BIOMETRICAL AND TRANSFORMATION STUDIES IN TOMATO (*Solanum lycopersicum* L.)

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1. INTRODUCTION

Tomato (*Solanum lycopersicum* L., syn. *Lycopersicon esculentum,* 2n=24) of nightshade or Solanaceae family with primary center of origin in Mexico-Peru-Equador region was once considered inedible but has evolved into globally leading popular vegetable. It is highly worked crop by the horticulturists and biotechnologists. It has wide range of variation in terms of growth habit, morphological traits and uses making it a repository of glowing traits in its armory. It has determinate vs indeterminate types, cherry to table type fruits, canning to juice type fruits, smooth to ridged fruits, acidic to sweet type fruits, red to orange yellow to striped color fruits, etc., But whatever may be the type botanically it is same and they are crossable. Its nutritional importance is enlarged with antioxidant properties of lycopene and its anticancerous properties. Growing consumption of tomato in processed or fresh form is driven by its versatile, palatable, culinary and attractive properties apart from its health benefits.

It was introduced in India in 17^{th} century by Europeans and today it has become part and parcel of Indian food besides becoming one of the leading vegetable with lot of research work and outcomes seen in it. Globally, India is the third largest producer of tomato after China and USA. Karnataka too is one of the leading producers of tomato. Year round cultivation has created new challenges to the varietal development and disease management. These challenges are reinforcing themselves owing to the climatic or weather changes and evolving race dynamics of pathogens. This calls for continuous work in tomato improvement in terms of varietal or F_1 hybrids development, identification, and management. Many institutions are working on these aspects at national level and are coming out with new genotypes. These new genotypes could be tested for suitability and adaptability in other regions besides using them for hybrid development or getting desirable segregants. Continuously there is a need to evaluate new genotypes in new environments as genetic information of them changes with changing composition of genotypes and new environmental conditions each year.

Botanical nomenclature of tomato has seen a lot of debate, research work and change. It's nomenclature has changed from previously widely used *Lycopersicon esculentum* Miller in *Lycopersicon* genus (named by Phillip Miller in 1768) to originally named *Solanum lycopersicum* L. in *Solanum* genus (named in 1753 by Linnaeus; *lyco* = wolf, *persicum* = peach i.e., wolf-peach) due to recent work of Peralta and Spooner (2001).

Challenges in tomato productions are need of new varieties or hybrids for dynamic production systems and disease resistant varieties. For meeting these we need to develop superior and stable varieties and also for development of hybrids with better yield and quality.

This calls for generating information on variability, heritability, genetic advance, character association, path analysis, diversity, and stability of tomato genotypes for identifying suitable variety to grow or for taking up heterosis breeding through hybridization to either develop suitable F_1 hybrids or generate desirable transgressive segregants which could be used in further improvement programmes.

Tomato diseases have compelled development of resistant varieties. Among fungal disease, early blight, late blight, powdery mildew, *Sclerotium* wilt are major ones, while in viral group, tomato leaf curl virus , tomato spotted wilt virus , are severe ones. Resistant varieties have compelled pathogens to evolve new races and overcome resistance in varieties. This is a never ending engagement of vegetable breeders and pathogens for existence. Non-complacency will keep one abreast in this engagement and development of newer strategies is the answer. With the exhaustion of available resistance gene sources among cultivated related species it leaves us with option to explore introducing new genes from other living organisms or artificial gene constructs that hinder pathogen from causing disease in the plant system. The gene transfer could be done with the help of biotechnological tools. One important disease i.e., tomato leaf curl virus is one which calls for greater focused work. To tackle this disease, genetic transformation attempts are needed.

Looking to these realities in tomato cultivation, identification of high yielding stable varieties, the development of F_1 hybrids and genetic transformation for disease resistance is taken up for investigations under the title 'Biometrical and transformation studies in tomato (*Solanum lycopersicum* L.) with the following objectives:

1. To study variability, divergence, character association and stability in tomato for horticultural traits.
2. To study heterosis and combining ability for growth, yield, quality and disease incidence traits in tomato.
3. To transform tomato with antiviral gene constructs.

2. REVIEW OF LITERATURE

Review of literature relevant to the investigation on "Biometrical and transformation studies in tomato (*Solanum lycopersicum.* L.)" has been collected and presented (from 1908 to 2010). There has been voluminous literature on biometrical and transformation aspects in tomato crop. Discretion has been exercised to retain only relevant representative few citations and omitting others looking to limitation of quoting here. For improvement of traits in tomato there is a need of having knowledge of genetics of different traits to initiate modifications for our situation specific requirements. Conventional approach of breeding involving utilizing existing genotypes after adequate evaluation to know their performance and expression for desirable traits at particular location is indispensible even with present day complementing biotechnological tools of tackling insurmountable handicaps in tomato crop more specifically like susceptibility to viral diseases like tomato leaf curl virus and tomato spotted wilt virus. Hence, the investigations in the present study involved evaluation of tomato genotypes for three seasons, hybridization to develop F_1's from parents with horticultural traits from diverse background to identify heterotic combinations after subjecting data to statistical analysis to elicit information on variability, correlation, path analysis, divergence, stability analysis, heterosis and combining ability and transformation of tomato with antiviral peptide gene constructs to modify them genetically to introduce resistance to viral disease .

Looking to these outlines of the present investigation, the literature that was reviewed on tomato is presented under following headings:

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation and path analysis

2.3 Genetic divergence

2.4 Stability analysis

2.5 Heterosis

2.6 Combining ability

2.7 Transformation in tomato

2.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

Variability is the foundation stone for initiating vegetable improvement programme. Utilization of the existing variability pool needs complete exploration and exploitation before trying to create new range of variations after recombination from hybridization or through mutations. Thorough estimate and study of genetic variability is a pre-requisite for initiating appropriate breeding procedures in crop improvement programmes, which demands wide range of variability in a population. The determination of genetic variability and its partitioning into various components in crop plants is necessary to have an insight into genic nature of yield and its components. The degree to which variability of a character may be transmitted to the progeny is referred to as its heritability. The heritable variation is marked by non-heritable components hence, it is necessary to split the overall heritability using genetic parameters.

Heritability in broad sense is the ratio of genotypic variance to total variance in non-segregating population (Hanson *et al*., 1956). A high heritability is not always accompanied by high genetic advance but, in the presence of fixable gene effects high genetic advance should be expected (Panse and Sukhatme, 1967). Genetic advance under selection is the improvement in the mean genotypic value of the selected families over base population which depends upon the genetic variability existing in the population, the heritability of the character under selection and the intensity of selection. Hence, the components of variances and heritable components with genetic parameters, such as genetic coefficient of variation, heritability estimate and genetic advance are important tools for the breeders to plan suitable breeding strategy.

High heritability, genotypic coefficient of variability, genetic advance has been reported in a study involving 21 tomato genotypes (Singh, 2009).

Significant variability (GCV & PCV) was seen among 30 tomato genotypes evaluated for 19 quantitative traits (Shashikanth, 2008).

Wide range of variability, high heritability high GAM were observed for many of the growth and yield attributes like number of fruits per plant, average fruit weight, fruit yield per plant from a study involving forty four tomato genotypes (Revanasidappa, 2008).

'DMT-2' a new high acid content tomato variety derivative of the cross 'CA-1' x '20/6 Alcobasa' had superior yields of 26.74 t/ha compared to 'Pusa Ruby' (11.45 t/ha) and 'Megha' (22.71 t/ha). It was 0.94% acid content, 65.07 g fruit weight, 3.87 kg fruit yield per plant with thin pericarp. It recorded 13.62 to 18.87% increase in yield over 'Megha' and upto 50% over 'Pusa Ruby' in farm trials in different districts of North Karnataka (Dharmatti *et al.,* 2008).

High variability was generated in populations J/S, S/J, J/G, G/J obtained by attempting biparental mating among selected F_2 generation of three commercial hybrids (JK-Des (J), Shivaji (G), Sasya-54 (S)). Population G/J exhibited high GCV, h^2 & GA for main yield attributing traits, J/G for fruit related characters. Populations involving J and G had potential to release variability from cross combinations (Sivaprasad, 2008).

Biparental progenies (derived from inter and intra-population mating) and selfed progenies when advanced through different methods of selection i.e., Individual plant selection (IPS) and bulk (BP) method to compare their efficiency to improve fruit yield and yield component traits indicated that inter-population mating had higher values / estimates of genetic parameter compared to intra-population mating indicating that inter-population mating can be a better tool for exploiting variability available in the crop and to pool the desirable genes from both the populations. In all the crosses estimates of genetic parameters and frequency of superior segregants were high in bulk method compared to IPS. Change in the association pattern was observed for yield and its component traits indicating that biparental mating had resulted in breakage of undesirable associations and creation of larger variability in the population when advanced through different selection methods (Revanasidappa, 2008),

Biparental mating in tomato to assess the variability generated and compare the efficiency of inter-population biparental mating over intra-population biparental mating over intra-population biparental mating and of biparental mating over selected population for yield and its components. Intra-population mating involved the crosses within each F_2 population of MHTM-256 and S-4-14 while inter-population mating was carried out between selected F_2 plants of MHTM-256 as male with selected F_2 plants of 'S-4-14' and vice-versa. Of the two the best F_2 population (S-4-14) was selfed to get F_3 progeny. It revealed that mean values were high in F_3 than BIPs because of wider variability generated in BIPs especially inter-mating populations. The magnitudes of GCV, PCV, heritability and GA were enhanced in BIPs for all characters studied than the selfed population. Among BIPs inter-populations mating exhibited high heritability and GA for plant height, fruit weight and yield. Biparental mating showed shift in magnitude as well as direction of correlation coefficient. Inter-population mating showed high frequency of superior segregants in yield (Kulkarni, 2006).

A bird view of the reports on these aspects is presented in Table 1.

2.2 CORRELATION AND PATH COEFFICIENT ANALYSIS

2.2.1 Correlation

Correlation study measures the natural relationship between various characters and helps in determining the component characters on which selection can be based on for yield improvement. Correlation coefficient measures the degree of association either in positive or negative direction. Phenotypic correlation is the observable correlation between two variables, which includes both genotypic and environmental effects. Genotypic correlation on the other hand, is the inherent association between two variables and it may be either due to pleotropic action of genes or linkage or both.

A crisp review of literature on correlation studies are presented in Table 2.

2.2.2 Path coefficient analysis

Correlation coefficient alone when considered as the criterion for selection for high yield, would be misleading, as such a character may not be directly correlated with yield but may further depend on other characters. As a result, the direct contribution of each of the component character to the yield and the indirect effects it has through its association with

Table 1. Literature showing the genetic variability, heritability and genetic advance for various characters in tomato.

Sl. No.	Character	PCV (%)	GCV (%)	h^2_{bs}	GA	GAM (%)	References
1.	Plant height	53.54	51.65	93.08	105.73	102.66	Nandpuri *et al.* (1977)
		258.91	101.06	39.03	9.78	17.12	Narendrakumar and Arya (1995)
		1343.57	1303.03	96.98	71.81	74.67	Pujari *et al.* (1995)
		11.89	9.53	65.50	8.80	15.94	Patil (1996)
		5.16	3.55	46.66	1.96	4.95	Shashikanth (2008)
		16.48	17.48	88.90	24.15	32.11	Shalini (2009)
2.	Number of branches per plant	-	18.04	83.00	4.34	33.91	Paranjothi and Muthukrishnan (1979)
		16.32	13.36	66.97	19.63	218.59	Patil (1996)
		36.93	30.98	70.40	8.70	53.53	Veershetty (2004)
		45.40	42.29	86.78	3.84	81.16	Revanasiddappa (2008)
		28.36	26.60	93.76	3.20	54.79	Sivaprasad (2008)
3.	Days to 50% flowering	35.03	26.75	76.37	8.58	10.10	Pujari *et al.* (1995)
		8.59	5.00	33.90	3.08	6.00	Patil (1996)
		11.51	8.82	58.80	3.93	13.94	Veershetty (2004)
		1.74	1.01	33.90	-	1.21	Mehta and Asati (2008)
5.	Number of fruits per cluster	163.15	126.31	62.48	44.08	232.04	Srivastava and Sachan (1973)
		18.79	16.27	75.00	-	29.21	Bora *et al.* (1993)
		37.07	33.79	83.05	21.97	749.83	Patil (1996)
		26.35	18.65	49.00	0.73	26.52	Sivaprasad (2008)
6.	Number of fruits per plant	78.74	68.69	76.09	96.85	123.43	Nandpuri *et al.* (1977)
		-	37.20	93.00	36.07	73.76	Paranjothi and Muthukrishnan (1979)
		169.15	167.85	98.47	89.95	343.13	Revanasiddappa (2008)
		43.90	37.32	85.00	20.78	76.88	Sivaprasad (2008)
7.	Yield per plant	-	29.04	83.00	0.68	54.71	Paranjothi and Muthukrishnan (1979)
		52.52	18.57	12.50	0.16	11.03	Narendrakumar and Arya (1995)
		57.48	55.05	90.90	0.87	106.60	Tiwari and Lal (2005)
		97.22	92.77	91.06	1846.48	182.36	Revanasiddappa (2008)
		48.26	39.51	81.85	855.04	81.39	Sivaprasad (2008)
8.	Average fruit weight	67.45	65.70	94.88	63.88	131.84	Nandpuri *et al.* (1977)
		38.57	38.10	97.60	68.15	77.52	Prashanth *et al.* (2006)
		49.19	46.19	89.18	35.77	89.33	Revanasiddappa (2008)

Contd...

Sl. No.	Character	PCV (%)	GCV (%)	h^2_{bs}	GA	GAM (%)	References
		24.79	19.33	77.98	15.68	39.82	Sivaprasad (2008)
9.	Pericarp thickness	24.56	21.97	82.01	0.41	100.74	Bhutani *et al.* (1983)
		42.28	35.09	68.96	3.32	5.61	Patil (1996)
		19.74	19.07	95.98	0.21	37.95	Sivaprasad (2008)
10.	Number of locules per fruit	-	36.00	85.00	2.60	68.48	Paranjothi and Muthukrishnan (1979)
		66.25	55.78	70.88	4.49	96.73	Revanasiddappa (2008)
		38.93	35.96	85.33	2.66	68.44	Sivaprasad (2008)
11.	Fruit length	14.38	10.58	54.15	0.46	10.50	Sahu and Mishra (1995)
		18.64	18.24	95.79	1.92	36.71	Das *et al.* (1998)
		20.58	19.19	87.00	8.12	-	Krishnaprasad and Rai (1999)
12.	Fruit width	20.29	17.61	75.35	1.50	31.47	Rattan *et al.* (1983)
		24.72	22.81	85.00	8.72	-	Krishnaprasad and Rai (1999)
		16.05	15.04	87.8	1.43	29.06	Shalini (2009)

Table 2. Review of literature on correlations among the different characters of tomato.

Sl. No.	Character	Plant height	No. of branches/ plant	Days to 50% flowering	No. of clusters/plant	No.of flowers/ cluster	No. of fruits / cluster	No. of fruits / plant	Total yield / plant	Avg. fruit weight	No. of locules per fruit	Pericarp thickness	Fruit length	Fruit width	Fruit shape index	No. of ridges on fruit	References
1.	Plant height							P-- G-	P-- G--								Nandapuri *et al.* (1976)
			P++ G++	G--		G--		P++ G++	P++ G--	G--	G-	G--	P-- G--				Prashanth (2003)
					G+				G+								Veershetty (2004)
				G++													Mehta and Asati (2008)
2.	Number of branches per plant							G+	G++					G+			Supe and Kale (1992)
						P++ G++	P++ G++	P++ G++	P+ G+	P-- G--							Raijadhav *et al.* (1996)
								G-	G--	G-			G-	G-			Mala and Vadivel (1999)
3.	Days to 50 per cent flowering	P-	P-							P+			P+				Mulge and Aravindakumar (2003)
										G+						G+	Veershetty (2004)
									G-								Mehta and Asati (2008)
4.	Number of clusters per plant								G++								Veershetty (2004)
								G+		G++							Mehta and Asati (2008)
5.	Number of flowers per cluster							P++ G++		P-- G--							Reddy and Gulshanlal (1987)
							P++ G++		P-- G--	P-- G--		P-- G--	P-- G--	P-- G--			Prashanth (2003)
6.	Number of fruits per cluster								P-- G--			P-- G--					Fageria and Kohli (1996)
								P++									Dhankar *et al.* (2001)
				G-													Mehta and Asati (2008)
7.	Number of fruits per plant									P-- G--				P-			Srivastava and Sachan (1973)
						P--	P++		P++	P-							Dhankar *et al.* (2001)
									P++ G++	P-- G--							Mohanty (2003)
										G-	G-						Parsanna *et al.* (2005)
8.	Total yield per plant	P--															Verma *et al.* (1976)
								P+		P+							Dudi and Kalloo (1982)
			P+ G+														Reddy and Gulshanlal (1987)
								P++ G++		P-							Raijadhav *et al.* (1996)

Contd.

Sl. No.	Character	Plant height	No. of branches/ plant	Days to 50% flowering	No. of clusters/plant	No.of flowers/ cluster	No. of fruits / cluster	No. of fruits / plant	Total yield / plant	Avg. fruit weight	No. of locules per fruit	Pericarp thickness	Fruit length	Fruit width	Fruit shape index	No. of ridges on fruit	References
9.	Average fruit weight								P-					P--			Srivastava and Sachan (1973)
											P++ G++		P++ G++	P++ G++			Krishnaprasad and Rai (1999)
									G++							P+ G++	Veershetty (2004)
10.	Number of locules per fruit												P++ G++	P++ G++			Singh *et al.* (1974)
									P+ G++	P++ G++							Prashanth (2003)
									P++ G++								Anitha *et al.* (2007)
11.	Pericarp thickness	G--					G--		G++								Fageria and Kohli (1996)
							P-- G--	P-- G--	P++ G++	P++ G++							Prashanth (2003)
12	Fruit length								G--					G-			Supe and Kale (1992)
									G+					G++			Mala and Vadivel (1999)
							P-	P--	P++ G++	P++ G++		P++		P++			Prashanth (2003)
13.	Fruit width								P++ G++								Srivastava and Sachan (1973)
									G++								Mala and Vadivel (1999)
							P-- G--	P-- G--	P++ G++	P++ G ++	P++ G++	P++ G++					Prashanth (2003)
14.	Fruit shape index								G++								Veershetty (2004)

Note: G+ and G++ denote genotypic positive association at 5 and 1 per cent significant level; G- and G-- denote genotypic negative association at 5 and 1 per cent significant level
P+ and P++ denote phenotypic positive association at 5 and 1 per cent significant level; P- and P-- denote phenotypic negative association at 5 and 1 per cent significant level

other components cannot be differentiated from correlation studies. The technique of path coefficient analysis was developed by Wright (1921) and demonstrated by Dewey and Lu (1959) as a means of separating direct and indirect contribution of various characters. It is a standardized partial regression coefficient analysis and as such, it measures the direct influence of one variable upon other and permits the separation of correlation coefficient into components of direct and indirect effects. The use of this technique requires cause and effect situation among the variables (Singh and Chaudhary, 1977).

Number of fruits per plant had the highest positive direct effect on yield (Padda *et al.*, 1971; Bhutani and Kalloo, 1989, Rathod, 1997 and Patil, 1998).

Bhutani and Kalloo (1991) reported that number of locules per fruit and plant height had direct positive effects on yield but its effect was counter balanced mostly by indirect negative effects via number of fruits. A negative and low indirect effect of pericarp thickness on yield of fruits per plant was noticed through number of locules (Patil, 1998).

Supe and Kale (1992) and Sonone *et al.* (1987) revealed that the number of primary branches per plant had the highest positive direct effect as the major yield contributing trait for enhancing yield. But, Patil (1998) noticed indirect effect of number of branches per plant through number of fruits per plant on yield was high.

Domani and Maya (1997) observed number of fruits per plant was most important character having direct effect on yield.

Pericarp thickness had positive direct effect on yield mainly due to positive indirect effects through number of fruits per plant and number of branches per plant (Patil, 1998).

Dhankar *et al.* (2001) reported that the average fruit weight under normal condition showed the highest positive effect on yield, therefore selection for average fruit weight, fruit shape index, number of fruits per plant and number of fruits per cluster is important for improvement of fruit yield.

Mohanty (2002) reported that the number of branches per plant, number of ridges on fruit and average fruit weight exerted high positive direct effect on yield and high positive indirect effect with each other.

Prashanth (2003) recorded high direct positive effects of number of flowers per cluster, average fruit weight and number of fruits per cluster on total yield per plant.

Kant and Mani (2004) observed that, path coefficient analysis indicated the importance of fruits per plant, fruit width, days to 50 per cent flowering and fruits per bunch as these characters showed higher direct positive effects on fruit yield.

The maximum direct positive effect on fruit yield per plant was exhibited by number of fruits per plant followed by number of fruits per cluster (Veershetty, 2004).

Locule number registered its positive indirect effect through yield per plant (Anitha *et al*., 2007).

Mehta and Asati (2008) reported that plant height had the highest positive direct effect on fruit yield at genotypic level which was followed by weight of fruit per plant.

Sivaprasad (2008) revealed that number of fruits per plant and average fruit weight had high direct and indirect effect on yield per plant in all the populations.

The fruits per plant showed maximum direct effect on fruit yield per plant in all the populations (Revanasidappa, 2008)

2.3 GENETIC DIVERGENCE

The magnitude of divergence between two groups under consideration is provided by D^2 statistic developed by Mahalanobis (1936). It considers the variation produced by any character and their consequent effect that it bears on other characters.

The technique in the form of generalized distance was first used by Mahalanobis (1936), in an anthropometric survey of the united province in India.

D^2 analysis can be extended to the situations where overlapping species need to be discriminated. It is also utilized when the discrimination at sub-species level is needed. Thus, the technique was subsequently used in different vegetable crops (Murthy and Pavate, 1962).

Genetic diversity involving 17 tomato advanced breeding lines showed contribution of nine quantitative traits to diversity. Seven clusters were formed with four solitary clusters indicating they are highly diverse from other genotypes. RAPD and SRAP primers were used to analyze molecular diversity among these 17 lines. Seven clusters and five clusters were formed in RAPD and SRAP diversity analysis. SARP markers showed more polymorphism, consistency and repeatability compared to RAPD, hence could be more useful markers (Mane, 2009).

Divergence study involving 70 tomato genotypes with high variability were grouped into seven clusters in D^2 analysis (Yashvantakumar *et. al*., 2009a).

Study to assess extent of genetic diversity among 10 ruling productive commercial hybrids in tomato lead to grouping into three clusters and this was done to understand diverse hybrids for exploitation of double cross hybrids. Average fruit weight and TSS contributed maximum (20% each) towards genetic divergence followed by number of flowers per cluster, plant height and number of locules per fruit. 'JK-Desi' and other six hybrids were in cluster I, 'Sasya' in cluster II and 'Shivaji' in cluster III (Sekhar *et al,* 2008).

30 tomato genotypes were grouped into 10 clusters in D^2 analysis. Major traits contributing to diversity were day to 50% flowering, TSS, fruits per cluster, and yield per plant (Shashikanth, 2008).

Sachan and Sharma (1971) while studying genetic divergence in 20 varieties of tomato from diverse geographical source reported substantial divergence of an indigenous material 'Jaipuri' from both exotics 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.

Bhattacharya *et al.* (1979) attempted to know the species differentiation in tomato based on the results of genetic divergence by D^2 analysis using 50 tomato genotypes comprising of wild collections and rest of them were common cultivars belonging to different geographical areas and were evaluated for 17 characters. Genotypes were grouped into 16 clusters on the basis of relative magnitude of D^2 values. The four wild collections of which three belonging to *Lycopersicon peruvianum* and one to *Lycopersicon pimpinellifolium* were grouped into three distant clusters, which were highly diverse from all the other clusters comprising only the cultivars of *Lycopersicon esculentum* Mill. The major contribution to the divergence was by the fruit number per plant which helped in species differentiation. Shape index was useful for varietal differentiation in the *Lycopersicon esculentum* Mill.

Singh and Singh (1980) studied 21 Indian and 9 foreign varieties of tomato using Mahalanobis's D^2 statistic. Maximum divergence resulted from number of fruits per plant followed by fruit size and number of primary branches per plant. The varieties were grouped into 8 clusters.

Chaurasia and Majorsingh (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. Considering the cluster distances and cluster means the genotypes KS-7, DVRT-2, Antey and PS-1 were recorded as potential parents for hybridization.

Rai *et al.* (1998) reported, 37 tomato genotypes of different geographical origin were assessed under field condition and determined the nature and magnitude of genetic divergence using non-hierarchical clustering approach with the help of Mahalanobis's D^2 analysis for yield and its contributing characters. The population was grouped into 4 clusters. The clustering pattern indicates that there was no association between genotypical distribution of genotypes and genetic divergence. The characters namely number of primary

branches, days to flowering, pericarp thickness, plant height and average fruit weight contributed maximum to the divergence.

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 were 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.

Sharma and Verma (2001) reported 18 genotypes of tomato were studied for genetic divergence. The genotypes were grouped in cluster irrespective of geographic divergence indicating no parallelism of fruit genetic divergence and geographical divergence. The characters like fruit yield per plant, pericarp thickness and fruit diameter plays an important role in divergence between the populations.

A study was conducted with 23 genotypes of tomato in Meghalaya. There was considerable diversity among genotypes for 8 morphological characters. Among them plant height, fruit number and fruit size contributed to the divergence. Crosses involving L-964 and L-154 with Arka Abha and LE-79 were recommended for improved yield and better fruit size as reported by Parthasarathy and Aswath (2002).

Arun *et al.* (2003) studied the nature and magnitude of genetic divergence in 73 tomato genotypes of different origin for quantitative characters and they grouped genotypes into 15 clusters indicated the presence of wide range of genetic diversity among the genotypes, cluster 5 having 6 genotypes. The mean fruit yield per plant (1034 g/plant) and average fruit weight (102.76 g) were the highest in cluster 5 and 3 respectively. The plant height (135.91 cm), harvest duration (37.77 days) were maximum in cluster 15 and lowest number of leaves (20280) was recorded in cluster 9 and cluster 6 consists of highest number of fruits per cluster (4.90).

Sixty-seven genotypes of tomato were grouped into seven clusters by following Mahalanobis's D^2 analysis. The cluster IV showed maximum intra cluster distance and the maximum inter-cluster distance was observed between cluster V and VI. Among the 21 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 (Prashanth, 2003).

Veershetty (2004) reported divergence for 32 tomato genotypes by following Mahalanobis's D^2 analysis for 16 productivity traits. The traits like number of fruits per cluster, plant height and number of clusters per plant contributed greatly towards divergence.

2.4 STABILITY ANALYSIS

Stability analysis for growth, yield and yield attributing traits and quality are very important from the point of stable production of tomatoes and to avoid glut or scarcity in the market. Literature on these aspects is reviewed in this chapter and presented under different headings.

2.4.1 Genotype x Environment interaction and models of stability analysis

A specified genotype does not exhibit the same phenotypic characters including yield in all environments. The failure of a genotype to give the same phenotypic performance when tested under different environments is the reflection of genotype x environment interaction. Genotype x Environment interactions are of major importance to the plant breeder in developing stable varieties (Eberhart and Russell, 1966). Vegetable breeders are mainly interested in increasing the level of production with minimum fluctuations in the crop performance as it influences prices of these perishable commodities in the market. It is here that stability has played a pivotal role.

Adaptation is the property of a genotype, which permits subsequent alteration of the norms of the adaptations in response to changed selection pressure (Simmonds, 1962). Lewis (1954) defined stability as the ability of an individual to produce a certain narrow range of phenotypes in different environments. Genotype-environment interaction exists whenever the differences between a numbers of genotypes change with changes in the environment (Ceccarelli, 1989).

There are basically two different approaches towards genotype-environment interaction. The first is to select for low genotype-environment interaction and high yield. This approach has resulted in the development of genotypes, which although classified as widely adapted are actually adapted to environments, where high yield potential can be expressed. The second approach towards genotype-environment interaction is to make use of it. This is possible by breeding for maximum yield and stability within macro-environment (Ceccarelli, 1989).

Effect of environmental variation on genotype performance suggests that, genotype selection is not possible from one environment (either year or location) but the genotypes must be evaluated in diverse environments.

Selection for stable genotypes that interact less with the environments in which they are grown, are known to reduce genotype environment interaction to considerable extent (Allard and Bradshaw, 1964). Genotypes, which interact less with the environment, are selected and it helps the breeder in developing stable genotypes.

A dynamic approach to the interaction of varietal adaptation to varying environments was developed by Finlay and Wilkinson (1963). It led to the discovery that the components of a genotype and environmental interaction were linear in relation to environmental effects.

The above technique was improved further by Eberhart and Russell (1966) by adding another stability parameter, *viz*., deviation from regression. From stability point of view, the variance due to genotype-environmental interaction being the most important. Perkins and Jinks (1968) proposed that, a regression of genotype environment interaction on environmental index should be obtained rather than regression of mean performance (Y_{ij}) on the later as done in the Eberhart and Russell model. With respect to the stability parameters, the same two parameters, regression coefficient and the deviation from regression are used as the parameters of stability. In comparison to Eberhart and Russell model, the regression coefficient in Perkins and Jinks (1968) model is different. Perkins and Jinks (1968) proposed to calculate the regression of genotype-environment interaction value on the environmental index. The relative ranking of different genotypes in this model will in no way be different from that of Eberhart and Russell model. In Perkins and Jinks model, the sum of squares is further divided into two parts, i.e. (i) sum of squares due to heterogeneity between regression which is the same as sum of squares due to variety x environment (linear) of Eberhart and Russell model and (ii) remainder sum of squares, which is the sum of squares due to pooled deviation of Eberhart and Russell's model.

Eberhart and Russell (1966) model is equally efficient as the other two models for deciding stability of genotypes (Luthra and Singh, 1974) and it was recommended for its simplicity and effectiveness. Luthra and Singh (1974) recommended that the breeding material should be evaluated both for sensitivity to the environment and for relative mean performance. In practice, there are wide deviations from linearity and the regression.

2.4.2 Stability for growth parameters

16 advanced breeding lines with Megha (L-15) as check were tested for their stability at three locations. Pooled analysis of variance revealed significant difference among the genotypes and environments for all the characters indicating that genotypes and environments tested are diverse in nature. G x E interaction was significant for most of the characters suggesting genotypes interacted significantly with environments. TS-1, TS-6, TS-11, TS-14, TS-15 and T-16 were found to be most stable genotypes for yield attributing traits with high mean performance across locations. TS-15 had highest lycopene. TS-7, L-15 and TS-9, had highest total titratable acidity, ascorbic acid content and pH respectively. TS-3 had highest juice recovery and TSS (Mane, 2009).

'Arka Alok' x' SP-2-2',' Arka Alok' x 'L-101' and 'Sonali' x' SP-2-2' were high yielding (2.65, 2.45, 2.29 kg fruit per plant) heterotic promising hybrids with resistance to bacterial wilt from among fifty hybrids developed in LXT crossings and evaluated for four years i.e., 2003-06 (Dharmatti *et al*., 2009).

Genotypes 'PTR-1', 'PTB-4', 'PTR-6' and 'Arka Ashish' were most stable tomato genotypes for yield from among 10 genotypes studied (Jothi, 2008).

Significant genotype x environment effects were observed in tomato for plant height, when advanced lines and varieties were evaluated for four years (Kalloo *et al*., 1998). The genotypes identified stable for plant height were Sel-7, H-36, H-24, DVRT-1 and Sel-10. The genotypes, H-24, Sel-7, Pant-T-4, Anand T-1, ATV-2 and NDT-96 showed below average response with regression coefficient more than unity and non-significant deviation from regression, while rest of the lines showed above average response (b_i>1).

The stability of 5 cultivars (Arka Meghali, Arka Vikas, Arka Ashish, Pusa Ruby and Megha) and 6 hybrids (Rashmi, S-72, NS-815, Shivaji, F1-124 and BSS-211) of tomatoes for growth was determined. Significant genotype x environment interaction was observed for plant height and number of primary branches in tomato and Arka Meghali was stable for plant height (Mulge and Aravindakumar, 2003).

Cuartero and Cubero (1982) reported that the performance of the hybrids was generally higher than that of parents for leaves between clusters.

The variance for genotype x environment (linear) and pooled deviations were significant for plant height and number of branches per plant in tomato, when seven varieties and their all possible diallel crosses (21) excluding reciprocals were tested for stability in three different environments by Pandey (1983). Significant genotype x environment effects were observed in tomato for plant height and number of primary branches, when eighteen advanced generation lines of tomato including 'Megha' were evaluated under four subset of environments (Patil, 1994). Selection 10 (L-15 x 79B 1390/2-6), Selection 13 (L-15 x 79B 1390/4-11-2) and selection 18 (Megha) were stable with regression coefficient near unity and non-significant deviation from regression, while selection-4 (UC204B x 79 B 1390/7-17-1) was stable for number of primary branches. Peter and Rai (1976) observed phenotypic stability with respect to number of primary branches per plant in twenty-five tomato varieties they studied. Mandal *et al.* (2000) observed non-significant genotype x environment interactions for plant height and number of primary branches per plant in tomato.

Significant differences among the genotypes and Genotype x Environment interactions were observed for plant height when nine varieties were tested for stability during *rabi* season of two different years. The genotypes H-88 had maximum plant height followed by NDT-VR-60 and H-86. These three genotypes possessed higher mean values with non-significant b_i values more than unity indicating their stability and responsive to favorable environments (Dhaduk *et al*., 2004).

Significant Genotype x Environment linear was recorded for plant height and number of branches by using eight tomato genotypes (Prasanna *et al*., 2007). For plant height all the genotypes had b_i value non-significant from units (b_i =1) indicating average response across the environments. Except VR-20 all the genotypes had non-significant S^2d_i values close to zero indicating genotypes were stable across the environments for these traits. For, number of branches all the genotypes had non-significant S^2d_i values from zero (S^2d_i =0) and were thus considered stable over the environment for this trait.

2.4.3 Stability for yield and yield contributing traits

Twenty varieties and genotypes of tomato were evaluated for yield and its components for four years (Kalloo *et al*., 1998). They observed significant genotype x environment interactions for average fruit weight and yield. Genotype x environment (linear) interaction were significant for yield. The lines DVRT-1 and DVRT-2 were identified as stable genotypes for higher yield with regression coefficient around unity and non-significant deviation from regression and higher performance for fruit size and average fruit weight, while the genotypes NDT-96, Arka Vikas and JT-99 were stable for pericarp thickness with regression coefficient around unity and minimum non-significant deviation from regression.

Stability for fruit yield of six tomato genotypes over three seasons were investigated by Kumarswamy and Madalageri (1989). Highly significant difference was observed with regard to marketable fruit yield. UC-204B and L-15 were the two genotypes with a mean yield greater than general mean and had the regression (b_i) value around unity and very low deviation from regression. Gaurish and Gotovtseva (1990) tested four tomato hybrids and the most variable in yield in different zones was F_1 Solina, while, Rusich and Strizh showed low variation in yield. Rusich gave good yields in all zones.

In tomato, genotype x environment interaction was studied for yield of eight varieties. Highly significant differences among genotypes, environments and genotype x environment interactions were found. Variety HS-101 exhibited the best performance under favourable environment with regression coefficient more than one and non-significant deviation from regression (Kalloo and Pandey, 1979). According to Peter and Rai (1976), tomato varieties HS-101 and Marglobe were suitable for high yielding environments (D_i>1), whereas Pusa Early Dwarf, Roma and B-2247 were suitable for poor environments (b_i<1).

Ten fresh market tomato genotypes were evaluated for yield stability in seven environments (Stoffella *et al*., 1984). They reported that yield stability differences occur among fresh market tomato genotypes. Sunny, Castlehy 1035, Burgis, FTE 12 and Duke were stable and high yielding due to regression coefficient near or to unity and non-significant deviation from regression, while the genotype Hayslip, D76127, Flora-Dade and Walter PF had regression coefficient more than one and below grand mean yields and would be considered unstable and low yielding.

Cuartero and Cubero (1982) conducted an experiment to study the genotype x environment interaction in twelve varieties and their hybrids of tomato in four environments. Genotype x environment interactions were significant for early maturity and early harvesting. All hybrids showed significant regression slopes. Early maturity was noticed in Mellilero and early harvesting in Pearson showed parent and hybrid differences. In both cases parents being earlier than hybrids.

Nine open pollinated and six hybrid tomato genotypes and most representative local tomato cultivars were evaluated at twenty Latin America and the Caribbean (LAC) locations (Ortiz and Izquierdo, 1994). They reported that Narita and Dina RPs (open-pollinated) were the most stable genotypes for marketable fruit yield. However, their stability characteristic regression coefficient was regarded as inconsistent because of significant deviation from regression. Flora Dade, an open pollinated genotype that is grown widely in Latin America and the Caribbean had unstable market fruit yield (significant b_i and S^2d_i). Neither heterogenous composition of an open pollinated genotype nor heterozygosity *per se* of the hybrids could explain the yield stability across environments. Therefore, alleles that confer broader adaptation might be required to achieve tomato yield stability across environments.

Poysa *et al*. (1986) assessed processing varieties of tomato for stability and genotype x environment interactions. Genotype IND-792 (b_i =1.01 and S^2d_i=-7.67) and Ohio-8243 (b_i=1.10 and S^2d_i=-2.12) were the best sources of yield stability combined with high yields for use in a new breeding programme.

The varieties Punjab Chhuhara and Punjab Kesari had unit regression coefficient and non-significant deviation from regression, there by showing an average stability. The mean values of these varieties were above the overall population mean value, which indicated their general adaptability (Sharma and Nandapuri, 1984). Pandey (1983) observed that, in general, in tomato, the F_1's were more productive as well as stable as compared to the parents. Relative stability of the crosses was associated with the stability of parents. Considering the yield and yield attributing characters, the most stable crosses were SI x PD, PR x PD, PR x Sx and parents SI-120, Pusa Early Dwarf and Sioux should be exploited for development of stable and high yielding genotypes.

Twenty tomato genotypes were tested under three environments for stability analysis following the model of Eberhart and Russell (1966). Relative judgment of the genotypes from the stability parameters (i.e., b_i and S^2d_i) revealed that Punjab Chhuhara, Kalyani Eunish, Pusa Ruby and Sel-7 were adapted specifically to rich environments and Arka Vikas, Marglobe Supreme, KBT-1 and Anand T-1 were adapted specifically to poor environments (Mandal *et al*., 2000).

Stability in yield was studied in tomato crosses and parental cultivars. Talallkhin x Dokhodny, Povarek x Radek, Talallkhin x Povarek and Dokhodny x Linia 7 exhibited high commodity yield and stability under weather conditions (Kilchevsky and Babak, 2001).

Upadhyay *et al*. (2001), studied genotype environment interaction and stability analysis in tomato. Significant mean squares due to genotype x environment interaction were observed for all traits except number of marketable fruits per plant and marketable fruit yield

per plant. Cultivars Rupali and Pant T-3 were the only stable genotypes for marketable fruit yield per plant.

Stability of fruit yield of nine varieties were investigated during *rabi* seasons of two different years (Dhaduk *et al*., 2004). They observed significant differences among the genotypes and G x E interactions for fruit yield in tomato. Five genotypes *viz*., NDT-VR-60, Bilahi-2, H-86, Sel-7 and Punjab Chhuhara were stable for yield as evident from their non-significant S^2d_i values. Out of these 5 genotypes, NDTVR-60 possessed higher mean yield with b_i more than unity indicating its stability and suitability for favourable environments, whereas H-86 recorded higher mean fruit with b_i less than unity revealing its suitability under poor/unfavourable environments.

Identification of stable variety for yield was studied in tomato by using eight genotypes. Genotypes VR-20 and Kashi Sharad had significant b_i values greater than the unity indicating better adaptation to the favourable conditions. But all the genotypes had S^2d_i values non-significant from zero thus could be considered stable for this trait (Prasanna *et al*., 2007).

Hosamani *et al.* (2003) studied stability analysis for yield in tomatoes during summer seasons by involving seven tomato varieties. The yield was recorded along with TLCV incidence. Pooled analysis of variances indicated significant differences among the genotypes, environments and genotype x environmental interaction. 'H-24' recorded highest mean yield of 17.69 t/ha. It was found to have below average stability (b_i=5.05) and with minimum unpredictable part of stability (S^2d_i=0.59). Megha (L-15) with second highest mean fruit yield (17.34 t/ha) was found to be of below average stability (b_i=0.27) and with least unpredictable part of stability (S^2d_i=0.19). Based on TLCV scoring 'H-24' classified as highly resistant while Megha (L-15) as moderately resistant. This study reveals 'H-24' can be recommended for cultivation under high yielding or favourable environments, while 'Megha (L-15)' can be recommended for cultivation under low yielding or unfavourable environments during summer season.

2.4.4 Stability for quality parameters

Investigation over six years of eight tomato cultivars for stability of soluble solids showed a wide range of variation for per cent soluble solids (Berry *et al*., 1988). The cultivar 'Ohio-7870' was least variable in soluble solids and 'Heinz 2653' most variable. Gull *et al.* (1989) reported that Walter (b_i=1.07 and S^2d_i=0.099) was stable variety for TSS content as indicated by unit regression coefficient and non-significant deviation from regression for TSS.

Patil (1994) reported that Selection-6 (DWD-1 x 79 B1390/Sp-2-2) was least variable for TSS due to around unit regression and non-significant deviation from regression. According to Cuartero and Cubero (1982), locules per fruit was very consistent due to non-significant regression slopes, but when interaction did exist, the number of locules was higher in less protected environments.

Aravindakumar *et al.* (2001) conducted a field experiment over eight environments to study the stability differences among tomato genotypes for fruit quality parameters. Mean squares of genotype x environment and genotype x environment (linear) were significant for fruit volume, flesh thickness, number of locules and total soluble solids. NS-815, Arka Meghali, Rashmi, Shivaji and F1-124 were found stable with high mean values for fruit volume, whereas S-72, NS-815, F1-124, Shivaji and Arka Ashish were found stable with high mean value for flesh thickness. Stability with high mean values for number of locules was observed in Arka Vikas, Pusa Ruby and Shivaji while, Arka Ashish was identified as a stable cultivar for total soluble solids.

Prasanna *et al.* (2007) reported the significant G x E linear for the traits fruit length, fruit width, number of locules and TSS. For all these traits, all the genotypes namely Kashi Visesh, Kashi Amrit, Kashi Anupam, Kashi Hemard, Kashi Sharad, Sel-7, VR-20 and VR-415 had S^2d_i values non-significant from zero and were thus considered stable over the environments.

2.5 HETEROSIS

When two inbred lines were crossed, the *per se* performance of the F_1 may be superior to mid parental value. This superiority over mean is called as heterosis (Shull, 1908).

The magnitude of heterosis depends on accumulation of favourable dominant alleles in the F_1 population. If the parental populations differ from each other for favourable dominant alleles, the magnitude of heterosis will be proportionally higher. This relationship is evidenced in the basic formula for heterosis (Falconer, 1981).

$$\text{Heterosis in } F_1 = \sum dy^2$$

Where,

d = Magnitude of dominance

y = Difference between the parental population for allelic frequencies at the locus

Though tomato is a self pollinated crop where degree of heterosis was theoretically observed that it has been attributed to the fact that tomato was basically a highly out crossing genus which was later evolved into a self pollinated one (Rick, 1965).

'Arka Alok' x' SP-2-2',' Arka Alok' x 'L-101' and 'Sonali' x' SP-2-2' were high yielding (2.65, 2.45, 2.29 kg fruit per plant) heterotic promising hybrids with resistance to bacterial wilt from among 50 hybrids developed in LXT crossings and evaluated for four years i.e., 2003-06 (Dharmatti *et al*., 2009).

In a study involving 24 crosses with wild species, two hybrids 'EC 520076' (*S. pimpinellifolium*) x 'DVRT-2' (*S. lycopersicum*), 'EC520078' (*S. pimpinellifolium)* x 'DVRT-2' were highly resistant to ToLCV with a coefficient of infection of 9.45 and 6.00 respectively (Singh *et al*., 2009).

' S-05'x'BFL', 'S-61' x ' Arka Alok', ' S-61' x 'BFL', and 'S-05' x'DMT-1' were heterotic crosses among 36 F_1's produced in LxT design (Yashvantakumar, 2008).

ToLCV resistant gene 'Ty-2' marker from "H-24' and 'Fla-478' was incorporated with 'H-86' by hybridization and backcrossing in tomato. The homozygous lines for 'Ty-2' marker was used to identify superior progenies (IIVRT-2, IIVRT-3 and IIVRT-4) in F_4 plants (Datta *et al.,* 2009).

Based on reports of various scientists, the heterosis of some traits is presented in Table 3.

2.6 COMBINING ABILITY

The combining ability generates valuable information on potential of genetic stocks involved, thus enabling plant breeder to take critical decisions regarding the selection of parents and employing suitable procedures in various crop improvement programmes. The concept of general combining ability (GCA) and specific combining ability (SCA) was proposed for the first time by Sprague and Tatum (1942) in relation to single cross of corn, but later the concept has been widely used in other crops.

According to Sprague and Tatum (1942), GCA is the average performance of a line across all across combinations and SCA refers to the deviation of specific cross from the average performance of the lines involved.

The line x tester technique developed by Kempthrone (1957) is a good approach to determine GCA and SCA effects. Thus it is possible to estimate the potential of crosses and also to assign the cause for this superiority in terms of GCA and SCA effects. Griffing (1956), showed the relationship between various components of variance *viz*., GCA and SCA variances. Thus, GCA variance is due to additive variances as well as additive inter-allelic interaction, whereas SCA variance is due to those of dominance and at the three epistatic variances. Hence, GCA and SCA variances act as diagnostic tools in selection of suitable parents as well as cross combinations.

KS-29, Pant Bahar and Kalyanpur Type-1 were good general combiners while KS-16 x KS-29, Kalyanpur Type-1 x KS-29 and Pant Bahar x KS-16 were best specific combiners for fruit yield. (Singh *et. al*., 2010b)

'S-61' x ' BFL', ' S-05' x 'DMT-1' and 'S-05' x 'BFL' had highly negative *sca* effects for tomato spotted wilt virus symptom severity (Yashvantakumar *et. al*., 2009b).

Table 3. Review of literature on heterosis for various traits in tomato

Sl. No.	Characters	Range of per cent heterosis over			References
		Mid parent	Better parent	Commercial check	
1.	Plant height	-	53.73-36.33	-	Bhutani *et al.* (1973)
		-65.52-81.27	-50.98-60.45	-58.82-148.64	Dharmatti (1995)
		-6.22-6.51	-	3.10-15.30	Patil (1997)
		-18.94-20.45	-20.98-17.57	48.89-0.07	Kulkarni (2003)
		-6.33-38.59	-17.21-28.56	-5.36-28.45	Sajjan (2001)
		-22.52-44.19	-35.99-26.02	-40.99-4.73	Yashavantakumar (2008)
2.	Number of branches per plant	5.71-76.00	1.77-67.20	-	Mishra and Khanna (1977)
		-18.88-21.82	-25.35-1.01	-21.30-8.26	Sajjan (2001)
		-38.07-55.52	-42.15-39.46	-65.10-15.86	Yashavantakumar (2008)
3.	Days to 50 per cent flowering	-	2.43 to 22.2	-	Patil (1996)
		-10.25 to 8.98	-	-22.93 to 12.10	Patil (1997)
		-13.38 to 9.89	-13.10 to 20.64	-14.28 to 3.41	Kulkarni (2003)
4.	Number of clusters per plant	-	3.30 to 67.40	-	Singh *et al.* (1976)
		-	-27.36 to 23.70	-	Kumar *et al.* (1988)
		-11.01 to 74.66	-13.41 to 29.57	-10.54 to 43.89	Prabhushankar (1990)
		-25.81 to 120.73	-36.41 to 92.25	-21.91 to 58.01	Sajjan (2001)
		-30.42-107.41	-35.99-105.94	-69.26- -1.09	Yashavanthakumar (2008)
5.	Number of flowers per cluster	-	1.64 to 7.64	31.90 to 39.75	Peter and Rai (1978)
		-22.81 to 30.00	-25.80 to 20.55	-14.00 to 32.60	Kulkarni (2003)
		14.22 to 43.97	8.93 to 37.22	-4.56 to 20.43	Sajjan (2001)
6.	Number of fruits per cluster	-20.19 to 33.58	-32.12 to 37.45	-12.24 to 35.57	Prashanth (2004)
		-31.20 to 63.36	-40.00 to 43.28	-11.59 to 111.11	Prabhushankar (1990)
		-27.78 to 181.52	-40.50 to 123.39	-40.41 to 181.51	Kulkarni (2003)
		5.90-248.9	25.9-153.8	15.9-137.5	Tiwari and Lal (2004)
		-18.45-232.37	-30.37-215.77	-63.11-24.41	Yashavantakumar (2008)
7.	Total yield per plant	-	0.40 to 60.36	-	Dixit *et al.* (1980)
		-25.39-88.85	27.87-72.89	-37.55-44.98	Dundi (1991)
		-40.74 to 93.13	-41.30 to 87.41	-47.06 to 65.36	Kulkarni (2003)
		0.06-179.45	-38.99-177.84	-	Premalakshmi *et al.* (2006)
		-30.94-333.45	-43.67-310.91	-69.58-42.40	Yashavantakumar (2008)
8.	Average fruit weight	-25.80 to 35.63	-32.63 to 22.77	-38.52 to 59.48	Prabhushankar (1990)
		-42.54 to 52.92	-45.97 to 29.66	-51.80 to 55.37	Prashanth (2004)
		-	-26.79 to 7.33	9.43 to 35.85	Fageria *et al.* (2001)

Sl. No.	Characters	Range of per cent heterosis over			References
		Mid parent	Better parent	Commercial check	
		-70.83 to 53.65 -30.50-30.50	-76.29 to 42.40 -37.76-30.05	-73.55 to 19.21 -28.71-32.84	Sajjan (2001) Yashavantakumar (2008)
9.	Number of locules per fruit	77.05 -44.83-37.50 -44.88-19.28 -12.22-14.47	60.40 -27.97-133.33 -28.10-36.25 -100.00-87.36	- -45.50-99.82 -36.10-68.37 -18.98-8.48	Anbu *et al*. (1981) Dundi (1991) Tendulkar (1994) Patil (1997)
10.	Pericarp thickness	-7.57-73.29 -43.71 to 94.10 -23.92 to 58.02 -12.00 to 40.74 -25.00-57.89 -	-17.22-63.16 -45.73 to 73.22 -29.50 to 5.93 -13.95 to 37.83 -30.77-66.67 -41.82-24.20	-44.40-55.5 -67.17 to 26.16 -26.18 to 40.14 8.82 to 50.00 - -42.04-9.60	Dundi (1991) Kulkarni (2003) Prashanth (2004) Sajjan (2001) Kumar *et al*. (2006) Sharma and Thakur (2008)
11.	Total soluble solids	-11.14-2.79 -13.13-55.13 -100.00-386.07 -4.87 to 12.73 -24.22-25.52	-21.27-5.88 -32.82-65.28 -100.00-282.59 -7.46 to 12.51 -26.51-10.98	- -7.14-126.19 -100.0-68.11 7.90 to 23.97 5.17-89.66	Kanthaswamy and Balakrishnan (1989) Dundi (1991) Dharmatti (1995) Sajjan (2001) Yashavantakumar (2008)
12.	Fruit length	-	-43.46 to 29.16	-38.15 to 26.23	Mahendrakar (2004)
13.	Fruit width	-	-37.14 to 23.36	-27.30 to 23.68	Mahendrakar (2004)
15.	Fruit shape index	3.66	-3.18	-	Ashwathappa (1980)
16.	TLCV incidence	-32.42 to 146.91 -85.02 to 5.28	-26.23 to 205.81 -79.21 to 8.16	-52.02 to 70.68 -89.09 to 17.10	Dharmatti (1995) Sajjan (2001)

Tester ‘d’ and Line ‘D” were good general combiners for yield, maximum *sca* was seen in ‘Hyb-13’ (for no. of fruits and yield), ‘Hyb-14’ (fruit weight) and ‘Hy-22’ (for titrable acidity and TSS). ‘Hy-23’ had higher economic segregants for yield in a study involving 25 three way F_1’s ,10 parents and 2 checks (Dhadde,2008).

‘S-22’ x ‘ L-15’, ‘ S-22’ x ‘ Sivayp’ and ‘CO-3’ x ‘ Solan Vajra’ were heterotic hybrids for yield and best specific combiners while ‘S-22’, ‘ Solan Vajra’, ‘ L-15’ were good general combiners from a study involving 7 seven parents in diallel mating (Kulkarni, 2006).

40 F_1 hybrids involving 8 females and five males developed in Line x Tester mating design were evaluated. Females showed diversity for bacterial wilt resistance and males were diverse for horticultural traits. DMT-6 x DMT-D, DMT-2 x IMP-B, DMT-5 x DMT- D were heterotic crosses. Sca variance was greater than gca for yield and for bacterial wilt resistance indicating predominance of non-additive gene action (Virupannavar, 2009).

Literature pertaining to combining ability for various traits in *Solanum lycopersicum* L., is summarized in Table 4.

2.7 Transformation studies in tomato:

Hypocotyl and cotyledon segments as ex-plants from five tomato genotypes [H-24 (Hissar Anmol), H-86 (Kashi vishesh), Sel-7 (Hissar Arun), DVRT-1 (Kashi Amrit) and DVRT-2 (Kashi Anupam)] were used in a study on *in vitro* regeneration potential. Among two cytokines, i.e., BAP (0.0-3.0 mgl^{-1}) in combination or without kinetin (0.5-1.0 mgl^{-1}) in MS medium revealed highest frequency shoot regeneration (96-6 and 92.2%) as well as maximum shoots per explant (10.2 and 8.4) from hypocotyls and cotyledon explant respectively in H-86 genotype. Among explants tested hypocotyls segment was more responsive compared to cotyledon segment. The order of genotype response was H -86>H-24>DVRT-1>Sel-7 > DVRT-2 with regard to shoot organogenesis and multiplication frequency (Singh *et al*., 2010a).

The cultures on this medium were green and showed good shoot bud regeneration. The individual shootlets were separated and inoculated on growth regulator free –MS medium. After two weeks of root induction, the individual plantlets were transferred to glass jars filled with autoclavable polypropylene (PP) caps filled with sterile peat:vermiculite (2:1). This hardening strategy lead to over 90.0% plant survival at green house stage (Singh *et al*., 2010a).

Post-transcriptional gene silencing (PTGS) / RNAi is a novel gene regulatory mechanism that limits the transcript level by either suppressing transcription or by activating a sequence-specific RNA degradation process. Dharwad local ToLCV isolate coat-protein (*TCP*), replicase (*TRP*) and suppressor of PTGS (*TRS*) genes were cloned and characterized as well as constructs were developed using all three genes (viz *TCP, TRP, TRS*) for gene silencing strategies viz sense (*s*), antisense (*as*), ihp (*sas*) and HUTR (heterologous 3-untranslated region). Coat-protein (*TCP*) gene was cloned and expressed in prokaryotic system. Plant expression vectors carrying *TCP, TRP* and *TRS* gene were used as different strategies transgenic development through *Agrobacterium*. Analysis of putative T_o-transgenics showed positive for PCR, GUS, Dot blot and southern blot analysis. PCR analysis of plants from TRP constructs showed drastic reduction in the virus inoculums compared to non-transgenic plants. The T_1-generation transgenic plants obtained from TRP constructs were positive for PCR and Dot blot analysis. Among different strategies tested for resistance to ToLCV in transgenics, those with *sas/ihp* construct showed significant resistance against ToLCV followed by HUTR, anti-sense (*as*) and sense (*as*). Among the three different genes tested, silencing was more in TRS constructs followed by TRP and TCP (Krishnamurthy, 2006).

In vitro response of leaf explants of tomato was genotype dependent and differed significantly with the kind and concentration of the growth regulators. Maximum percent plant regeneration was in ‘IPA-3’ (84.11%) followed by ‘VFN-8’ (83.10), ‘Punjab Upma’ (75.91%) and ‘Castle rock’ (78.99%) in media MS + BAP 2.0 mg $l\ 1^{-1}$ + kinetin 1 mg l^{-1}. With increase in the concentration of BAP in the nutrient media there was increase per plant regeneration (Devi *et al*., 2009).

Table 4. Review of literature on combining ability variances and effects for different traits in tomato.

Sl. No.	Characters	Combining ability	References
1.	Plant height	Significant GCA and SCA variance	Kalloo *et al.* (1974), Peter and Rai (1980), Patil (1984),
		SCA variance > GCA variance	Anbu *et al.* (1981), Sharma *et al.* (1999), Singh *et al.* (2008)
		GCA variance > SCA variance	Pradeepkumar *et al.* (1997), Rai *et al.* (2003)
		Significant gca and sca effects	Prabhushankar (1990), Dharmatti (1995),
		Higher sca effect	Asati *et al.* (2007), Yashavantakumar (2008)
2.	Number of branches per plant	SCA variance > GCA variance	Dharmatti (1995), Patil (1997), Yashavantakumar (2008)
		GCA variance > SCA variance	Dundi (1991), Patil (1984), Rai *et al.* (2003)
		Significant gca and sca effects	Kulkarni (2003), Mahendrakar *et al.* (2007),
3.	Days to 50% flowering	Higher SCA variance	Anbu *et al.* (1981), Tendulkar (1994)
		GCA variance > SCA variance	Roopa *et al.* (2001), Mahendrakar (2004)
		SCA variance > GCA variance	Patil (1984), Kulkarni (2003)
		Significant negative gca and sca effects	Srivastava *et al.* (1998), Mahendrakar (2004)
		Higher sca effect	Singh *et al.* (2008)
4.	Number of clusters per plant	SCA variance > GCA variance	Sajjan (2001), Roopa *et al.* (2001)
		GCA variance > SCA variance	Kavitha *et al.* (2007), Yashavantakumar (2008)
		Higher sca effect	Dharmatti (1995), Kulkarni (2003)
		Significant gca and sca effects	Tendulkar (1994)
5.	Number of flowers per cluster	SCA variance > GCA variance	Kulkarni (2003)
		Significant gca and sca effects	Sajjan (2001), Kulkarni (2003)
6.	Number of fruits per cluster	SCA variance > GCA variance	Dundi (1991), Dharmatti (1995), Mahendrakar (2004)
		Higher sca effects	Bhatt *et al.* (2001), Yashavantakumar (2008)
		Higher GCA variance	Joshi *et al.* (2004), Roopa *et al.* (2001)
7.	Number of fruits per plant	Significant GCA variance> SCA variance	Kalloo *et al.* (1974),Tendulkar (1994), Sajjan (2001)
		High SCA variance	Prabhushankar (1990), Dundi (1991), Joshi *et al.* (2004)
		SCA variance > GCA variance	Srivastava *et al.* (1998), Pandey *et al.* (2006)
		Significant gca and sca effects	Nandpuri and Tyagi (1976), Premalakshmi *et al.*(2006)
		Higher gca effects	Asati *et al.* (2007)
8.	Total yield per plant	Significant of GCA and SCA variance	Prabhushankar (1990), Dundi (1991)
		High GCA variance	Dixit *et al.* (1980), Sidhu *et al.* (1981), Asati *et al.* (2007)

Contd...

Sl. No.	Characters	Combining ability	References
		High SCA variance	Anbu *et al.*(1981), Kavitha *et al.* (2007), Singh *et al.* (2008)
		Significant gca and sca effects	Joshi *et al.* (2004), Yashavantakumar (2008)
9.	Average fruit weight	Higher GCA variance > SCA variance	Dod *et al.* (1995), Patil (1996), Mahendrakar (2004)
		SCA variance > GCA variance	Patil (1984), Dharmatti (1995), Sajjan (2001)
		Significant gca and sca effects	Prashanth (2004), Joshi *et al.* (2004), Kavitha *et al.* (2007)
10.	Number of locules per fruit	Significant gca and sca effects	Chadha *et al.* (2002), Joshi and Kohli (2006)
		Significant GCA variance > SCA variance	Thakur and Kohli (2005), Rai *et al.* (2003)
		Significant SCA variance > variance	Pradeepkumar *et al.* (1997), Roopa *et al.*(2001),
		Higher sca effects	Singh *et al.* (2008)
11.	Pericarp thickness	GCA variance > SCA variance	Patil (1984), Patil (1996),
		Higher SCA variance	Thakur and Kholi (2005), Singh *et al.* (2008)
		Significant gca and sca effects	Sharma *et al.* (1999), Mahendrakar (2004)
12.	Total soluble solids (TSS)	Significant SCA > GCA variance	Prabhushankar (1990), Dundi (1991)
		SCA variance > GCA variance	Anbu *et al.* (1981), Patil (1984), Singh *et al.* (2008)
		GCA variance > SCA variance	Sharma *et al.* (1996), Patil (1997), Dod *et al.* (1995)
		Significant gca and sca effects	Patil (1996), Dharmatti (1995), Mahendrakar (2004)
13.	Fruit length	GCA variance > SCA variance	Rai *et al.* (2003), Mahendrakar (2004), Singh *et al.* (2005)
		SCA variance > GCA variance	Pandey *et al.* (2006),
		Significant gca and sca effect	Mahendrakar (2004), Singh *et al.* (2005)
14.	Fruit width	GCA variance > SCA variance	Mahendrakar (2004), Singh *et al.* (2005)
		SCA variance > GCA variance	Rai *et al.* (2003)
		Significant gca and sca effects	Mahendrakar (2004), Singh *et al.* (2005)
		Significant gca and sca effects	Sajjan (2001)
15.	TLCV incidence	Higher SCA variance	Dharmatti (1995), Sajjan (2001)
		Significant gca and sca effects	Dharmatti (1995), Sajjan (2001)

'*npr1*' gene from mustard was transferred to tomato using *Agrobacterium* mediated transformation. Transformants were selected on Kanamycin (200 mg/l) and were confirmed by PCR with *nptII* positive plants screened, 7 plants were positive for *npr*1 specific primer bioassay using *Alternaria* spp in positive plants. The nonexpresser of PR genes (*npr*1) also known as *N1M1* and *SAI1* is a key regulator of SA mediated systemic acquired resistance (SAR) in plants. (Chandrabanu, 2008).

Tomato variety 'Pusa Ruby' was transformed using a new promoter trapping vector pNU435 using *Agrobacterium* mediated transformation i.e. using *Agrobacterium* strain LBA4404 carrying pNU485.

Plant transformation vector pRAGS carrying both *ech42* and *bgn* under single T-DNA was constructed. pRAGS121 vector was developed by cloning *ech42* from pSAG1 [*ech42* (pSUM1) cloned into pYES2/CT] cloned into *KpnI* and *XhoI* . This vector could be used to transform crop plants to enhance resistance to fungal diseases since the genes encoding chitinase and glucanase act synergistically (Sharma, 2009).

2.7.1 Transformation studies:

The plant transformation is a process where DNA is introduced into plant cells. Several procedures have been reported, so far, to accomplish gene transfer and they have been categorized into two broad categories.

a) *Agrobacterium* mediated transfer.

b) Artificial delivery system/Direct DNA transfer

2.7.1.1 *Agrobacterium* mediated DNA transfer

Agrobacterium mediated DNA transfer is the most common and widely used method for the transformation of dicotyledonous plants. The first set of transgenic plants of *Nicotiana tobaccum* were produced via *Agrobacterium* mediated transformation by Horsch *et al.,* (1984). Though host range is the greatest limitation of this method, recently, *Agrobacterium* has been successfully employed for transformation of monocots also.

Agrobacterium tumefaciens is a gram negative soil bacteria and a useful plant pathogen, which induces crown gall disease in plants by transferring a discrete portion of its plasmid DNA. Two regions are essential for transformation: oncogenic T-DNA with 25 bp direct repeat sequence flanking T-DNA and the *vir*ulence (*vir)* genes, which encode proteins for T-DNA transfer. The T-DNA is capable of inducing tumor in a transformed plant accomplished by products of three genes, which code for auxins and Cytokinin. T-DNA in this process is transferred to the host genome as its integral part.

Agrobacterium tumefaciens plasmid transfers only T-DNA. In principle, desired genetic DNA sequence can be intentionally introduced into plant genomes. The oncogenic T-DNA region is deleted from *Agrobacterium* strain in order to prevent overproduction of phytohormones, which interferes generation from tissues and with normal plant development. The strains with disarmed T-DNA has only the *vir* region and it is a suitable host strain for plant transformation. A variety of Ti plasmid vectors have been constructed for gene transfer. Some examples are pLBA4404, pGV3850 and pEHA101. Alterations in the virulence and effective host range of commonly used *Agrobacterium* strains have also been reported.

2.7.1.2 Plant Transformation vectors

Vectors used for transformation are designed with the following basic features:

1. Must function in three organisms; E. *coli, Agrobacterium tumefaciens* and plant cells.
2. Must have T-DNA with direct repeat border sequences in proper orientation.
3. A suitable marker gene and convenient restriction enzyme sites.

Two vector systems are in use; co-integrating and binary vectors. Co-integrate vectors rely upon recombination and co-integration with a disarmed Ti plasmid and they can integrate into a limited number of Ti plasmids. Binary vectors replicate autonomously in

Agrobacterium. Agrobacterium harboring T-DNA region and the '*vir*' region of the Ti plasmid on separate replicons can efficiently transfer their T-DNA to plants. Thus binary vectors systems are easiest to handle and widely used. Presently, we have conjugal type of plasmids where *vir* region of the plasmids are replaced by *tra* and *mob* genes, overcoming the need for two plasmids.

A suitable marker gene allows the preferential growth of transformed cells in the presence of the corresponding selective agent. Many antibiotics and herbicide genes are used as selectable markers. Selection efficiency depends on the size and developmental state of the plant cells, regeneration response and the concentration of the selective agent.

Kanamycin has proven to be the most widely applicable selective agent but the concentration is species specific. Species like *Lycopersicum esculentum*, *Brassica napus* are selected at low concentration of kanamycin (15-100 mg/l) whereas *Beta vulgaris* needs relatively high concentration of kanamycin (400 mg/l).

The neomycin phosphotransferase type-II (*npt II)* gene has been used in transformation of more plants species than any other selectable marker. The original coding sequence of *npt II* was from bacterial transposon, Tn5 Npt5 II provides resistance to certain aminoglycoside antibiotics such as kanamycin, paramomycin and geneticin, but kanamycin is the most widely used. NPT II coding sequence has been fused to constitutively regulated promoters such as the napoline synthase (nos) and cauliflower mosaic virus (CaMV) 35 S regulatory sequences and later cloned into plant transformation and expression vectors by many researchers.

2.7.1.3 Reporter genes

In all transformation protocols, invariably many non-transformed plants (escapes) are noticed along with transgenic plants. The transformed plants can be identified by southern blot analysis of the DNA isolated from them, recallusing assay, enzymatic assay, antibody assay and by detecting the selectable markers gene products. But these assays are laborious, time consuming and require radioactive substrate, antibodies, etc.

These drawbacks can be overcome by including an independent reporter gene in the gene transfer cassette whose presence can be easily visualized/measured. A reporter gene product should be stable, tolerate amino terminal fusions, have simple and versatile assays and that it should not have intrinsic background activity in the organisms. Two genes are widely used as reporters; β-glucuronidase (*gus*) and luciferase (*lux*).

GUS activity can be quantified using either fluorometric or spectrometric assays, both of which are reasonably simple and cheap. Localization of GUS expression is possible histochemically also. However the histochemical assay is expensive and needs destructive sampling. GUS reporter is widely used for studies on transformation in tomato.

2.7.1.4 Plant transformation in tomato

The transformation protocol involves three major steps; concentration of bacteria for co-cultivation, co-cultivation time, elimination of bacteria, selection of transformed, confirmation of transgenic individuals and expression analysis.

To increase the frequency of transformation concentration of bacteria, length of co-cultivation and elimination of bacteria are important factors.

Elimination of *Agrobacterium tumefaciens* after co-cultivation is one of the major problems in *Agrobacterium mediated* transformation. If the *A. tumefaciens* not eliminated, it will overgrow the tissue and destroy it. Antibodies are used for this purpose but the levels of antibiotics needed to kill the organism may have deleterious effects on plant regeneration. So the level of antibiotic requirement is to be standardized for individual crops. Although many antibiotics have been used for effective elimination of *Agrobacterium* cells, carbenicillin and cefotaxime have minimal toxicity on most plant tissues and efficiently eliminate *Agrobacterium* cells. However, both antibiotics show plant hormone like activity especially at lower concentration, Cefotaxime is the most common antibiotic used for the purpose. A strain of *A. tumefaciens* sensitive to a given antibiotic can be used. Out of 10 antibiotics tested, cefotaxime was the most effective against LBA4404 and Oxalactam against EHA101.

Usually bacteria at 10^8 -10^9 CFU/ml are used for co-cultivation. Tomato explants co-cultivated with five concentrations of bacteria indicated that eighty percent of the cotyledons with $5x10^8$ bacteria per ml produced shoots on a selective medium; however when the concentration of bacteria was increased or decreased five fold the rate of transformation was reduced by at least 20%.

Length of co-cultivation time employed varies widely from a few hours to a few days, depending upon the species, explant and culture conditions. An average of sixty percent of the cotyledons co-cultivated for 48 hrs produced kanamycin resistant shoots, while the average transformation rate was observed after cotyledons were co-cultivated for 24 and 72 hours was only 24 and 44% respectively.

2.7.1.5 Tomato Transformation

Species from the Solanaceae family have so far used for biotechnological approaches. First attempts in culture of plant tissue and dells an also in gene transfers have been done with some genera of this family, mainly with tobacco as a model plant species. This family contains many useful and cultivated plants. Tomato is one of the most favored crops of Solanaceae family used for studying plant transformation techniques and biology. Tomato is susceptible to *Agrobacterium* infection and therefore has been successfully adopted for such studies. A novel leaf disc transformation/regulation method was developed. Transformation was carried out with an *Agrobacterium* strain in which the phytohormone gene was deleted and replaced with a chimeric gene for kanamycin resistance. Shoot generation occurred after 2-4 weeks on selection media, allowing the application of leaf disc transformation. In an earlier study, Transformation protocol wherein both leaf explants and cotyledon sections were used in transformation was developed. The results showed evidence for both single and multicopy insertion of T-DNA. A comparison between binary T-DNA vector and cointegrate T-DNA vector revealed reduced efficiency of transformation with binary T-DNA vector. Cotyledons of tomato were transformed with *A. tumefaciens* harboring a binary vector with Neomycin phosphotransferase genes and a mutant aroA gene. *AroA* gene confers tolerance to the herbicide glyphosate. Seven percent of transformed cells/tissues expressed both *NPTII* enzyme and the aroA protein. The progeny of *AroA* positive plants were tolerant to 0.84 kg active ingredient of glyphosate/hectare.

Analysis of the events in tomato transformation using *Agrobacterium tumefaciens* carrying a binary vector with NPTII and a reporter (GUS intron (p355S) chimeric gene was done. Subepidermal cells were more susceptible to transformation than epidermal cells. Optimal transformation rate was observed with a preculture time of 1-2 days. Varietal differences were observed in transformation rates, which varied between 8-14%. *Agrobacterium* mediated transformation were studied. Tomato was transformed using *A. rhizogenes* containing two independent plasmids; the wild type Ri-plasmid and the vector plasmid, pARC8 having bacterial CAT gene with *CaMV* 35S promoter have been transformed using leaf discs of cultivar *L. esculentum* 462 with the help of Ti-plasmid of *A. tumefaciens*. The maize transposable element Ac was transferred to tomato plants via *A. tumefaciens*..

Stably transformed tomato (*L. esculentum,* var.Better boy) with a gene consisting of the open reading frame of a prosystemin DNA under *CaMV* 35S promoter was achieved. Transformation ot the tomato plants via *A. tumefaciens* with a chimeric tobacco *anionic peroxidase* (E.C1.11.1.7) gene joined to the *CaMV* 35S promoter was achieved. DNA sequencing corresponding to the 5' region of two tomato (*L. esculentum*) genes encoding homologous anionic peroxidases were fused, inserted into a pTi-based plasmid designed to express a composite antisense transcript and introduced into tomato via *A. tumefaciens* mediated transformation.

2.7.1.6 Engineering resistance to viral diseases

The application of transgene technology to engineer desired traits to crops has revolutionized the development of new crop varieties. With the knowledge of many genes and their products, molecular breeding seems to be straightforward and fast. This is usually not a common practice. Transgenes are inserted into the genome in a random fashion and their expression varies considerably. Additionally, stability of expression in subsequent generations is a major concern, as the multi-copy insertions lead to homologous recombinations. Although, transgene silencing is a major problem in the development of transgenics. The

discovery that transgenes under certain circumstances can silence the expression of homologous genes located elsewhere in the genome, led development of major technology of post-transcriptional gene silencing (PTGS) for selective silencing of genes.

Use of gene silencing as a tool to develop tomato resistant to tomato leaf curl virus (ToLCV) is of importance. The strategies for the management of viral diseases normally include control of vector population using insecticides, use of virus-free propagation material, appropriate cultural practices and resistant cultivars. However, each of these methods, mentioned above has its own drawbacks. Advances in the techniques used in molecular biology have resulted in cloning and analysis of the genomes of many plant viruses. Protocols developed for transformation of number of crop plants, have opened up the possibility of engineering crops towards controlling plant viruses. Engineering genetic resistance remains a viable alternative to protect tomato against ToLCV, One method is through introduction of pathogen-derived resistance (PDR), either by allowing transgenic tomato to produce truncated version of the viral protein (protein-mediated resistance) or RNA (RNA-mediated resistance).

Three questions have guided the study of RNA silencing for nearly a decade: what is the molecular nature of the silencing trigger?, what are the silencing targets?, and what proteins comprise the RNAi machinery?. These questions continue to drive the study of RNA silencing, even as new questions emerge about the broader fabric of cell metabolism and development.

RNA-mediated interference (RNAi) is an evolutionarily conserved gene silencing mechanism that recognizes double-stranded RNA (dsRNA) as a signal to trigger the sequence-specific degradation of homologous mRNA. Arguably the most important advance in biology has been the discovery that RNA molecules can regulate the expression of both endogenous and exogenous genes.

3. MATERIAL AND METHODS

The investigation on "Biometrical and transformation studies in tomato (*Solanum lycopersicum*. L.)" were carried out at the AICRP (Vegetable) block, Main Agricultural Research Station, Division of Horticulture, and in the laboratory of the Institute of Agri-Biotechnology, University of Agricultural Sciences, Dharwad, India, during 2007 to 2010. The details of the material used for the study, experimental designs adapted, statistical procedures followed and methodology adopted are described here under.

3.1 LOCATION AND CLIMATE

Geographically, the main campus of University of Agricultural Sciences, Dharwad is situated in the agro-climatic zone-8 (northern transitional zone) of Karnataka state, at 15°26'N latitude, 75°07'E longitude at an altitude of 678 m above the mean sea level. The meteorological data is presented in Appendix I.

3.2 EXPERIMENTAL SITE

Experiments were conducted on black cotton soils /vertisols block of AICRP on Vegetables, Division of Horticulture, at the Main Agricultural Research Station, University of Agricultural Sciences, Dharwad (Plate 1). The physical and chemical properties of the soil are presented in Appendix II.

The investigations done were as below:

A. Biometrical studies in tomato:

Experiment I: Evaluation of 41 tomato genotypes during *kharif* 2007, *kharif* 2008 and *rabi* 2008,

Experiment II: Evaluation of 25 F_1 hybrids developed by Line x Tester method during *rabi* 2008

B. Transformation studies in tomato

3.3 EXPERIMENT I: EVALUATION OF 41 TOMATO GENOTYPES DURING *KHARIF* 2007, *KHARIF* 2008 AND *RABI* 2008,

Fortyone genotypes available in tomato gene pool maintained at the All India Coordinated Vegetable Improvement Research Project, University of Agricultural Sciences, Dharwad were used to evaluate for variability, correlation analysis, path analysis, divergence and stability analysis in three different seasons *viz*., *kharif* 2007, *kharif* 2008 and *rabi* 2008 and the source of the genotypes is presented in Table 5.

The details of the experiment are as below:

Number of Genotypes (Treatments)	:	Forty one genotypes
Replications	:	Three
Spacing	:	60 cm x 60 cm
Plot size	:	2.4 m x 3.0 m
Plant population		20 plants per plot of each entry
Design	:	Randomized Block Design (RBD)

3.4 EXPERIMENT II: DEVELOPMENT OF F_1 HYBRIDS AND THEIR EVALUATION

Inbred lines of ten divergent parents were selected from the evaluated genotypes and crossed in line x tester mating design as suggested by Kempthorne (1957) to produce 25 hybrids in *kharif* 2008 and evaluated during *rabi* 2008. This involves five females (lines) and five males (testers). They are as follows,

Tomato Nursery beds

Grown up seedlings

Flower emasculation

Field view of tomato experimental block

Baged Plants

Fruiting tomato Experimental crop

Plate.1. View of experimental plot wherein investigations on tomato were taken up

Lines	Testers
1) CO-3	1) VR-35
2) DVRT-2	2) KS-227
3) H-24	3) Dwd-T-1
4) Megha (L-15)	4) Dwd-T-3
5) Pant-T-10	5) Dwd-T-6

3.4.1 Hybridization programme

The seeds of the above said parents were sown in nursery and transplanted in separate crossing block.

Healthy flower buds in a cyme preferably of the first flush of the female parents, which were expected to open next day were emasculated before their opening, between 3 to 6 pm and bagged to prevent out crossing. Pollination was done next morning using pollen grains from desired freshly opened male parent flowers. Crossed flower buds were covered with butter paper bags till fruits were set and labelled. Simultaneously, flower buds of parents were selfed and it was ensured by bagging the flower buds. Seeds were extracted from red ripe fruits by fermentation method.

3.4.2 Evaluation of F_1 hybrids

The evaluation of twenty five F_1 hybrids along with their parents and commercial check (ARTH-3) for various traits was taken up in *rabi* 2008. The details of experiment are as under,

Treatments	:	25 hybrids + 10 parents + commercial check (ARTH-3)
Replication	:	Three
Design	:	Randomized Block Design (RBD)
Spacing	:	60 cm x 60 cm
Plot size	:	2.4 m x 3.0 m
Population	:	20 plants per plot or of each entry

3.5 CULTURAL PRACTICES

3.5.1 Raising of seedlings

The seedlings of all the aforesaid genotypes and developed F_1's along with parents were brought up in raised nursery beds. Recommended cultural and plant protection measures were taken up before and after sowing of the seeds.

3.5.2 Field preparation and layout of the experiment

The experimental fields were ploughed and brought to fine tilth. FYM @ 25 tones per ha and 115:100:60 kg NPK per ha were applied in the recommended manner. The experiment was laid out during *kharif* 2007, Kharif 2008 and *rabi* 2008 seasons.

3.5.3 Transplanting and after care

Thirty days old seedlings were transplanted to the main field. Top dressing was done with 50 per cent nitrogen after one month of planting. Timely irrigation was given and recommended package of practices followed.

The dates of nursery sowing and transplanting of genotypes/hybrids done in different seasons are as below:

Table 5. Sources of 41 tomato genotypes used in the investigations.

Sl.No.	Genotype	Source
1	ALT-02-39	AAU, Anand, Gujarat
2	VR-20	IIVR, Varanasi, Uttar Pradesh
3	CO-3	TNAU, Coimbatore, TAMIL Nadu
4	DVRT-2	IIVR, Varanasi, Uttar Pradesh
5	H-24	CCSHAU, Hissar, Haryana
6	HADT-294	VPKAS Almora, Uttaranchal
7	HAT-121	HARP,Ranchi, Jharkhand
8	HAT-20	HARP,Ranchi, Jharkhand
9	KS-227	CSAUTA, Kalyanapur, Uttar Pradesh
10	KS-229	CSAUTA, Kalyanapur, Uttar Pradesh
11	Megha (L-15)	AICVIP, UAS, Dharwad, Karnataka
12	NDT-9	NDUAT, Faizabad, Uttar Pradesh
13	PANT-T-10	GBPUAT, Pantnagar, Uttaranchal
14	PANT-T-11	GBPUAT, Pantnagar, Uttaranchal
15	PAU-2371	PAU, Ludhiana, Punjab
16	PAU-2372	PAU, Ludhiana, Punjab
17	PAU-2373	PAU, Ludhiana, Punjab
18	PAU-2374	PAU, Ludhiana, Punjab
19	Arka Vikas	IIHR, Bengaluru, Karnataka
20	Dwd-T-11	AICVIP, UAS, Dharwad, Karnataka
21	VR-35	IIVR, Varanasi, Uttar Pradesh
22	VR-415	IIVR, Varanasi, Uttar Pradesh
23	VRCT-155	VPKAS Almora, Uttaranchal
24	VRCT-17	VPKAS Almora, Uttaranchal
25	VTG-106	VPKAS Almora, Uttaranchal
26	VTG-85	VPKAS Almora, Uttaranchal
27	VTG-86	VPKAS Almora, Uttaranchal
28	VTG-89	VPKAS Almora, Uttaranchal
29	VTG-90	VPKAS Almora, Uttaranchal
30	VTG-93	VPKAS Almora, Uttaranchal
31	VTG-95	VPKAS Almora, Uttaranchal
32	Dwd-T-1	AICVIP, UAS, Dharwad, Karnataka
33	Dwd-T-2	AICVIP, UAS, Dharwad, Karnataka
34	Dwd-T-3	AICVIP, UAS, Dharwad, Karnataka
35	Dwd-T-4	AICVIP, UAS, Dharwad, Karnataka
36	Dwd-T-5	AICVIP, UAS, Dharwad, Karnataka
37	Dwd-T-6	AICVIP, UAS, Dharwad, Karnataka
38	Dwd-T-7	AICVIP, UAS, Dharwad, Karnataka
39	Dwd-T-8	AICVIP, UAS, Dharwad, Karnataka
40	Dwd-T-9	AICVIP, UAS, Dharwad, Karnataka
41	Dwd-T-10	AICVIP, UAS, Dharwad, Karnataka

Year	Season	Material evaluated	Nursery sowing date	Transplanting date
2007	*Kharif*	41 Genotypes	10.07.2007	03.08.2007
2008	*Kharif*	41 Genotypes	23.06.2008	23.07.2008
2008	*Rabi*	41 Genotypes ;	11.11.2008	06.12.2008
2008	*Rabi*	25 hybrids + 10 parents + 1 commercial check (ARTH-3)	28.11.2008	29.12.2008

3.6 OBSERVATIONS RECORDED

Five random competitive plants per treatment were selected, tagged and observations were recorded.

Observations for all the 19 characters described below were recorded for each of the genotypes and developed F_1 hybrids.

3.6.1 Plant growth parameters

3.6.1.1 Plant height

Height of the plants from the base to the tip of the plant was measured in five plants and expressed in centimeter (cm) and the average was used for computation.

3.6.1.2 Number of branches per plant

Number of branches per plant was counted in five plants in each genotype and the average was calculated.

3.6.1.3 Days to 50 per cent flowering

Number of days from transplanting to first flower appearance in 50 per cent of the plants in each row was recorded and the average was computed.

3.6.1.4 Number of fruits per cluster

Before first picking, three fruit bunches were chosen at random in each of labelled plant to calculate the average number of fruits per cluster.

3.6.2 Fruit physical parameters

Fully grown mature representative fruits of each genotype/hybrid were selected to measure fruit parameters. Five fruits were used for recording these traits and average was taken from them

3.6.2.1 Fruit length (Polar diameter)

The length of fruit was measured in centimeters (cm) from the base of the calyx to tip of fruit with the help of vernier calipers.

3.6.2.2 Fruit width (Equatorial diameter)

Diameter of the fruit was measured in centimeters (cm) with the help of a vernier calipers at the center (equatorial length) of the fruit.

3.6.2.3 Pericarp thickness

The fruits were cut transversely in the middle and were used for measuring pericarp thickness. The pericarp thickness was measured in centimeter (cm).

3.6.2.4 Number of locules per fruit

Number of locules was counted by cutting the fruit transversely in the middle and the average was calculated.

3.6.2.5 Single fruit weight (g)

Well developed individual fruit weight was recorded in grams by weighing on a sensitive balance.

3.6.3 Fruit quality parameters

The fruits utilized for recording pericarp thickness were used for TSS.

3.6.3.1 Total soluble solids (TSS)

A drop of juice was used to record the TSS (%) with the help of Erma hand refractometer at ambient temperature.

3.6.4 Plant yield parameters

3.6.4.1 Number of fruits per plant

Total number of fruits harvested from all the pickings was pooled and the average number of fruits was calculated.

3.6.4.2 Yield per plant

Fruit yield was determined by adding the total fruit weight over all the pickings from each reference plant and expressed in kilograms (kg).

3.6.4.3 Yield per hectare

Yield per hectare was determined by adding the total fruit weight over all the pickings from each plot of a genotype/hybrid and converted to hectare . It is expressed in tonnes (t) per hectare (ha).

3.6.5 Disease incidence:

Field incidence of following diseases was recorded using appropriate grade scales and percentage incidence were used during the crop period with the help of the Department of Plant Pathology, UAS, Dharwad.

1. Early blight
2. Late blight
3. Powdery mildew
4. Tomato leaf curl virus
5. Tomato spotted wilt virus
6. *Sclerotium* wilt

3.7 STATISTICAL ANALYSIS

3.7.1 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 significance of differences among all the genotypes was tested by 'F' test.

ANOVA

Sources	df	MSS	Expected MSS	F-ratio
Replications	r-1	RMSS	-	
Genotypes	g-1	VMSS	$\sigma^2_e + r\sigma^2_g$	VMSS/EMSS
Error	(r-1) (g-1)	EMSS	σ^2_e	
Total	(rg-1)			

Where,

r = Number of replications

g = Number of genotypes

$$\text{S. Em} = \text{Standard error mean} = \frac{\sqrt{\text{EMSS}}}{r}$$

3.7.2 Estimation of genetic parameters

To identify and ascertain the genetic variability among genotypes and to assess the extent of environmental effect on various characteristics, different genetic parameters were estimated.

3.7.2.1 Estimation of variance components

Genotypic and phenotypic components of variance were estimated with the help of following formulae.

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{VMSS} - \text{EMSS}}{r}$$

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

$$\text{Error } (\sigma^2_e) = \text{EMSS}$$

3.7.2.2 Coefficient of variability

Both genotypic and phenotypic coefficients of variability were computed for each character as per method suggested by Burton and Devane (1953).

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sigma_g}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sigma_p}{\bar{x}} \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{x}$ = Grand mean of the character

PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) as follows;

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

3.7.2.3 Heritability (h^2) in broad sense

Heritability (h^2_{bs}) in broad sense was computed for each character as the ratio of genotypic variance to the total variance as suggested by Hanson *et al.* (1956) and expressed in percentage.

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

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949).

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

3.7.2.4 Genetic advance

Genetic advance (GA) for each character was computed by adopting the formula given by Johnson *et al.* (1955).

$$GA = h^2_{bs} (i) (\sigma_p)$$

Where,

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

i = Selection differential which is equal to 2.06 at 5 per cent selection intensity (Lush, 1949)

σ_p = Phenotypic standard deviation

3.7.2.5 Genetic advance over mean (GAM)

Genetic advance over mean (GAM) was computed by the formula,

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

Where,

GA = Genetic advance

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

The genetic advance as per cent of mean was categorized into low, moderate and high by Johnson *et al*. (1955) and is as follows.

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

3.7.3 Estimation of correlations

The correlation coefficient analysis among all possible character combination at phenotypic (r_p) and genotypic (r_g) level were estimated employing the following formula (Al-Jibouri *et al.*, 1958).

$$\text{Phenotypic correlation } V_{xy(p)} = \frac{COV_{xy(p)}}{\sqrt{[V_{x(p)} \times V_{y(p)}]}}$$

$$\text{Genotypic correlation } V_{xy(g)} = \frac{COV_{xy(g)}}{\sqrt{[V_{x(g)} \times V_{y(g)}]}}$$

Where,

$COV_{xy(p)}$ = Phenotypic co-variance between variables x and y

$COV_{xy(g)}$ = Genotypic co-variance between variables x and y

$V_{x(p)}$ = Phenotypic variance for the variable x

$V_{x(g)}$ = Genotypic variance for the variable x

$V_{y(p)}$ = Phenotypic variance for the variable y

$V_{y(g)}$ = Genotypic variance for the variable y

Significance of correlation coefficient at both phenotypic and genotypic levels were tested by comparing table 'r' value with obtained value.

3.7.4 Path coefficient analysis

The estimates of direct and indirect effect of component characters on fruit yield were computed using appropriate correlation coefficient of different component characters as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). Thus the correlation coefficient of any character with fruit yield was split into direct and indirect effects adopting the standard formula.

$$r_{iy} = r_{1i}P_1 + r_{2i}P_2 + r_{3i}P_3 + \ldots + r_{ni}P_n + \ldots . r_{ii}P_1$$

Where,

r_{iy} = Correlation of the i^{th} character with fruit yield

r_{ni} = Correlation between n^{th} character with i^{th} character

n = Number of independent variables (component characters)

P_i = Direct effect of i^{th} character on fruit yield

Direct effects of different component character on fruit yield were obtained by solving the following equations.

$r_{iy} = [P_I] [r_{ij}]$ which can also be rearranged as

$$[P_I] = [r_{iy}]^{-1} [r_{ij}]$$

Where,

$[P_I]$ = Matrix of direct effect

$[r_{ij}]$ = Matrix of correlation coefficients among all the n components characters

$[r_{iy}]$ = Matrix of correlation of all component characters with fruit yield

r_{il} = Indirect effect of i^{th} character on fruit yield through first characters

The residual effect was obtained by the following formula.

Residual effect = $P_R = \sqrt{1 - P_i r_{iy}}$

Where,

P_i and r_{iy} are as given above

3.7.5 Genetic diversity

3.7.5.1 Mahalanobis D^2 analysis

Mahalanobis (1936) D^2 analysis was used for assessing the genetic divergence among the test entries involving quantitative characters. The generalized distance between any two population is given by the formula.

$$D^2 = \sum\sum \lambda_{ij}\, \sigma_{ai}\sigma_{aj}$$

Where,

D^2 = square of generalized distance

λ_{ij} = Reciprocal of the common dispersal matrix

$\sigma_{ai} = (\mu_{i1} - \mu_{i2})$

$\sigma_{aj} = (\mu_{j1} - \mu_{j2})$

μ = General mean

Since, the formula for computation requires inversion of higher order determinant, transformation of the original correlated unstandardized character mean (Xs) to standardized uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the sum of squares of the differences between pairs of corresponding uncorrelated (γs) values of any two uncorrelated genotypes (Rao, 1952).

3.7.5.2 Cluster of D^2 values

All n(n-1)/2 D^2 values were clustered using Tocher's method described by Rao (1952).

3.7.5.3 Intra cluster distance

The intra cluster distances were calculated by the formula given by Singh and Choudhary (1977).

$$\text{Square of the inter cluster distance} = \frac{\sum D^2_i}{n}$$

Where,

$\sum D^2_i$ is the sum of distance between all possible combinations of the entries included in a cluster.

n = Number of all possible combinations

3.7.5.4 Inter cluster distance

The inter cluster distances were calculated by the formula described by Singh and Choudhary (1977).

$$\text{Square of the intra cluster distance} = \frac{\sum D^2_i}{n_i n_j}$$

Where,

$\sum D^2_i$ is the sum of distances between all possible combinations ($n_i n_j$) of the entries included in the clusters study.

n_i =Number of entries of cluster i

n_j =Number of entries of cluster j

3.7.6 Stability analysis

3.7.6.1 Phenotypic stability (regression procedure)

Only when a significant genotype X environment interaction occurred, stability parameters for each genotype were determined using regression procedure of Eberhart and Russell (1966).

The model:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

Y_{ij} = Mean of i^{th} genotype at j^{th} environment

μ_i = i^{th} genotype mean over all the environments

β_i = Regression coefficient that measures the response of the i^{th} genotype to the varying environment

I_j = Environmental index obtained as the deviation of mean of all the environment from the grand mean where $\sum_{ij} = 0$

δ_{ij} = Deviation from regression of the i^{th} genotype at j^{th} environment

ANOVA for estimating stability parameters as suggested by Eberhart and Russell (1966) is given below.

Source	d.f.	SS	MSS	Cal F
Total	(S.t-1)	$\sum_i \sum_j Y^2_{ij}$ - CF		
Genotypes	(t-1)	$1/n \sum_j Y^2_i$ – CF	MSS1	MSS1/ MSS3
Environment	(S-1)	$t(n-1) \sum_i \sum_j Y^2_{ij} - \sum y^2/in$		
Environment (linear)	1	$1/t (\sum_j Y_i I_i)^2 / \sum_j I^2_j$		
Genotypes x Environment (linear)	(t-1)	$\sum_i (\sum_j Y_{ij} I_j)^2 / \sum_j I^2_j$	MSS2	MSS2/ MSS3
Pooled deviation	t (S-2)	$\sum_i \sum_j \delta^2_{ij}$	MSS3	
Pooled error	S (t-1) (r-1)			

If these values are significantly deviating from zero, the expected genotypes cannot be predicted satisfactorily (unstable). When deviations are not significant the conclusion may be drawn by considering jointly the mean yield and regression value (Finley and Wilkinson, 1963 and Eberhart and Russell, 1966) as follows.

Regression coefficient (b_i)	Mean value of character (μ)	Stability	Remarks
$b_i = 1$	High	Average	Well adopted to all environments
$b_i = 1$	Low	Average	Poorly adopted to all environments
$b_i > 1$	High	Below average	Specificially adopted to favourable environments
$b_i < 1$	High	Below average	Specifically adopted to unfavourable environments

Unit regression is interpreted as average stability since the slope over all genotypes on the environment index will be one.

3.7.6.2 Stability parameters

The stability parameters were estimated by the following formulae.

$$m = \sum_j Y_{ij}/n$$

$$b_i = \sum_j Y_{ij} I_j / I^2_j$$

$$S^2d_i = [\sum_j S^2_{ij}/n-2] - S^2e/r$$

Where,

n = Number of environments

$\sum_j S^2_{ij}$ = Sum of the squares of deviation from the regression

S^2e/r = Estimate of pooled error

The deviation from unity of the regression coefficient was tested by the 't' test where t = 1-b/SEb and comparing it against table 't' values. The appropriate F test ($F \approx (\sum_i b_{ij}/n-2)$/pooled error) was used to evaluate deviation from regression mean square for each genotype (Eberhart and Russell, 1966).

1. Mean yield of overall environment (μ)
2. Regression coefficient (b_i) : and
3. Deviation from regression (mean square) (S^2d_i)

According to Eberhart and Russell (1966), the highly stable variety is one with high mean above the grand mean (μ), regression coefficient (b_i) = 1.00 and non-significant deviation from regression (S^2d_i) = 0.

The estimates of deviation from regression (using F test) suggests the degree of reliance that should be put to linear regression in interpretation of the data.

3.7.7 Line x Tester analysis

3.7.7.1 Analysis of variance

Analysis of variance (ANOVA) for individual character was carried out on the basis of mean value per treatment per replication following the procedure described by Panse and Sukhatme (1967) from randomized block design (RBD). Analysis was carried out only to know the significance or otherwise of the difference seen between means of parents and hybrids.

Significance of treatments was tested at 5 and 1 per cent probability. The model of analysis of variance table adopted is given below.

ANOVA table for parents and hybrids

Source of variation	Degrees of freedom	Mean sum of squares
Replication	(r-1)	
Treatments	(e-1)	
Parents	(p-1)	
Parents Vs Crosses	1	
Crosses	(lt-1)	
Lines	(l-1)	M_1
Testers	(t-1)	M_2
Lines x Testers	1	M_3
Error	(e-1) (r-1)	M_4
Total	(ltr-1)	

Where,

r = Number of replication

e = Number of treatments

l = Number of lines

t = Number of testers

3.7.7.2 Estimation of heterosis

The magnitude of heterosis was estimated in relation to mid parent (MP), better parent (BP) and commercial check (CC) as percentage increase or decrease of F_1's over the respective mid parent value/better parent value/commercial check.

Average values over replications were used for estimating the heterosis over mid parent, better parent and the commercial check (economic heterosis). The designation of a cross as heterotic depended upon the trait.

Per cent heterosis of F_1's over MP,BP, and CC was calculated using the methods of Turner (1953) and Hayes *et al.* (1955).

Mid parent (MP) value = $\frac{P_1 + P_2}{2}$

a) Heterosis over mid parent (MP) (%) = $\frac{F_1 - \overline{MP}}{\overline{MP}} \times 100$

b) Heterosis over better parent (BP) (%) = $\frac{F_1 - \overline{BP}}{\overline{BP}} \times 100$

c) Economic heterosis (CC) (%) = $\frac{F_1}{C} \times 100$

Testing whether heterosis was significant or not was done by comparing the mean deviations with values of critical difference (CD) obtained separately from MP and CC by using the formulae.

CD for heterosis over MP = $\sqrt{\frac{3 \times \text{ErMSS} \times \text{'t' value}}{2 \times r}}$

CD for heterosis over BP&CC = $\sqrt{\frac{2 \times \text{ErMSS} \times \text{'t' value}}{r}}$

Where,

r = Number of replications

t = Table 't' value at error degrees of freedom

ErMSS = Error mean sum of squares

3.7.7.3 Combining ability analysis

3.7.7.3.1 Analysis of variance for combining ability

For combining ability analysis, only crosses were considered and analyzed based on the line x tester analysis as proposed by Kempthrone (1957) and emphasized by Arunachalam (1974). Analysis of variance adopted for combining ability is given below.

ANOVA for combining ability

Source	d.f.	MSS	Expectation
Replications	(r-1)	-	
Crosses	(dt-1)	-	
Lines	(d-1)	M_1	$\sigma^2e + r\sigma^2_d + tr\sigma^2_1$
Testers	(t-1)	M_2	$\sigma^2e + r\sigma^2_d + dr\sigma^2_t$
Lines x testers	(d-1) (t-1)	M_3	$\sigma^2e + r\sigma^2_d$
Error (LT)	(r-1) (dt-1)	M_4	σ^2e

Where,

d = number of lines

t = number of testers

COV (half sibs) and COV (full sibs) were estimated by equating the observed mean squares to their expectations. Since number of lines and testers used were different, weighed average of COV (half sibs) was computed by deriving least square estimates as proposed by Arunachalam (1974). Least square estimates were derived as follows.

$$Y = \text{COV (half sibs)} = \frac{Y_2 [t(a+c-2b) + d (b+c-2a)}{dt-t^2-d^2}$$

$$X = \text{COV (full sibs)} = \frac{[t(a+c-2b) + d (b+c-2a) - 1/2 [t^2(a+c)+d^2(b+c)-d+(a+b)]]}{dt-t^2-d^2}$$

where,

$a = (M_2-M_4)/r$, $b=(M_1-M_4)/r$, $c=(M_3-M_4)/r$

The least square estimates of X and Y were used to compute components of combining ability variances as follows.

$\sigma^2_{gca} = Y$ and $\sigma^2_{gca} = X - 2Y$

3.7.7.3.2 Estimation of combining ability effects

The combining ability effects were estimated as follows:

General combining ability effects (gca effects) of i^{th} line

$$g_i = \frac{x_i..}{tr} - \frac{x...}{dtr}$$

where,

$x_i..$ = Total of i^{th} line over all testers and replication and

$x.../dtr$ = Overall mean

General combining ability effects (gca effects) of j^{th} tester

$$g_j = \frac{x_{.j}..}{dr} - \frac{x...}{dtr}$$

where,

x.j. = Total of j^{th} tester over all the lines and replications

Specific combining ability effects (sca) due to ij^{th} cross

$$S_{ij} = \frac{x_{ij}.}{r} - \frac{x...}{dtr} - \frac{x.j.}{dr} - \frac{x...}{dtr}$$

where,

$x_{ij}.$ = Total of ij^{th} cross over all the lines and replications

3.7.7.3.3 Standard errors of combining ability estimates

The variance of different estimates was calculated by multiplying the error variance by their respective coefficients as shown below.

Error variance = M_4 = Error mean squares from combining ability analysis

$$\text{Variance of } (g_i) \text{ lines} = \frac{M_4}{rt}$$

$$\text{Variance of } (g_j) \text{ lines} = \frac{M_4}{rd}$$

$$\text{Variance of hybrids } (S_{ij}) = \frac{M_4}{r}$$

The square root of variance of the estimates was used as standard error meant for testing the significance of combining ability effects.

3.7.7.3.4 Proportion contribution of lines, testers and their interaction

$$\text{Contribution of lines} = \frac{SS(d)}{SS(c)} \times 100$$

where,

SS(d) = Sum of squares due to lines effect

SS(t) = Sum of squares due to crosses

$$\text{Contribution of testers} = \frac{SS(t)}{SS(c)} \times 100$$

where,

SS(t) = Sum of squares due to testers effect.

$$\text{Contribution of (line x tester)} = \frac{SS(dxt)}{SS(c)} \times 100$$

where,

SS(dxt) = Sum of squares due to interaction

For statistical analysis of raw data ‘Windostat Statistical Software’ was utilized.

B. TRANSFORMATION STUDIES IN TOMATO:

3.8 TRANSGENIC TOMATO DEVELOPMENT

Agrobacterium cells containing construct; pCAMBIA with TRP sas/ihp (Krishnamurthy, 2006) developed for post transcriptional silencing of replicase gene of ToLCV was used for transformation of tomato (DMT-2) using protocol of McCormick (1991) with some modifications.

Agrobacterium tumefaciens LBA4404 transformed with pCAMBIA constructs were grown in YEM (yeast extract mannitol) with streptomycin (100 µg/ml), rifampicin (25 µg/ml) and kanamycin (50 µg/ml) at 28^0C for 24 hr. Seven-days-old cotyledonary leaves of tomato were surface sterilized with 0.1 percent mercuric chloride for 1 min and rinsed with sterilized distilled water 3 to 4 times to remove the traces of the mercuric chloride. The cotyledonary leaves were pre-cultured on MS plain medium for two days. The cotyledonary leaves were cut at ends and infected with *Agrobacterium* culture treated with 200 µM of acetosyringone. Cultures were left for 20 minutes for agroinfection under dark with gentle shaking. These co-cultivated explants were blot dried on sterile filter paper and then placed on solid MS (Murashige and Skoog, 1962) medium without any hormones and incubated in dark for 2 days. The cotyledonary leaves were then transferred to solid MS medium containing 3% sucrose, 2mg/l Zeatin, 0.1mg/l IAA, 200 µg/ml cefotaxime to prevent further growth of *Agrobacterium* and hygromycin at 7.5 µg/ml was used in the medium for selection of transformants. The cultures were incubated at 25^0C under 16 hr photoperiod for 3 to 4 weeks, with subculturing at every 15-20 days. Young shoots were then transferred to MS medium containing 3% sucrose, 0.1 mg/l Zeatin, 0.1 mg/l IAA and hygromycin at 7.5 µg/ml for shoot elongation. The shoots so obtained were transferred to MS medium with 0.2 mg/l of NAA for rooting.

The T_0-transgenic plants obtained from TRP sas/ihp constructs were analysed for transgenes through testing for presence of *hptII,* the marker gene using CITAB method (Sambrook, *et.al*., 1989).

3.9 TRANSGENE EXPRESSION ANALYSIS

3.9.1 PCR analysis

DNA isolated from putative transgenic lines from each construct was tested for the presence of insert. PCR was performed using *hpt*II specific primers in a 20µl PCR reaction containing 1U of Taq DNA polymerase, 2mM dNTP mix, 5 pmoles of each primer, 1xTaq assay buffer. For PCR standard protocol was followed except the annealing temperature (55^0C for 1 min). Vector DNA and non-transgenic plant DNA were used as negative and positive control, respectively. The following primer combination was used for *hpt*II amplification;

Forward-5' CGACCTGATGCAGCTCTCGGAGGC 3';

reverse-5' CGATTGCGTCGCATCGACCCTGCGC3'.

Amplicons were visualized by running 1% agarose gels. Similarly, the total DNA isolated from T_1-transgenic plants obtained from TRP constructs were subjected to PCR analysis using *hpt*II specific primer pair.

4. EXPERIMENTAL RESULTS

The results of the experiments conducted under "Biometrical and transformation studies in tomato (*Solanum lycopersicum.* L.)" at the AICRP (Vegetable) block, Main Agricultural Research Station, Division of Horticulture, and at the laboratory of the Institute of Agri-Biotechnology, University of Agricultural Sciences, Dharwad during 2007 to 2010 are presented under following headings:

A. Biometrical studies in tomato:

Experiment I: Evaluation of tomato genotypes during *kharif* 2007, *kharif* 2008 and *rabi* 2008,

4.1.1 Analysis of variance

4.1.2 Genetic variability, heritability and genetic advance

4.1.3 Association analysis

4.1.4 Path coefficient analysis

4.1.5 Genetic diversity analysis

4.1.6 Stability analysis

Experiment II: Evaluation of F_1 hybrids developed by Line x Tester method during *rabi* 2008

4.2.1 Heterosis

4.2.3 Combining ability

B. Transformation studies in tomato

A. BIOMETRICAL STUDIES IN TOMATO:

4.1 EXPERIMENT I: EVALUATION OF TOMATO GENOTYPES.

4.1.1 ANALYSIS OF VARIANCE

The results of seasonwise analysis of variance for nineteen characters of 41 tomato genotypes evaluated during *kharif* 2007, *kharif* 2008 and *rabi* 2008 is presented in Tables 6. The results indicated highly significant variation among the genotypes for all the characters in *kharif* 2007, *kharif* 2008 and *rabi* 2008 environments.

4.1.2 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The estimates of genetic variability including character mean, mean minimum, mean maximum, genotypic and phenotypic variance, genotypic and phenotypic coefficient of variability, heritability, genetic advance, genetic advance as per cent mean for different characters are presented season wise for *kharif* 2007, *kharif* 2008 and *rabi* 2008 in Table 7.

4.1.2.1 Plant height

The range observed for plant height among genotypes was 62.90 to 154.33 cm, 63.67 to 161.30 cm and 70.39 to 166.10 cm with a mean of 99.44 cm, 99.66 cm and 102.08 cm for *kharif* 2007, *kharif* 2008 and *rabi* 2008 seasons respectively.

The high GCV (21, 23, 22 %) , high PCV (21, 23, 23 %) , very high heritability (97, 98, 99 %) with a high GAM (42.40, 46, 45.93 %) were noticed in *kharif* 2007, *kharif* 2008 and *rabi* 2008 seasons respectively .

4.1.2.2 Number of branches per plant

Across three environments minimum, maximum and mean value for number of primary branches per plant ranged from 2.33 - 2.63, 5.41 - 6.21 and 3.56 - 3.58 respectively. It

Table 6 . Analysis of variance for various characters in 41 tomato genotypes during *kharif* 2007, *kharif* 2008 *and rabi* 2008.

Sl No	Characters	Mean sum of squares								
		Kharif 2007			*Kharif* 2008			*Rabi* 2008		
	Source of Var. →	Replicate	Treatments	Error	Replicate	Treatments	Error	Replicate	Treatments	Error
	df →	2	40	80	2	40	80	2	40	80
1	Plant height (cm)	183.34	1335.83**	40.29	103.08	1535.95**	25.16	90.58	1597.35**	21.85
2	No. of branches	0.08	1.45**	0.29	0.03	1.06**	0.29	0.79	1.10**	0.21
3	Days to 50% flowering	28.50	34.25**	5.10	9.35	23.30**	3.33	16.72	26.89**	2.00
4	No. of fruits / cluster	0.93	14.98**	0.46	0.06	17.81**	0.42	1.55	21.14**	0.23
5	Fruit length (cm)	0.39	2.63**	0.08	0.04	2.41**	0.05	0.12	2.70**	0.03
6	Fruit width (cm)	0.78	3.25**	0.10	0.06	3.07**	0.05	0.28	3.41**	0.03
7	Pericarp thickness (cm)	0.001	0.019*	0.002	0.007	0.015**	0.001	0.008	0.016*	0.001
8	No. of locules / fruit	0.50	4.19**	0.14	0.11	3.45**	0.15	0.20	3.61**	0.16
9	Single fruit weight (g)	167.97	2200.42**	34.43	16.53	2106.91**	11.81	12.17	2214.18**	11.98
10	TSS (%)	0.01	3.41**	0.07	0.03	3.22**	0.07	0.13	3.27**	0.05
11	No. of fruits / plant	18.67	8123.87**	29.76	26.64	7897.01**	27.23	75.23	9030.67**	20.57
12	Yield / plant (kg)	0.03	0.19**	0.02	0.02	0.17**	0.02	0.02	0.23*	0.02
13	Yield / ha (t)	0.70	52.84**	3.78	2.13	66.48**	3.80	33.06	98.68**	3.97
14	Early Blight	0.08	1.19**	0.15	0.32	0.83**	0.19	0.15	1.64**	0.31
15	Late Blight	1.28	1.35**	0.30	0.63	1.43**	0.25	0.10	0.38*	0.31
16	Powdery Mildew	0.04	0.34**	0.10	0.04	0.42**	0.12	1.28	2.16**	0.33
17	Tomato Leaf curl Virus	43.38	93.95**	21.35	53.89	179.52**	18.04	5.39	22.52**	3.53
18	Tomato Spotted Wilt Virus	3.18	18.68**	4.25	31.95	47.21*	4.41	2.33	3.18**	0.45
19	*Sclerotium* wilt	21.26	24.52**	3.77	6.84	57.98**	5.83	22.84	79.47**	8.57

* Significant at 5% probability ** Significant at 1% probability

Table 7. Variability studies in 41 tomato genotypes for various characters during *kharif* 2007, *kharif* 2008 *and rabi* 2008.

Sl.	Characters	Year	Mean	Mean range		Genotypicvariance (σ^2_g)	Phenotypicvariance (σ^2_p)	Genotypiccoefficientof variation (GCV %)	Phenotypiccoefficient of variation (PCV %)	Heritability (h^2_{bs})	Genetic advance (GA)	Geneticadvance overmean(GAM)
				Minimum	Maximum							
1	Plant height (cm)	2007K	99.44	62.90	154.33	431.85	445.28	21	21	97	42.16	42.40
		2008K	99.66	63.67	161.30	503.59	511.98	23	.23	98	45.85	46.00
		2008R	102.08	70.39	166.10	525.16	532.45	22	23	99	46.88	45.93
2	No. of branches per plant	2007K	3.58	2.33	6.21	0.39	0.48	17	19	80	1.14	31.95
		2008K	3.56	2.63	5.41	0.26	0.35	14	17	73	0.89	25.06
		2008R	3.58	2.41	5.49	0.30	0.37	15	17	81	1.01	28.21
3	Days to 50% flowering	2007K	32.70	24.67	38.67	9.72	11.42	10	10	85	5.92	18.12
		2008K	33.53	25.00	38.33	6.66	7.77	8	8	86	4.92	14.68
		2008R	35.60	29.00	42.00	8.30	8.96	8	8	93	5.71	16.04
4	No. of fruits per	2007K	4.38	2.11	10.56	4.84	4.99	50	51	97	4.46	102.02
	cluster	2008K	4.29	2.09	11.40	5.80	5.94	56	57	98	4.90	114.16
		2008R	4.41	2.44	11.66	6.97	7.05	60	60	99	5.41	122.79
5	Fruit length (cm)	2007K	4.25	2.03	6.13	0.85	0.88	22	22	97	1.87	44.02
		2008K	4.27	2.07	6.04	0.79	0.80	21	21	98	1.81	42.35
		2008R	4.49	2.12	6.35	0.89	0.90	21	21	99	1.93	43.01
6	Fruit width (cm)	2007K	4.44	2.05	6.39	1.05	1.08	23	23	97	2.08	46.86
		2008K	4.54	2.03	6.32	1.00	1.02	22	22	98	2.05	45.13
		2008R	4.68	2.11	6.64	1.13	1.14	23	23	99	2.18	46.54
7	Pericarp thickness (cm)	2007K	0.44	0.30	0.57	0.006	0.006	17.4	18.3	90.9	0.150	34.173
		2008K	0.43	0.30	0.59	0.004	0.005	15.4	16.2	90.7	0.131	30.239
		2008R	0.46	0.31	0.60	0.005	0.005	15.3	15.8	94.0	0.141	30.625
8	No. of locules per fruit	2007K	3.61	2.00	7.22	1.35	1.40	32	33	97	2.35	65.11
		2008K	3.67	2.12	7.07	1.10	1.15	29	29	96	2.11	57.63
		2008R	3.69	2.15	7.40	1.15	1.20	29	30	95	2.16	58.56
9	Single fruit weight (g)	2007K	64.57	10.22	118.50	721.99	733.47	42	42	98	54.92	85.05
		2008K	65.45	10.40	108.93	698.36	702.30	40	40	99	54.29	82.94
		2008R	69.12	10.88	114.63	734.07	738.06	39	39	99	55.66	80.53
10	Total soluble solids (%)	2007K	4.38	3.21	7.62	1.11	1.14	24	24	98	2.15	49.08
		2008K	4.34	3.12	8.00	1.05	1.07	24	24	98	2.09	48.07
		2008R	4.67	3.50	7.93	1.08	1.09	22	22	99	2.12	45.38
11	No. of fruits per plant	2007K	58.10	20.44	210.71	2698.04	2707.96	89	90	100	106.81	183.84
		2008K	60.09	18.97	196.00	2623.26	2632.34	85	85	100	105.33	175.27
		2008R	66.40	24.81	226.11	3003.37	3010.22	83	83	100	112.77	169.82
12	Yield per plant (kg)	2007K	1.308	0.726	1.93	0.06	0.06	18	19	88	0.45	34.75
		2008K	1.435	0.982	1.972	0.05	0.06	16	17	89	0.44	30.47
		2008R	1.732	1.077	2.154	0.07	0.08	15	16	90	0.52	29.76

Contd...

Sl.	Characters	Year	Mean	Mean range		Genotypicvariance (σ^2_g)	Phenotypicvariance (σ^2_p)	Genotypiccoefficientof variation (GCV %)	Phenotypiccoefficient of variation (PCV %)	Heritability (h^2_{bs})	Genetic advance (GA)	Geneticadvance overmean(GAM)
				Minimum	Maximum							
13	Yield / hectare (t)	2007K	27.82	19.76	38.73	16.35	17.61	15	15	93	8.03	28.85
		2008K	30.58	17.25	38.82	20.89	22.16	15	15	94	9.14	29.90
		2008R	36.29	21.97	45.08	31.57	32.89	15	16	96	11.34	31.25
14	Early Blight	2007K	1.14	0.13	3.11	0.34	0.40	51	55	87	1.13	98.80
		2008K	1.19	0.10	2.41	0.21	0.28	38	44	77	0.83	69.51
		2008R	2.26	0.17	4.00	0.44	0.55	29	33	81	1.23	54.58
15	Late Blight	2007K	2.37	0.85	4.20	0.35	0.45	25	28	78	1.08	45.51
		2008K	2.28	0.58	4.33	0.39	0.48	27	30	82	1.17	51.36
		2008R	0.56	0.04	1.96	0.02	0.13	28	64	19	0.14	25.14
16	Powdery mildew	2007K	0.66	0.08	1.86	0.08	0.11	43	51	70	0.48	73.59
		2008K	0.68	0.06	1.75	0.10	0.14	47	55	72	0.55	81.48
		2008R	2.71	0.70	4.85	0.61	0.72	29	31	85	1.48	54.68
17	Tomato leaf curl	2007K	12.81	1.33	29.58	24.20	31.32	38	44	77	8.91	69.57
	virus (TLCV) (%)	2008K	13.63	2.67	43.22	53.83	59.84	54	57	90	14.33	105.18
		2008R	1.37	0.02	13.97	6.33	7.51	184	200	84	4.76	348.04
18	Tomato spotted wilt virus (TSWV) (%)	2007K	2.91	0.37	14.10	4.81	6.23	75	86	77	3.97	136.51
		2008K	4.09	0.33	16.37	14.27	15.74	92	97	91	7.41	180.95
		2008R	0.69	0.02	4.37	0.91	1.06	138	149	86	1.82	262.95
19	*Sclerotium* wilt (%)	2007K	4.76	0.27	13.33	6.92	8.17	55	60	85	4.98	104.74
		2008K	6.31	0.02	18.33	17.38	19.33	66	70	90	8.15	129.00
		2008R	9.92	1.74	24.26	23.64	26.49	49	52	89	9.46	95.34

2007K = *kharif* 2007, 2008K = *kharif* 2008, 2008R = *rabi* 2008

exhibited moderate GCV (14 -17 %), moderate PCV (17 - 19 %) with high heritability (73 - 81%) and high GAM (25.06 - 31.95%).

4.1.2.3 Days to 50 per cent flowering

Days required for 50 per cent flowering ranged from 24.67 - 29.00 days for minimum days, 38.33 - 42.00 days for maximum and 32.70 - 35.60 days for mean. The range estimates of PCV, GCV, heritability and GAM were 8 -10, 8-10, 86 - 93 and 14.68 -18.12 per cent respectively over three seasons of evaluation.

4.1.2.4 Number of fruits per cluster

It varied from 2.09 - 2.44, 10.56 - 11.40 and 4.29 - 4.41 for minimum, maximum and mean number of fruits per cluster respectively for three evaluations done. High PCV, high GCV, high heritability and very high GAM (51-60%, 50 - 60 %, 97-99 % and 102 - 122 % respectively) was observed.

4.1.2.5 Fruit length

Fruit polar diameter ranged from 2.03 - 2.12 cm to 6.04 - 6.35 cm with a grand means of 4.25 - 4.49 cm. The PCV, GCV, were 21 - 22, and 21 - 22 per cent respectively. Very high heritability in broad sense of 97 - 99 per cent coupled with high GAM 42.35 - 44.02 % was observed observed.

4.1.2.6 Fruit width

Fruit equatorial diameter had a range 2.03 - 2.11 to 6.32 - 6.64 cm. The mean fruit width was 4.44 - 4.68 cm. High PCV and GCV were recorded. Heritability was very high (97 - 99 %) with high GAM (45.13 - 46.86 %).

4.1.2.7 Pericarp thickness

Pericarp thickness had a range of 0.30-0.31 to 0.57-0.60 cm. The mean thickness recorded was 0.43 - 0.46 cm. Moderate estimates of PCV (15.8 - 18.3 %) and GCV (15.3-17.4 %), very high heritability (90.7 - 94.0 %) and high GAM (30.2 - 34.1%) were noticed.

4.1.2.8 Number of locules per fruit

The maximum and minimum number of locules per fruit were 7.07 - 7.40 and 2.00- 2.15 respectively. The mean value was 3.61 - 3.69. The high PCV (29 - 33 %) and GCV (29 - 32 %) coupled with very high heritability (95 - 97 %) and high GAM (57.63 - 65.11 %) were exhibited by this trait.

4.1.2.9 Single fruit weight

Single fruit weight ranged from 10.22 - 10.88 g to 108.93 - 118.50 g with an average of 64.57 - 69.12 g. High PCV (39 - 42 %) and GCV (39 - 42 %) with high broad sense heritability (98 - 99 %) and GAM (80.53 - 85.05 %) were recorded.

4.1.2.10 Total soluble solids

TSS ranged from 3.12-3.50^0 Brix to 7.62-8.00^0 Brix with a mean of 4.34 - 4.67^0 Brix. The GCV and PCV were 22 - 24 per cent and 22 - 24 per cent respectively. The values of heritability and GAM were high with 98 - 99 per cent and 45.38 - 49.08 per cent respectively.

4.1.2.11 Number of fruits per plant

The maximum, lowest and mean number of fruits ranges was 196 - 226.11, 18.97 - 24.81 and 58.10 - 66.40 respectively. The very high PCV, very high GCV with high heritability and GAM have been recorded by this trait.

4.1.2.12 Yield per plant

The minimum and maximum range limits of 0.726 - 1.077 kg to 1.93-2.154 kg with an average fruit yield per plant of 1.308-1.732 kg was recorded. The moderate PCV (16 - 19 %) and moderate GCV (15 - 18 %) with high heritability (88 - 90 %) and GAM (29.76 - 34.75 %) were observed.

4.1.2.13 Yield per hectare

The highest and lowest range limits of 38.82-45.08 t/ha to 17.25-21.97 t/ha with an average yield per hectare of 27.82-36.29 t/ha was recorded. The moderate PCV (15-16 %) and GCV (15 %) with very high heritability (93 - 96 %) and high GAM (28.85 -31.25 %) were observed.

4.1.2.14 Early blight incidence

The minimum, maximum and mean range of early blight incidence in different tomato genotypes were 0.10-0.17, 2.41 - 4.00 and 1.14 - 2.26 severity grades. High PCV (33-55%), high GCV (29-51%), coupled with high heritability (77 -87 %) and high GAM (54.58 - 98.80 %) were exhibited by this parameter.

4.1.2.15 Late blight incidence

The lowest, highest and mean range of late blight incidence in different tomato genotypes were 0.04 -0.85, 1.96 - 4.33 and 0.56-2.37 severity grades. High PCV (28-64%), high GCV (25 - 28%), coupled with low to high heritability (19 -78 %) and high GAM (25.14-51.36 %) were exhibited for this disease.

4.1.2.16 Powdery mildew incidence

The range of disease noticed was from 0.06-0.70 to 1.75-4.85 with a mean of 0.66-2.71 severity scale. The PCV (31-55%) and GCV (29-47%) were high with higher heritability (70-85 %) and GAM (54.68-81.48%).

4.1.2.17 Tomato leaf curl virus incidence

TLCV incidence ranged from 0.02-2.67 per cent to 13.97-43.22 per cent with a mean of 1.37-13.63 per cent. High PCV (44-200%) and moderate to high GCV (38-184%) were combined with higher heritability (77-90 %) and very high GAM.

4.1.2.18 Tomato spotted wilt virus incidence

TSWV incidence ranged from 0.02-0.37 per cent to 4.37-16.37 per cent with a mean of 0.69-4.09 per cent. High PCV (86-149%) and moderate to high GCV (75-138 %) were combined with higher heritability (77-91 %) and extremely high GAM.

4.1.2.19 *Sclerotium* wilt incidence

The highest, lowest and mean range of *Sclerotium* wilt incidence in different tomato genotypes were 13.33 - 24.26 %, 0.02-1.74% and 4.76-9.92%. High PCV (52-70%), high GCV (49-66%), coupled with low to high heritability (85-90 %) and high GAM (95.34-129.00 %) were noticed in this disease.

4.1.3 ASSOCIATION ANALYSIS

The twelve growth, quality and yield traits (plant height, no. of branches per plant, days to 50% flowering, no. of fruits per cluster, fruit length, fruit width, pericarp thickness, no. of locules per fruit, total soluble solids, single fruit weight , no. of fruits per plant, yield per plant) were involved in the association analysis to know their phenotypic and genotypic correlations among themselves for the tomato evaluations of *kharif* 2007, *kharif* 2008 and *rabi* 2008 . The results of the analysis i.e., phenotypic and genotypic correlations are presented season wise in Table 8.

Yield per plant showed positive significant association with number of fruits per plant57,0.38,0.23; 0.68, 0.44, 0.26), TSS (0.44, 0.27,0.26; 0.53,0.32,0.31), and number of fruits (0. Per cluster (0.64,0.31,0.20; 0.64,0.36,0.23) at both phenotypic (normal number) and genotypic (bold values) levels during three seasons. It also recorded negative significant association with days to 50 % flowering (-0.17,-0.32,-0.25; -0.26,-0.46,-0.32,) at both the levels.

Table 8. Genotypic and phenotypic correlation values of different traits on yield per plant in tomato from varietal evaluation done during *kharif* 2007, *kharif* 2008 and *rabi* 2008.

Sl No	Character	Season	Plant height	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length	Fruit width	Pericarp thickness	No. of locules per fruit	Single fruit weight	Total soluble solids	No. of fruits per plant	Yield per plant
1	Plant height	2007K	1.00	0.36**	0.01	0.55**	-0.37**	-0.54**	-0.19*	-0.11	-0.35**	0.55**	0.50**	0.47**
		2008K	1.00	0.39**	0.19*	0.55**	-0.36**	-0.55**	-0.25**	-0.18*	-0.36**	0.56**	0.47**	0.20*
		2008R	1.00	0.31**	0.24**	0.46**	-0.37**	-0.48**	-0.37**	-0.05	-0.32**	0.53**	0.43**	0.06
2	No. of branches	2007K	.26**	1.00	-0.38**	0.43**	-0.52**	-0.27**	-0.31**	0.01	-0.32**	0.54**	0.48**	0.35**
		2008K	0.28**	1.00	-0.23*	0.41**	-0.50**	-0.36**	-0.41**	0.14	-0.29**	0.59**	0.49**	0.19**
		2008R	0.22*	1.00	-0.22*	0.47**	-0.40**	-0.18*	-0.47**	0.18*	-0.20*	0.47**	0.51**	0.35**
3	Days to 50% flowering	2007K	0.02	-0.24**	1.00	-0.36**	0.21*	0.22*	0.08	0.15	0.18*	-0.34**	-0.40**	-0.26*
		2008K	0.14	-0.16	1.00	-0.29**	0.11	0.18*	0.18*	0.00	0.22*	-0.32**	-0.39**	-0.46**
		2008R	0.22 *	-0.11	1.00	-0.26**	0.11	0.29**	0.21*	0.21	0.30**	-0.21**	-0.31**	-0.32**
4	No. of fruits per cluster	2007K	0.49**	0.30**	-0.63**	1.00	-0.67**	-0.84**	-0.47**	-0.27**	-0.79**	0.89**	0.94**	0.64**
		2008K	0.52**	0.32**	-0.25**	1.00	-0.69**	-0.90**	-0.49**	-0.33**	-0.85**	0.91**	0.95**	0.36**
		2008R	0.44**	0.35**	-0.24**	1.00	-0.74**	-0.86**	-0.60**	-0.28**	-0.85**	0.87**	0.98**	0.23*
5	Fruit length	2007K	-0.34**	-0.37**	-0.77**	0.68**	1.00	0.69**	0.73**	0.07	0.70**	-0.55**	-0.75**	-0.30**
		2008K	-0.35**	-0.35**	0.08	-0.65**	1.00	0.70**	0.72**	0.09	0.71**	-0.54**	-0.74**	-0.17*
		2008R	-0.35**	-0.27**	0.09	-0.72**	1.00	0.65**	0.69**	0.04	0.71**	-0.53**	-0.71**	-0.01
6	Fruit width	2007K	-0.49**	-0.17	-0.40**	0.59**	0.68**	1.00	0.53**	0.55**	0.86**	-0.76**	-0.81**	-0.37**
		2008K	-0.52**	-0.23**	0.16	-0.85**	0.68**	1.00	0.56**	0.61**	0.93**	-0.81**	-0.89**	-0.19*
		2008R	-0.47**	-0.14	0.25**	-0.83**	0.64**	1.00	0.59**	0.58**	0.92**	-0.78**	-0.84**	-0.14
7	Pericarp thickness	2007K	-0.16	-0.20*	-0.24**	0.04	0.60**	0.42**	1.00	0.04	0.55**	-0.45**	-0.58**	-0.40**
		2008K	-0.21*	-0.22*	0.14	-0.42**	0.63**	0.49**	1.00	0.10	0.66**	-0.46**	-0.59**	0.00
		2008R	-0.32**	-0.35**	0.18	-0.55**	0.62**	0.54**	1.00	0.15	0.68**	-0.54**	-0.63**	0.07

Sl No	Character	Season	Plant height	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length	Fruit width	Pericarp thickness	No. of locules per fruit	Single fruit weight	Total soluble solids	No. of fruits per plant	Yield per plant
8	No. of	2007K	-0.09	0.02	-0.73**	0.66**	0.04	0.49**	0.02	1.00	0.53**	-0.37**	-0.22*	-0.07
	locules per	2008K	-0.17	0.13	-0.02	-0.29**	0.07	0.55**	0.08	1.00	0.54**	-0.44**	-0.28**	0.09
	fruit	2008R	-0.04	0.13	0.18*	-0.26**	0.05	0.55**	0.13	1.00	0.53**	-0.39**	-0.27*	0.06
9	Single	2007K	-0.32**	-0.21*	0.82**	-0.52**	0.66**	0.82**	0.48**	0.49**	1.00	-0.67**	-0.80**	-0.32**
	fruit	2008K	-0.34**	-0.19*	0.18	-0.81**	0.68**	0.90**	0.57**	0.50**	1.00	-0.71**	-0.83**	-0.07
	weight	2008R	-0.31**	-0.14	0.27**	-0.83**	0.69**	0.89**	0.61**	0.50**	1.00	-0.71**	-0.84**	0.01
10	Total	2007K	0.49**	0.39**	0.89**	-0.71**	-0.52**	-0.71**	-0.37**	-0.35**	-0.64**	1.00	0.82**	0.53**
	soluble	2008K	0.53**	0.37**	-0.22*	0.84**	-0.51**	-0.76**	-0.39**	-0.40**	-0.68**	1.00	0.85**	0.32**
	solids	2008R	0.52**	0.35**	-0.18*	0.85**	-0.50**	-0.75**	-0.48**	-0.35**	-0.68**	1.00	0.83**	0.31**
11	No. of	2007K	0.48**	0.35**	0.50	-0.24	-0.71**	-0.77**	-0.51**	-0.21*	-0.77**	0.79**	1.00	0.68**
	fruits per	2008K	0.46**	0.33**	-0.32**	0.92**	-0.71**	-0.86**	-0.51**	-0.26**	-0.82**	0.81**	1.00	0.44**
	plant	2008R	0.42**	0.38**	-0.28**	0.96**	-0.69**	-0.83**	-0.57**	-0.25**	-0.83**	0.81**	1.00	0.26*
12	Yield per	2007K	0.38**	0.27**	-0.17*	0.64**	-0.24*	-0.30**	-0.23*	-0.08	-0.28**	0.44**	0.57**	1.00
	plant	2008K	0.16	0.15	-0.32**	0.31**	-0.14	-0.15	-0.01	0.07	-0.06	0.27**	0.38**	1.00
		2008R	0.05	0.27**	-0.25*	0.20*	0.00	-0.11	0.07	0.05	0.02	0.26*	0.23*	1.00

(Genotypic correlation values are above diagonal and Phenotypic correlation values are below diagonal i.e. bold values are separators)

*, **: Indicates significant at 5 and 1% level of probability respectively, 2007K = *kharif* 2007, 2008K = *kharif* 2008, 2008R = *rabi* 2008

Plant height exhibited significant positive association with number of primary branches per plant 0.26,0.28,0.22; 0.36,0.39,0.31), number of fruits per cluster (0.49,0.52,0.44; 0.55,0.55,0.46), TSS (0.49,0.53,0.52; 0.55,0.56,0.53), and number of fruits per plant (0.48,0.46,0.42; 0.5,0.47,0.43) both at phenotypic and genotypic levels but highly significant negative correlation was observed with fruit length (-0.34,-0.35,-0.35;-0.37,-0.36,-0.37), fruit width (-0.49,-0.52,-0.47;-0.54,-0.55,-0.48), single fruit weight at phenotypic and genotypic levels. It also showed negative correlation with pericarp thickness and number of locules per fruit only at genotypic level.

Number of branches per plant was correlated positively and significantly with number of fruits per cluster (0.30, 0.32, 0.35; 0.46, 0.43, 0.41), TSS (0.39, 0.37, 0.35; 0.54, 0.59, 0.47), number of fruits per plant (0.48, 0.49, 0.51; 0.35, 0.33, 0.38) both at phenotypic and genotypic levels.

Number of fruits per plant exhibited highly significant positive correlation with TSS (0.79,0.81,0.81; 0.82,0.85,0.83), and yield per (0.57, 0.38. 0.2; 0.68, 0.44, 0.26) plant and significant negative correlation was seen with fruit length (-0.71, -0.71, -0.69; -0.75, 0.74, 0.71), fruit width (-0.77, -0.86, -0.83; -0.81, -0.89, -0.84), pericarp thickness (-0.51, -0.51, -0.57; -0.58, -0.59, -0.63) no of locules per fruit (-0.21, 0.26, -0.25; -0.22, -0.28, -0.27) , single fruit weight (-0.77,-0.82,-0.83; --0.80, -0.83, -0.84) both at phenotypic and genotypic levels.

Single fruit weight was positively and significantly associated with number of locules per fruit (0.66, 0.68, 0.69; 0.70, 0.71, 0.71), fruit length (0.66, 0.68, 0.69; 0.70, 0.71, 0.71) and fruit width (0.82,0.90, 0.89; 0.86,0.93,0.92), pericarp thickness (0.48, 0.57, 0.61; 0.55, 0.66, 0.68), number of locules per fruit (0.49, 0.50, 0.50 ; 0.53, 0.54, 0.53) at phenotypic and genotypic levels, while negatively and significantly correlated with Plant height, number of fruits per cluster, TSS, number of fruits per plant both at phenotypic and genotypic levels .

4.1.4 PATH COEFFICIENT ANALYSIS

Relative contribution of different traits towards fruit yield through partitioning of genotypic and phenotypic correlation into direct and indirect effects of component characters was computed with path coefficient analysis. The direct and indirect effects of ten traits on fruit yield per plant at phenotypic and genotypic levels for tomato genotypes evaluated in three environments is presented in Table 9. The results are presented as:

4.1.4.1. Direct effect of characters on yield

4.4.1.2 Indirect effect of different characters

4.1.4.1. Direct effect of characters on yield

The three season results indicate that the yield was directly affected mainly by two traits out of ten i.e., single fruit weight (0.37, 0.67, 0.68 ; 0.93, 0.25, 0.68) and number of fruits per plant (1.08, 1.13, 0.43; 1.21, 2.02, 0.79) in positive direction at phenotypic and genotypic levels in all environments while it varied in positive direction for two seasons for fruit width (0.26, 0.34, -0.49; 0.97, 1.38, -0.97) and plant height (0.14, 0.08, -0.13; 0.26, 0.45, -0.25). Highest direct effect on yield was recorded by number of fruits per plant with values 2.02, and 1.21 at genotypic level followed by 1.13 and 1.08 as phenotypic path values during *kharif* 2008 and *kharif* 2007 respectively.

Positive correlation of plant height, number of branches per plant, number of fruits per plant, total soluble solids and number of fruits per plant is pronouncedly shown along with negative correlations of days to 50 % flowering and fruit width on yield per plant.

4.4.1.2 Indirect effect of different characters

Indirect effects on yield per plant in positive direction at phenotypic and genotypic levels in all three seasons in an appreciable magnitude was recorded in:

(i) number of fruits per plant through plant height (0.52,0.51, 0.18; 0.61, 0.95, 0.34), number of branches per plant (0.39, 0.38, 0.16; 0.59, 0.99, 0.40), number of fruits per cluster (0.97, 1.04, 0.42; 1.15, 1.93, 0.77) and TSS (0.85, 0.92, 0.35; 0.99, 1.72, 0.65);

(ii) Single fruit weight through fruit length (0.25, 0.46, 0.47; 0.66, 0.18, 0.48), fruit width (0.31, 0.60, 0.61; 0.80, 0.23, 0.62), pericarp thickness (0.18, 0.38, 0.42; 0.51, 0.16, 0.46), number of

Table 9. Genotypic and phenotypic path values of different traits on yield per plant in tomato from varietal evaluation done during *kharif* 2007, *kharif* 2008 and *rabi* 2008.

Sl.	Characters	Level	Season	Plant height	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length	Fruit width	Pericarp thickness	No. of locules per fruit	Single fruit weight	Total soluble solids	No. of fruits per plant	Yield per plant	Partial R^2
1	Plant height	Phenotypic	2007	0.14	0.04	0.00	0.07	-0.05	-0.07	-0.02	-0.01	-0.05	0.07	0.07	0.38	0.05
			2008	0.08	0.02	0.01	0.04	-0.03	-0.04	-0.02	-0.01	-0.03	0.04	0.04	0.16	0.01
			2008	-0.13	-0.03	-0.03	-0.06	0.05	0.06	0.04	0.01	0.04	-0.07	-0.06	0.05	-0.01
		Genotypic	2007	0.26	0.09	0.00	0.14	-0.09	-0.14	-0.05	-0.03	-0.09	0.14	0.13	0.47	0.12
			2008	0.45	0.18	0.08	0.25	-0.16	-0.24	-0.11	-0.08	-0.16	0.25	0.21	0.20	0.09
			2008	-0.25	-0.08	-0.06	-0.11	0.09	0.12	0.09	0.01	0.08	-0.13	-0.11	0.06	-0.01
2	No. of branches per lant	Phenotypic	2007	0.02	0.08	-0.02	0.02	-0.03	-0.01	-0.02	0.00	-0.02	0.03	0.03	0.27	0.02
			2008	0.00	-0.02	0.00	-0.01	0.01	0.00	0.00	0.00	0.00	-0.01	-0.01	0.15	0.00
			2008	0.04	0.18	-0.02	0.06	-0.05	-0.02	-0.06	0.02	-0.02	0.06	0.07	0.27	0.05
		Genotypic	2007	0.09	0.26	-0.10	0.11	-0.13	-0.07	-0.08	0.00	-0.08	0.14	0.13	0.35	0.09
			2008	-0.08	-0.20	0.05	-0.08	0.10	0.07	0.08	-0.03	0.06	-0.12	-0.10	0.19	-0.04
			2008	0.09	0.27	-0.06	0.13	-0.11	-0.05	-0.13	0.05	-0.05	0.13	0.14	0.35	0.10
3	Days to 50% flowering	Phenotypic	2007	0.00	-0.03	0.11	-0.03	0.01	0.02	0.01	0.01	0.01	-0.03	-0.04	-0.17	-0.02
			2008	-0.02	0.03	-0.17	0.04	-0.01	-0.03	-0.02	0.00	-0.03	0.04	0.05	-0.32	0.05
			2008	-0.04	0.02	-0.19	0.05	-0.02	-0.05	-0.03	-0.04	-0.05	0.04	0.05	-0.25	0.05
		Genotypic	2007	0.00	-0.09	0.24	-0.09	0.05	0.05	0.02	0.04	0.04	-0.08	-0.10	-0.26	-0.06
			2008	-0.06	0.07	-0.31	0.09	-0.03	-0.06	-0.06	0.00	-0.07	0.10	0.12	-0.46	0.14
			2008	-0.04	0.04	-0.18	0.05	-0.02	-0.05	-0.04	-0.04	-0.06	0.04	0.06	-0.32	0.06
4	No. of Fruits pe r cluster	Phenotypic	2007	0.07	0.04	-0.04	0.13	-0.08	-0.10	-0.05	-0.03	-0.10	0.11	0.12	0.50	0.07
			2008	0.06	0.04	-0.03	0.12	-0.08	-0.10	-0.05	-0.03	-0.10	0.10	0.11	0.31	0.04
			2008	-0.07	-0.06	0.04	-0.17	0.12	0.14	0.09	0.04	0.14	-0.14	-0.16	0.20	-0.03
		Genotypic	2007	0.88	0.68	-0.57	1.60	-1.07	-1.34	-0.76	-0.44	-1.25	1.42	1.51	0.64	1.02
			2008	-0.26	-0.20	0.14	-0.48	0.33	0.43	0.23	0.16	0.40	-0.43	-0.45	0.36	-0.17
			2008	-0.50	-0.51	0.28	-1.08	0.80	0.93	0.65	0.30	0.92	-0.94	-1.06	0.23	-0.25
5	Fruit length	Phenotypic	2007	-0.07	-0.08	0.03	-0.13	0.21	0.14	0.13	0.01	0.14	-0.11	-0.15	-0.24	-0.05
			2008	0.02	0.02	0.00	0.03	-0.05	-0.03	-0.03	0.00	-0.03	0.03	0.04	-0.14	0.01
			2008	-0.01	-0.01	0.00	-0.02	0.02	0.01	0.01	0.00	0.02	-0.01	-0.02	0.00	0.00
		Genotypic	2007	-0.17	-0.24	0.10	-0.31	0.46	0.32	0.34	0.03	0.33	-0.26	-0.35	-0.30	-0.14
			2008	0.11	0.15	-0.03	0.20	-0.29	-0.20	-0.21	-0.03	-0.21	0.16	0.22	-0.17	0.05
			2008	0.01	0.02	0.00	0.03	-0.04	-0.02	-0.03	0.00	-0.03	0.02	0.03	-0.01	0.00
6	Fruit width	Phenotypic	2007	-0.13	-0.04	0.03	-0.20	0.17	0.26	0.11	0.13	0.21	-0.18	-0.20	-0.30	-0.08
			2008	-0.17	-0.08	0.05	-0.29	0.23	0.34	0.17	0.18	0.30	-0.26	-0.29	-0.15	-0.05
			2008	0.23	0.07	-0.12	0.41	-0.31	-0.49	-0.26	-0.27	-0.44	0.37	0.41	-0.11	0.05
		Genotypic	2007	-0.52	-0.27	0.22	-0.82	0.67	0.97	0.51	0.54	0.84	-0.74	-0.79	-0.37	-0.36
			2008	-0.76	-0.49	0.25	-1.24	0.97	1.38	0.78	0.84	1.29	-1.11	-1.22	-0.19	-0.26
			2008	0.46	0.18	-0.28	0.83	-0.62	-0.97	-0.57	-0.57	-0.88	0.75	0.81	-0.14	0.14
7	Pericarp thicknees	Phenotypic	2007	0.01	0.01	0.00	0.02	-0.03	-0.02	-0.06	0.00	-0.03	0.02	0.03	-0.23	0.01
			2008	-0.02	-0.02	0.01	-0.04	0.06	0.04	0.09	0.01	0.05	-0.03	-0.04	-0.01	0.00
			2008	-0.07	-0.08	0.04	-0.13	0.14	0.12	0.23	0.03	0.14	-0.11	-0.13	0.07	0.02
		Genotypic	2007	0.12	0.19	-0.05	0.29	-0.45	-0.33	-0.62	-0.02	-0.34	0.28	0.36	-0.40	0.24
			2008	-0.08	-0.13	0.06	-0.15	0.23	0.18	0.32	0.03	0.21	-0.14	-0.19	0.00	0.00

			2008	-0.15	-0.19	0.09	-0.25	0.28	0.24	0.41	0.06	0.28	-0.22	-0.26	0.07	0.03
8	No. of locules per fruit	Phenotypic	2007	0.02	0.00	-0.02	0.04	-0.01	-0.09	0.00	-0.19	-0.09	0.07	0.04	-0.08	0.01
			2008	0.03	-0.03	0.00	0.06	-0.01	-0.10	-0.01	-0.19	-0.10	0.08	0.05	0.07	-0.01
			2008	0.00	0.01	0.02	-0.03	0.01	0.07	0.02	0.12	0.06	-0.04	-0.03	0.05	0.01
		Genotypic	2007	0.09	-0.01	-0.12	0.22	-0.06	-0.45	-0.03	-0.80	-0.42	0.30	0.17	-0.07	0.06
			2008	0.08	-0.06	0.00	0.14	-0.04	-0.25	-0.04	-0.41	-0.22	0.18	0.11	0.09	-0.04
			2008	-0.02	0.06	0.07	-0.10	0.01	0.20	0.05	0.34	0.18	-0.13	-0.09	0.06	0.02
9	Single fruit weight	Phenotypic	2007	-0.12	-0.08	0.05	-0.27	0.25	0.31	0.18	0.18	0.37	-0.24	-0.29	-0.28	-0.11
			2008	-0.23	-0.13	0.12	-0.55	0.46	0.60	0.38	0.34	0.67	-0.46	-0.55	-0.06	-0.04
			2008	-0.21	-0.09	0.18	-0.57	0.47	0.61	0.42	0.34	0.68	-0.46	-0.57	0.02	0.01
		Genotypic	2007	-0.32	-0.30	0.17	-0.73	0.66	0.80	0.51	0.49	0.93	-0.63	-0.74	-0.32	-0.30
			2008	-0.09	-0.07	0.05	-0.21	0.18	0.23	0.16	0.13	0.25	-0.18	-0.20	-0.07	-0.02
			2008	-0.22	-0.13	0.20	-0.58	0.48	0.62	0.46	0.36	0.68	-0.48	-0.57	0.01	0.01
10	Total soluble solids	Phenotypic	2007	-0.07	-0.06	0.04	-0.12	0.08	0.11	0.05	0.05	0.09	-0.15	-0.12	0.44	-0.07
			2008	-0.09	-0.06	0.04	-0.15	0.09	0.13	0.07	0.07	0.12	-0.17	-0.14	0.27	-0.05
			2008	0.14	0.10	-0.05	0.23	-0.14	-0.21	-0.13	-0.10	-0.19	0.28	0.22	0.26	0.07
		Genotypic	2007	-0.57	-0.56	0.35	-0.92	0.57	0.79	0.47	0.39	0.70	-1.04	-0.85	0.53	-0.55
			2008	-0.05	-0.05	0.03	-0.08	0.05	0.07	0.04	0.04	0.06	-0.09	-0.07	0.32	-0.03
			2008	0.33	0.29	-0.13	0.55	-0.33	-0.49	-0.34	-0.24	-0.44	0.63	0.52	0.31	0.20
11	No. of fruits per plant	Phenotypic	2007	0.52	0.39	-0.35	0.97	-0.77	-0.83	-0.55	-0.23	-0.84	0.85	1.08	0.57	0.62
			2008	0.51	0.38	-0.36	1.04	-0.80	-0.97	-0.58	-0.29	-0.92	0.92	1.13	0.38	0.43
			2008	0.18	0.16	-0.12	0.42	-0.30	-0.36	-0.25	-0.11	-0.36	0.35	0.43	0.23	0.10
		Genotypic	2007	0.61	0.59	-0.49	1.15	-0.91	-0.98	-0.71	-0.26	-0.97	0.99	1.21	0.68	0.83
			2008	0.95	0.99	-0.78	1.93	-1.50	-1.79	-1.20	-0.56	-1.68	1.72	2.02	0.44	0.89
			2008	0.34	0.40	-0.25	0.77	-0.56	-0.67	-0.50	-0.21	-0.66	0.65	0.79	0.26	0.21

(Numbers in bold are direct effects on yield per plant)

	Phenotypic		Genotypic	
	R^2	Residual effect	R^2	Residual effect
2007K	0.47	0.73	0.95	0.22
2008K	0.38	0.78	0.62	0.62
2008R	0.32	0.83	0.49	0.72

2007K = *kharif* 2007, 2008K = *kharif* 2008, 2008R = *rabi* 2008

locules per fruit (0.18, 0.34, 0.34; 0.49, 0.13, 0.36), days to 50% flowering (0.05, 0.12, 0.18; 0.17, 0.05, 0.20).

Indirect effects on yield per plant in positive direction at phenotypic in all three seasons in an appreciable magnitude was recorded in:

(i) number of locules per fruit through plant height (0.02, 0.03, 0.000) ,

(ii) number of branches per plant through plant height (0.02, 0.00, 0.04) and

(iii) fruit length through days to 50 % flowering through

Indirect effects on yield per plant in negative direction at both phenotypic and genotypic levels in all three seasons in an appreciable magnitude was recorded in:

(i) number of fruits per plant through days to 50 % flowering (-0.35, -0.36, -0.12; -0.49, -0.78, -0.25), fruit length (-0.77, -0.80, -0.30; -0.91, -1.50, -0.56) , fruit width (-0.83, -0.97, -0.36; -0.98, -1.79, -0.67), pericarp thickness (-0.55, -0.58, -0.25, ; -0.71, -1.20, -0.50) , number. of locules per fruit (-0.23, -0.29, -0.11; -0.26, -0.56, -0.21), single fruit weight (-0.84, -0.92, -0.36; -0.97, -1.68, -0.66),

(ii) Single fruit weight through plant height (-0.12, -0.23, -0.21; -0.32, -0.09, -0.22), number of branches per plant (-0.08,-0.13, -0.09; -0.30, -0.07,-0.13), number of fruits per cluster (-0.27 -0.55, -0.57; -0.73, -0.21, -0.58), number of fruits per plant (-0.29, -0.55. -0.57; -0.74, -0.20, -0.57), total soluble solids (-0.24, -0.46, -0.46; -0.63, -0.18, -0.48).

The direct effects and indirect effects of eleven quantitative traits from path analysis for tomato evaluations done during *kharif* 2007, *kharif* 2008 and *rabi* 2008 are presented as phenotypic and genotypic path diagrams for yield per plant in Fig. 1, Fig. 2 and Fig. 3 respectively.

4.1.5 GENETIC DIVERSITY

Selection of parents for hybridization programme based on their genetic divergence is beneficial in getting heterotic hybrids and also to get desirable segregants. The 41 tomato genotypes evaluated were subjected to Mahalanobis D^2 analysis using twelve quantitative traits to assess the genetic diversity from which 10 parents were used for developing 25 F_1 hybrids in Line x Tester method for heterosis and combining ability study. The results are presented as follow:

4.1.5.1 Characters contribution to divergence

4.1.5.2 Group constellation

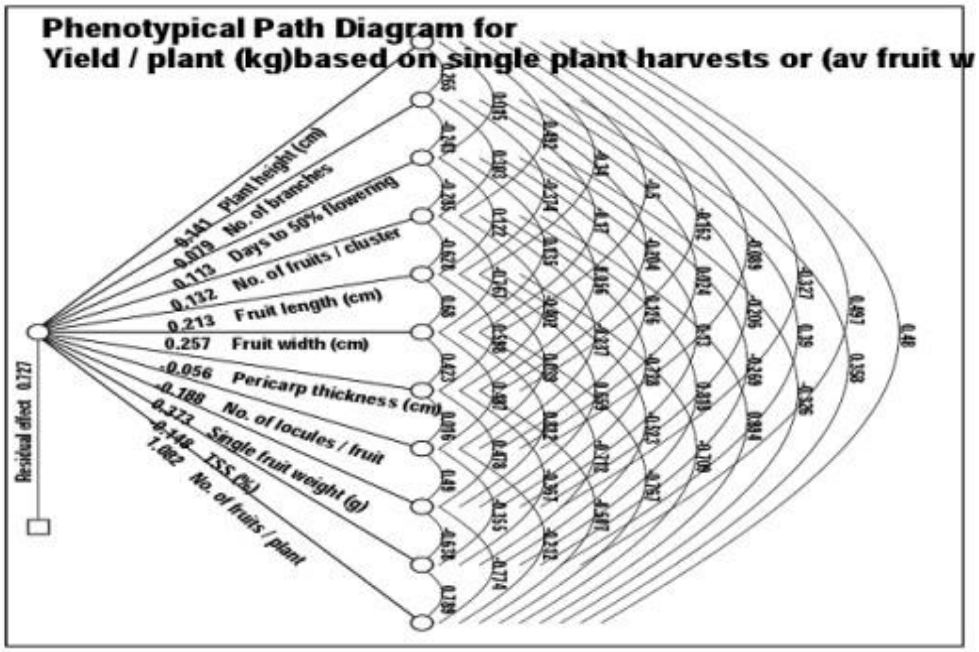
4.1.5.3 Inter relation of clusters

4.1.5.4 Cluster means

4.1.5.1 Characters contribution to divergence

All twelve quantitative traits included in the analysis have contributed to the diversity. The contribution of these traits to divergence in three seasons is tabulated in Table 10.

The relative contributions range vary as 0.49 - 33.29 % (branches per plant, number of fruits p(branches per plant, er plant), 0.12 - 29.51 % (branches per plant, single fruit weight) and 0.00 - 29.51 % (branches per plant,number of fruits per plant) during *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. The major contributors to divergence in order of magnitude are number of fruits per plant (33.29, 28.90 and 29.51 %), single fruit weight (9.51, 29.51, 16.22 %), plant height (12.56, 18.41, 18.05 %), fruit length (8.17, 11.59, 12.68 %) during three season evaluation. Bar graph of relative characters contribution to divergence is given in Fig. 4.



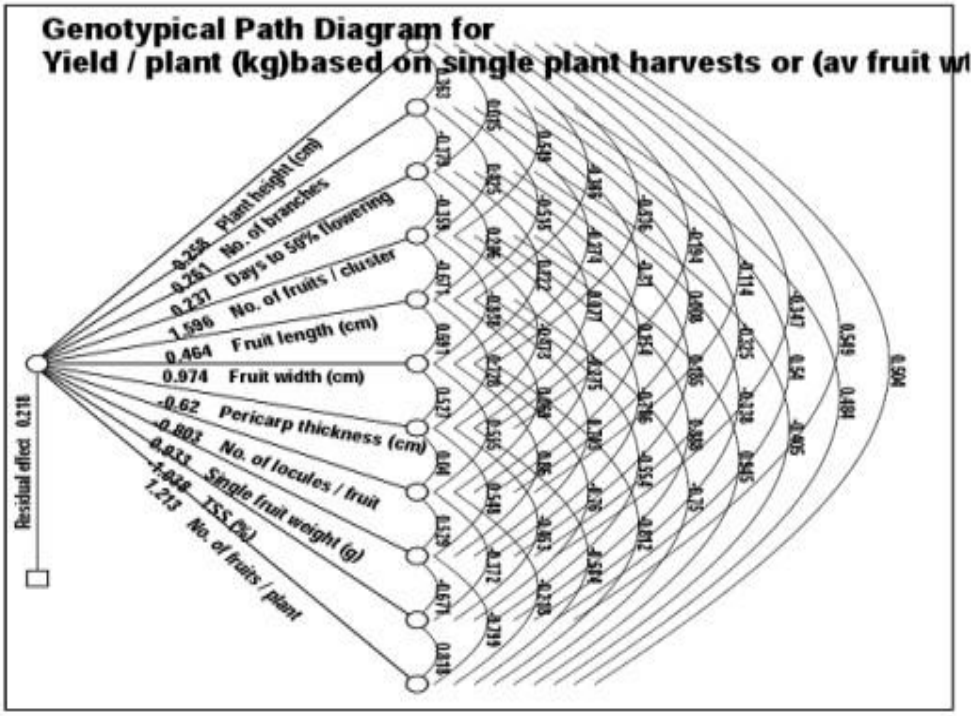
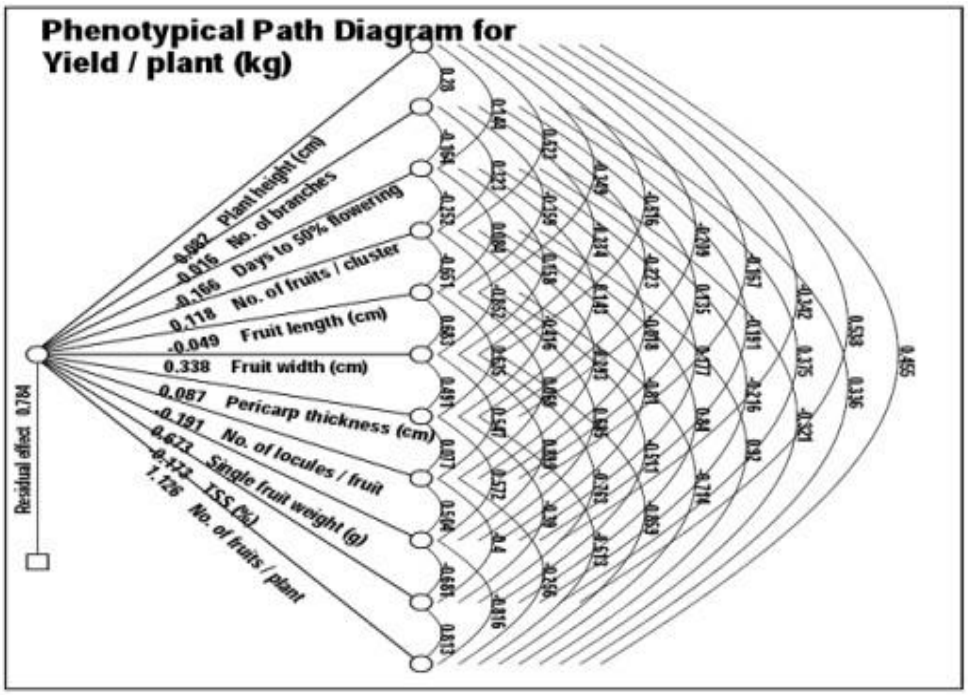


Figure.1. Phenotypic (top) and genotypic (bottom) path diagram for tomato yield per plant during kharif 2007



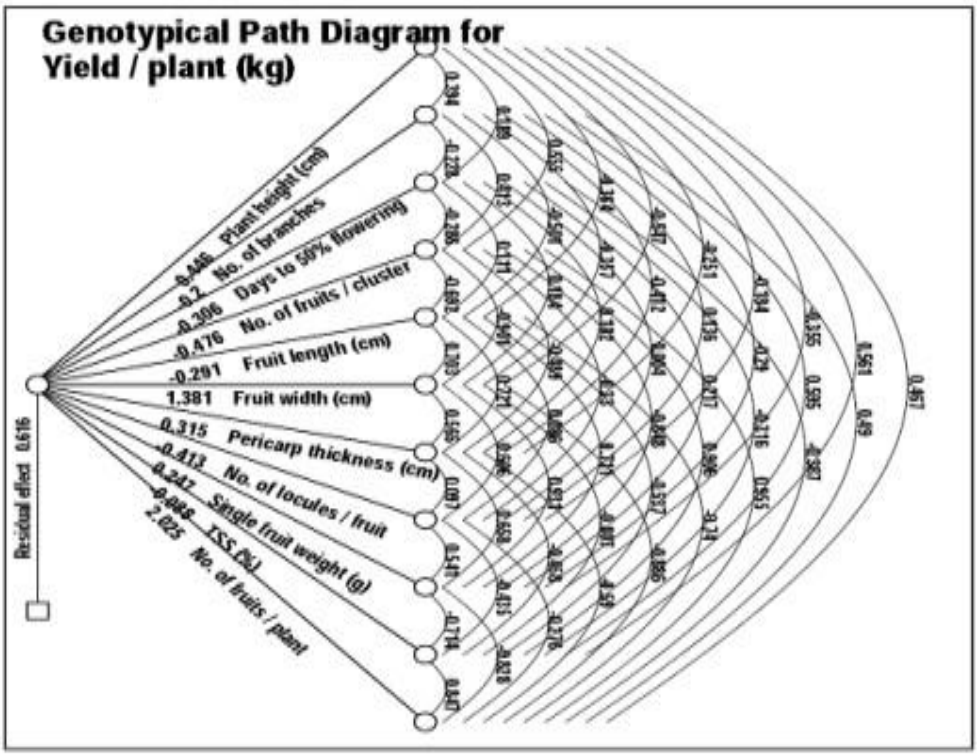
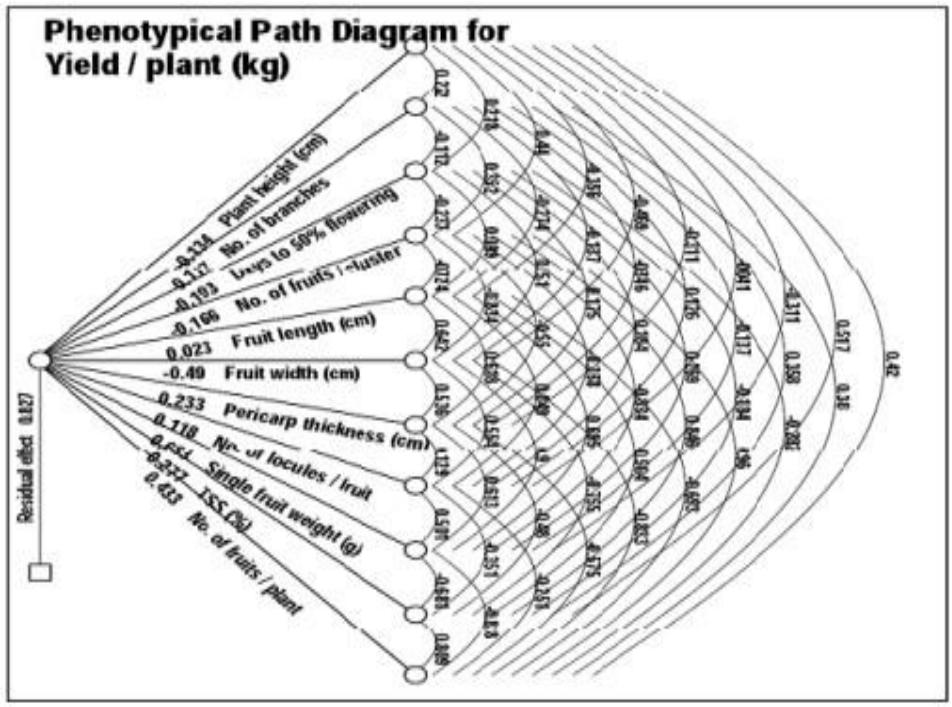


Figure.2. Phenotypic (top) and genotypic (bottom) path diagram for tomato yield per plant during kharif 2008



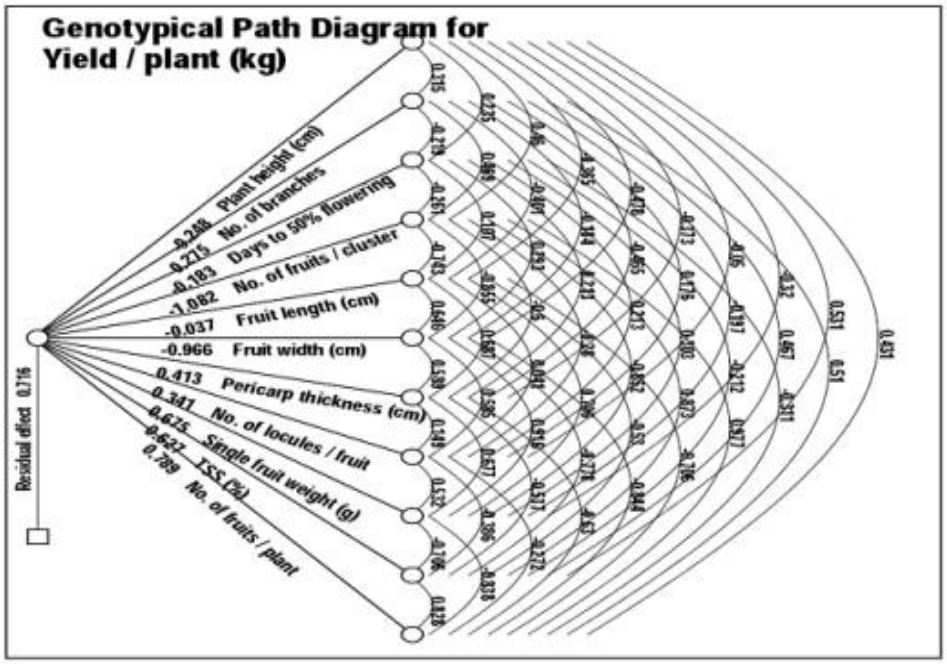


Figure.3. Phenotypic (top) and genotypic (bootom) path diagram for tomato yield per pant during rabi 2008

4.1.5.2 Cluster constellation

Based on the D^2 values the 41 tomato genotypes were grouped into six, five and nine clusters on the basis of *kharif* 2007, *kharif* 2008 and *rabi* 2008 evaluations respectively (Table 11) using Tocher's method (Rao , 1952).

Cluster I was the biggest group with 27, 26, 26 genotypes followed by Cluster V with six genotypes in each of three seasons .The same genotypes were in Cluster V in all the three seasons. There were three, one and six solitary clusters with single tomato genotype in *kharif* 2007, *kharif* 2008 and *rabi* 2008 groupings. Dendrograms clustering of 41 tomato genotypes in *kharif* 2007, *kharif* 2008 and *rabi* 2008 are presented in Fig. 5, Fig. 6 and Fig. 7 respectively.

4.1.5.3 Inter relation of clusters

The D^2 values for inter and intra clusters are given in the Table 12.

The inter cluster D^2 value was maximum (25.11, 28.21, 33.84) between clusters III & V, III & V , V &VII followed by clusters IV & V, IV&V and V& IX (24.33, 24.50 and 31.02) for *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. The minimum distance observed was 6.51, 8.79 and 5.78 between clusters I & II, I & II and VI & VII for three seasons respectively. Cluster V in all three groupings was the most diverse as many clusters showed maximum inter cluster distances with it.

The intra cluster distance was observed in clusters I, III & V in *kharif* 2007; Clusters I, II, III & V in *kharif* 2008 and Clusters I, IV, & V in *rabi* 2008 as remaining clusters contained only one genotype each. Remaining clusters showed zero intra cluster distances as they were solitary genotype containers.

4.1.5.4 Cluster mean analysis

The mean values of 12 characters for six, five and nine clusters of three seasons evaluations are summarized in Table 13. Comparison of cluster means for the different characters indicated considerable differences between clusters for all the characters. During *kharif* 2007, Cluster V had greater mean values for yield per plant (1.66 kg), number of fruits per plant (179.11), TSS (6.54%). Cluster V in *kharif* 2008 had highest mean values for yield per plant (1.64 kg), number of fruits per plant (180.10), TSS (6.46%) while in *rabi* 2008 Cluster VI had highest mean values for yield per plant (1.96kg).

Cluster I which was having maximum number of genotypes in it recorded plant heights of 93.49,90.17, and 93.83 cm; single fruit weight of 67.97 , 71.26 and 45.23 g ; number of fruits per plant 37.47, 45.56, and 45.23; and yield per plant of 1.22, 1.38 and 1.74 kg in *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. Highest fruit weight was in cluster III (107.66 g), III (103.49 g) and VI (106.46 g) during three seasons sequentially.

4.1.6 STABILITY ANALYSIS

Stability of a genotype indicates its adaptability and performance with predictability with least variations in performance or phenotype under different environments. It is a prerequisite for identifying an entry for utility in vegetable improvement. Identifying stability is challenging in presence of environmental influences and genotype x environment interactions by splitting into components. It is achieved by selecting entries with high mean yield, deviations from mean value approaching zero and regression coefficient value equal to one as suggested by Eberhart and Russell (1966).

Results of stability analysis done for 41 tomato genotypes evaluations in three environments (*kharif* 2007, *kharif* 2008 and *rabi* 2008 seasons) is presented under following headings:

4.1.6.1 Pooled analysis of variance

4.1.6.2 Stability parameters

Table 10. Relative contribution of different characters towards divergence in tomato during *kharif* 2007, *kharif* 2008, *and rabi* 2008.

Sl.	Characters	Contribution to divergence		
		Kharif 2007	*Kharif* 2008	*Rabi* 2008
1	Plant height (cm)	12.56%	18.41%	18.05%
2	No. of branches per plant	0.49%	0.12%	0.00%
3	Days to 50% flowering	1.95%	1.22%	2.56%
4	No. of fruits per cluster	0.61%	0.24%	0.00%
5	Fruit length (cm)	8.17%	11.59%	12.68%
6	Fruit width (cm)	6.10%	0.98%	16.59%
7	Pericarp thickness (cm)	3.17%	0.49%	0.98%
8	No. of locules per fruit	16.71%	4.51%	1.46%
9	Single fruit weight (g)	9.51%	29.51%	16.22%
10	Total soluble solids (%)	5.49%	3.17%	0.98%
11	No. of fruits per plant	33.29%	28.90%	29.51%
12	Yield per plant (kg)	1.95%	0.85%	0.98%

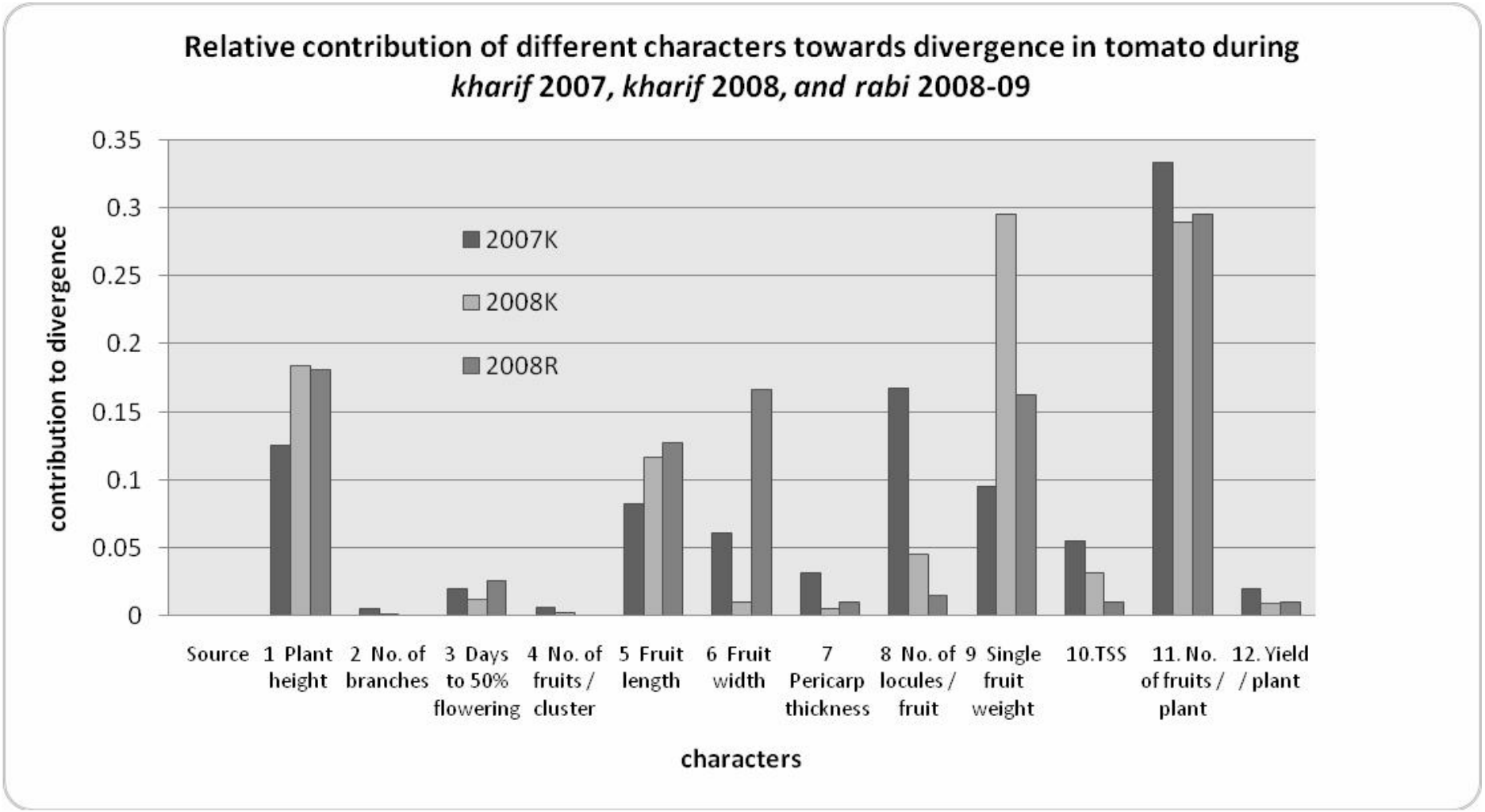
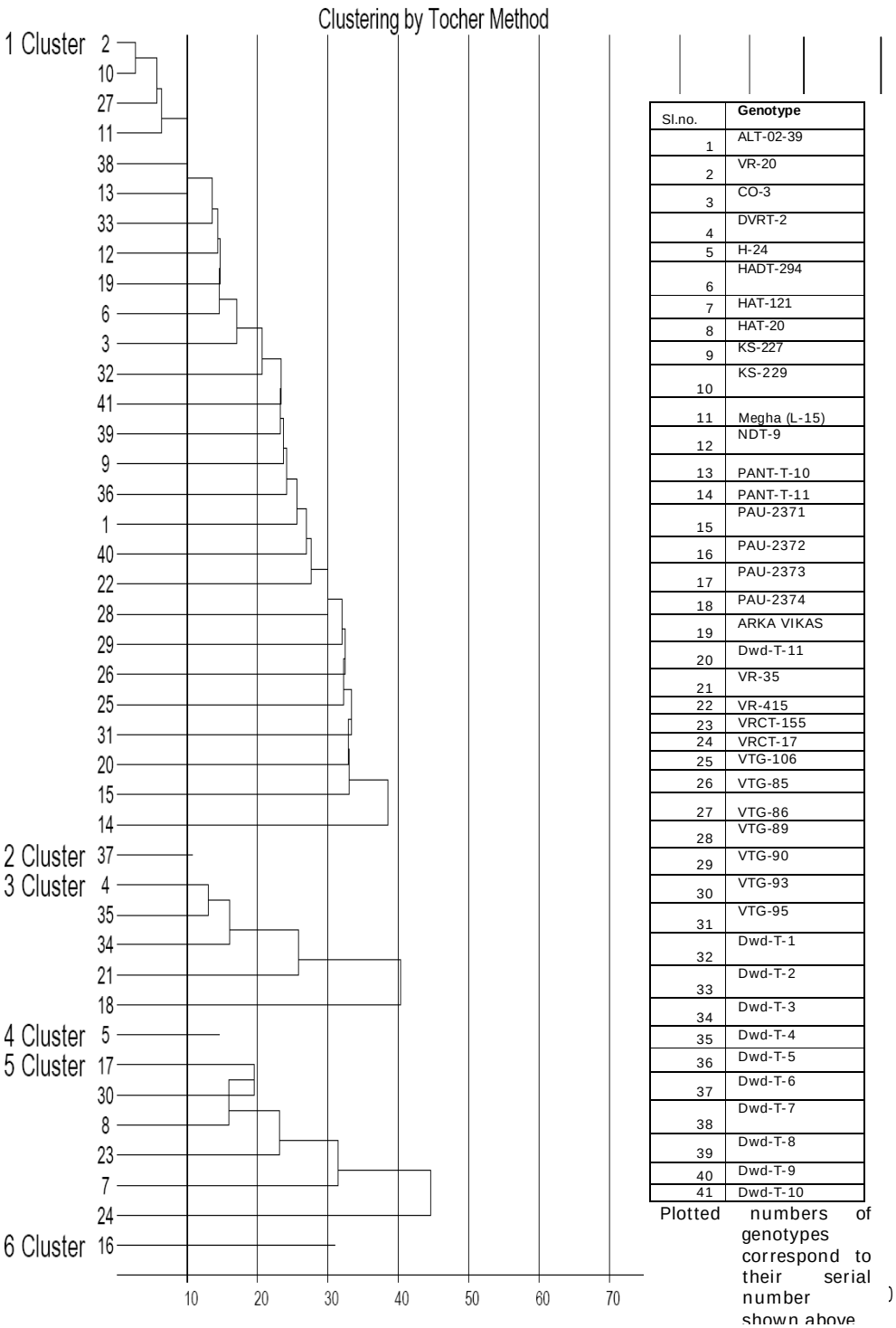


Figure.4. Relative contribution of different characters towards divergence in tomato

Table 11. Grouping of tomato genotypes under different clusters during *kharif* 2007*, kharif* 2008*, and rabi* 2008.

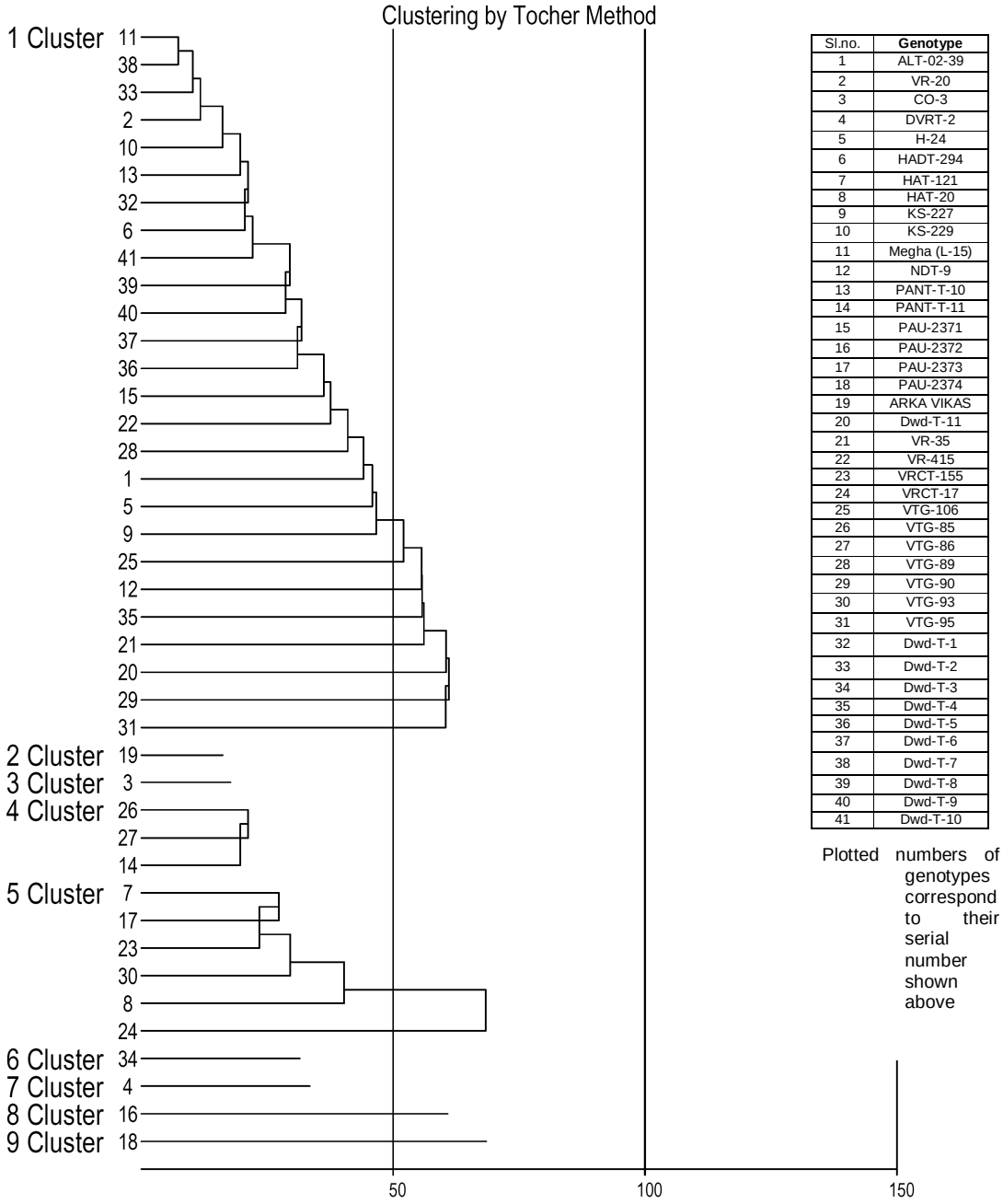
Sl.	Cluster	Number of genotypes	Name of the genotypes
Kharif, 2007			
1	I	27	ALT-02-39, VR-20,CO-3, HADT-294, KS-227, KS-229, Megha (L-15), NDT-9, PANT-T-10, PANT-T-11, PAU-2371, ARKA VIKAS, Dwd-T-11, VR-415, VTG-106, VTG-85, VTG-86, VTG-89, VTG-90, VTG-95, Dwd-T-1, Dwd-T-2, Dwd-T-5, Dwd-T-7, Dwd-T-8, Dwd-T-9, Dwd-T-10
2	II	1	Dwd-T-6
3	III	5	DVRT-2, PAU-2374, VR-35, Dwd-T-3, Dwd-T-4
4	IV	1	H-24
5	V	6	HAT-121, HAT-20, PAU-2373, VRCT-155, VRCT-17, VTG-93
6	VI	1	PAU-2372
Kharif, 2008			
1	I	26	ALT-02-39, VR-20, CO-3, HADT-294, KS-227, KS-229, Megha (L-15), NDT-9, PANT-T-10, PANT-T-11, PAU-2371, ARKA VIKAS, Dwd-T-11, VR-415, VTG-106, VTG-85, VTG-86, VTG-89, Dwd-T-1, Dwd-T-2, Dwd-T-5, Dwd-T-6, Dwd-T-7, Dwd-T-8, Dwd-T-9, Dwd-T-10
2	II	3	PAU-2372, VTG-90, VTG-95
3	III	5	DVRT-2, PAU-2374, VR-35, Dwd-T-3, Dwd-T-4
4	IV	1	H-24
5	V	6	HAT-121, HAT-20, PAU-2373, VRCT-155, VRCT-17, VTG-93
Rabi, 2008			
1	I	26	ALT-02-39, VR-20, H-24, HADT-294, KS-227, KS-229, Megha (L-15), NDT-9, PANT-T-10, PAU-2371, Dwd-T-11, VR-35, VR-415, VTG-106, VTG-89, VTG-90, VTG-95, Dwd-T-1, Dwd-T-2, Dwd-T-4, Dwd-T-5, Dwd-T-6, Dwd-T-7, Dwd-T-8, Dwd-T-9, Dwd-T-10
2	II	1	ARKA VIKAS
3	III	1	CO-3
4	IV	3	PANT-T-11, VTG-85, VTG-86
5	V	6	HAT-121, HAT-20, PAU-2373, VRCT-155, VRCT-17, VTG-93
6	VI	1	Dwd-T-3
7	VII	1	DVRT-2
8	VIII	1	PAU-2372
9	IX	1	PAU-2374



Sl.no.	Genotype
1	ALT-02-39
2	VR-20
3	CO-3
4	DVRT-2
5	H-24
6	HADT-294
7	HAT-121
8	HAT-20
9	KS-227
10	KS-229
11	Megha (L-15)
12	NDT-9
13	PANT-T-10
14	PANT-T-11
15	PAU-2371
16	PAU-2372
17	PAU-2373
18	PAU-2374
19	ARKA VIKAS
20	Dwd-T-11
21	VR-35
22	VR-415
23	VRCT-155
24	VRCT-17
25	VTG-106
26	VTG-85
27	VTG-86
28	VTG-89
29	VTG-90
30	VTG-93
31	VTG-95
32	Dwd-T-1
33	Dwd-T-2
34	Dwd-T-3
35	Dwd-T-4
36	Dwd-T-5
37	Dwd-T-6
38	Dwd-T-7
39	Dwd-T-8
40	Dwd-T-9
41	Dwd-T-10

Plotted numbers of genotypes correspond to their serial number shown above

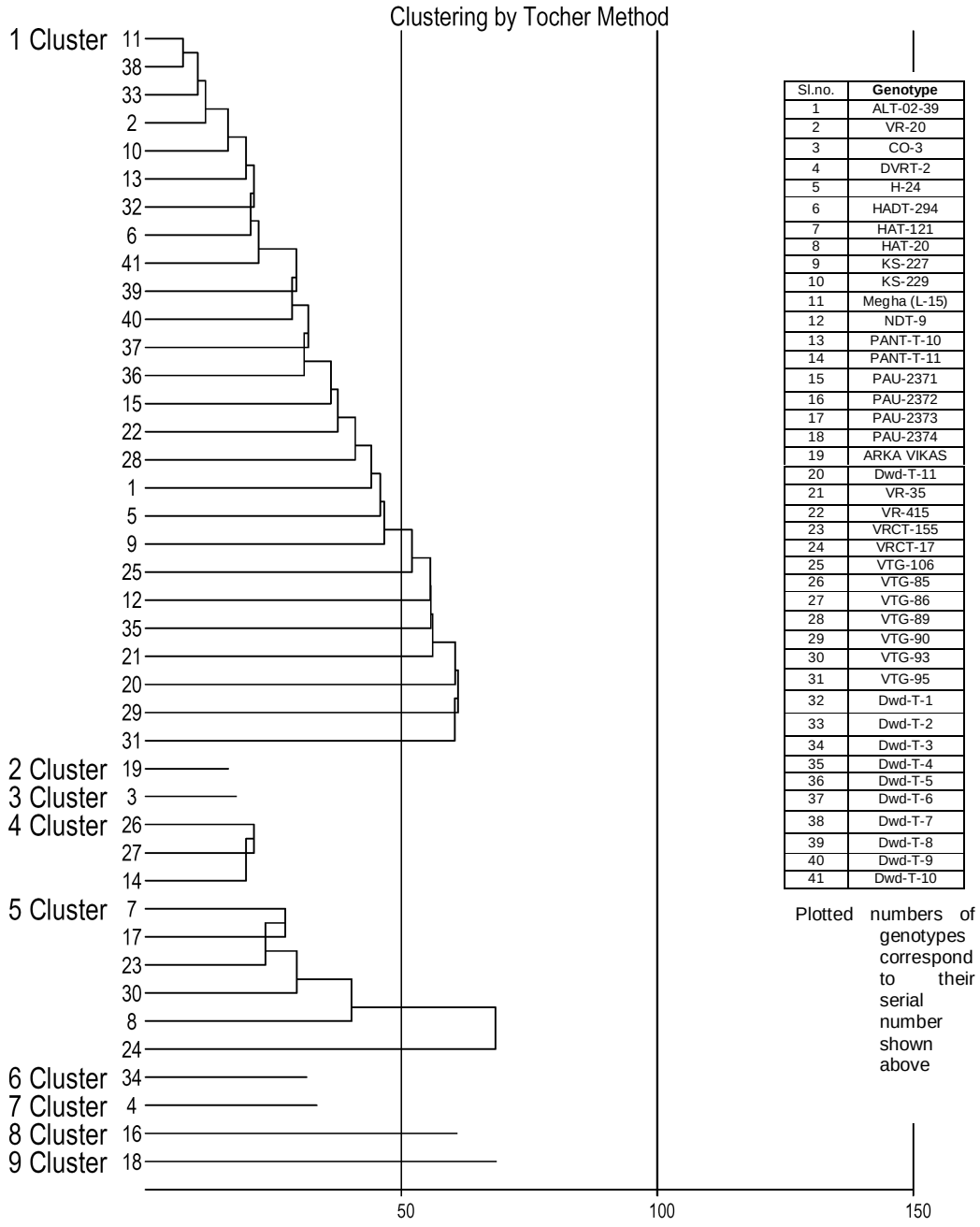
Figure 5. Clustering of 41 tomato genotypes into six groups in a divergence study based on evaluation during *kharif* 2007.



Sl.no.	Genotype
1	ALT-02-39
2	VR-20
3	CO-3
4	DVRT-2
5	H-24
6	HADT-294
7	HAT-121
8	HAT-20
9	KS-227
10	KS-229
11	Megha (L-15)
12	NDT-9
13	PANT-T-10
14	PANT-T-11
15	PAU-2371
16	PAU-2372
17	PAU-2373
18	PAU-2374
19	ARKA VIKAS
20	Dwd-T-11
21	VR-35
22	VR-415
23	VRCT-155
24	VRCT-17
25	VTG-106
26	VTG-85
27	VTG-86
28	VTG-89
29	VTG-90
30	VTG-93
31	VTG-95
32	Dwd-T-1
33	Dwd-T-2
34	Dwd-T-3
35	Dwd-T-4
36	Dwd-T-5
37	Dwd-T-6
38	Dwd-T-7
39	Dwd-T-8
40	Dwd-T-9
41	Dwd-T-10

Plotted numbers of genotypes correspond to their serial number shown above

Figure 6. Clustering of 41 tomato genotypes into five groups in divergence study based on evaluation during *kharif* 2008.



Sl.no.	Genotype
1	ALT-02-39
2	VR-20
3	CO-3
4	DVRT-2
5	H-24
6	HADT-294
7	HAT-121
8	HAT-20
9	KS-227
10	KS-229
11	Megha (L-15)
12	NDT-9
13	PANT-T-10
14	PANT-T-11
15	PAU-2371
16	PAU-2372
17	PAU-2373
18	PAU-2374
19	ARKA VIKAS
20	Dwd-T-11
21	VR-35
22	VR-415
23	VRCT-155
24	VRCT-17
25	VTG-106
26	VTG-85
27	VTG-86
28	VTG-89
29	VTG-90
30	VTG-93
31	VTG-95
32	Dwd-T-1
33	Dwd-T-2
34	Dwd-T-3
35	Dwd-T-4
36	Dwd-T-5
37	Dwd-T-6
38	Dwd-T-7
39	Dwd-T-8
40	Dwd-T-9
41	Dwd-T-10

Figure 7. Clustering of 41 tomato genotypes into nine groups in divergence study based on evaluation during *rabi* 2008.

Table 12. Intra and inter cluster distance of various clusters in divergence study of 41 genotypes of tomato during *kharif* 2007, *kharif* 2008, *and rabi* 2008.

Kharif 2007

Cluster	I	II	III	IV	V	VI
I	5.38	6.51	8.53	6.71	21.97	7.88
II		0.00	10.24	6.52	20.73	9.58
III			6.05	10.06	25.11	10.85
IV				0.00	24.33	11.24
V					6.24	20.14
VI						0.00

Kharif 2008

Cluster	I	II	III	IV	V
I	5.62	8.79	9.19	7.01	23.22
II		5.61	12.78	11.17	21.57
III			5.79	11.03	28.21
IV				0.00	24.50
V					6.04

Rabi 2008

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	6.94	8.41	8.34	9.32	26.67	10.18	13.56	12.08	12.92
II		0.00	7.16	13.01	27.33	7.72	9.47	10.13	8.27
III			0.00	13.69	27.89	8.43	9.56	13.52	12.06
IV				5.17	28.98	13.48	17.34	14.69	15.61
V					7.43	30.39	33.84	25.51	31.02
VI						0.00	5.78	15.18	9.16
VII							0.00	17.42	9.74
VIII								0.00	12.82
IX									0.00

Diagonal bold values are intra-cluster distances and off- diagonal values are inter-cluster distances

Table 13 . Cluster mean values of the characters in tomato divergence study done during *kharif* 2007, *kharif* 2008, *and rabi* 2008.

Sl.	Year (Season)	Cluster	Plant height (cm)	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules per fruit	Single fruit weight (g)	Total soluble solids (%)	No. of fruits per plant	Yield per plant (kg)
1	2007	I	93.49	3.38	33.11	3.52	4.53	4.64	0.46	3.39	67.97	4.10	37.47	1.22
	Kharif	II	62.90	3.78	26.00	3.88	4.09	4.70	0.31	2.67	70.66	3.72	53.00	1.46
		III	102.29	3.62	33.53	3.49	4.93	5.88	0.48	5.75	107.66	3.73	35.30	1.44
		IV	64.67	3.87	33.33	2.89	3.67	4.77	0.41	4.11	56.78	3.36	20.77	0.73
		V	126.56	4.39	30.17	9.40	2.59	2.46	0.34	2.99	12.83	6.54	179.11	1.66
		VI	154.33	3.41	38.67	3.67	3.70	3.19	0.37	3.14	69.62	4.04	45.56	1.37
2	2008	I	90.17	3.44	33.43	3.29	4.56	4.80	0.44	3.52	71.26	4.01	40.95	1.38
	Kharif	II	140.07	3.30	36.96	4.17	4.43	4.05	0.46	2.71	61.73	4.21	40.37	1.36
		III	98.65	3.50	34.10	3.14	4.69	5.85	0.49	5.59	103.49	3.78	35.72	1.63
		IV	66.70	3.52	35.00	3.14	3.96	5.03	0.43	4.66	50.66	3.29	18.97	0.98
		V	126.92	4.22	31.54	9.85	2.67	2.45	0.34	3.03	12.89	6.46	180.10	1.64
3	2008	I	93.83	3.50	35.16	3.38	4.71	4.93	0.48	3.61	74.80	4.34	45.23	1.74
	Rabi	II	123.73	3.74	38.44	3.41	4.12	5.18	0.45	3.56	93.11	5.00	40.93	1.81
		III	90.66	3.40	37.67	3.15	3.74	5.63	0.45	4.23	67.15	3.85	30.04	1.20
		IV	87.45	2.77	36.04	3.37	6.26	4.92	0.53	3.00	79.22	4.37	49.44	1.70
		V	128.12	4.23	34.28	10.63	2.79	2.54	0.35	3.03	13.99	6.81	193.66	1.86
		VI	93.44	4.04	38.00	3.59	4.63	6.18	0.58	5.60	106.46	3.59	47.33	1.96
		VII	97.45	3.89	42.00	2.63	4.27	6.64	0.51	5.67	114.63	3.60	26.04	1.28
		VIII	166.10	3.15	38.00	3.34	3.92	3.66	0.36	3.66	73.78	3.95	51.41	1.59
		IX	143.33	4.00	37.67	2.85	5.56	6.55	0.43	7.40	112.26	4.85	40.48	1.79

4.1.6.1 Pooled analysis of variance

Pooled analysis of variance for nineteen quantitative traits across three different seasons is presented in the Table 14. The results revealed that there were significant differences among the genotypes tested at both the 5 and 1 per cent level of significance for all the characters studied. The environment in which all the observations were recorded also differed significantly (both at 5 and 1% probability) to influence significant variation in all the characters recorded except for number of branches per plant, number of fruits per cluster, and number of locules per fruit.

The differences due to genotype × environment interaction were found to be highly significant for yield per plant and powdery mildew. The genotype × environment interactions differed significantly for the traits *viz.,* fruit width, yield per hectare, early blight and *Sclerotium* wilt incidence.

In order to know the magnitude of linear and non linear components of variations which provide information on predictable and unpredictable sources of variations respectively, contributing to genotype × environment interactions for all characters the partitioning was done as per Eberhart and Russell (1966) model.

The mean sum of squares due to G × E (linear) interactions were tested against pooled deviation mean sum of square to find out significant effects due to genotype and environment separately. The effects due to environments (linear) were highly significant for all the characters at 5 and 1 per cent probability level except for number of branches per plant, number of fruits per cluster, pericarp thickness, number of locules per fruit, TSS, late blight, and tomato leaf curl incidence.

The variance due to variety/genotype × environment (linear) were found to be significant at both 5 and 1 per cent level of significance for the seven characters *viz.,* fruit width, TSS , yield per plant, yield per hectare, early blight, powdery mildew and *Sclerotium* wilt.

The mean sum of squares due to pooled deviation was also found significant for all the characters except days to 50 % flowering, number of locules per fruit, TSS, number of fruits per plant, and powdery mildew incidence both at 1 and 5 per cent probability levels, which indicates the non linear or unpredictable portion of G × E interaction when tested against pooled error.

Since the G × E interactions were found significant for most of the characters, the data of all the nineteen characters were subjected to stability analysis.

4.1.6.2 Stability parameters

Table 15 has environmental indices and Table 16 to Table 23 has three stability parameters [*viz.*, mean, regression coefficient (b_i) and mean square deviation from linear regression line (S^2di)] estimated for nineteen characters as per Eberhart and Russell model.

4.1.6.2.1 Environmental Indices

Table 15 has environmental indices. The environmental indices for nineteen traits indicate significant variations or differences across three seasons or environments. Number of branches per plant had lowest values of environmental indices (0.01, -0.02, 0.01) while tomato leaf curl virus incidence had highest values of environmental indices (03.54, 4.36, -7.90), followed by number of fruits per plant (-3.43, -1.44, 4.87) and yield per hectare (-3.74, -0.98, 4.72) for three environments of evaluations.

4.1.6.2.2 Mean, regression coefficients (b_i), and mean square deviation from linear regression line (S^2d_i)

Table 16 to Table 23 has three stability parameters [*viz.*, mean, regression coefficient (b_i) and mean square deviation from linear regression line (S^2d_i)] for all the nineteen traits recorded.

Table 14. ANOVA for stability parameters in tomato.

Sl.	Character	Source of variation (mean sum of squares)									
		Rep within Env.	Varieties	Env.+ (Var.* Env.)	Environ ments	Var.* Env.	Environments (Lin.)	Var.* Env.(Lin.)	Pooled Deviation	Pooled Error	Total
	Degrees of freedom	6	40	82	2	80	1	40	41	240	122
1	Plant height	41.91	1444.31**	24.30	88.19*	22.70	176.38**	24.87	20.03**	9.70	489.88
2	No. of branches per plant	0.10	0.95**	0.12	0.01	0.13	0.02	0.12	0.13*	0.09	0.39
3	Days to 50% flowering	6.06**	23.15**	4.68**	91.76**	2.50	183.52**	3.34*	1.62	1.16	10.73
4	No. of fruits per cluster	0.28	17.61**	0.19	0.14	0.19	0.28	0.14	0.23**	0.12	5.90
5	Fruit length	0.06	2.48**	0.06*	0.74**	0.05	1.49**	0.06*	0.03**	0.02	0.86
6	Fruit width	0.12**	3.13**	0.07**	0.61**	0.05*	1.22**	0.07**	0.03**	0.02	1.07
7	Pericarp thickness	0.002*	0.015**	0.001	0.009**	0.001	0.017**	0.001	0.001*	0.000	0.006
8	No. of locules per fruit	0.09	3.66**	0.05	0.06	0.05	0.11	0.05	0.04	0.05	1.23
9	Total soluble solids	21.85*	2148.64**	18.10**	238.26**	12.60	476.53**	6.99**	8.01	6.47	716.64
10	Single fruit weight	0.02	3.21**	0.07*	1.34**	0.04	2.68**	0.04	0.04**	0.02	1.10
11	No. of fruits per plant	13.39	8319.10**	34.12**	770.61**	15.71	1541.23**	20.92*	10.24	8.62	2750.51
12	Yield per plant	0.01	0.15**	0.07**	1.94**	0.02**	3.88**	0.03**	0.01 *	0.01	0.10
13	Yield per hectare	3.99	58.92**	25.34**	763.95**	6.87*	1527.89**	9.86**	3.79**	1.28	36.35
14	Early Blight	0.06	0.817**	0.59**	16.34***	0.20*	32.67**	0.28**	0.12*	0.07	0.67
15	Late Blight	0.22	0.59**	1.27**	42.79**	0.23	85.58**	0.26	0.19**	0.10	1.05
16	Powdery mildew	0.15	0.33**	1.70**	56.94**	0.32**	13.87**	0.56**	0.08	0.06	1.25
17	Tomato leaf curl virus	11.41	51.80**	69.83**	1925.93**	23.43	3851.85**	28.08	18.32**	4.77	63.92
18	Tomato spotted wilt virus	4.16	12.17**	8.28**	122.35**	5.43	244.69**	6.91*	3.85**	1.01	9.56
19	*Sclerotium* wilt	5.66	33.82**	16.86**	287.82**	10.08*	575.64**	13.94**	6.07**	2.02	22.42

* Significant at 5% probability ** Significant at 1% probability

Table 15. Environmental indices for *kharif* 2007, k*harif* 2008 and *rabi* 2008 seasons during which evaluation of tomato genotypes was done in stability analysis.

Sl No.	Character	Environment 1 (*Kharif* 2007)	Environment 2 (*Kharif* 2008)	Environment 3 (*Rabi* 2008)
1	Plant height	-0.96	-0.73	1.69
2	No. of branches per plant	0.01	-0.02	0.01
3	Days to 50% flowering	-1.25	-0.41	1.66
4	No. of fruits per cluster	0.02	-0.07	0.05
5	Fruit length	-0.09	-0.06	0.16
6	Fruit width	-0.11	-0.02	0.13
7	Pericarp thickness	0.00	-0.01	0.02
8	No. of locules per fruit	-0.04	0.01	0.03
9	Total soluble solids	-1.81	-0.93	2.74
10	Single fruit weight	-0.08	-0.12	0.21
11	No. of fruits per plant	-3.43	-1.44	4.87
12	Yield per plant	-0.18	-0.06	0.24
13	Yield per hectare	-3.74	-0.98	4.72
14	Early Blight	-0.39	-0.34	0.73
15	Late Blight	0.63	0.55	-1.18
16	Powdery mildew	-0.69	-0.67	1.36
17	Tomato leaf curl virus	3.54	4.36	-7.90
18	Tomato spotted wilt virus	0.34	1.53	-1.87
19	*Sclerotium* wilt	-2.24	-0.68	2.92

Table 16. Mean performance and stability parameters of 41 tomato genotypes for plant height and number of branches per plant

No.	enotype	Plant height (cm)			No. of branches per plant		
		Mean	b_i	s^2d_i	Mean	b_i	s^2d_i
1	ALT-02-39	77.64	2.02	14.50	3.61	-23.38	-0.01
2		89.43	-2.80	84.4 **	3.16	0.15	-0.08
3		90.41	0.01	4.40	3.46	-16.51	-0.05
4	DVRT-2	96.39	0.60	-9.90	4.00	4.78	-0.02
5		67.25	1.90	-9.20	3.53	-1.82	0.13
6	HADT-294	95.43	0.77	-4.60	3.47	-5.70	0.17
7	HAT-121	144.51	-5.17	48.8 *	4.38	-0.02	-0.07
8	HAT-20	123.06	1.60	-7.30	4.76	-38.66	0.02
9	'	106.02	1.53	-3.00	3.29	5.19	-0.05
10	)	98.56	3.54	-7.00	3.34	-18.32	0.00
11	Megha (L-15)	81.19	-0.22	-2.30	3.42	-6.02	-0.08
12		107.81	2.73*	-10.50	3.69	-4.00	-0.07
13	PANT-T-10	83.02	0.94	-10.40	2.88	-3.49	-0.03
14	PANT-T-11	82.39	-0.83*	-10.40	2.78	-10.96	0.16
15	PAU-2371	94.06	1.27	-10.00	3.06	4.13	-0.07
16	PAU-2372	10.58	3.43	8.90	3.31	-4.57	-0.06
17	PAU-2373	116.70	3.80	-4.90	5.45	40.78	0.31*
18	PAU-2374	130.71	7.40	-6.50	3.94	6.95	-0.09
19	ARKA VIKAS	114.81	5.71	123.3**	4.07	-8.08	0.05
20	Dwd-T-11	125.67	4.57	-9.90	4.04	3.41	0.13
21		99.68	1.01	18.30	3.59	1.68	-0.09
22	5	76.39	0.98	47.2 *	2.82	-1.06	-0.05
23	VRCT-155	142.50	4.47	20.80	3.76	-7.96	-0.08
24	VRCT-17	124.47	-1.71	-9.50	4.02	28.87	0.07
25	VTG-106	113.97	2.10	73.7 **	3.12	12.56	0.85**
26	VTG-85	91.68	-0.71	-0.90	2.73	0.47	0.17
27	VTG-86	88.94	0.70	70.3 **	3.25	-3.41	0.11
28	VTG-89	88.21	0.34	-0.70	2.76	-0.58	-0.09
29	VTG-90	122.51	-1.02	-6.90		17.81	-0.09
30	VTG-93	111.96	0.30	-8.30	3.30	-6.82	-0.08
31	VTG-95	127.47	-0.24	70.4 **	3.74	-11.97	0.27*
32	Dwd-T-1	73.64	1.36	-4.00	3.10	-12.58	-0.01
33	Dwd-T-2	85.70	1.55*	-10.50	3.56	16.63*	-0.09
34	Dwd-T-3	96.62	-2.06	14.10	3.46	16.92	0.29 *
35	Dwd-T-4	86.07	0.97	-9.30	3.34	18.53	0.01
36	Dwd-T-5	80.93	-3.42*	-10.40	3.48	19.75	0.19
37	Dwd-T-6	65.80	2.99*	-10.50	3.53	31.43*	-0.09
38	Dwd-T-7	88.23	-1.30	-3.40	3.84	6.98	-0.08
39	Dwd-T-8	85.39	0.93	-7.20	4.14	4.33	-0.08
40	Dwd-T-9	92.09	1.43	-9.70	4.05	12.55	0.19
41	Dwd-T-10	88.18	-0.48*	-10.50	4.36	-26.85	0.14
	Mean	100.40		1.00	3.57		1.00
	S.Ed+	3.20		2.20	0.26		16.45
	C.D. @ 5%	6.14			0.54		

*, **: Indicates significant at 5 and 1% level of probability respectively

4.1.6.2.2.1 Plant height (cf. Table 16)

The genotype ‘PAU-2372’ recorded highest mean plant height (160.58 cm) while, lowest mean plant height was recorded in ‘Dwd-T-6’ (65.80 cm) and average plant height over environments was 100.40 cm.

The genotypes ‘Pant-T-11’, ‘Dwd-T-2’ and ‘Dwd-T-10’ recorded significant regression coefficient values around unity though in all seven genotypes had significant regression coefficient values. The deviation from regression value was significantly more than zero for the six genotypes.

4.1.6.2.2.2 Number of branches per plant (cf. Table 16)

The maximum number of branches was recorded by the genotype ‘PAU-2373’ (5.45) and minimum was recorded by the genotype ‘VTG-85’ (2.73) with a population mean of 3.57.

Regression coefficient value differed significantly for the genotype ‘Dwd-T-2’ and ‘Dwd-T-6’. The deviation from regression values was significantly near zero for the four genotypes ‘PAU-2373’, ‘VTG-106’, ‘VTG-85’ and ‘Dwd-T-3’.

4.1.6.2.2.3 Days to 50 per cent flowering (cf. Table 17)

The genotypes ‘Dwd-T-8’ (26.56 days) was earlier in 50 per cent flowering and the genotype ‘PAU-2373’ (38.33 days) was recorded as late to 50 per cent flowering over the three environments. The population mean was 33.95 days.

The regression coefficient values were significant around unity for three genotypes ‘PAU-2372’ , ‘PAU-2374’ and ‘Dwd-T-2’ .The deviation from regression value was significantly more than zero for the six genotypes.

4.1.6.2.2.4 Number of fruits per clusters (cf. Table 17)

The mean number of fruits per cluster over three environments was 4.36. The maximum number of fruits per cluster was recorded by ‘HAT-121’ (11.21) and minimum was observed by the genotype ‘DVRT-2’ (2.28).

Though four genotypes showed significant regression coefficient values ‘Megha (L-15) and ‘H-24’ had values -0.04 and -2. The deviation from regression values were significantly different in six entries but was around zero to $\pm$ 1.00 for five genotypes (‘HAT-121’, ‘HAT-20’, ‘VRCT-155’, ‘VTG-106’).

4.1.6.2.2.5 Fruit length (cf. Table 17)

The fruit length was maximum in the genotype ‘VTG-85’ (6.16 cm) and minimum was recorded in ‘HAT-20’ (2.07cm).

The genotype ‘Dwe-T-8’ showed significant regression coefficient value lesser than unity and deviation from regression coefficient was significant for seven genotypes of which three were near zero (CO-3, Dwd-T-11, VTG-85).

4.1.6.2.2.6 Fruit width (cf. Table 18)

The maximum fruit width was observed in ‘APU-2374’ (6.36 cm) , minimum was observed in ‘VTG-93’ (2.13 cm) with a population mean of 4.55 cm .

Regression coefficient was significant for four genotypes but ‘KS-229’, ‘Arka Vikas’, ‘Dwd-T-5’ having values around unity and deviation from regression were significant for four genotypes (‘DVRT-2’, ‘VR-35’, ‘VTG-106’, ‘Dwd-T-6’) with values nearing zero.

4.1.6.2.2.7 Pericarp thickness (cf. Table 18)

The mean pericarp thickness of population was 0.44 cm. The maximum pericarp thickness was recorded by the genotype ‘VTG-85’ and ‘VR-35’ (0.56 cm) and minimum was recorded by the ‘HAT-20’ (0.31 cm).

The regression coefficient values were significant for two genotypes ‘VTG-89’ and ‘Dwd-T-5’ that were more nearer unity and positive. And the deviation from regression values was significantly very near zero for five genotypes.

Table 17. Mean performance and stability parameters of 41 tomato genotypes for days to 50 per cent flowering, number of fruit of fruits per cluster and fruit length.

Sl.	Genotype	Days to 50% flowering			No. of fruits per cluster			Fruit length (cm)		
		Mean	β_i	$\sigma^2 d_i$	Mean	β_i	$\sigma^2 d_i$	Mean	β_i	$\sigma^2 d_i$
1	ALT-02-39	36.00	1.20	0.90	3.15	4.03	0.15	4.93	0.75	-0.01
2	VR-20	34.11	-0.80	-0.32	3.16	-1.41	-0.13	4.24	1.50	-0.02
3	CO-3	35.89	0.99	-0.91	2.72	5.11	-0.03	3.66	0.33	0.09*
4	DVRT-2	38.33	2.01	0.92	2.28	3.81	-0.04	4.40	-1.12	0.23**
5	H-24	35.11	1.21	-1.04	2.95	-2.87*	-0.13	3.98	2.26	0.01
6	HADT-294	35.33	-0.10	3.35	3.57	4.42	-0.11	3.77	2.03	0.01
7	HAT-121	32.18	0.91	-1.27	11.21	-0.44	0.54 *	2.96	0.60	0.00
8	HAT-20	32.67	1.58	0.26	8.56	1.58	0.88**	2.07	0.30	-0.02
9	KS-227	34.00	0.87	-1.07	3.79	-6.60	0.37	5.07	0.06	-0.01
10	KS-229	34.22	1.58	-0.75	3.42	1.78	-0.10	4.71	0.83	-0.01
11	Megha (L-15)	32.81	0.87	-0.80	2.89	-0.04*	-0.13	4.49	2.06	-0.02
12	NDT-9	37.00	1.76	-1.16	3.62	-3.75	-0.11	3.76	1.26	-0.02
13	PANT-T-10	35.26	1.03	-0.88	3.78	0.71	-0.11	3.97	0.94	-0.02
14	PANT-T-11	37.81	0.97	8.01**	3.47	-4.79	-0.08	6.06	0.28	0.00
15	PAU-2371	37.22	0.03	-1.21	3.52	-3.50	0.17	5.07	0.85	-0.01
16	PAU-2372	38.33	-0.22*	-1.27	3.67	-5.41	-0.11	3.81	0.70	-0.01
17	PAU-2373	31.67	2.35	-1.06	10.04	6.06	0.29	3.50	1.31	0.09*
18	PAU-2374	34.67	1.82*	-1.26	3.02	-2.71	-0.12	5.29	1.77	-0.01
19	ARKA VIKAS	35.37	2.05	0.79	3.01	3.91	0.01	3.96	1.12	-0.01
20	Dwd-T-11	34.78	1.57	-1.21	2.54	0.42	0.01	4.88	1.44	0.06*
21	VR-35	34.61	0.82	-1.25	3.75	5.02	-0.12	5.28	1.33	0.24**
22	VR-415	34.23	-0.69	0.56	3.30	5.16	-0.08	4.86	1.16	-0.02
23	VRCT-155	31.00	0.74	-1.07	10.70	-0.57	0.46 *	2.41	1.42	0.00
24	VRCT-17	30.22	1.70	-1.24	8.88	12.62	1.34**	2.61	0.68	-0.02
25	VTG-106	35.55	3.27	0.75	2.68	5.39	0.59*	5.16	-0.15	-0.01
26	VTG-85	32.57	1.02	-0.03	3.96	-8.46*	-0.13	6.16	1.00	-0.01
27	VTG-86	32.44	0.93	-1.27	3.09	1.53	0.06	5.37	6.43	0.04
28	VTG-89	31.54	0.78	3.75 *	4.94	-1.93	0.34	4.41	-0.81	0.05*
29	VTG-90	35.08	0.01	-0.14	3.92	-7.49	0.36	4.93	0.12	-0.02
30	VTG-93	34.22	1.11	-1.19	10.38	6.13	0.01	2.54	0.00	-0.01
31	VTG-95	36.89	1.42	5.28 *	4.03	-4.19	-0.09	4.80	0.47	0.04
32	Dwd-T-1	36.36	0.15	-0.49	3.10	1.71	-0.11	3.99	2.56	0.02
33	Dwd-T-2	35.78	-0.25*	-1.25	2.96	-1.16	-0.10	4.41	0.03	-0.01
34	Dwd-T-3	35.11	1.98	1.71	3.80	-0.23	0.00	4.52	0.69	-0.02
35	Dwd-T-4	32.63	0.60	5.37 *	3.73	4.60	0.52 *	4.65	-2.05*	-0.02
36	Dwd-T-5	31.89	-0.09	0.09	3.29	2.26	-0.04	4.23	1.87	-0.01
37	Dwd-T-6	27.66	1.07	-0.95	3.59	6.59	-0.08	4.11	0.66	-0.01
38	Dwd-T-7	35.89	0.06	1.00	3.41	1.78	0.14	4.44	2.68	-0.01
39	Dwd-T-8	26.56	1.30	0.38	3.40	3.67	-0.10	5.05	0.14*	-0.02
40	Dwd-T-9	27.67	1.33	4.35 *	3.47	2.54	-0.09	4.78	1.69	-0.01
41	Dwd-T-10	31.11	2.07	-0.40	3.95	5.59	0.11	4.52	1.82	0.12 **
	Mean	33.95		1.00	4.36		1.00	4.34		1.00
	S.Ed±	0.90		0.60	0.34		5.77	0.13		0.97
	C.D. @ 5%	1.75			0.71			0.27		

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 18. Mean performance and stability parameters of 41 tomato genotypes for days to 50 fruit width, pericarp thickness and number of locules per fruit.

Sl.	Genotype	Fruit width (cm)			Pericarp thickness (cm)			No. of locules per fruit		
		Mean	β_i	σ^2d_i	Mean	β_i	σ^2d_i	Mean	β_i	σ^2d_i
1	ALT-02-39	4.81	1.60	-0.02	0.53	1.91	-0.0004	4.08	-4.15	0.12
2	VR-20	4.66	1.29	-0.01	0.46	1.22	-0.0005	3.62	3.75	-0.04
3	CO-3	5.36	1.43	0.06	0.43	1.70	0.004**	4.19	-0.37	-0.04
4	DVRT-2	6.30	1.39	0.25**	0.49	1.34	-0.0004	5.74	-5.54	-0.03
5	H-24	4.97	1.36	-0.01	0.43	0.53	-0.0003	4.41	6.25	0.00
6	HADT-294	5.01	1.07	-0.02	0.45	1.90	-0.0004	4.30	0.29	0.01
7	HAT-121	2.14	1.19	-0.01	0.33	0.45	-0.0001	2.09	2.17	-0.05
8	HAT-20	2.38	-0.32	-0.02	0.31	0.37	-0.0004	2.76	4.10	-0.02
9	KS-227	4.40	0.94	0.03	0.48	1.34	-0.0001	3.58	-0.57	0.02
10	KS-229	4.92	1.54*	-0.02	0.44	1.44	0.0002	3.49	3.33	-0.04
11	Megha (L-15)	4.95	1.69	-0.02	0.34	0.83	0.0003	3.53	-0.84	-0.05
12	NDT-9	4.93	2.01	-0.02	0.43	0.98	-0.0004	4.42	0.35	-0.02
13	PANT-T-10	4.85	1.18	-0.02	0.44	3.17	0.0000	2.70	4.09	-0.04
14	PANT-T-11	4.83	3.30	-0.02	0.49	-1.05	-0.0003	3.15	3.11	-0.02
15	PAU-2371	4.62	2.35	0.06	0.45	2.30	-0.0001	2.17	4.60	-0.04
16	PAU-2372	3.51	1.80	0.04	0.37	-0.78	-0.0003	3.33	5.84	0.02
17	PAU-2373	2.95	0.45	-0.02	0.38	-1.15	-0.0005	2.61	3.80	-0.04
18	PAU-2374	6.36	1.44	-0.02	0.39	1.92	0.015*	7.23	1.38	0.00
19	ARKA VIKAS	5.12	0.50*	-0.02	0.46	-0.64	-0.0001	3.70	1.95	0.07
20	Dwd-T-11	4.52	3.27	0.05	0.49	1.35	0.0042**	2.99	0.26	0.14
21	VR-35	5.61	-2.13	0.19 **	0.56	-1.57	0.0002	3.54	3.83	0.01
22	VR-415	4.42	1.41	0.00	0.46	3.90	-0.0003	2.58	2.24	-0.01
23	VRCT-155	2.44	0.61	-0.02	0.34	0.99	-0.0001	4.02	-1.96*	-0.05
24	VRCT-17	2.83	0.03	-0.01	0.33	2.44	-0.0005	3.63	2.34	-0.03
25	VTG-106	4.66	0.38	0.07 *	0.51	0.02	0.0007	2.58	6.18	-0.05
26	VTG-85	5.01	-3.44	0.01	0.56	2.41	-0.0002	2.74	-2.86	-0.03
27	VTG-86	4.67	1.58	-0.02	0.48	2.44	-0.0005	3.17	-1.34	-0.05
28	VTG-89	4.15	0.63	-0.02	0.50	-1.35*	-0.0005	2.74	3.37	-0.03
29	VTG-90	4.21	1.01	-0.01	0.52	0.15	-0.0004	2.73	-9.96	-0.02
30	VTG-93	2.13	0.08	-0.01	0.38	-0.12	-0.0004	2.97	-6.43	-0.04
31	VTG-95	4.42	-2.53	-0.01	0.51	0.68	-0.0001	2.53	7.64	0.25 *
32	Dwd-T-1	5.08	1.28	-0.02	0.43	4.07	0.0014 *	4.89	-2.03	-0.03
33	Dwd-T-2	5.19	-0.62	0.03	0.48	1.59	-0.0004	4.23	-5.15*	-0.05
34	Dwd-T-3	5.64	4.84	0.05	0.56	1.43	-0.0004	5.51	-0.34	-0.02
35	Dwd-T-4	5.72	-2.09	0.09 *	0.47	1.55	-0.0004	6.28	-8.38*	-0.05
36	Dwd-T-5	4.34	1.43*	-0.02	0.33	-1.64	0.0018 *	3.41	3.13	0.03
37	Dwd-T-6	4.76	1.14	0.00	0.35	3.35	0.0007	2.74	1.57	-0.05
38	Dwd-T-7	4.78	3.07*	-0.02	0.36	1.40	0.0012	3.32	-1.63	0.02
39	Dwd-T-8	5.45	0.50	-0.01	0.53	-1.03	-0.0005	3.54	9.56	-0.01
40	Dwd-T-9	4.69	2.06	-0.02	0.47	0.53	-0.0003	3.95	6.72	-0.05
41	Dwd-T-10	4.90	2.31	-0.01	0.48	0.62	0.0014	4.68	0.63	-0.05
	Mean	4.55		1.00	0.44		1.00	3.66		1.00
	S.Ed+	0.13		1.06	0.02		1.29	0.15		3.97
	C.D. @ 5%	0.26			0.04			0.29		

*, **: Indicates significant at 5 and 1% level of probability respectively

4.1.6.2.2.8 Number of locules per fruit (cf. Table 18)

The number of locules per fruit was maximum in 'PAU-2374' (7.23) while minimum number of locules per fruit was observed in 'HAT-121' (2.09). Mean was 3.66.

Significant regression coefficient that more than unity was observed in three genotypes. The deviation from regression values was significantly very near zero one genotype 'VTG-95'.

4.1.6.2.2.9 Single fruit weight (cf. Table 19)

Single fruit weight was maximum in 'PAU-2374' (113.23 g) and minimum in 'HAT-121' (10.73 g). Mean single fruit weight was 66.38 g.

The genotypes 'HAT-121, HAT-20, VR-415, and Megha (L-15)' recorded significant regression coefficient values near unity. The deviation from regression value was significantly more than zero for four genotypes.

4.1.6.2.2.10 Total soluble solids (cf. Table 19)

TSS was maximum in 'HAT-121' (7.85) and minimum in 'DVRT-2' (3.37). Mean was 4.46.

The genotypes 'Pant-T-11', 'PAU-2373'and 'VTG-89' recorded significant regression coefficient values near unity. The deviation from regression value was significantly more nearing zero for five genotypes.

4.1.6.2.2.11 Number of fruits per plant (cf. Table 19)

The highest number of fruits per plant was recorded by the genotype 'VRCT-17'(210.94) and lowest was recorded by 'H-24' (21.52) with a population mean of 61.53 .

The regression coefficient values were significant for four genotypes 'Pant-T-10', 'Arka Vikas', VTG-106', and 'Dwd-T-1' that were significantly around unity and positive. Three genotypes 'HAT-121', 'VRCT-155' and 'VRCT-17' showed the significant deviation from regression values that were more than the zero.

4.1.6.2.2.12 Yield per plant (cf. Table 20)

Mean yield per plant for three seasons were 1.308, 1.435, and 1.732 kg. The grand population mean was 1.492 kg. The genotype 'VR-35' recorded highest mean yield of 1.964 kg/plant and lowest mean yield was recorded by the genotype 'H-24' with 0.955 kg over three seasons. The highest yielders in *kharif* 2007, *kharif* 2008 and *rabi* 2008 were 'VRCT-17', 'VR-35', and 'Dwd-T-8' with 1.930, 1.972 and 2.154 kg/plant respectively. The environmental indices for *kharif* 2007, *kharif* 2008 and *rabi* 2008 were -0.18, -0.06 and 0.24 respectively indicating the environments varied significantly with regard to yield per plant.

None of the genotypes recorded significant values for regression coefficient and three entries ('Megha (L-15)', 'PAU-2373' and 'Dwd-T-4') were having significant deviation from regression nearing zero. Distribution of 41 tomato genotypes graphically for yield per plant trait stability parameters like mean, regression coefficients, deviations from regression values and environmental indices through scatter graphs is shown in Fig. 8.

4.1.6.2.2.13 Yield per hectare (cf. Table 21)

Mean yield per hectare for three seasons were 27.82, 30.58 and 36.29 t/ha. The grand population mean was 31.56 t/ha. The genotype 'PAU-2372' recorded highest mean yield of 39.25t/ha and lowest mean yield was recorded by the genotype 'H-24' with 19.86 t/ha over three seasons. The highest yielders in *kharif* 2007, *kharif* 2008 and *rabi* 2008 were 'PAU-2372', 'VR-35', and 'Pant-T-11' with 38.73, 38.82 and 45.08 t/ha respectively. The environmental indices for *kharif* 2007, *kharif* 2008 and *rabi* 2008 were -3.74,-0.98 and 4.72 respectively indicating the environments varied significantly with regard to yield per hectare. One genotype ('CO-3') recorded significant values for regression coefficient of 0.41 and twelve were having significant deviation from regression values higher than zero.

Distribution of 41 tomato genotypes graphically for yield per hectare trait stability parameters like mean, regression coefficients, deviations from regression values and environmental indices through scatter graphs is shown in Fig. 9.

Table 19. Mean performance and stability parameters of 41 tomato genotypes for single fruit weight, total soluble solids and number of fruits per plant.

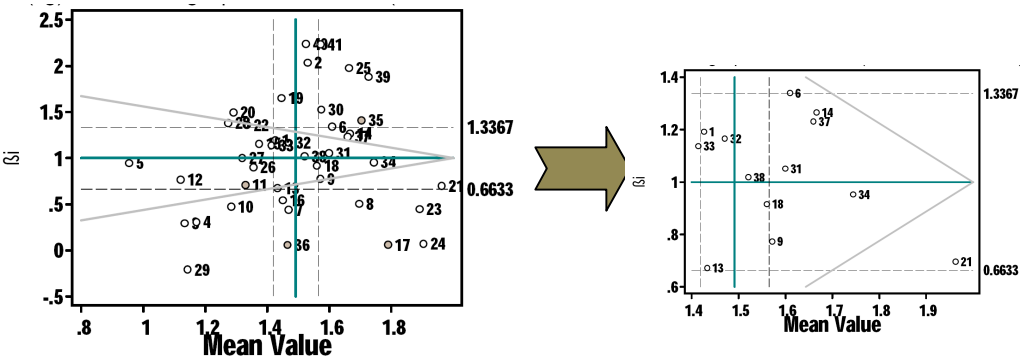
Sl. No.	Genotype	Single fruit weight (g)			Total soluble solids (%)			No. of fruits per plant		
		Mean	β_i	σ^2d_i	Mean	β_i	σ^2d_i	Mean	β_i	σ^2d_i
1	ALT-02-39	88.54	1.83	-5.99	4.26	0.46	0.001	34.90	0.59	-8.50
2	VR-20	61.06	0.56	-6.78	3.79	0.92	0.003	37.12	1.07	-3.70
3	CO-3	61.72	2.15	2.94	3.69	0.83	-0.012	26.84	0.65	-8.69
4	DVRT-2	107.15	2.59	0.10	3.37	1.03	-0.011	23.57	0.48	-8.31
5	H-24	55.00	0.67	16.39	3.38	0.56	-0.020	21.52	0.59	-4.03
6	HADT-294	75.82	0.70	-5.29	4.23	0.76	-0.018	30.85	0.91	-7.69
7	HAT-121	10.73	0.30*	-6.84	7.85	0.24	0.056	166.15	2.75	54.83 **
8	HAT-20	11.42	-0.02*	-6.82	6.26	1.49	0.068*	165.97	-1.32	-0.89
9	KS-227	60.68	0.93	-4.77	3.65	0.94	-0.021	36.17	0.70	-7.59
10	KS-229	62.60	1.10	-6.12	3.62	1.19	0.005	35.84	0.49	-7.13
11	Megha (L-15)	55.62	1.916*	-6.83	4.03	1.17	0.018	45.17	0.76	-7.07
12	NDT-9	77.55	0.92	-6.82	4.07	0.54	-0.008	33.62	0.91	-5.38
13	PANT-T-10	71.92	1.43	-6.70	4.13	0.501*	-0.021	36.10	0.367*	-8.71
14	PANT-T-11	69.96	1.35	2.06	4.12	0.653*	-0.021	39.57	1.02	-2.45
15	PAU-2371	74.46	1.08	-5.36	5.09	0.69	-0.021	35.41	0.72	-8.31
16	PAU-2372	71.63	0.83	-6.16	3.94	0.15	0.001	48.49	0.65	-7.26
17	PAU-2373	16.69	0.73	-6.71	7.09	0.112*	-0.021	183.34	2.60	-4.99
18	PAU-2374	113.23	-0.70	34.63*	4.68	0.91	0.014	38.67	0.34	-8.02
19	ARKA VIKAS	89.44	1.37	-6.60	4.53	2.14	0.123**	37.00	0.80*	-8.73
20	Dwd-T-11	77.02	1.31	-6.02	4.15	1.72	0.013	28.13	1.82	-2.90
21	VR-35	101.28	-0.62	-5.44	4.22	0.87	-0.021	46.25	0.91	2.69
22	VR-415	67.16	1.545*	-6.83	4.73	1.67	0.148**	58.19	1.27	-8.68
23	VRCT-155	11.87	0.33	-6.75	6.88	2.83	0.378**	194.84	2.26	33.93 *
24	VRCT-17	17.93	0.24	-5.51	5.14	0.52	-0.021	210.94	2.56	198.61**
25	VTG-106	82.80	0.67	-6.49	4.47	3.27	-0.019	29.36	1.42*	-8.73
26	VTG-85	79.18	0.87	-5.31	4.17	0.70	0.001	36.12	0.70	-2.97
27	VTG-86	66.69	6.16	3.56	4.03	2.18	0.212**	57.44	1.54	-6.81
28	VTG-89	50.87	-0.40	-6.57	3.98	-0.63*	-0.021	51.01	0.54*	-8.71
29	VTG-90	56.06	0.42	0.99	4.03	1.42	-0.021	40.87	1.13	-8.69
30	VTG-93	10.80	0.04	-6.77	6.38	0.80	-0.010	184.49	2.24	3.67
31	VTG-95	61.89	1.46	-6.64	4.84	0.45	0.055	34.19	0.50	-8.61
32	Dwd-T-1	70.07	3.36	27.29*	3.47	2.07	0.001	43.62	0.26*	-8.73
33	Dwd-T-2	66.00	1.40	57.79 **	3.68	0.90	0.016	45.29	0.86	14.03
34	Dwd-T-3	108.72	-1.27	59.59 **	3.41	0.78	0.015	43.89	0.76	-6.91
35	Dwd-T-4	98.61	0.01	-5.78	3.68	1.80	0.025	33.55	0.83	-8.67
36	Dwd-T-5	67.39	1.10	-5.71	4.24	-0.12	-0.012	59.82	0.69	-8.18
37	Dwd-T-6	69.20	0.75	13.80	3.88	1.25	-0.016	59.68	1.81	-8.15
38	Dwd-T-7	66.85	1.96	-5.85	4.29	0.77	-0.021	43.20	1.06	-8.56
39	Dwd-T-8	84.53	0.74	-3.10	4.77	1.70	0.035	39.01	1.30	-8.68
40	Dwd-T-9	88.70	0.93	-4.12	4.73	-0.13	0.095*	47.73	0.72	-6.83
41	Dwd-T-10	82.71	0.29	3.21	4.09	0.91	-0.020	58.93	0.75	-7.91
	Mean	66.38		1.00	4.46		1.00	61.53		1.00
	S.Ed+	2.00		0.83	0.15		0.82	2.26		0.52
	C.D. @ 5%	4.19			0.31			4.73		

*, **: Indicates significant at 5 and 1% level of probability respectively

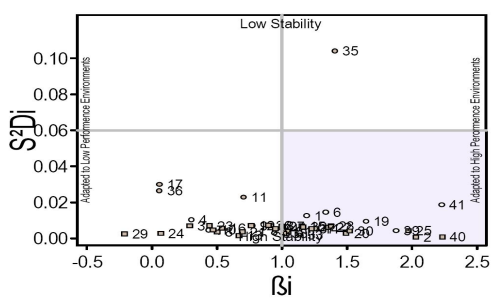
Table 20. *Per se* performance and stability parameters of 41 tomato genotypes for yield per plant.

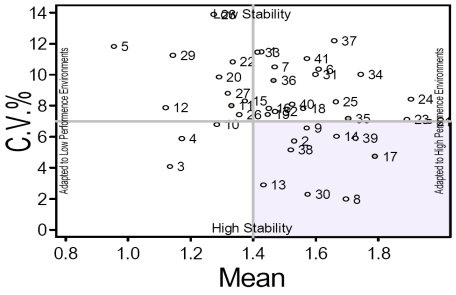
Sl. No.	Genotype	Yield per plant (kg)					
		Env 1	Env 2	Env 3	Mean	β_i	$\sigma^2 d_i$
1	ALT-02-39	1.287	1.247	1.746	1.427	1.191	0.013
2	VR-20	1.113	1.481	2.000	1.531	2.032	-0.001
3	CO-3	1.070	1.133	1.200	1.134	0.292	-0.007
4	DVRT-2	1.190	1.050	1.277	1.172	0.304	0.010
5	H-24	0.726	0.982	1.158	0.955	0.944	0.003
6	HADT-294	1.447	1.417	1.967	1.610	1.338	0.014
7	HAT-121	1.449	1.358	1.600	1.469	0.437	0.005
8	HAT-20	1.570	1.717	1.803	1.697	0.503	-0.004
9	KS-227	1.497	1.433	1.786	1.572	0.773	0.007
10	KS-229	1.227	1.217	1.410	1.284	0.472	-0.005
11	Megha (L-15)	1.298	1.153	1.542	1.331	0.707	0.022 *
12	NDT-9	0.973	1.088	1.301	1.121	0.765	-0.007
13	PANT-T-10	1.268	1.456	1.577	1.433	0.672	-0.002
14	PANT-T-11	1.410	1.630	1.960	1.667	1.264	-0.005
15	PAU-2371	1.151	1.326	1.647	1.374	1.154	-0.007
16	PAU-2372	1.374	1.387	1.590	1.450	0.541	-0.006
17	PAU-2373	1.887	1.633	1.850	1.790	0.059	0.03 *
18	PAU-2374	1.403	1.493	1.785	1.561	0.915	-0.007
19	ARKA VIKAS	1.073	1.456	1.812	1.447	1.648	0.009
20	Dwd-T-11	0.980	1.260	1.634	1.291	1.494	-0.003
21	VR-35	1.802	1.972	2.116	1.964	0.696	-0.004
22	VR-415	1.105	1.230	1.670	1.335	1.358	-0.006
23	VRCT-155	1.820	1.853	2.003	1.892	0.445	-0.007
24	VRCT-17	1.930	1.847	1.937	1.905	0.069	-0.003
25	VTG-106	1.333	1.509	2.152	1.665	1.974	-0.004
26	VTG-85	1.187	1.310	1.570	1.356	0.899	-0.007
27	VTG-86	1.150	1.243	1.566	1.320	1.000	-0.007
28	VTG-89	1.032	1.180	1.610	1.274	1.379	-0.007
29	VTG-90	1.143	1.211	1.077	1.144	-0.210	-0.002
30	VTG-93	1.327	1.443	1.954	1.575	1.524	-0.004
31	VTG-95	1.440	1.493	1.866	1.600	1.051	-0.004
32	Dwd-T-1	1.240	1.429	1.743	1.471	1.165	-0.006
33	Dwd-T-2	1.259	1.274	1.710	1.414	1.136	0.002
34	Dwd-T-3	1.545	1.726	1.963	1.745	0.952	-0.005
35	Dwd-T-4	1.260	1.890	1.963	1.704	1.408	0.10**
36	Dwd-T-5	1.353	1.609	1.436	1.466	0.057	0.03 *
37	Dwd-T-6	1.459	1.555	1.966	1.660	1.230	-0.005
38	Dwd-T-7	1.297	1.518	1.750	1.521	1.018	-0.003
39	Dwd-T-8	1.323	1.706	2.154	1.728	1.879	0.004
40	Dwd-T-9	1.160	1.334	2.081	1.525	2.235	-0.001
41	Dwd-T-10	1.073	1.573	2.070	1.572	2.231	0.019
	Mean	1.31	1.44	1.73	1.49		1.00
	S.Ed±	0.12	0.11	0.13	0.07		0.34
	C.D. @ 5%	0.25	0.22	0.25	0.15		
	C.V. %	11.57	9.46	8.92			
	Enviromental Index	-0.18	-0.06	0.24			

*, **: Indicates significant at 5 and 1% level of probability respectively

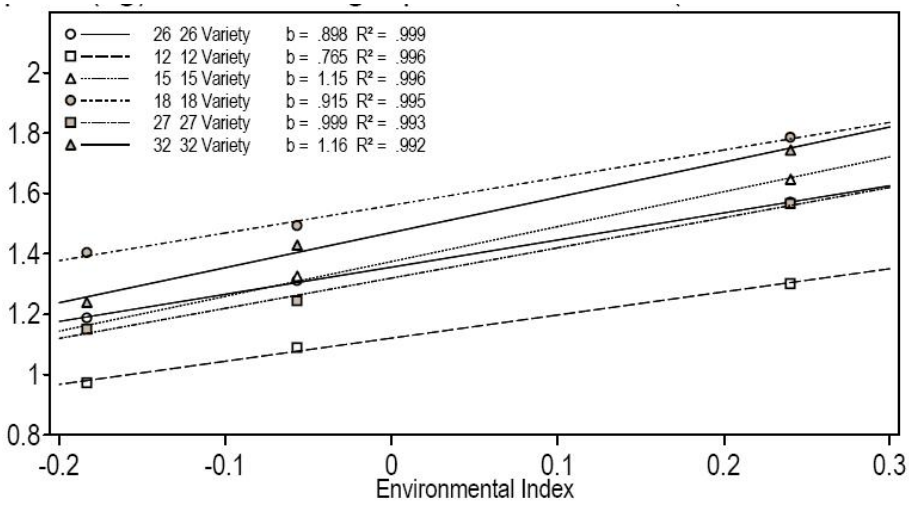


(a) Plotting of genotypes on mean and b_i





(b).Plotting genotypes on b_i and s^2 d_i (c) Plotting of genotypes with mean and C.V.



Legend:

Sl.	Genotype
1	ALT-02-39
2	VR-20
3	CO-3
4	DVRT-2
5	H-24
6	HADT-294
7	HAT-121
8	HAT-20
9	KS-227
10	KS-229
11	Megha (L-15)
12	NDT-9
13	PANT-T-10
14	PANT-T-11
15	PAU-2371
16	PAU-2372
17	PAU-2373
18	PAU-2374
19	ARKA VIKAS
20	Dwd-T-11
21	VR-35
22	VR-415
23	VRCT-155
24	VRCT-17
25	VTG-106
26	VTG-85
27	VTG-86
28	VTG-89
29	VTG-90
30	VTG-93
31	VTG-95
32	Dwd-T-1
33	Dwd-T-2
34	Dwd-T-3
35	Dwd-T-4
36	Dwd-T-5
37	Dwd-T-6
38	Dwd-T-7
39	Dwd-T-8
40	Dwd-T-9
41	Dwd-T-10

Plotted numbers of genotypes correspond to their serial number shown above

Figure 8. Distribution of tomato genotypes with respect to b_i values, S^2d_i , C.V. and environmental index in yield per plant trait stability study based on evaluation in *kharif* 2007, *kharif* 2008 and *rabi* 2008.

4.1.6.2.2.14 Disease incidence (cf. Table 22 to Table 23)

Stability parameters for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence has presented in above mentioned tables. The environmental indices of these traits indicate the environments differed significantly. There were two, one, four, two, three and three genotypes showing significant regression coefficient values for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence respectively. There were two, four, three, ten, nine and nine genotypes showing significant deviation from regression values for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence respectively.

Some of the entries that were evaluated and their variability is presented in plates 2 and plate 3.

4.2 EXPERIMENT II: EVALUATION OF F_1 HYBRIDS DEVELOPED BY LINE X TESTER METHOD DURING *RABI* 2008

4.2.1 HETEROSIS

4.2.1.1 Analysis of variance

Results of the analysis of variance for 19 characters of F_1's evaluated with commercial check and local check are presented in Table 24.

It is revealed from the results that all the entries (treatments) comprising parents and hybrids showed significant difference for all the characters. All traits of parents except for late blight incidence were differing significantly. Among the parents, lines (females) exhibited significant differences for all the characters except for late blight incidence. Similarly, the testers (males) also differed significantly for all the characters except for late blight, TLCV, and tomato spotted wilt virus incidence. The contribution of lines Vs tester showed significant variation for all the characters except for number of branches per plant, number of locules per fruit, TSS and late blight. Variance, for parents vs. hybrids was significant for all the characters except for number of branches per plant, days to 50 % flowering, number of fruits per cluster, fruit length, number of locules per fruit, early blight and powdery mildew. Within crosses all traits exhibited significant variation for all traits except pericarp thickness, and tomato leaf curl virus incidence.

4.2.1.2 *Per se* performance and magnitude of heterosis

Results from statistical analysis of F_1's data with regard to the *per se* performance of the parents (i.e., lines & testers), F_1's , commercial check/(ARTH-3) and local check [Megha (L-15)], per cent heterosis over mid parent (MP), better parent (BP), and commercial check (CC) for the nineteen characters studied are presented in Tables 25 to 34.While highlighting the results of each trait under subsequent sub headings focus will be on *per se* values and commercial heterosis percentages as they would of utility and average heterosis or heterobeltiosis would be of academic interest that could is indicated in values from corresponding tables.

4.2.1.2.1 Plant height (cf. Table 25)

Among the parents, the maximum plant height was recorded in 'KS-227' (108.78 cm) and the minimum in 'H-24' (70.39 cm) whereas in F_1s higher and lower values for plant height were registered by 'DVRT-2' x 'KS-227' (104.58 cm) and 'CO-3'x 'Dwd-T-6' (71.25 cm) respectively.

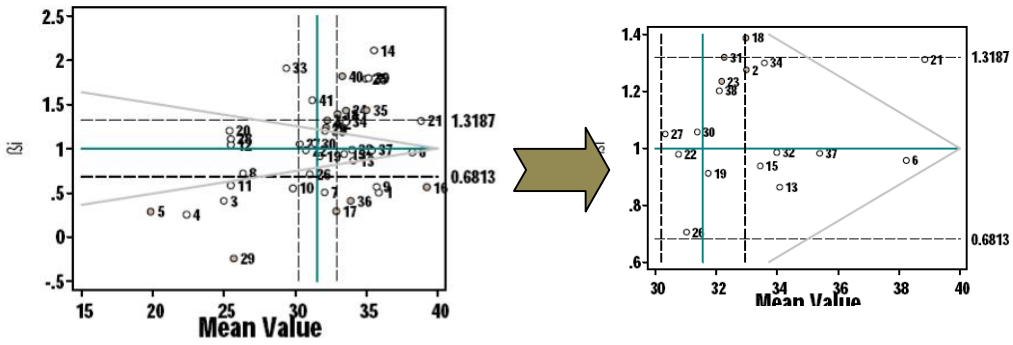
The range of heterosis over mid parent value was from -16.71 to 9.58 per cent. Out of 25 F_1s, three showed significant positive heterosis, while ten had significant negative heterosis for this trait. Heterosis in F_1s over their respective better parent ranged from -31.40 to 8.31 per cent.

All significant fifteen crosses for heterosis over better parent were negative. Five and three crosses had significant positive and negative heterosis over commercial check.

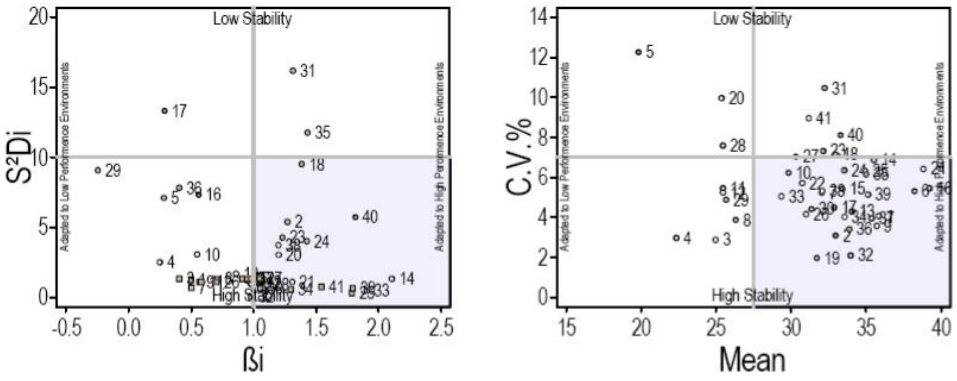
Table 21. *Per se* performance and stability parameters of 41 tomato genotypes for yield per hectare.

Sl. No.	Genotype	Yield per hectare (t)					
		Env 1	Env 2	Env 3	Mean	b_i	s^2d_i
1	ALT-02-39	33.84	35.61	38.17	35.87	0.50	-1.27
2	VR-20	26.83	33.82	38.33	32.99	1.27	5.39 *
3	CO-3	23.41	24.69	26.89	25.00	0.41*	-1.33
4	DVRT-2	22.48	20.55	24.07	22.37	0.25	2.51
5	H-24	20.36	17.25	21.97	19.86	0.29	7.10 *
6	HADT-294	34.85	37.03	42.85	38.24	0.96	-1.23
7	HAT-121	30.63	30.92	34.66	32.07	0.50	-0.68
8	HAT-20	23.78	25.44	29.77	26.33	0.72	-1.30
9	KS-227	33.89	34.78	38.54	35.74	0.57	-1.10
10	KS-229	28.93	27.63	33.00	29.85	0.55	3.07
11	Megha (L-15)	23.57	24.50	28.36	25.48	0.58	-1.10
12	NDT-9	21.30	24.89	30.26	25.48	1.04	-1.07
13	PANT-T-10	29.92	34.63	37.71	34.09	0.86	1.67
14	PANT-T-11	26.77	34.78	45.08	35.54	2.11	1.32
15	PAU-2371	30.04	32.38	37.92	33.45	0.94	-1.32
16	PAU-2372	38.73	36.34	42.67	39.25	0.56	7.32 *
17	PAU-2373	33.87	29.54	35.25	32.88	0.29	13.30 **
18	PAU-2374	26.01	34.25	38.67	32.98	1.39	9.51**
19	ARKA VIKAS	28.24	30.97	36.00	31.74	0.91	-1.32
20	Dwd-T-11	19.76	25.88	30.52	25.38	1.20	3.04
21	VR-35	33.10	38.82	44.63	38.85	1.31	1.11
22	VR-415	27.92	28.58	35.78	30.76	0.98	0.96
23	VRCT-155	28.84	29.07	38.62	32.18	1.23	4.27 *
24	VRCT-17	29.48	30.32	40.92	33.58	1.43	4.01 *
25	VTG-106	27.73	34.03	43.15	34.97	1.79	-0.30
26	VTG-85	28.11	30.75	34.22	31.03	0.71	-1.08
27	VTG-86	26.46	29.21	35.31	30.33	1.05	-1.34
28	VTG-89	21.71	23.85	30.88	25.48	1.11	-0.89
29	VTG-90	24.86	28.51	23.70	25.69	-0.24	9.05 **
30	VTG-93	27.88	29.67	36.59	31.38	1.06	-0.65
31	VTG-95	29.59	27.62	39.58	32.26	1.32	16.15**
32	Dwd-T-1	29.70	33.93	38.35	33.99	0.98	-0.08
33	Dwd-T-2	21.51	28.59	38.04	29.38	1.91	0.49
34	Dwd-T-3	28.24	33.02	39.48	33.58	1.30	-0.56
35	Dwd-T-4	27.71	36.51	40.85	35.02	1.43	11.74**
36	Dwd-T-5	30.75	35.93	35.04	33.91	0.41	7.80**
37	Dwd-T-6	31.80	34.33	40.07	35.40	0.98	-1.33
38	Dwd-T-7	26.39	32.72	37.18	32.10	1.20	3.73
39	Dwd-T-8	27.99	34.07	43.43	35.16	1.80	-0.65
40	Dwd-T-9	27.95	29.40	42.59	33.31	1.82	5.71 *
41	Dwd-T-10	25.84	29.07	38.71	31.21	1.55	-0.75
	Mean	27.82	30.58	36.29	31.56		1.00
	S.Ed+	1.59	1.59	1.63	1.38		0.32
	C.D. @ 5%	3.16	3.17	3.24			
	C.V. %	6.99	6.37	5.49			
	Enviromental Index	-3.74	-0.98	4.72			

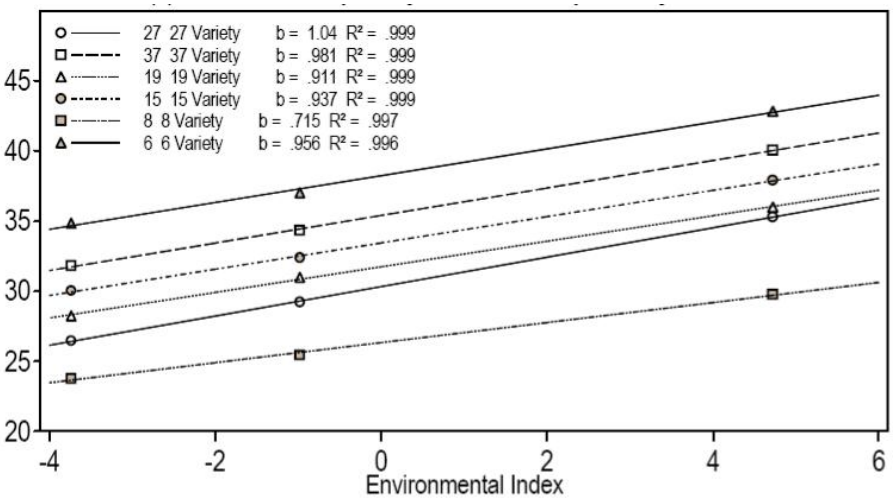
*, **: Indicates significant at 5 and 1% level of probability respectively



(a) Plotting of genotypes on mean and b_i



(b).Plotting genotypes on b_i and s^2 d_i (c) Plotting of genotypes with mean and C.V.



Legend:

Sl.	Genotype
1	ALT-02-39
2	VR-20
3	CO-3
4	DVRT-2
5	H-24
6	HADT-294
7	HAT-121
8	HAT-20
9	KS-227
10	KS-229
11	Megha (L-15)
12	NDT-9
13	PANT-T-10
14	PANT-T-11
15	PAU-2371
16	PAU-2372
17	PAU-2373
18	PAU-2374
19	ARKA VIKAS
20	Dwd-T-11
21	VR-35
22	VR-415
23	VRCT-155
24	VRCT-17
25	VTG-106
26	VTG-85
27	VTG-86
28	VTG-89
29	VTG-90
30	VTG-93
31	VTG-95
32	Dwd-T-1
33	Dwd-T-2
34	Dwd-T-3
35	Dwd-T-4
36	Dwd-T-5
37	Dwd-T-6
38	Dwd-T-7
39	Dwd-T-8
40	Dwd-T-9
41	Dwd-T-10

Plotted numbers of genotypes correspond to their serial number shown above

Figure 9. Distribution of tomato genotypes with respect to b_i values, S^2d_i, C.V., and environmental index in yield per hectare trait stability study based on evaluation in *kharif* 2007, *kharif* 2008 and rabi 2008.

Table 22. Mean performance and stability parameters of 41 tomato genotypes for field incidence of early blight, late blight and powdery mildew.

Sl.	Genotype	Early Blight			Late Blight			Powdery mildew		
		Mean	β_i	$\sigma^2 d_i$	Mean	β_i	$\sigma^2 d_i$	Mean	β_i	$\sigma^2 d_i$
1	ALT-02-39	2.68	1.83	-0.02	1.84	1.16	1.13**	1.25	0.80	-0.06
2	VR-20	1.13	0.93	-0.06	1.73	1.15	-0.07	1.98	2.11	0.04
3	CO-3	2.03	-0.75	0.17	2.46	1.71	0.07	1.57	1.87*	-0.06
4	DVRT-2	2.63	0.23	0.60 **	2.29	1.77	1.24**	1.98	1.99*	-0.06
5	H-24	2.26	-0.22	0.06	2.23	1.59	-0.09	1.49	1.11	-0.02
6	HADT-294	1.13	1.35	-0.06	1.34	0.94	0.27	1.06	1.12	-0.05
7	HAT-121	1.93	1.24	0.11	1.65	1.18	-0.10	1.18	1.28	-0.04
8	HAT-20	1.32	1.46	0.08	1.37	1.09	-0.08	1.09	1.00	0.14
9	KS-227	0.14	0.05*	-0.07	1.26	0.86	0.21	0.63	0.06	0.01
10	KS-229	1.40	2.02	0.18	1.67	1.34	-0.07	1.57	1.33	-0.06
11	Megha (L-15)	1.62	1.53	-0.07	1.75	1.12	-0.06	1.30	1.10	0.03
12	NDT-9	1.58	1.02	0.04	2.09	1.05	0.10	1.71	0.95	-0.04
13	PANT-T-10	1.83	1.46	-0.06	2.14	1.11	0.11	1.79	0.93	0.97**
14	PANT-T-11	2.11	1.57	0.04	1.62	1.04	0.22	1.07	1.17	-0.06
15	PAU-2371	1.44	1.43	-0.06	1.46	1.13	0.33*	1.46	0.88	-0.05
16	PAU-2372	1.03	0.30	-0.03	1.75	1.21	0.02	0.56	0.62	-0.05
17	PAU-2373	1.59	0.83	-0.06	1.99	1.11	-0.10	1.42	1.30	0.07
18	PAU-2374	1.18	0.42	-0.07	1.76	0.94	-0.10	1.01	0.40	-0.04
19	ARKA VIKAS	1.70	0.89	0.10	2.81	2.00	0.25	1.46	0.89	-0.03
20	Dwd-T-11	0.62	0.62	-0.05	1.73	0.80	-0.02	1.36	1.12	-0.04
21	VR-35	0.69	0.18	-0.05	0.60	0.23	-0.08	0.74	0.01*	-0.06
22	VR-415	1.74	1.53	-0.07	1.89	1.14	0.06	1.35	1.43	0.00
23	VRCT-155	1.77	1.75*	-0.07	1.52	0.93	0.02	1.43	0.99	-0.04
24	VRCT-17	2.44	1.12	-0.06	1.59	0.56*	-0.10	1.54	1.02	-0.06
25	VTG-106	0.68	1.14	-0.04	1.47	0.89	0.04	0.82	1.06	-0.06
26	VTG-85	1.65	1.31	-0.03	1.95	0.91	-0.01	1.56	1.00	-0.06
27	VTG-86	1.35	0.67	-0.04	1.63	1.03	0.16	1.43	0.88	-0.05
28	VTG-89	1.50	1.54	-0.07	1.83	0.89	0.01	1.08	1.05	-0.02
29	VTG-90	1.21	0.97	-0.05	1.57	0.93	-0.09	1.25	1.02	-0.06
30	VTG-93	1.48	1.49	-0.02	1.76	0.72	-0.05	1.63	1.14	-0.06
31	VTG-95	1.55	1.27	0.05	2.24	1.16	-0.06	1.53	1.38	-0.06
32	Dwd-T-1	1.84	0.86	0.15	1.33	0.68	0.16	1.41	0.98	-0.01
33	Dwd-T-2	1.48	0.57	-0.05	2.55	0.50	-0.09	1.40	0.76	0.00
34	Dwd-T-3	1.40	0.77	-0.05	1.90	1.08	-0.09	1.51	0.99	-0.05
35	Dwd-T-4	1.93	1.12	1.35**	1.74	0.61	-0.06	1.79	0.70	0.07
36	Dwd-T-5	1.16	1.15	-0.06	0.85	0.57	-0.02	0.95	0.07*	-0.06
37	Dwd-T-6	1.42	1.16	-0.06	1.95	0.93	0.63 **	1.72	0.44	0.14
38	Dwd-T-7	1.67	1.10	0.20	0.69	0.57	0.23	1.03	0.38	0.30 *
39	Dwd-T-8	0.96	0.21	0.03	1.70	0.46	0.18	1.25	1.17	0.12
40	Dwd-T-9	1.85	1.58	-0.04	1.53	0.81	-0.07	1.52	1.17	-0.06
41	Dwd-T-10	1.74	1.31	0.10	1.99	1.14	-0.09	1.38	1.33	0.31 *
	Mean	1.53		1.00	1.74		1.00	1.35		1.00
	S.Ed±	0.24		0.39	0.31		0.31	0.21		0.17
	C.D. @ 5%	0.51			0.63			0.44		

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 23. Mean performance and stability parameters of 41 tomato genotypes for field incidence of tomato leaf curl virus, tomato leaf spotted virus and *Sclerotium* wilt.

Sl.	Genotype	Tomato leaf curl virus (TLCV) (%)			Tomato spotted wilt virus (TSWV) (%)			*Sclerotium* wilt (%)		
		Mean	β_i	$\sigma^2 d_i$	Mean	β_i	$\sigma^2 d_i$	Mean	β_i	$\sigma^2 d_i$
1	ALT-02-39	18.86	1.80	30.42**	6.44	2.81	2.00	13.50	-1.18	23.45**
2	VR-20	7.36	0.92	32.71 **	2.02	0.62	-0.17	10.10	2.27	6.29 *
3	CO-3	17.41	2.058*	-4.30	5.63	2.29	8.39**	11.10	4.21	10.71 *
4	DVRT-2	14.34	1.85	25.45 *	6.64	3.13	16.64**	2.89	1.23	-2.04
5	H-24	3.61	0.38	-4.55	3.23	-0.13*	-1.07	6.89	1.56	-1.93
6	HADT-294	21.10	2.70	226.0 **	3.10	0.69	6.08*	1.39	0.61	-1.71
7	HAT-121	8.88	1.05	16.53 *	1.75	0.59	1.13	1.94	0.16*	-2.07
8	HAT-20	12.87	1.61	-3.03	6.83	4.31	30.68**	10.23	1.91	-1.73
9	KS-227	10.36	1.28*	-4.90	2.47	0.86	6.57**	3.07	-0.13	-1.19
10	KS-229	11.70	1.45	11.39	1.81	0.93	-1.03	2.43	0.03*	-2.03
11	Megha (L-15)	3.42	-0.33	-3.57	1.34	0.76	-0.81	5.68	0.49	-2.01
12	NDT-9	7.86	0.84	3.47	0.99	0.50	-1.07	10.81	1.37	1.40
13	PANT-T-10	7.70	0.90	12.54	3.47	0.11	-0.41	9.21	2.23	1.70
14	PANT-T-11	11.17	1.31	9.59	1.05	0.44	-0.63	12.89	0.15	33.25**
15	PAU-2371	13.73	-0.05	1.38	7.79	3.00	42.13**	11.67	1.19	1.35
16	PAU-2372	7.70	0.97	2.70	1.74	0.78	-0.89	5.68	0.85	-1.63
17	PAU-2373	15.27	1.02	36.99**	5.01	2.54	6.02*	7.75	1.31	-0.65
18	PAU-2374	5.71	0.49	52.56**	2.94	0.48	-1.02	2.80	-0.31	-1.30
19	ARKA VIKAS	12.22	1.35	2.65	7.56	3.91	6.66**	8.36	-1.77	33.73**
20	Dwd-T-11	7.55	0.88	4.36	1.94	0.66	-0.77	3.13	0.72	-1.73
21	VR-35	11.11	1.34	13.73	2.29	1.38	1.62	5.64	0.98	-2.10
22	VR-415	8.62	1.07	5.14	1.51	0.62	-1.06	4.00	-0.19	-1.64
23	VRCT-155	8.45	0.98	25.21 *	1.47	0.67	-0.64	9.77	2.16	-0.53
24	VRCT-17	7.72	0.99	1.96	1.65	0.55	-0.44	4.65	0.77	-0.37
25	VTG-106	9.38	1.07	0.92	1.61	0.81	-1.02	10.88	0.92	20.05**
26	VTG-85	11.97	0.57	-4.32	3.22	-0.30	3.48*	10.52	1.29	14.33**
27	VTG-86	8.24	1.00	-4.25	1.73	0.76*	-1.09	7.67	1.30	-1.02
28	VTG-89	9.02	1.08	-0.76	1.44	0.40	-0.04	10.02	1.16	-1.04
29	VTG-90	9.11	1.13	-2.10	1.70	0.55	-0.95	7.42	1.04	0.12
30	VTG-93	7.22	0.85	28.32 **	1.19	0.37	-1.04	8.43	1.81	0.15
31	VTG-95	7.43	0.92	-0.44	1.06	0.40	0.09	7.35	1.47	24.69**
32	Dwd-T-1	9.11	1.14	-4.74	1.45	0.38	-1.04	7.37	0.68	8.28*
33	Dwd-T-2	6.43	0.75	30.28**	1.71	0.65	0.05	3.95	1.09	-1.44
34	Dwd-T-3	8.94	1.10	-3.44	2.27	1.07	-0.25	4.81	0.99	1.85
35	Dwd-T-4	11.25	1.35	4.07	2.69	1.57	2.88	9.53	1.24	0.44
36	Dwd-T-5	7.14	0.88	-4.52	1.11	0.43	-1.01	7.74	1.52	0.77
37	Dwd-T-6	3.77	0.36	2.65	0.27	0.10	-1.05	2.42	0.72	3.62
38	Dwd-T-7	1.73	0.23	-2.20	0.42	0.23	-1.06	3.20	0.42	-1.58
39	Dwd-T-8	4.29	0.49	8.27	0.96	0.38	-0.49	9.83	1.84	10.20*
40	Dwd-T-9	4.98	0.61	7.56	0.60	0.22*	-1.09	2.67	0.87	-2.06
41	Dwd-T-10	5.23	0.64	-0.88	1.06	0.50	-0.96	7.58	2.04*	-2.09
	Mean	9.27		1.00	2.57		1.00	7.00		1.00
	S.Em±	3.03		0.44	1.39		0.80	1.74		0.66
	C.D. @ 5%	6.05			2.96			3.67		

*, **: Indicates significant at 5 and 1% level of probability respectively

VR-35

CO-3

PAU-2371

VTG 106

PAU 2372

HADT-294

Plate.2. Fruits of some of the tomato genotypes that were evaluated

HAT-121

PAU 2371

VRCT-17

FRUIT VARIABILITY

PAU 2373

HAT 20

FRUITING CLUSTER

Plate.3. Fruit and fruiting variability in evaluated tomatoes

Table 24. Analysis of variance in respect of 19 traits in line x tester study of tomato

Sl.	Character	Source of Variation (Mean Sum of squares)												
		Replicates	Treatments	Parents	Lines	Testers	Lines vs Testers	Parents vs Crosses	Crosses	Line Effect	Tester Effect	Line x Tester Effect	Error	Total
	d.f. →	2	34	9	4	4	1	1	24	4	4	16	68	104
1	Plant height	31.33	253.23**	518.86**	312.27**	802.81**	209.46**	169.84**	157.09**	374.58**	291.42*	69.14**	15.71	93.66
2	No. of branches per plant	0.70**	0.31**	0.49**	0.33*	0.70**	0.29	0.19	0.25**	0.35*	0.74**	0.11	0.10	0.18
3	Days to 50% flowering	6.04*	26.72**	31.09**	24.16**	33.44**	49.40**	0.28	26.18**	81.46**	54.67**	5.23**	1.93	10.11
4	No. of fruits per cluster	0.64**	0.41**	0.67**	0.55**	0.53**	1.67**	0.01	0.34*	1.56**	0.21*	0.07	0.13	0.23
5	Fruit length	0.16	0.43**	0.80**	0.45**	0.86**	1.96**	0.11	0.31**	0.75**	0.68**	0.11*	0.06	0.18
6	Fruit width	0.13	0.59**	1.18**	1.36**	1.19**	0.39**	0.67**	0.37**	0.59*	0.95**	0.17**	0.06	0.23
7	Pericarp thickness	0.013**	0.009**	0.014**	0.012**	0.012**	0.028**	0.00005.	0.01	0.02	0.01	0.00	0.00	0.00
8	No. of locules per fruit	0.15	1.76**	3.32**	3.34**	4.12**	0.08	0.06	1.24E+09	3.17**	3.43**	0.21	0.12	0.66
9	Total soluble solids	0.17*	0.27**	0.31**	0.39**	0.29**	0.05	0.17*	0.26**	1.09**	0.27**	0.05	0.04	0.12
10	Single fruit weight	40.03	659.33**	1222.66**	1602.12**	1005.95**	571.68**	145.70*	469.48**	1525.87**	609.02**	170.49**	22.56	231.07
11	No. of fruits per plant	28.19*	297.91**	527.90**	304.70**	357.28*	2103.21**	342.48**	209.81**	404.45**	644.23**	52.55**	7.78	103.03
12	Yield per plant	0.04	0.22**	0.35**	0.11**	0.07*	2.39**	1.44**	0.12**	0.29*	0.13	0.07**	0.02	0.09
13	Yield per hectare	14.03	102.71**	186.33**	110.40**	19.77**	1156.30**	862.04**	39.71**	97.56*	20.83	29.97*	5.05	37.15
14	Early Blight	0.26	1.37**	2.43**	1.05**	2.98**	5.78**	0.68	1.00**	0.60	3.15**	0.57**	0.21	0.59
15	Late Blight	0.15	0.26**	0.13	0.14	0.15	0.02	1.25**	0.27**	0.25	0.46	0.22	0.11	0.16
16	Powdery mildew	0.27	1.88**	4.72**	2.05**	3.39**	20.67**	0.10	0.89**	1.82	0.62	0.73**	0.25	0.79
17	Tomato leaf curl virus	0.18	2.97**	9.76**	18.04**	0.19	14.91**	1.33**	0.50	1.09	0.08	0.45	0.42	1.25
18	Tomato spotted wilt virus	0.34	2.29**	6.04**	7.88**	0.23	21.91**	10.88**	0.53*	0.23	0.38	0.64*	0.30	0.95
19	*Sclerotium* wilt	24.42*	60.13**	117.04**	162.20	28.20**	291.78**	364.47**	26.11**	46.08	32.89	19.42**	7.01	24.71

* Significant at 5% probability ** Significant at 1% probability

4.2.1.2.2 Number of branches per plant (cf. Table 25)

Minimum and maximum number of branches among the parents were 2.78 ('Dwd-T-1') and 4.04 ('Dwd-T-3'). Among F_1s it was 2.67, ('C0-3'x 'Dwd-T-1') and 3.86 ('Pant-T-10' x 'Dwd-T-3').

The extent of heterosis over mid parent was -17.16 to 10.71 per cent. Out of 25 crosses, three showed significant negative heterosis. Heterosis over better parent ranged from -21.65 to 4.00 per cent. The heterosis over commercial check varied from -14.80 to 23.22 per cent.

4.2.1.2.3 Days to 50 per cent flowering (cf. Table 26)

'Dwd-T-6' flowered earlier (29.30 days) and 'DVRT-2' took longest time (42.00 days) among parents. The F_1's showed variation which ranged from 30.58 days ('Megha (L-15)' x 'Dwd-T-6') to 44.00 days ('DVRT-2'x 'Dwd-T-3'). The commercial check took 36.74 days for 50 per cent flowering.

The heterosis over mid parent ranged from -10.09 to 10.00 per cent. All six crosses that showed significance heterosis over better parent were negative. However, six crosses exhibited significant negative heterosis over commercial check while four were significant with positive commercial heterosis.

4.2.1.2.4 Number of fruits per clusters (cf. Table 26)

Per se values for number of fruits per cluster ranged from 2.63 ('DVRT-2') to 4.04 ('VR-35') among the parents. Highest number of fruits per cluster was 3.97 in 'Pant-T-10'x 'Dwd-T-6' and lowest (2.82) was noticed in 'CO-3 x Dwd-T-1' among the F_1s. whereas commercial check recorded 3.81 fruits per cluster.

Heterosis over mid parent and better parent ranged from -11.34 and 12.80 to -26.82 and 5.98 per cent respectively. Significant negative heterosis was noticed in seven crosses over better parent. Whereas over commercial check 17 crosses registered only significant negative heterosis.

4.2.1.2.5 Fruit length (cf. Table 27)

Values for fruit length ranged from 3.74 cm ('CO-3') to 5.53 cm ('VR-35') among the parents. Two crosses recorded maximum of 4.88 cm and minimum was 3.66 cm fruit length among the hybrids.

Mid parent heterosis for fruit length varied from -13.67 to 12.27 per cent. Only one and three F_1 exhibited significance heterosis over mid parent heterosis in positive and negative direction respectively. Heterosis over better parent ranged from -23.13 to 4.53 per cent. Only ten F_1 exhibited significance heterosis over better parent heterosis that too in negative direction. Significant negative heterosis over commercial check was recorded in six F_1s.

4.2.1.2.6 Fruit width (cf. Table 27)

'DVRT-2' recorded maximum (6.64 cm) fruit width and 'KS-227' recorded minimum (4.45 cm) fruit width among the parents. The hybrids recorded fruit width in the range of 4.50 cm ('CO-3' x 'Dwd-T-6') to 6.00 cm ('CO 3' x 'Dwd-T-3').

Per cent average heterosis ranged from -15.82 to 10.28 per cent. Out of 25 crosses, one and nine crosses showed significant positive and negative heterosis over mid parent respectively. All twelve significant crosses had negative heterosis over better parent. And heterosis over commercial check varied from -10.60 ('CO-3' x 'Dwd-T-6') to 19.28 ('CO-3' x 'Dwd-T-3') per cent.

4.2.1.2.7 Pericarp thickness (cf. Table 28)

The range in parents was from 0.34 cm ['Megha (L-15')] to 0.58 cm ('Dwd-T-3'). The maximum pericarp thickness was noticed in 'Pant-T-10' x 'KS-227' (0.61 cm) and minimum in 'Megha (L-15)' x 'VR-35' and 'Megha (L-15) x 'Dwd-T-6' and 'Megha (L-15)' x 'VR-3' (0.39 cm) among the hybrids.

The significant heterosis over mid parent was exhibited by one hybrid. Whereas, heterosis over better parent was significant in five and one crosses for negative and positive direction.

Table 25. *Per se* performance and magnitude of heterosis for plant height and number of branches per plant

Sl.	Parents and F_1 hybrid	Plant height (cm)				Number of branches per plant			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se* value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	90.66				3.40			
2	DVRT-2	97.45				3.89			
3	H-24	70.39				3.21			
4	Megha L-15	81.00				3.30			
5	PANT-T-10	84.63				3.00			
	Testers								
1	VR-35	101.71				3.63			
2	KS-227	108.78				3.48			
3	Dwd-T-1	75.78				2.78			
4	Dwd-T-3	93.44				4.04			
5	Dwd-T-6	70.85				3.84			
	F_1 hybrids								
1	CO-3 X VR 35	87.15	-9.39 **	-14.31 **	5.47	3.32	-5.59	-8.54	6.07
2	CO-3 X KS- 227	94.92	-4.81	-12.74 **	14.87 **	2.85	-17.05 *	-17.93 *	-8.84
3	CO-3 X Dwd-T-1	78.30	-5.91	-13.63 **	-5.24	2.67	-13.75	-21.65 **	-14.80
4	CO-3 X Dwd-T-3	86.18	-6.38 *	-7.77 *	4.3	3.60	-3.40	-11.05	14.91
5	CO-3 X Dwd-T-6	71.25	-11.77 **	-21.41 **	-13.77 **	3.18	-12.24	-17.26 *	1.60
6	DVRT-2 X VR 35	87.75	-11.88 **	-13.72 **	6.19	3.11	-17.16 **	-19.90 **	-0.53
7	DVRT-2 X KS- 227	104.58	1.43	-3.85	26.56 **	3.59	-2.49	-7.63	14.70
8	DVRT-2 X Dwd-T-1	86.30	-0.36	-11.44 **	4.44	3.25	-2.40	-16.30 *	3.94
9	DVRT-2 X Dwd-T-3	92.69	-2.88	-4.88	12.17 **	3.77	-4.83	-6.68	20.55 *
10	DVRT-2 X Dwd-T-6	82.68	-1.75	-15.16 **	0.05	3.22	-16.77 **	-17.24 *	2.77
11	H-24 X VR 35	76.03	-11.64 **	-25.24 **	-7.99 *	3.54	3.61	-2.39	13.21
12	H-24 X KS- 227	74.62	-16.71 **	-31.40 **	-9.70 *	3.44	2.99	-0.96	10.01
13	H-24 X Dwd-T-1	76.92	5.25	1.51	-6.91	3.01	0.39	-6.33	-3.94
14	H-24 X Dwd-T-3	83.65	2.12	-10.47 **	1.23	3.45	-4.96	-14.76 *	10.12
15	H-24 X Dwd-T-6	76.74	8.66 *	8.31	-7.13	3.47	-1.70	-9.80	10.76
16	Megha (L-15) X VR 35	80.69	-11.67 **	-20.66 **	-2.35	3.21	-7.31	-11.57	2.56
17	Megha (L-15) X KS- 227	85.63	-9.76 **	-21.28 **	3.62	3.59	5.91	3.16	14.59
18	Megha (L-15) X Dwd-T-1	80.48	2.67	-0.64	-2.61	3.11	2.36	-5.66	-0.64
19	Megha (L-15) X Dwd-T-3	89.75	2.91	-3.95	8.62 *	3.56	-3.00	-11.95	13.74
20	Megha (L-15) X Dwd-T-6	81.07	6.78	0.09	-1.89	3.38	-5.32	-12.06	7.99
21	Pant-T-10 X VR 35	86.84	-6.79 *	-14.61 **	5.09	3.43	3.52	-5.51	9.58
22	Pant-T-10 X KS- 227	87.86	-9.15 **	-19.23 **	6.32	3.58	10.71	3.07	14.48
23	Pant-T-10 X Dwd-T-1	87.18	8.70 *	3.01	5.5	3.12	7.91	4.00	-0.43
24	Pant-T-10 X Dwd-T-3	91.85	3.16	-1.71	11.15 **	3.86	9.56	-4.62	23.22 **
25	Pant-T-10 X Dwd-T-6	85.19	9.58 *	0.66	3.09	3.76	10.04	-2.08	20.23 *
	ARTH-3 (Comercial check)	82.63				3.13			
	Megha (L-15) (Local check)	81.00				3.30			
	Mean	85.26	-2.78	-10.18	2.45	3.38	-2.44	-8.86	7.43
	Minimum	70.39	-16.71	-31.40	-13.77	2.67	-17.16	-21.65	-14.80
	Maximum	108.78	9.58	8.31	26.57	4.04	10.71	4.00	23.22
	No of F_1's better than CC	16.00				19			
	No of F_1's better than OPC	17.00				15			
	S.Ed. ±		2.80	3.24	3.24		0.23	0.26	
	CD at 5 %		5.64	6.51	6.51		0.45	0.52	
	CD at 1 %		7.52	8.68	8.68		0.60	0.69	

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 26. *Per se* performance and magnitude of heterosis for days to 50% flowering and number of fruits per cluster.

Sl.	Parents and F_1 hybrid	Days to 50% flowering				Number of fruits per cluster			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se* value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	37.67				3.15			
2	DVRT-2	42.00				2.63			
3	H-24	37.00				2.82			
4	Megha L-15	34.10				2.89			
5	PANT-T-10	37.11				3.74			
	Testers								
1	VR-35	36.00				4.04			
2	KS-227	35.33				3.07			
3	Dwd-T-1	36.41				3.11			
4	Dwd-T-3	38.00				3.59			
5	Dwd-T-6	29.30				3.78			
	F_1 hybrids								
1	CO-3 X VR 35	36.65	-0.49	-2.69	-0.23	3.22	-10.52	-20.38 **	-15.65 *
2	CO-3 X KS- 227	35.85	-1.78	-4.82	-2.41	3.20	2.84	1.48	-16.17 *
3	CO-3 X Dwd-T-1	33.30	-10.09 **	-11.59 **	-9.35 **	2.82	-10.06	-10.58	-26.14 **
4	CO-3 X Dwd-T-3	36.77	-2.81	-3.24	0.09	3.23	-4.25	-10.12	-15.38 *
5	CO-3 X Dwd-T-6	33.46	-0.08	-11.18 **	-8.93 **	3.20	-7.51	-15.18	-16.00 *
6	DVRT-2 X VR 35	41.73	7.00 **	-0.64	13.59 **	2.96	-11.34	-26.82 **	-22.47 **
7	DVRT-2 X KS- 227	40.14	3.82	-4.42	9.27 **	2.97	4.15	-3.26	-22.20 **
8	DVRT-2 X Dwd-T-1	39.85	1.65	-5.11	8.48 **	2.92	1.68	-6.21	-23.43 **
9	DVRT-2 X Dwd-T-3	44.00	10.00 **	4.76	19.77 **	3.22	3.54	-10.31	-15.56 *
10	DVRT-2 X Dwd-T-6	35.00	-1.82	-16.67 **	-4.73	3.11	-2.91	-17.65 *	-18.44 *
11	H-24 X VR 35	36.48	-0.05	-1.41	-0.70	3.34	-2.67	-17.33 *	-12.41
12	H-24 X KS- 227	34.17	-5.52 *	-7.65 *	-6.99 *	3.21	9.11	4.78	-15.73 *
13	H-24 X Dwd-T-1	37.05	0.93	0.13	0.84	2.85	-3.87	-8.35	-25.17 **
14	H-24 X Dwd-T-3	38.85	3.60	2.24	5.75	3.17	-1.04	-11.61	-16.78 *
15	H-24 X Dwd-T-6	36.33	9.60 **	-1.80	-1.10	3.15	-4.44	-16.50 *	-17.31 *
16	Megha (L-15) X VR 35	34.92	-0.36	-2.99	-4.94	3.15	-9.19	-22.11 **	-17.48 *
17	Megha (L-15) X KS- 227	33.44	-3.69	-5.37	-8.98 **	3.25	9.12	5.98	-14.77
18	Megha (L-15) X Dwd-T-1	34.73	-1.50	-4.62	-5.47	2.97	-1.05	-4.60	-22.12 **
19	Megha (L-15) X Dwd-T-3	35.89	-0.45	-5.56	-2.31	3.51	8.44	-2.14	-7.87
20	Megha (L-15) X Dwd-T-6	30.58	-3.53	-10.32 **	-16.76 **	2.97	-11.00	-21.45 **	-22.20 **
21	Pant-T-10 X VR 35	36.85	0.80	-0.71	0.30	3.90	0.21	-3.55	2.19
22	Pant-T-10 X KS- 227	35.81	-1.14	-3.50	-2.52	3.52	3.38	-5.89	-7.78
23	Pant-T-10 X Dwd-T-1	36.04	-1.97	-2.89	-1.91	3.86	12.80	3.39	1.31
24	Pant-T-10 X Dwd-T-3	39.00	3.85	2.63	6.16	3.92	7.01	4.91	2.80
25	Pant-T-10 X Dwd-T-6	33.26	0.16	-10.38 **	-9.47 **	3.97	5.68	5.12	4.11
	ARTH-3 (Comercial check)	36.74				3.81			
	Megha (L-15) (Local check)	34.10				2.89			
	Mean	36.32	0.24	-4.31	0.74	3.27	-0.48	-8.33	-14.35
	Minimum	29.30	-10.09	-16.67	-15.38	2.63	-11.34	-26.82	-26.07
	Maximum	44.00	10.00	4.76	21.75	4.04	12.80	5.98	4.20
	No of F_1's better than CC	9				4			
	No of F_1's better than OPC	20				23			
	S.Ed. $\pm$		0.98	1.13			0.25	0.29	
	CD at 5 %		1.97	2.28			0.50	0.58	
	CD at 1 %		2.63	3.04			0.67	0.77	

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 27. *Per se* performance and magnitude of heterosis for fruit length and fruit width

Sl.	Parents and F_1 hybrid	Fruit length (cm)				Fruit width (cm)			
		per se	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se*	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	3.74				5.63			
2	DVRT-2	4.27				6.64			
3	H-24	4.32				5.11			
4	Megha L-15	4.81				5.19			
5	PANT-T-10	4.11				5.01			
	Testers								
1	VR-35	5.53				5.48			
2	KS-227	5.07				4.45			
3	Dwd-T-1	4.37				5.27			
4	Dwd-T-3	4.63				6.18			
5	Dwd-T-6	4.22				5.05			
	F_1 hybrids								
1	CO-3 X VR 35	4.61	-0.50	-16.59 **	0.51	5.18	-6.69 *	-7.93 *	3.05
2	CO-3 X KS- 227	3.90	-11.50 **	-23.13 **	-14.97 **	4.52	-10.32 **	-19.72 **	-10.14 *
3	CO-3 X Dwd-T-1	4.01	-1.15	-8.24	-12.65 **	5.08	-6.76 *	-9.77 **	0.99
4	CO-3 X Dwd-T-3	4.70	12.27 **	1.51	2.40	6.00	1.61	-2.91	19.28 **
5	CO-3 X Dwd-T-6	3.66	-7.92	-13.12 **	-20.13 **	4.50	-15.82 **	-20.13 **	-10.60 **
6	DVRT-2 X VR 35	4.57	-6.77	-17.37 **	-0.44	5.49	-9.43 **	-17.36 **	9.15 *
7	DVRT-2 X KS- 227	4.21	-9.95 **	-17.08 **	-8.28	5.37	-3.19	-19.17 **	6.76
8	DVRT-2 X Dwd-T-1	4.25	-1.58	-2.67	-7.34	5.69	-4.51	-14.40 **	13.06 **
9	DVRT-2 X Dwd-T-3	4.46	0.34	-3.53	-2.69	5.98	-6.78 *	-10.04 **	18.82 **
10	DVRT-2 X Dwd-T-6	4.15	-2.28	-2.89	-9.59 *	5.29	-9.60 **	-20.42 **	5.10
11	H-24 X VR 35	4.88	-0.78	-11.64 **	6.47	5.34	0.82	-2.55	6.16
12	H-24 X KS- 227	4.77	1.60	-5.98	4.00	5.27	10.28 **	3.13	4.84
13	H-24 X Dwd-T-1	4.30	-0.88	-1.45	-6.18	5.22	0.58	-0.89	3.78
14	H-24 X Dwd-T-3	4.41	-1.38	-4.68	-3.85	5.26	-6.85 *	-14.89 **	4.57
15	H-24 X Dwd-T-6	4.43	3.75	2.55	-3.49	4.98	-2.03	-2.61	-0.99
16	Megha (L-15) X VR 35	4.82	-6.71 *	-12.73 **	5.16	5.11	-4.28	-6.81	1.52
17	Megha (L-15) X KS-227	4.90	-0.88	-3.42	6.83	5.15	6.78	-0.83	2.32

18	Megha (L-15) X Dwd-T-1	4.75	3.41	-1.39	3.49	5.23	0.03	-0.70	3.98
19	Megha (L-15) X Dwd-T-3	4.88	3.32	1.32	6.32	5.26	-7.48 *	-14.89 **	4.57
20	Megha (L-15) X Dwd-T-6	4.41	-2.33	-8.38 *	-3.85	5.17	0.94	-0.39	2.78
21	Pant-T-10 X VR 35	4.56	-5.39	-17.49 **	-0.58	5.15	-1.84	-6.08	2.32
22	Pant-T-10 X KS-227	4.44	-3.27	-12.42 **	-3.13	4.96	4.83	-1.00	-1.46
23	Pant-T-10 X Dwd-T-1	4.18	-1.42	-4.27	-8.87 *	5.20	1.30	-1.20	3.45
24	Pant-T-10 X Dwd-T-3	4.49	2.75	-2.95	-2.11	5.47	-2.21	-11.49 **	8.75 *
25	Pant-T-10 X Dwd-T-6	4.17	0.12	-1.11	-9.08 *	4.75	-5.57	-6.00	-5.57
	ARTH-3 (Comercial check)	4.59				5.03			
	Megha (L-15) (Local check)	4.81				5.19			
	Mean	4.47	-1.18	-6.59	-3.35	5.27	-3.05	-8.36	3.86
	Minimum	3.66	-13.67	-23.13	-20.19	4.45	-15.82	-20.42	-10.60
	Maximum	5.53	12.27	4.53	6.75	6.64	10.28	3.13	19.28
	No of F_1's better than CC	8				20			
	No of F_1's better than OPC	4				14			
	S.Ed. $\pm$		0.17	0.20			0.17	0.19	
	CD at 5 %		0.34	0.40			0.34	0.39	
	CD at 1 %		0.46	0.53			0.45	0.52	

*, **: Indicates significant at 5 and 1% level of probability respectively

4.2.1.2.8 Number of locules per fruit (cf. Table 28)

The greater range of variation was observed among the parents 2.77 ('Dwd-T-6') to 5.67 (DVRT-2). Hybrids varied from 2.78 to 5.37. The commercial check had 4.11 locules per fruit.

Among hybrids, average heterosis ranged from -11.70 to 23.28 per cent and heterobeltiosis ranged from -30.26 to 20.65 per cent. Out of 25 crosses, four and seven crosses showed significant positive and negative heterosis over commercial check respectively.

4.2.1.2.9 Total soluble solids (cf. Table 29)

TSS exhibited wider variation among the parents 3.50 ('H-24') to 4.40 per cent ('VR-35'). The F_1s showed wider range of variation from 3.23 per cent ('CO-3' x 'Dwd-T-3') to 4.33 per cent ('Megha (L-15)' x 'VR-35').

Per cent average heterosis ranged from -13.34 to 8.48 per cent. There were one and two hybrids exhibited significant positive and negative heterosis over mid parents respectively. There were nine hybrids exhibited significant negative heterosis over better parents. There were fifteen hybrids that exhibited significant negative heterosis over commercial check.

4.2.1.2.10 Single fruit weight (cf. Table 29)

Minimum single fruit weight was recorded in 'H-24' (57.56 g) and maximum in 'DVRT-2'(114.63 g) while, among the crosses 'CO-3' x 'Dwd-T-6' weighed minimum (62.82 g) as against maximum weight of fruit in cross 'DVRT-2' x 'VR-35' weighed minimum (107.18 g).

Mid parent heterosis exhibited by the hybrids varied from -24.55 to 14.64 per cent. Out of 25 hybrids, one and sixteen crosses had significant negative and positive heterosis over better parent. Four and sixteen crosses had significant positive and negative heterosis over commercial check.

4.2.1.2.11 Number of fruits per plant (cf. Table 30)

Among the parents, 'H-24' (24.81) produced least number of fruits per plant and 'Dwd-T-6' (68.37) produced highest fruits per plant. The F_1s showed variation which ranged from 35.10 ('H-24' x 'KS-227') to 70.83 ('Pant-T-10' x 'Dwd-T-6').

With regard to heterosis over mid parent and better parent, the fruits ranged from -10.97 to 33.28 and -25.74 to 16.59 per cent respectively. The maximum heterosis over commercial check was manifested by Pant-T-10' x 'Dwd-T-6' (48.71%).

4.2.1.2.12 Yield per plant (cf. Table 30)

The total yield per plant among the parents ranged from 1.158 kg in 'H-24' to 2.116 kg in 'VR-35'.

Among the F_1s, the highest of 2.375 kg was registered by 'DVRT-2' x 'VR-35' followed by 'Pant-T-10'' x 'VR-35' (2.135 kg), 'Pant-T-10' x 'Dwd-T-6' (2.126 kg) and 'DVRT-2' x 'KS-227' (2.108 kg). Commercial check had a yield of 1.751 kg and local check 'Megha (L-15)' yielded 1.542 kg/plant.

Mid parent heterosis for total yield per plant ranged from -1.23 to 40.01 per cent. There were fourteen crosses which exhibited significant positive heterosis over their mid parents out of 25 crosses. Heterosis over better parent and commercial check ranged from -22.00 to 18.01 per cent and -12.32 to 35.68 respectively. Seven hybrids 'DVRT-2' x 'VR-35' (35.68%), 'Pant-T-10' x 'VR-35' (21.93%), 'Pant-T-10' x 'Dwd–T-6' (21.46%), 'DVRT-2' x 'KS-227' (20.39%), 'Pant-T-10' x 'Dwd-T-3' (18.51%), 'DVRT-2' x 'Dwd-T-6' (16.13%) and 'Megha (L-15)' x 'Dwd-T-3' (16.30%) with 2.375, 2.135, 2.126, 2.108, 2.075, 2.033 and 2.036 kg/plant respectively exhibited positive significant heterosis over commercial check .

4.2.1.2.13 Yield per hectare (cf. Table 31)

The total yield per hectare among the parents ranged from 21.97 t/ha in 'H-24' to 44.63 t/ha in 'VR-35'.

Table 28 . *Per se* performance and magnitude of heterosis for fruit pericarp thickness and number of locules per fruits.

Sl.	Parents and F_1 hybrid	Pericarp thickness (cm)				Number of locules per fruit			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se* value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	0.45				4.23			
2	DVRT-2	0.51				5.67			
3	H-24	0.44				4.46			
4	Megha L-15	0.34				3.48			
5	PANT-T-10	0.50				2.89			
	Testers								
1	VR-35	0.54				3.51			
2	KS-227	0.50				3.41			
3	Dwd-T-1	0.51				4.92			
4	Dwd-T-3	0.58				5.60			
5	Dwd-T-6	0.41				2.77			
	F_1 hybrids								
1	CO-3 X VR 35	0.48	-3.05	-11.18	-6.54	3.68	-4.91	-13.07	-10.53
2	CO-3 X KS- 227	0.43	-9.47	-14.57	-15.69 *	3.62	-5.41	-14.57 *	-12.07
3	CO-3 X Dwd-T-1	0.49	2.10	-3.95	-4.58	4.81	5.14	-2.17	16.94 *
4	CO-3 X Dwd-T-3	0.47	-9.39	-20.00 **	-8.50	4.78	-2.81	-14.65 **	16.13 *
5	CO-3 X Dwd-T-6	0.41	-4.28	-8.21	-19.61 *	3.27	-6.67	-22.83 **	-20.58 **
6	DVRT-2 X VR 35	0.52	-0.96	-3.73	1.31	4.46	-2.80	-21.34 **	8.43
7	DVRT-2 X KS- 227	0.50	-1.65	-1.97	-2.61	4.56	0.48	-19.52 **	10.94
8	DVRT-2 X Dwd-T-1	0.48	-4.61	-4.61	-5.23	5.17	-2.27	-8.76	25.77 **
9	DVRT-2 X Dwd-T-3	0.57	4.59	-2.29	11.76	5.37	-4.62	-5.23	30.63 **
10	DVRT-2 X Dwd-T-6	0.43	-6.18	-15.13 *	-15.69 *	4.33	2.73	-23.57 **	5.35
11	H-24 X VR 35	0.49	1.37	-8.07	-3.27	3.97	-0.33	-10.99	-3.48
12	H-24 X KS- 227	0.49	4.96	-1.99	-3.27	4.07	3.39	-8.74	-1.05
13	H-24 X Dwd-T-1	0.50	5.30	-1.97	-2.61	4.43	-5.58	-9.97	7.62
14	H-24 X Dwd-T-3	0.47	-8.50	-20.00 **	-8.50	4.44	-11.70 *	-20.67 **	7.94
15	H-24 X Dwd-T-6	0.43	0.79	-2.29	-16.34 *	3.46	-4.34	-22.50 **	-15.96 *
16	Megha (L-15) X VR 35	0.39	-10.61	-26.71 **	-22.88 **	3.68	5.49	5.04	-10.45
17	Megha (L-15) X KS- 227	0.42	-1.57	-17.22 *	-18.30 *	3.27	-5.18	-6.04	-20.58 **
18	Megha (L-15) X Dwd-T-1	0.44	3.53	-13.16	-13.73	4.27	1.75	-13.15 *	3.81
19	Megha (L-15) X Dwd-T-3	0.49	5.04	-16.57 *	-4.58	4.44	-2.20	-20.73 **	7.86
20	Megha (L-15) X Dwd-T-6	0.39	2.65	-5.69	-24.18 **	2.78	-11.05	-20.13 *	-32.50 **
21	Pant-T-10 X VR 35	0.52	0.96	-2.48	2.61	3.29	2.97	-6.08	-19.94 **
22	Pant-T-10 X KS- 227	0.61	20.93 **	20.53 **	18.95 *	3.71	17.61 *	8.59	-9.89
23	Pant-T-10 X Dwd-T-1	0.51	1.99	1.32	0.65	3.74	-4.10	-23.86 **	-9.00
24	Pant-T-10 X Dwd-T-3	0.53	-2.77	-9.71	3.27	3.90	-8.01	-30.26 **	-5.11
25	Pant-T-10 X Dwd-T-6	0.46	0.37	-8.67	-10.46	3.49	23.28 *	20.65 *	-15.24 *
	ARTH-3 (Comercial check)	0.51				4.11			
	Megha (L-15) (Local check)	0.34				3.48			
	Mean	0.47	-0.35	-7.94	-6.73	4.04	-0.76	-12.18	-1.72
	Minimum	0.34	-10.61	-26.71	-24.18	2.77	-11.70	-30.26	-32.44
	Maximum	0.61	20.93	20.53	18.95	5.67	23.28	20.65	30.74
	No of F_1's better than CC	6				11			
	No of F_1's better than OPC	25				20			
	S.Ed. $\pm$		0.03	0.04			0.25	0.28	
	CD at 5 %		0.07	0.08			0.50	0.57	
	CD at 1 %		0.09	0.10			0.66	0.76	

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 29. *Per se* performance and magnitude of heterosis for total soluble solids and single fruit weight.

Sl.	Parents and F_1 hybrid	Total soluble solids (%)			Single fruit weight (g)				
		per se value	eterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se* svalue	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	3.85				67.15			
2	DVRT-2	3.60				114.63			
3	H-24	3.50				57.56			
4	Megha L-15	4.29				60.88			
5	PANT-T-10	4.23				75.77			
	Testers								
1	VR-35	4.40				99.41			
2	KS-227	3.84				63.44			
3	Dwd-T-1	3.89				78.41			
4	Dwd-T-3	3.59				106.46			
5	Dwd-T-6	4.15				71.93			
	F_1 hybrids								
1	CO-3 X VR 35	3.89	-5.69	-11.58 **	-9.25 *	82.85	-0.52	-16.66 **	-0.06
2	CO-3 X KS-227	3.70	-3.85	-3.98	-13.75 **	66.25	1.46	-1.34	-20.08 **
3	CO-3 X Dwd-T-1	3.77	-2.63	-3.08	-12.12 **	70.18	-3.56	-10.49 *	-15.33 **
4	CO-3 X Dwd-T-3	3.23	-13.34 **	-16.26 **	-24.79 **	92.63	6.71	-12.99 **	11.75 *
5	CO-3 X Dwd-T-6	3.69	-7.75 *	-11.01 **	-13.99 **	62.82	-9.66	-12.67 *	-24.22 **
6	DVRT-2 X VR 35	3.98	-0.58	-9.69 *	-7.30	107.18	0.15	-6.50	29.30 **
7	DVRT-2 X KS- 227	3.68	-1.16	-4.34	-14.30 **	91.77	3.07	-19.95 **	10.70 *
8	DVRT-2 X Dwd-T-1	3.51	-6.32	-9.85 *	-18.26 **	72.83	-24.55 **	-36.47 **	-12.14 *
9	DVRT-2 X Dwd-T-3	3.62	0.60	0.56	-15.70 **	102.73	-7.07 *	-10.38 **	23.93 **
10	DVRT-2 X Dwd-T-6	3.85	-0.47	-7.07	-10.18 *	89.27	-4.30	-22.13 **	7.69
11	H-24 X VR 35	3.74	-5.23	-14.99 **	-12.74 **	66.25	-15.58 **	-33.35 **	-20.07 **
12	H-24 X KS-227	3.51	-4.27	-8.59	-18.10 **	66.66	10.19	5.08	-19.58 **
13	H-24 X Dwd-T-1	3.50	-5.32	-10.11 *	-18.49 **	70.44	3.62	-10.16 *	-15.02 **
14	H-24 X Dwd-T-3	3.46	-2.30	-3.62	-19.27 **	68.78	-16.13 **	-35.39 **	-17.03 **
15	H-24 X Dwd-T-6	3.66	-4.23	-11.74 **	-14.69 **	63.70	-1.60	-11.43 *	-23.15 **
16	Megha (L-15) X VR 35	4.33	-0.42	-1.67	0.93	67.20	-16.15 **	-32.40 **	-18.93 **
17	Megha (L-15) X KS- 227	4.03	-0.94	-6.13	-6.06	71.26	14.64 **	12.33 *	-14.03 **
18	Megha (L-15) X Dwd-T-1	3.95	-3.38	-7.92 *	-7.85 *	72.51	4.11	-7.52	-12.53 *
19	Megha (L-15) X Dwd-T-3	4.04	2.37	-5.98	-5.91	72.19	-13.72 **	-32.19 **	-12.91 **
20	Megha (L-15) X Dwd-T-6	4.20	-0.39	-2.10	-2.02	66.74	0.50	-7.21	-19.49 **

21	Pant-T-10 X VR 35	4.29	-0.69	-2.65	-0.08	83.59	-4.56	-15.91 **	0.84
22	Pant-T-10 X KS- 227	3.99	-1.16	-5.67	-6.99	71.07	2.11	-6.20	-14.26 **
23	Pant-T-10 X Dwd-T-1	4.08	0.49	-3.55	-4.90	80.16	3.99	2.24	-3.29
24	Pant-T-10 X Dwd-T-3	4.24	8.48 *	0.32	-1.09	92.92	1.98	-12.72 **	12.10 *
25	Pant-T-10 X Dwd-T-6	4.20	0.20	-0.79	-2.18	71.89	-2.66	-5.13	-13.28 **
	ARTH-3 (Comercial check)	4.29				82.89			
	Megha (L-15) (Local check)	4.29				60.88			
	Mean	3.89	-2.32	-6.46	-10.36	77.39	-2.70	-13.58	-7.16
	Minimum	3.23	-13.34	-16.26	-24.79	57.56	-24.55	-36.47	-24.22
	Maximum	4.40	8.48	0.56	0.93	114.63	14.64	12.33	29.31
	No of F_1's better than CC	1				7			
	No of F_1's better than OPC	1				25			
	S.Ed. $\pm$		0.14	0.17			3.36	3.88	
	CD at 5 %		0.29	0.33			6.75	7.80	
	CD at 1 %		0.38	0.44			9.01	10.40	

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 30. *Per se* performance and magnitude of heterosis for number of fruits per plant and yield per plant.

Sl.	Parents and F_1 hybrid	Number of fruits per plant				Yield per plant (kg)			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se* value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	30.04				1.200			
2	DVRT-2	26.04				1.277			
3	H-24	24.81				1.158			
4	Megha L-15	49.11				1.542			
5	PANT-T-10	37.91				1.577			
	Testers								
1	VR-35	51.29				2.116			
2	KS-227	39.77				1.786			
3	Dwd-T-1	44.88				1.743			
4	Dwd-T-3	47.33				1.963			
5	Dwd-T-6	68.37				1.966			
	F_1 hybrids								
1	CO-3 X VR 35	44.33	9.03	-13.56 **	-6.91	1.829	10.30	-13.58 *	4.47
2	CO-3 X KS- 227	42.78	22.56 **	7.56	-10.18 *	1.926	28.98 **	7.82	10.00
3	CO-3 X Dwd-T-1	35.77	-4.51	-20.30 **	-24.90 **	1.535	4.32	-11.93	-12.32
4	CO-3 X Dwd-T-3	42.18	9.04	-10.87 *	-11.44 *	1.984	25.43 **	1.05	13.31
5	CO-3 X Dwd-T-6	56.15	14.12 **	-17.87 **	17.89 **	1.646	3.96	-16.29 *	-6.00
6	DVRT-2 X VR 35	45.90	18.71 **	-10.52 *	-3.63	2.375	40.01 **	12.24 *	35.68 **
7	DVRT-2 X KS- 227	36.82	11.89	-7.43	-22.70 **	2.108	37.64 **	18.01 *	20.39 **
8	DVRT-2 X Dwd-T-1	35.95	1.38	-19.90 **	-24.52 **	1.716	13.63	-1.57	-2.00
9	DVRT-2 X Dwd-T-3	36.90	0.60	-22.03 **	-22.52 **	2.000	23.49 **	1.90	14.26
10	DVRT-2 X Dwd-T-6	54.86	16.23 **	-19.75 **	15.19 **	2.033	25.39 **	3.41	16.13 *
11	H-24 X VR 35	41.88	10.07	-18.34 **	-12.06 *	1.651	0.82	-22.00 **	-5.71
12	H-24 X KS- 227	35.15	8.86	-11.62 *	-26.19 **	1.712	16.33 *	-4.12	-2.19
13	H-24 X Dwd-T-1	38.85	11.47 *	-13.45 *	-18.44 **	1.850	27.57 **	6.16	5.69
14	H-24 X Dwd-T-3	38.03	5.42	-19.65 **	-20.16 **	1.625	4.11	-17.24 **	-7.20
15	H-24 X Dwd-T-6	50.77	8.97 *	-25.74 **	6.60	1.791	14.64 *	-8.92	2.28
16	Megha (L-15) X VR 35	54.11	7.78	5.49	13.61 **	1.969	7.67	-6.95	12.49
17	Megha (L-15) X KS- 227	45.44	2.25	-7.47	-4.58	1.913	14.98 *	7.11	9.27
18	Megha (L-15) X Dwd-T-1	42.56	-9.45 *	-13.34 **	-10.65 *	1.811	10.27	3.90	3.45
19	Megha (L-15) X Dwd-T-3	51.44	6.68	4.74	8.01	2.036	16.19 *	3.72	16.30 *
20	Megha (L-15) X Dwd-T-6	52.29	-10.97 **	-23.51 **	9.80 *	1.732	-1.23	-11.89	-1.05
21	Pant-T-10 X VR 35	46.58	4.43	-9.19 *	-2.20	2.135	15.61 *	0.87	21.93 **
22	Pant-T-10 X KS- 227	46.37	19.39 **	16.59 **	-2.63	1.877	11.66	5.11	7.24
23	Pant-T-10 X Dwd-T-1	52.22	26.15 **	16.35 **	9.65 *	1.837	10.67	5.39	4.93
24	Pant-T-10 X Dwd-T-3	50.66	18.87 **	7.05	6.38	2.075	17.22 **	5.69	18.51 *
25	Pant-T-10 X Dwd-T-6	70.83	33.28 **	3.60	48.71 **	2.126	20.04 **	8.16	21.46 **
	ARTH-3 (Comercial check)	47.63				1.751			
	Megha (L-15) (Local check)	49.11				1.542			
	Mean	45.00	9.69	-8.93	-3.52	1.808	15.99	-0.96	8.03
	Minimum	24.81	-10.97	-25.74	-26.19	1.158	-1.23	-22.00	-12.34
	Maximum	70.83	33.28	16.59	48.70	2.375	40.01	18.01	35.66
	No of F_1's better than CC	9				18			
	No of F_1's better than OPC	9				24			
	S.Ed. $\pm$		1.97	2.28			0.11	0.13	
	CD at 5 %		3.97	4.58			0.22	0.25	
	CD at 1 %		5.29	6.11			0.29	0.34	

*, **: Indicates significant at 5 and 1% level of probability respectively

Among the F_1s, the highest of 48.47 t/ha was registered by 'DVRT-2' x 'VR-35' followed by 'Pant-T-10'' x 'VR-35' (45.65 t/ha), 'DVRT-2' x 'KS-227' (45.09t/ha), Pant-T-10' x 'Dwd-T-3'(43.74 t/ha), 'DVRT-2' x 'Dwd-T-6'(43.71 t/ha), 'CO-3' x 'Dwd-T-3' (43.47 t/ha) and 'Pant-T-10' x 'Dwd-T-6' (42.78 t/ha) . Commercial check had a yield of 35.80 t/ha and local check 'Megha (L-15)' yielded 28.36 t/ha.

Mid parent heterosis for total yield per plant ranged from -1.25 to 44.03 per cent. There were twenty crosses which exhibited significant positive heterosis over their mid parents out of 25 crosses. Heterosis over better parent and commercial check ranged from -26.33 to 16.99 and -8.14 to 35.39 per cent respectively. Seven hybrids 'DVRT-2' x 'VR-35' (35.39%), 'Pant-T-10' x 'VR-35' (27.54%), 'DVRT-2' x 'KS-227'(25.97), Pant-T-10' x 'Dwd–T-3' (22.19%), 'DVRT-2' x 'Dwd-T-6' (22.10) 'CO-3 X Dwd-T-3' (21.43) 'Pant-T-10' x 'Dwd-T-6' (19.50%), and 'Megha (L-15)' x 'Dwd-T-3' (18.87%) with 48.47, 45.65, 45.09, 43.74, 43.71, 43.47, 42.78 and 42.55 kg/plant respectively exhibited positive significant heterosis over commercial check .16 hybrids showed positive significant commercial heterosis . In all 22 and 25 hybrids recorded higher yield than commercial check and local check respectively. High yielding hybrids with high positive heterosis over commercial check are 'DVRT-2' x 'VR-35' (35.39%), 'Pant-T-10'' x 'VR-35' (27.54%), 'DVRT-2' x 'KS-227' (25.97%), Pant-T-10' x 'Dwd-T-3'(22.19%), 'DVRT-2' x 'Dwd-T-6'(22.10%), 'CO-3' x 'Dwd-T-3' (21.43%) and 'Pant-T-10' x 'Dwd-T-6' (19.50%).

4.2.1.2.14 Disease incidence (cf. Table 31 to Table 34)

Per se values and heterosis for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence of F_1 hybrids in comparison to their mid parent, better parent and commercial check has been presented in above mentioned tables.

The average heterosis of all crosses for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence is 9.02, 49.58, -2.51, -23.94, -68.00, and -41.24 per cent respectively (Appendix IV).

Among the 25 hybrids two, three, none, none, none, and none had significant negative heterosis over commercial check for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence.

Graphical presentation of average heterosis for hybrids evaluated for disease incidence and other growth, yield and quality parameters is presented in Fig. 10.

4.2.2 COMBINING ABILITY

4.2.2.1 Analysis of variance

The analysis of variance for combining ability with respect to 19 traits is presented in Table 35.

Crosses showed highly significant differences for all the traits except for number of branches per plant which was just significant. Differences among lines were significant only for 14 traits out of 19 except for early blight, late blight, powdery mildew, tomato leaf curl virus and tomato spotted wilt incidence. Differences testers were significant only for twelve traits out of 19 except for yield per plant, yield per hectare, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt incidence. For all the characters line x tester variance was significant except five i.e., number of branches per plant, number of fruits per cluster, fruit length, pericarp thickness and TSS.

Contribution of line was more for plant height, days to 50 % flowering, number of fruits per cluster, fruit length, pericarp thickness, TSS, single fruit weight, and yield per plant. While, maximum contribution recorded by testers for number of branches per plant, fruit width, number of locules per fruit, and early blight. The contribution of line x tester was of higher in magnitude than either line or tester for yield per hectare, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus, and *Sclerotium* wilt incidence.

The estimates of GCA variance was higher for plant height, days to 50% flowering, single fruit weight, and number of fruits per plant.

The estimates of SCA variance were greater in magnitude than those of GCA variance for yield per hectare, powdery mildew, tomato spotted wilt virus, and *Sclerotium* wilt virus.

Table 31. *Per se* performance and magnitude of heterosis for yield per hectare and incidence of early blight.

Sl.	Parents and F_1 hybrid	Yield per hectare (t/ha)				Early Blight			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se* value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	26.89				1.51			
2	DVRT-2	24.07				2.82			
3	H-24	21.97				2.12			
4	Megha L-15	28.36				2.73			
5	PANT-T-10	37.71				2.89			
	Testers								
1	VR-35	44.63				0.81			
2	KS-227	38.54				0.17			
3	Dwd-T-1	38.35				2.48			
4	Dwd-T-3	39.48				1.96			
5	Dwd-T-6	40.07				2.26			
	F_1 hybrids								
1	CO-3 X VR 35	40.14	12.25 **	-10.07 *	12.13 *	1.29	11.65	-14.16	-39.84 *
2	CO-3 X KS- 227	40.51	23.84 **	5.11	13.18 *	1.66	97.62 *	10.18	-22.79
3	CO-3 X Dwd-T-1	35.30	8.22	-7.95	-1.40	2.93	46.82 **	18.01	36.12 *
4	CO-3 X Dwd-T-3	43.47	30.98 **	10.09 *	21.43 **	3.05	75.94 **	55.71 **	41.71 *
5	CO-3 X Dwd-T-6	37.99	13.48 **	-5.19	6.13	2.85	51.46 **	26.29	32.56
6	DVRT-2 X VR 35	48.47	41.08 **	8.59 *	35.39 **	1.68	-7.62	-40.54 **	-22.02
7	DVRT-2 X KS- 227	45.09	44.03 **	16.99 **	25.97 **	1.48	-1.34	-47.64 **	-31.32
8	DVRT-2 X Dwd-T-1	38.17	22.29 **	-0.47	6.62	2.88	8.55	2.01	33.80
9	DVRT-2 X Dwd-T-3	40.92	28.78 **	3.65	14.32 **	2.71	13.61	-3.78	26.20
10	DVRT-2 X Dwd-T-6	43.71	36.28 **	9.08	22.10 **	2.78	9.65	-1.30	29.46
11	H-24 X VR 35	32.88	-1.25	-26.33 **	-8.14	2.15	46.70 *	1.42	-0.16
12	H-24 X KS- 227	37.93	25.38 **	-1.58	5.97	1.40	22.56	-33.70	-34.73
13	H-24 X Dwd-T-1	41.10	36.28 **	7.17	14.81 **	2.74	19.22	10.48	27.44
14	H-24 X Dwd-T-3	34.44	12.10 *	-12.76 **	-3.78	2.14	5.24	1.26	-0.31
15	H-24 X Dwd-T-6	37.26	20.12 **	-7.01	4.09	2.56	16.92	13.29	18.91
16	Megha (L-15) X VR 35	40.60	11.25 *	-9.03 *	13.43 *	2.11	18.91	-22.93	-2.02
17	Megha (L-15) X KS- 227	40.17	20.08 **	4.22	12.22 *	1.30	-10.55	-52.44 **	-39.53 *
18	Megha (L-15) X Dwd-T-1	39.97	19.83 **	4.22	11.65 *	2.92	12.02	6.83	35.81 *
19	Megha (L-15) X Dwd-T-3	42.55	25.44 **	7.77	18.87 **	2.28	-2.77	-16.59	6.05
20	Megha (L-15) X Dwd-T-6	36.98	8.09	-7.70	3.32	1.56	-37.34 **	-42.80 **	-27.29
21	Pant-T-10 X VR 35	45.65	10.89 **	2.29	27.54 **	1.82	-1.44	-36.91 **	-15.19
22	Pant-T-10 X KS- 227	40.44	6.08	4.93	12.98 *	2.00	30.79	-30.68 *	-6.82
23	Pant-T-10 X Dwd-T-1	38.47	1.17	0.33	7.48	2.07	-23.03	-28.49 *	-3.88
24	Pant-T-10 X Dwd-T-3	43.74	13.33 **	10.78 *	22.19 **	1.78	-26.41	-38.29 **	-17.05
25	Pant-T-10 X Dwd-T-6	42.78	10.00 *	6.75	19.50 **	1.67	-35.10 **	-42.21 **	-22.33
	ARTH-3 (Comercial check)	35.80				2.15			
	Megha (L-15) (Local check)	28.36				2.73			
	Mean	38.19	19.20	0.55	12.71	2.12	13.68	200.69	0.11
	Minimum	21.97	-1.25	-26.33	-8.15	0.17	-37.34	-30.72	-39.84
	Maximum	48.47	44.03	16.99	35.38	3.05	97.62	1055.77	41.71
	No of F_1's better than CC	22				15			
	No of F_1's better than OPC	25				18			
	S.Ed. ±		1.59	1.84			0.32	0.37	
	CD at 5 %		3.20	3.69			0.65	0.75	
	CD at 1 %		4.26	4.92			0.87	1.00	

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 32. *Per se* performance and magnitude of heterosis for incidence of Late blight and powdery mildew.

Sl.	Parents and F_1 hybrid	Late blight				Powdery mildew			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se*	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	0.43				4.11			
2	DVRT-2	0.24				4.70			
3	H-24	0.36				3.00			
4	Megha L-15	0.44				2.80			
5	PANT-T-10	0.81				3.07			
	Testers								
1	VR-35	0.34				0.76			
2	KS-227	0.27				0.70			
3	Dwd-T-1	0.51				2.74			
4	Dwd-T-3	0.63				2.86			
5	Dwd-T-6	0.83				2.31			
	F_1 hybrids								
1	CO-3 X VR 35	0.72	87.07	66.92	-23.32	2.56	4.92	-37.84 **	24.31
2	CO-3 X KS- 227	0.44	26.67	2.31	-53.00	2.92	21.38	-28.93 **	42.14 *
3	CO-3 X Dwd-T-1	0.55	16.20	7.14	-41.70	2.47	-27.92 **	-39.95 **	20.10
4	CO-3 X Dwd-T-3	0.96	81.76	53.72	2.12	3.18	-8.74	-22.61 *	54.78 **
5	CO-3 X Dwd-T-6	1.20	89.97 *	44.58	27.21	3.52	9.44	-14.51	70.99 **
6	DVRT-2 X VR 35	0.52	77.14	51.96	-45.23	2.19	-19.90	-53.48 **	6.32
7	DVRT-2 X KS- 227	0.31	20.26	15.00	-67.49 *	3.56	31.77 *	-24.26 **	73.10 **
8	DVRT-2 X Dwd-T-1	1.08	186.34 **	111.04 *	14.84	3.33	-10.57	-29.22 **	61.75 **
9	DVRT-2 X Dwd-T-3	0.67	53.26	6.38	-29.33	3.05	-19.44 *	-35.18 **	48.14 *
10	DVRT-2 X Dwd-T-6	1.30	141.61 **	56.22	37.46	3.19	-8.94	-32.06 **	55.27 **
11	H-24 X VR 35	0.26	-26.07	-28.44	-72.44 *	2.85	51.60 **	-5.00	38.57
12	H-24 X KS- 227	0.60	89.42	64.22	-36.75	2.26	21.87	-24.78	9.72
13	H-24 X Dwd-T-1	0.90	106.08 *	75.97	-4.24	2.22	-22.65	-26.00	7.94
14	H-24 X Dwd-T-3	0.55	11.78	-11.70	-41.34	2.45	-16.32	-18.22	19.29
15	H-24 X Dwd-T-6	0.97	62.01	16.47	2.47	2.90	9.03	-3.44	40.84 *
16	Megha (L-15) X VR 35	0.72	82.98	61.65	-24.03	3.15	76.78 **	12.38	53.00 *
17	Megha (L-15) X KS- 227	0.86	141.31 *	93.23	-9.19	1.83	4.47	-34.64 *	-11.02
18	Megha (L-15) X Dwd-T-1	0.44	-7.32	-13.64	-53.00	2.12	-23.47	-24.29	3.08
19	Megha (L-15) X Dwd-T-3	0.19	-64.49	-69.68	-79.86 **	2.45	-13.60	-14.55	18.96
20	Megha (L-15) X Dwd-T-6	0.54	-15.18	-34.94	-42.76	2.63	2.74	-6.19	27.71
21	Pant-T-10 X VR 35	0.53	-8.67	-35.25	-44.17	0.63	-33.62	-58.59 **	-38.25
22	Pant-T-10 X KS- 227	0.99	83.95	22.13	5.30	2.86	51.55 **	-6.85	38.90
23	Pant-T-10 X Dwd-T-1	0.97	46.23	19.26	2.83	2.46	-15.38	-19.89	19.45
24	Pant-T-10 X Dwd-T-3	0.96	32.87	17.62	1.41	2.07	-30.30 *	-32.61 *	0.49
25	Pant-T-10 X Dwd-T-6	1.00	21.70	20.48	6.01	2.49	-7.31	-18.70	21.23
	ARTH-3 (Comercial check)	0.94				2.06			
	Megha (L-15) (Local check)	0.44				2.80			
	Mean	0.66	53.48	114.06	-22.45	3.44	-0.24	98.53	25.60
	Minimum	0.19	-64.49	-57.14	-79.79	0.70	-67.07	-27.82	-69.71
	Maximum	1.30	186.34	432.88	37.94	3.56	76.78	405.92	71.15
	No of F_1's better than CC	16				1			
	No of F_1's better than OPC	3				13			
	S.Ed. $\pm$		0.23	0.27			0.35	0.41	
	CD at 5%		0.46	0.54			0.71	0.82	
	CD at 1%		0.62	0.72			0.95	1.10	

*, **: Indicates significant at 5 and 1% level of probability respectively

Table 33. *Per se* performance and magnitude of heterosis for incidence of tomato leaf curl virus and tomato spotted wilt virus.

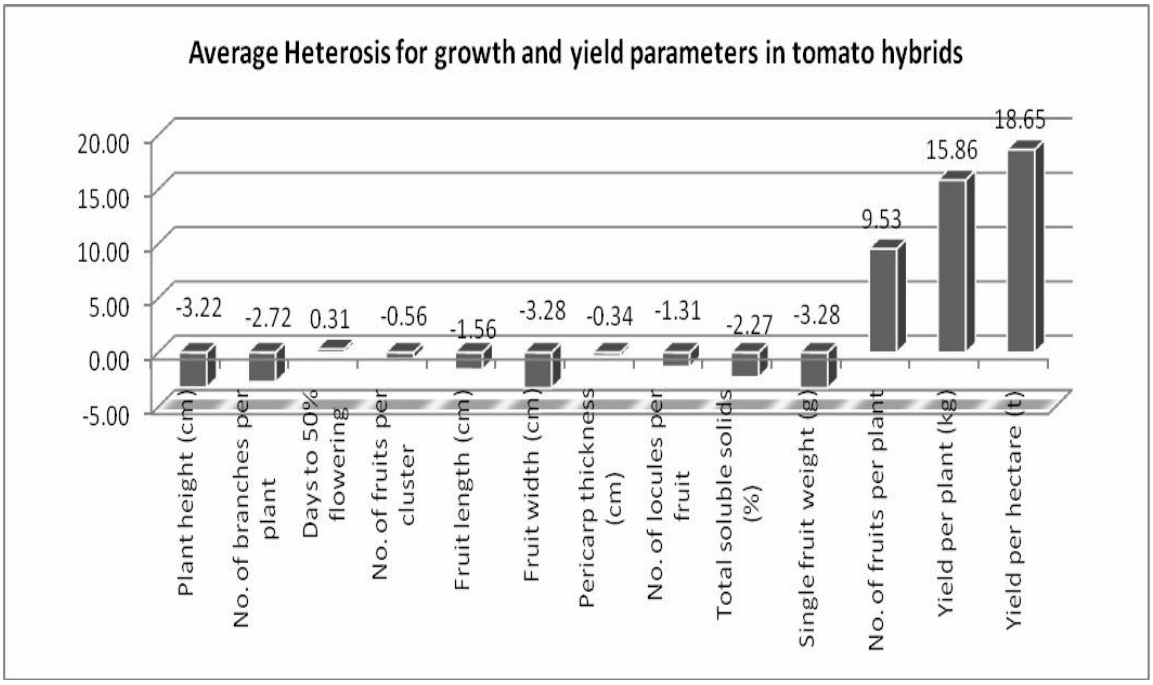
Sl.	Parents and F_1 hybrid	Tomato leaf curl virus (%)				Tomato spotted wilt virus (%)			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC	*per se* value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines								
1	CO-3	1.19				0.47			
2	DVRT-2	0.03				1.96			
3	H-24	0.68				3.51			
4	Megha L-15	6.07				0.07			
5	PANT-T-10	0.77				3.50			
	Testers								
1	VR-35	0.32				0.17			
2	KS-227	0.22				0.08			
3	Dwd-T-1	0.15				0.67			
4	Dwd-T-3	0.23				0.02			
5	Dwd-T-6	0.77				0.02			
	F_1 hybrids								
1	CO-3 X VR 35	1.71	126.55 *	43.82	103.98	0.02	-94.85	-96.48	-95.58
2	CO-3 X KS- 227	1.01	43.74	-14.61	21.12	0.55	100.00	16.90	46.90
3	CO-3 X Dwd-T-1	0.85	27.50	-28.37	1.59	0.29	-48.84	-56.44	-22.12
4	CO-3 X Dwd-T-3	1.07	51.42	-9.83	27.89	0.22	-10.81	-53.52	-41.59
5	CO-3 X Dwd-T-6	0.78	-20.61	-34.55	-7.17	0.26	5.41	-45.07	-30.97
6	DVRT-2 X VR 35	0.02	-88.46	-93.75	-97.61	0.01	-98.75 **	-99.32 **	-96.46
7	DVRT-2 X KS- 227	0.58	366.67	161.19	-30.28	0.47	-53.67	-75.89 **	25.66
8	DVRT-2 X Dwd-T-1	0.09	0.00	-40.91	-89.64	0.19	-85.84 **	-90.49 **	-50.44
9	DVRT-2 X Dwd-T-3	0.80	534.21	254.41	-3.98	0.02	-98.32 *	-99.15 **	-95.58
10	DVRT-2 X Dwd-T-6	0.65	62.34	-16.02	-22.71	1.70	71.76	-13.24	352.21 **
11	H-24 X VR 35	0.34	-31.33	-49.51	-58.96	0.12	-93.48 **	-96.58 **	-68.14
12	H-24 X KS- 227	0.77	71.22	13.73	-7.57	0.22	-87.73 **	-93.73 **	-41.59
13	H-24 X Dwd-T-1	1.38	233.06 *	102.45	64.54	1.48	-29.03	-57.70 **	293.81 *
14	H-24 X Dwd-T-3	0.06	-87.50	-91.67	-93.23	0.44	-74.86 **	-87.36 **	17.70
15	H-24 X Dwd-T-6	1.03	42.07	33.77	23.11	0.02	-99.05 **	-99.52 **	-95.58
16	Megha (L-15) X VR 35	0.82	-74.44 **	-86.55 **	-2.39	0.63	408.11	261.54	66.37
17	Megha (L-15) X KS- 227	1.06	-66.31 **	-82.54 **	26.69	0.22	182.61	170.83	-42.48
18	Megha (L-15) X Dwd-T-1	0.86	-72.33 **	-85.83 **	2.79	0.41	10.71	-38.61	9.73
19	Megha (L-15) X Dwd-T-3	1.41	-55.32 **	-76.83 **	68.13	0.02	-64.29	-77.27	-95.58
20	Megha (L-15) X Dwd-T-6	1.04	-69.59 **	-82.87 **	24.30	0.02	-57.14	-72.73	-94.69
21	Pant-T-10 X VR 35	0.63	14.63	-18.97	-25.10	0.33	-82.02 **	-90.56 **	-12.39
22	Pant-T-10 X KS- 227	0.57	14.38	-26.29	-31.87	0.25	-86.02 **	-92.85 **	-33.63
23	Pant-T-10 X Dwd-T-1	0.57	23.19	-26.72	-32.27	0.38	-81.93 **	-89.23 **	0.00
24	Pant-T-10 X Dwd-T-3	0.73	46.00	-5.60	-12.75	0.03	-98.29 **	-99.14 **	-92.04
25	Pant-T-10 X Dwd-T-6	1.01	30.45	30.17	20.32	0.08	-95.26 **	-97.62 **	-77.88
	ARTH-3 (Comercial check)	0.84				0.38			
	Megha (L-15) (Local check)	6.07				0.07			
	Mean	1.00	44.72	495.98	-5.62	0.52	-26.46	631.09	-11.75
	Minimum	0.02	-88.48	-75.00	-97.62	0.01	-99.05	-92.31	-96.49
	Maximum	6.07	532.55	2839.02	103.17	3.51	408.11	8416.67	348.25
	No of F_1's better than CC	14				18			
	No of F_1's better than OPC	25				7			
	S.Ed. ±		0.46	0.53			0.39	0.45	
	CD at 5 %		0.92	1.06			0.78	0.90	
	CD at 1 %		1.23	1.42			1.04	1.20	

*, **: Indicates significant at 5 and 1% level of probability respectively

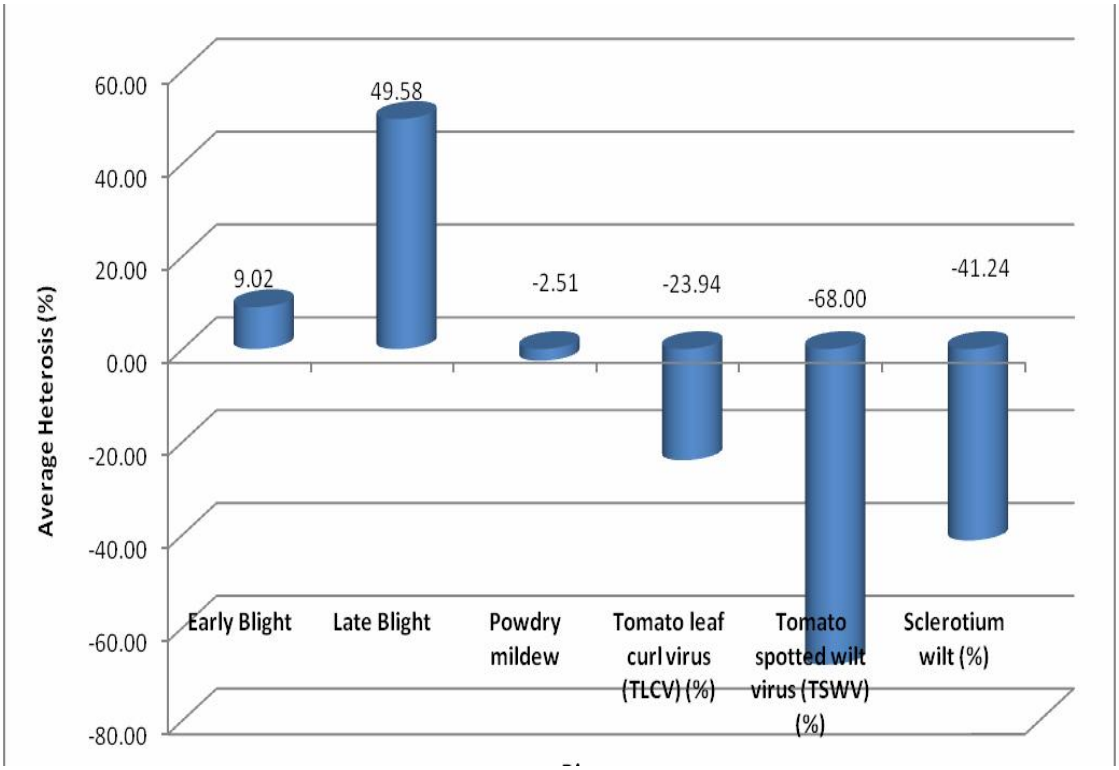
Table 34 . *Per se* performance and magnitude of heterosis for incidence of Sclerotium wilt.

Sl.	Parents and F_1 hybrid	Sclerotium wilt (%)			
		per se value	Heterosis per cent over MP	Heterosis per cent over BP	Heterosis per cent over CC
	Lines				
1	CO-3	24.26			
2	DVRT-2	6.56			
3	H-24	11.55			
4	Megha L-15	7.03			
5	PANT-T-10	16.20			
	Testers				
1	VR-35	8.52			
2	KS-227	2.48			
3	Dwd-T-1	10.14			
4	Dwd-T-3	8.19			
5	Dwd-T-6	5.09			
	F_1 hybrids				
1	CO-3 X VR 35	4.44	-72.89 **	-81.68 **	-4.85
2	CO-3 X KS- 227	8.12	-39.28 **	-66.54 **	73.80
3	CO-3 X Dwd-T-1	8.82	-48.74 **	-63.66 **	88.79
4	CO-3 X Dwd-T-3	9.99	-38.40 **	-58.81 **	113.99 *
5	CO-3 X Dwd-T-6	7.78	-46.98 **	-67.93 **	66.60
6	DVRT-2 X VR 35	5.56	-26.18	-34.68	19.13
7	DVRT-2 X KS- 227	3.90	-13.73	-40.57	-16.56
8	DVRT-2 X Dwd-T-1	13.47	61.42 **	32.92	188.51 **
9	DVRT-2 X Dwd-T-3	10.70	45.11	30.66	129.05 **
10	DVRT-2 X Dwd-T-6	2.29	-60.72	-65.12	-51.03
11	H-24 X VR 35	8.55	-14.80	-25.98	83.01
12	H-24 X KS- 227	4.00	-42.95	-65.36 **	-14.35
13	H-24 X Dwd-T-1	6.73	-37.96 *	-41.74 *	44.04
14	H-24 X Dwd-T-3	6.19	-37.30	-46.42 *	32.48
15	H-24 X Dwd-T-6	3.85	-53.71 *	-66.66 **	-17.56
16	Megha (L-15) X VR 35	6.67	-14.13	-21.64	42.90
17	Megha (L-15) X KS- 227	5.82	22.48	-17.17	24.63
18	Megha (L-15) X Dwd-T-1	6.89	-19.67	-32.00	47.61
19	Megha (L-15) X Dwd-T-3	3.49	-54.12 *	-57.37 *	-25.27
20	Megha (L-15) X Dwd-T-6	2.67	-55.92	-62.00 *	-42.83
21	Pant-T-10 X VR 35	6.07	-50.86 **	-62.51 **	30.05
22	Pant-T-10 X KS- 227	3.74	-59.99 **	-76.93 **	-19.99
23	Pant-T-10 X Dwd-T-1	2.13	-83.80 **	-86.83 **	-54.32
24	Pant-T-10 X Dwd-T-3	2.79	-77.12 **	-82.78 **	-40.26
25	Pant-T-10 X Dwd-T-6	2.22	-79.11 **	-86.28 **	-52.39
	ARTH-3 (Comercial check)	4.67			
	Megha (L-15) (Local check)	7.03			
	Mean	6.99	-35.97	9.14	25.81
	Minimum	2.13	-83.80	-78.95	-54.32
	Maximum	24.26	61.42	227.73	188.51
	No of F_1's better than CC	11			
	No of F_1's better than OPC	18			
	S.Ed. ±		1.87	2.16	
	CD at 5 %		3.76	4.35	
	CD at 1 %		5.02	5.80	

*, **: Indicates significant at 5 and 1% level of probability respectively



a) Average heterosis for growth and yield parameters in tomato hybrids



b) Average heterosis for disease incidence in tomato hybrids

Fig.10. Average heterosis for (a) growth and yield parameters and (b) disease incidence in tomato hybrids developed by line x tester method

Table 35. Analysis of variance for combining ability

Sl.	Character	Source of Variation for Mean sum of squares							Per cent contribution			Random effect			Heritability (h^2_{ns})	Genetic Advance (%)
		Replicates	Crosses	Lines	Testers	Line x Testers	Errors	Total	Lines	Tester	Line x	σ^2_{gca}	σ^2_{sca}	$\sigma^2_{gca}/\sigma^2_{sca}$		
	Degrees of freedom	2	24	4	4	16	48	74								
1	Plant height	22.59	157.09**	374.57**	291.42*	69.14**	17.87	63.15	39.74	30.92	29.34	84.60	71.234	1.188	64.73	10.78
2	anches / plant	0.59**	0.25*	0.35*	0.74**	0.11	0.12	0.17	23.04	48.39	28.56	0.11	0.01	11.765	61.95	0.394
3	Days to 50% flowering	3.97	26.18**	81.47**	54.68**	5.24**	2.07	9.94	51.86	34.80	13.34	17.63	4.414	3.996	83.47	5.589
4	No. of fruits /cluster	0.60**	0.34**	1.56**	0.21**	0.07	0.10	0.19	76.09	10.48	13.42	0.20	-0.075	-2.716	81.59	0.594
5	Fruit length	0.09	0.31**	0.75**	0.68**	0.11	0.07	0.15	39.83	36.12	24.05	0.17	0.072	2.423	69.86	0.508
6	Fruit width	0.09	0.37**	0.59*	0.95**	0.17**	0.06	0.16	26.48	42.24	31.28	0.19	0.158	1.204	61.95	0.5
7	Pericarp thickness	0.015*	0.01**	0.02**	0.01*	0.00	0.00	0.00	45.71	29.30	24.99	0.004	0.001	3.411	68.01	0.08
8	No. of locules per fruit	0.08	1.24**	3.17**	3.43**	0.20**	0.08	0.46	42.66	46.19	11.16	0.84	0.114	7.422	85.98	1.244
9	Total soluble solids	0.18*	0.26**	1.09**	0.27**	0.05	0.05	0.12	70.55	17.73	11.71	0.172	0.006	30.042	85.00	0.557
10	uit weight	63.46	469.48**	1525.87**	609.02*	170.49**	20.87	167.52	54.17	21.62	24.21	278.6	197.243	1.413	71.02	20.492
11	No. of fruits per plant	31.30**	209.81**	404.45**	644.23**	52.55**	8.23	74.23	32.13	51.18	16.70	137.7	59.69	2.308	79.72	15.265
12	Yield per plant	0.02	0.12**	0.29*	0.13	0.07**	0.03	0.05	41.55	18.21	40.25	0.04	0.062	0.793	51.30	0.231
13	Yield per hectare	5.88	39.70**	97.56*	20.83	29.97**	6.23	17.08	40.95	8.74	50.31	14.43	33.221	0.435	41.95	3.585
14	Early Blight	0.20	1.00**	0.60	3.15**	0.57**	0.15	0.43	9.99	52.24	37.77	0.44	0.479	0.928	53.93	0.713
15	Late Blight	0.11	0.27**	0.25	0.46	0.22**	0.08	0.14	15.79	28.53	55.68	0.06	0.155	0.427	30.81	0.208
16	Powdery mildew	0.11	0.89**	1.82	0.62	0.73**	0.23	0.44	33.84	11.62	54.55	0.25	0.644	0.402	34.64	0.437
17	Tomato leaf curl virus	0.11	0.49**	1.09	0.08	0.45*	0.21	0.30	36.81	2.79	60.40	0.04	0.04	1.139	13.11	0.112
18	Tomato spotted wilt virus	0.05	0.53**	0.23	0.38	0.64**	0.08	0.23	7.10	12.02	80.89	0.00	0.461	0.003	0.35	0.003
19	Sclerotium wilt (%)	1.50	26.11**	46.09**	32.89	19.42**	6.34	12.62	29.42	20.99	49.59	8.66	16.548	0.523	40.081	2.714

* Significant at 5% probability ** Significant at 1% probability

The estimates of ratio of GCA variance to SCA variance was higher for number of branches per plant, number of fruits per cluster, fruit length, fruit width, pericarp thickness, number of locules per fruit, TSS, yield per plant, early blight, late blight and tomato leaf curl virus.

Heritability in narrow sense was high plant height, number of branches per plant, days to 50 % flowering, number of fruits per cluster, fruit length, fruit width, pericarp thickness, number of locules per fruit, TSS and number of fruits per plant. It was moderate for six traits *viz.* yield per plant, yield per hectare, early blight, late blight, powdery mildew, and *Sclerotium* wilt incidence. For two traits i.e., tomato leaf curl virus and tomato spotted wilt virus incidence it was low.

Genetic advance over mean was moderate for three traits i.e., plant height, single fruit weight and number of fruits per plant and for rest of the traits it was low.

4.2.2.2 Combining ability effects (cf Tables 36 & Table 37)

Combining effects are of two types: general combining effects and specific combining effects. These are basis or important in selecting or identifying the suitable parents for hybridization programme. The estimates of general combining ability (*gca*) and specific combining ability (*sca*) effects for all the nineteen characters are presented in Table 4.24 and 4.25 respectively. In each trait their role is highlighted as below:

4.2.2.2.1 Plant height

Two of lines (DVRT-2, Pant-T-10) and two of the testers (KS-227, Dwd-T-3) showed significant positive *gca* effects while there were few with significant negative values. The lines possessed significant *gca* and *sca* effects. The highest (-7.06) significant negative gca effect was exhibited by the line 'H-24' followed by tester 'Dwd-T-6' (-5.27).

A total of five crosses showed significant positive and negative *sca* effects. The highest (8.91) significant positive *sca* effect exhibited by the cross 'DVRT-2' x 'KS-227' which involved the parents showing significant positive general combiners, whereas 'H-24' x 'KS-227' recorded highest significant negative *sca* effect involved parents one with negative gca effect and other with positive significant *gca* effect respectively.

4.2.2.2.2 Number of branches per plant

One of the lines and testers had negative ('CO-3' & VR-35) other one positive (Pant-T-10, Dwd-T-3) significant *gca* effects and two of the testers (KS-227, Dwd-T-3) showed significant positive *gca* effects.

The *sca* effects were non- significant for all the crosses.

4.2.2.2.3 Days to 50 per cent flowering

Three parents in lines and testers had significant *gca* effects. Among all the parents highest significant negative *gca* effect (-2.68) was noticed in 'Dwd-T-6' followed by 'Megha (L-15)' with -2.49 which happened to be from testers and lines respectively. This is an ideal character for earliness. 'DVRT-2' was found to be significant positive general combiner with a higher value of 3.74 among the lines and among testers 'Dwd-T-3' had high significant positive *gca* effect (2.49).

Among the crosses, two crosses were found to have significant negative *sca* effect with highest specific cross 'DVRT-2' x 'Dwd-T-6' (-2.46) whose the parents having significant positive and negative *gca* effects respectively. The other crosses which revealed significant negative *sca* effects were 'H-24' x 'KS-227' (-1.88) and 'CO-3' x 'Dwd-T-1' (-1.69).

4.2.2.2.4 Number of fruits per cluster

Significant *gca* effect was observed for two parents from lines and none from testers side. Among lines, 'DVRT-2' had negative *gca* of -0.22 and 'Pant-T-10' had positive *gca* effect of 0.57.

None among the 25 crosses were having significant *sca* effects.

Table 36 . Estimates of general combining ability effects of parents for different traits in line x tester study of tomato.

Sl.	Parents	Plant height	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length	Fruit width	Pericarp thickness	No. of locules per fruit	Total soluble solids	Single fruit weight	No. of fruits per plant	Yield per plant	Yield per hectare	Early Blight	Late Blight	Powdery mildew	Tomato leaf curl virus	Tomato spotted wilt virus	Sclerotium wilt
	Lines																			
1	CO-3	-1.09	-0.24**	-1.20**	-0.13	-0.26**	-0.17**	-0.02	-0.01	-0.19**	-2.01	-1.71 *	-0.11 **	-0.87	0.20	0.05	0.29 *	0.29	-0.07	1.95**
2	DVRT-2	6.15**	0.03	3.74**	-0.22*	-0.11	0.34**	0.02	0.74**	-0.12 *	15.80**	-3.87**	0.15**	2.92**	0.15	0.05	0.42**	-0.36*	0.14	1.31
3	H-24	-7.06**	0.02	0.17	-0.12	0.12	-0.01	0.00	0.03	-0.27**	-9.79**	-5.02**	-0.17**	-3.63**	0.05	-0.07	-0.10	-0.08	0.12	-0.01
4	Megha L-15	-1.13	0.01	-2.49**	-0.09	0.31**	-0.04	-0.05**	-0.35**	0.26**	-6.97**	3.21**	0.00	-0.30	-0.12	-0.18 *	-0.20	0.24	-0.08	-0.77
5	PANT-T-10	3.13**	0.19 *	-0.22	0.57**	-0.07	-0.12	0.05**	-0.41**	0.31**	2.97 *	7.38**	0.12 **	1.87**	-0.28 *	0.16	0.41**	-0.09	-0.12	-2.48**
	S.Ed. (g_i)	1.02	0.08	0.36	0.09	0.06	0.06	0.01	0.09	0.05	1.23	0.72	0.04	0.58	0.12	0.08	0.13	0.17	0.14	0.68
	CD @ 5%	2.06	0.17	0.72	0.18	0.13	0.12	0.02	0.18	0.11	2.47	1.45	0.08	1.17	0.24	0.17	0.26	0.34	0.28	1.37
	CD @1%	2.75	0.22	0.96	0.25	0.17	0.17	0.03	0.24	0.14	3.29	1.93	0.11	1.56	0.32	0.23	0.35	0.45	0.38	1.83
	S.Ed. (gi-gj)	1.45	0.12	0.51	0.13	0.09	0.09	0.02	0.13	0.07	1.73	1.02	0.06	0.82	0.17	0.12	0.18	0.24	0.14	0.97
	CD @ 5%	2.91	0.23	1.02	0.26	0.18	0.18	0.03	0.26	0.15	3.49	2.05	0.11	1.65	0.34	0.24	0.37	0.48	0.28	1.94
	CD @1%	3.88	0.31	1.36	0.35	0.24	0.23	0.05	0.34	0.20	4.65	2.73	0.15	2.20	0.45	0.32	0.49	0.63	0.28	2.59
	Testers																			
1	VR-35	-0.96	-0.04	0.92*	0.05	0.25**	0.03	0.01	-0.22*	0.20**	4.46**	0.61	0.10 *	1.20 *	-0.34 **	-0.18 *	-0.24	-0.09	-0.11	0.39
2	KS-227	4.87**	0.05	-0.52	-0.04	0.01	-0.17**	0.01	-0.19*	-0.06	-3.55**	-4.64**	0.02	0.48	-0.58**	-0.09	0.05	0.01	0.01	-0.76
3	Dwd-T-1	-2.82**	-0.33**	-0.21	-0.18	-0.14 *	0.06	0.01	0.44**	-0.08	-3.73**	-4.88**	-0.14**	-1.75 **	0.55**	0.06	-0.12	-0.05	0.22	1.73*
4	Dwd-T-3	4.17**	0.28**	2.49**	0.15	0.15*	0.37**	0.03 *	0.55**	-0.13 *	8.89**	-2.11**	0.05	0.68	0.241 *	-0.06	0.00	0.02	-0.19	0.76
5	Dwd-T-6	-5.27**	0.04	-2.68**	0.02	-0.27**	-0.29**	-0.05**	-0.57**	0.08	-6.07**	11.03**	-0.03	-0.61	0.13	0.27 **	0.31*	0.11	0.08	-2.11**
	S.Ed. (g_j)	1.02	0.08	0.36	0.09	0.06	0.06	0.01	0.09	0.05	1.23	0.72	0.04	0.58	0.12	0.08	0.13	0.17	0.14	0.68
	CD @ 5%	2.06	0.17	0.72	0.18	0.13	0.12	0.02	0.18	0.11	2.47	1.45	0.08	1.17	0.24	0.17	0.26	0.34	0.28	1.37
	CD @1%	2.75	0.22	0.96	0.25	0.17	0.17	0.03	0.24	0.14	3.29	1.93	0.11	1.56	0.32	0.23	0.35	0.45	0.38	1.83
	S.Ed. (g_i-g_j)	1.45	0.12	0.51	0.13	0.09	0.09	0.02	0.13	0.07	1.73	1.02	0.06	0.82	0.17	0.12	0.18	0.24	0.14	0.97
	CD @ 5%	2.91	0.23	1.02	0.26	0.18	0.18	0.03	0.26	0.15	3.49	2.05	0.11	1.65	0.34	0.24	0.37	0.48	0.28	1.94
	CD @1%	3.88	0.31	1.36	0.35	0.24	0.23	0.05	0.34	0.20	4.65	2.73	0.15	2.20	0.45	0.32	0.49	0.63	0.38	2.59

* Significant at 5% probability ** Significant at 1% probability

Table 37 . Estimates of specific combining ability effects of 19 characters in tomato hybrids developed by line x tester method.

Sl. No.	F_1 hybrid	Plant height	No. branches /plant	Days to flowering	No. fruits/ cluster	Fruit length	Fruit width	Pericarp thickness	No. of locules / fruit	TSS	Single fruit weight	No. fruits /plant	Yield per plant	Yield per hectare	Early Blight	Late Blight	Powdery mildew	Tomato leaf curl virus	Tomato spotted wilt virus	Sclerotium wilt
1	CO-3 X VR 35	4.55	0.24	0.53	0.04	0.18	0.10	0.02	-0.13	0.04	3.44	-0.52	-0.06	-0.54	-0.72**	0.13	-0.14	0.71	-0.14	4.77*
2	CO-3 X KS- 227	6.49**	-0.32	1.17	0.10	-0.28*	-0.36*	-0.04	-0.22	0.11	-5.14	3.18	0.13	0.55	-0.11	-0.24	-0.05	-0.08	0.28	-4.05
3	CO-3 X Dwd-T-1	-2.44	-0.13	-1.69*	-0.14	-0.03	-0.04	0.02	0.34	0.20	-1.03	-3.58*	-0.11	-2.44	0.02	-0.29	-0.34	-0.19	-0.19	-0.75
4	CO-3 X Dwd-T-3	-1.55	0.19	-0.93	-0.05	0.37*	0.57**	-0.02	0.20	-0.30*	8.79**	0.05	0.15	3.31*	0.45	0.25	0.25	-0.03	0.14	1.41
5	CO-3 X Dwd-T-6	-7.04**	0.02	0.93	0.05	-0.24	-0.27	0.01	-0.19	-0.04	-6.06*	0.88	-0.11	-0.89	0.36	0.15	0.28	-0.41	-0.09	2.06
6	DVRT-2 X VR 35	-2.09	-0.24	0.66	-0.13	-0.01	-0.10	0.01	-0.10	0.05	9.97**	3.21	0.23*	3.99**	-0.29	-0.08	-0.64*	-0.32	-0.35	-2.01
7	DVRT-2 X KS- 227	8.91 **	0.15	0.52	-0.03	-0.13	-0.02	-0.02	-0.02	0.01	2.56	-0.63	0.05	1.34	-0.25	-0.38	0.45	0.15	-0.01	-2.53
8	DVRT-2 X Dwd-T-1	-1.68	0.20	-0.08	0.06	0.06	0.07	-0.02	-0.05	-0.14	-16.19**	-1.25	-0.19*	-3.35*	0.02	0.25	0.38	-0.30	-0.51	4.56**
9	DVRT-2 X Dwd-T-3	-2.28	0.10	1.36	0.04	-0.02	0.05	0.04	0.05	0.02	1.08	-3.08	-0.10	-3.02*	0.17	-0.04	-0.02	0.36	-0.27	2.76
10	DVRT-2 X Dwd-T-6	-2.86	-0.21	-2.46**	0.06	0.09	0.01	-0.02	0.13	0.05	2.59	1.75	0.01	1.04	0.35	0.25	-0.18	0.11	1.14**	-2.78
11	H-24 X VR 35	-0.60	0.20	-1.02	0.15	0.07	0.10	0.01	0.12	-0.03	-5.37	0.34	-0.18	-5.04**	0.29	-0.22	0.55	-0.28	-0.22	2.30
12	H-24 X KS- 227	-7.84**	0.01	-1.88*	0.10	0.20	0.23	0.01	0.19	0.00	3.05	-1.14	-0.03	0.73	-0.21	0.03	-0.33	0.05	-0.24	-1.10
13	H-24 X Dwd-T-1	2.14	-0.04	0.68	-0.12	-0.12	-0.06	0.01	-0.09	0.01	7.00*	2.79	0.27**	6.12**	-0.01	0.19	-0.20	0.71	0.811 *	-0.87
14	H-24 X Dwd-T-3	1.89	-0.22	-0.22	-0.12	-0.30*	-0.32*	-0.04	-0.18	0.02	-7.28*	-0.80	-0.15	-2.95*	-0.30	-0.04	-0.08	-0.68	0.18	-0.43
15	H-24 X Dwd-T-6	4.41	0.05	2.44**	-0.01	0.14	0.05	0.01	-0.04	0.01	2.61	-1.19	0.09	1.14	0.23	0.04	0.05	0.21	-0.52	0.10
16	Megha (L-15) X VR 35	-1.87	-0.12	0.09	-0.07	-0.18	-0.11	-0.04	0.22	0.02	-7.24*	4.33**	-0.02	-0.65	0.42	0.35	0.95**	-0.13	0.48	1.18
17	Megha (L-15) X KS- 227	-2.77	0.17	0.05	0.12	0.14	0.14	-0.02	-0.23	-0.02	4.83	0.92	0.01	-0.37	-0.15	0.39*	-0.65*	0.02	-0.05	1.47
18	Megha (L-15) X Dwd-T-1	-0.23	0.07	1.03	-0.02	0.13	-0.01	0.01	0.14	-0.07	6.26*	-1.73	0.06	1.66	0.33	-0.17	-0.20	-0.13	-0.06	0.05
19	Megha (L-15) X Dwd-T-3	2.06	-0.09	-0.52	0.20	-0.03	-0.29*	0.03	0.20	0.05	-6.68*	4.38**	0.09	1.82	0.01	-0.30	0.01	0.35	-0.05	-2.38
20	Megha (L-15) X Dwd-T-6	2.81	-0.03	-0.65	-0.22	-0.07	0.28	0.02	-0.34	0.02	2.83	-7.90**	-0.13	-2.47	-0.60*	-0.28	-0.12	-0.10	-0.32	-0.33
21	Pant-T-10 X VR 35	0.02	-0.08	-0.26	0.02	-0.06	0.01	-0.01	-0.11	-0.07	-0.80	-7.36**	0.03	2.24	0.30	-0.18	-0.72*	0.02	0.23	2.30
22	Pant-T-10 X KS- 227	-4.79 *	-0.02	0.14	-0.28	0.07	0.02	0.07*	0.28	-0.11	-5.30	-2.32	-0.15	-2.26	0.72**	0.19	0.58*	-0.14	0.03	1.11
23	Pant-T-10 X Dwd-T-1	2.21	-0.10	0.06	0.21	-0.05	0.04	-0.02	-0.33	0.01	3.97	3.77*	-0.03	-1.99	-0.36	0.02	0.35	-0.09	-0.05	-2.99
24	Pant-T-10 X Dwd-T-3	-0.11	0.02	0.31	-0.06	-0.03	-0.01	-0.03	-0.27	0.21	4.10	-0.56	0.01	0.85	-0.33	0.13	-0.16	0.01	0.01	-1.36

Sl. No.	F_1 hybrid	Plant height	No. branches /plant	Days to flowering	No. fruits/ cluster	Fruit length	Fruit width	Pericarp thickness	No. of locules / fruit	TSS	Single fruit weight	No. fruits /plant	Yield per plant	Yield per hectare	Early Blight	Late Blight	Powdery mildew	Tomato leaf curl virus	Tomato spotted wilt virus	Sclerotium wilt
25	Pant-T-10 X Dwd-T-6	2.67	0.18	-0.25	0.12	0.07	-0.07	-0.02	0.43*	-0.04	-1.97	6.47**	0.14	1.17	-0.33	-0.16	-0.04	0.20	-0.21	-0.95
	S.Ed. S_{ij}	2.29	0.18	0.80	0.20	0.14	0.14	0.03	0.20	0.12	2.74	1.61	0.09	1.30	0.26	0.19	0.29	0.37	0.32	1.53
	CD @ 5%	4.60	0.37	1.61	0.41	0.28	0.28	0.05	0.40	0.24	5.51	3.24	0.18	2.61	0.53	0.38	0.58	0.75	0.63	3.07
	CD @1%	6.14	0.49	2.15	0.55	0.38	0.37	0.07	0.54	0.31	7.36	4.32	0.24	3.48	0.71	0.51	0.77	1.00	0.85	4.10
	S. Ed.(S_{ij} - S_{ik}) $\pm$	3.24	0.26	1.13	0.29	0.20	0.19	0.04	0.28	0.17	3.88	2.28	0.13	1.84	0.37	0.27	0.41	0.53	0.45	2.16
	CD @ 5%	6.51	0.52	2.28	0.58	0.40	0.39	0.08	0.57	0.33	7.80	4.58	0.25	3.69	0.75	0.54	0.82	1.06	0.90	4.35
	CD @1%	8.68	0.70	3.04	0.77	0.53	0.52	0.10	0.76	0.44	10.40	6.11	0.34	4.92	1.00	0.72	1.10	1.42	1.20	5.80
	S. Ed.(S_{ij} - S_{ik}) $\pm$	3.55	0.28	1.24	0.32	0.22	0.21	0.04	0.31	0.18	4.25	2.50	0.14	2.01	0.41	0.29	0.45	0.58	0.49	2.37
	CD @ 5%	7.13	0.57	2.50	0.64	0.44	0.43	0.08	0.63	0.36	8.54	5.02	0.28	4.04	0.82	0.59	0.90	1.16	0.98	4.76
	CD @1%	9.51	0.76	3.33	0.85	0.58	0.57	0.11	0.84	0.49	11.40	6.69	0.37	5.39	1.10	0.78	1.20	1.55	1.31	6.35

* Significant at 5% probability ** Significant at 1% probability

4.2.2.2.5 Fruit length

Significant positive *gca* effect was observed in 'Megha (L-15) with 0.31 among the lines. All except 'KS 227' had significant *gca* effect among testers. While, maximum significant negative *gca* effect was observed in 'Dwd-T-6' (-0.27) among testers followed by CO-3 (-0.26) among lines.

Only three crosses showed significant *sca* effects. The highest significant positive *sca* effect was recorded by 'CO-3' x 'Dwd-T-3' (0.37).

4.2.2.2.6 Fruit width

Significant positive *gca* effect was observed in 'DVRT-2' (0.34) and negative effects in 'CO-3' (-0.17) among the lines while 'Dwd-T-3' (0.37) and 'Dwd-T-6' (-0.29) & 'KS-227' (-0.17) among the testers.

Out of 25 hybrids, only one and three exhibited significant positive and negative *sca* effects respectively. The cross which showed significant positive *sca* effect was ''CO-3' x 'Dwd-T-3' (0.57) and highest significant negative *sca* effect was recorded by the cross 'CO-3' x 'KS-227' (-0.36), H-24 x 'Dwd-T-3' (-0.32) and 'Megha (L-15) x 'Dwd-T-3' (-0.29).

4.2.2.2.7 Perciarp thickness

Two each in lines and testers showed significant *gca* effect. Significant positive *gca* effect was observed in 'Pant-T-10' (0.05) and 'Dwd-T-3' (0.03) among the testers and lines respectively in parents. While, significant negative *gca* effect was observed in 'Megha (L-15)' (-0.05) and 'Dwd-T-6' (-0.05) among the testers and lines respectively in parents.

Out of 25 hybrids, only one ['Pant-T-10' x 'KS-227' (0.07)] showed significant *sca* effect in positive direction.

4.2.2.2.8 Number of locules per fruit

Three lines and all testers had significant *gca* effect. Among testers three and two were having negative and positive *gca* effects. Among lines 'Pant-T-10' (-0.41) showed highest significant negative *gca* effect while among testers 'Dwd-T-6' (-0.57) showed significant *gca* effect. 'DVRT-2' (0.74) followed by 'Dwd-T-3' (0.55) and 'Dwd-T-1' (0.44) had significant positive *gca* effect.

Out of 25 hybrids, only one ['Pant-T-10' x 'Dwd-T-6' (0.43)] showed significant *sca* effect in positive direction.

4.2.2.2.9 Total soluble solids

All in lines and two testers showed significant *gca* effect. Two and one in lines and testers were with positive *gca* effects i.e., 'Pant-T-10' (0.31) and 'Megha (L-15)' (0.26) in lines, and 'VR-35' (0.20) in testers had significant *gca* effects.

Out of 25 hybrids, only one ['CO-3' x 'Dwd-T-3' (-0.30)] showed significant sca effect in negative direction.

4.2.2.2.10 Single fruit weight

This trait had highest *gca* and *sca* values amongst all the 19 traits in present study. 'DVRT-2' (15.80) and 'Dwd-T-3' (8.89) amongst lines and testers recorded highest significant positive *gca* effects ever recorded for in any trait in this study.

'DVRT-2' x 'Dwd-T-1' (-16.19) and 'DVRT-2' x 'VR-35' (9.97) recorded highest significant gca effects ever recorded for in any trait in this study.

All lines except one and all tester showed significant *gca* effects. The female parents 'DVRT-2' (15.80) followed by 'Pant-T-10' (2.97) and in male parents 'Dwd-T-3' (8.89) followed by 'VR-35' (4.46) exhibited significant positive *gca* effect.

'H-24' (-9.79), Megha (L-15) (-6.97) and 'CO-3' (-2.01) among lines and 'Dwd-T-6' (-6.07) , 'Dwd-T-1'(-3.73), 'KS-227' (-3.55) among testers recorded significant negative *gca* effects. Estimates of *sca* effects were significant for nine crosses of which four were in positive direction. The crosses 'DVRT-2' x 'VR-35' (9.97), 'CO-3' x 'Dwd-T-3' (8.79), 'H-24'x 'Dwd-T-1'

(7.00), and ‘Megha (L-15)’ x ‘Dwd-T-1’ (6.26) had significant positive *sca* effects. ‘ DVRT-2’ x ‘Dwd-T-1’ (-16.19) , ‘H-24’ x ‘Dwd-T-3’ (-7.28), ‘Megha (L-15)’ x ‘VR-35’ (-7.24), ‘Megha (L-15)’ x ‘Dwd-T-3’ (-6.68) , ‘CO-3’ x ‘Dwd-T-6’ (-6.06) had significant negative *sca* effects.

4.2.2.2.11 Number of fruits per plant

All the lines and four testers had significant gca effects. Six crosses showed significant *sca* effects.

Significant positive general combining ability effect was observed in three parents *viz.*, ‘Pant-T-10’ (7.38) and ‘Megha (L-15)’ (3.21) in lines while highest *gca* in ‘Dwd-T-6’ (11.03) among testers. ‘H-24’ (-5.02), ‘DVRT-2’ (-3.87) and ‘CO-3’ (-1.71) in lines and ‘Dwd-T-1’ (-4.88), ‘KS-227’ (-4.64) and ‘Dwd-T-3’ (-2.11) among testers showed negative *gca* effect.

Out of 25 crosses, 7 crosses showed significant *sca* effects of which 4 were in positive direction. The best cross with highest positive *sca* effect was in ‘Pant-T-10’ x ‘Dwd-T-6’ (6.47) followed by ‘Megha (L-15)’ x ‘Dwd-T-3’ (4.38), ‘Megha (L-15)’x ‘VR-35’ (4.33) and ‘Pant-T-10’ x ‘Dwd-T-1’ (3.77). ‘Megha (L-15)’ x ‘Dwd-T-6’ (-7.90), ‘Pant-T-10’ x ‘VR-35’ (-7.36) and ‘CO-3’ x ‘Dwd-T-1’ (-3.58) had significant negative *sca* effects

4.2.2.2.12 Yield per plant

Four lines and two testers had significant *gca* effects amongst parents. ‘DVRT-2’ (0.15) and ‘Pant-T-10’ (0.12) among lines and ‘VR-35’ (0.10) in testers recorded significant positive *gca* effects for the yield per plant. The genotypes ‘H-24’ (-0.17), and ‘CO-3’ (-0.11) amongst lines and tester ‘Dwd-T-1’ (-0.14) exhibited significant negative *gca* effects for this character.

Three crosses manifested significant *sca* effect of which two were positive and one in negative direction. The highest significant positive *sca* effect was observed in ‘H-24’ x ‘Dwd-T-1’ (0.27) followed by ‘DVRT-2’ x ‘VR-35’ (0.23). Only one significant negative *sca* effect was noticed in the cross combination ‘DVRT-2’ x ‘Dwd-T-1’ (-0.19).

4.2.2.2.13 Yield per hectare

There were three and two significant gca effects in lines and testers respectively. Two lines [‘DVRT-2’ (2.92), ‘Pant-T-10’ (1.87)] and one tester [‘VR-35’ (1.20)] had positive *gca* effects for the yield per hectare. ‘H-24’ (-3.63) in lines and ‘Dwd-T-1’ (-1.75) in testers exhibited significant negative *gca* effects for this character.

Seven crosses manifested significant *sca* effect of which three were positive and 4 in negative direction. The highest significant positive *sca* effect was observed in ‘H-24’ x ‘Dwd-T-1’ (6.12) followed by ‘DVRT-2’ x ‘VR-35’ (3.99) and ‘CO-3’ x ‘Dwd-T-3’ (3.31). ‘H-24’ x ‘VR-35’(-5.04), ‘DVRT-2’ x ‘Dwd-T-1’ (-3.35), ‘DVRT-2’ x ‘Dwd-T-3’ (-3.02) and ‘H-24’ x ‘Dwd-T-3’ (-2.95) had significant negative *sca* effect .

4.2.2.2.14 Diseases incidence

Combing ability effects both *gca* and *sca* for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence in F_1 hybrids and their parents has been presented in Tables 36 and Table 38

There were five, three, four, one, none and four parents with significant *gca* effects for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence respectively. There were one ,one, none, one and one amongst lines while in testers two, one, none, none and one with significant negative *gca* effect for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence respectively.

There were two, one , five, none, two and two crosses with significant *sca* effects for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence respectively. Two [‘CO-3’ x ‘VR-35’ (-0.75) and ‘Megha (L-15)’ x ‘Dwd-T-6’ (-0.60)], none , three [‘Pant-T-10’ x ‘VR-35’ (-0.72), ‘Megha (L-15)’ x ‘KS-227’ (-0.65) and ‘DVRT-2’ x ‘VR-35’ (-64)], none, none and one [‘CO-3’ x ‘VR-35’ (-3.77)] crosses showed significant negative sca effects for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence respectively.

Fig.11. The gca effects of parents for total Soluble solids (TSS) in line x tester study of tomato

Fig.12. The gca effects of parents for single fruit weight in line x tester study of tomato

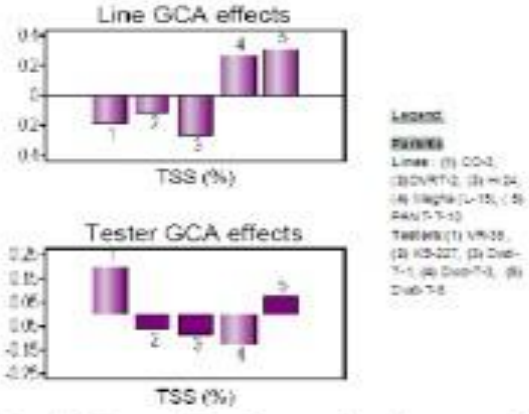


Figure 11. The gca effects of parents for total soluble solids (TSS) in line x tester study of tomato.

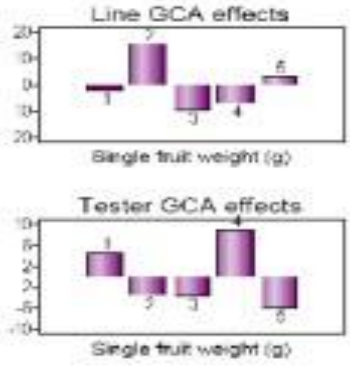


Figure 12. The gca effects of parents for single fruit weight in line x tester study of tomato.

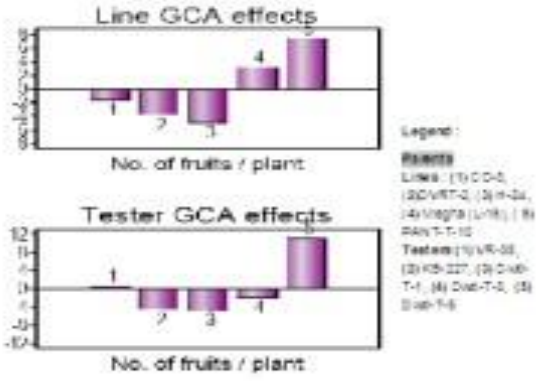


Figure 13. The gca effects of parents for number of fruits per plant in line x tester study of tomato.

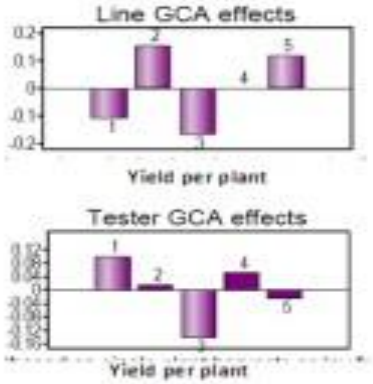
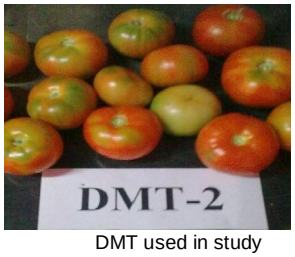


Figure 14. The gca effects of parents for yield per plant in line x tester study of tomato.

Fig.13. The gca effects of parents for number of fruits per plant in line x tester study of tomato

Fig.14. The gca effects of parents for yield per plant in line x tester study of tomato



DMT used in study

Raising seedlings in culture

7 day old cotyledon leaf explant

Preculturing of xexplant

Co cultivation
Of explant

callus and multiple shoots from transformed explants

callus

Shoot development on MS medium

Rooting on MS medium

Complete rooted plants

Plate.4. Agrobacterium mediated transformation of tomato with TRP sas/ihp gene construct

Graphical presentation of *gca* effects of parents, heterosis in hybrids, and hybrid distribution for TSS, single fruit weight, yield per plant is presented in Fig. 11 to Fig. 14.

B. Transformation studies in tomato

4.3 DEVEOPMENT OF TRANSGENIC TOMATO

Agrobacterium tumefaciens LBA4404 (pCAMBIA 1305.1) constructs carrying –TRP sas/ihp gene were used to asses their utility to induce resistance to T_0LCV in tomato. They were grown in yeast extract mannitol (YEMA) broth with streptomycin (100 µg/ml), rifampicin (25 µg/ml) and kanamycin (50 µg/ml), at 28^0C for 16 hrs. Seven-days-old precultured cotyledonary explants of 'DMT-2' (Plate 4) were infected with *Agrobacterium* and co-cultivated on MS medium (Plate 4). The untransformed explants turned white on selection medium (Plate 4). The treated explants produced multiple shoots within 4 weeks (Plate 4). Majority of the shoots excised and transferred to shooting medium turned albino on both multiple shoot induction and shoot elongation medium. Surviving green shoots having well developed root system were transferred to sterile peat and shifted to green house .

Direct shoot initiation rather than the callus was frequently observed at the proximal end of the explants. About 40% of the selected explants showed multiple shoot induction. Each surviving explant produced a number of shoots. Healthy shoots were subsequently transformed to fresh selection medium for shoot elongation. About 24.6%, of transformed shoots survived selection pressure during shoot elongation. The elongated shoots were cultured in rooting medium,

Root development from shoots was achieved with reduced level (5mg/l) of hygromycin. Rooted transgenic plants were hardened in peat and under green house conditions. About 40% of the rooted shoots survived the hardening process. Surviving plants; were maintained in glasshouse, along with a set of control plants.

4.4 PCR analysis of transformed plants

Screening of transgenic plants (T_0) by PCR using *hpt* II specific primers resulted in 25.0% (1/5) of the transformed plants from TRP (s), and T_0LCV inoculated (positive control) plants gave an expected PCR amplicon of ~800 bp, but no such amplicon was observed in untransformed (negative control) plants (Plate 5) .

Plate.5 PCR confirmation of primary transgenic plants

5. DISCUSSION

Discussion on the results obtained from the investigations done on 'Biometrical and Transformation studies in Tomato (*Solanum lycopersicum* L.)' is presented in this section with a critical analysis and interpretation of the outcomes in the present context and in the limelight of the findings of the previous workers and available information documented in the review of literature and the methodology adopted to study the material used or generated.

This investigation has come out with results on (i) variability, heritability, genetic advance, correlation, path analysis, genetic divergence, stability parameters from the evaluation of 41 tomato genotypes for three seasons during *kharif* 2007, *kharif* 2008 and *rabi* 2008, (ii) heterosis in F_1's and combining ability *i.e.*, general combining ability and specific combining ability effects from the evaluation of 25 F_1's during *rabi* 2008 and (iii) genetic transformation of tomato with RNAi anti-viral [TRP (SAS)] gene construct to develop resistance against tomato leaf curl virus disease.

In this study it was attempted to continue with the ever demanding need to identify new tomato genotypes with better performance for the location specific needs at Dharwad either from available material (genotypes evaluation) or generation of new ones (F_1's and transformants) needed for changing requirements in tomato cultivation.

Tomato is an important vegetable being grown in our country and state throughout the year for fresh and processing purposes. This vegetable which is being grown year round experiences different kinds of biotic stresses seasonally and uncertainties. They cause an impact on crop health affecting production with compounded fluctuations in weather parameters from the normal pattern supposedly due to global climatic variations attributable to global warming. As it is, tomato has many challengers from the group of biotic stresses i.e., fungal diseases, bacterial diseases, viral diseases nematodes, insect pests, etc greatly limiting plant potential and inserting risk into farmers earnings. Many a varieties have been developed taking these risks into account to make tomato production a secure and safe venture by trying to make a kind of insurance against all the uncertainties that could be perceived. This is seen in gluts in markets on account of over production than what the market can absorb and also due to the perishable nature of the tomato produce unlike like field crops produces like grains that could be stored among other things.

This does not indicate us to be complacent as recent fluctuations in weather nearly wiped out tomato in *kharif* as also other solanaceous vegetables like potato crop in Karnataka due to out break of fungal diseases like early blight, late blight, besides recurring problem of tomato leaf curl virus disease and gaining prominence hitherto minor or unknown disease in our region i.e., tomato spotted wilt virus disease. This calls for refocused work on these angles for ever live or real problems besides need of meeting the consumption requirements of growing population on one hand and raw material needed for the expanding tomato processing industries.

Production problems can be over come with improvement of yield and its contributory traits and resistance for diseases as a viable and long lasting measure. These traits are mainly governed by quantitative genes. Tomato improvement for yield and quality needs a sound knowledge on the genetic architecture of the crop and inheritance of economic characters that are of interest to the breeder. Disease resistance breeding has contributed new varieties. Resistant varieties performance has been highly variable and short duration stable owing to the changing environmental conditions influencing genotype x environmental interaction and emergence of new races. Sources of resistance within the species and genera has been exploited but is not foolproof and long lasting. This calls for exploring and introducing genes from other sources through genetic engineering or application of biotechnological tools and approaches .

New genotypes or varieties are being developed across the country by different tomato breeders on a continuous basis so also selections are being made locally by vegetable breeders. These newer identified selections or genotypes needs to be exploited for their potential use at other places in general and Dharwad in particular as a first step in tomato improvement. This has been attempted in this study. The forty-one tomato genotypes included for the study were blend of genotypes developed at different national institutions

spread across the country implying diverse geographical background accounting for nearly 75% of entries and rest of the other entries were selections made in tomato for various traits for local conditions which were maintained at the AICVIP , UAS, Dharwad. This made genotypes picked for the study well composed and suited for the objectives of the investigation for eliciting genetic information on various parameters. The traits selected for study were more pertinent for growth, yield, quality and field performance against diseases. The evaluation in three seasons during *kharif* 2007, *kharif* 2008 and *rabi* 2008 represented different environments as seen in meteorological data recorded and was having significant differences on expression of traits in these seasons. The diverse nature of selected genotypes, the selected traits contributing to variability and the divergence in tomato genotypes reinforces the suitability of selected tomato genotypes for the study. It is supported from the results got in the correlation and path analysis and divergence results based on Mahalanobis D^2 analysis of *per se* performance of tomato genotypes in each of three seasons. As seasons vary the genotype x environment interaction vary and is reflected in varied performance of a genotype. Hence, selection of a genotype with predictable performance with wider adaptability and greater stability becomes very difficult but is inevitable. This aspect too was taken up in this study through stability analysis as suggested by Eberhart and Russell (1966). This has been of great help in identifying stable variety for different environments with respect to their performance.

Heterosis is a potential phenomenon in tomato that is exploited commercially to harness higher yields with buffering against stresses by pooling of favorable genes for these and contributing traits. Selection of parents for hybridization programme is a pre-requisite for successful exploitation of heterosis in F_1 hybrids. Choice of parents with some genetic basis is essential to add weight to choice as also the likely outcome in terms of hybrids *per se* performance. The selected parents were drawn from sufficient diverse background as seen from the divergence study results which placed the parents in clusters with varying inter-cluster distances and characters means of the clusters. It can be expressed in terms of combining ability. The development of F_1's in a particular fashion or design achieves certain objective. Line x tester method makes it possible involving maximum number of parents in hybridization programme. This method was used in the present study. For this five lines i.e., female parents selected were locally adapted as well as widely grown varieties viz., 'Megha (L-15)', 'CO-3', 'H-24', 'DVRT-2' and 'Pant-T-10'. 'Megha (L-15)', 'CO-3', 'H-24', 'DVRT-2' and 'Pant-T-10' have hardiness with resistance to nematode, well adapted, resistant to tomato leaf curl virus, bigger sized fruits with good yield and good yielder respectively. Testers or male parents selected for the study were with high yield potential with good fruits. These hybrids were evaluated for their field performance during *rabi* 2008. Information on combining ability was elicited.

Tomato leaf curl virus belonging to Gemini virus group is an important disease causing pathogen in tomato. This causes yield losses up to 90 per cent depending on stage of infection and severity. It is a disease that needs attention for improvement and was taken up in the present study. Incorporating resistance in tomato against TLCV through use of RNAi technology's Post-Transcriptional Gene Silencing (PTGS) has been attempted. The work at the Institute of Agri-Biotechnology, University of Agricultural Sciences, Dharwad on PTGS has resulted in the development of many gene constructs for the purpose. Some of these gene constructs, i.e., tomato replicase (TRP) sense and anti-sense (SAS) gene constructs has been used in genetic transformation of tomato in present investigations.

The discussion of the results will be followed as below:

A. Biometrical studies in tomato:

Experiment I: Evaluation of tomato genotypes during *kharif* 2007, *kharif* 2008 and *rabi* 2008,

5.1 Analysis of variance, genetic variability, heritability and genetic advance

5.2 Association and Path coefficient analysis

5.3 Genetic diversity analysis

5.4 Stability analysis

Experiment II: Evaluation of F_1 hybrids developed by Line x Tester method during *rabi* 2008

5.5 Heterosis

5.6 Combining ability

5.7 Top performers

B. Transformation studies in tomato

A. Biometrical studies in tomato:

EXPERIMENT I: EVALUATION OF TOMATO GENOTYPES

5.1 ANALYSIS OF VARIANCE, GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The presence of genetic variability among the genotypes studied is shown from the results of analysis of variance for nineteen characters of 41 tomato genotypes. It indicated highly significant variation among the genotypes for all the characters in *kharif* 2007, *kharif* 2008 and *rabi* 2008 environments (Table 6).

The information on the estimates of variability with respect to yield and its heritable components in the material with which the tomato breeder is working is essential for chalking out selection strategies. Partitioning the total variability into heritable and non-heritable components *viz.,* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and further to compute heritability and genetic advances for various metric traits of interest to the breeder also has to be done for gaining insight to formulate selection strategies for tomato improvement.

One of the ways in which variability is assessed is through simple approach of examining the range of variation. In all the seasons the wider range of variation was recorded for the characters such as plant height, single fruit weight, days to 50% flowering, number of fruits per plant, yield per plant, yield per hectare, TLCV incidence, tomato spotted wilt virus, and *Sclerotium* wilt in all the genotypes. This is mainly because the experiment consists of genotypes of different genetic background and also different groups of genotypes (inter group variation). The characters showing wide range of variation offer ample scope for efficient selection of desirable types.

Absolute variability values of different characters do not reveal which of the characters are showing high variability. This could only be assessed through standardized values of the phenotypic and genotypic variance estimates by obtaining the coefficients of variability.

The coefficient of variability indicates only the extent of variability present for a character and does not demarcate the variability into heritable and non-heritable portion. The extent to which variability could be transferred from parent to offspring would suggest how far variation is heritable which has close bearing on response to selection.

As expected the PCV was invariably higher than GCV for all the characters. The coefficient of variation indicates only the extent of variability present in different characters but do not indicate their heritable position. Heritability estimates provides the assessment of amount of transmissible genetic variation to total variability. The parameter, genetic advance as per cent of mean is a more reliable index for understanding the effectiveness of selection in improving the traits.

High heritability, genetic advance over mean, GCV and PCV were observed for plant height, number of fruits per cluster, number fruits per plant, number of locules per fruit, TSS, fruit length, fruit width, early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt incidence in all the seasons. The magnitude of difference between PCV and GCV in case of these traits has been very small indicating this

category of characters are least affected by the environment. Hence, these traits could be used as selection criteria for selection of individual plants from the population. These characters can be further improved through simple selection, recurrent selection and hybridization for heterosis breeding. High heritability, high genetic advance over mean, moderate GCV and PCV were observed for yield per plant, yield per hectare, pericarp thickness and branches per plant. High heritability, moderate genetic advance over mean, moderate GCV and PCV were observed for days to 50 per cent flowering. It is evident from the above observations that there is lack of genetic variability for the improvement of days to 50 per cent flowering. So, there is need to create variability. Similar findings were also noted by Kumar *et al.* (2006) for number of fruits per plant, Mehta and Asati (2008) ; Prashanth *et al.* (2006) for average fruit weight and total yield per plant; Prashanth *et al.* (2007) for number of locules per fruit, pericarp thickness; Joshi *et al.* (2004) for fruit length and fruit width .

These provide clear picture regarding the effectiveness of selection in improving the plant characters.

5.2 ASSOCIATION AND PATH ANALYSIS

5.2.1 Association analysis

Correlation studies provide information on the nature and extent of association between only two pairs of metric characters and from this it would be possible to bring about genetic upgradation in one character by selection of the other of a pair. Obviously, knowledge about character associations will surely help to identify the character to make selection for higher yield. Determining the extent and nature of relationship prevailing among yield contributing characters is attempted in this study. For a rational approach towards the improvement of yield selection has to be made for the components of yield.

The twelve growth, quality and yield traits (plant height, no. of branches per plant, days to 50% flowering, no. of fruits per cluster, fruit length, fruit width , pericarp thickness , no. of locules per fruit, total soluble solids , single fruit weight , no. of fruits per plant, yield per plant) were involved in the association analysis to know their phenotypic and genotypic correlations among themselves for the tomato evaluations of *kharif* 2007, *kharif* 2008 and *rabi* 2008 . From the results of the analysis it shows that genotypic correlations are having higher values than phenotypic correlations indicating high heritable nature of the traits (Table 8).

Yield per plant improvement could be achieved through selection for number of fruits per plant, TSS, and number of fruits per cluster as they showed positive significant associations at both phenotypic and genotypic levels during three seasons. This is indicates selection could be done in any season and is reliable to accomplish yield enhancement. It also recorded negative significant association with days to 50 per cent flowering.

Plant height exhibited significant positive association with number of primary branches per plant, number of fruits per cluster, TSS, and number of fruits per plant both at phenotypic and genotypic levels but highly significant negative correlation was observed with fruit length, fruit width, and single fruit weight phenotypic. It also showed negative correlation with pericarp thickness and number of locules per fruit only at genotypic level. Number of branches per plant was correlated positively and significantly with number of fruits per cluster, TSS, number of fruits per plant, both at phenotypic and genotypic levels.

Number of fruits per plant exhibited highly significant positive correlation with TSS and yield per plant and significant negative correlation was seen with fruit length, fruit width, and pericarp thickness, no of locules per fruit, single fruit weight both at phenotypic and genotypic levels.

Single fruit weight was positively and significantly associated with number of locules per fruit, fruit length and fruit width, pericarp thickness, number of locules per fruit while negatively and significantly correlated with Plant height, number of fruits per cluster, TSS, number of fruits per plant.

The variation between the three seasons in respect of intensity and direction of association for different traits with some of the characters may be attributed to response to the environmental fluctuations. Similar trend observed that plant height had positive correlation with number of fruits per plant (Raijadhav *et al.,* 1996 and Prashant, 2003) at both

the levels, total yield per plant (Veershetty, 2004 and Mala and Vadivel, 1999) at genotypic level, number of clusters per plant (Veershetty, 2004) at genotypic level and average fruit weight (Mala and Vadivel, 1999) at genotypic level.

5.2.2 Path coefficient analysis:

Relative contribution of different traits towards fruit yield through partitioning of genotypic and phenotypic correlation into direct and indirect effects of component characters was computed with path coefficient analysis. The path coefficient analysis, a statistical device developed by Wright (1921), which takes into account the cause and effect relation between the variation into direct and indirect effect through other independent variables. The path coefficient analysis also measures the relative importance of causal factors involved. This is simply standardized partial regression analysis, wherein total correlation value is subdivided into causal scheme. Li (1956) emphasized the importance of path diagram which facilitates the understanding of the nature of cause and effect system. The direct and indirect effects of ten traits on fruit yield per plant at phenotypic and genotypic levels for tomato genotypes evaluated in three environments (Table 9 and path diagrams Fig. 1, 2 and 3) are presented as:

5.2.2.1. Direct effect of characters on yield

The three season results indicate that the yield was directly affected mainly by two traits out of ten i.e., single fruit weight and number of fruits per plant in positive direction at phenotypic and genotypic levels in all environments while it varied in positive direction for two seasons for fruit width and plant height. Highest direct effect on yield was recorded by number of fruits per plant during *kharif* 2008 and *kharif* 2007 respectively. Shalini (2009), Shashikanth (2008), Veershetty (2004), Patil (1998) and Domani and Maya (1997) reported similar reports

Positive correlation of plant height, number of branches per plant, number of fruits per plant, total soluble solids and number of fruits per plant is pronouncedly shown along with negative correlations of days to 50 % flowering and fruit width on yield per plant.

5.2.2.2 Indirect effect of different characters

Indirect effects on yield per plant in positive direction at phenotypic and genotypic levels in all three seasons in an appreciable magnitude was recorded in:

(i) number of fruits per plant through plant height, number of branches per plant, number of fruits per cluster and TSS ;

(ii) Single fruit weight through fruit length, fruit width, pericarp thickness, number of locules per fruit, days to 50% flowering.

Indirect effects on yield per plant in positive direction at phenotypic in all three seasons in an appreciable magnitude was recorded in: (i) number of locules per fruit through plant height,(ii) number of branches per plant through plant height and (iii) fruit length through days to 50 % flowering through

Indirect effects on yield per plant in negative direction at both phenotypic and genotypic levels in all three seasons in an appreciable magnitude was recorded in:

(i) number of fruits per plant through days to 50 % flowering , fruit length , fruit width , pericarp thickness , number of locules per fruit , single fruit weight .

(ii) single fruit weight through plant height ,number of branches per plant ,number of fruits per cluster , number of fruits per plant , total soluble solids .

5.3 GENETIC DIVERSITY

Determination of genetic diversity existing within and between groups of germplasm is of utmost significance and particularly useful in proper choice of parents for realizing higher heterosis and obtaining useful recombinants. Several methods have been advocated by various workers to estimate the genetic divergence in crop plants (Rai *et al.,* 1998). Of the several methods available, Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is an unique tool for disseminating populations considering a set of parameters together rather than inferring from indices based upon morphological similarities, eco-geographical diversity and phylogenetic relationships.

Genetic diversity between genotypes indicates differences in the gene frequencies. Mahalanobis generalized distance is the most widely used technique in plant breeding to know the distance between the genotypes. This statistical module has been employed widely to resolve genetic divergence at inter varietal and species level on classifying crop plants. This is possible by clustering the entries based on D^2 values as it represents the index of genetic diversity among the genotypes and clusters.

Selection of parents for hybridization programme based on their genetic divergence is beneficial in getting heterotic hybrids and also to get desirable segregants. The 41 tomato genotypes evaluated were subjected to Mahalanobis D^2 analysis using twelve quantitative traits to assess the genetic diversity from which 10 parents were used for developing 25 F_1 hybrids in Line x Tester method for heterosis and combining ability study.

All twelve quantitative traits included in the analysis have contributed to the diversity. The contribution of these traits to divergence in three seasons is tabulated in (Table 10).

During *kharif* 2007, *kharif* 2008 and *rabi* 2008, the major contributors to divergence in order of their over all magnitude are number of fruits per plant, single fruit weight, plant height, fruit length during three season evaluation. Bar graph of relative characters contribution to divergence is given in Fig. 4.

The contribution to the total divergence by these attributes indicate their role in maintaining variability in natural population and hence selection of best genotypes for such traits would be helpful in breeding programme.

Based on the D^2 values the 41 tomato genotypes were grouped into six, five and nine clusters on the basis of *kharif* 2007, *kharif* 2008 and *rabi* 2008 evaluations respectively (Table 11) using Tocher's method (Rao , 1952).

Cluster I was the biggest group with 27, 26, 26 genotypes followed by Cluster V with six genotypes in each of three seasons .The same genotypes were in Cluster V in all the three seasons. There were three, one and six solitary clusters with single tomato genotype in *kharif* 2007, *kharif* 2008 and *rabi* 2008 groupings. Dendrograms clustering of 41 tomato genotypes in *kharif* 2007, *kharif* 2008 and *rabi* 2008 are presented in Fig. 5, Fig. 6 and Fig. 7 respectively.

This similarity or dissimilarity of the constituents in a cluster, that is, differences in clustering pattern in such cases is attributed to differences in environmental conditions in the three seasons which might have shown their influence in the process of discrimination.

From this study, it was concluded that, in general, there was no parallelism in genetic diversity in all the three seasons. For genetic diversity geographical diversity is not an index, which is observed by clustering pattern. This indicates that clustering pattern is because of the maximum differences in characters contributing towards diversity. The role of different plant traits in the inter cluster divergence can be studied by comparing cluster means for different traits in three seasons.

The D^2 values for inter and intra clusters are given in the Table 12. Based on the cluster means for each character it was possible to group the cluster according to their average performance for a particular character.

The inter cluster D^2 value was maximum between clusters III & V, III & V , V &VII followed by clusters IV & V, IV&V and V& IX for *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. The minimum distance observed was between clusters I & II, I & II and VI & VII for three seasons respectively. Cluster V in all three groupings was the most diverse as many clusters showed maximum inter cluster distances with it.

The intra cluster distance was observed in clusters I, III & V in *kharif* 2007; Clusters I, II, III & V in *kharif* 2008 and Clusters I, IV, & V in *rabi* 2008 as remaining clusters contained only one genotype each. Remaining clusters showed zero intra cluster distances as they were solitary genotype containers.

It could be observed that the higher magnitude of distance between clusters indicating the genotypes between these clusters were more divergent. The minimum distance observed between clusters indicated that the genotypes of these individual cluster pairs were comparatively closer to each other.

The mean values of 12 characters for six, five and nine clusters of three seasons evaluations are summarized in Table 4.8. Comparison of cluster means for the different characters indicated considerable differences between clusters for all the characters. During *kharif* 2007, Cluster V had greater mean values for yield per plant, number of fruits per plant, TSS. Cluster V in *kharif* 2008 had highest mean values for yield per plant, number of fruits per plant, TSS while in *rabi* 2008 Cluster VI had highest mean values for yield per plant.

Cluster I which was having maximum number of genotypes in it recorded plant heights of 93.49, 90.17 and 93.83 cm; single fruit weight of 67.97 , 71.26 and 74.80 g ; number of fruits per plant 37.47, 40.95 and 45.23; and yield per plant of 1.22, 1.38 and 1.74 kg in *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. Highest single fruit weight was in cluster III (107.66 g), III (103.49 g) and VI (106.46 g) during three seasons sequentially while for number of fruits, yield per plant and TSS Cluster V was having highest character values in all seasons except as second highest in *rabi* 2008 for yield. It indicates that the mean values for each trait for three seasons changes as genotypes grouped within the cluster vary so also the trait *per se* values. Cluster V had in all six number of same genotypes in all three season divergence clustering but the individual traits values varied in magnitude. It indicates effect of environment and cluster genotypes constitution on the trait or character values.

The D^2 matrix values ranges and magnitude were 8.93-909.30, 4.23-1072.55 and 14.92-1398.49 for three seasons i.e., *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. The major contributors to divergence over three seasons in order of their over all range and magnitude are number of fruits per plant (28.9-33.29 %), single fruit weight (9.51-29.51 %) , plant height (12.5-18.41 %) , fruit length (8.17-12.68 %), and yield per plant (0.85-1.95 %). These traits i.e., number of fruits per plant , single fruit weight, plant height, fruit length , and yield per plant had GCV of 83-89 %, 39-42 %, 21-23 %, 21-22 %, and 15-18 % respectively ; PCV of 83-90 %, 39-42 %, 21-23 %, 21-22 %, and 16-19 % respectively; *per se* value ranges of 18.97-226.11, 10.22-118.50 g, 62.90-166.10 cm, 2.03-2.12-6.35 cm, 0.726-2.154 kg/pl respectively and *per se* mean values of 58.10-66.40, 64.57-69.12 g, 99.44-102.08 cm, 4.27-4.49 cm, 1.308-1.732 kg/pl respectively across seasons. This indicates that the major contributors to divergence had higher GCV, PCV and mean values. Traits with higher values of GCV and PCV are going to be the major contributors to divergence in the same proportion.

Maximum inter-cluster distances were 25.11 (between cluster V and III), 28.21 (between cluster V and III) and 23.84 (between cluster V and VII) while minimum inter-cluster distances were 6.51 (between cluster I and II), 7.01 (between cluster I and IV) and 5.78 (between cluster VI and VII) during three seasons i.e., *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. Maximum intra-cluster distances were 6.24 (cluster V), 6.04 (cluster V) and 7.34 (cluster V) while minimum intra-cluster distance of zero was in three (II, IV, VI), one (IV) and six (II, III, VI, VII,VIII and IX) clusters with solitary genotype during three seasons i.e., *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. Higher magnitude of inter-cluster distances were recorded by cluster V with other clusters during all three seasons. For number of fruits, yield per plant and TSS Cluster V was having highest character values in all seasons except as second highest in *rabi* 2008 for yield. This shows that the cluster with maximum values of major traits contributing divergence also has higher magnitude of inter-cluster distances with other clusters and could be the source of diverse genotypes.

Irrespective of the seasons, the crosses between genotypes of diverse background reflected in higher cluster distances of each pairs may create some useful transgressive segregants. The diverse cluster V though had higher values for major traits, it could not be utilized for selecting parents as the genotypes in it had small sized fruits. Looking to the marketable size of fruits with good yield contributing traits like fruit weight, fruit size, number of fruits per plant, yield per plant and their consistence in performance i.e., *per se* performance along with information obtained from divergence study was used in selecting parents. The parents selected for crossing programme in this study were spread out in four clusters [cluster I (CO-3, Megha (L-15), Pant-T-10, KS-227, Dwd-T-1), Cluster II (Dwd-T-6), Cluster III (DVRT-2, VR-35, Dwd-T-3), Cluster IV (H-24)], three clusters [cluster I (CO-3, KS-227, Megha (L-15), Pant-T-10, Dwd-T-1, Dwd-T-6), Cluster III (DVRT-2, VR-35, Dwd-T-3), Cluster IV (H-24)] and four clusters [cluster I (H-24, KS-227, Megha (L-15), Pant-T-10, VR-35, Dwd-T-1, Dwd-T-6), Cluster III (CO-3), Cluster VI (Dwd-T-3), Cluster VII (DVRT-2)] during *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively. Solitary clusters constituted by some of these parents were seen and to indicate them are underlined in the previous sentence. The

lines fell in Clusters I, III, IV in *kharif* 2007, in Clusters II, III, *kharif* 2008 and clusters I, III,VII *rabi* 2008 respectively. The testers fell in clusters II, III in *kharif* 2007, in clusters I, III, *kharif* 2008 and clusters I, IV, *rabi* 2008 respectively.

These observations are in accordance with the observations of Shalini (2009), Shashikanth (2008), Mane (2008), Sekhar *et al.,* (2008), Veershetty (2004), Sharma and Verma (2001), Dharmatti *et al.,* (2001) and Rai *et al.* (1998).

5.4 STABILITY ANALYSIS

Stability of a genotype indicates its adaptability and performance with predictability with least variations in performance or phenotype under different environments. It is a prerequisite for identifying an entry for utility in vegetable improvement. Identifying stability is challenging in presence of environmental influences and genotype x environment interactions by splitting into components. It is achieved by selecting entries with high mean yield, deviations from mean value approaching zero and regression coefficient value equal to one as suggested by Eberhart and Russell (1966).
Discussions on results of stability analysis done for 41 tomato genotypes evaluations in three environments (*kharif* 2007, *kharif* 2008 and *rabi* 2008 seasons) is presented under following headings:

5.4.1 Pooled analysis of variance
5.4.2 Stability parameters

5.4.1 Pooled analysis of variance

Pooled analysis of variance for nineteen quantitative traits across three different seasons revealed that there were significant differences among the genotypes tested for all the characters studied. The environment in which all the observations were recorded also differed significantly to influence significant variation in all the characters recorded except for number of branches per plant, number of fruits per cluster, and number of locules per fruit.

The differences due to genotype × environment interaction were found to be highly significant for yield per plant and powdery mildew. The genotype × environment interactions differed significantly for the traits viz., fruit width, yield per hectare, early blight and *Sclerotium* wilt incidence.

In order to know the magnitude of linear and non linear components of variations which provide information on predictable and unpredictable sources of variations respectively, contributing to genotype × environment interactions for all characters the partitioning was done as.

The effects due to environments (linear) were highly significant for all the characters except for number of branches per plant, number of fruits per cluster, pericarp thickness, number of locules per fruit, TSS, late blight, and tomato leaf curl incidence. The variance due to variety/genotype × environment (linear) were found to be highly significant for the seven characters viz., fruit width, TSS , yield per plant, yield per hectare, early blight, powdery mildew and Sclerotium wilt. The mean sum of squares due to pooled deviation was also found significant for all the characters except days to 50 % flowering, number of locules per fruit, TSS, number of fruits per plant, and powdery mildew incidence, which indicates the non linear or unpredictable portion of G × E interaction when tested against pooled error.

Since the G × E interactions were found significant for most of the characters, the data of all the nineteen characters were subjected to stability analysis. This indicated that the performance can not be predicted over the environments for these traits. Pandey (1983) reported significant G x E (linear) interaction for plant height and number of branches. A genotypes x environment (linear) interaction significant for number of locules per fruit was observed Aravindakumar *et al.* (2001).

5.4.2 Stability parameters

Once the genotype × environment interactions were found to be significant, the next task is to identify stable genotypes. The stable genotypes are one which interact less with the

environments giving a near consistent performance across different environments. Many stability models have been developed to identify the stable genotypes. Eberhart and Russell (1966) model is the one which has been used in tomato and in other crops by several workers. According to Eberhart and Russell (1966), a variety is said to be stable when regression coefficient (b_i) is equal to one and deviation from regression (S^2d_i) as close to zero as possible with high mean performance. Selection of stable genotypes that interact less with environments in which they are to be grown with a view to reduce the genotype × environment interaction to a considerable extent.

The above three measures of assessing the stability of genotype *viz.,* mean, regression coefficient (b_i) and the mean square deviation (S^2d_i) were employed in assessing the stability of genotypes included in the present study. The linear regression (b_i) could simply be regarded as the measure of response of a particular genotype and if it is greater than one then, the genotype is said to be sensitive to environmental changes but adapted to favorable environments. If it is less than one then it indicates above average stability. If this is accompanied by a high mean value then, the genotype is said to be better adapted to widely differing conditions or unfavorable environments and if the mean value is low, greater G × E interaction indicated (Finlay and Wilkinson, 1963). On the other hand, deviation around the regression line is considered as a better measure of stability. With respect to the non linear component of the G × E interaction, the genotype with the lowest standard deviations will be the most stable and vice- versa.

Table 15 has environmental indices and Table 16 to Table 23 has three stability parameters [*viz*., mean, regression coefficient (b_i) and mean square deviation from linear regression line (S^2d_i)] estimated for nineteen characters as per Eberhart and Russell model. The results pertaining to these stability parameters are discussed for most important characters below:

5.4.2.1 Environmental Indices

Nineteen traits recorded significant variations or differences across three seasons or environments as reflected in the environmental indices (Table 15). Number of branches per plant had the lowest values of environmental indices while tomato leaf curl virus incidence had the highest values of environmental indices, followed by number of fruits per plant and yield per hectare for three environments of evaluations. In all *rabi* 2008 was a favorable environment for all traits compared to other seasons as indicated by positive values of environmental indices.

5.4.2.2 Mean, regression coefficients (b_i), and mean square deviation from linear regression line (S^2d_i)

Table 16 to Table 23 has three stability parameters [viz., mean, regression coefficient (b_i) and mean square deviation from linear regression line (S^2d_i)] for all the nineteen traits recorded.

However, of all the nineteen traits used for stability analysis, the yield per plant and yield per hectare are utmost important characters. Hence only these traits are taken up for discussion as other traits could be glanced in above mentioned tables.

5.4.2.2.1 Yield per plant (cf. Table 20)

Mean yield per plant across three seasons was 1.492 kg. The genotype 'VR-35' recorded the highest mean yield of 1.964 kg per plant and the lowest mean yield was recorded by the genotype 'H-24' with 0.955 kg over three seasons.

Ten tomato genotypes i.e., 'CO-3', 'HADT-294', 'Pant-T-11', 'VTG-106', 'VTG-93', 'Dwd-T-4', 'Dwd-T-6', 'Dwd-T-8' and 'Dwd-T-9' were specially adapted to favorable environments as they had higher yield per plant than the mean yield , more than one regression coefficient value and non significant deviation from the regression values. These could be grown with high input management conditions.

Seven tomato genotypes i.e., 'HAT-121', 'HAT-20', 'KS-227', 'PAU-2374', 'Arka Vikas', 'VTG-95', 'Dwd-T-3' and 'Dwd-T-7' were specially adapted to unfavorable (poor)

environments as they had higher yield per plant than the mean yield, more than one regression coefficient value and non significant deviation from the regression values. These could be grown with low input management conditions.

Five tomato genotypes i.e., 'PAU-2374', 'Arka Vikas', 'VTG-95', 'Dwd-T-3' and 'Dwd-T-7' were well adapted to all the environments as they had higher yield per plant than the mean yield , more than one regression coefficient value around one and non significant deviation from the regression values. These could be grown under all management conditions without much fluctuation on account least genotype x environmental interaction in them.

The stable genotypes for yield per plant were reported by earlier workers like Shalini (2009), Mane (2009), Prasanna *et al.* (2007), Dhaduk *et al.* (2004), Hosamani *et al.* (2003) Upadhyay *et al.* (2001), Kilchevsky and Babak (2001) and Mandal *et al.* (2000).

Distribution of 41 tomato genotypes graphically for yield per plant trait stability parameters like mean, regression coefficients, deviations from regression values and environmental indices through scatter graphs is shown in Fig. 8.

5.4.2.2.2 Yield per hectare (cf. Table 21)

Mean yield per hectare for three seasons were 27.82, 30.58 and 36.29 t/ha. The grand population mean was 31.56 t/ha. Two of the three seasons recorded lower than the favourable environment of *rabi* 2008. The genotype 'PAU-2372' recorded highest mean yield of 39.25t/ha and lowest mean yield was recorded by the genotype 'H-24' with 19.86 t/ha over three seasons. The highest yielders in kharif 2007, kharif 2008 and rabi 2008 were 'PAU-2372', 'VR-35', and 'Pant-T-11'.

Six tomato genotypes i.e., 'ATL-02-39', 'Pant-T-11', 'VTG-106', 'Dwd-T-3' 'Dwd-T-7', and 'Dwd-T-8' were specially adapted to favorable environments as they had higher yield per hectare than the mean yield, more than one regression coefficient value and non significant deviation from the regression values. These could be grown with high management conditions.

Three tomato genotypes i.e., 'HAT-121', 'Pant-T-10' and 'PAU-2372', were specially adapted to unfavorable (poor) environments as they had higher yield per plant than the mean yield , more than one regression coefficient value and non significant deviation from the regression values. These could be grown with low input management conditions.

Four tomato genotypes i.e., 'HADT-294', 'PAU-2371', 'Dwd-T-1' and 'Dwd-T-6' were well adapted to all the environments as they had higher yield per plant than the mean yield , more than one regression coefficient value around one and non significant deviation from the regression values. These could be grown under all management conditions without much fluctuation on account of least genotype x environmental interaction in them.

The stable genotypes for yield per hectare were reported by earlier workers like Hosamani *et al.* (2003), Upadhyay *et al.* (2001), Kilchevsky and Babak (2001) and Mandal *et al.* (2000).

EXPERIMENT II: EVALUATION OF F_1 HYBRIDS DEVELOPED BY LINE X TESTER METHOD DURING *RABI* 2008

5.5 HETEROSIS

Heterosis is superiority of F_1 produced from crossing between two diverse parents in the desired direction in a trait of interest. Heterosis breeding has been employed to achieve enhanced yields coupled with stress resistances and quality parameters. Tomato is one of the leading vegetable crops in which it has been exploited to the maximum. Involvement of 10 diverse parents (i.e., 5 lines and 5 testers) in Line x Tester mating design was done to generate 25 hybrids. They were evaluated during *rabi* 2008 along nationally recommended commercial hybrid check 'ARTH-3' and local open pollinated check 'Megha (L-15)'. Observation for 19 growth, quality, yield and disease parameters were recorded and used for analysis to generate information on heterosis and combining ability.

5.5.1 Analysis of variance

All the entries (treatments) comprising parents and hybrids showed significant difference for all the characters as seen from the ANOVA (Table 24). All traits of parents except for late blight incidence were differing significantly. Among the parents, lines (females) exhibited significant differences for all the characters except for late blight incidence. Similarly, the testers (males) also differed significantly for all the characters except for late blight, TLCV, and tomato spotted wilt virus incidence. The contribution of lines Vs tester showed significant variation for all the characters except for number of branches per plant, number of locules per fruit, TSS and late blight. Variance, for parents vs. hybrids was significant for all the characters except for number of branches per plant, days to 50 % flowering, number of fruits per cluster, fruit length, number of locules per fruit, early blight and powdery mildew. Within crosses all traits exhibited significant variation for all traits except pericarp thickness, and tomato leaf curl virus incidence.

5.5.2 *Per se* performance and magnitude of heterosis

The *per se* performance of the parents (i.e., lines & testers), F_1's , commercial check (ARTH-3) and local check [Megha (L-15)], per cent heterosis over mid parent (MP), better parent (BP), and commercial check (CC) for the nineteen characters were studied (Tables 25 to 34). While highlighting the results of each trait under subsequent sub headings focus will be on *per se* values and commercial heterosis percentages as they would of utility and average heterosis or heterobeltiosis would be of academic interest that could is indicated in values from corresponding tables. Discussion on yield per plant and yield per hectare would be focused as it is more important parameter.

The range of average heterosis in nineteen characters varied from -3.28 per cent recorded in fruit width and single fruit weight to 18.65 per cent in yield per hectare while it was 15.86 per cent for yield per plant (Appendix IV).

Single fruit weight: Minimum single fruit weight was recorded in 'KS-227' (63.44 g) and maximum in 'DVRT-2'(114.63 g) while, among the crosses 'CO-3' x 'Dwd-T-6' weighed minimum (62.82 g) as against maximum weight of fruit in cross 'DVRT-2' x 'VR-35' weighed (107.18 g). Seven crosses had higher fruit weight than the commercial check. Out of 25 hybrids four crosses had significant positive heterosis over commercial check.

Number of fruits per plant: Out of 25 hybrids six crosses had significant positive heterosis over commercial check. The maximum heterosis over commercial check was manifested by 'Pant-T-10' x 'Dwd-T-6' (48.17%).

Yield per plant: The total yield per plant among the parents ranged from 1.158 kg in 'H-24' to 2.116 kg in 'VR-35'. Among the F_1s, the highest of 2.375 kg was registered by 'DVRT-2' x 'VR-35' followed by 'Pant-T-10'' x 'VR-35' (2.135 kg), 'Pant-T-10' x 'Dwd-T-6' (2.126 kg) and 'DVRT-2' x 'KS-227' (2.108 kg). Commercial check had a yield of 1.751 kg and local check 'Megha (L-15)' yielded 1.542 kg/plant. Heterosis over commercial check ranged from -12.32 to 35.68 respectively. Seven hybrids 'DVRT-2' x 'VR-35' (35.68%), 'Pant-T-10' x 'KS-227' (21.93%), 'Pant-T-10' x 'Dwd–T-6' (21.46%), 'DVRT-2' x 'KS-227' (20.39%), 'Pant-T-10' x 'Dwd-T-3' (18.51%), 'DVRT-2' x 'Dwd-T-6' (16.13%) and 'Megha (L-15)' x 'Dwd-T-3' (16.30%) with 2.375, 2.135, 2.126, 2.108, 2.075, 2.033 and 2.036 kg/plant respectively exhibited positive significant heterosis over commercial check .

Yield per hectare: The total yield per hectare among the parents ranged from 21.97 t/ha in 'H-24' to 44.63 t/ha in 'VR-35'. Among the F_1s, the highest of 48.47 t/ha was registered by 'DVRT-2' x 'VR-35' followed by 'Pant-T-10'' x 'VR-35' (45.65 t/ha), 'DVRT-2' x 'KS-227' (45.09t/ha), Pant-T-10' x 'Dwd-T-3'(43.74 t/ha), 'DVRT-2' x 'Dwd-T-6'(43.71 t/ha), 'CO-3' x 'Dwd-t-3' (43.47 t/ha) and 'Pant-T-10' x 'Dwd-T-6' (42.78 t/ha) . Commercial check had a yield of 35.80 t/ha and local check 'Megha (L-15)' yielded 28.36 t/ha. Heterosis over commercial check ranged from -8.15 to 35.38 respectively. Seven hybrids 'DVRT-2' x 'VR-35' (35.39%), 'Pant-T-10' x 'VR-35' (27.54%), 'DVRT-2' x 'KS-227'(25.97%), Pant-T-10' x 'Dwd–T-3' (22.19%), 'DVRT-2' x 'Dwd-T-6' (22.10%), 'CO-3 X Dwd-T-3' (21.43%), 'Pant-T-10' x 'Dwd-T-6' (19.50%), and 'Megha (L-15)' x 'Dwd-T-3' (18.87%) with 48.47, 45.65, 45.09, 43.74, 43.71, 43.47, 42.78 and 42.55 t/ha respectively exhibited positive significant heterosis over commercial check .16 hybrids showed positive significant commercial heterosis . In all 22 and 25 hybrids recorded higher yield than commercial check and local check respectively.

High yielding hybrids with high positive heterosis over commercial check are 'DVRT-2' x 'VR-35' (35.39%), 'Pant-T-10' x 'VR-35' (27.54%), 'DVRT-2' x 'KS-227'(25.97%), Pant-T-10' x 'Dwd–T-3' (22.19%), 'DVRT-2' x 'Dwd-T-6' (22.10%), 'CO-3 X Dwd-T-3' (21.43%), 'Pant-T-10' x 'Dwd-T-6' (19.50%) and 'Megha (L-15)' x 'Dwd-T-3' (18.87%) . The foregoing discussion on yield and yield components indicated the role of non-additive and additive gene effect in governing these traits.

Heterosis never concerns directly to the whole plant organization, but occurs in the development of individual traits. Therefore, the sources of heterosis are essentially formed and located in separate systems, enclosed in the cell apparatus of the hybrid progenies. These sources represent on altered genetic system brought about by the interaction of heterogeneous genetic background. The interaction does so through complementation and mutual intensification of structural genes (such as changes in gene dose, position effect, production of extra DNA copies *etc.*) and through improvement of the balance of genetic factors controlling the regulatory mechanisms of the cell (Sharma, 1994). Shalini (2009), Yeshvanthkumar (2008), Prashanth (2004) and many other workers have recorded heterosis for various growth and yield parameters.

Among the 25 hybrids two, three, none, none, none, and none had significant negative heterosis over commercial check for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt disease incidence.

Graphical presentation of average heterosis for hybrids evaluated for disease incidence and other growth, yield and quality parameters is presented in Fig. 10.

5.6 COMBINING ABILITY

The combining ability analysis gives an indication of the variance due to GCA and SCA which represent a relative measure of additive and non-additive gene effect, respectively. Several workers have shown that dominance is a component of additive genetic variance. If *sca* effect is the main cause for superiority of a cross, it is inferred that superiority of the cross cannot be fixed through selection. Hence, this necessitates combining ability studies, which helps in choosing potential parents for hybridization based on general combining ability and potential crosses based on their specific combining ability.

5.6.1 Analysis of variance for combining ability

Crosses showed highly significant differences for all the traits except for number of branches per plant which was just significant. Differences among lines were significant only for 14 traits out of 19 except for early blight, late blight, powdery mildew, tomato leaf curl virus and tomato spotted wilt incidence. Differences testers were significant only for twelve traits out of 19 except for yield per plant, yield per hectare, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and Sclerotium wilt incidence. For all the characters line x tester variance was significant except for five i.e., number of branches per plant, number of fruits per cluster, fruit length, pericarp thickness and TSS.

Contribution of line was more for plant height, days to 50 % flowering, number of fruits per cluster, fruit length, pericarp thickness, TSS, single fruit weight, and yield per plant. While, maximum contribution recorded by testers for number of branches per plant, fruit width, number of locules per fruit, and early blight. The contribution of line x tester was of higher in magnitude than either line or tester for yield per hectare, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus, and Sclerotium wilt incidence indicating predominance of non-additive gene action for these traits.

The estimates of GCA variance were higher for plant height, days to 50% flowering, single fruit weight, and number of fruits per plant.

The estimates of SCA variance were greater in magnitude than those of GCA variance for yield per hectare, powdery mildew, tomato spotted wilt virus, and Sclerotium wilt virus.

The estimates of ratio of GCA variance to SCA variance was higher for number of branches per plant, number of fruits per cluster, fruit length, fruit width, pericarp thickness, number of locules per fruit, TSS, yield per plant, early blight, late blight and tomato leaf curl virus.

Heritability in narrow sense was high for plant height, number of branches per plant, days to 50 % flowering, number of fruits per cluster, fruit length, fruit width, pericarp thickness, number of locules per fruit, TSS and number of fruits per plant. It was moderate for six traits viz. yield per plant, yield per hectare, early blight, late blight, powdery mildew, and Sclerotium wilt incidence. For two traits i.e., tomato leaf curl virus and tomato spotted wilt virus incidence it was low.

Genetic advance over mean was moderate for three traits i.e., plant height, single fruit weight and number of fruits per plant and for rest of the traits it was low.

5.6.2 Combining ability effects

Combining effects are of two types: general combining effects and specific combining effects. These are basis or important in selecting or identifying the suitable parents for hybridization programme. The estimates of general combining ability (gca) and specific combining ability (*sca*) effects for all the nineteen characters are presented in Table 36 and 37 respectively. In each trait their role is highlighted as below:

Single fruit weight: This trait had highest *gca* and *sca* effect values amongst all the 19 traits in present study. 'DVRT-2' (15.80) and 'Dwd-T-3' (8.89) amongst lines and testers recorded highest significant positive *gca* effects ever recorded for in any trait in this study. ' DVRT-2' x 'Dwd-T-1' (-16.19) and 'DVRT-2' x 'VR-35' (9.97) recorded highest significant positive *gca* effects ever recorded for in any trait in this study. All lines except one and all tester showed significant *gca* effects. The female parents 'DVRT-2' (15.80) followed by 'Pant-T-10' (2.97) and in male parents 'Dwd-T-3' (8.89) followed by 'VR-35' (4.46) exhibited significant positive *gca* effect. The crosses 'DVRT-2' x 'VR-35' (9.97), 'CO-3' x 'Dwd-T-3' (8.79), 'H-24'x 'Dwd-T-1' (7.00), and 'Megha (L-15)' x 'Dwd-T-1' (6.26) had significant positive *sca* effects. These effects indicate predominance of additive and non-additive factors respectively in expression of this trait.

Number of fruits per plant: Significant positive general combining ability effect was observed in three parents viz., 'Pant-T-10' (7.38) and 'Megha (L-15)'(3.21) in lines while highest *gca* in 'Dwd-T-6' (11.03) among testers. The best cross with highest positive *sca* effect was in 'Pant-T-10' x 'Dwd-T-6' (6.47) followed by 'Megha (L-15)' x 'Dwd-T-3' (4.38), 'Megha (L-15)'x 'VR-35' (4.33) and 'Pant-T-10' x 'Dwd-T-1' (3.77). These effects indicate predominance of additive and non-additive factors respectively in expression of this trait.

Yield per plant: 'DVRT-2' (0.15) and 'Pant-T-10' (0.12) among lines and 'VR-35' (0.10) in testers recorded significant positive *gca* effects for the yield per plant. Three crosses manifested significant *sca* effect of which two were positive .The highest significant positive *sca* effect was observed in 'H-24' x 'Dwd-T-1' (0.27) followed by 'DVRT-2' x 'VR-35' (0.23). These effects indicate predominance of additive and non-additive factors respectively in expression of this trait.

Yield per hectare: Two lines ['DVRT-2' (2.92), 'Pant-T-10' (1.87)] and one tester ['VR-35' (1.20)] had positive *gca* effects for the yield per hectare. 'H-24' (-3.63) in lines and 'Dwd-T-1' (-1.75) in testers exhibited significant negative gca effects for this character. The highest significant positive *sca* effect was observed in 'H-24' x 'Dwd-T-1' (6.12) followed by 'DVRT-2' x 'VR-35' (3.99) and 'CO-3' x 'Dwd-T-3' (3.31). These effects indicate predominance of additive and non-additive factors respectively in expression of this trait.

Diseases incidence: There were one ,one, none, one and one amongst lines while in testers two, one, none, none and one with significant negative *gca* effect for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and Sclerotium wilt disease incidence respectively. Two ['CO-3' x 'VR-35' (-0.75) and 'Megha (L-15)' x 'Dwd-T-6' (-0.60)], none , three ['Pant-T-10' x 'VR-35' (-0.72), 'Megha (L-15)' x 'KS-227' (-0.65) and 'DVRT-2' x 'VR-35' (-0.64)], none, none and one ['CO-3' x 'VR-35' (-3.77)] crosses showed significant negative *sca* effects for early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and Sclerotium wilt disease incidence respectively.

Graphical presentation of *gca* effects of parents, heterosis in hybrids, and hybrid distribution for TSS, single fruit weight, yield per plant is presented in Fig. 11 to Fig. 14.

These findings are in agreement with Shalini (2009), Yeshwanthkumar (2008), Singh *et al.* (2008), Premalakshmi *et al.* (2006), Singh *et al.* (2005), Mahendrakar (2004), Kulkarni (2003), Sajjan (2001), Dharmatti (1995) and Dod *et al.* (1995).

The *sca* effect, being a estimate, may be biased, as it is based on certain assumptions. The *per se* performance on the other hand is the actual realized mean. For improving the traits, heterosis breeding is the best approach as there was more non-additivity. Traits governed by both additive and non-additive gene effects, as this trait has equal magnitude of dominance and additive variances, inter-mating followed by recurrent selection should be followed for improvement.

Improvements in individual component and certain associated traits may be better approach for raising yield potential of the crop. For exploitation of heterosis the information on *gca* should be supplemented with *sca* and hybrid *per se* performance.

5.6.3 INFLUENCE OF OVERALL COMBINING ABILITY EFFECTS OF THE PARENTS ON HETEROTIC HYBRIDS

Ascertaining the status of a parent with respect to *gca* over a number of component characters assumes importance as often we observe *gca* effects in desirable direction for a particular parent in respect of some characters and in undesirable direction for others. Classification of the ten parents involved in twentyfive crosses as low (L), average (A) and high (H) general combiners are presented in Table 38 as suggested by Arunachalam and Bandopadhya (1979).

'DVRT-2', 'H-24', 'Megha (L-15), Dwd-T-3', and 'Dwd-T-6' were the five parents out of ten parents that were found in the category of overall high general combiners (H). The parents 'Dwd-T-1' scored equal number of positive and negative points and obtained a status of average performer (A). The four parents 'CO-3', 'Pant-T-10', 'VR-35' and 'KS-227' were overall low (L) combiners.

'DVRT-2', 'H-24' and 'Dwd-T-1' could be exploited for yield per plant.

We are often interested in identifying the potential biological systems as the characters are inter-related in vegetable improvement. This assessment is meaningful when it is made over all the characters considered to be useful as components of yield and other economic traits at a time. Crosses were classified as heterotic or otherwise taking 19 characters at a time as suggested by Arunachalam and Bandopadhya (1979) are presented in Table 39 and also giving *gca* status of the crosses.

It was noticed that out of twentyfive crosses, all crosses scored equal or more than 4 B's implying that the amount of heterosis registered by these crosses over all the characters is more, but in order to identify the superior hybrids, crosses showing significantly superior heterosis over better parental values were scored and added over all the 19 characters. The crosses which scored more than overall mean were considered to be most heterotic. Accordingly, all the crosses were found to be most heterotic.

For better insight into the genetics of heterosis, the information on combining ability and heterosis considered together would be more meaningful. That is (i) if the heterotic hybrids involve parents with high *gca* effects, it implies that the parental contribution to heterosis is mainly through additive gene effects, (ii) if it involved parents with low into high *gca* effects , it implies that the parental contribution to heterosis is through additive and non-additive gene effects and (iii) if it involved parents with low into low *gca* effects , it implies that the parental contribution to heterosis is through non-additive gene effects. Each cross was scored with respect to their parental *gca* status over 19 characters. All the twentyfive crosses were highly heterotic. Out of these crosses, 10 were of high and low (H x L or L x H) parents, three were of high and average (H x A or A x H) parents, six were of high and high (H x H) parents, two were of low and average (L x A or A x L) parents and four were of low and low (L x L) parents. Obtaining highly heterotic hybrids (heterosis over their better parent) was possible from the parents with any cross combination of parental overall *gca* status, *i.e.* H x H, H x L, L x H, L x L, H x A, L x A. In general, the frequency of heterotic hybrids was comparatively more in H x L or L x H type of crosses *gca* status, indicating role of non-additive gene effects and additive gene effects.

TABLE 38. POOLED *GCA* EFFECTS OF PARENTS FOR 19 CHARACTERS USED IN HYBRIDS DEVELOPMENT BY LINE X TESTER METHOD.

SL. NO.	PARENTS	PLANT HEIGHT	NO. OF BRANCHES PER PLANT	DAYS TO 50% FLOWERING	NO. OF FRUITS PER CLUSTER	FRUIT LENGTH	FRUIT WIDTH	PERICARP THICKNESS	NO. OF LOCULES PER FRUIT	TOTAL SOLUBLE SOLIDS	SINGLE FRUIT WEIGHT	NO. OF FRUITS PER PLANT	YIELD PER PLANT	YIELD PER HECTARE	EARLY BLIGHT	LATE BLIGHT	POWDERY MILDEW	TOMATO LEAF CURL VIRUS	TOMATO SPOTTED WILT VIRUS	SCLEROTIUM WILT	TOTAL POSITIVE	TOTAL NEGATIVES	GCA STATUS
	LINES																						
1	CO-3	0.	-1	-1	0	+1	-1	0	0	-1	0	-1	-1	0	0	0	-1	0	0	-1	1	7	L
2	DVRT-2	+1	0	+1	-1	0	+1	0	+1	-1	+1	-1	+1	+1	0	0	+1	+1	0	0	9	3	H
3	H-24	+1	0	0	0	0	0	0	0	+1	+1	+1	+1	+1	0	0	0	0	0	0	6	0	H
4	MEGHA L-15	0	0	+1	0	+1	0	+1	-1	+1	+1	-1	0	+1	0	-1	0	0	0	0	6	3	H
5	PANT-T-10	-1	-1	0	+1	0	0	+1	-1	+1	-1	+1	-1	-1	-1	0	+1	0	0	+1	6	7	L
	TESTERS																						
1	VR-35	0	0	-1	0	+1	0	0	-1	-1	-1	0	-1	-1	-1	-1	0	0	0	0	1	8	L
2	KS-227	+1	0	0	0	0	-1	0	-1	0	-1	-1	0	0	+1	0	0	0	0	0	2	4	L
3	DWD-T-1	-1	+1	0	0	-1	0	0	+1	0	-1	+1	+1	-1	+1	0	0	0	0	-1	5	5	A
4	DWD-T-3	+1	+1	+1	0	-1	+1	-1	+1	-1	+1	-1	0	0	-1	0	0	0	0	0	6	5	H
5	DWD-T-6	+1	0	+1	0	+1	+1	+1	+1	0	-1	+1	0	0	0	+1	-1	0	0	+1	9	2	H

CLASSIFICATION OF ALL THE TEN PARENTS INVOLVED IN TWENTY FIVE CROSSES:. FOR THIS PURPOSE, THE PARENTAL *GCA* WAS ASSESSED FOR EACH CHARACTER USING A NORM 'M' EQUAL TO THE MEAN OF THE SIGNIFICANT *GCA* EFFECTS OF PARENTS FOR THAT CHARACTER. THE NON-SIGNIFICANT *GCA* EFFECTS WERE GIVEN A STATUS OF ZERO. THE PARENTS WHOSE *GCA* EFFECTS WAS GREATER THAN OR EQUAL TO 'M WERE CLASSIFIED AS HIGH (H) AND ASSIGNED A SCORE OF +1. OTHERS WERE CLASSIFIED AS LOW (L) WITH A SCORE OF -1. CONSIDERING THE NEGATIVE EFFECTS TO BE MORE IMPORTANT FOR CHARACTERS SUCH AS DAYS TO 50 PER CENT FLOWERING AND DISEASES INCIDENCE, A PARENT WITH LESS THAN 'M' WAS CLASSIFIED AS H. ALL THE FIFTEEN PARENTS WERE THUS SCORED FOR EACH CHARACTER AND FINAL SCORE WAS COMPUTED FOR EACH OF THEM OVER TWENTY ONE CHARACTERS. FINALLY, THE PARENTS WERE SCORED AS H (HIGH), L (LOW) AND A (AVERAGEI.E., WHEN EQUAL NUMBER OF POSITIVE AND NEGATIVE) (ARUNACHALAM AND BANDOPADHYA , 1979).

TABLE 39. CLASSIFICATION OF CROSSES FOR HETEROSIS OVER 19 CHARACTERS IN TOMATO HYBRIDS DEVELOPED BY LINE X TESTER METHOD.

SL. NO.	F_1 HYBRID	PLANT HEIGHT	NO. BRANCHES /PLANT	DAYS TO FLOWERING	NO. FRUITS/ CLUSTER	FRUIT LENGTH	FRUIT WIDTH	PERICARP THICKNESS	NO. OF LOCULES / FRUIT	TSS	SINGLE FRUIT WEIGHT	NO. FRUITS /PLANT	YIELD PER PLANT	YIELD PER HECTARE	EARLY BLIGHT	LATE BLIGHT	POWDERY MILDEW	TLCV	TSWV	SCLEROTIUM WILT	TOTAL B+B*	TOTAL W	STATUS OF CROSSS	GCA STATUS
1	CO-3 X VR 35	W	W	W	W	W	W	W	W	W	W	W	W	W	B	W	B*	W	B	B*	4	15	H	L X L
2	CO-3 X KS- 227	W	W	W	B	W	W	W	W	W	W	B	B	B	W	W	B*	B	W	B*	7	12	H	L X L
3	CO-3 X DWD-T-1	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	B*	B	B	B*	4	15	H	L X A
4	CO-3 X DWD-T-3	W	W	W	W	B	W	W	W	W	W	W	B	B*	W	W	B*	B	B	B*	7	12	H	L X H
5	CO-3 X DWD-T-6	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	B	B	B	B*	4	15	H	L X H
6	DVRT-2 X VR 35	W	W	W	W	W	W	W	W	W	W	W	B*	B*	B*	W	B*	B	B*	B	7	12	H	H X L
7	DVRT-2 X KS- 227	W	W	W	W	W	W	W	W	W	W	W	B*	B**	B*	W	B*	B	B*	B	7	12	H	H X L
8	DVRT-2 X DWD-T-1	W	W	W	W	W	W	W	W	W	W	W	W	W	W	W	B*	B	B*	B	4	15	H	H X A
9	DVRT-2 X DWD-T-3	W	W	B	W	W	W	W	W	B	W	W	B	B	B	W	B*	W	B*	W	7	12	H	H X H
10	DVRT-2 X DWD-T-6	W	W	W	W	W	W	W	W	W	W	W	B	B	B	W	B*	B	B	B	7	12	H	H X H
11	H-24 X VR 35	W	W	W	W	W	W	W	W	W	W	W	W	W	W	B	B	B	B*	B	5	14	H	H X L
12	H-24 X KS- 227	W	W	W	B	W	B	W	W	W	B	W	W	W	B	W	B	W	B*	B*	7	12	H	H X L
13	H-24 X DWD-T-1	B	W	B	W	W	W	W	W	W	W	W	B	B	W	W	B	W	B*	B*	7	12	H	H X A
14	H-24 X DWD-T-3	W	W	B	W	W	W	W	W	W	W	W	W	W	W	B	B	B	B*	B*	7	12	H	H X H
15	H-24 X DWD-T-6	B	W	W	W	B	W	W	W	W	W	W	W	W	W	W	B	W	B*	B*	5	14	H	H X H
16	MEGHA (L-15) X VR 35	W	W	W	W	W	W	W	B	W	W	B	W	W	B	W	B	B*	W	B	5	14	H	H X L
17	MEGHA (L-15) X KS- 227	W	B	W	B	W	W	W	W	W	B	W	B	B	B*	W	B*	B*	W	B	9	10	H	H X L
18	MEGHA (L-15) X DWD-T-1	B	W	W	W	W	W	W	W	W	W	W	B	B	W	B	B	B*	B	B	8	11	H	H X A
19	MEGHA (L-15) X DWD-T-3	W	W	W	W	B	W	W	W	W	W	B	B	B	B	B	B	B*	B	B*	10	9	H	H X H
20	MEGHA (L-15) X DWD-T-6	B	W	W	W	W	W	W	W	W	W	W	W	W	B*	B	B	B*	B	B*	7	12	H	H X H
21	PANT-T-10 X VR 35	W	W	W	W	W	W	W	W	W	W	W	B	B	B*	B	B*	B	B*	B*	8	11	H	L X L
22	PANT-T-10 X KS- 227	W	B	W	W	W	W	B*	B	W	W	B*	B	B	B*	W	B	B	B*	B*	11	8	H	L X L
23	PANT-T-10 X DWD-T-1	B	B	W	B	W	W	B	W	W	B	B*	B	B	B*	W	B	B	B*	B*	13	6	H	L X A
24	PANT-T-10 X DWD-T-3	W	W	B	B	W	W	W	W	B	W	B	B	B*	B*	W	B*	B	B*	B*	10	9	H	L X H
25	PANT-T-10 X DWD-T-6	B	W	W	B	W	W	W	B*	W	W	B	B	B	B*	W	B	W	B*	B*	10	9	H	L X H

THE METHOD TO DECIDE A CROSS AS HETEROTIC OR OTHERWISE WAS EMPLOYED TAKING NUMBER OF CHARACTERS AT A TIME. UNDER THIS SCHEME, FOR EVERY CHARACTER, A CROSS WAS ASSIGNED A STATUS 'B' IF ITS VALUE EXCEEDED THAT OF THE SUPERIOR PARENT, OTHERWISE, A STATUS OF 'W'. ARUNACHALAM AND BANDOPADHYA (1979) HAVE THEORIZED THAT IF P_1 IS THE MEAN OF SUPERIOR AND P_2 THAT OF THE OTHER PARENT, M THE VALUE OF THE MID-PARENT AND F, THE VALUE OF THE F_1 HYBRID, THEN FOUR POSSIBILITIES EXIST.I. $F \geq P_1$, II. $P_1 \geq F > M$, III. $M \geq F \geq P_2$,IV. $P_2 > F$THE PROBABILITY THAT THE F_1 EXCEEDS BETTER PARENT BEING 0.25, AND WHEN CROSS IS SCORED FOR HETEROSIS OVER TWENTY-ONE CHARACTERS, THE NUMBER OF B'S THAT IT WILL SCORE, WILL BE DETERMINED BY THE BINOMIAL DISTRIBUTION $(3/4 + 1/4)^{21}$, WHERE PROBABILITY OF B=3/4, AND PROBABILITY OF W=1/4. THE MEAN OF THIS DISTRIBUTION IS 'NP'=19X1/4 = 4.75. THUS, IT WAS DECIDED THAT IF A CROSS HAS SCORED AT LEAST 4 B'S IT WAS CONSIDERED TO BE HETEROTIC (H).

5.7 TOP TOMATO VARIETIES AND HYBRID PERFORMERS

Crystallizing the out comes from the investigations on 'Biometrical and transformation studies in tomato (*Solanum lycopersicum* L.)' in which evaluation of 41tomato genotypes during *kharif,* 2007, *kharif* 2008 and *rabi* 2008 coupled with evaluation of 25 F_1 hybrids during *rabi* 2008 were done in field experiments is a sure and logical way of utilizing the information generated for further tomato crop improvement work. Hence, top performers for important traits are attempted here.

Among 41 tomato genotypes evaluated for three seasons toppers based on the mean *per se* performance were: 'PAU-2372', 'VR-35', 'HADT-294 and 'ALT-02-39' were higher yielders per hectare. Further it was noticed that, 'VR-35' scored higher for yield per plant and single fruit weight. Highest single fruit weight was noticed in 'PAU-2374', 'Dwd-T-3', 'DVRT-2' and 'VR-35'. For quality traits, 'HADT-294', 'PAU-2373'and 'VRCT-155' were good TSS containers, (Table 40).

Top F_1 hybrids, divergence, combining ability and mean performance:

Among the F_1s, 'DVRT-2' x 'VR-35' (48.47 t), 'Pant-T-10' x 'VR-35' (45.65 t), 'DVRT-2' x KS-227' (45.09 t) and 'DVRT-2' x 'Dwd-T-6' (43.71 t) were top yielders per hectare and incidentally yield per plant too was high in these. Higher yield of 'Pant-T-10' x 'VR-35' was contributed by its higher nuber of fruits per plant, fruits per cluster and higher TSS. Whereas 'Megha (L-15)' x 'VR-35' followed by 'Pant-T-10' x 'VR-35' recorded more TSS content. It is evident that not all the varieties or hybrids are consistent for all the traits under study.

Yield per plant was highest in crosses 'DVRT-2' x 'VR-35'(2.375 kg) , 'Pant-T-10' x 'VR-35' (2.135 kg), 'Pant-T-10' x 'Dwd-T-6' (2.126 kg) and 'DVRT-2' x 'KS-227' (2.108 kg) .

'DVRT-2' x 'VR-35'(2.375 kg/pl) parents were (i) from diverse background from cluster VII and I with a inter-cluster distance of 13.56 in *rabi* 2008 D^2 analysis while they belonged to same cluster III with intra cluster distance of 6.05 in *kharif* 2007 D^2 analysis, (ii) with H x L *gca* effects and (iii) fruit yield of 1.277 kg/pl and 2.116 kg/pl respectivey. This cross had single fruit weight of 107.18 g that was highest and total number of fruits per plant was 45.90.

'Pant-T-10' x 'VR-35' (2.135 kg) parents were (i) from diverse background from cluster I and III with a inter-cluster distance of 8.53 in *kharif* 2007 D^2 analysis while they belonged to same cluster I with intra cluster distance of 6.94 in *rabi* 2008D^2 analysis, (ii) with L x L *gca* effects and (iii) fruit yield of 1.577 kg/pl and 2.116 kg/pl respectivey. This cross had single fruit weight of 83.59 g and 46.58 number of fruits per plant.

'Pant-T-10' x 'Dwd-T-6' (2.126 kg) parents were (i) from diverse background from cluster I and II with a inter-cluster distance of 10.24 in *kharif* 2007 D^2 analysis while they belonged to same cluster I with intra cluster distance of 6.94 in *rabi* 2008D^2 analysis, (ii) with L x H *gca* effects and (iii) fruit yield of 1.577 kg/pl and 1.966 kg/pl respectivey. This cross had single fruit weight of 82.89 g and 47.63 number of fruits per plant.

'DVRT-2' x 'KS-227' (2.108 kg) parents were (i) from diverse background from cluster VII and I with a inter-cluster distance of 13.56 in *rabi* 2008 D^2 analysis while they belonged to cluster III and I with a inter-cluster distance of 8.53 in *kharif* 2007 D^2 analysis, (ii) with H x L *gca* effects and (iii) fruit yield of 1.277 kg/pl and 1.786 kg/pl respectivey. This cross had single fruit weight of 91.77 g and total number of fruits per plant was 36.82.

Above top hybrids when looked from divergence, *gca* effects, and *per se* mean of parents , it indicates that though *gca* effects , divergence and *per se* values are informative and indicative but not very definite explanation for high performance of hybrids. Broadly, it can be accepted that parents of diverse background are likely to give heterotic crosses and parents with H x L *gca* effects crosses were more heterotic than other combinations. Ultimately, it is *per se* performance that needs to be looked at for assessing the worth of the hybrids.

These best or top performing genotypes and F_1 hybrids could be utilized for those traits, for certain purposes and used in hybridization programme.

Table 40. *Per se* performance toppers among tomato genotypes and hybrids.

Sl. No.	Characters	Genotypes	Hybrids
1.	Plant height (cm)	Tall- PAU-2372 Dwarf- Dwd-T-6	DVRT-2 x KS-227
2.	Days to 50% flowering	Earliness – Dwd-T-8 Late – PAU-2373	Megha(L-15) x Dwd-T-6
3.	No. of fruits per cluster	HAT-121	Pant-T-10x Dwd-T-6
4.	No. of fruits per plant	VRCT-155	Pant-T-10x Dwd-T-6
5.	Yield per plant	VR-35 (1.964 kg) VRCT-17 (1.902 kg) VRCT-155 (1.892 kg) PAU-2373 (1.790 kg)	DVRT-2 x VR-35(2.375 kg) Pant-T-10 x VR-35 (2.135 kg) Pant-T-10 x Dwd-T-6 (2.126 kg) DVRT-2 x KS-227 (2.108 kg)
6.	Yield per hectare (t)	‘PAU-2372 (39.25 t) VR-35 (38.85 t) HADT-294 (38.24 t) ALT-02-39 (38.87t)	DVRT-2 x VR-35(48.47 t) Pant-T-10 x VR-35 (45.65 t) DVRT-2 x KS-227 (45.09 t) DVRT-2 x Dwd-T-6 (43.71 t)
7.	Single fruit weight	PAU-2374 (113.24 g) Dwd-T-3 (108.72 g) DVRT-2 (107.15 g) VR-35 (101.28 g)	DVRT-2 x VR-35(107.18 g) DVRT-2 x Dwd-T-3 (102.73 g) CO-3 x Dwd-T-3 (92.63 g) DVRT-2 x KS-227 (91.77 g)
8.	Total soluble solids	HADT-294 (7.85 %) PAU-2373 (7.09%) VRCT-155 (6.88%)	Megha (L-15) x VR- 35 (4.33%) Pant-T-10 x VR-35 (4.29%) Pant-T-10 x Dwd-T-3 (4.24 %)

B. TRANSFORMATION STUDIES IN TOMATO:

Antisense mediated gene silencing and PTGS are remarkable strategies to tackle viruses. Both forms of silencing are involved in production of 20-25nt long degraded RNS (siRNA), which ultimately lead to PTGS. However, PTGS works only when both sense and antisense RNAs are simultaneously present in the plant cell. Transgenic constructs engineered to produce dsRNA as opposed to single stranded sense (s) or antisense (as) RNA cause higher level of RNA silencing (Baulcombe, 2004a; Klahre *et al*., 2002; Smith *et al*., 2000). In addition, a vector construct containing an inverted repeat of the 3'-UTR (SHUTR) has been shown to operate effectively in *Arabidopis* and tomato (Brummel *et al*., 2003), suggesting utility of this approach. However, in plant species that are difficult to transform stable, transitive RNA silencing methods using virus induced gene silencing (VIGS) would be valuable in overcoming this limitation (Liu *et al*., 2002; Smith *et al*., 2006). Therefore, we attempted to develop constructs for different gene silencing, using three major genes of T_0LCV (TCP, TRP and TRS).

A local isolate of T_0LCV from Dharwad was used as a source of genes for developing a TRP sas/ihp gene construct for silencing the expression of genes encoding the replicase of ToLCV(Krishnamurthy, 2006). Based on the available information of nucleotide sequences of T_0LCV, primers were designed for T_0LCV- replicase (TRP). TRP sas/ihp gene construct was employed for developing transgenics in native cultivar 'DMT-2'.

The transgene integration in plant genome was confirmed through PCR amplification of *hpt* II gene. The presence of single ~800bp amplicon in transformed plants corresponding to positive control indicated the integration of transgene (T-DNA). Whereas, it was absent in the negative control (untransformed plant). Among different types of transformed plants tested, the transformation efficiency by PCR analysis was 45.0% under hygromycin selection pressure. The plants developed during the study needs to be now advanced in order to understand their ability to resist ToLCV.

FUTURE LINE OF WORK

1. Multilocation testing of stable and top performers among tomato genotypes may be done for top performers as they are better performers over seasons in one location.
2. Testing the suitability of other genotypes in hybridization programme is needed.
3. Parents with high gca can be used in multiple crosses and segregating population obtained thereof can be screened for segregants which pool all the favorable alleles distributed among the parents. The segregants thus obtained can reveal still higher level of combining ability which could be used to produce better hybrids
4. Superior lines of transgressive segregants including disease resistance could be selected from segregating material
5. The transgenic plants with sequences meant for inhibiting replicase gene transcription needs to be further validated.

6. SUMMARY AND CONCLUSION

An investigation on 'Biometrical and Transformation studies in Tomato (*Solanum lycopersicum* L.)' was carried out at the Main Agricultural Research, University of Agricultural Sciences, Dharwad, Karnataka, India. It has come out with results on (i) variability, heritability, genetic advance, correlation, path analysis, genetic divergence, stability parameters from the evaluation of 41 tomato genotypes for three seasons during *kharif* 2007, *kharif* 2008 and *rabi* 2008, (ii) heterosis and combining ability from the evaluation of 25 F_1's during *rabi* 2008 and (iii) genetic transformation of tomato with RNAi anti-viral [TRP (sas/ihp)] gene constructs to develop transgenic tomato resistant to tomato leaf curl virus disease.

In this study it was attempted to continue with the ever demanding need to identify new tomato genotypes with better performance for the location specific needs at Dharwad either from available material (genotypes evaluation) or generation of new ones (F_1's and transformants) needed for changing requirements in tomato cultivation.

Brief summary of the findings in these investigations are presented below:

- There was highly significant variation among the 41 tomato genotypes evaluated for all the characters in *kharif* 2007, *kharif* 2008 and *rabi* 2008 environments .
- There was wider range of variation recorded for the characters such as plant height, single fruit weight, days to 50% flowering, number of fruits per plant, yield per plant, yield per hectare, TLCV incidence, tomato spotted wilt virus, and *Sclerotium* wilt in all the genotypes.
- PCV was invariably higher than GCV for all the characters.
- High heritability, genetic advance over mean, GCV and PCV were observed for plant height, number of fruits per cluster, number fruits per plant, number of locules per fruit, TSS, fruit length, fruit width, early blight, late blight, powdery mildew, tomato leaf curl virus, tomato spotted wilt virus and *Sclerotium* wilt incidence in all the seasons. The magnitude of difference between PCV and GCV in case of these traits has been very small indicating this category of characters are least affected by the environment. Hence, these traits could be used as selection criteria for selection of individual plants from the population.
- The twelve growth, quality and yield traits were involved in the association and path analysis to know their phenotypic and genotypic correlations among themselves for the tomato evaluations of *kharif* 2007, *kharif* 2008 and *rabi* 2008.
- Yield per plant improvement could be achieved through selection for number of fruits per plant, TSS, and number of fruits per cluster as they showed positive significant associations at both phenotypic and genotypic levels during three seasons.
- The three season path analysis results showed that the yield was directly affected mainly by two traits out of ten i.e., single fruit weight and number of fruits per plant in positive direction at phenotypic and genotypic levels in all environments while it varied in positive direction for two seasons for fruit width and plant height.
- Indirect effects on yield per plant was by: (i) number of fruits per plant through plant height, number of branches per plant, number of fruits per cluster and TSS and (ii) Single fruit weight through fruit length, fruit width, pericarp thickness, number of locules per fruit, days to 50% flowering at both genotypic and phenotypic level.
- The 41 tomato genotypes evaluated were subjected to Mahalanobis D^2 analysis using twelve quantitative traits to assess the genetic diversity from which 10 parents were used for developing 25 F_1 hybrids in Line x Tester method for heterosis and combining ability study.
- All twelve quantitative traits included in the analysis have contributed to the diversity.
- During *kharif* 2007, *kharif* 2008 and *rabi* 2008, the major contributors to divergence in order of their over all magnitude are number of fruits per plant, single fruit weight, plant height, fruit length during three season evaluation.
- Based on the D^2 values the 41 tomato genotypes were grouped into six, five and nine clusters on the basis of *kharif* 2007, *kharif* 2008 and *rabi* 2008 evaluations respectively using Tocher's method.

- Cluster I was the biggest group with 27, 26, 26 genotypes followed by Cluster V with six genotypes in each of three seasons .The same genotypes were in Cluster V in all the three seasons. There were three, one and six solitary clusters with single tomato genotype in *kharif* 2007, *kharif* 2008 and *rabi* 2008 groupings.
- The inter cluster D^2 value was maximum between clusters III & V, III & V , V &VII followed by clusters IV & V, IV&V and V& IX for *kharif* 2007, *kharif* 2008 and *rabi* 2008 respectively.
- Stability analysis as suggested by Eberhart and Russell (1966) done for 41 tomato genotypes evaluations in three environments (*kharif* 2007, *kharif* 2008 and *rabi* 2008 seasons) : (i) Pooled analysis of variance for nineteen quantitative traits across three different seasons revealed that there were significant differences among the genotypes tested for all the characters studied.
- Among all seasons, *rabi* 2008 was a favorable environment for all traits compared to other seasons as indicated by positive values of environmental indices.
- Six tomato genotypes i.e., ATL-02-39, Pant-T-11, VTG-106, Dwd-T-3 Dwd-T-7, and Dwd-T-8 were specially adapted to favorable environments.
- Three tomato genotypes i.e., HAT-121, Pant-T-10, PAU-2372, and Dwd-T-1 were specially adapted to unfavorable (poor) environments.
- Four tomato genotypes i.e., HADT-294, PAU-2371, Dwd-T-1 and Dwd-T-6 were well adapted to all the environments
- Involvement of 10 diverse parents (i.e., 5 lines and 5 testers) in Line x Tester mating design was done to generate 25 hybrids. They were evaluated during *rabi* 2008 along with nationally recommended commercial hybrid check ARTH-3 and local open pollinated check Megha (L-15).
- All the entries (treatments) comprising parents and hybrids showed significant difference for all the characters.
- The range of average heterosis in nineteen characters varied from -3.28 per cent recorded in fruit width and single fruit weight to 18.65 per cent in yield per hectare while it was 15.86 per cent for yield per plant.
- Out of 25 hybrids, six crosses had significant positive heterosis over commercial check for number of fruits per plant. The maximum heterosis over commercial check was manifested by Pant-T-10' x 'Dwd-T-6' (48.17%) for fruit number per plant.
- Among the F_1s, the highest yield per plant of 2.375 kg was registered by 'DVRT-2' x 'VR-35' followed by 'Pant-T-10'' x 'VR-35' (2.135 kg), 'Pant-T-10' x 'Dwd-T-6' (2.126 kg) and 'DVRT-2' x 'KS-227' (2.108 kg). Commercial check, ARTH- 3 had a yield of 1.751 kg and local check 'Megha (L-15)' yielded 1.542 kg/plant.
- Among the F_1s, the highest of 48.47 t/ha was registered by 'DVRT-2' x 'VR-35' followed by 'Pant-T-10'' x 'VR-35' (45.65 t/ha), 'DVRT-2' x 'KS-227' (45.09t/ha), Pant-T-10' x 'Dwd-T-3'(43.74 t/ha), 'DVRT-2' x 'Dwd-T-6'(43.71 t/ha), 'CO-3' x 'Dwd-t-3' (43.47 t/ha) and 'Pant-T-10' x 'Dwd-T-6' (42.78 t/ha) . Commercial check had a yield of 35.80 t/ha and local check 'Megha (L-15)' yielded 28.36 t/ha. Heterosis over commercial check ranged from -8.15 to 35.38 respectively.
- The estimates of GCA variance were higher for plant height, days to 50% flowering, single fruit weight, and number of fruits per plant.
- The estimates of SCA variance were greater in magnitude than those of GCA variance for yield per hectare, powdery mildew, tomato spotted wilt virus, and Sclerotium wilt virus.
- The estimates of ratio of GCA variance to SCA variance was higher for number of branches per plant, number of fruits per cluster, fruit length, fruit width, pericarp thickness, number of locules per fruit, TSS, yield per plant, early blight, late blight and tomato leaf curl virus.
- Heritability in narrow sense was high for plant height, number of branches per plant, days to 50 % flowering, number of fruits per cluster, fruit length, fruit width, pericarp thickness, number of locules per fruit, TSS and number of fruits per plant.

- Single fruit weight had highest *gca* and sca effect values amongst all the 19 traits in present study. The female parents 'DVRT-2' (15.80) followed by 'Pant-T-10' (2.97) and in male parents 'Dwd-T-3' (8.89) followed by 'VR-35' (4.46) exhibited significant positive *gca* effect for single fruit weight. The crosses 'DVRT-2' x 'VR-35' (9.97), 'CO-3' x 'Dwd-T-3' (8.79), 'H-24'x 'Dwd-T-1' (7.00), and 'Megha (L-15)' x 'Dwd-T-1' (6.26) had significant positive *sca* effects.
- Significant positive general combining ability effect was observed in three parents viz., 'Pant-T-10'(7.38) and 'Megha (L-15)'(3.21) in lines while highest *gca* in 'Dwd-T-6' (11.03) among testers for number of fruits per plant. The best cross with highest positive *sca* effect was in 'Pant-T-10' x 'Dwd-T-6' (6.47) followed by 'Megha (L-15)' x 'Dwd-T-3' (4.38), 'Megha (L-15)'x 'VR-35' (4.33) and 'Pant-T-10' x 'Dwd-T-1' (3.77).
- 'DVRT-2' (0.15) and 'Pant-T-10' (0.12) among lines and 'VR-35' (0.10) in testers recorded significant positive *gca* effects for the yield per plant. The highest significant positive *sca* effect was observed in 'H-24' x 'Dwd-T-1' (0.27) followed by 'DVRT-2' x 'VR-35' (0.23). These effects indicate predominance of additive and non-additive factors respectively in expression of this trait.
- Among 41 tomato genotypes evaluated for three seasons toppers based on the mean *per se* performance were: 'PAU-2372', 'VR-35', 'HADT-294 and 'ALT-02-39' were higher yielders per hectare. Further it was noticed that, 'VR-35' scored higher for yield per plant and higher single fruit weight.
- Highest single fruit weight was noticed in 'PAU-2374', 'Dwd-T-3', 'DVRT-2' and 'VR-35'. For quality traits, 'HADT-294', 'PAU-2373'and 'VRCT-155' were good TSS containers.
- Among the F_1s, DVRT-2 x VR-35(48.47 t), Pant-T-10 x VR-35 (45.65 t), DVRT-2 x KS-227 (45.09 t) and DVRT-2 x Dwd-T-6 (43.71 t) were top yielders per hectare and incidentally yield per plant too was higher in these.
- 'Megha (L-15) x VR-35' followed by Pant-T-10 x VR-35 recorded more TSS content.
- Above top hybrids when looked from divergence, *gca* effects, and *per se* mean of parents, it indicates that though *gca* effects, divergence and *per se* values are informative and indicative but not very definite explanation for high performance of hybrids. Broadly, it can be accepted that parents of diverse background are likely to give heterotic crosses and parents with H x L *gca* effects crosses were more heterotic than other combinations. Ultimately, it is *per se* performance that needs to be looked at for assessing the worth of the hybrids.
- The transgenic 'DMT-2' tomato plants were obtained through *Agrobacterium* mediated transformation with sas/ihp TRP construct for silencing the transcription of ToLCV gene encoding replicase.

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*Originals not seen

APPENDIX

Appendix I. Meteorological data recorded at MARS, UAS, Dharwad, Karnataka for the years 2007, 2008 and 2009.

Sl. No	Meteorological Periods		2007					2008					2009				
			Temperature (^{0}C)		Rainfall	Relative humidity		Temperature (^{0}C)		Rainfall	Relative humidity		Temperature (^{0}C)		Rainfall	Relative humidity	
	From	To	Mean Max.	Mean min.	(mm)	Max (%)	Min. (%)	Mean Max.	Mean min.	(mm)	Max (%)	Min. (%)	Mean Max.	Mean min.	(mm)	Max (%)	Min. (%)
1	Jan 01	Jan 15	29.27	12.54	00.00	85.07	56.33	29.52	12.87	00.00	70.27	28.53	28.47	13.29	0.00	73.33	38.80
2	Jan 16	Jan 31	31.53	15.43	00.00	84.19	61.13	29.96	12.92	00.00	61.88	24.19	30.96	13.26	0.00	60.31	30.06
3	Feb 01	Feb 15	31.47	15.37	00.00	79.73	61.07	29.57	16.27	00.00	74.33	40.67	32.38	16.03	0.00	57.33	27.40
4	Feb 16	Feb 28	32.35	16.13	00.00	79.08	48.69	32.86	17.14	00.00	56.86	25.07	34.25	17.62	0.00	57.62	18.92
5	Mar 01	Mar 15	34.27	18.24	00.00	66.53	24.20	33.37	17.51	14.00	51.80	26.20	35.37	19.82	0.00	71.13	23.27
6	Mar 16	Mar 31	36.28	21.16	12.80	81.06	26.06	31.53	20.15	97.00	87.38	46.50	34.75	20.01	29.00	74.94	26.31
7	Apr 01	Apr 15	37.13	21.49	28.40	83.00	25.20	33.62	18.83	26.20	75.53	30.20	36.34	20.97	5.40	78.73	27.93
8	Apr 16	Apr 30	36.15	21.33	50.60	78.33	30.47	35.74	22.03	02.60	85.20	34.47	36.61	21.21	26.80	83.60	30.13
9	May 01	May 15	34.84	21.25	48.40	83.33	46.27	36.20	20.35	01.20	81.80	31.40	37.40	21.58	89.20	78.47	28.00
10	May 16	May 31	34.39	21.36	16.60	80.56	38.75	32.07	19.69	54.60	82.81	43.81	33.76	21.35	58.40	89.06	46.00
11	June 01	June 15	32.27	21.83	50.10	88.93	55.20	29.04	20.76	69.60	92.40	76.33	31.38	21.39	92.40	90.33	57.73
12	June 16	June 30	27.17	20.88	170.00	92.27	82.40	28.39	21.15	32.00	91.27	73.40	29.37	20.41	145.40	90.40	68.47
13	July 01	July 15	26.35	21.51	159.00	91.07	80.40	28.50	20.77	18.60	90.33	69.47	25.81	20.76	111.40	93.93	85.87
14	July 16	July 31	29.41	22.07	52.60	96.33	83.53	26.06	19.28	121.00	86.63	71.69	26.16	21.08	13.40	92.56	80.31
15	Aug 01	Aug 15	25.77	20.52	132.20	93.53	81.87	25.23	20.45	202.20	95.00	86.33	28.03	20.67	58.80	89.80	67.73
16	Aug 16	Aug 31	28.27	20.44	43.80	90.25	71.88	26.96	18.53	11.00	82.38	60.56	28.10	20.51	45.60	90.19	72.88
17	Sept 01	Sept 15	27.45	20.47	39.80	93.20	76.13	27.98	20.57	65.20	92.73	75.53	27.74	20.55	40.4	92.93	71.53
18	Sept 16	Sept 30	26.96	20.23	141.00	91.33	73.53	29.48	20.96	97.20	97.20	70.75	29.33	20.64	183.40	92.93	73.20
19	Oct 01	Oct 15	30.33	19.54	4.00	76.25	60.31	30.57	20.27	50.80	87.67	55.47	27.57	19.93	141.00	89.40	68.40
20	Oct 16	Oct 31	29.08	19.32	70.80	77.25	60.31	30.05	17.63	9.60	79.56	45.50	31.02	17.69	0.00	75.75	38.88
21	Nov 01	Nov 15	30.19	16.90	54.00	74.00	41.13	30.65	14.05	0.00	73.47	33.07	29.08	18.47	31.40	85.07	55.67
22	Nov 16	Nov 30	28.87	13.17	00.00	62.40	34.60	27.99	17.69	72.20	85.33	60.87	28.86	17.58	14.60	83.00	55.53
23	Dec 01	Dec 15	28.36	14.26	00.00	82.93	48.07	28.47	13.29	0.00	73.33	38.80	29.07	14.38	0.00	75.93	40.87
24	Dec 16	Dec 31	28.91	14.91	00.00	79.50	46.21	30.65	12.99	0.00	62.14	32.43	27.52	16.48	76.40	88.94	59.56
	TOTAL				1081.10					945.00					1163.00		

Appendix II. Physical and chemical characteristic of the soil

Sl. No.	Particulars	Value obtained	Rating	Method employed
I	Physical properties			
	Coarse sand (%)	6.26	Clayey soil	International Pipette Method (Piper, 1966)
	Fine sand (%)	14.26		
	Silt (%)	27.50		
	Clay (%)	51.98		
	Bulk density (gm^{-3})	1.32		Core sampler method (Dastane, 1967)
II.	Chemical properties			
	Total nitrogen (%)	0.06		Modified Kjeldhal method (Jackson, 1967)
	Available nitrogen (kg ha^{-1})	220.00	Low	Subbaiah and Asija (1956)
	Available phosphorus (kg ha^{-1})	32.86	Medium	Olsen's method (Jackson, 1967)
	Available potassium (kg ha^{-1})	328.60	High	Flame photometer (Jackson, 1967)
	Organic carbon (%)	0.51	Medium	Wet oxidation method (Jackson, 1967)
	Soil pH 1:2.5 (Soil : water ratio)	7.60	Normal	pH meter (Piper, 1966)

Appendix III. Characters means of tomato genotypes evaluated during *kharif* 2007, *kharif* 2008 and *rabi* 2008.

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
1	ALT-02-39	2007K	72.33	3.65	35.33	3.63	4.79	4.60	0.53	4.33	84.67	4.33	33.18	1.287	33.84	1.81	3.33	0.74	29.58	6.00	13.33
		2008K	79.84	4.00	34.33	2.77	4.96	4.84	0.51	3.70	87.55	4.11	33.68	1.247	35.61	2.22	1.67	0.68	22.67	11.67	18.33
		2008R	80.74	3.18	38.33	3.03	5.03	5.00	0.56	4.20	93.40	4.34	37.85	1.746	38.17	4.00	0.51	2.33	4.33	1.67	8.85
		Mean	77.64	3.61	36.00	3.15	4.93	4.81	0.53	4.08	88.54	4.26	34.90	1.427	35.87	2.68	1.84	1.25	18.86	6.44	13.50
2	VR-20	2007K	98.67	3.22	35.67	3.11	4.08	4.45	0.45	3.44	59.89	3.60	32.10	1.113	26.83	0.85	2.33	0.74	6.15	1.46	3.41
		2008K	84.31	3.15	33.67	3.26	4.18	4.73	0.44	3.74	60.73	3.78	37.33	1.481	33.82	0.73	2.48	0.33	15.57	3.47	10.85
		2008R	85.30	3.11	33.00	3.11	4.47	4.79	0.48	3.67	62.55	4.00	41.93	2.000	38.33	1.82	0.37	4.85	0.37	1.14	16.03
		Mean	89.43	3.16	34.11	3.16	4.24	4.66	0.46	3.62	61.06	3.79	37.12	1.531	32.99	1.13	1.73	1.98	7.36	2.02	10.10
3	CO-3	2007K	93.00	3.21	35.00	2.57	3.85	5.33	0.48	4.22	55.89	3.69	24.74	1.070	23.41	2.67	3.26	0.34	24.11	8.90	3.67
		2008K	87.56	3.78	35.00	2.45	3.39	5.11	0.37	4.12	62.12	3.52	25.74	1.133	24.69	1.93	3.69	0.26	26.92	7.52	5.37
		2008R	90.66	3.40	37.67	3.15	3.74	5.63	0.45	4.23	67.15	3.85	30.04	1.200	26.89	1.51	0.43	4.11	1.19	0.47	24.26
		Mean	90.41	3.46	35.89	2.72	3.66	5.36	0.43	4.19	61.72	3.69	26.84	1.134	25.00	2.03	2.46	1.57	17.41	5.63	11.10
4	DVRT-2	2007K	96.33	4.22	36.67	2.11	4.83	6.39	0.49	6.00	104.11	3.21	22.30	1.190	22.48	3.11	4.20	0.54	16.85	4.33	0.27
		2008K	95.40	3.89	36.33	2.09	4.10	5.85	0.47	5.56	102.72	3.31	22.37	1.050	20.55	1.96	2.42	0.70	26.15	13.63	1.84
		2008R	97.45	3.89	42.00	2.63	4.27	6.64	0.51	5.67	114.63	3.60	26.04	1.277	24.07	2.82	0.24	4.70	0.03	1.96	6.56
		Mean	96.39	4.00	38.33	2.28	4.40	6.30	0.49	5.74	107.15	3.37	23.57	1.172	22.37	2.63	2.29	1.98	14.34	6.64	2.89
5	H-24	2007K	64.67	3.87	33.33	2.89	3.67	4.77	0.41	4.11	56.78	3.36	20.77	0.726	20.36	2.60	3.29	0.87	4.48	3.08	3.63
		2008K	66.70	3.52	35.00	3.14	3.96	5.03	0.43	4.66	50.66	3.29	18.97	0.982	17.25	2.08	3.04	0.60	5.67	3.11	5.49
		2008R	70.39	3.21	37.00	2.82	4.32	5.11	0.44	4.46	57.56	3.50	24.81	1.158	21.97	2.12	0.36	3.00	0.68	3.51	11.55
		Mean	67.25	3.53	35.11	2.95	3.98	4.97	0.43	4.41	55.00	3.38	21.52	0.955	19.86	2.26	2.23	1.49	3.61	3.23	6.89
6	HADT-294	2007K	96.33	3.81	36.67	3.56	3.48	4.93	0.44	4.33	75.34	4.12	27.11	1.447	34.85	0.68	1.52	0.21	19.55	5.49	0.37
		2008K	93.08	3.52	33.67	3.31	3.77	4.93	0.43	4.11	74.22	4.17	30.33	1.417	37.03	0.59	2.29	0.40	43.22	2.74	0.47
		2008R	96.88	3.08	35.67	3.85	4.07	5.18	0.48	4.45	77.92	4.39	35.11	1.967	42.85	2.11	0.21	2.58	0.52	1.06	3.34
		Mean	95.43	3.47	35.33	3.57	3.77	5.01	0.45	4.30	75.82	4.23	30.85	1.610	38.24	1.13	1.34	1.06	21.10	3.10	1.39
7	HAT-121	2007K	144.25	4.47	31.00	10.56	2.81	2.05	0.34	2.00	10.22	7.62	151.97	1.449	30.63	1.15	2.44	0.18	9.23	3.15	1.70

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Appendix III. Contd….

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
		2008K	153.96	4.36	31.88	11.40	3.03	2.03	0.31	2.13	10.40	8.00	168.43	1.358	30.92	1.81	2.26	0.44	16.64	1.87	1.67
		2008R	135.31	4.30	33.67	11.66	3.04	2.32	0.33	2.15	11.56	7.93	178.06	1.600	34.66	2.81	0.26	2.92	0.78	0.22	2.44
		Mean	144.51	4.38	32.18	11.21	2.96	2.14	0.33	2.09	10.73	7.85	166.15	1.469	32.07	1.93	1.65	1.18	8.88	1.75	1.94
8	HAT-20	2007K	120.33	4.74	30.00	7.79	2.03	2.46	0.31	2.55	11.37	5.91	168.85	1.570	23.78	0.48	1.97	0.08	17.55	3.78	5.61
		2008K	123.19	5.41	33.00	8.66	2.07	2.33	0.30	2.96	11.55	6.27	170.07	1.717	25.44	1.11	2.07	0.74	20.81	16.37	9.41
		2008R	125.66	4.13	35.00	9.22	2.12	2.37	0.31	2.77	11.33	6.60	159.00	1.803	29.77	2.37	0.09	2.44	0.26	0.33	15.67
		Mean	123.06	4.76	32.67	8.56	2.07	2.38	0.31	2.76	11.42	6.26	165.97	1.697	26.33	1.32	1.37	1.09	12.87	6.83	10.23
9	KS-227	2007K	106.41	3.18	32.67	4.22	5.01	4.18	0.46	3.56	59.88	3.58	34.41	1.497	33.89	0.13	2.19	0.39	14.77	4.99	2.82
		2008K	102.89	3.22	34.00	4.08	5.13	4.58	0.47	3.78	58.70	3.52	34.33	1.433	34.78	0.10	1.33	0.78	16.08	2.33	3.92
		2008R	108.78	3.48	35.33	3.07	5.07	4.45	0.50	3.41	63.44	3.84	39.77	1.786	38.54	0.17	0.27	0.70	0.22	0.08	2.48
		Mean	106.02	3.29	34.00	3.79	5.07	4.40	0.48	3.58	60.68	3.65	36.17	1.572	35.74	0.14	1.26	0.63	10.36	2.47	3.07
10	KS-229	2007K	96.44	3.00	32.67	3.33	4.70	4.75	0.45	3.33	61.14	3.40	34.92	1.227	28.93	0.26	2.40	0.71	19.78	1.93	2.51
		2008K	94.59	3.70	33.00	3.34	4.57	4.90	0.40	3.63	60.92	3.58	34.15	1.217	27.63	1.08	2.53	0.63	15.27	3.36	2.20
		2008R	104.66	3.33	37.00	3.60	4.84	5.12	0.45	3.52	65.74	3.88	38.44	1.410	33.00	2.85	0.09	3.38	0.05	0.13	2.59
		Mean	98.56	3.34	34.22	3.42	4.71	4.92	0.44	3.49	62.60	3.62	35.84	1.284	29.85	1.40	1.67	1.57	11.70	1.81	2.43
11	Megha (L-15)	2007K	83.33	3.44	31.33	2.89	4.33	4.79	0.35	3.56	52.22	3.79	43.33	1.298	23.57	1.08	2.59	0.32	1.41	1.18	4.41
		2008K	79.25	3.52	33.00	2.89	4.33	4.88	0.31	3.56	53.77	4.02	43.07	1.153	24.50	1.04	2.22	0.78	2.78	2.77	5.59
		2008R	81.00	3.30	34.10	2.89	4.81	5.19	0.34	3.48	60.88	4.29	49.11	1.542	28.36	2.73	0.44	2.80	6.07	0.07	7.03
		Mean	81.19	3.42	32.81	2.89	4.49	4.95	0.34	3.53	55.62	4.03	45.17	1.331	25.48	1.62	1.75	1.30	3.42	1.34	5.68
12	NDT-9	2007K	105.33	3.55	35.00	3.44	3.63	4.71	0.43	4.37	75.80	4.11	29.41	0.973	21.30	1.41	2.45	0.96	12.96	1.27	6.70
		2008K	105.66	3.78	36.00	3.89	3.70	4.87	0.42	4.55	76.82	3.93	33.74	1.088	24.89	1.00	2.99	1.18	9.56	1.67	11.36
		2008R	112.44	3.75	40.00	3.52	3.96	5.20	0.45	4.33	80.03	4.18	37.69	1.301	30.26	2.33	0.85	3.00	1.06	0.02	14.36
		Mean	107.81	3.69	37.00	3.62	3.76	4.93	0.43	4.42	77.55	4.07	33.62	1.121	25.48	1.58	2.09	1.71	7.86	0.99	10.81
13	PANT-T-10	2007K	82.33	2.67	34.33	3.89	3.85	4.72	0.41	2.56	69.11	4.08	34.93	1.268	29.92	1.18	2.52	1.86	7.84	2.85	5.30
		2008K	82.11	2.96	34.33	3.70	3.96	4.83	0.42	2.66	70.88	4.07	35.45	1.456	34.63	1.42	3.08	0.44	14.49	4.08	6.13
		2008R	84.63	3.00	37.11	3.74	4.11	5.01	0.50	2.89	75.77	4.23	37.91	1.577	37.71	2.89	0.81	3.07	0.77	3.50	16.20

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Appendix III. Contd….

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
		Mean	83.02	2.88	35.26	3.78	3.97	4.85	0.44	2.70	71.92	4.13	36.10	1.433	34.09	1.83	2.14	1.79	7.70	3.47	9.21
14	PANT-T-11	2007K	83.33	2.33	38.33	3.56	6.13	4.47	0.51	2.99	65.67	4.07	34.59	1.410	26.77	1.73	2.67	0.30	18.59	1.75	9.26
		2008K	82.85	3.03	35.00	3.74	5.93	4.74	0.50	3.33	71.00	4.04	40.07	1.630	34.78	1.33	1.78	0.24	14.29	1.37	17.52
		2008R	81.00	2.99	40.11	3.12	6.11	5.27	0.47	3.14	73.21	4.26	44.07	1.960	45.08	3.27	0.41	2.67	0.62	0.03	11.89
		Mean	82.39	2.78	37.81	3.47	6.06	4.83	0.49	3.15	69.96	4.12	39.57	1.667	35.54	2.11	1.62	1.07	11.17	1.05	12.89
15	PAU-2371	2007K	93.33	2.99	37.33	3.89	5.06	4.22	0.42	2.00	73.27	5.04	32.56	1.151	30.04	0.82	2.62	0.76	15.41	14.10	10.04
		2008K	92.59	3.00	37.00	3.64	4.94	4.81	0.43	2.12	72.52	4.99	34.89	1.326	32.38	1.02	1.60	0.96	11.82	8.92	9.37
		2008R	96.25	3.19	37.33	3.04	5.21	4.84	0.49	2.37	77.59	5.23	38.78	1.647	37.92	2.48	0.15	2.66	13.97	0.33	15.59
		Mean	94.06	3.06	37.22	3.52	5.07	4.62	0.45	2.17	74.46	5.09	35.41	1.374	33.45	1.44	1.46	1.46	13.73	7.79	11.67
16	PAU-2372	2007K	154.33	3.41	38.67	3.67	3.70	3.19	0.37	3.14	69.62	4.04	45.56	1.374	38.73	0.77	2.28	0.21	9.11	2.37	4.15
		2008K	161.30	3.37	38.33	4.00	3.82	3.67	0.39	3.19	71.49	3.82	48.52	1.387	36.34	1.08	2.66	0.06	13.81	2.70	4.55
		2008R	166.10	3.15	38.00	3.34	3.92	3.66	0.36	3.66	73.78	3.95	51.41	1.590	42.67	1.24	0.32	1.41	0.18	0.15	8.33
		Mean	160.58	3.31	38.33	3.67	3.81	3.51	0.37	3.33	71.63	3.94	48.49	1.450	39.25	1.03	1.75	0.56	7.70	1.74	5.68
17	PAU-2373	2007K	114.67	6.21	29.00	9.64	3.15	2.89	0.38	2.44	15.15	7.09	173.26	1.887	33.87	1.18	2.66	0.26	14.14	3.74	4.15
		2008K	112.18	4.66	30.33	9.77	3.66	2.96	0.40	2.73	16.30	7.07	181.11	1.633	29.54	1.39	2.62	0.81	24.11	10.29	7.82
		2008R	123.26	5.49	35.67	10.70	3.67	3.00	0.36	2.67	18.63	7.12	195.63	1.850	35.25	2.19	0.68	3.19	7.55	1.01	11.29
		Mean	116.70	5.45	31.67	10.04	3.50	2.95	0.38	2.61	16.69	7.09	183.34	1.790	32.88	1.59	1.99	1.42	15.27	5.01	7.75
18	PAU-2374	2007K	94.33	3.56	31.33	2.78	4.62	4.50	0.47	3.22	53.55	3.48	52.99	1.150	26.46	1.21	1.93	0.89	12.37	1.99	5.33
		2008K	123.81	3.81	34.00	3.18	5.24	6.32	0.39	7.07	108.93	4.44	37.52	1.493	34.25	0.99	2.26	0.62	2.67	3.80	2.30
		2008R	143.33	4.00	37.67	2.85	5.56	6.55	0.43	7.40	112.26	4.85	40.48	1.785	38.67	1.49	0.66	1.56	1.50	2.11	2.11
		Mean	130.71	3.94	34.67	3.02	5.29	6.36	0.39	7.23	113.23	4.68	38.67	1.561	32.98	1.18	1.76	1.01	5.71	2.94	2.80
19	ARKA VIKAS	2007K	101.56	4.30	32.00	2.78	3.78	5.06	0.48	3.56	86.67	4.06	34.26	1.073	28.24	1.07	3.67	0.70	15.00	6.67	9.00
		2008K	119.13	4.18	35.67	2.83	3.96	5.11	0.46	4.00	88.55	4.51	35.80	1.456	30.97	1.70	4.33	1.00	20.00	15.00	14.33
		2008R	123.73	3.74	38.44	3.41	4.12	5.18	0.45	3.56	93.11	5.00	40.93	1.812	36.00	2.33	0.44	2.67	1.67	1.01	1.74
		Mean	114.81	4.07	35.37	3.01	3.96	5.12	0.46	3.70	89.44	4.53	37.00	1.447	31.74	1.70	2.81	1.46	12.22	7.56	8.36
20	Dwd-T-11	2007K	120.78	4.41	32.67	2.26	4.55	4.02	0.54	2.89	75.22	4.15	20.44	0.980	19.76	0.48	2.04	0.48	8.45	2.62	1.86

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Appendix III. Contd….

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
		2008K	122.89	3.93	34.33	2.59	5.00	4.67	0.44	3.33	75.11	3.82	27.40	1.260	25.88	0.29	2.37	0.72	13.48	2.66	2.15
		2008R	133.33	3.77	37.33	2.78	5.07	4.86	0.50	2.73	80.74	4.49	36.55	1.634	30.52	1.07	0.77	2.89	0.73	0.55	5.37
		Mean	125.67	4.04	34.78	2.54	4.88	4.52	0.49	2.99	77.02	4.15	28.13	1.291	25.38	0.62	1.73	1.36	7.55	1.94	3.13
21	VR-35	2007K	102.33	3.57	33.67	3.78	5.49	6.08	0.54	3.33	101.67	4.14	45.15	1.802	33.10	0.52	0.85	0.69	19.00	1.44	3.48
		2008K	94.99	3.56	34.15	3.44	4.82	5.26	0.59	3.77	102.77	4.12	42.30	1.972	38.82	0.74	0.62	0.78	14.00	5.26	4.92
		2008R	101.71	3.63	36.00	4.04	5.53	5.48	0.54	3.51	99.41	4.40	51.29	2.116	44.63	0.81	0.34	0.76	0.32	0.17	8.52
		Mean	99.68	3.59	34.61	3.75	5.28	5.61	0.56	3.54	101.28	4.22	46.25	1.964	38.85	0.69	0.60	0.74	11.11	2.29	5.64
22	VR-415	2007K	70.33	2.67	34.33	3.22	4.73	4.18	0.44	2.45	64.44	4.90	53.96	1.105	27.92	1.10	2.89	0.54	14.71	1.59	4.04
		2008K	81.26	2.86	35.59	3.00	4.81	4.52	0.43	2.77	65.63	4.25	56.18	1.230	28.58	1.26	2.22	0.21	11.10	2.55	4.67
		2008R	77.59	2.93	32.78	3.66	5.04	4.55	0.53	2.52	71.41	5.04	64.44	1.670	35.78	2.85	0.55	3.29	0.04	0.40	3.29
		Mean	76.39	2.82	34.23	3.30	4.86	4.42	0.46	2.58	67.16	4.73	58.19	1.335	30.76	1.74	1.89	1.35	8.62	1.51	4.00
23	VRCT-155	2007K	142.00	3.67	30.33	10.08	2.37	2.39	0.32	4.10	11.48	7.12	190.96	1.820	28.84	1.07	2.35	0.63	7.92	2.24	4.23
		2008K	135.11	3.91	30.33	10.89	2.23	2.41	0.34	4.00	11.33	6.11	186.48	1.853	29.07	1.19	1.77	0.88	16.48	2.15	9.29
		2008R	150.40	3.71	32.33	11.11	2.64	2.53	0.36	3.97	12.82	7.41	207.08	2.003	38.62	3.04	0.44	2.78	0.95	0.02	15.80
		Mean	142.50	3.76	31.00	10.70	2.41	2.44	0.34	4.02	11.87	6.88	194.84	1.892	32.18	1.77	1.52	1.43	8.45	1.47	9.77
24	VRCT-17	2007K	125.44	3.93	28.00	8.15	2.57	2.89	0.32	3.56	18.22	5.08	210.71	1.930	29.48	1.93	1.95	0.88	9.29	2.49	3.66
		2008K	126.44	3.55	29.67	8.30	2.54	2.73	0.30	3.55	16.82	5.09	196.00	1.847	30.32	2.13	1.89	0.82	13.81	2.07	3.07
		2008R	121.52	4.59	33.00	10.18	2.72	2.88	0.37	3.77	18.75	5.25	226.11	1.937	40.92	3.25	0.92	2.93	0.05	0.41	7.21
		Mean	124.47	4.02	30.22	8.88	2.61	2.83	0.33	3.63	17.93	5.14	210.94	1.905	33.58	2.44	1.59	1.54	7.72	1.65	4.65
25	VTG-106	2007K	105.78	2.47	30.67	3.44	5.22	4.47	0.54	2.33	81.22	4.23	24.44	1.333	27.73	0.35	1.78	0.10	14.92	2.11	6.21
		2008K	119.18	3.00	35.33	2.15	5.11	4.90	0.49	2.63	82.63	4.03	27.37	1.509	34.03	0.17	2.22	0.08	12.39	2.72	14.00
		2008R	116.96	3.88	40.66	2.44	5.14	4.61	0.51	2.78	84.55	5.14	36.26	2.152	43.15	1.52	0.41	2.26	0.84	0.02	12.43
		Mean	113.97	3.12	35.55	2.68	5.16	4.66	0.51	2.58	82.80	4.47	29.36	1.665	34.97	0.68	1.47	0.82	9.38	1.61	10.88
26	VTG-85	2007K	94.44	3.11	30.67	3.77	6.13	5.49	0.57	2.89	76.84	4.00	32.30	1.187	28.11	0.99	2.73	0.88	14.55	1.40	9.89
		2008K	89.92	2.67	33.03	4.52	6.04	4.93	0.53	2.59	79.33	4.18	37.00	1.310	30.75	1.35	2.22	0.88	13.92	3.89	6.41
		2008R	90.66	2.41	34.00	3.58	6.32	4.62	0.60	2.74	81.37	4.33	39.07	1.570	34.22	2.59	0.88	2.92	7.43	4.37	15.26

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Appendix III. Contd….

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
		Mean	91.68	2.73	32.57	3.96	6.16	5.01	0.56	2.74	79.18	4.17	36.12	1.356	31.03	1.65	1.95	1.56	11.97	3.22	10.52
27	VTG-86	2007K	94.33	3.56	31.33	2.78	4.62	4.50	0.47	3.22	53.55	3.48	52.99	1.150	26.46	1.21	1.93	0.89	12.37	1.99	5.33
		2008K	81.81	3.26	32.00	3.07	5.14	4.63	0.46	3.19	63.44	4.07	54.15	1.243	29.21	1.00	2.56	0.77	12.03	2.89	5.95
		2008R	90.67	2.93	34.00	3.41	6.35	4.88	0.52	3.11	83.07	4.52	65.19	1.566	35.31	1.85	0.40	2.63	0.33	0.30	11.73
		Mean	88.94	3.25	32.44	3.09	5.37	4.67	0.48	3.17	66.69	4.03	57.44	1.320	30.33	1.35	1.63	1.43	8.24	1.73	7.67
28	VTG-89	2007K	90.00	2.78	29.30	5.44	4.66	4.10	0.51	2.63	51.92	4.04	49.25	1.032	21.71	0.96	2.63	0.51	14.33	2.40	7.99
		2008K	85.66	2.77	33.00	4.92	4.26	4.11	0.51	2.67	50.85	4.05	50.11	1.180	23.85	0.92	2.08	0.22	12.33	1.51	8.40
		2008R	88.98	2.74	32.33	4.45	4.31	4.24	0.48	2.93	49.84	3.85	53.67	1.610	30.88	2.63	0.79	2.51	0.40	0.41	13.67
		Mean	88.21	2.76	31.54	4.94	4.41	4.15	0.50	2.74	50.87	3.98	51.01	1.274	25.48	1.50	1.83	1.08	9.02	1.44	10.02
29	VTG-90	2007K	122.20	3.11	35.67	4.33	4.95	4.15	0.52	3.11	57.04	3.92	36.86	1.143	24.86	0.93	2.10	0.48	11.88	2.19	5.92
		2008K	124.66	2.63	34.23	4.26	4.89	4.11	0.51	2.75	53.52	3.85	39.41	1.211	28.51	0.77	2.14	0.64	15.18	2.34	5.52
		2008R	120.67	3.12	35.33	3.15	4.95	4.38	0.52	2.34	57.63	4.33	46.35	1.077	23.70	1.92	0.48	2.63	0.26	0.56	10.81
		Mean	122.51	2.95	35.08	3.92	4.93	4.21	0.52	2.73	56.06	4.03	40.87	1.144	25.69	1.21	1.57	1.25	9.11	1.70	7.42
30	VTG-93	2007K	112.67	3.33	32.67	10.20	2.60	2.07	0.38	3.26	10.55	6.40	178.89	1.327	27.88	0.74	2.36	0.88	14.44	1.51	5.22
		2008K	110.66	3.41	34.00	10.05	2.48	2.22	0.39	2.81	10.97	6.22	178.51	1.443	29.67	1.14	2.00	0.81	7.00	1.65	6.00
		2008R	112.56	3.16	36.00	10.89	2.55	2.11	0.38	2.85	10.88	6.54	196.08	1.954	36.59	2.55	0.93	3.18	0.21	0.43	14.07
		Mean	111.96	3.30	34.22	10.38	2.54	2.13	0.38	2.97	10.80	6.38	184.49	1.575	31.38	1.48	1.76	1.63	7.22	1.19	8.43
31	VTG-95	2007K	121.63	4.11	33.67	4.11	4.92	4.76	0.52	2.32	59.52	4.60	32.67	1.440	29.59	1.29	3.11	0.62	9.14	2.07	6.93
		2008K	134.26	3.89	38.33	4.26	4.59	4.37	0.49	2.19	60.18	4.97	33.19	1.493	27.62	0.86	2.74	0.56	12.89	1.10	2.22
		2008R	126.51	3.23	38.67	3.71	4.89	4.12	0.51	3.08	65.96	4.96	36.70	1.866	39.58	2.48	0.88	3.41	0.26	0.02	12.89
		Mean	127.47	3.74	36.89	4.03	4.80	4.42	0.51	2.53	61.89	4.84	34.19	1.600	32.26	1.55	2.24	1.53	7.43	1.06	7.35
32	Dwd-T-1	2007K	70.63	3.22	35.67	3.22	3.63	4.97	0.38	5.00	60.36	3.41	42.67	1.240	29.70	1.83	1.41	0.89	12.81	1.75	7.63
		2008K	74.52	3.29	37.00	2.96	3.96	5.00	0.41	4.75	71.44	3.12	43.30	1.429	33.93	1.20	2.06	0.60	14.37	1.92	4.33
		2008R	75.78	2.78	36.41	3.11	4.37	5.27	0.51	4.92	78.41	3.89	44.88	1.743	38.35	2.48	0.51	2.74	0.15	0.67	10.14
		Mean	73.64	3.10	36.36	3.10	3.99	5.08	0.43	4.89	70.07	3.47	43.62	1.471	33.99	1.84	1.33	1.41	9.11	1.45	7.37
33	Dwd-T-2	2007K	84.23	3.67	36.00	2.81	4.44	5.37	0.46	4.44	58.48	3.75	39.52	1.259	21.51	1.15	2.81	0.69	13.40	2.79	1.97

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Appendix III. Contd….

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
		2008K	84.55	3.26	36.00	3.07	4.36	5.01	0.47	4.18	70.89	3.44	47.79	1.274	28.59	1.41	2.89	1.08	5.63	2.14	2.55
		2008R	88.33	3.74	35.33	3.00	4.42	5.18	0.51	4.08	68.64	3.85	48.56	1.710	38.04	1.89	1.96	2.44	0.25	0.19	7.33
		Mean	85.70	3.56	35.78	2.96	4.41	5.19	0.48	4.23	66.00	3.68	45.29	1.414	29.38	1.48	2.55	1.40	6.43	1.71	3.95
34	Dwd-T-3	2007K	101.93	3.11	31.67	4.08	4.45	4.96	0.56	5.55	116.07	3.21	40.48	1.545	28.24	1.00	2.63	0.92	13.71	3.38	3.69
		2008K	94.48	3.22	35.67	3.75	4.48	5.78	0.54	5.37	103.62	3.44	43.85	1.726	33.02	1.24	2.44	0.76	12.89	3.42	2.55
		2008R	93.44	4.04	38.00	3.59	4.63	6.18	0.58	5.60	106.46	3.59	47.33	1.963	39.48	1.96	0.63	2.86	0.23	0.02	8.19
		Mean	96.62	3.46	35.11	3.80	4.52	5.64	0.56	5.51	108.72	3.41	43.89	1.745	33.58	1.40	1.90	1.51	8.94	2.27	4.81
35	Dwd-T-4	2007K	85.87	3.22	33.33	4.44	4.81	5.79	0.45	6.62	97.96	3.37	30.55	1.260	27.71	0.67	2.00	1.05	18.23	1.63	7.63
		2008K	84.56	3.04	30.33	3.26	4.81	6.03	0.45	6.18	99.40	3.60	32.55	1.890	36.51	2.41	2.21	1.58	15.11	6.13	7.40
		2008R	87.78	3.74	34.21	3.48	4.33	5.34	0.49	6.03	98.48	4.07	37.56	1.963	40.85	2.70	1.01	2.74	0.41	0.32	13.55
		Mean	86.07	3.34	32.63	3.73	4.65	5.72	0.47	6.28	98.61	3.68	33.55	1.704	35.02	1.93	1.74	1.79	11.25	2.69	9.53
36	Dwd-T-5	2007K	84.05	3.22	32.67	3.56	4.01	4.18	0.30	3.33	66.07	4.18	57.00	1.353	30.75	0.80	1.00	0.92	10.70	1.03	3.40
		2008K	83.59	3.19	31.00	3.08	4.18	4.31	0.38	3.22	65.55	4.32	59.41	1.609	35.93	0.67	1.36	0.89	10.52	1.92	8.05
		2008R	75.15	4.04	32.00	3.22	4.52	4.52	0.32	3.67	70.55	4.23	63.06	1.436	35.04	2.00	0.17	1.04	0.19	0.38	11.76
		Mean	80.93	3.48	31.89	3.29	4.23	4.34	0.33	3.41	67.39	4.24	59.82	1.466	33.91	1.16	0.85	0.95	7.14	1.11	7.74
37	Dwd-T-6	2007K	62.90	3.78	26.00	3.88	4.09	4.70	0.31	2.67	70.66	3.72	53.00	1.459	31.80	0.88	1.95	1.11	7.07	0.46	2.14
		2008K	63.67	2.97	27.67	3.11	4.02	4.63	0.33	2.78	65.00	3.77	57.67	1.555	34.33	1.12	3.07	1.75	3.48	0.33	0.02
		2008R	70.85	3.84	29.30	3.78	4.22	4.95	0.41	2.77	71.93	4.15	68.37	1.966	40.07	2.26	0.83	2.31	0.77	0.02	5.09
		Mean	65.80	3.53	27.66	3.59	4.11	4.76	0.35	2.74	69.20	3.88	59.68	1.660	35.40	1.42	1.95	1.72	3.77	0.27	2.42
38	Dwd-T-7	2007K	91.26	3.96	36.67	3.85	4.15	4.43	0.32	3.33	62.68	4.24	39.30	1.297	26.39	1.60	1.44	0.35	1.33	0.37	1.85
		2008K	87.22	3.71	34.67	3.19	4.32	4.74	0.37	3.51	65.79	4.18	42.00	1.518	32.72	0.92	0.58	1.21	3.85	0.85	3.49
		2008R	86.21	3.86	36.33	3.19	4.85	5.18	0.39	3.11	72.07	4.45	48.29	1.750	37.18	2.49	0.04	1.54	0.02	0.03	4.25
		Mean	88.23	3.84	35.89	3.41	4.44	4.78	0.36	3.32	66.85	4.29	43.20	1.521	32.10	1.67	0.69	1.03	1.73	0.42	3.20
39	Dwd-T-8	2007K	83.28	4.10	25.67	3.34	5.04	5.35	0.54	3.11	82.00	4.81	34.41	1.323	27.99	0.66	1.63	0.74	8.65	1.71	3.77
		2008K	86.03	4.07	25.00	3.19	5.04	5.52	0.54	3.81	85.33	4.41	37.33	1.706	34.07	1.13	2.33	0.16	3.92	1.14	11.37
		2008R	86.85	4.25	29.00	3.67	5.07	5.48	0.51	3.70	86.25	5.10	45.30	2.154	43.43	1.11	1.14	2.85	0.28	0.02	14.36

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Appendix III. Contd….

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
		Mean	85.39	4.14	26.56	3.40	5.05	5.45	0.53	3.54	84.53	4.77	39.01	1.728	35.16	0.96	1.70	1.25	4.29	0.96	9.83
40	Dwd-T-9	2007K	90.13	3.74	24.67	3.66	4.58	4.47	0.46	3.67	86.00	5.00	44.44	1.160	27.95	1.11	2.15	0.74	9.71	0.68	0.85
		2008K	91.70	3.88	29.00	3.26	4.73	4.63	0.47	4.07	89.11	4.52	47.77	1.334	29.40	1.44	1.85	0.71	5.22	0.95	1.91
		2008R	94.45	4.52	29.33	3.48	5.04	4.97	0.48	4.12	91.00	4.67	50.97	2.081	42.59	2.99	0.58	3.10	0.03	0.18	5.26
		Mean	92.09	4.05	27.67	3.47	4.78	4.69	0.47	3.95	88.70	4.73	47.73	1.525	33.31	1.85	1.53	1.52	4.98	0.60	2.67
41	Dwd-T-10	2007K	88.72	3.82	28.00	4.43	4.10	4.60	0.51	4.67	80.22	4.04	55.81	1.073	25.84	1.52	2.66	0.89	8.95	1.52	3.07
		2008K	88.46	4.89	31.00	3.48	4.69	4.94	0.45	4.63	84.88	3.95	58.56	1.573	29.07	1.00	2.67	0.06	6.64	1.63	6.07
		2008R	87.37	4.38	34.34	3.94	4.77	5.17	0.48	4.74	83.04	4.27	62.41	2.070	38.71	2.71	0.64	3.19	0.10	0.03	13.59
		Mean	88.18	4.36	31.11	3.95	4.52	4.90	0.48	4.68	82.71	4.09	58.93	1.572	31.21	1.74	1.99	1.38	5.23	1.06	7.58
	Mean	2007K	99.44	3.58	32.70	4.38	4.25	4.44	0.44	3.61	64.57	4.38	58.10	1.308	27.82	1.14	2.37	0.66	12.81	2.91	4.76
		2008K	99.66	3.56	33.53	4.29	4.27	4.54	0.43	3.67	65.45	4.34	60.09	1.435	30.58	1.19	2.28	0.68	13.63	4.09	6.31
		2008R	102.08	3.58	35.60	4.41	4.49	4.68	0.46	3.69	69.12	4.67	66.40	1.732	36.29	2.26	0.56	2.71	1.37	0.69	9.92
		Mean	100.39	3.57	33.95	4.36	4.34	4.55	0.44	3.66	66.38	4.46	61.53	1.492	31.56	1.53	1.74	1.35	9.27	2.57	7.00
	Minimum	2007K	62.90	2.33	24.67	2.11	2.03	2.05	0.30	2.00	10.22	3.21	20.44	0.726	19.76	0.13	0.85	0.08	1.33	0.37	0.27
		2008K	63.67	2.63	25.00	2.09	2.07	2.03	0.30	2.12	10.40	3.12	18.97	0.982	17.25	0.10	0.58	0.06	2.67	0.33	0.02
		2008R	70.39	2.41	29.00	2.44	2.12	2.11	0.31	2.15	10.88	3.50	24.81	1.077	21.97	0.17	0.04	0.70	0.02	0.02	1.74
		Mean	65.80	2.73	26.56	2.28	2.07	2.13	0.31	2.09	10.73	3.37	21.52	0.955	19.86	0.14	0.60	0.56	1.73	0.27	1.39
	Maximum	2007K	154.33	6.21	38.67	10.56	6.13	6.39	0.57	7.22	118.50	7.62	210.71	1.930	38.73	3.11	4.20	1.86	29.58	14.10	13.33
		2008K	161.30	5.41	38.33	11.40	6.04	6.32	0.59	7.07	108.93	8.00	196.00	1.972	38.82	2.41	4.33	1.75	43.22	16.37	18.33
		2008R	166.10	5.49	42.00	11.66	6.35	6.64	0.60	7.40	114.63	7.93	226.11	2.154	45.08	4.00	1.96	4.85	13.97	4.37	24.26
		Mean	160.58	5.45	38.33	11.21	6.16	6.36	0.56	7.23	113.23	7.85	210.94	1.964	39.25	2.68	2.81	1.98	21.10	7.79	13.50
	Environmental Index	2007K	-0.96	0.01	-1.25	0.02	-0.09	-0.11	0.00	-0.04	-1.81	-0.08	-3.43	-0.18	-3.74	-0.39	0.63	-0.69	3.54	0.34	-2.24
		2008K	-0.73	-0.02	-0.41	-0.07	-0.06	-0.02	-0.01	0.01	-0.93	-0.12	-1.44	-0.06	-0.98	-0.34	0.55	-0.67	4.36	1.53	-0.68
		2008R	1.69	0.01	1.66	0.05	0.16	0.13	0.02	0.03	2.74	0.21	4.87	0.24	4.72	0.73	-1.18	1.36	-7.90	-1.87	2.92
	C.V. (%)	2007K	6.38	15.01	6.90	15.42	6.66	6.95	9.55	10.32	9.09	6.07	9.39	11.57	6.99	34.25	23.05	48.88	36.08	70.87	40.81
		2008K	5.03	15.15	5.44	15.15	5.06	5.02	8.52	10.48	5.25	6.16	8.68	9.46	6.37	36.63	22.00	50.82	31.16	51.28	38.24

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Appendix III. Contd….

Sl. No.	Genotype	Seasons	Plant height (cm)	No. of branches	Days to 50% flowering	No. of fruits / cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules / fruit	Single fruit weight (g)	TSS (%)	No. of fruits / plant	Yield / plant (kg)	Yield / ha (t)	Early Blight	Late Blight	Powdery Mildew	Tomato Leaf curl Virus (%)	Tomato Spotted Wilt Virus (%)	*Sclerotium* wilt (%)
		2008R	4.58	12.67	3.97	10.90	3.77	3.38	6.72	11.02	5.01	4.67	6.83	8.92	5.49	24.63	99.58	21.30	137.38	97.22	29.49
	S.Em±.	2007K	5.18	0.44	1.84	0.55	0.23	0.25	0.03	0.31	4.79	0.22	4.45	0.12	1.59	0.32	0.45	0.26	3.77	1.68	1.59
		2008K	4.10	0.44	1.49	0.53	0.18	0.19	0.03	0.31	2.81	0.22	4.26	0.11	1.59	0.36	0.41	0.28	3.47	1.71	1.97
		2008R	3.82	0.37	1.15	0.39	0.14	0.13	0.03	0.33	2.83	0.18	3.70	0.13	1.63	0.45	0.45	0.47	1.53	0.55	2.39
		Mean	3.20	0.26	0.90	0.34	0.13	0.13	0.02	0.15	2.00	0.15	2.26	0.07	1.38	0.24	0.31	0.21	3.03	1.39	1.74
	CD @ 5%	2007K	10.31	0.87	3.67	1.10	0.46	0.50	0.07	0.61	9.54	0.43	8.86	0.25	3.16	0.64	0.89	0.52	7.51	3.35	3.16
		2008K	8.15	0.88	2.96	1.06	0.35	0.37	0.06	0.63	5.59	0.44	8.48	0.22	3.17	0.71	0.82	0.56	6.90	3.41	3.92
		2008R	7.60	0.74	2.30	0.78	0.28	0.26	0.05	0.66	5.62	0.36	7.37	0.25	3.24	0.90	0.90	0.94	3.05	1.09	4.76
	C D @ 1%	2007K	13.68	1.16	4.86	1.45	0.61	0.66	0.09	0.80	12.64	0.57	11.75	0.33	4.19	0.84	1.18	0.69	9.95	4.44	4.18
		2008K	10.81	1.16	3.93	1.40	0.47	0.49	0.08	0.83	7.41	0.58	11.24	0.29	4.20	0.94	1.08	0.74	9.15	4.52	5.20
		2008R	10.07	0.98	3.04	1.04	0.36	0.34	0.07	0.88	7.46	0.47	9.77	0.33	4.29	1.20	1.20	1.24	4.05	1.45	6.31

* Significant at 5% probability ** Significant at 1% probability , 2007K = *kharif* 2007, 2008K = *kharif* 2008, 2008R = *rabi* 2008

Appendix IV. *Per se* means, ranges and average heterosis of tomato parents and hybrids evaluated during *rabi* 2008.

Sl. No.	Parents and Hybrids	Plant height (cm)	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules per fruit	Total soluble solids (%)	Single fruit weight (g)	No. of fruits per plant	Yield per plant (kg)	Yield per hectare (t)	Early Blight	Late Blight	Powdry mildew	Tomato leaf curl virus (TLCV) (%)	Tomato spotted wilt virus (%)	Sclerotium wilt (%)
	Lines																			
1	CO-3	90.66	3.40	37.67	3.15	3.74	5.63	0.45	4.23	3.85	67.15	30.04	1.200	26.89	1.51	0.43	4.11	1.19	0.47	24.26
2	DVRT-2	97.45	3.89	42.00	2.63	4.27	6.64	0.51	5.67	3.60	114.63	26.04	1.277	24.07	2.82	0.24	4.70	0.03	1.96	6.56
3	H-24	70.39	3.21	37.00	2.82	4.32	5.11	0.44	4.46	3.50	57.56	24.81	1.158	21.97	2.12	0.36	3.00	0.68	3.51	11.55
4	Megha L-15	81.00	3.30	34.10	2.89	4.81	5.19	0.34	3.48	4.29	60.88	49.11	1.542	28.36	2.73	0.44	2.80	6.07	0.07	7.03
5	PANT-T-10	84.63	3.00	37.11	3.74	4.11	5.01	0.50	2.89	4.23	75.77	37.91	1.577	37.71	2.89	0.81	3.07	0.77	3.50	16.20
	Testers																			
1	VR-35	101.71	3.63	36.00	4.04	5.53	5.48	0.54	3.51	4.40	99.41	51.29	2.116	44.63	0.81	0.34	0.76	0.32	0.17	8.52
2	KS-227	108.78	3.48	35.33	3.07	5.07	4.45	0.50	3.41	3.84	63.44	39.77	1.786	38.54	0.17	0.27	0.70	0.22	0.08	2.48
3	Dwd-T-1	75.78	2.78	36.41	3.11	4.37	5.27	0.51	4.92	3.89	78.41	44.88	1.743	38.35	2.48	0.51	2.74	0.15	0.67	10.14
4	Dwd-T-3	93.44	4.04	38.00	3.59	4.63	6.18	0.58	5.60	3.59	106.46	47.33	1.963	39.48	1.96	0.63	2.86	0.23	0.02	8.19
5	Dwd-T-6	70.85	3.84	29.30	3.78	4.22	5.05	0.41	2.77	4.15	71.93	68.37	1.966	40.07	2.26	0.83	2.31	0.77	0.02	5.09
	Crosses / Hybrids																			
1	CO-3 X VR 35	87.15	3.32	36.65	3.22	4.61	5.18	0.48	3.68	3.89	82.85	44.33	1.829	40.14	1.29	0.72	2.56	1.71	0.02	4.44
2	CO-3 X KS- 227	94.92	2.85	35.85	3.20	3.90	4.52	0.43	3.62	3.70	66.25	42.78	1.926	40.51	1.66	0.44	2.92	1.01	0.55	8.12
3	CO-3 X Dwd-T-1	78.30	2.67	33.30	2.82	4.01	5.08	0.49	4.81	3.77	70.18	35.77	1.535	35.30	2.93	0.55	2.47	0.85	0.29	8.82
4	CO-3 X Dwd-T-3	86.18	3.60	36.77	3.23	4.70	6.00	0.47	4.78	3.23	92.63	42.18	1.984	43.47	3.05	0.96	3.18	1.07	0.22	9.99
5	CO-3 X Dwd-T-6	71.25	3.18	33.46	3.20	3.66	4.50	0.41	3.27	3.69	62.82	56.15	1.646	37.99	2.85	1.20	3.52	0.78	0.26	7.78
6	DVRT-2 X VR 35	87.75	3.11	41.73	2.96	4.57	5.49	0.52	4.46	3.98	107.18	45.90	2.375	48.47	1.68	0.52	2.19	0.02	0.01	5.56
7	DVRT-2 X KS- 227	104.58	3.59	40.14	2.97	4.21	5.37	0.50	4.56	3.68	91.77	36.82	2.108	45.09	1.48	0.31	3.56	0.58	0.47	3.90
8	DVRT-2 X Dwd-T-1	86.30	3.25	39.85	2.92	4.25	5.69	0.48	5.17	3.51	72.83	35.95	1.716	38.17	2.88	1.08	3.33	0.09	0.19	13.47
9	DVRT-2 X Dwd-T-3	92.69	3.77	44.00	3.22	4.46	5.98	0.57	5.37	3.62	102.73	36.90	2.000	40.92	2.71	0.67	3.05	0.80	0.02	10.70
10	DVRT-2 X Dwd-T-6	82.68	3.22	35.00	3.11	4.15	5.29	0.43	4.33	3.85	89.27	54.86	2.033	43.71	2.78	1.30	3.19	0.65	1.70	2.29
11	H-24 X VR 35	76.03	3.54	36.48	3.34	4.88	5.34	0.49	3.97	3.74	66.25	41.88	1.651	32.88	2.15	0.26	2.85	0.34	0.12	8.55

Appendix IV. Contd....

Sl. No.	Parents and Hybrids	Plant height (cm)	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules per fruit	Total soluble solids (%)	Single fruit weight (g)	No. of fruits per plant	Yield per plant (kg)	Yield per hectare (t)	Early Blight	Late Blight	Powdry mildew	Tomato leaf curl virus (TLCV) (%)	Tomato spotted wilt virus (%)	Sclerotium wilt (%)
12	H-24 X KS- 227	74.62	3.44	34.17	3.21	4.77	5.27	0.49	4.07	3.51	66.66	35.15	1.712	37.93	1.40	0.60	2.26	0.77	0.22	4.00
13	H-24 X Dwd-T-1	76.92	3.01	37.05	2.85	4.30	5.22	0.50	4.43	3.50	70.44	38.85	1.850	41.10	2.74	0.90	2.22	1.38	1.48	6.73
14	H-24 X Dwd-T-3	83.65	3.45	38.85	3.17	4.41	5.26	0.47	4.44	3.46	68.78	38.03	1.625	34.44	2.14	0.55	2.45	0.06	0.44	6.19
15	H-24 X Dwd-T-6	76.74	3.47	36.33	3.15	4.43	4.98	0.43	3.46	3.66	63.70	50.77	1.791	37.26	2.56	0.97	2.90	1.03	0.02	3.85
16	Megha (L-15) X VR 35	80.69	3.21	34.92	3.15	4.82	5.11	0.39	3.68	4.33	67.20	54.11	1.969	40.60	2.11	0.72	3.15	0.82	0.63	6.67
17	Megha (L-15) X KS-227	85.63	3.59	33.44	3.25	4.90	5.15	0.42	3.27	4.03	71.26	45.44	1.913	40.17	1.30	0.86	1.83	1.06	0.22	5.82
18	Megha (L-15) X Dwd-T-1	80.48	3.11	34.73	2.97	4.75	5.23	0.44	4.27	3.95	72.51	42.56	1.811	39.97	2.92	0.44	2.12	0.86	0.41	6.89
19	Megha (L-15) X Dwd-T-3	89.75	3.56	35.89	3.51	4.88	5.26	0.49	4.44	4.04	72.19	51.44	2.036	42.55	2.28	0.19	2.45	1.41	0.02	3.49
20	Megha (L-15) X Dwd-T-6	81.07	3.38	30.58	2.97	4.41	5.17	0.39	2.78	4.20	66.74	52.29	1.732	36.98	1.56	0.54	2.63	1.04	0.02	2.67
21	Pant-T-10 X VR 35	86.84	3.43	36.85	3.90	4.56	5.15	0.52	3.29	4.29	83.59	46.58	2.135	45.65	1.82	0.53	1.27	0.63	0.33	6.07
22	Pant-T-10 X KS-227	87.86	3.58	35.81	3.52	4.44	4.96	0.61	3.71	3.99	71.07	46.37	1.877	40.44	2.00	0.99	2.86	0.57	0.25	3.74
23	Pant-T-10 X Dwd-T-1	87.18	3.12	36.04	3.86	4.18	5.20	0.51	3.74	4.08	80.16	52.22	1.837	38.47	2.07	0.97	2.46	0.57	0.38	2.13
24	Pant-T-10 X Dwd-T-3	91.85	3.86	39.00	3.92	4.49	5.47	0.53	3.90	4.24	92.92	50.66	2.075	43.74	1.78	0.96	2.07	0.73	0.03	2.79
25	Pant-T-10 X Dwd-T-6	85.19	3.76	33.26	3.97	4.17	4.75	0.46	3.49	4.20	71.89	70.83	2.126	42.78	1.67	1.00	2.49	1.01	0.08	2.22
	ARTH-3 (Com. check)	82.63	3.13	36.74	3.81	4.59	5.03	0.51	4.11	4.29	82.89	47.63	1.751	35.80	2.15	0.94	2.06	0.84	0.38	4.67
	Megha (L-15) (local check)	81.00	3.30	34.10	2.89	4.81	5.19	0.34	3.48	4.29	60.88	49.11	1.542	28.36	2.73	0.44	2.80	6.07	0.07	7.03
	Mean	85.26	3.38	36.32	3.27	4.47	5.27	0.47	4.04	3.89	77.39	45.00	1.808	38.19	2.12	0.66	2.65	1.00	0.52	6.99
	Minimum	70.39	2.67	29.30	2.63	3.66	4.45	0.34	2.77	3.23	57.56	24.81	1.158	21.97	0.17	0.19	0.70	0.02	0.01	2.13

Appendix IV. Contd….

Sl. No.	Parents and Hybrids	Plant height (cm)	No. of branches per plant	Days to 50% flowering	No. of fruits per cluster	Fruit length (cm)	Fruit width (cm)	Pericarp thickness (cm)	No. of locules per fruit	Total soluble solids (%)	Single fruit weight (g)	No. of fruits per plant	Yield per plant (kg)	Yield per hectare (t)	Early Blight	Late Blight	Powdry mildew	Tomato leaf curl virus (TLCV) (%)	Tomato spotted wilt virus (%)	Sclerotium wilt (%)
	Maximum	108.78	4.04	44.00	4.04	5.53	6.64	0.61	5.67	4.40	114.63	70.83	2.375	48.47	3.05	1.30	4.70	6.07	3.51	24.26
	Parental Mean	87.47	3.46	36.29	3.28	4.51	5.40	0.48	4.09	3.93	79.56	41.96	1.63	34.01	1.97	0.49	2.71	1.04	1.05	10.00
	Cross Mean	84.65	3.36	36.41	3.26	4.44	5.22	0.48	4.04	3.85	76.96	45.95	1.89	40.35	2.15	0.73	2.64	0.79	0.34	5.88
	Lines Mean	84.83	3.36	37.58	3.05	4.25	5.52	0.45	4.15	3.89	75.20	33.58	1.351	27.80	2.41	0.46	3.54	1.75	1.90	13.12
	Testers Mean	90.11	3.55	35.01	3.52	4.76	5.29	0.51	4.04	3.98	83.93	50.33	1.915	40.22	1.54	0.52	1.88	0.34	0.19	6.88
	Hybrid Mean	84.65	3.36	36.41	3.26	4.44	5.22	0.48	4.04	3.85	76.96	45.95	1.892	40.35	2.15	0.73	2.64	0.79	0.34	5.88
	Hybrid Minimum	71.25	2.67	30.58	2.82	3.66	4.50	0.39	2.78	3.23	62.82	35.15	1.535	32.88	1.29	0.19	1.27	0.02	0.01	2.13
	Hybrid Maximum	104.58	3.86	44.00	3.97	4.90	6.00	0.61	5.37	4.33	107.18	70.83	2.375	48.47	3.05	1.30	3.56	1.71	1.70	13.47
	No of F_1's > CC	16	19	9	4	8	20	6	11	1	7	9	18	22	15	16	2	14	18	11
	No of F_1's > OPC	17	15	20	23	4	14	25	20	1	25	9	24	25	18	3	14	25	7	18
	Average Heterosis (%)	-3.22	-2.72	0.31	-0.56	-1.56	-3.28	-0.34	-1.31	-2.27	-3.28	9.53	15.86	18.65	9.02	49.58	-2.51	-23.94	-68.00	-41.24
	S. Em. $\pm$	2.80	0.22	0.99	0.25	0.17	0.17	0.03	0.25	0.14	3.36	1.97	0.11	1.59	0.32	0.23	0.35	0.46	0.39	1.87
	CD @ 5%	5.64	0.45	1.97	0.50	0.34	0.34	0.07	0.50	0.29	6.75	3.97	0.22	3.20	0.65	0.46	0.71	0.92	0.78	3.76
	CD @1%	7.52	0.60	2.64	0.67	0.46	0.45	0.09	0.66	0.38	9.01	5.29	0.29	4.26	0.87	0.62	0.95	1.23	1.04	5.02

* Significant at 5% probability ** Significant at 1% probability , 2007K = *kharif* 2007, 2008K = *kharif* 2008, 2008R = *rabi* 2008

BIOMETRICAL AND TRANSFORMATION STUDIES IN TOMATO (*Solanum lycopersicum* L.)

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ABSTRACT

Biometrical and transformation studies in tomato (*Solanum lycopersicum* L.) were conducted at the University of Agricultural Sciences, Dharwad, India during 2007-2010 to find high yielding genotypes, F_1 hybrids and to develop genetic transformation. Variability, heritability, genetic advance, correlation, path analysis, genetic divergence, stability parameters were studied from evaluation of 41 tomato genotypes during *kharif* 2007, *kharif* 2008 and *rabi* 2008. Heterosis and combining ability was estimated from evaluating 25 F_1's developed in line x tester method during *rabi* 2008. Genetic transformants (T_0) with 'TRP sas/ihp' gene construct to develop resistance against tomato leaf curl virus disease in 'DMT-2'variety were identified.

Genotypes had highly significant variation amongst themselves for all the 19 characters in all seasons.High GCV, PCV, heritability and GAM were observed for plant height, fruits per cluster, fruits per plant, locules per fruit, TSS, fruit length and width in all the seasons. Yield had significant positive association with number of fruits per plant, TSS and number of fruits per cluster. Yield was directly affected mainly by single fruit weight and number of fruits per plant in positive direction.

D^2 analysis indicated that number of fruits per plant, single fruit weight, plant height, fruit length were major contributors to divergence over seasons. Genotypes were grouped into six, five and nine clusters in three seasons.

Stability analysis showed that 'HADT-294', 'PAU-2371', 'Dwd-T-1' and 'Dwd-T-6' were well adapted to all the environments. 'PAU-2372', 'VR-35', 'HADT-294' and 'ALT-02-39' were higher yielders per hectare. 'VR-35' had high yield per plant and higher single fruit weight.

The average heterosis in nineteen characters varied from -3.28 to 18.65 per cent. It was 15.86 per cent for yield per plant. Single fruit weight had highest *gca* and *sca* effect values. 'DVRT-2', 'H-24', 'Megha (L-15)', 'Dwd-T-3', and 'Dwd-T-6' were overall high general combiners. Among the F_1's, DVRT-2 x VR-35 (48.47 t), Pant-T-10 x VR-35 (45.65 t), DVRT-2 x KS-227 (45.09 t) and DVRT-2 x Dwd-T-6 (43.71 t) were top yielders per hectare and incidentally yield per plant too was higher in these hybrids.

The transgenic 'DMT-2' tomato plants (T_0) were obtained through *Agrobacterium* mediated transformation with 'TRP sas/ihp' gene construct for silencing the transcription of ToLCV gene encoding replicase. The transgene integration in plant genome was confirmed through PCR amplification of *hpt* II gene.