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Research Article

Gene action studies in cherry tomato for yield and yield attributing traits in open and protected environment

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ABSTRACT

The present study was undertaken to learn more about the the nature and magnitude of gene action for various yield and yield attributing traits in cherry tomato. Ten different lines of cherry tomato were crossed in diallel fashion (excluding reciprocals) and tested for gene action investigations in open and protected environment. Analysis of variance of the components of genetic variation and their ratios and differences revealed that the additive variance component ($\hat{D}$) was significant for all the traits in the individual as well as pooled data analysis, except for number of primary branches plant^{-1} in E_2. The dominance components ($\hat{H}_1$ and $\hat{H}_2$) showed the significant difference for all the traits except for plant height in E_2. This shows the involvement of both additive and non-additive type of gene action in the inheritance of the traits. Hence, reliance should be placed on reciprocal recurrent selection and the development of superior lines with several desirable genes.

Keywords: Gene action, Additive variance, Cherry tomato, Inheritance.

INTRODUCTION

Cherry tomato (*Solanum lycopersicum* var. *cerasiforme*), the ancestor of the cultivated tomato, is one of the most promising vegetable crops grown throughout the world due to its commercial and dietary value, widespread adaptability, possibility of growing in a variety of farming environments, relatively short life cycle, good productivity, seed production ability and resistance to some pests and diseases. For these and other desirable features like relatively small genome size, lack of gene duplication, easy way of controlling pollination and hybridization, ability of asexual propagation by grafting and possibility to regenerate whole plant from different explants, it is used as a model plant for both basic and applied research programmes (Bai and Lindhout, 2007; Prema *et al*., 2011b; Venkadeswaran *et al*., 2018). Because of its widespread distribution in Central America and the existence of reduced style length in the flower, it is thought to be the ancestor of the cultivated tomato (Cox, 2000; Grandillo *et al*., 2011). 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).

In the present study, efforts were made to understand the effects of genes in governing various yield and yield attributing traits and to gain information on the mode of inheritance of desirable traits. The early knowledge of essential genetic parameters involved in the expression of trait also helps in choosing the most suitable method for selection.

MATERIALS AND METHODS

The gene action studies in cherry tomato were carried out at Vegetable Experimental Farm, Division of Vegetable Science, SKUAST-Kashmir, Shalimar, India during 2019-20 (*Rabi* and *Kharif* season), in two environments namely open environment (E_1) and protected environment (E_2). A total of 10 parental lines were crossed in diallel fashion (excluding reciprocals) during

Rabi season, 2019. The resultant 45 F_1's was then evaluated along with their ten parents and two standard checks (Local cherry tomato-1 and Local cherry tomato-2) during *Kharif* season, 2020 for various quantitative traits in Augmented Block Design. The seeds of all accessions and their crosses were first sown in nursery and then transplanted to the main field at a spacing of 60 x 60 cm between rows and plants respectively. Recommended package of practices was followed to raise a healthy crop. The observations were recorded on 16 quantitative traits viz., plant height, number of primary branches plant^{-1}, days to first flowering, days to first fruit set, days to first fruit maturity, number of clusters plant^{-1}, number of flowers cluster^{-1}, number of fruits cluster^{-1}, number of fruits plant^{-1}, number of locules fruit^{-1}, fruit length, fruit diameter, average fruit weight, pericarp thickness, fruit yield plant^{-1} and fruit yield hectare^{-1} by selecting five random plants and the average was worked out.

RESULTS AND DISCUSSION

Analysis of variance of the components of genetic variation (Table 1.0-1.3) and their ratios and differences (Table 2.0-2.3) revealed that the additive variance component ($\hat{D}$) was significant for all the traits in the individual as well as pooled data analysis, except for number of primary branches plant^{-1} in E_2. The dominance components ($\hat{H}_1$ and $\hat{H}_2$) showed the significant difference for all the traits except for plant height in E_2. This shows the involvement of both additive and dominance components in the inheritance of these traits.

Net dominance effect component ($\hat{h}^2$) was found significant and positive for all the traits except for plant height in E_1 and E_2 and number of flowers cluster^{-1}; number of primary branches plant^{-1} and fruit yield hectare^{-1} in E_2; number of fruits plant^{-1} in E_1 and data pooled over environments; days to first flowering, pericarp thickness and fruit yield plant^{-1} in E_2 and data pooled over environments; days to first fruit set, number of clusters plant^{-1}, number of fruits cluster^{-1}, number of locules fruit^{-1}, fruit length, fruit diameter and average fruit weight in the individual as well as data pooled over environments, indicating significantly high dominance effect in heterozygote over all loci and presence of directional dominance (positive) for all these traits.

$\hat{F}$ value was found significant and positive for all the traits except for plant height in E_1 and E_2; days to first fruit set, days to first fruit maturity, number of flowers cluster^{-1} and pericarp thickness in E_1; number of locules fruit^{-1} in E_2; number of clusters plant^{-1}, number of fruits cluster^{-1}, number of fruits plant^{-1} and fruit yield plant^{-1} in E_1 and data pooled over environments; number of primary branches plant^{-1} and fruit diameter in E_2 and data pooled over environments; fruit length, average fruit weight and fruit yield hectare^{-1} in the individual as well as data pooled over environments, depicting the higher frequency of dominant alleles in the parents with respect to these traits. For the traits, where $\hat{F}$ value is positive but non-significant, the relative frequency of dominant and recessive alleles was proportionally equal in the parental genotypes.

Estimates of $\hat{E}$ value were also found non- significant for all the traits except for number of primary branches plant^{-1} in the individual as well as data pooled over environments; number of flowers cluster^{-1} and number of fruits cluster^{-1} in E_1, indicating that the environment plays no role in the expression of these traits.

Average degree of dominance $(\hat{H}_1 / \hat{D})^{1/2}$ was found to be greater than unity for all the traits reflecting the over dominance in the expression of these traits. The estimates of $\hat{H}_2 / 4\hat{H}_1$ were found to be less than 0.25 for all the traits indicating the asymmetrical distribution of alleles with positive and negative effect in the parents with reference to these traits. If this ratio is equal to 0.25, then there is symmetrical distribution of positive and negative alleles. The negative effects of alleles in parents were compensated by positive alleles in the hybrid resulting in over-dominance. Hence, selecting the parent with high positive alleles, the dominant genes exhibit dominance in hybrid. The KD / KR component estimates were found to be greater than unity for all the traits indicating the excess of dominant genes in parents as compared to the recessive genes. The values of $\hat{h}^2 / \hat{H}_2$ were found to be less than 0.50 for all the traits except for number of primary branches plant^{-1} in E_1, depicting the less proportion of dominance gene groups, while as the value of $\hat{h}^2 / \hat{H}_2$ was found to be more than 0.50 in number of primary branches plant^{-1} in E_1, depicting the greater proportion of dominant gene groups for this trait.

Estimates of $\hat{h}^2$ (n.s) (heritability in narrow sense) were found to be high (>50%) for plant height in the individual as well as pooled data analysis, days to first flowering and days to first fruit maturity in E_1 and pooled data analysis, days to first fruit set in E_1, fruit diameter, average fruit weight and pericarp thickness in E_2; medium (31 to 50%) for number of clusters plant^{-1} and fruit length in E_1, number of flowers cluster^{-1}, number of fruits cluster^{-1}, number of fruits plant^{-1}, fruit diameter, average fruit weight in E_1 and pooled data analysis, days to first flowering, days to first fruit maturity, fruit yield plant^{-1} and fruit yield hectare^{-1} in E_2, days to first fruit set in E_2 and pooled data analysis and pericarp thickness in pooled data analysis; low (11 to 30%) for number of locules fruit^{-1} in the individual as well as pooled data analysis, pericarp thickness in E_1, number of primary branches plant^{-1}, fruit yield plant^{-1} and fruit yield hectare^{-1} in E_1 and pooled data analysis, number of flowers cluster^{-1}, number of fruits cluster^{-1} and number of fruits plant^{-1} in E_2 and number of clusters plant^{-1} in E_2 and pooled data analysis and fruit length in pooled data analysis and very low (0.01 to 10%) for number of primary branches plant^{-1} and fruit length in E_2.

Table-1.0: Estimates of components of genetic variation for yield and yield attributing traits in Cherry tomato.

Components	Plant height (cm)			Number of primary branches plant^{-1}			Days to first flowering			Days to first fruit set		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$\hat{D}$	228.22*	16095.99*	8162.10*	0.09*	0.01	0.04*	16.60*	39.26*	27.92*	16.58*	37.55*	27.06*
	± 126.97	± 2179.52	± 1153.24	± 0.05	± 0.04	± 0.04	± 2.95	± 3.64	± 3.29	± 3.09	± 3.66	± 3.37
$\hat{H}_1$	1060.58*	30179.68	15620.12*	0.29*	0.38*	0.33*	17.93*	51.61*	34.76*	24.33*	47.56*	35.94*
	± 270.26	± 4639.31	± 2454.78	± 0.11	± 0.07	± 0.08	± 6.28	± 7.76	± 7.01	± 6.58	± 7.80	± 7.18
$\hat{H}_2$	979.71*	22777.84	11878.77*	0.21*	0.36*	0.28*	15.55*	38.35*	26.94*	21.69*	36.39*	29.03*
	± 229.69	± 3942.90	± 2086.29	± 0.10	± 0.06	± 0.07	± 5.34	± 6.59	± 5.96	± 5.59	± 6.63	± 6.10
$\hat{h}^2$	52.38	7095.80	3574.08*	0.15*	-0.01	0.06*	3.81*	0.85	2.32	2.92	0.75	1.83
	± 153.75	± 2639.23	± 1396.48	± 0.07	± 0.04	± 0.05	± 3.57	± 4.41	± 3.98	± 3.74	± 4.44	± 4.08
$\hat{F}$	117.36	19048.40	9582.87*	0.12*	0.01	0.06	3.40	40.31*	21.85*	4.88	36.21*	20.54*
	± 292.95	± 5028.81	± 2660.87	± 0.12	± 0.08	± 0.09	± 6.81	± 8.41	± 7.60	± 7.13	± 8.45	± 7.78
$\hat{E}$	4.32	119.05	61.68	0.05*	0.05*	0.04*	0.12	0.05	0.08	0.12	0.12	0.11
	± 38.28	± 657.15	± 347.71	± 0.02	± 0.01	± 0.01	± 0.89	± 1.20	± 1.04	± 0.93	± 1.11	± 1.01

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

Table-1.1: Estimates of components of genetic variation for yield and yield attributing traits in Cherry tomato.

Components	Days to first fruit maturity			Number of clusters plant^{-1}			Number of flowers cluster^{-1}			Number of fruits cluster^{-1}		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$\hat{D}$	16.99*	107.65*	62.31*	126.83*	9.64*	68.23*	1.05*	2.64*	1.84*	0.76*	1.97*	1.36*
	± 2.96	± 12.51	± 7.73	± 69.73	± 3.08	± 36.40	± 0.21	± 1.16	± 0.68	± 0.17	± 0.93	± 0.54
$\hat{H}_1$	18.15*	215.78*	116.96*	594.88*	38.19*	316.53*	3.13*	11.13*	7.12*	2.47*	8.89*	5.67*
	± 6.31	± 26.64	± 16.47	± 148.43	± 6.56	± 77.49	± 0.45	± 2.47	± 1.45	± 0.36	± 1.98	±1.16
$\hat{H}_2$	15.68*	173.78*	94.72*	490.62*	27.74*	259.17*	2.54*	8.84*	5.68*	1.86*	7.10*	4.47*
	± 5.36	± 22.64	± 13.99	± 126.15	± 5.57	± 65.85	± 0.39	± 2.10	± 1.24	± 0.30	± 1.68	± 0.98
$\hat{h}^2$	3.96*	29.25*	16.60*	5.36	2.21	3.78	0.05	1.80*	0.92*	-0.03	0.19	0.07
	± 3.59	± 15.15	± 9.36	± 84.44	± 3.73	± 44.08	± 0.26	± 1.40	± 0.82	± 0.20	± 1.13	± 0.66
$\hat{F}$	3.35	74.09*	38.71*	102.34	16.29*	59.31	0.29	3.52*	1.90*	0.27	2.22*	1.24
	± 6.83	± 28.87	± 17.84	± 160.90	± 7.11	± 84.00	± 0.49	± 2.67	± 1.57	± 0.39	± 2.15	± 1.26
$\hat{E}$	0.12	0.12	0.11	0.12	0.12	0.11	0.12*	0.12	0.11	0.12*	0.12	0.11
	± 0.89	± 3.77	± 2.32	± 21.03	± 0.93	± 10.97	± 0.06	± 0.35	± 0.20	± 0.05	± 0.28	± 0.16

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

Table-1.2: Estimates of components of genetic variation for yield and yield attributing traits in Cherry tomato.

Components	Number of fruits plant^{-1}			Number of locules fruit^{-1}			Fruit length (cm)			Fruit diameter (cm)		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$\hat{D}$	2139.87*	133.68*	1136.77*	0.476*	0.012*	0.237*	0.15*	0.46*	0.30*	0.19*	0.40*	0.29*
	± 706.34	± 57.05	± 381.69	± 0.253	± 0.015	± 0.127	± 0.07	± 0.17	± 0.11	± 0.05	± 0.14	± 0.09
$\hat{H}_1$	7968.51*	412.37*	4190.43*	1.367*	0.077*	0.715*	0.66*	1.65*	1.15*	0.62*	1.37*	0.99*
	± 1503.52	± 121.44	± 812.47	± 0.540	± 0.032	± 0.279	± 0.15	± 0.36	± 0.25	± 0.10	± 0.30	± 0.19
$\hat{H}_2$	6503.68*	342.69*	3423.18*	0.996*	0.064*	0.523*	0.55*	1.24*	0.89*	0.51*	1.03*	0.76*
	± 1277.83	± 103.21	± 690.51	± 0.459	± 0.027	± 0.236	± 0.13	± 0.30	± 0.21	± 0.09	± 0.25	± 0.16
$\hat{h}^2$	184.07	74.81*	129.43	0.008	-0.001	-0.004	0.04	0.04	0.03	0.05	0.07	0.05
	± 855.33	± 69.08	± 462.20	± 0.307	± 0.018	± 0.156	± 0.09	± 0.20	± 0.14	± 0.06	± 0.17	± 0.11
$\hat{F}$	817.80	144.82*	481.30	0.652*	0.019	0.329*	0.13	0.30	0.21	0.12*	0.12	0.11
	± 1629.75	± 131.63	± 880.68	± 0.585	± 0.035	± 0.303	± 0.16	± 0.39	± 0.27	± 0.11	± 0.32	± 0.21
$\hat{E}$	0.12	0.12	0.11	0.005	0.004	-0.003	0.00	0.00	0.00	0.00	0.00	0.00
	± 212.97	± 17.20	± 115.08	± 0.076	± 0.005	± 0.034	± 0.02	± 0.05	± 0.03	± 0.02	± 0.04	± 0.02

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

Table-1.3: Estimates of components of genetic variation for yield and yield attributing traits in Cherry tomato.

Components	Average fruit weight (g)			Pericarp thickness (mm)			Fruit yield plant^{-1} (Kg)			Fruit yield hectare^{-1} (q)		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$\hat{D}$	155.72*	650.15*	402.93*	0.30*	2.29*	1.29*	0.15*	0.63*	0.38*	16710.05*	48787.80*	32748.92*
	± 54.97	± 404.25	± 229.60	± 0.24	± 0.45	± 0.34	± 0.10	± 0.32	± 0.20	± 11399.14	± 24753.15	± 18076.14
$\hat{H}_1$	747.66*	3656.98*	2202.31*	2.35*	5.45*	3.89*	1.87*	3.29*	2.57*	208081.90*	253752.30*	230917.09*
	± 117.00	± 860.48	± 488.73	± 0.51	± 0.96	± 0.73	± 0.22	± 0.68	± 0.44	± 24264.13	± 52689.39	± 38476.75
$\hat{H}_2$	594.13*	2761.03*	1677.57*	2.12*	3.93*	3.02*	1.76*	2.48*	2.11*	195909.80*	191411.30*	193660.54*
	± 99.44	± 731.31	± 415.37	± 0.43	± 0.82	± 0.62	± 0.19	± 0.58	± 0.38	± 20621.82	± 44780.14	± 32700.97
$\hat{h}^2$	48.24	343.57	195.90	0.67*	0.03	0.34	0.39*	0.08	0.23	42827.78*	5917.69	24372.73*
	± 66.56	± 489.51	± 278.03	± 0.29	± 0.55	± 0.41	± 0.12	± 0.39	± 0.25	± 13803.45	± 29974.09	± 21888.76
$\hat{F}$	122.88	97.04	109.95	0.14	1.67*	0.90*	0.10	0.74*	0.41	10978.02	57054.97	34016.49
	± 126.82	± 932.72	± 529.76	± 0.55	± 1.04	± 0.79	± 0.24	± 0.68	± 0.45	± 26301.24	± 57112.96	± 41707.09
$\hat{E}$	0.35	0.35	0.34	0.00	0.00	0.00	0.01	0.00	0.00	530.98	97.49	314.23
	± 16.57	± 121.89	± 69.22	± 0.07	± 0.14	± 0.10	± 0.03	± 0.10	± 0.06	± 3436.97	± 7463.36	± 5450.16

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

Table-2.0: Proportion of related genetic parameters of variation for yield and yield attributing traits in Cherry tomato.

Proportion	Plant height (cm)			Number of primary branches plant^{-1}			Days to first flowering			Days to first fruit set		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]$½	2.156	1.369	1.756	1.793	5.978	3.879	1.039	1.146	1.086	1.212	1.125	1.162
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.231	0.189	0.203	0.183	0.238	0.204	0.217	0.186	0.195	0.223	0.191	0.200
$\frac{KD}{KR}$	1.271	2.522	1.890	2.118	1.203	1.654	1.219	2.621	1.913	1.276	2.499	1.881
$\frac{\hat{h}^2}{\hat{H}^2}$	0.053	0.312	0.176	0.720	-0.002	0.352	0.245	0.022	0.127	0.134	0.021	0.071
$\hat{h}^2$ (n.s)	0.278	0.277	0.271	0.196	0.055	0.119	0.660	0.388	0.517	0.564	0.404	0.477
b	0.192	0.462	0.320	-0.020	0.081	0.024	0.465	0.515	0.483	0.526	0.485	0.499
b-0/S.E.(b)	± 0.154	± 0.209	± 0.175	± 0.230	± 0.163	± 0.190	± 0.299	± 0.234	± 0.260	± 0.286	± 0.231	± 0.252
b-1/S.E.(b)	-1.241	-2.213	-1.734	0.085	-0.497	-0.213	-1.554	-2.196	-1.882	-1.839	-2.102	-1.978
t^2	5.236**	2.575**	3.899**	4.431**	5.645**	5.031**	1.791**	2.070**	1.924**	1.659**	2.231**	1.938**

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

Table-2.1: Proportion of related genetic parameters of variation for yield and yield attributing traits in Cherry tomato.

Proportion	Days to first fruit maturity			Number of clusters plant^{-1}			Number of flowers cluster^{-1}			Number of fruits cluster^{-1}		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]$½	1.033	1.416	1.218	2.166	1.990	2.071	1.725	2.053	1.882	1.804	2.124	1.957
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.216	0.201	0.202	0.206	0.182	0.187	0.203	0.198	0.194	0.189	0.200	0.188
$\frac{KD}{KR}$	1.211	1.642	1.420	1.458	2.476	1.960	1.176	1.960	1.561	1.219	1.724	1.465
$\frac{\hat{h}^2}{\hat{H}^2}$	0.252	0.168	0.203	0.011	0.080	0.039	0.018	0.203	0.104	-0.018	0.026	-0.003
$\hat{h}^2$ (n.s)	0.666	0.464	0.558	0.344	0.212	0.271	0.472	0.233	0.346	0.483	0.288	0.379
b	0.480	0.736	0.601	0.042	0.262	0.145	0.601	0.143	0.365	0.767	0.112	0.433
	± 0.295	± 0.265	± 0.273	± 0.186	± 0.298	± 0.235	± 0.250	± 0.265	± 0.251	± 0.330	± 0.241	± 0.279
b-0/S.E.(b)	-1.630	-2.780	-2.212	-0.225	-0.879	-0.559	-2.404	-0.539	-1.479	-2.325	-0.464	-1.402
b-1/S.E.(b)	1.763**	0.998**	1.374**	5.165**	2.479**	3.815**	1.593**	3.231**	2.405 **	0.706	3.680**	2.186**
t^2	0.016	0.037	0.020	3.795**	0.139	1.960*	0.075	0.617*	0.339	0.484	1.167**	0.819*

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

The higher estimate of heritability in narrow sense concluded the presence of low degree of non-additive gene action, the moderate estimate of heritability in narrow sense concluded the presence of medium degree of non-additive gene action and the low to very low estimate of heritability in narrow sense concluded the high degree of non-additive gene action.

Significant deviation of regression coefficient from unity along with the significant value of t^2 in the individual as well as in pooled data analysis revealed the presence of epistasis in all traits except for days to first flowering, days to first fruit set and days to first fruit maturity in the individual as well as in pooled data analysis; number of fruits cluster^{-1} and number of fruits plant^{-1} in E_1; number of flowers cluster^{-1} in E_1 and pooled data analysis; number of clusters plant^{-1} in E_2.

Similar, findings have been reported by Thakur and Kholi (2005), Hannan *et al.* (2007a), Saleem *et al.* (2009), Patel *et al.* (2013), Chaudhari *et al.* (2018), Bindal *et al.* (2019) and Zorb *et al.* (2020).

Table-2.2: Proportion of related genetic parameters of variation for yield and yield attributing traits in Cherry tomato.

Proportion	Number of fruits plant^{-1}			Number of locules fruit^{-1}			Fruit length (cm)			Fruit diameter (cm)		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]$½	1.930	1.756	1.836	1.696	2.579	2.131	2.098	1.889	1.987	1.809	1.857	1.826
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.204	0.208	0.199	0.182	0.207	0.188	0.206	0.188	0.190	0.205	0.187	0.189
$\frac{KD}{KR}$	1.220	1.892	1.549	2.356	1.950	2.146	1.521	1.405	1.456	1.413	1.179	1.289
$\frac{\hat{h}^2}{\hat{H}^2}$	0.028	0.218	0.116	0.008	-0.021	-0.014	0.077	0.028	0.046	0.096	0.072	0.077
$\hat{h}^2$ (n.s)	0.461	0.254	0.351	0.278	0.121	0.193	0.333	0.035	0.177	0.417	0.548	0.476
b	0.353 ± 0.281	-0.243 ± 0.242	0.048 ± 0.255	-0.005 ± 0.167	-0.069 ±0.147	-0.044 ± 0.150	0.040 ± 0.177	0.262 ± 0.197	0.144 ± 0.180	0.225 ± 0.140	0.212 ± 0.148	0.212 ± 0.137
b-0/S.E.(b)	-1.259	1.003**	-0.135	0.028	0.471**	0.243	-0.226	-1.334	-0.787	-1.609	-1.438	-1.531
b-1/S.E.(b)	2.304**	5.139**	3.715**	6.002**	7.296**	6.642**	5.408**	3.754**	4.574**	5.548**	5.341**	5.438**
t^2	0.190	0.959**	0.568*	5.370**	7.895**	6.626**	4.420**	2.505**	3.456**	8.056**	7.007**	7.525**

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

Table-2.3: Proportion of related genetic parameters of variation for yield and yield attributing traits in Cherry tomato.

Proportion	Average fruit weight (g)			Pericarp thickness (mm)			Fruit yield plant^{-1} (Kg)			Fruit yield hectare^{-1} (q)		
	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled	E_1	E_2	Pooled
$[\frac{\hat{H}_1}{\hat{D}}]$½	2.191	2.372	2.275	2.800	1.544	2.165	3.525	2.280	2.896	3.529	2.281	2.898
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.199	0.189	0.187	0.225	0.180	0.196	0.235	0.188	0.205	0.235	0.189	0.205
$\frac{KD}{KR}$	1.439	1.065	1.245	1.183	1.622	1.396	1.206	1.690	1.441	1.205	1.690	1.441
$\frac{\hat{h}^2}{\hat{H}^2}$	0.081	0.124	0.096	0.317	0.006	0.155	0.219	0.031	0.118	0.219	0.031	0.118
$\hat{h}^2$ (n.s)	0.385	0.512	0.442	0.269	0.521	0.388	0.153	0.361	0.250	0.153	0.361	0.250
b	0.230 ± 0.111	0.250 ± 0.108	0.233 ± 0.103	0.124 ± 0.093	0.326 ± 0.196	0.218 ± 0.138	0.111 ± 0.227	0.151 ± 0.191	0.124 ± 0.202	0.114 ± 0.226	0.150 ± 0.191	0.125 ± 0.202
b-0/S.E.(b)	-2.067	-2.303	-2.192	-1.327	-1.668	-1.505	-0.490	-0.793	-0.649	-0.502	-0.785	-0.651
b-1/S.E.(b)	6.905**	6.914**	6.903**	9.412**	3.444**	6.421**	3.992**	4.441**	4.210**	3.915**	4.450**	4.176**
t^2	14.457**	15.108**	14.776**	24.157**	2.254**	13.199**	1.617**	3.213**	2.408**	1.624**	3.222**	2.416**

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

CONCLUSION

From the study, it is concluded that both additive and non-additive type of gene action is involved in the inheritance of traits. Hence, reliance should be placed on reciprocal recurrent selection and the development of superior lines with several desirable genes.

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