



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2022; 11(12): 3635-3638

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www.thepharmajournal.com

Received: 25-09-2022

Accepted: 02-11-2022

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Gene action studies in tomato for yield and yield attributing traits using diallel analysis

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Abstract

The goal of the current study was to better understand the type and extent of gene action in tomato for different yield and yield contributing traits. Twelve different lines of tomato were crossed in diallel fashion (excluding reciprocals) and tested for gene action investigations in three different environments. Analysis of variance of the components of genetic variation revealed that the additive variance component (\hat{D}) and those of dominance components (\hat{H}_1 and \hat{H}_2) were found to be significant in all environments and data pooled over environments. This demonstrates how both additive and non-additive gene action are involved in the inheritance of characteristics. Hence, reliance should be placed on the development of superior lines with several desirable genes.

Keywords: Gene action, yield, diallel analysis

Introduction

Tomato (*Solanum lycopersicum* L.), is one of the most promising vegetable crops grown throughout the world due to its commercial value, widespread adaptability, relatively short life cycle, good productivity, seed production ability and resistance to some pests and diseases. The tomato is a sexually reproduced herbaceous plant with bisexual flowers that is both annual and perennial. After sweet potato and potato, it is the third most important vegetable crop in the world, but it is the most popular canned vegetable. It was introduced in India during British period in the year 1828. In India, it is commonly referred as to 'Poor Man's Orange'. It is believed to be of Peru-Ecuador origin. The wild species of tomato originated in the western part of South America in the area stretching from southern Colombia to northern Chile and from the pacific coast to the western foothills of the Andes. It was introduced to Spain from Mexico in the first half of the 16th century, then to European countries, other continents and later on to India by Portuguese explorers.

Plant breeding relies heavily on combining ability since it gives information on the nature of gene action. The knowledge of genetic structure and mode of inheritance of different characters helps breeders to employ suitable breeding methodology for their improvement (Kiani *et al.*, 2007) [1].

Materials and Methods

The gene action studies in tomato was carried out at three locations *viz.*, E₁: Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar; E₂: Vegetable Seed Multiplication Farm, SKUAST-Kashmir, Shuhama and E₃: Faculty of Agriculture, SKUAST-Kashmir, Wadura Sopore. During 2021-2022. Twelve parental lines were crossed in diallel fashion (excluding reciprocals) during 2021. The resultant 66 crosses were then evaluated along with their twelve parents and two standard checks (Shalimar Hybrid-1) and (Shalimar Hybrid-2) during 2022, for various quantitative traits in RCBD. The seeds of all parental lines and their crosses were first sown in nursery and then transplanted to the main field at a spacing of 60 x 45 cm between rows and plants respectively. Recommended package of practices was followed to raise a healthy crop. The observations were recorded on 18 quantitative traits *viz.*, number of days to 1st flowering, number of days to 1st fruit set, number of days to 1st fruit harvest, number of pickings, number of fruits cluster⁻¹, number of fruit plant⁻¹, fruit length (cm), fruit diameter (cm), number of locules fruit⁻¹, pericarp thickness (mm), number of primary branches plant⁻¹, plant height (cm), average fruit weight (g), fruit yield plant⁻¹ (kg), fruit yield hectare⁻¹ (q), seed yield fruit⁻¹ (g), seed yield plant⁻¹ (g) and 100-seed weight (g).

Results and Discussion

Analysis of variance of the components of genetic variation revealed that the estimates of additive components (\hat{D}) and those of dominance components (\hat{H}_1 and \hat{H}_2) were found to be significant in all environments and data pooled over environments. This shows the involvement of both additive and dominance components in the inheritance of these traits, however greater magnitude of dominance component than its corresponding additive component of variance demonstrated greater role of dominance component in the inheritance of traits studied, which was also found while estimating variance arising due to dominance deviation through combining ability analysis by Griffing (1956a,b) approach. As, the magnitude of dominance component is more in comparison with the additive component, the breeders can then go for inter-mating of the selected plants in segregating population or recurrent selections may be practiced to improve the yield component. Also, such genetic variation among the parents will help in the identification of genotypes, carrying genes with the positive effects for the traits of interest in the plant improvement programmes.

The net dominance effect component (h^2) was found non-significant and positive for all the traits except for number of days to first fruit harvest in E_3 and pooled environment; fruit length in E_1, E_2, E_3 and pooled environments; fruit diameter in E_1, E_3 and pooled environments; number of primary branches in E_1, E_2, E_3 and pooled environments; plant height in E_2, E_3 and pooled environments, indicating absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance (positive) for all these traits. While as the net dominance effect component (h^2) was found positive and significant for number of days to first flowering in E_1 and E_2 ; number of locules fruit⁻¹ in E_1, E_2, E_3 and pooled

environments indicating the presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance (positive) for these traits.

The F^* value was found to be positive and significant for various traits viz., number of days to first flowering, number of days to first fruit harvest, number of pickings, number of fruits plant⁻¹, number of locules fruit⁻¹, number of fruits cluster⁻¹, plant height, fruit yield plant⁻¹, fruit yield hectare⁻¹, seed yield fruit⁻¹, seed yield plant⁻¹, 100 seed weight, number of first fruit set in E_1 , pericarp thickness in E_2 and number of primary branches in E_1 and E_3 depicting the higher frequency of dominant alleles in the parents with respect to these traits. The F^* value was found positive and non-significant for various traits viz., fruit length, fruit diameter, average fruit weight, number of days to first fruit set in E_2, E_3 and pooled environments, pericarp thickness in E_1, E_3 and pooled environments, number of primary branches in E_2 and pooled environments. For the traits, where F^* value is positive but non-significant, the relative frequency of dominant and recessive alleles was proportionally equal in the parental genotypes.

The estimates of E^* value were also found non-significant for all the traits except for number of days to first flowering in pooled environments; number of days to first fruit set in pooled environments; number of primary branches plant⁻¹ in E_1, E_2 and pooled environments; number of fruits cluster⁻¹ in E_3 and pooled environments indicating that the environment plays no role in the expression of these traits.

These findings were in accordance with the findings of Shankar *et al.*, (2013) [6], Shankar *et al.*, (2014) [7], Triveni *et al.*, (2017) [2], Dharva *et al.* (2018) [3], Kumar *et al.* (2018) [4], Rajkumar *et al.* (2018) [5], Veena *et al.* (2019) [8] and Vekariya *et al.* (2019) [9] and Bindal *et al.* (2019) [10].

Table 1(a): Estimates of components of genetic variation for no. of days to first flowering, no. of days to first fruit set, no. of days to first fruit harvest and no. of pickings in Tomato (*Solanum lycopersicum* L.) [Individual and pooled data over environments]

Components	No. of days to first flowering				No. of days to first fruit set				No. of days to first fruit harvest				No. of pickings			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	11.35* ±2.65	11.27* ±2.18	10.77* ±2.53	7.68* ±2.42	9.98* ±3.89	10.54* ±4.12	8.61* ±3.48	6.28 ±3.82	30.51* ±6.04	32.00* ±5.88	26.63* ±6.68	26.34* ±6.08	11.15* ±2.53	7.98* ±2.17	5.48* ±1.20	7.52* ±1.88
\hat{H}_1	36.44* ±5.30	35.15* ±4.37	37.94* ±5.06	26.07* ±4.85	43.72* ±7.78	44.87* ±8.25	41.29* ±6.98	33.15* ±7.64	113.13* ±12.09	110.25* ±11.77	101.15* ±13.37	99.01* ±12.17	33.59* ±5.07	23.92* ±4.34	15.03* ±2.40	21.89* ±3.77
\hat{H}_2	27.28* ±4.41	26.96* ±3.63	28.94* ±4.21	20.27* ±4.03	35.47* ±6.47	35.84* ±6.86	33.71* ±5.80	27.7* ±6.36	84.78* ±10.06	83.47* ±9.79	79.10* ±11.12	76.05* ±10.12	23.07* ±4.22	16.21* ±3.61	10.38* ±2.00	14.91* ±3.14
\hat{h}^2	3.20* ±2.95	2.61* ±2.43	1.81 ±2.81	1.53 ±2.70	0.66 ±4.32	3.62 ±4.58	2.59 ±3.88	1.06 ±4.25	0.14 ±6.72	0.58 ±6.54	-0.11 ±7.43	-0.76 ±6.77	0.63 ±2.82	0.11 ±2.41	0.15 ±1.33	0.13 ±2.10
\hat{F}	18.82* ±6.01	17.53* ±4.95	17.34* ±5.73	12.08* ±5.50	12.77* ±8.81	13.62 ±9.34	10.29 ±7.90	6.52 ±8.66	37.29* ±13.70	36.38* ±13.34	25.98 ±15.15	27.61* ±13.79	19.96* ±5.75	14.56* ±4.92	9.11* ±2.72	13.35* ±4.28
\hat{E}	0.31 ±0.73	0.35 ±0.60	0.27 ±0.70	3.53* ±0.67	0.29 ±1.07	0.25 ±1.14	0.35 ±0.96	3.65* ±1.06	0.28 ±1.67	2.28 ±1.63	0.40 ±1.85	3.21 ±1.68	0.07 ±0.70	0.05 ±0.60	0.06 ±0.33	0.48 ±0.52

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

E1: Div. of Vegetable Science (SKUAST-K, Shalimar) E2: Vegetable SMF (SKUAST-K, Shuhama) E3: FOA (SKUAST-K, Wadura)

Table 1(b): Estimates of components of genetic variation for no. of fruits cluster⁻¹, no. of fruits plant⁻¹, fruit length and fruit diameter in Tomato (*Solanum lycopersicum* L.) [Individual and pooled data over environments]

Components	No. of fruits cluster ⁻¹				No. of fruits plant ⁻¹				Fruit length (cm)				Fruit diameter (cm)			
	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled	E ₁	E ₂	E ₃	Pooled
\hat{D}	0.54* ±0.10	0.50* ±0.06	0.19* ±0.04	0.32* ±0.06	713.09* ±110.21	670.86* ±96.55	506.57* ±65.30	618.42* ±89.69	0.87* ±0.32	0.84* ±0.30	0.45* ±0.21	0.62* ±0.26	1.22* ±0.39	1.15* ±0.41	0.74* ±0.28	0.94* ±0.35
\hat{H}_1	1.03* ±0.20	0.83* ±0.12	0.57* ±0.08	0.58* ±0.12	1410.57* ±220.48	1325.56* ±193.16	905.57* ±130.64	1176.85* ±179.43	4.34* ±0.65	3.97* ±0.61	2.67* ±0.42	3.37* ±0.53	4.88* ±0.79	4.52* ±0.82	3.13* ±0.56	3.92* ±0.70
\hat{H}_2	0.77* ±0.17	0.62* ±0.10	0.39* ±0.06	0.42* ±0.10	869.84* ±183.40	795.49* ±160.68	515.71* ±108.67	700.21* ±149.25	3.63* ±0.54	3.20* ±0.51	2.33* ±0.35	2.86* ±0.44	4.13* ±0.66	3.80* ±0.68	2.76* ±0.46	3.39* ±0.58

\hat{h}^2	0.02 ±0.11	0.03 ±0.06	0.03 ±0.04	0.01 ±0.06	68.92 ±122.62	80.95 ±107.43	60.73 ±72.65	69.57 ±99.79	-0.04 ±0.36	-0.01 ±0.34	-0.04 ±0.23	-0.02 ±0.29	-0.01 ±0.44	0.02 ±0.45	-0.02 ±0.31	-0.01 ±0.39
\hat{F}	0.69* ±0.23	0.58* ±0.14	0.34* ±0.09	0.42* ±0.13	1172.82* ±249.79	1132.07* ±218.84	851.20* ±148.00	1032.53* ±203.28	1.09 ±0.74	1.15 ±0.70	0.53 ±0.48	0.75 ±0.60	1.46 ±0.90	1.38 ±0.93	0.79 ±0.63	1.05 ±0.80
\hat{E}	0.03 ±0.02	0.02 ±0.01	0.02* ±0.01	0.07* ±0.01	0.71 ±30.56	0.60 ±26.78	0.66 ±18.11	8.05 ±24.87	0.02 ±0.09	0.02 ±0.08	0.02 ±0.05	0.07 ±0.07	0.02 ±0.11	0.01 ±0.11	0.02 ±0.07	0.07 ±0.09

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

E1: Div. of Vegetable Science (SKUAST-K, Shalimar) E2: Vegetable SMF (SKUAST-K, Shuhama) E3: FOA (SKUAST-K, Wadura)

Table 1(c): Estimates of components of genetic variation for no. of locules fruit⁻¹, pericarp thickness, no. of primary branches plant⁻¹ and plant height in Tomato (*Solanum lycopersicum* L.) [Individual and pooled data over environments]

Components	No. of locules fruit ⁻¹				Pericarp thickness (mm)				No. of primary branches plant ⁻¹				Plant height (cm)			
	E1	E2	E3	Pooled	E1	E2	E3	Pooled	E1	E2	E3	Pooled	E1	E2	E3	Pooled
\hat{D}	1.36* ±0.32	1.18* ±0.28	0.86* ±0.27	1.06* ±0.28	2.18* ±0.78	2.01* ±0.72	1.07 ±0.72	1.60* ±0.72	0.28* ±0.03	0.25* ±0.03	0.38* ±0.04	0.10* ±0.02	599.62* ±106.13	492.72* ±94.76	529.92* ±103.18	537.99* ±100.77
\hat{H}_1	4.96* ±0.65	4.46* ±0.56	3.60* ±0.54	4.09* ±0.57	8.83* ±1.56	8.18* ±1.45	5.52* ±1.44	7.03* ±1.44	0.56* ±0.06	0.54* ±0.07	0.51* ±0.08	0.17* ±0.05	1611.85* ±212.32	1428.47* ±189.58	1505.90* ±206.42	1508.59* ±201.59
\hat{H}_2	3.93* ±0.54	3.49* ±0.47	2.90* ±0.45	3.25* ±0.47	6.93* ±1.30	6.24* ±1.21	4.34* ±1.19	5.49* ±1.20	0.50* ±0.05	0.48* ±0.06	0.43* ±0.06	0.22* ±0.04	1054.85* ±176.61	990.19* ±157.70	1008.82* ±171.71	1013.46* ±167.69
\hat{h}^2	0.59* ±0.36	0.51* ±0.31	0.35* ±0.30	0.46* ±0.32	0.17 ±0.87	0.08 ±0.81	0.10 ±0.80	0.09 ±0.80	-0.01 ±0.03	-0.02 ±0.04	-0.01 ±0.04	-0.03 ±0.02	0.36 ±118.08	-0.51 ±105.43	-0.26 ±114.80	-0.87 ±112.12
\hat{F}	1.98* ±0.74	1.75* ±0.64	1.26* ±0.62	1.55* ±0.65	3.28 ±1.77	3.29* ±1.65	1.72 ±1.63	2.51 ±1.63	0.21* ±0.07	0.17 ±0.08	0.30* ±0.09	0.02 ±0.06	1105.09* ±240.54	888.16* ±214.78	981.41* ±233.86	987.77* ±228.39
\hat{E}	0.02 ±0.09	0.02 ±0.07	0.01 ±0.07	0.07 ±0.07	0.02 ±0.21	0.03 ±0.20	0.01 ±0.19	0.11 ±0.20	0.03* ±0.00	0.02* ±0.01	0.01 ±0.01	0.13* ±0.00	1.80 ±29.43	3.01 ±26.28	2.60 ±28.61	2.92 ±27.94

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

E1: Div. of Vegetable Science (SKUAST-K, Shalimar) E2: Vegetable SMF (SKUAST-K, Shuhama) E3: FOA (SKUAST-K, Wadura)

Table-1(d): Estimates of components of genetic variation for average fruit weight, fruit yield plant⁻¹ and fruit yield hectare⁻¹ in Tomato (*Solanum lycopersicum* L.) [Individual and pooled data over environments]

Components	Average fruit weight(g)				Fruit yield plant ⁻¹ (kg)				Fruit yield hectare ⁻¹ (q)			
	E1	E2	E3	Pooled	E1	E2	E3	Pooled	E1	E2	E3	Pooled
\hat{D}	276.84* ±96.37	254.32* ±95.69	230.44* ±93.46	245.01* ±94.91	0.43* ±0.11	0.37* ±0.09	0.21* ±0.06	0.30* ±0.08	60049.36* ±15202.92	50811.50* ±13229.94	29145.01* ±8729.95	41926.00* ±12054.59
\hat{H}_1	1206.40* ±192.81	1141.90* ±191.43	1088.11* ±186.97	1123.76* ±189.87	1.80* ±0.22	1.48* ±0.19	0.83* ±0.12	1.25* ±0.17	248098.40* ±30413.97	203220.80* ±26466.95	114814.20* ±17464.57	178676.10* ±24115.61
\hat{H}_2	1069.46* ±160.38	1009.72* ±159.24	966.82* ±155.53	999.96* ±157.94	1.43* ±0.18	1.16* ±0.16	0.66* ±0.10	1.00* ±0.14	197420.80* ±25299.20	160221.30* ±22015.95	90855.01* ±14527.52	138473.50* ±20060.05
\hat{h}^2	21.94 ±107.23	23.54 ±106.47	13.42 ±103.99	17.48 ±105.60	0.05 ±0.12	0.07 ±0.10	0.03 ±0.07	0.04 ±0.09	8137.24 ±16915.27	9898.92 ±14720.06	4811.91 ±9713.23	6514.72 ±13412.32
\hat{F}	269.55 ±218.43	261.78 ±216.88	234.67 ±211.83	241.87 ±215.11	0.68* ±0.25	0.57* ±0.21	0.32* ±0.14	0.47* ±0.19	93336.63* ±34456.52	79326.70* ±29984.87	45257.31* ±19785.92	64892.80* ±27321.01
\hat{E}	1.69 ±26.73	1.68 ±26.54	1.67 ±25.92	7.92 ±26.32	0.01 ±0.03	0.02 ±0.02	0.01 ±0.01	0.02 ±0.02	327.80 ±4216.53	349.33 ±3669.32	211.71 ±2421.25	3378.63 ±3343.34

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

E1: Div. of Vegetable Science (SKUAST-K, Shalimar) E2: Vegetable SMF (SKUAST-K, Shuhama) E3: FOA (SKUAST-K, Wadura)

Table-1(e): Estimates of components of genetic variation for seed yield fruit⁻¹, seed yield plant⁻¹ and 100 seed weight in Tomato (*Solanum lycopersicum* L.) [Individual and pooled data over environments]

Components	Seed yield fruit ⁻¹ (g)				Seed yield plant ⁻¹ (g)				100 Seed weight			
	E1	E2	E3	Pooled	E1	E2	E3	Pooled	E1	E2	E3	Pooled
\hat{D}	0.03* ±0.02	0.02* ±0.01	0.04* ±0.02	0.03* ±0.02	11.83* ±2.46	10.43* ±2.06	6.89* ±1.25	9.34* ±1.89	0.03* ±0.01	0.08* ±0.02	0.06* ±0.02	0.04* ±0.01
\hat{H}_1	0.06* ±0.05	0.08* ±0.02	0.09* ±0.04	0.07* ±0.04	29.94* ±4.93	26.24* ±4.12	15.80* ±2.51	22.82* ±3.78	0.08* ±0.02	0.11* ±0.05	0.09* ±0.04	0.08* ±0.06
\hat{H}_2	0.05* ±0.02	0.06* ±0.03	0.08* ±0.04	0.09* ±0.05	21.08* ±4.10	18.15* ±3.43	10.47* ±2.09	15.70* ±3.14	0.07* ±0.02	0.09* ±0.06	0.12* ±0.06	0.09* ±0.06
\hat{h}^2	0.04 ±0.06	0.02 ±0.01	0.01 ±0.02	0.06 ±0.08	0.41 ±2.74	0.64 ±2.29	0.42 ±1.40	0.41 ±2.10	0.03 ±0.01	0.02 ±0.04	0.04 ±0.03	0.06 ±0.02
\hat{F}	0.03* ±0.01	0.01* ±0.03	0.04* ±0.01	0.02* ±0.04	18.33* ±5.59	16.58* ±4.67	11.05* ±2.85	11.73* ±4.28	0.04* ±0.02	0.03* ±0.01	0.04* ±0.02	0.06* ±0.04
\hat{E}	0.03 ±0.01	0.04 ±0.01	0.04 ±0.02	0.04 ±0.01	0.02 ±0.68	0.02 ±0.57	0.01 ±0.34	0.26 ±0.52	0.01 ±0.02	0.03 ±0.04	0.06 ±0.01	0.04 ±0.02

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

E1: Div. of Vegetable Science (SKUAST-K, Shalimar) E2: Vegetable SMF (SKUAST-K, Shuhama) E3: FOA (SKUAST-K, Wadura)

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