



Combining ability, gene action and heritability analysis for early blight resistance, yield and quality traits in tomato (*Solanum lycopersicum* L.)

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Abstract: Nine tomato genotypes were crossed in Line × Tester fashion to develop 18 hybrids, which, along with their parents and checks were evaluated for early blight resistance, fruit yield and quality of tomato (*Solanum lycopersicum*) to know extent of combining ability for the same. IIHR1816 was found to be the best general combiner with significant highest GCA (General Combining Ability) in desirable direction for per cent disease index (-15.71), carotenoids (3.46), lycopene (2.43) and yield (13.13); while, for plant height (3.94), average fruit weight (25.93), fruit length (0.54), fruit breadth (0.63) and pericarp thickness (1.71), the line IIHR2848 was best general combiner. The tester IIHR2852 was a best general combiner for traits like days to 50% flowering (-0.83) and fruit firmness (0.51). The crosses viz., IIHR2891 × IIHR2853 (11.61), IIHR2850 × IIHR2852 (11.40) and IIHR2892 × IIHR2890 (11.19) were found to be superior specific combiners for yield. IIHR2892 × IIHR2852 was a superior specific combiner for fruit quality traits like fruit firmness (0.98), total carotenoids (6.95) and lycopene (4.52). Best specific combiners for early blight resistance were IIHR2850 × IIHR2852 (-9.58), IIHR2891 × IIHR2890 (-9.58) and IIHR2892 × IIHR2890 (-6.82). The experiment helped in identifying these superior general combiners and specific combiners for early blight resistance, coupled with good yield and quality of the crop, which can be used in further breeding undertakings.

Keywords: Combining ability, Early blight, Gene action, Heritability, Tomato

INTRODUCTION

Tomato (*Solanum lycopersicum* L., 2n=24) is one of the most remunerable and widely grown vegetables in the world with the global productivity of 34.66tonne/ha (Anonymous, 2016). It belongs to the family Solanaceae and is native of Peru, Ecuador region (Rick, 1969). Ripe tomato fruit is an important culinary ingredient of Indian cuisine, also consumed fresh as salad and utilized in the manufacture of wide range of processed products. In addition, fresh and processed tomatoes are the richest sources of the antioxidant lycopene, which is known to protect cells from cancer causing oxidants (Rao and Rao, 2007). It is also a source of other compounds with antioxidant activities, including chlorogenic acid, plastoquinones, rutin, tocopherol and xanthophylls (Leonardi *et al.*, 2000). Since tomato is a very good source of income to small and marginal farmers in India, it ranks third in area immediately after the potato and onion crop and second in production immediately after the potato Crop (Anon., 2016). However, the average national productivity is very low (20.70 t/ha as compared to other countries like USA (88 t/ha), Spain (82.1 t/ha) and Brazil (60.7 t/ha) mainly because of disease and pests. Tomato is susceptible to over 200 diseases (Lukyanenko, 1991) caused by

pathogenic fungi, bacteria, viruses or nematodes. Early blight is one of the major disease symptoms caused by the fungus *Alternaria solani* (Ellis and Martin) Sorauer causing yield loss of about 15- 100% (Sohi, 1984). Numerous fungicides suggested to control early blight is known to be inconsistent and insufficient to deal with the disease and may also cause human and environment hazards. Therefore, it is economical and ethical to concentrate on the development of cultivars that are resistant to early blight through breeding efforts like hybridization and selection or other methods. The success of hybridization depends upon the selection of suitable parental genotypes and heterotic performance of their cross combinations. Since the selection made on phenotypic performance alone does not lead to expected degree of heterosis, combining ability is an effective tool, which gives useful genetic information for the choice of parents in relation to the performance of their hybrids (Chezhian *et al.*, 2000). The term “general combining ability (GCA)” is used to designate the average performance of a line in hybrid combinations (Sprague and Tatum, 1942). While, the term “specific combining ability (SCA)” is used to entitle those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines in-

volved (Sprague and Tatum, 1942). GCA estimates the magnitude of the additive portion of the genetic effect, and means that particular line has good genes in general, while the specific combining ability was the result of the dominance, epistasis and genotype improvement interactions. The Line \times Tester design given by Kempthorne (1957) is basically an extension of the top-cross analysis where instead of one tester (as used in top-crossing), more than one tester is used and it is a useful tool for evaluation of genotypes for use in hybridization programme with a view to identify good combiners, which may be used to build up a population with favourable and fixable genes. Therefore, the main objectives of the present investigation are to know the importance of gene actions through the estimation of both the general and specific combining abilities of nine tomato genotypes in L \times T fashion.

MATERIALS AND METHODS

Site selection: The investigation was undertaken during *rabi* (crossing program) of 2013-14 and *summer* (evaluation of genotypes and hybrids) of the year 2014 with the objective to study the traits like resistance to early blight, yield and quality parameters in tomato. The experiment was conducted at Experimental plot (Block-8), Division of vegetable crops, Indian Institute of Horticultural Research (IIHR), Hessaraghatta, Bengaluru. The experimental field was located at an altitude of 890 meters above MSL, 130.58' N latitude and 770.37' E longitude.

Selection of genotypes: Materials for this study comprised of 9 genotypes (IIHR977, IIHR1816, IIHR2848, IIHR2850, IIHR2891, IIHR2892, IIHR2852, IIHR2853 and IIHR2890) that were selected from IIHR

collection based on their diversity for various traits. These 9 parental lines were crossed in Line \times Tester fashion comprising 6 lines and 3 testers. Resultant 18 hybrids along with the parents, resistant (Arka Rakshak) and susceptible (IIHR 2202) checks for early blight and a commercial check (Abhinav) were transplanted on February 2014 in randomized block design with three replications. Each entry was represented by 4 rows of 10 plants each spaced at 100 cm apart between rows and 45 cm within row. The plants were managed by following all the package of practices recommended by IIHR for tomato crop, excluding the fungicidal spray.

Observations recorded: The observations were recorded on five randomly selected plants in each replication for days to 50 per cent flowering, days to first fruit maturity, plant height (cm), number of primary branches, flower clusters per plant, fruit clusters per plant, fruits per cluster, fruit set per cent, fruit yield per hectare (t/ha). Whereas five fruits were selected to record the observation on average fruit weight (g), fruit length (cm), fruit breadth (cm), firmness (kg/cm²), number of locules per fruit, pericarp thickness (mm), TSS ($^{\circ}$ Brix), ascorbic acid (mg/100 g), total carotenoids (mg/100 g) and lycopene (mg/100 g). Physiologically mature leaf of test genotype was detached from plant and placed in moisture maintained petridish, leaf was then inoculated with the virulent strain of *Alternaria solani* and severity was recorded after 7 days of inoculation employing the disease scale suggested by Devananthan and Ramanujam (1995) and PDI was calculated by using the following formula.

PDI = Sum of numerical ratings/Total number of leaves assessed \times Maximum disease rating \times 100

Table 1. Analysis of variance in respect of various characters for combining ability.

S.N.	Source	Replication	Crosses	Lines	Tester	Line \times tester	Error
	Degrees of freedom	2	17	5	2	10	34
1	Days to 50 % flowering	0.39	4.07**	5.29	9.72*	2.34*	0.82
2	Plant height (cm)	27.09	80.16**	66.43	329.98**	37.07**	11.85
3	Number of branches	1.70**	1.03**	1.43	0.16	1.00**	0.24
4	Flower clusters/plant	25.20	144.16**	277.39	98.48	86.68**	7.89
5	Fruits/cluster	1.77**	0.36*	0.90**	0.15	0.14	0.16
6	Fruit length	0.06	1.29**	1.30	5.31**	0.47**	0.14
7	Fruit breadth	0.05	1.29**	2.35	1.41	0.74**	0.20
8	Fruit clusters/plant	7.95	21.68**	28.82*	74.32**	7.58	4.86
9	Fruit set per cent	71.98	88.83	211.67**	142.21**	16.73	47.20
10	Average fruit weight	860.55	2552.56 **	3916.87	3849.84	1610.95 **	509.40
11	Firmness	0.48	2.05**	1.98	5.44	1.41**	0.43
12	Number of locules	0.004	2.24**	2.57	2.32	2.06**	0.20
13	TSS	0.001	0.24**	0.51*	0.30	0.10	0.09
14	Pericarp thickness	0.04	3.28**	9.16**	2.38*	0.50	0.48
15	Days to first fruit maturity	5.69	11.20**	24.21*	1.19	6.70*	2.55
16	Vitamin C	0.31	21.88**	31.10	14.20	18.82**	0.25
17	Carotenoids	0.03	80.46**	62.67	211.04	63.25**	0.59
18	Lycopene	0.00	35.11**	27.14	94.32	27.26**	0.25
19	PDI	1.05	542.35**	1223.42**	549.63	200.372**	22.47
20	Yield/ha	28.209	483.277 **	1096.031 *	330.875	207.380 **	58.81

*P<0.05, **P<0.01, TSS: Total soluble solids, PDI: Per cent disease index

Table 2. Estimates of variance components, degree of dominance and narrow sense heritability.

S.N.	Characters	Var.G CA	Var.SC A	Var.GCA : Var.SCA	Var. A	Var. D	Var.A / Var.D	Degree of dominance	h_{ns}^2 (%)
1	Days to 50 % flowering	0.38	0.49	0.77	0.76	0.49	1.57	0.80	49.45
2	Plant height	11.94	7.97	1.49	23.87	7.97	3.00	0.58	65.89
3	Number of branches	-0.015	0.23	-0.06	-0.03	0.23	-0.13	2.76	-10.05
4	Flower clusters/plant	7.50	26.37	0.28	15.00	26.37	0.57	1.33	34.17
5	Fruits/cluster	0.030	-0.0002	-141	0.06	0.00	-226.76	0.07	54.61
6	Fruit length	0.21	0.10	2.1	0.42	0.10	4.10	0.49	72.76
7	Fruit breadth	0.09	0.17	0.52	0.17	0.17	1.00	0.99	40.72
8	Fruit clusters/plant	3.26	0.78	4.18	6.52	0.78	8.41	0.34	72.07
9	Fruit set per cent	11.87	-9.46	-1.25	23.73	-9.46	-2.51	0.63	80.97
10	Average fruit weight	168.33	375.28	0.44	336.65	375.28	0.90	1.06	38.53
11	Firmness	0.170	0.29	0.58	0.34	0.29	1.17	0.92	41.97
12	Number of locules	0.03	0.60	0.05	0.06	0.60	0.10	3.23	7.71
13	TSS	0.023	0.007	3.28	0.05	0.01	6.79	0.38	58.59
14	Pericarp thickness	0.39	0.036	10.83	0.78	0.04	21.69	0.21	82.44
15	Days to first fruit maturity	0.45	1.23	0.36	0.89	1.23	0.72	1.18	28.48
16	Vitamin C	0.28	6.20	0.05	0.57	6.21	0.09	3.31	8.30
17	Carotenoids	5.45	20.88	0.26	10.91	20.86	0.52	1.38	34.09
18	Lycopene	2.48	8.99	0.27	4.96	8.98	0.55	1.35	35.31
19	PDI	50.83	59.97	0.84	101.65	59.97	1.70	0.77	60.35
20	Yield/ha	37.49	49.52	0.76	74.97	49.52	1.514	0.81	52.02

Var.GCA: Variance due to general combining ability, Var.SCA: Variance due to specific combining ability, Var. A: Additive variance, Var. D: Dominance variance, h_{ns}^2 : Narrow sense heritability

Table 3. Estimates of general combining ability (GCA) effects for various characters.

Genotypes	DFP	PH	NB	FLRC	FPC	FRUC	FSP	AFW	FL	FB
LINES										
IIHR977	1.00**	0.75	0.76**	4.33**	0.55**	0.37	1.92	-19.86*	-0.02	-0.63**
IIHR1816	0.89**	-3.56**	-0.13	1.97*	-0.10	-0.10	1.71	22.31**	-0.13	-0.13
IIHR2848	0.22	3.94**	-0.014	-10.01**	-0.36**	-1.25	4.47	25.93**	0.54**	0.63**
IIHR2850	0.00	-1.01	-0.41*	-2.71**	-0.21	-2.53**	0.073	-0.11	0.10	0.49**
IIHR2891	0.89**	1.83	-0.12	1.97*	0.08	2.68**	-9.45**	-24.42**	0.13	-0.46**
IIHR2892	0.56	-1.95	-0.08	4.46**	0.05	0.83	1.28	-3.83	-0.62**	0.10
CD 95%	0.63	2.46	0.37	1.86	0.25	1.55	4.55	14.92	0.27	0.33
CD 99%	0.85	3.30	0.50	2.50	0.34	2.08	6.11	20.03	0.36	0.44
TESTERS										
IIHR2852	-0.83**	2.87**	0.06	2.32**	0.04	2.34**	3.00	-0.57	0.29**	-0.11
IIHR2853	0.56*	2.05*	-0.11	0.03	-0.10	-1.19*	-2.57	14.90**	0.33**	0.31**
IIHR2890	0.28	-4.92**	0.05	-2.35**	0.07	-1.15*	-0.42	-14.33**	-0.62**	-0.21
CD 95%	0.45	1.74	0.26	1.31	0.18	1.09	3.21	10.55	0.19	0.23
CD 99%	0.60	2.33	0.35	1.76	0.24	1.47	4.32	14.16	0.26	0.32
Genotypes	FRM	LOC	TSS	PT	DFFM	AA	CAR	LYC	PDI	YLD
LINES										
IIHR 977	0.13	-0.86**	-0.16	-0.2	-0.96	2.75**	0.42	0.053	-6.70**	-15.81**
IIHR1816	-0.82**	0.42*	-0.21*	0.01	-0.96	0.67**	3.46**	2.43**	-15.71**	13.13**
IIHR2848	0.42	0.24	0.17	1.71**	2.70**	-1.36**	-3.15**	-2.04**	0.88	-8.48**
IIHR2850	0.09	0.48**	0.25**	0.42	1.370*	-2.27**	-3.13**	-1.95**	-3.23*	-1.78
IIHR2891	-0.23	-0.42*	0.21*	-0.77**	-1.29*	-0.93**	1.070**	0.77**	6.49**	2.78
IIHR2892	0.41	0.13	-0.26**	-1.15**	-0.85	1.14**	1.33**	0.73**	18.28**	10.17**
CD 95%	0.5	0.34	0.18	0.42	1.174	0.3	0.55	0.37	3.06	5.19
CD 99%	0.67	0.46	0.25	0.57	1.57	0.41	0.75	0.5	4.11	6.97
TESTERS										
IIHR2852	0.51**	-0.39**	0.02	0.42**	0.15	-0.99**	2.11**	1.40**	3.35**	-0.8
IIHR2853	0.06	0.30*	-0.13*	-0.2	0.15	0.71**	1.83**	1.23**	3.02**	4.63*
IIHR2890	-0.57**	0.09	0.12	-0.22	-0.3	0.27*	-3.95**	-2.64**	-6.37**	-3.83*
CD 95%	0.35	0.24	0.13	0.3	0.83	0.21	0.39	0.26	2.16	3.67
CD 99%	0.47	0.33	0.18	0.4	1.11	0.29	0.53	0.35	2.9	4.93

* $P < 0.05$, ** $P < 0.01$, DFP; days to 50 per cent flowering, DFFM; days to first fruit maturity, PH; plant height, NB; number of primary branches, FLRC; flower clusters per plant, FRUC; fruit clusters per plant, FPC; fruits per cluster, FSP; fruit set per cent, AFW; average fruit weight, FL; fruit length, FB; fruit breadth; FRM; firmness, LOC; number of locules per fruit, PT; pericarp thickness, TSS; total soluble solids, AA; ascorbic acid, CAR; total carotenoids, LYC; lycopene, PDI; per cent disease index; YLD; fruit yield per hectare.

Table 4. Estimates of specific combining ability (SCA) effects for various characters.

Crosses	DFE	PH	NB	FLRC	FPC	FRUC	FSP	AFW	FL	FB
IIHR977 × IIHR2852	-0.83	-2.34	-0.39	2.48	-0.13	-0.32	-0.22	4.6	0.22	0.04
IIHR977 × IIHR2853	1.44*	4.894 *	0.01	-3.26*	0.19	-0.39	0.06	-2.6	-0.46	-0.46
IIHR977 × IIHR2890	-0.61	-2.55	0.38	0.79	-0.05	0.71	0.15	-2.0	0.23	0.42
IIHR1816 × IIHR2852	0.72	2.38	0.28	1.67	-0.17	1.01	-2.74	-17.9	-0.02	-0.58*
IIHR1816 × IIHR2853	-0.67	-1.63	-0.43	-0.41	0.37	0.35	2.43	-13.5	-0.03	0.54
IIHR1816 × IIHR2890	-0.06	-0.75	0.15	-1.26	-0.20	-1.36	0.31	31.44*	0.05	0.05
IIHR2848 × IIHR2852	0.61	-4.87	-0.04	4.35**	-0.04	-1.17	-1.03	-13.34	-0.65**	0.15
IIHR2848 × IIHR2853	-0.44	2.20	-0.68*	3.04	-0.10	-0.03	1.64	37.08**	0.72**	-0.25
IIHR2848 × IIHR2890	-0.17	2.67	0.725*	-7.39**	0.15	1.20	-0.61	-23.75	-0.07	0.09
IIHR2850 × IIHR2852	0.17	3.82	0.29	3.09	0.08	2.69*	0.81	24.37	0.06	-0.01
IIHR2850 × IIHR2853	-0.56	-3.36	0.35	1.45	-0.19	-1.55	-1.53	0.93	0.09	0.59*
IIHR2850 × IIHR2890	0.39	-0.47	-0.64	-4.53**	0.11	-1.15	0.72	-25.30	-0.15	-0.58*
IIHR2891 × IIHR2852	-0.28	-1.51	-0.02	-4.99**	0.26	-0.30	4.32	-2.65	0.33	-0.13
IIHR2891 × IIHR2853	-0.67	0.56	0.75*	-1.98	-0.21	-0.27	-1.74	-10.99	-0.08	-0.24
IIHR2891 × IIHR2890	0.94	0.95	-0.73*	6.97**	-0.05	0.57	-2.59	13.64	-0.24	0.37
IIHR2892 × IIHR2852	-0.39	2.52	-0.11	-6.58**	0.01	-1.91	-1.14	4.94	0.06	0.53
IIHR2892 × IIHR2853	0.89	-2.66	-0.01	1.166	-0.05	1.89	-0.87	-10.92	-0.24	-0.18
IIHR2892 × IIHR2890	-0.50	0.14	0.13	5.42**	0.04	0.02	2.01	5.99	0.19	-0.35
CD 95%	1.10	4.26	0.65	3.229	0.44	2.69	7.88	25.84	0.48	0.58
CD 99%	1.48	5.71	0.86	4.33	0.89	3.61	10.58	34.69	0.64	0.78
Crosses	FRM	LOC	TSS	PT	DFM	AA	CAR	LYC	PDI	YLD
IIHR977 × IIHR2852	-0.06	-0.16	0.03	-0.18	1.41	0.28	4.31**	2.84**	8.42**	-3.5
IIHR977 × IIHR2853	-0.43	-0.2	-0.01	-0.37	-0.26	2.87 **	-2.52**	-1.68**	-5.78*	0.79
IIHR977 × IIHR2890	0.5	0.36	-0.03	0.54	-1.15	-3.15**	-1.78**	-1.16**	-2.63	2.79
IIHR1816 × IIHR2852	-0.07	-0.46	-0.05	0.19	-0.59	-1.37**	-0.83	-0.49	-3.35	-0.75
IIHR1816 × IIHR2853	0.53	1.00**	0.05	0.26	-0.59	-3.31**	1.89**	1.18**	-3.02	2.21
IIHR1816 × IIHR2890	-0.46	-0.55	0	-0.45	1.19	4.68**	-1.06*	-0.69*	6.37*	-1.46
IIHR2848 × IIHR2852	0.33	-0.05	0.1	0.1	-1.93	1.54**	-3.56**	-2.29**	0.84	-2.01
IIHR2848 × IIHR2853	-0.34	-0.31	-0.17	-0.06	0.74	-0.94**	1.34**	0.95**	-0.87	3.50
IIHR2848 × IIHR2890	0.01	0.36	0.07	-0.04	1.19	-0.60*	2.22**	1.34**	0.02	-1.49
IIHR2850 × IIHR2852	-0.97*	0.32	0.2	-0.05	1.07	-0.54*	0.28	0.18	-9.58**	11.40*
IIHR2850 × IIHR2853	0.08	0.56	-0.08	0.24	1.41	0.66*	0.06	-0.09	-3.05	-8.05
IIHR2850 × IIHR2890	0.88*	-0.88**	-0.12	-0.19	-2.481 *	-0.12	-0.34	-0.09	12.64**	-3.35
IIHR2891 × IIHR2852	-0.21	-0.71*	-0.12	-0.42	0.07	-0.53*	-7.15**	-4.77**	3.57	-3.92
IIHR2891 × IIHR2853	0.41	-0.42	0.28	0.43	-0.93	1.60**	4.50**	3.04**	6.01*	11.61*
IIHR2891 × IIHR2890	-0.21	1.13**	-0.16	-0.01	0.85	-1.06**	2.64**	1.73**	-9.58**	-7.68
IIHR2892 × IIHR2852	0.98*	1.06**	-0.17	0.36	-0.04	0.62*	6.95**	4.52**	0.09	-1.11
IIHR2892 × IIHR2853	-0.25	-0.64*	-0.06	-0.52	-0.37	-0.87**	-5.28**	-3.40**	6.72*	-10.07*
IIHR2892 × IIHR2890	-0.73	-0.42	0.24	0.16	0.41	0.25	-1.67**	-1.12**	-6.82*	11.19*
CD 95%	0.86	0.6	0.32	0.73	2.03	0.525	0.963	0.646	5.308	8.99
CD 99%	1.16	0.8	0.44	0.98	2.73	0.7	1.29	0.87	7.126	12.08

*P<0.05, **P<0.01

Yield per hectare was obtained by conversion of yield obtained by 40 plants in each replication to hectare by considering the spacing given. Statistical analysis of combining ability and narrow sense heritability in Line × Tester mating design was performed following the method given by Kempthorne (1957) using statistical software INDOSTAT version 8.0. Significance of the combining ability effects was determined at 1% and 5% probability. Combining ability values for the characters like days to 50 per cent flowering, days to first fruit maturity, PDI of early blight disease and number of locules per fruit are to be considered desirable only if they are in negative direction. For rest of the traits studied, combining ability values in positive direction are preferred as desirable.

RESULTS AND DISCUSSION

ANOVA: Variance due to lines (female parents)

revealed significant differences for the characters like number of fruits per cluster(0.90), fruit clusters per plant(28.82), fruit set per cent(211.67), TSS(0.51), pericarp thickness(9.16), days to first fruit maturity (24.21), PDI(1223.42) and yield per hectare(1096.03) (Table 1). Whereas, Variance due to testers (male parents) was found to be significant for the characters like days to 50% flowering(9.72), plant height(329.98), fruit length(5.31), number of fruit clusters per plant (74.32), fruit set per cent(142.21) and pericarp thickness(2.38). The Line × Tester interaction was found significant for all the traits except for fruits per cluster, fruit clusters per plant, per cent fruit set, TSS and pericarp thickness, representing specific combining ability. Presence of significant variance among the lines, testers or Line × Tester implies that there is significant difference at 5% and 1% level of significance for that particular character, diverse parents are the basic re-

quirements for better hybrid development.

Variance and gene action: Variance due to SCA had greater estimates than variance due to GCA and the ratio of additive variance and non-additive genetic variance is less than unity, establishing the predominance of non-additive gene action in the inheritance of traits like flower clusters per plant, average fruit weight, number of locules per fruit, days to first fruit maturity, vitamin C, total carotenoids and lycopene (Table 2). These results are in a harmony with the findings of El-Gabry *et al.* (2014) for plant height, number of branches, yield per plant and Shankar *et al.*, 2013 for TSS and titrable acidity. The presence of non-additive gene action for these traits requires maintenance of heterozygosity in the population. Hence, it is necessary to follow modified breeding methods such as biparental cross or triple test cross design or recurrent selection method in early generations. However, the traits like plant height (3.00), fruit length (4.10), fruit clusters per plant (8.41), TSS (6.79) and pericarp thickness (21.69) had greater values of additive variance over non-additive variance, which indicates the operation of additive gene action. Hence, for improvement of this type of characters simple selection procedures or conventional breeding methods such as pedigree and bulk selection can be employed in segregating generations. The results obtained for additive gene action are in line with the results obtained by Shankar *et al.*, 2013 for number of locules per fruit and Hosamani (2010) for pericarp thickness, and total soluble solids. The greater values of additive variance than non-additive variance and greater SCA variance than GCA variance revealed the involvement of both additive and non-additive gene action in the inheritance of days to 50 per cent flowering, fruit firmness, PDI and yield per hectare and, similar type of results was obtained by Shankar *et al.* (2013) for ascorbic acid. Such a type of trait can be improved by reciprocal recurrent selection or bi parental mating.

Narrow sense heritability [h^2_{ns}] percentage: For the various studied characters, h^2_{ns} % was found to be highly variable with-10.05% for number of primary branches to 82.44% for fruit pericarp thickness (Table 2). Narrow sense heritability estimates for the characters fruit clusters per plant, fruit length, fruit set per cent and pericarp thickness were found to be relatively as high as 72.07%, 72.76, 80.97% and 82.44%, respectively. Whereas yield per hectare, fruits per cluster, TSS, PDI and plant height were found to be having relatively high to intermediate estimates of 52.02%, 54.61%, 58.59%, 60.35% and 65.89%, respectively. The estimates of h^2_{ns} % for rest of ten traits under study showed relatively low or low percentage of heritability. However, the estimates of narrow sense heritability percentages for number of branches found to be negative, which could be considered indifferent from zero. The traits with low heritability are not suitable for se-

lection procedure since selection is purely based on physical performance of an entry and is successful under high heritability. Similar findings for the narrow sense heritability estimates were reported by Hosamani (2010) and by Mehta and Asati (2008) and El-Gabry *et al.* (2014).

Combining ability: The estimate of GCA of a parent is an important indicator of its potential for generating superior breeding populations (Dey *et al.*, 2014) and it represents a strong evidence of favourable gene flow from parents to offspring at high frequency and gives information about the concentration of predominantly additive genes (Franco *et al.*, 2001). The estimates of GCA effects of lines and testers (Table 3) suggested that, among six lines, IIHR977 was good general combiner for number of branches, flower clusters per plant, fruits per cluster, PDI, number of locules per fruit and ascorbic acid in desirable direction. Whereas, IIHR1816 was best general combiner for traits like PDI, total carotenoids, lycopene content and yield per hectare in desirable direction. For the characters like average fruit weight and pericarp thickness, IIHR2848 was found to be a best general combiner while, IIHR2892 was found to be the good general combiner for flower clusters per plant, ascorbic acid, total carotenoids, lycopene and yield per hectare. Among the testers, IIHR2852 was the good general combiner for flower clusters per plant, fruit clusters per plant and for fruit quality traits like fruit length, firmness, number of locules, pericarp thickness, total carotenoids and lycopene and IIHR2853 was found to be a good general combiner for yield attributing traits like average fruit weight, fruit length, breadth and total yield per hectare along with the fruit quality attributes like ascorbic acid, total carotenoids and lycopene content. However for early blight resistance, IIHR2890 was found to be a good general combiner among testers. Results from the analysis of data from 18 hybrids (Table 4) revealed significant SCA effects in desirable direction in 3 crosses for flower clusters per plant, 2 crosses for average fruit weight, 14 crosses for PDI, 3 crosses for yield per hectare and one cross each for fruit length and breadth. Among fruit quality traits significant positive SCA effects were observed in 2 crosses for fruit firmness, 3 crosses for number of locules per fruit, 6 crosses for ascorbic acid and 7 crosses each for total carotenoids and lycopene. However, for PDI of early blight, highest significant SCA in desirable direction was observed in the crosses IIHR2850 \times IIHR2852 and IIHR2891 \times IIHR2890 followed by IIHR2892 \times IIHR2890 and IIHR977 \times IIHR2853. The hybrid IIHR2848 \times IIHR2853 exhibited highest significant positive SCA for average fruit weight followed by the cross IIHR1816 \times IIHR2890. For fruit firmness, highest SCA in positive direction was observed in cross IIHR2892 \times IIHR2852 followed by IIHR2850 \times IIHR2890. Highest significant SCA effect for ascorbic

acid content was recorded in the hybrid, IIHR 1816 × IIHR 2890 followed by IIHR 977 × IIHR 2853. For both total carotenoids and lycopene content, highest significant SCA effect in positive direction were observed in the same set of hybrids IIHR 2892 × IIHR 2852 followed by IIHR 2891 × IIHR 2853. The cross IIHR 2850 × IIHR 2890 was found to be the only best specific combiner for days to first fruit maturity. None of the hybrids found to be a significant specific combiner in desirable direction for the traits like days to 50 per cent flowering; fruits per cluster, fruit set per cent, TSS and pericarp thickness (Table 4).

Conclusion

From this study, it can be concluded that, combining ability estimates can be used to select the parents to be involved in hybrid combinations to predict the best hybrid. Present investigation suggests that none of the single parent or cross found to be superior for all the studied traits. Amongst the parents, IIHR 1816 was found to be a good general combiner for flower clusters per plant, average fruit weight, PDI for early blight, ascorbic acid, total carotenoids, lycopene and yield per hectare. However, the combination IIHR 2891 × IIHR 2853 was best specific combiner for number of branches, ascorbic acid, total carotenoids, lycopene and yield per hectare. Whereas the cross IIHR 2892 × IIHR 2890 was found to be the best specific combination for flower clusters per plant, PDI of early blight and yield per hectare. Identified general combiners for resistance to early blight can be used as parent to obtain early blight tolerant hybrids coupled with yield and quality. Similarly, better specific combiners can be used as hybrids since their performance as a combination is superior.

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