 x TSH-7	3.45	2.00	6.00	0.51	0.15	20.60	11.23	29.72	0.44	12.61
		TSH-2 x TSH-3	3.05	2.00	5.00	0.29	0.02	20.90	12.95	38.38	0.50	16.52
8	Average fruit weight (g)	TSH-8 x TSH-7	41.47	10.00	150.00	23807.62	23730.48	38.56	35.62	85.33	28.10	67.77
		TSH-2 x TSH-3	43.78	10.00	162.50	22568.69	22493.58	38.90	36.83	89.65	31.45	71.84
9	Fruit yield per plant (kg)	TSH-8 x TSH-7	0.22	0.02	1.01	6.74	5.44	68.85	54.11	61.78	0.20	87.62
		TSH-2 x TSH-3	0.24	0.02	0.81	0.41	0.09	62.80	54.81	76.18	0.24	98.56

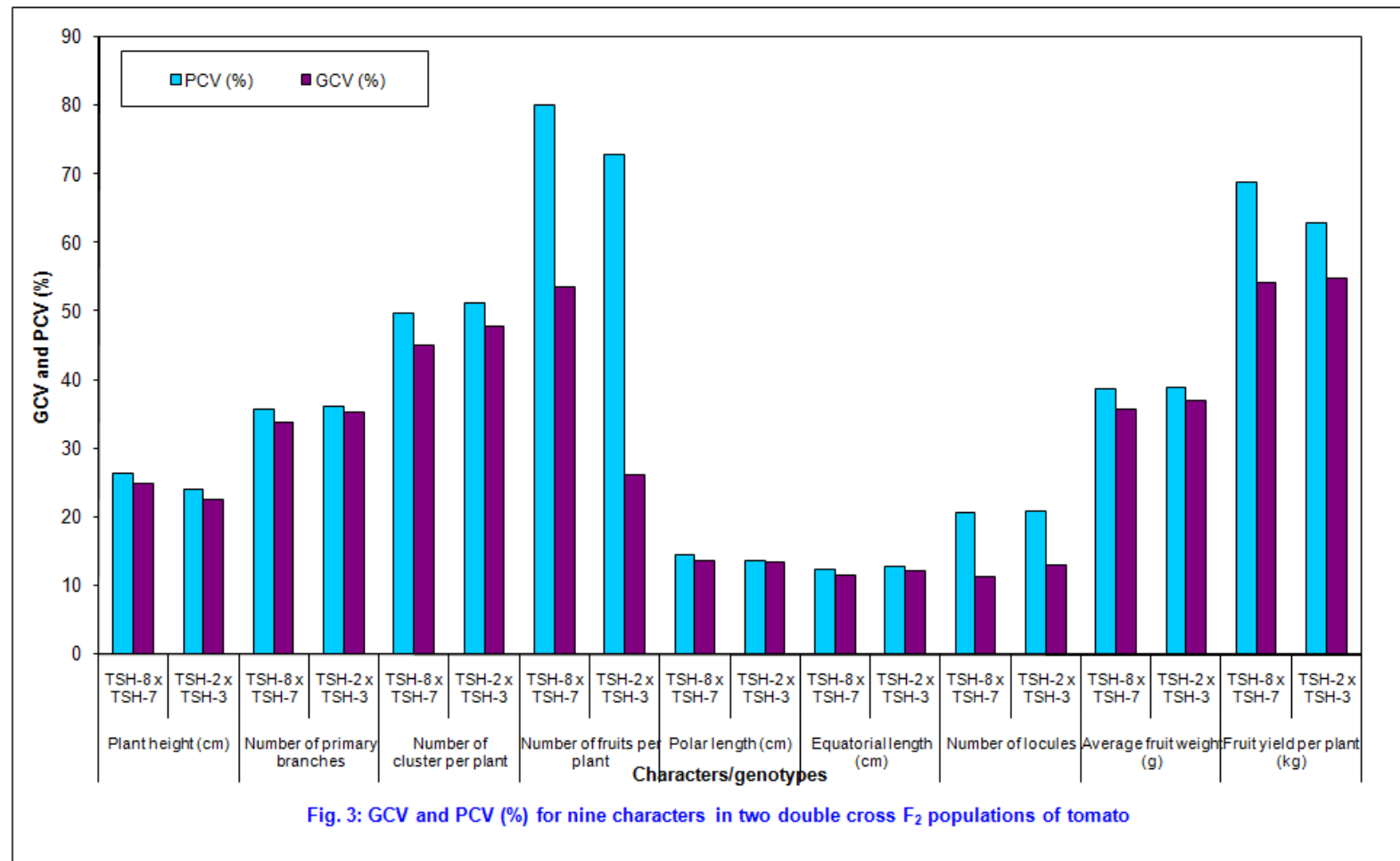


Fig. 3: GCV and PCV (%) for nine characters in two double cross F_2 populations of tomato

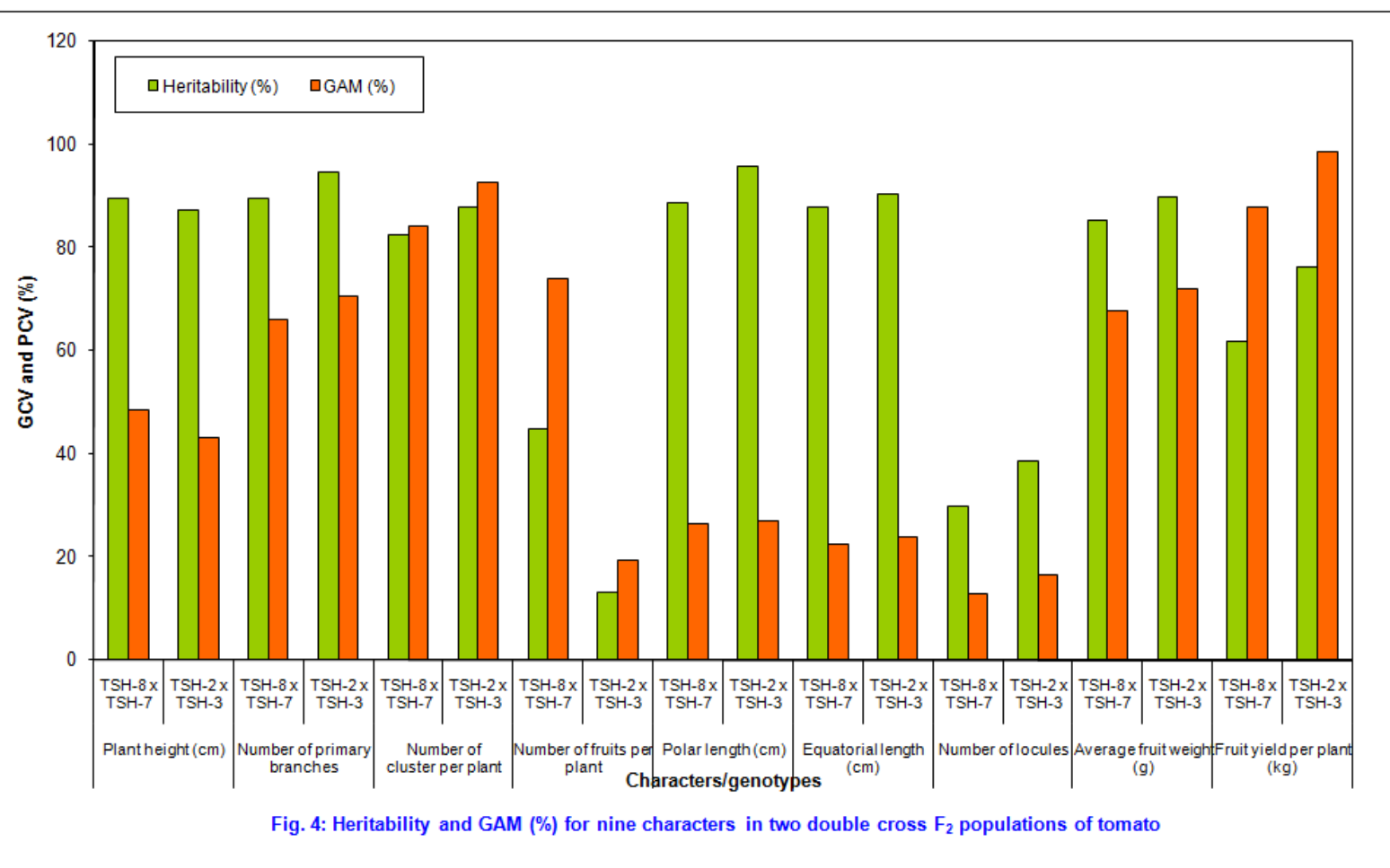


Fig. 4: Heritability and GAM (%) for nine characters in two double cross F_2 populations of tomato

4.3.2 Number of branches

Among double cross F_2 population, number of primary branches ranged from 1 (TSH-8 x TSH-7) to 14 (TSH-2 x TSH-3) branches with an average mean of 4.81 branches from both the double cross F_2 population. This character exhibited high PCV and GCV, heritability and GAM. In the F_2 population of the double cross TSH-2 x TSH-3 higher PCV (36.19 %), higher GCV (35.16 %), heritability (94.54 %) and GAM (70.49 %) were recorded.

4.3.3 Number of clusters

The number of clusters ranged from 1 (TSH-2 x TSH-3, TSH-8 x TSH-7) to 19 (TSH-8 x TSH-7) clusters with mean value of 6.78 clusters with high GCV and PCV in double cross F_2 populations. Highest GCV (47.86 %) and PCV (51.07 %), high heritability (87.84 %) were exhibited in TSH-2 x TSH-3 respectively. Genetic advance as per cent over mean were high in both TSH-2 x TSH-3 (92.41 %) and TSH-8 x TSH-7 (84.02 %) double cross F_2 populations for this trait.

4.3.4 Number of fruits per plant

Both double cross F_2 populations exhibited high PCV and GCV. Among the double crosses F_2 populations, the double cross F_2 population of TSH-8 x TSH-7 hybrid recorded relatively higher PCV (80.06 %) and GCV (53.59 %), moderate high heritability (44.80 %) and high GAM (73.89 %).

4.3.5 Polar length (cm)

In both double cross F_2 populations, fruit length ranged from 2.00 cm to 7.00 cm with an average mean of 3.88 cm. Both the double cross F_2 populations recorded moderate PCV, GCV and high GAM. Moderately higher PCV (14.49 %) and GCV (13.64 %) was recorded in TSH-8 x TSH-7 double cross F_2 population. but higher heritability (95.62 %) and GAM (26.8 %) was recorded in TSH-2 x TSH-3 double cross F_2 population.

4.3.6 Equatorial length (cm)

In double cross F_2 populations the fruit length ranged from 2 cm (TSH-8 x TSH-7) to 5.70 cm (TSH-8 x TSH-7) with an average mean of 4.22 cm. For this trait moderate coefficients of variation, high heritability and high GAM were recorded. The moderate PCV (12.28 %), GCV (11.51 %), high heritability (87.85 %) and GAM (22.22 %) were recorded in F_2 population of TSH-8 x TSH-7 double cross and other double cross TSH-2 x TSH-3 F_2 populations recorded moderate PCV (12.75 %), GCV (12.12 %), high heritability (90.34 %) and moderate GAM (23.73 %).

4.3.7 Number of locules per plant

In double cross F_2 populations, a minimum of 2 locules (both double cross F_2 populations) and maximum of 6 (TSH-8 x TSH-7) with an average of 3.76 locules were observed. The moderate PCV (20.96 %) and GCV (12.95 %), moderate heritability (23.96 %) along with high GAM (15.36 %) were observed in cross TSH-2 x TSH-3 double cross F_2 population.

4.3.8 Average fruit weight (g)

In double cross F_2 populations, the fruit weight ranged from 10 g (both double cross F_2 population) to 162.25 g (TSH-2 x TSH-3 double cross F_2 population) with an average mean of 42.62 g. F_2 population of the double cross TSH-2 x TSH-3 exhibited high PCV (38.73 %) and GCV (36.22 %) with high heritability (87.49 %) and genetic advance (71.84 %).

4.3.9 Fruit yield per plant (kg)

In the double cross F_2 population, the yield per plant ranged from 0.02 (in both F_2 population) to 1.01 kg (TSH-8 x TSH-7) with an average mean of 0.23 kg. The high PCV (62.80 %), GCV (54.81 %), heritability (76.18 %) and GAM (98.56 %) were recorded in cross TSH-2 x TSH-3 double cross F_2 population compared to other double cross F_2 population.

4.4 Phenotypic correlation coefficients for yield and yield contributing traits

Analysis of simple correlation coefficients of yield components with fruit yield and among themselves in respect of segregating populations are presented in Table 21.

4.4.1 Character association in double cross F_2 populations of TSH-8 x TSH-7 hybrid

Fruit yield per plant recorded positive correlation with plant height, number of clusters, number of fruits per plants, number of primary branches and equatorial length. High correlation was observed for number of fruits per plant (0.8586), number of clusters (0.4220) and number of primary branches (0.2259) followed by plant height (0.2058) and equatorial length (0.1704).

Plant height recorded significant positive correlation with number of clusters (0.3254), number of primary branches (0.3421) and equatorial length (0.1945). Number of primary branches was positively associated with number of cluster per plant (0.3784), number of fruits (0.1919) and equatorial length (0.1757) and also number of cluster was positively correlated with number of fruits (0.4168) while, number of fruits per plant was negatively correlated with average fruit weight (-0.3354). Average fruit weight was positively correlated with polar length (0.4288) and equatorial length (0.2958). It was found that polar length was positively associated with equatorial length (0.3330).

4.4.2 Character association in double cross F_2 populations of TSH-2 x TSH-3 hybrid

In the double cross F_2 population of TSH-2 x TSH-3 hybrid, it was found that plant height, number of clusters, number of fruits per plant, number of branches, polar length and equatorial length, plant height was positively correlated with primary branches (0.2943), number of clusters (0.3148), average fruit weight (0.1218) and equatorial length (0.1277). Highest correlation was observed for number of fruits (0.8746) followed number of per cluster (0.5542), primary branches (0.4065), followed by equatorial length (0.3026), polar length (0.1719) and plant height (0.1444).

Primary branches was found positively correlated with number of cluster (0.647), number of fruits (0.3148), polar length (0.1639) and equatorial (0.2680). Number of clusters was positively correlated with number of fruits (0.4771), polar length (0.1344) and equatorial length (0.2578), there was significant negative correlation of number of fruits with average fruit weight (-0.3271), it was found that average fruit weight had significant positive correlation with polar (0.4874) and equatorial length (0.3518). Polar length had positive significant correlation with equatorial length (0.5744), equatorial length had significant positive association with locule counts (0.2660).

Table 21: Phenotypic correlations among different quantitative traits in F₂ population of double cross hybrids of tomato

	Double cross F ₂ population	Plant height (cm)	Primary branch	Number of cluster	Number of fruits	Average fruit weight (g)	Polar length (cm)	Equatorial length (cm)	Number of locules	Yield (kg)
Plant height (cm)	TSH-8 x TSH-7	1	0.3421**	0.3254**	0.0797	0.0516	0.1072	0.1945**	0.0272	0.2058**
	TSH-2 x TSH-3	1	0.2943**	0.3148**	0.0992	0.1218*	0.0882	0.1277*	-0.0209	0.1444*
Primary branch	TSH-8 x TSH-7		1	0.3784**	0.1919**	0.0114	-0.0261	0.1757**	0.0481	0.2259**
	TSH-2 x TSH-3		1	0.647**	0.3197**	0.0426	0.1639**	0.2680**	0.0675	0.4065**
Number of cluster	TSH-8 x TSH-7			1	0.4168**	-0.0767	-0.0703	0.073	0.024	0.4220**
	TSH-2 x TSH-3			1	0.4771**	0.0175	0.1344*	0.2578**	0.0563	0.5542**
Number of fruits	TSH-8 x TSH-7				1	-0.3354 **	-0.0779	-0.0096	0.0589	0.8586**
	TSH-2 x TSH-3				1	-0.3271 **	-0.0442	0.1127	0.024	0.8746**
Average fruit weight (g)	TSH-8 x TSH-7					1	0.4288**	0.2985**	-0.0964	0.0375
	TSH-2 x TSH-3					1	0.4874**	0.3518**	0.1471*	0.0404
Polar length (cm)	TSH-8 x TSH-7						1	0.3330**	0.0929	0.0734
	TSH-2 x TSH-3						1	0.5744**	0.1226	0.1719**
Equatorial length (cm)	TSH-8 x TSH-7							1	-0.0308	0.1704**
	TSH-2 x TSH-3							1	0.2660**	0.3026**
Number Of locules	TSH-8 x TSH-7								1	-0.0136
	TSH-2 x TSH-3								1	0.0765

*, ** Significant at 5 per cent and 1 per cent level of significance

4.5 Path coefficient analysis for various yield and yield attributing traits in F_2 populations of double cross hybrids of tomato.

The path coefficient analysis was done to partition the correlation coefficient into direct and indirect effects. The phenotypic correlation coefficients of various characters were subjected to path coefficient analysis to estimate the direct and indirect effects of component traits on fruit yield considered as the dependent variable in the analysis. The direct and indirect effects of various traits on yield are presented in Table 22 and same depicted in Fig. 5 and Fig. 6.

4.5.1 Path coefficient analysis for yield and yield attributing traits in F_2 population of TSH-8 x TSH-7 double cross hybrid

4.5.1.1 Plant height (cm)

In the F_2 population of TSH-8 x TSH-7 double cross hybrid plant height had positive direct effect (0.053) on fruit yield per plant, but it had positive indirect effect through primary branches (0.0156), number of clusters (0.02959), number of fruits per plants (0.0053), average fruit weight (0.0064), polar length (0.0047) and equatorial length (0.0068). There was negative effect via number of locules (-0.0011).

4.5.1.2 Number of branches

Number of branches had positive direct effect (0.0008) on fruit yield per plant. It had indirect negative effect through number of cluster (0.0003), number of fruits (0.0001), and equatorial length (0.0001).

4.5.1.3 Number of clusters

Number of clusters also had positive direct effect (0.0258) on fruit yield per plant and positive indirect effects for all character studied except average fruit weight (-0.002) and polar length (-0.0018) which recorded negative indirect effect.

4.5.1.4 Number of fruits per plant

Number of fruits per plant exhibited positive direct effect (0.9565) on number of fruits per plant. It had positive indirect effect through plant height (0.0949), primary branches (0.1835) number of clusters (0.3987) and number of locules (0.0564) but negative indirect via average weight (-0.3208), polar length (-0.0746) and equatorial length (-0.0092).

4.5.1.5 Average fruit weight (g)

Positive direct effect was observed for number of fruits per cluster (0.3373) on fruit yield per plant and it had negative indirect effects through number of cluster (-0.0259), number of fruits (-0.1131), number of locules (-0.0325), while positive indirect effect through plant height (0.0411), primary branches (0.0038) polar length (0.1446) and equatorial length (0.1007).

4.5.1.6 Polar length (cm)

Polar length recorded negative direct effect (-0.0094) on fruit yield per plant. It also recorded negative indirect effect on fruit yield through plant height (-0.0019), average weight (-0.0094), equatorial length (-0.0073) and number of locules (-0.002). Rest character had positive indirect effect.

Table 22: Direct and indirect effects of different quantitative traits on fruit yield in F₂ population of single cross hybrids of tomato

	F2 population	Plant height (cm)	Primary branch	Number of cluster	Number of fruits	Average fruit weight (g)	Polar length (cm)	Equatorial length (cm)	Number of locules	Correlation with yield (kg)
Plant height (cm)	TSH-8 x TSH-7	0.053	0.0156	0.0167	0.0053	0.0064	0.0047	0.0068	-0.0011	0.2058**
	TSH-2 x TSH-3	0.0095	0.0032	0.0031	0.0008	0.0005	0.001	0.0018	0.0003	0.1444*
Primary branch	TSH-8 x TSH-7	0.0002	0.0008	0.0003	0.0001	0	0	0.0001	0	0.2259**
	TSH-2 x TSH-3	0.012	0.0351	0.0227	0.0112	0.0015	0.0058	0.0094	0.0024	0.4065**
Number of cluster	TSH-8 x TSH-7	0.0081	0.0098	0.0258	0.0108	-0.002	-0.0018	0.0019	0.0006	0.4220**
	TSH-2 x TSH-3	0.0207	0.0412	0.0636	0.0304	0.0011	0.0086	0.0164	0.0036	0.5542**
Number of fruits	TSH-8 x TSH-7	0.0949	0.1835	0.3987	0.9565	-0.3208	-0.0746	-0.0092	0.0564	0.8586**
	TSH-2 x TSH-3	0.0742	0.2977	0.4443	0.9313	-0.3046	-0.0411	0.105	0.0224	0.8746**
Average weight (g)	TSH-8 x TSH-7	0.0411	0.0038	-0.0259	-0.1131	0.3373	0.1446	0.1007	-0.0325	0.0375
	TSH-2 x TSH-3	0.0164	0.0136	0.0056	-0.1042	0.3186	0.1553	0.1121	0.0469	0.0404
Polar length (cm)	TSH-8 x TSH-7	-0.0019	0.0006	0.0015	0.0017	-0.0094	-0.0094	-0.0073	-0.002	0.0734
	TSH-2 x TSH-3	0.0014	0.0021	0.0018	-0.0006	0.0064	0.0131	0.0075	0.0016	0.1719**
Equatorial length (cm)	TSH-8 x TSH-7	0.0098	0.0134	0.0056	-0.0007	0.0228	0.0255	0.0764	-0.0024	0.1704**
	TSH-2 x TSH-3	0.0106	0.0146	0.014	0.0061	0.0191	0.0312	0.0544	0.0145	0.3026**
Number of locules	TSH-8 x TSH-7	0.0007	-0.0016	-0.0008	-0.0019	0.0031	-0.003	0.001	-0.0326	-0.0136
	TSH-2 x TSH-3	-0.0004	-0.001	-0.0008	-0.0004	-0.0022	-0.0018	-0.004	-0.015	0.0765

Residual effect: TSH-8 x TSH-7 double cross F₂ population = 0.3636

TSH-2 x TSH-3 F₂ double cross population = 0.3227

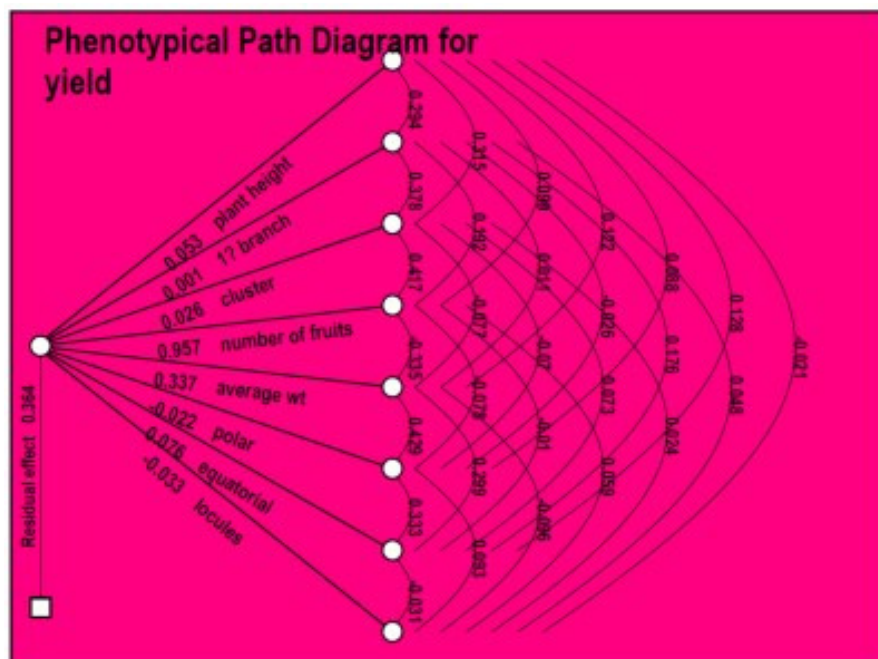


Fig. 5: Phenotypic path diagram for yield (kg/plant) in double cross F₂ population of TSH-8 x TSH-7

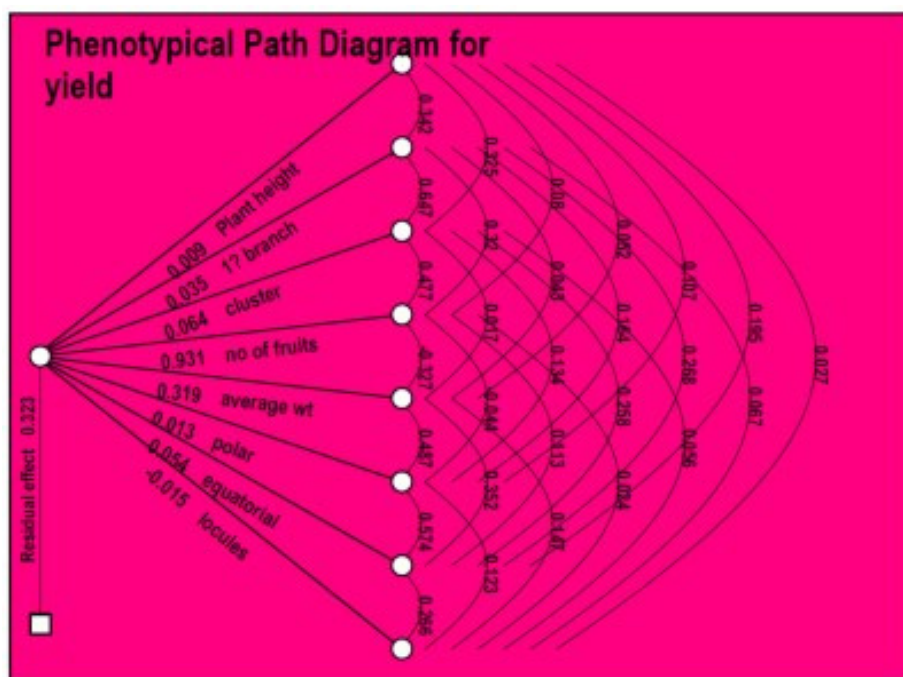


Fig. 6: Phenotypic path diagram for yield (kg/plant) in double cross F_2 population of TSH-2 x TSH-3

4.5.1.7 Equatorial length (cm)

Fruit diameter exhibited positive direct effect (0.0764) on fruit yield per plant. It had indirect positive effect through number of plant height (0.0098), primary branches (0.0134), number of cluster (0.0056), average fruit weight (0.0228) and polar length (0.0255). Equatorial length had indirect effect through number of fruits (-0.0007) and number of locules (-0.0024).

4.5.1.8 Number of locules

Number of locules recorded negative direct effect (-0.0326) on fruit yield per plant. However, it exhibited positive indirect effect through other characters. It also recorded indirect negative effect on yield through primary branches (-0.0016), number of cluster (-0.0008), number of fruits (-0.0019) and polar length (-0.003).

4.5.2 Path coefficient analysis for yield and yield attributing traits in double cross F₂ population of TSH-2 x TSH-3 double cross hybrid

4.5.2.1 Plant height (cm)

In the F₂ population of TSH-2 x TSH-3 hybrid plant height had positive direct effect (0.0095) on fruit yield per plant and positive indirect effect through primary branches (0.0032), number of clusters (0.0031), number of fruits (0.0008), average weight (0.0005), polar length (0.001), equatorial length (0.0018) and number of locules (0.0003) .

4.5.2.2 Number of primary branches

Number of primary branches had positive direct effect (0.0351) on fruit yield per plant and indirect positive effect through plant height (0.012), number of clusters (0.0227), number of fruits (0.0112), average fruit weight (0.0015), polar length (0.0058), equatorial length(0.0094) and number of locules (0.0024) .

4.5.2.3 Number of clusters

Number of clusters also had positive direct effect (0.0636) on fruit yield per plant and positive indirect effects through plant height (0.0207), number of primary branches (0.0412), number of fruits (0.0304) and average fruit weight (0.0011), polar length(0.0086), equatorial length(0.0164) and number of locules (0.0036).

4.5.2.4 Number of fruits per plant

Number of fruits per plant exhibited significant positive correlation with fruit yield per plant and recorded positive direct effect (0.9313) on it. It also had positive indirect effect through plant height (0.0742), primary branches (0.2977), number of cluster (0.0015), number of fruits (0.0017) and it had negative indirect effect through polar length (0.00172), fruit diameter (0.01427), pericarp thickness (0.01529) and total soluble solids (0.01326) and negative indirect effects through other characters.

4.5.2.5 Average fruit weight (g)

Positive direct effect was observed for average fruit weight (0.3186) on fruit yield per plant and it had positive indirect effects observed for all characters [plant height (0.0164), primary branches (0.0136), number of clusters (0.0056), polar length (0.1553), equatorial length (0.1121) and number of locules (0.0469)] except negative indirect effects were observed through number of fruits (-0.1042).

4.5.2.6 Polar length (cm)

Polar length recorded positive direct effect (0.0131) on fruit yield per plant and recorded positive indirect direct effect on fruit yield through plant height (0.0014), primary branches (0.0021), number of cluster (0.0018), average fruit weight (0.0064), equatorial length (0.0075) and number of locules (0.0016). But number of fruits had negative indirect effect.

4.5.2.7 Equatorial length (cm)

Equatorial length exhibited positive direct effect (0.0544) on fruit yield per plant. It had indirect positive effect through plant height (0.0106), number of primary branches (0.0146), number of cluster per plant (0.014), number of fruit (0.0061), average fruit weight (0.0191), polar length (0.0312) and number of locules (0.0145).

4.5.2.8 Number of locules

Number of locules recorded negative direct effect (-0.015) on fruit yield per plant. It also recorded indirect negative effect on fruit yield through plant height (-0.0004), primary branches (-0.001), number of cluster (-0.0008), number of fruits (-0.0004), average fruit weight (-0.0022), polar length (-0.0018) and equatorial length (-0.004).

5. DISCUSSION

Tomato (*Solanum lycopersicum* L.) is an important vegetable crop for the farmers, consumers and processing industries. There is a necessity to improve the productivity in India (21 t/ha) on par with world productivity (33 t/ha). This can be achieved either through the development of high yielding varieties or hybrids. In addition, the price fluctuation is the major problem which receives the wrath of either farmers or consumers. The handling of tomatoes during market glut is burning issue which requires cultivation of tomato cultivars fit for industrial uses. Keeping these things in view study was planned and executed to know the genetic diversity and variability for nutraceuticals traits, industrial quality traits and yield components. This helps to identify the suitable genotype for industrial processing and also to develop new genotypes with higher nutraceuticals and yield.

Understanding the type and extent of genetic diversity and variability is pre-requisite before planning for improvement of specific trait or development of genotype with combination of several good traits. Understanding the type of dependency between characters also helps to redesign the plant type. Hence in the present study popular hybrids and varieties along with few selected germplasms were used to assess the genetic diversity and variability for nutraceuticals and industrial quality traits. Efforts were also made to understand dependency of these characters with fruit yield per plant and its components. The results obtained were discussed in the following chapter.

5.1 Genetic diversity for nutraceuticals, industrial quality traits and yield components in popular hybrids, varieties and germplasm

5.1.1 Genetic diversity among twenty eight genotypes of tomato

In the present study the material used consisted of thirteen popular hybrids, eight varieties and seven germplasm. A total of twelve divergent clusters were formed using Tochers method. The cluster II followed by cluster I had maximum intracluster distance indicating that the genotypes in these clusters were more divergent than other clusters. The clusters II had least intra cluster distance indicating less divergence. Similarly highest inter cluster distance was observed between VIII and IX clusters. Therefore, the genotypes falling in these two clusters may have wider genetic diversity.

Among the 14 quantitative characters studied, the maximum contribution to the total divergence was from β -carotene followed by TSS, ascorbic acid, pH and fruit yield per plant.

Analysis of cluster means indicated substantial variation among the five clusters grouped according to D^2 analysis. Based on the cluster means, it is possible to know the characters influencing divergence. In the present study the cluster XI and IX had high yielding genotypes, whereas clusters VIII was comprised of less yielding genotypes.

It was observed that genotypes producing maximum lycopene content was in X and XI while, lowest lycopene content was found in cluster VI. Highest β -carotene content was found in cluster XI and XII, whereas lower ascorbic content was found in cluster IX and X. Maximum β -carotene content was found in cluster VI and VIII while minimum β -carotene content was noticed in cluster IX and X. Minimum pH was found in II and maximum in cluster III. Maximum TSS content was found in cluster VIII and minimum in cluster IX. The highest intercluster distance was found between clusters VIII and IX. Hence, it could be expected that the cross combinations involving genotypes from each of these

clusters as parents might produce maximum heterosis. Also the probability of isolating superior or transgressive segregants in advanced generations could be high. Interestingly out of twelve clusters ten were solitary indicating distinctness of genotypes.

5.2 Assessing variability for nutraceuticals and industrial quality traits in popular hybrids, varieties and germplasm

All forms of plant improvement activities through breeding contemplate an eventual boost in genetic potential for yield. Since yield is polygenically controlled and highly influenced by environment, selection based on yield alone is not effective. The breeder hence proposes to select for high yield indirectly through yield associated and highly heritable characters after eliminating environmental component of phenotypic variation. An attempt to improve a character by selection would be futile unless a major portion of variation is heritable. This depends entirely on the magnitude of genetic variability in the source population in respect of yield and its heritable components. Although, range can provide a preliminary idea about variability, the coefficient of variation is reliable as it is independent of unit of measurement. In general the characters having high range also exhibited high genotypic and phenotypic coefficients of variations. Hence, it is necessary to partition the total variability into heritable and nonheritable components *viz.*, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance.

In this study, for all the characters the difference between genotypic coefficient of variability and phenotypic coefficient of variation was very less, which indicates lesser environmental influence in the expression of character. Individual character wise variation of GCV and PCV are discussed below and best performing top five genotypes for nutraceuticals and industrial quality traits are presented in Table 17.

5.2.1 Plant height (cm)

High phenotypic and genotypic coefficients of variation were recorded for plant height, similar findings were found by Tasnia *et al.* (2015), Muhammad *et al.* (2013), Osekita and Ademiluyi (2014), Adhishankara *et al.* (2013)

5.2.2 Number of primary branches

Phenotypic and genotypic coefficients of variation was found high for primary branches per plant which was similar to results obtained by Firas *et al.* (2012), Mohamed *et al.* (2012), Gosh *et al.* (2010), Dhankhar and Dhankhar (2006) and Samadia *et al.* (2006).

5.2.3 Number of cluster per plant.

Number of cluster per plant recorded high GCV and PCV values, these findings were similar findings were obtained by Khaidem *et al.* (2014), Rajshekar *et al.* (2013), Islam *et al.* (2012), Gosh *et al.* (2010) and Veerashetty (2004).

5.2.4 Number of fruits per plant.

This trait showed higher phenotypic and genotypic coefficient of variation these findings were in accordance with the results of Tasnia *et al.* (2015), Khaidem *et al.* (2014), Muhammad *et al.* (2013) and Rajshekar *et al.* (2013).

5.2.5 Average fruit weight (g)

This trait showed higher genotypic and phenotypic coefficient of variation these results were in accordance with findings of Tasnia *et al.* (2015) Khaidem *et al.* (2014), Muhammad *et al.* (2013) and Rajshekar *et al.* (2013).

5.2.6 Fruit yield per plant (kg)

Higher GCV and PCV was obtained for fruit yield, similar findings were noted by Tasnia *et al.* (2015), Khaidem *et al.* (2014), Adhishankara *et al.* (2013), Muhammad *et al.* (2013), Rajshekar *et al.* (2013) and Gosh *et al.* (2010).

5.2.7 Number of locules

This trait showed moderate PCV and GCV such a results were obtained by Osekita and Ademiluyi (2014), Adhishankara *et al.* (2013), Veershetty (2004) and Aradhana and Singh (2003).

5.2.8 Polar length (cm)

Phenotypic and genotypic variation for this trait was found moderate, similar results was obtained by Adhishankara *et al.* (2013), Rajshekar *et al.* (2013), Jiregna (2013) and Kumar *et al.* (2006).

5.2.9 Equatorial length (cm)

This trait had shown low PCV and GCV, such a findings were obtained by Upadhyay *et al.* (2005).

5.2.10 Lycopene (mg/100g of fruit)

This trait showed moderate to high GCV and PCV similar to results obtained by Ravindra *et al.* (2015) and Ruskar and Jag (2010).

5.2.11 β -carotene (mg/100g of fruit)

Estimates of phenotypic and genotypic coefficient of variation was found high, such an estimate was also obtained by Ruskar and Jag (2010).

5.2.12 Ascorbic acid (mg/100g of fruit)

Higher GCV and PCV coupled was shown by this trait, such a similar results were obtained by Adhishankara *et al.* (2013), Rajsekhar *et al.* (2013) and Kumar *et al.* (2006).

5.2.13 Total soluble solids (%)

Estimates of coefficient of variation for this trait was found high similar to results obtained by Adhishankara *et al.* (2013), Ruskar and Jag (2010), Jiregna (2013) and Kumar *et al.* (2006).

A greater phenotypic coefficient of variability (PCV) was observed than genotypic coefficient of variation (GCV) for all the traits which indicated that the apparent variation is not only due to genotypes but also due to the influence of environment. Since the difference between values of PCV and GCV were less for all traits. It indicated that major portion of variations observed was genetic in nature and influence of environment was less. The characters yield per plant, number of fruits per plant, number of clusters, β -carotene, ascorbic acid, average fruit weight, plant height, number of primary branches, TSS and number of locules showed higher values of genotypic and phenotypic coefficients variation, indicating the presence of exploitable variability among studied genotypes to improve these characters through selection.

5.3 Nature of variability in F_2 population of double cross hybrids

Improvement of any character in a population depends on the magnitude of variability, heritability and GAM. For this information of genotypic and phenotypic coefficient of variations together with genetic advance as per cent over mean would be useful for improving the efficiency of selection in segregating populations.

One of the ways in which the variability is assessed is through simple approach of examining the range of variation. For most of the characters range was broader in double cross F_2 populations which indicate that more variability is released from segregating generations of double cross hybrids. These higher means and larger magnitude of genotypic and phenotypic variances seen in F_2 population of multiple crosses may be attributed to the release of hidden genetic variability, breaking of linkage and free exchange of favorable genes.

In this study, for all the characters the difference between genotypic coefficient of variability and phenotypic coefficient of variation was very less in both double cross F_2 populations, which indicates lesser environmental influence in the expression of a particular character.

5.3.1 Plant height (cm)

High phenotypic and genotypic coefficients of variation were recorded for plant height in the TSH-8 x TSH-7 than the TSH-2 x TSH-3 F_2 populations of double cross hybrids, such a high estimates of coefficients of variation were found by Tasnia *et al.* (2015), Muhammad *et al.* (2013), Osekita and Ademiluyi (2014), Adhishankara *et al.* (2013), Jiregna (2013), Mohamed *et al.* (2012) and Pradeep *et al.* (2001). Higher heritability coupled with high GAM (both F_2 population) was shown by this character which was similar to findings of Tasnia *et al.* (2015), Muhammad *et al.* (2013), Osekita and Ademiluyi (2014), Adhishankara *et al.* (2013), Mohamed *et al.* (2012) and Pradeep *et al.* (2001).

5.3.2 Number of primary branches

Coefficients of variation was found high for primary branches per plant in both F_2 populations of double cross hybrids but TSH-2 x TSH-3 F_2 population had little higher estimates, such a high results was obtained by Dhankhar and Dhankhar (2006), Gosh *et al.* (2010), Firas *et al.* (2012) and Mohamed *et al.* (2012). Even higher heritability and higher GAM obtained F_2 populations of double cross hybrids which were similar to results obtained by Khaidem *et al.* (2014), Adhishankara *et al.* (2013), Firas *et al.* (2012), Mohamed *et al.* (2012), Gosh *et al.* (2010), Dhankhar and Dhankhar (2006) and Samadia *et al.* (2006). High values of GAM, heritability and GCV indicated that number of primary branches per plant was controlled by additive gene action and selection based on phenotype might be effective in both double cross F_2 populations.

5.3.3 Number of cluster per plant

High PCV and GCV was recorded for number of cluster per plant even higher heritability and GAM was found in TSH-2 x TSH-3 F_2 population of double cross hybrid, similar findings of high estimates were obtained by Khaidem *et al.* (2014), Rajshekar *et al.* (2013), Islam *et al.* (2012), Gosh *et al.* (2010) and Veerashetty (2004).

5.3.4 Number of fruits per plant

Higher phenotypic and genotypic coefficient of variation and high heritability coupled with high GAM was obtained in TSH-8 x TSH-7 F_2 population of double cross hybrid, which was similar to findings of Tasnia *et al.* (2015), Khaidem *et al.* (2014), Muhammad *et al.* (2013) and Rajshekar *et al.* (2013). Coefficients of variation and heritability estimates of TSH-2 x TSH-3 F_2 population was also high but slightly less in comparison.

5.3.5 Average fruit weight (g)

This trait also showed higher genotypic and phenotypic coefficient of variation along with high heritability and GAM in both the population both populations were on par with each other, such a high estimates of variation was found by Tasnia *et al.* (2015) Khaidem *et al.* (2014), Muhammad *et al.* (2013) and Rajshekar *et al.* (2013).

5.3.6 Fruit yield per plant (kg)

Both population showed higher GCV and PCV but heritability and GAM estimates were found high for TSH-2 x TSH-3 F_2 population of double cross hybrid, similar higher estimates of high coefficient of variation were noted by Tasnia *et al.* (2015), Khaidem *et al.* (2014), Adhishankara *et al.* (2013), Muhammad *et al.* (2013), Rajshekar *et al.* (2013) and Gosh *et al.* (2010).

5.3.7 Number of locules

This trait showed moderate PCV, GCV in both the F_2 populations of double cross hybrids such a results were obtained by Osekita and Ademiluyi (2014), Adhishankara *et al.* (2013), Veershetty (2004) and Aradhana and Singh (2003). This trait showed moderate heritability and GAM but the population TSH-2 x TSH-3 had higher results in comparison, such estimates of heritability and GAM were obtained by Osekita and Ademiluyi (2014), Kumar *et al.* (2006), Aradhana and Singh (2003) and Veerashetty (2004).

5.3.8 Polar length (cm)

Phenotypic and genotypic variation for this trait was found moderate in the F_2 populations of double cross hybrids, both population had same performance, similar results of moderate PCV and GCV was obtained by Adhishankara *et al.* (2013), Rajshekar *et al.* (2013), Jiregna (2013) and Kumar *et al.* (2006) but the heritability and GAM estimates was found high and both populations were on par with each other, such a high estimates of heritability and GAM Tasnia *et al.* (2015), Muhammad *et al.* (2013), Adhishankara *et al.* (2013) and Golani *et al.* (2007).

5.3.9 Equatorial length (cm)

Similar to polar length this trait also had moderate PCV and GCV with high heritability and GAM and both populations were on par, such moderate PCV and GCV with high heritability and GAM were obtained by Khaidem *et al.* (2014), Adhishankara *et al.* (2013), Muhammad *et al.* (2013) and Ravindra *et al.* (2015).

Comparison of variability of both population indicated that population TSH-8 x TSH-7 had higher variability for plant height, number of fruits, polar length and fruit yield per plant and population TSH-2 x TSH-3 had higher variability for number of primary branches and number of clusters per plant. But variability for equatorial length, number of locules and average fruit weight both population

were almost same. Presence of high values of GCV and heritability accompanied by high GAM suggest that improvement of number of fruits per plant, fruit yield per plant, number of cluster per plant, average fruit weight, number of primary branches and plant height would be effective through phenotypic selection in both double cross F_2 populations. Lower difference between PCV and GCV for all character except number of fruits per plant in both double cross F_2 populations indicate presence of low environmental effect and variation observed is due to genetic cause. Lower GCV, higher heritability and GAM in polar length, equatorial length and number of locules may be attributed to non-additive gene action and may be further improved through hybridization, which are in consistence with some of researchers like Haydar *et al.* (2007), Kashif *et al.* (2013) and Jiregna, 2013.

5.4 Correlation analysis for yield and yield contributing traits in tomato

Yield is a very complex trait that is why Griffing (1956) was at opinion that there are no genes as such governing yield. Therefore improving yield breeders often try to select on the basis of component characters which are less complex as compared to yield. Correlation analysis helps the breeder to take decision on the choice of the character as selection criteria.

Genetic variability and correlation among fruit yield per plant and yield attributes help in identifying a suitable genotype with desired characteristics. The success of selection depends on the choice of selection criteria for improvement of yield. Correlation coefficient analysis could establish significant relationship among the evaluated traits.

In the present study, in F_2 populations of two double cross hybrids were subjected to correlation studies. It was found that plant height and number of primary branches was positively associated with fruit yield per plant in both F_2 populations. Similar results were recorded by Ravindra *et al.* (2015) and Vinod *et al.* (2013). Even the number of cluster were positively associated with yield such a findings was noticed by Kashif *et al.* (2013). Number of fruits showed positive significance with yield such a similar findings were noted by Ravindra *et al.* (2015), Vinod *et al.* (2013) and Kashif *et al.* (2013). And also equatorial length showed positive significance with yield similar to findings of Islam *et al.* (2012).

This indicates that plant height, number of primary branches, number of clusters and fruits per plant are the most important yield contributing characters in tomato and therefore emphasis should be given for these traits while making selection.

Plant height had significant positive correlation with yield per plant and equatorial in both the F_2 populations of double cross hybrids which is in accordance with Ravindra *et al.* (2015), Muhammad *et al.* (2013) and Vinod *et al.* (2013). However, this trait also exhibited positive effects to number of primary branches similar to results of Ravindra *et al.* (2015) and Vinod *et al.* (2013).

In both F_2 population number of primary branches recorded significant positive correlation with the yield and plant height which is similar to findings of Ravindra *et al.* (2015) and Vinod *et al.* (2013). While number of fruits per plant also recorded significant positive correlation in both F_2 population as findings noted by Khaidem *et al.* (2014) and Rajesh *et al.* (2006). This indicates that simple phenotypic selection based on primary branches in these F_2 populations will help in yield improvement. Average fruit weight had positive correlation with yield similar to findings of Ravindra *et al.* (2015), Santosh *et al.* (2013) and Vinod *et al.* (2013). But it had significant negative correlation with number of fruits similar to findings of Santosh *et al.* (2013).

In the same lines even the number of fruits had positive significant correlation with yield and number of primary branches similar to findings of Vinod *et al.* (2015). Number of clusters had significant positive association with yield, plant height and number of fruits and such a findings were published by Islam *et al.* (2012). Equatorial length showed positive correleation with yield similar too results of Madhurina *et al.* (2012).

It was found that plant height, number of primary branches, number of cluster per plant, number of fruits per plant, fruit length, were associated among themselves in the F₂ populations of both double cross hybrids.

Correlation studies indicated that plant height, number of primary branches, number of fruits per plant, average fruit weight and number of fruits weight, deserve greater weightage during selection for enhancing fruit yield in tomato.

5.5 Path analysis for yield and yield contributing traits in tomato

The correlation values decide only the nature and degree of association existing between pairs of characters. A character like yield is dependent on several mutually associated component characters. The knowledge of correlation alone however is often misleading as the correlation observed may not reflect true nature of association, since two characters may show correlation just because they are correlated with a common third one (Jaiswal and Gupta, 1967). In such cases it becomes necessary to study a method which takes into account the causal relationship. The direct and indirect effect of different characters on fruit yield per plant in two F₂ populations of double cross hybrids is discussed below.

Number of fruits exhibited highest positive direct effect on yield per plant followed by average fruit weight, equatorial length, number of cluster per plant, followed by plant height and number of primary branches in both the F₂ population, number of locules showed negative direct effect in both population, whereas polar length showed negative direct effect in TSH-8 x TSH-7 population but positive direct effect in TSH-2 x TSH-3 population.

Number of fruits showed highest positive direct effect on yield per plant in both F₂ population, but this trait showed positive indirect effect through plant height, number of primary branches, number of clusters and number of locules. Earlier, similar results were reported by Kashif *et al.* (2013), Firas *et al.* (2012) and Gosh *et al.* (2010).

Both F₂ population showed a highest direct effect of average fruit weight on yield but only next highest after number of fruits per plant as it manifested indirect effect on yield through plant height, number of primary branches, equatorial and polar length, similar results were noted by Kashif *et al.* (2013), Firas *et al.* (2012) and Gosh *et al.* (2010). But results of highest positive direct effect through average fruit weight was found by Khapte and Jhansirani (2014a) and Santosh *et al.* (2013).

Number of clusters in both F₂ population showed higher positive direct effect but it showed indirect effect through plant height, number of primary branches, number of fruits and number of locules. Earlier such a findings of higher positive direct effect of number of clusters on fruit yield was reported by Kashif *et al.* (2013) and Gosh *et al.* (2010).

Number of locules showed highest negative direct effect on yield in both F_2 population but it showed negative indirect through primary branches, number of clusters, number of fruits per plant and polar length. Similar results were obtained by Kumar and Dudi (2011). On the other hand polar length in F_2 population of TSH-8 x TSH-7 showed negative direct effect.

Low residual effect indicated that the selection of traits for path coefficient analysis is appropriate and no characters were neglected. In the present investigation, plant height, number of primary branches per plant, number of inflorescence per plant, number of clusters, number of fruits per plant, and average fruit weight were formed as important components characters which must be given due weightage when a plant breeder practices selection.

Future line of work

The highlights of results obtained and inferences derived under different aspects of the study have given rise to some directions for future line of work as indicated below.

- Yield levels of superior genotypes for the quality traits (neutraceuticals and industrial quality traits) could be improved through recombination breeding.
- The lines superior for both neutraceuticals and industrial quality traits can be developed using available genetic variability.
- Intercluster distance was between clusters VIII and IX was very high, genotypes in these clusters could be used as parents and might produce maximum heterosis.
- High amount of variability in two F_2 population of double cross hybrids was observed which can be further exploited for isolation superior lines.
- The traits like number of fruits per plant and average fruit weight can be used for direct selection on account of their maximum positive direct effect with yield.

6. SUMMARY AND CONCLUSIONS

Present study involved two different experiments of which first was to find genetic diversity and variability for nutraceuticals, industrial quality traits, yield and yield components in popular hybrids, varieties and selected germplasm. The second experiment consisted of comparing the variability in two F_2 populations of double cross hybrids of tomato and understanding the nature and type of dependency between characters.

- Thirteen popular hybrids, eight varieties and seven germplasm were evaluated for genetic diversity and variability for nutraceuticals, industrial quality traits and yield components.
- Diversity studies indicated that intercluster distance was maximum between clusters VIII and IX. Hence, it could be expected that the cross combinations involving genotypes from each of these clusters as parents might produce heterotic hybrids.
- For lycopene, cross between the genotypes of cluster V and XI would produce maximum heterosis while for β -carotene cross between the genotype of cluster VI and VIII could produce better heterosis. Similarly genotypes between cluster III and XII may produce maximum heterosis for ascorbic acid content. The genotypes from between cluster II and III may produce good heterosis for pH. While cross between genotypes of cluster VIII and XI may produce good heterosis for TSS.
- Lycopene showed moderate to high coefficient of variation, whereas β -carotene, ascorbic acid and pH showed high PCV and GCV.
- Majority of yield related characters showed high PCV and GCV except polar length and equatorial length.
- Yield levels of best performing genotypes in terms of nutraceuticals or industrial quality traits was found low, which can be enhanced further by recombination breeding.
- Two double cross F_2 populations were subjected for variability, character association and path analysis. It was found that for all major characters had higher PCV and GCV in double cross F_2 populations except for polar length, equatorial length and number of locule.
- High heritability and genetic advance as per cent over mean was exhibited by both the populations for all characters except number of fruits per plant, number locules which exhibited low to moderate heritability and GAM.
- The number of fruits, number of clusters were positively and highly associated with fruit yield per plant in both F_2 populations, while number of primary branches, plant height and equatorial length were also positively associated with fruit yield per plant in both of the populations. Polar length showed significant correlation only in TSH-2 X TSH-3 F_2 but it was not significant in TSH-8 X TSH-7 double cross F_2 population.
- Path analysis revealed that number of fruits per plant exhibited highest positive direct effect on yield followed by average fruit weight, equatorial length, number of clusters, plant height and primary branches. Number of locules had exhibited significant negative direct effect on fruit yield per plant in both F_2 populations.

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GENETIC STUDIES ON NEUTRACEUTICALS, INDUSTRIAL QUALITY TRAITS AND YIELD COMPONENTS OF TOMATO (*Solanum lycopersicum* L.)

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ABSTRACT

Present study involved two different experiments of which first was to find genetic diversity and variability for neutraceuticals, industrial quality traits, yield and yield components in twenty eight genotypes of tomato. Diversity studies indicated that intercluster distance was maximum between clusters VIII and IX. Hence, it could be expected that the cross combinations involving genotypes from each of these clusters as parents might produce heterotic hybrids. Lycopene showed moderate to high coefficient of variation, whereas β -carotene, ascorbic acid and pH showed high PCV and GCV. Majority of yield related characters showed high PCV and GCV. The second experiment consisted of comparing the variability in two F_2 populations of double cross hybrids of tomato and understanding the nature and type of dependency between characters. It was found that all major characters had higher PCV and GCV in double cross F_2 populations. High heritability and genetic advance as per cent over mean was exhibited by both the populations for all characters except number of fruits per plant, number locules other wise which exhibited low to moderate heritability and GAM. The number of fruits and number of clusters were positively and highly associated with fruit yield per plant in both F_2 populations. Polar length showed significant correlation only in the cross TSH-2 X TSH-3 F_2 . Path analysis revealed that number of fruits per plant exhibited highest positive direct effect on yield followed by average fruit weight, equatorial length, number of clusters, plant height and primary branches. Number of locules had exhibited significant negative direct effect on fruit yield per plant in both F_2 populations.