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Diallel analysis over environments for yield and its attributing traits in tomato (*Solanum lycopersicum* L.)

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Abstract
Forty five F_1 hybrids produced in a diallel fashion and their 10 parents were grown in an RBD to generate information on the genetics of yield attributing traits following components of variation and diallel analysis. Components of variation analysis suggested that both fixable and non-fixable gene effects were involved in the inheritance. The component analysis revealed the preponderance of non-additive gene effects in the inheritance of traits. Net dominance effect was significant and positive for most of the traits indicating positive direction of dominance. Positive and significant 'F' values for number of primary branches/plant, flesh thickness, number of fruits per plant, average fruit weight and fruit yield/plant indicated positive direction of dominance. Average degree of dominance was more than unity in all the traits indicating over-dominance. Non-significant values of t^2 and deviation of regression coefficient from unity depicted the absence of epistasis for all the traits in all the environments and pooled analysis.

Keywords: diallel, yield, traits, tomato (*Solanum lycopersicum* L.)

Introduction
Tomato (*Solanum lycopersicum* L., 2n = 24) a member of solanaceae family, is one of the most important vegetable crops both because of its special nutritive value and also due to its worldwide cultivation in all kind of climates, like temperate, sub-tropical and tropical. Besides, fresh consumption, tomato ranks first among processed vegetables in the world (Dhaliwal *et al.*, 2002) [3].

In India, tomato is grown across all agro-ecological zones and occupies an area of about 865 thousand ha with an annual production of 16826 thousand metric tonnes (Anonymous, 2010-11) [1]. The average productivity is 19.50 mtha^{-1} in the country as against 27.20 t ha^{-1} in the world. Jammu and Kashmir State with its varied agro-climatic conditions favours the cultivation of tomato throughout the year. It occupies an area of 2120 hectares with an annual production of 4020 tonnes (Anonymous, 2010) [2]. In the present study, ten diverse lines of tomato (*Solanum lycopersicum* L.) were involved in a diallel crossing programme to generate information on genetic parameters and identification of superior cross combinations.

Materials and Methods
The present investigation was conducted during *Kharif* 2011 at three locations viz., Vegetable Experimental Farm, SKUAST-K, Shalimar; KVK, Malangpora and RRS & FOA Wadura. The basic materials consisted of ten diverse genotypes of Tomato (*Solanum lycopersicum* L.) viz., Arka Vikas, KS-227, VLT-32, DARL-63, DVRT-I, Local, Marglobe, Shalimar-II, Roma and Shalimar-I. These lines have been maintained by the Division of Vegetable Science, SKUAST-K, Shalimar and have been selected for the present study on the basis of genetic variability of various agronomic traits and maturity parameters. Forty five F_1 crosses were generated through 10 x 10 diallel mating design at Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-K, Shalimar during the year 2010. The final experimental materials consisting of ten parents and forty five F_1 crosses were evaluated during year 2011 at three locations i.e. (i) Vegetable Experimental Field, Division of Vegetable Science, SKUAST-K, Shalimar, (ii) Krishi Vigyan Kendra, Malangpora, (iii) Faculty of Agriculture, SKUAST-K, Wadura, Sopore, Baramulla. At each location the experiment was laid out in completely randomized block design with three replications. The row to row and plant to plant spacing was maintained at 60 x 45 cm. Recommended package of practices were adopted to raise a healthy crop at all the locations. The observations were recorded on five randomly

selected plants in each replication at all locations. Mean values were worked out for further statistical analysis. The observations were recorded on the following characters: days to first fruit set, days to first picking, plant height (cm), number of primary branches per plant, fruit size (cm^2), flesh thickness (mm), number of fruits per plant, average fruit weight (g), fruit yield per plant (kg) and number of locules.

Results and Discussion

Genetic variances are used for working out various genetic parameters. Six components of variance were worked out i.e., additive variance (D), dominance variance (H), proportion of positive and negative genes in parents (H_2), expected environmental component (E), mean of F.

Table 1.1: Estimates of components of genetic variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Components	Days to first fruit set				Days to first picking			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
$\hat{D}$	3.56 ±5.43	3.95 ±5.39	4.28 ±5.29	3.74 ±5.36	3.65* ±1.28	1.73 ±1.51	1.52 ±1.51	2.05 ±1.28
$\hat{H}_1$	48.58* ±11.57	42.79* ±11.48	38.87* ±11.27	42.42* ±11.42	19.16* ±2.74	14.35* ±3.22	20.28* ±3.22	14.66* ±2.72
$\hat{H}_2$	39.71* ±9.83	34.64* ±9.76	31.93* ±9.57	34.76* ±9.70	16.06* ±2.32	12.89* ±2.73	18.77* ±2.74	13.17* ±2.31
$\hat{h}^2$	44.04* ±6.58	37.77* ±6.53	30.00* ±6.41	37.09* ±6.49	5.14* ±1.56	2.07 ±1.83	0.31 ±1.83	2.10 ±1.55
$\hat{F}$	6.03 ±12.54	6.31 ±12.44	6.26 ±12.22	5.84 ±12.38	4.04 ±2.97	-1.84 ±3.49	-1.23 ±3.49	-0.08 ±2.95
$\hat{E}$	0.02 ±1.63	0.07 ±1.62	0.02 ±1.59	0.01 ±1.62	0.15 ±0.38	0.21 ±0.45	0.19 ±0.45	0.06 ±0.38

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.2: Estimates of components of genetic variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Components	Plant height (cm)				Number of primary branches plant^{-1}			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
$\hat{D}$	47.38 ±47.63	34.46 ±40.20	48.40 ±57.62	41.60 ±48.12	0.93* ±0.14	0.65* ±0.14	0.43* ±0.07	0.64* ±0.08
$\hat{H}_1$	527.72* ±101.39	525.29* ±85.57	542.39* ±122.66	520.49* ±102.42	3.06* ±0.31	2.28* ±0.29	1.44* ±0.16	1.91* ±0.16
$\hat{H}_2$	494.90* ±86.17	486.06* ±72.72	506.80* ±104.24	487.64* ±87.05	2.54* ±0.26	2.01* ±0.25	1.21* ±0.14	1.60* ±0.14
$\hat{h}^2$	163.08* ±57.68	153.54* ±48.68	114.34 ±69.77	142.92 ±58.27	1.38* ±0.17	0.99* ±0.16	1.46* ±0.09	1.28* ±0.09
$\hat{F}$	23.59* ±109.90	13.32 ±92.75	21.26 ±132.95	15.66 ±11.02	1.13* ±0.34	0.64* ±0.32	0.40* ±0.18	0.68* ±0.17
$\hat{E}$	0.21 ±14.36	0.33 ±12.12	0.32 ±17.37	0.10 ±14.51	0.01 ±0.04	0.01 ±0.04	0.009 ±0.02	0.004 ±0.02

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.3: Estimates of components of genetic variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Components	Fruit size (cm^2)				Flesh thickness (mm)			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
$\hat{D}$	13.42 ±8.63	10.98 ±7.71	11.07 ±7.58	11.76 ±7.85	0.66* ±0.18	0.88* ±0.18	0.74* ±0.16	0.71* ±0.15
$\hat{H}_1$	95.50* ±18.37	87.50* ±16.42	89.34* ±16.13	88.13* ±16.70	1.95* ±0.40	1.85* ±0.39	1.64* ±0.34	1.54* ±0.32
$\hat{H}_2$	80.30* ±15.62	73.49* ±13.96	76.55* ±13.71	74.37* ±14.19	1.61* ±0.34	1.20* ±0.34	1.23* ±0.29	1.13* ±0.27
$\hat{h}^2$	16.67* 10.45	18.46* ±9.34	16.13 ±9.18	17.08 ±9.50	0.86* ±0.23	0.16 ±0.22	0.26 ±0.19	0.39* ±0.18
$\hat{F}$	20.93 ±19.92	17.30 ±17.79	16.62 ±17.49	18.26 ±18.11	0.82 ±0.43	1.41* ±0.43	0.98* ±0.37	0.97* ±0.35
$\hat{E}$	0.03 ±2.60	0.04 ±2.32	0.04 ±2.28	0.01 ±2.37	0.01 ±0.05	0.01 ±0.06	0.02 ±0.04	0.006 ±0.04

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.4: Estimates of components of genetic variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Components	Number of fruits plant^{-1}				Av. fruit weight			
	E_1	**E_2**	**E_3**	**Pooled**	**E_1**	**E_2**	**E_3**	**Pooled**
$\hat{D}$	38.09* ±4.97	35.65* ±3.21	30.71* ±3.45	34.17* ±3.72	27.80* ±5.50	30.47* ±6.31	32.00* ±5.88	29.56* ±5.13
$\hat{H}_1$	71.92* ±10.58	66.58* ±6.84	68.58* ±7.35	66.98* ±7.592	117.89* ±11.70	119.25* ±13.44	110.78* ±12.53	107.74* ±10.93

$\hat{H}_2$	49.84* ±9.00	48.17* ±5.81	52.45* ±6.24	48.72* ±6.73	92.71* ±9.95	94.90* ±11.42	89.03* ±10.65	86.48* ±9.29
$\hat{h}^2$	70.44* ±6.02	107.21* ±3.89	134.17* ±4.18	102.21* ±4.51	228.09* ±6.66	271.25* ±7.64	244.95* ±7.13	247.82* ±6.22
$\hat{F}$	56.81* ±11.47	50.22* ±7.42	43.51* ±7.96	48.99* ±8.59	34.68* ±12.69	39.43* ±14.57	37.82* ±13.58	37.12* ±11.85
$\hat{E}$	0.03 ±1.50	0.03 ±0.97	0.04 ±1.04	0.01 ±1.12	0.03 ±1.65	0.066 ±1.90	0.056 ±1.77	0.02 ±1.54

*, ** Significant at 5 and 1 per cent levels, respectively

Table 1.5: Estimates of components of genetic variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Components	Fruit yield plant^{-1}				Locule number			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
$\hat{D}$	0.14* ±0.02	0.12* ±0.02	0.11* ±0.03	0.12* ±0.02	0.29* ±0.12	0.34* ±0.15	0.29* ±0.12	0.30* ±0.13
$\hat{H}_1$	0.56* ±0.05	0.58* ±0.05	0.58* ±0.06	0.57* ±0.05	1.10* ±0.27	1.27* ±0.32	1.14* ±0.26	1.13* ±0.28
$\hat{H}_2$	0.48* ±0.04	0.49* ±0.04	0.50* ±0.05	0.49* ±0.05	0.87* ±0.23	1.00* ±0.27	0.92* ±0.22	0.89* ±0.24
$\hat{h}^2$	2.32* ±0.02	2.60* ±0.03	2.69* ±0.04	2.54* ±0.03	0.002 ±0.15	0.03 ±0.18	0.002 ±0.15	0.01 ±0.16
$\hat{F}$	0.21* ±0.05	0.19* ±0.06	0.18* ±0.07	0.19* ±0.06	0.35 ±0.29	0.43 ±0.35	0.33 ±0.28	0.36 ±0.31
$\hat{E}$	0.002 ±0.007	0.000 ±0.007	0.000 ±0.009	0.00 ±0.01	0.009 ±0.03	0.013 ±0.04	0.012 ±0.03	0.004 ±0.04

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.1: Proportion of related genetic parameters of variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Proportion	Days to first fruit set				Days to first fruit picking			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]$½	3.69	3.29	3.01	3.37	2.29	2.88	3.65	2.67
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.20	0.20	0.20	0.20	0.21	0.22	0.23	0.22
$\frac{KD}{KR}$	1.59	1.64	1.64	1.60	1.64	0.69	0.80	0.99
$\frac{\hat{h}^2}{\hat{H}_2}$	1.11	1.09	0.94	1.07	0.32	0.16	0.02	0.16
Heritability (n.s)	0.24	0.25	0.24	0.24	0.24	0.42	0.30	0.35
B	0.11 ±0.09	0.10 ±0.09	0.13 ±0.09	0.11 ±0.09	0.18 ±0.34	0.09 ±0.11	0.29 ±0.10	0.16 ±0.16
b-0/SE(b)	-1.13	-1.03	-1.37	-1.20	-0.54	-0.88	-2.85	-1.04
b-1/S.E(b)	9.51	9.06	8.94	9.39**	2.41	8.01	6.80	5.27*
t^2	23.89	21.10	21.86	23.58	0.005	15.63	15.92	5.93

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.2: Proportion of related genetic parameters of variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Proportion	Plant height (cm)				Number of primary branches plant^{-1}			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]$½	3.34	3.90	3.35	3.54	1.81	1.84	1.82	1.73
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.23	0.23	0.23	0.23	0.21	0.22	0.21	0.21
$\frac{KD}{KR}$	1.16	1.10	1.14	1.12	2.00	1.72	1.68	1.88
$\frac{\hat{h}^2}{\hat{H}_2}$	0.33	0.32	0.23	0.29	0.55	0.49	1.20	0.79
Heritability (n.s)	0.18	0.19	0.20	0.19	0.20	0.21	0.29	0.25
B	-0.27 ±0.15	-0.18 ±0.13	-0.20 ±0.14	-0.23 ±0.14	0.89 ±0.25	0.64 ±0.23	0.75 ±0.16	0.84 ±0.15
b-0/SE(b)	1.76*	1.39	1.47	1.67*	-3.61	-2.79	-4.77	-5.77
b-1/S.E(b)	8.15	9.05	8.70	8.92	0.43	1.56	1.61	1.09
t^2	5.43	10.09	8.52	8.32	0.34	0.13	0.61	0.18

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.3: Proportion of related genetic parameters of variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Proportion	Fruit size (cm^2)				Flesh thickness (mm)			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]½$	2.67	2.82	2.84	2.74	1.71	1.45	1.48	1.48
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.21	0.21	0.21	0.21	0.21	0.16	0.19	0.18
$\frac{KD}{KR}$	1.83	1.77	1.72	1.79	2.14	3.46	2.59	2.75
$\frac{\hat{h}^2}{\hat{H}_2}$	0.21	0.25	0.21	0.23	0.53	0.14	0.21	0.34
Heritability (n.s)	0.16	0.17	0.16	0.16	0.17	0.16	0.22	0.20
B	0.06 ±0.20	-0.02 ±0.25	0.10 ±0.24	0.05 ±0.23	0.24 ±0.18	-0.09 ±0.26	0.24 ±0.18	0.16 ±0.21
b-0/SE(b)	-0.28	0.08	-0.42	-0.23	-1.30	0.34	-1.37	-0.78
b-1/S.E(b)	4.59	4.11	3.76	4.09*	4.20	4.23	4.25	4.05**
t^2	2.61	1.05	1.23	1.51	3.51	0.81	3.72	2.31

*, ** Significant at 5 and 1 per cent levels, respectively

Table 2.4: Proportion of related genetic parameters of variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Proportion	Number of fruits $plant^{-1}$				Av. fruit weight			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]½$	1.37	1.37	1.49	1.40	2.06	1.98	1.86	1.91
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.17	0.18	0.19	0.18	0.20	0.19	0.20	0.20
$\frac{KD}{KR}$	3.37	3.13	2.80	3.09	1.87	1.97	1.93	1.98
$\frac{\hat{h}^2}{\hat{H}_2}$	1.41	2.23	2.56	2.09	2.46	2.86	2.75	2.87
Heritability (n.s)	0.12	0.14	0.11	0.12	0.28	0.24	0.26	0.24
B	0.88 ±0.24	0.93 ±0.16	0.88 ±0.18	0.91 ±0.19	0.60 ±0.19	0.54 ±0.20	0.64 ±0.18	0.65 ±0.17
b-0/SE(b)	-3.69	-5.74	-4.78	-4.81*	-3.22	-2.68	-3.57	-3.84
b-1/S.E(b)	0.50	0.43	0.67	0.45	2.12	2.24	1.97	2.06*
t^2	0.23	0.05	0.01	0.11	0.91	0.84	0.80	1.04

Table 2.5: Proportion of related genetic parameters of variation for maturity and yield attributing traits in Tomato (*Solanum lycopersicum* L.)

Proportion	Fruit yield $plant^{-1}$				Locule number			
	E_1	E_2	E_3	Pooled	E_1	E_2	E_3	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]½$	2.04	2.19	2.26	2.17	1.92	1.92	1.95	1.93
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.21	0.21	0.22	0.21	0.19	0.20	0.20	0.19
$\frac{KD}{KR}$	2.21	2.15	2.08	2.15	1.88	1.98	1.77	1.87
$\frac{\hat{h}^2}{\hat{H}_2}$	4.82	5.23	5.32	5.20	0.003	0.03	0.002	1.01
Heritability (n.s)	0.05	0.04	0.05	0.04	0.29	0.25	0.29	0.28
B	0.73±0.18	0.65±0.14	0.58±0.15	0.65±0.16	0.32±0.25	0.17±0.27	0.35±0.27	0.27±0.27
b-0/SE(b)	-4.07	-4.67	-3.83	-4.12	-1.29	-0.65	-1.29	-1.01*
b-1/S.E(b)	1.53	2.55	2.76	2.25**	2.68	3.09	2.36	2.74
t^2	0.37	2.39	2.49	1.49	0.59	0.56	0.26	0.46

*, ** Significant at 5 and 1 per cent levels, respectively

over the array (F) and dominance effect (h^2). These estimates were used to generate some genetic ratios i.e., average degree of dominance $(\hat{H}_1 / \hat{D})^{1/2}$, ratio of dominant and recessive genes in the parents [(4DH1)1/2 + F]/ [(4DH1)1/2-F], the number of gene groups (h^2/H_2) and the proportion of positive and negative genes (H_2/4H1). Perusal of data pooled over environments indicated that additive genetic variance component ($\hat{D}$) was significant for number of primary branches $plant^{-1}$, flesh thickness, number of fruits $plant^{-1}$, average fruit weight, fruit yield $plant^{1}$, number of locules and non-significant for rest of the traits. Measures of dominance components ($\hat{H}_1$ and $\hat{H}_2$) were significant for all the traits. These results indicated the involvement of both additive and dominance components in the inheritance of these traits. However, the magnitude of dominance components, in general, was higher than the corresponding additive

component. This suggests the greater role of dominance component in the inheritance of these traits. Hannan *et al.* (2007a) [4] also reported higher magnitude of dominant genetic component than expressed additive effects in most of the traits studied. Asymmetrical distribution of genes with positive and negative effects in the parents was also reported by Hannan *et al.* (2007c) [5]. Such genetic variation among parents would help in identification of parents carrying genes with positive effects for traits of interest in improvement programme. The net dominance effect ($\hat{h}^2$) was significant and positive for days to first fruit set, number of primary branches plant^{-1}, number of fruits plant^{-1}, average fruit weight, fruit yield plant^{-1} suggesting significantly high dominance effect in heterozygote over all loci and positive direction of dominance for these traits. For rest of the traits, $\hat{h}^2$ was non-significant and positive suggesting absence of directional dominance. Hannan *et al.* (2007b) [6] suggested that overall effects of dominant genes in F_1's were in enhancing direction for traits under concern which could be utilized via hybrid seed production. $\hat{F}$ values were found to be positive and significant for number of primary branches plant^{-1}, flesh thickness, number of fruits plant^{-1}, average fruit weight, fruit yield plant^{-1}, depicting the higher frequency of dominant alleles in the parents with respect to these traits. For rest of the traits, $\hat{F}$ value was positive but non-significant depicting that the relative frequency of dominant and recessive alleles in the parents was proportionally equal. Availability of surplus dominant genes for all traits except fruit length as indicated by positive and significant $\hat{F}$ values was also reported by Hannan *et al.* (2007b) [6].

Average degree of dominance $(\hat{H}_1 / \hat{D})^{0.5}$ was greater than unity in all the characters indicating overdominance in the expression of these traits. The estimate of $\hat{H}_2 / 4\hat{H}_1$ was less than 0.25 in all the traits revealing asymmetrical distribution of genes in the parents with respect to these traits. Similar results have also been reported by Hannan *et al.* (2007c) [5]. The value of KD/KR ratio was greater than unity in all the traits except days to first picking indicating excess of dominant alleles as compared to recessive ones, whereas for days to first picking the ratio was less than unity indicating the excess of recessive alleles. The estimates of $\hat{h}^2 / \hat{H}_2$ were more than 0.50 for days to first fruit set, number of primary branches plant^{-1}, number of fruits plant^{-1}, average fruit weight and fruit yield plant^{-1} indicating the greater proportion of dominant genes or gene groups in these traits, whereas for rest of the traits the values were less than 0.50, indicating greater proportions of recessive genes. The heritability (narrow sense) estimates for days to first fruit set, plant height, number of primary branches plant^{-1}, fruit size, flesh thickness, number of fruits plant^{-1}, average fruit weight were low (10 to 26%), whereas for rest of the traits heritability (narrow sense) estimates were medium (31 to 53%). The low to medium heritability (narrow sense) indicates high degree of non-additive gene action. Hannan *et al.* (2007) [4] reported more than unity values of $\hat{h}^2 / \hat{H}_2$ for number of fruits plant^{-1}, fruit length and fruit yield plant^{-1}and low values of narrow sense heritability for some of the traits studied.

Non-significant value of t^2 along with non-significant deviation of regression coefficient from unity in all environments as well as in pooled data revealed the absence of epistasis in all traits.

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