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Research Paper

Gene action studies of biochemical traits in tomato under open field and protected conditions

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ABSTRACT

The goal of the current study was to understand the type and extent of gene action for different biochemical traits in tomato. Fourteen diverse lines of tomato were crossed in diallel fashion (excluding reciprocals) and tested for gene action investigations in two environments viz., open field and polyhouse. The analysis of variance revealed significant mean squares for all the traits under both the environments. The additive variance was higher than the dominance variance for most of the quality traits among all the crosses in both the environments. The gene action studies revealed greater magnitude of dominance component than additive component demonstrating greater role of dominance component in the inheritance of traits studied. The net dominance effect component showed absence of significantly high dominance effect in heterozygote and absence of directional dominance for all such traits. However, for total soluble sugars (TS) and lycopene content (Lyc) in both environments; total carotenoids content (Caro) and proline content (Pro) in E_1, significantly high dominance effect in heterozygote and presence of directional dominance was observe. The F value indicated higher frequency of dominant alleles in the parents for traits *viz.*, ascorbic acid content (AA), Lyc and Caro in both the environments; TS and titratable acidity (TA) in E_2. The average degree of dominance $[(H_1/D)^{1/2}]$ revealed over dominance range for all the traits under study in both the environments. The estimates of $H_2/4H_1$ (the proportion of genes with positive and negative effects on the parents) indicated the asymmetrical distribution of alleles with positive and negative effect in the parents for all the traits. The estimates of KD/KR (number of dominant and recessive genes in parents) revealed excess of dominant genes in parents as compared to the recessive genes. The estimates of h^2/H_2 (number of gene groups controlling that character and exhibiting dominance) depicted the less proportion of dominance gene groups for major traits however, for TS and Lyc in E_2 and indicated higher proportion of dominance gene groups. The estimates of h^2 (heritability n.s.) revealed that the genes were showing non-additive gene action for most of the traits in present set of material. The study highlights the importance of both additive and non-additive gene action involved in the inheritance of biochemical traits.

Key words: Biochemical, diallel, gene action, quality traits, tomato

Tomato *(Solanum lycopersicum* L.) is one of the most widely grown vegetable in India as well as throughout the world. The tomato is a sexually reproduced herbaceous plant with bisexual flowers which promotes the self-pollination. It is grown for its edible fruits, which can be consumed either fresh, cooked or in the form of various processed products like, juice, ketchup, sauce, puree etc. It is universally recognized as protective food having rich vitamins, minerals, organic acids, antioxidant property of ascorbic acid and lycopene content, which prevent cancer (Agarwal and Rao, 2000). Some other compounds with antioxidant activities, like chlorogenic acid, plastoquinones, rutin, tocopherol and xanthophylls are also available in tomato (Leonardi *et al*., 2000). Temperature stress is one of the major environmental factors limiting productivity and geographical distribution of tomato in Kashmir valley. Both high and low temperature affects vegetative and reproductive growth of tomato and requires specific temperatures at different growth stages. The optimum temperature ranges are 16-29 ºC, 21-24 ºC and 20-24 ºC for seed germination, seedling growth and fruit set and red colour (lycopene) development, respectively (Naika *et al.,* 2005). The variation in quantitative and qualitative traits under cold stress conditions is also genotype specific. Most cultivars of tomato are sensitive to temperature during different stages of plant development including seed germination, early and late vegetative growth, and reproductive phases (Foolad and Lin, 2000). Accumulation and synthesis of pigments (chlorophyll and lycopene) depletes with decrease in temperature below 20 ºC (Venema *et al.,* 1999; Brandt *et al.,* 2006; Meena *et al.,* 2017; Mesa *et al*., 2022), while, accumulation of phenol (Marsic *et al.,* 2012; Alhaithoul *et al.,* 2021; Shu *et al.,* 2023) and prolines (Khan *et al.,* 2015; Barrero *et al.,* 2016; Yang *et al.,* 2020; Shu *et al.,* 2023) increases by several folds under cold stress. Other quality parameters like, total soluble sugars, titratable acidity, ascorbic acid and carotenoids highly varies with cultivars and exhibits both increased and decreased levels under low temperature stress (Barrero *et al.,* 2016; Meena *et al.,* 2017; Yang *et al*., 2020; Mesa *et al*., 2022). Though, extensive studies have been done in tomato by evolving a larger number of varieties/hybrids, but still there is a lack of adequate information for a very strong improvement programme aimed for developing varieties or hybrids with high yield and superior quality and to extended availability of tomato in this climate sensitive temperate region. Since, the genetic information such as gene action, combining ability, heterosis etc. are very important, the evaluation of the parents for their capacity to transfer desirable genes to their offspring shall be a pre-requisite for planning of a systematic plant-breeding methodology and gives an insight for selection of superior parents for use in hybridization programmes and understanding the nature and magnitude of gene actions governing various traits (Kiani *et al.,* 2007).

MATERIALS AND METHODS

The present investigation was carried out during *Kharif,* 2020 under two different environments *viz.,* Vegetable Experimental Field, Division of Vegetable Science-Shalimar, SKUAST-Kashmir (E_1) and Polyhouse of Division of Vegetable Science-Shalimar, SKUAST-Kashmir (E_2). The experimental material for present study consists of fourteen diverse genotypes of tomato (*viz.,* Roma, Shalimar-1, Black Plum, H-88-78-1, IARI-4, CLN-1621, Sub-Arctic Plenty, VRT-01, Stupice, Superbug, Mortgage Lifter, Glacier, TOLCV-28 and S-22) maintained by Division of Vegetable Science, SKUAST-Kashmir, Shalimar. 91 F_1 crosses were generated through 14 x 14 diallel mating design (excluding reciprocals) during *Kharif,* 2019. The set of 105 genotypes *viz.,* crosses (91) along with their parents (14) were evaluated in augmented block design under both the environments during *Kharif,* 2020. The row to row and plant to plant spacing was maintained at 60 x 50 cm. Recommended package of practices were adopted to raise a healthy crop. Only single plant per hill was allowed to grow after establishment of transplant and plants were facilitated with single stem training in both environments. All the eight quality traits were estimated using the samples (fruits/leaves) collected during peak fruit harvest season from both the environments using standard procedures *viz.,* total soluble sugars (TS - mg/100g) and ascorbic acid content (AA - mg/100g) (Thimmaiah,1999); titratable acidity (TA - %) (Ranganna, 1986); lycopene content (Lyc - mg/100g) (Zuorro and Lavecchia, 2010); total carotenoid content (Caro - mg/100g) (Lakra *et al.,* 2018); total chlorophyll content (Chl - mg/100g) (Wellburn A. R., 1994); total phenol content (Phl - mg/100g) (Singleton and Rossi, 1965); proline content (Pro - µg/g fresh weight) (Bates *et al.*, 1973; Claussen, W., 2005). The obtained data on eight quality traits in all the parents and crosses were subjected data analysis to study the nature and magnitude of gene action involved in inheritance of these traits using TNAUSTAT-Statistical package of diallel analysis (Manivannan, 2014).

RESULTS AND DISCUSSION

Analysis of variance: The diallel analysis has been hailed by plant breeders as a long over-due biometrical technique for rationalizing the genetic study of continuous variation. The analysis of variance for all eight quality traits revealed that there were significant differences in mean squares due to hybrids under both environments (table 1). The variances due to replications were non-significant for all the traits in both environments. These significant differences indicated that the parents chosen and hybrids generated in this breeding programme were genetically diverse for different traits under investigation. Similar findings with respect to analysis of variance were also reported by Dagade *et al.* (2015), Amin *et al.* (2017), Thakur *et al.* (2019), Nayana *et al.* (2021), Izzo *et al.* (2022), Kamau *et al.* (2022) and Chandel *et al.* (2022).

Table 1: Analysis of variance for various quality traits of tomato (*Solanum lycopersicum* L.) in open field (E_1) and polyhouse (E_2) environments

Source of variation	d.f.	Total soluble sugars		Titratable acidity		Ascorbic acid content		Lycopene content	
		E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
Replications	2	4657.13	6307.91	0.00	0.00	0.10	1.07	0.05	0.38
Hybrids	104	234074.87 **	262888.18 **	0.06 **	0.08 **	40.23 **	36.05 **	61.35 **	63.58 **
Error	208	4665.05	2482.18	0.00	0.00	0.50	0.44	0.46	0.38

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

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Source of variation	d.f.	Total carotenoids content		Total chlorophyll content		Total phenol content		Proline content	
		E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
Replications	2	1.46	0.50	2.18	6.35	0.06	0.03	62.28	14.60
Hybrids	104	46.72 **	56.67 **	6464.15 **	13434.52 **	8.45 **	5.68 **	8380.50 **	6239.32 **
Error	208	0.56	0.45	9.85	19.23	0.03	0.03	25.98	31.96

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

The analysis of variance for combining ability revealed significant mean squares for all the traits under both the environments (table 2). The comparison of relative magnitude of *gca* and *sca* variances and Baker's ratio (*gca/sca*) indicated greater magnitude of *sca* variance than the corresponding *gca* variances for all the traits in both the environments signified the predominance of non-additive gene action in the inheritance of all the traits. Variances due to *sca* (σ^2_s) were higher in magnitude than the corresponding *gca* variances (σ^2_g) for all the traits also indicated the prevalence of non-additive components. Significance of both additive and non-additive gene action with preponderance of non-additive genes for major quality traits was also observed in tomato by Sprague and Tatum (1942), Dutta *et al.* (2013), Savale and Patel (2017), Mishra *et al.* (2020) and Chandel *et al.* (2022). However, the perusal of estimates of additive variance (σ^2_A) and dominance variance (σ^2_D) revealed that the magnitude of additive variance was higher than the dominance variance for TA, AA, Lyc, Caro and Phl under both the environments. The additive variance was also higher (compared to dominance variance) for Chl under open field and Pro content under protected conditions indicating prevalence of additive variance for these traits. However, the dominance variance was higher (as compared to additive variance) for TS under both the environments, Chl under protected conditions and Pro under open field conditions indicated the presence of dominance variance for respective traits. Similarly, Kalloo *et al.* (1974), Akhtar and Hazra (2013), Kaushik and Dhaliwal (2018) and Mishra *et al.* (2020) also reported importance of both additive and non-additive genetic variance for most of the quality traits. In general, all traits under study were controlled by both additive and non-additive gene action with preponderance of former for most of the quality traits in both the environments which can be exploited through population improvement programme. While, non-additive genes have greater significance for quality traits such as TS, Chl and Pro in tomato which can be exploited through hybrid breeding.

Table 2: Analysis of variance for various quality traits of tomato (*Solanum lycopersicum* L.) in open field (E_1) and polyhouse (E_2) environments

Source of variation	d.f.	Total soluble sugars		Titratable acidity		Ascorbic acid content		Lycopene content	
		E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
gca	13	489322.60 **	802266.29 **	0.16 **	0.19 **	76.30 **	74.56 **	133.04 **	124.73 **
sca	91	197610.91 **	185834.16 **	0.05 **	0.07 **	35.08 **	30.55 **	51.11 **	54.85 **
Residuals	208	4665.05	2482.18	0.00	0.00	0.50	0.44	0.46	0.38
***gca/sca* Ratio**	--	0.16	0.27	0.21	0.18	0.14	0.15	0.16	0.14
$\hat{\sigma}^2_g$	--	10097.03	16662.17	0.00	0.00	1.58	1.54	2.76	2.59
$\hat{\sigma}^2_s$	--	64315.29	61117.33	0.02	0.02	11.53	10.04	16.88	18.16
$\hat{\sigma}^2_A$	--	210.66	1866.07	0.75	0.76	26.35	24.52	19.78	16.96
$\hat{\sigma}^2_D$	--	10471.02	6502.92	0.74	0.75	26.18	21.89	11.85	7.79
$\hat{\sigma}^2_A/\hat{\sigma}^2_D$	--	0.02	0.29	1.00	1.02	1.01	1.12	1.67	2.18

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

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Source of variation	d.f.	Total carotenoids content		Total chlorophyll content		Total phenol content		Proline content	
		E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
gca	13	63.76 **	55.62 **	19084.75 **	47722.00 **	23.08 **	9.34 **	32213.59 **	19922.45 **
sca	91	44.29 **	56.82 **	4661.21 **	8536.31 **	6.35 **	5.16 **	4975.78 **	4284.59 **
Residuals	208	0.56	0.45	9.85	19.23	0.03	0.03	25.98	31.96
***gca/sca* Ratio**	--	0.09	0.06	0.26	0.35	0.23	0.11	0.41	0.29
$\hat{\sigma}^2_g$	--	1.32	1.15	397.39	993.81	0.48	0.19	670.58	414.39
$\hat{\sigma}^2_s$	--	14.58	18.79	1550.45	2839.03	2.11	1.71	1649.93	1417.54
$\hat{\sigma}^2_A$	--	28.67	24.95	82.16	684.18	6.00	5.97	179.60	185.32
$\hat{\sigma}^2_D$	--	28.10	21.73	38.98	1469.56	5.37	5.56	626.28	183.67
$\hat{\sigma}^2_A/\hat{\sigma}^2_D$	--	1.02	1.15	2.11	0.47	1.12	1.07	0.29	1.01

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

Gene action: The estimates of genetic components (table 3) of variance revealed that estimates of additive component (D) were significant for most of the traits in both environments except for Chl and Phl in E_1 whereas, the two measures of dominance component (H_1 and H_2) were significant for all the quality traits in both environments. This suggested the involvement of both the additive and dominance components in the inheritance of these traits, however greater magnitude of dominance component than its corresponding additive component demonstrated greater role of dominance component in the inheritance of traits studied, which was also noted while estimating variance arising due to dominance deviation through combining ability analysis by Griffing (1956a&b) approach.

Table 3: Estimates of components of genetic variation for various quality traits of tomato in open field-Shalimar (E_1) and polyhouse (E_2) environments

Components	Total soluble sugars		Titratable acidity		Ascorbic acid content		Lycopene content	
	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
$\hat{D}$	81196.08 *	121998.33 *	0.01 *	0.04 *	17.54 *	14.05 *	27.26 *	28.04 *
	± 27379.17	± 26095.51	± 0.01	± 0.01	± 3.67	± 3.26	± 4.83	± 5.98
$\hat{H}_1$	314741.78 *	299291.28 *	0.08 *	0.10 *	55.66 *	50.56 *	76.46 *	89.68 *
	± 52026.79	± 49587.55	± 0.01	± 0.02	± 6.98	± 6.19	± 9.18	± 11.36
$\hat{H}_2$	227258.28 *	232527.88 *	0.06 *	0.08 *	42.65 *	37.17 *	61.72 *	65.73 *
	± 42415.63	± 40427.00	± 0.01	± 0.01	± 5.69	± 5.05	± 7.49	± 9.26
$\hat{h}^2$	151506.64 *	89297.88 *	0.01	0.01	6.94	4.99	33.51 *	17.99 *
	± 28339.22	± 27010.55	± 0.01	± 0.01	± 3.80	± 3.37	± 5.00	± 6.19
$\hat{F}$	123011.18	126449.60 *	0.02	0.04 *	24.19 *	20.94 *	31.41 *	41.22 *
	± 61196.69	± 58327.52	± 0.01	± 0.02	± 8.21	± 7.28	± 10.80	± 13.36
$\hat{E}$	1553.27	839.38	0.00	0.00	0.17	0.15	0.15	0.13
	± 7069.27	± 6737.83	± 0.00	± 0.00	± 0.95	± 0.84	± 1.25	± 1.54

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

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Components	Total carotenoids content		Total chlorophyll content		Total phenol content		Proline content	
	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
$\hat{D}$	21.01 *	30.80 *	2247.49	4672.70 *	1.17	1.90 *	1554.25 *	1320.12 *
	± 3.60	± 5.71	± 1080.49	± 1110.67	± 0.70	± 0.59	± 596.54	± 510.54
$\hat{H}_1$	67.53 *	97.69 *	8254.11 *	12998.81 *	9.23 *	7.45 *	7638.18 *	6697.93 *
	± 6.85	± 10.84	± 2053.18	± 2110.54	± 1.33	± 1.12	± 1133.56	± 970.14
$\hat{H}_2$	54.74 *	67.97 *	5505.43 *	10776.28 *	8.16 *	6.64 *	6133.25 *	5209.32 *
	± 5.58	± 8.84	± 1673.88	± 1720.65	± 1.08	± 0.91	± 924.15	± 790.92
$\hat{h}^2$	9.44 *	-0.03	210.25	1624.89	0.28	0.32	1466.86 *	826.49
	± 3.73	± 5.91	± 1118.37	± 1149.62	± 0.72	± 0.61	± 617.46	± 528.44
$\hat{F}$	29.16 *	55.92 *	3156.62	2781.69	0.08	1.99	26.70	891.70
	± 8.05	± 12.76	± 2415.06	± 2482.53	± 1.56	± 1.32	± 1333.35	± 1141.13
$\hat{E}$	0.19	0.15	3.26	6.37	0.01	0.01	8.78	10.61
	± 0.93	± 1.47	± 278.98	± 286.78	± 0.18	± 0.15	± 154.03	± 131.82

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

As, the magnitude of dominance component was more in comparison with the additive component, the breeders can apply inter-mating of the selected plants in segregating population or practice recurrent selections to bring quality improvement in tomato. 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 crop improvement programmes. The net dominance effect component (h^2) was found non-significant and positive for most of the traits in both the environments, indicating absence of significantly high dominance effect in heterozygote over all loci and absence of directional dominance for all such traits. However, for TS and Lyc in both environments; Caro and Pro in E_1, the net dominance effect component (h^2) was found positive and significant indicating the presence of significantly high dominance effect in heterozygote over all loci and presence of directional dominance (positive) for the respective traits. The F value was found to be positive and significant for traits *viz.,* AA, Lyc and Caro in both the environments; TS and TA in E_2 indicating the higher frequency of dominant alleles in the parents with respect to these traits in respective environment. The F value was found positive and non-significant for the traits *viz.,* Chl, Phl and Pro in both the environments; TS and TA in E_1 indicating the relative frequency of dominant and recessive alleles was proportionally equal in the parental genotypes. The estimates of E value (environmental component of variation) were also found non-significant for all the traits in both the environments indicating that the environment had no/negligible role in the expression of these traits. The values of proportion of average degree of dominance $[(H_1/D)^{1/2}]$ measured form genetic components of variance were more than unity thus revealing over dominance range for all the traits under study in both the environments (table 4).

Table 4: Proportion of genetic components of variation for various quality traits of tomato open field-Shalimar (E_1) and polyhouse (E_2) environments

Parameters	Total soluble sugars		Titratable acidity		Ascorbic acid content		Lycopene content	
	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
$[\frac{\hat{H}_1}{\hat{D}}]^{½}$	1.57	1.97	1.69	2.35	1.90	1.78	1.79	1.67
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.19	0.18	0.20	0.19	0.18	0.19	0.18	0.20
$\frac{KD}{KR}$	1.99	2.25	2.03	1.66	2.29	2.26	2.40	2.05
$\frac{\hat{h}^2}{\hat{H}_2}$	0.38	0.67	0.08	0.18	0.13	0.16	0.27	0.54
$\hat{h}^2$ (n.s.)	0.35	0.28	0.29	0.35	0.26	0.23	0.25	0.25
B	0.07	0.13	0.50	0.16	0.21	0.01	0.41	0.43
b-0/S.E.(b)	0.30	0.46	2.92	0.78	0.59	0.05	2.18	2.74
b-1/S.E.(b)	4.17	3.11	2.97	4.22	2.28	4.57	3.10	3.64
t^2	0.78	0.01	1.44	1.53	0.51	1.03	1.10	2.76

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Parameters	Total carotenoids content		Total chlorophyll content		Total phenol content		Proline content	
	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
$[\frac{\hat{H}_1}{\hat{D}}]^{½}$	1.78	1.79	1.67	1.92	1.98	2.81	2.25	2.22
$\frac{\hat{H}_2}{4\hat{H}_1}$	0.17	0.20	0.21	0.17	0.23	0.22	0.19	0.20
$\frac{KD}{KR}$	3.08	2.26	1.43	2.16	1.72	1.02	1.35	1.01
$\frac{\hat{h}^2}{\hat{H}_2}$	-0.00	0.17	0.15	0.04	0.05	0.03	0.16	0.24
$\hat{h}^2$ (n.s.)	0.12	0.14	0.43	0.40	0.18	0.35	0.42	0.50
B	0.13	0.03	0.25	0.06	0.22	0.30	0.00	0.24
b-0/S.E.(b)	0.44	0.22	2.00	0.45	1.11	3.66	0.01	1.66
b-1/S.E.(b)	2.87	6.40	5.96	7.25	3.91	8.71	7.00	5.38
t^2	0.03	5.77	8.83	9.36	1.43	26.61	7.01	6.12

This dominance was due to high heterozygosity in F_1 indicating that parents selected were diverse and from different source population. The estimates of the proportion of genes with positive and negative effects on the parents ($H_2/4H_1$) were found to be less than 0.25 for all the traits in both E_1 and E_2 indicating the asymmetrical distribution of alleles with positive and negative effect in the parents with reference to the respective traits. Hence, selecting the parent with high positive alleles results in the dominant genes exhibit dominance in hybrid. The KD/KR (number of dominant and recessive genes in parents) component estimates were found to be greater than unity for all the traits in both the environments indicating the excess of dominant genes in parents as compared to the recessive genes. The values of h^2/H_2 were found to be less than 0.50 for almost all the traits depicting the less proportion of dominance gene groups for such traits. However, values of h^2/H_2 (number of gene groups controlling that character and exhibiting dominance) were found to be greater than 0.50 for TS and Lyc in E_2 indicated higher proportion of dominance gene groups for these traits. The estimates of h^2 (n.s.) (heritability in narrow sense) were found low (< 30 %) for traits *viz.,* AA, Lyc and Caro in both E_1 and E_2; TA and Phl in E_1; TS in E_2. While, estimates of h^2 (n.s.) were found medium (31 to 50 %) for traits *viz.,* Chl and Pro in both E_1 and E_2; TA and Phl in E_2; TS in E_1. The moderate estimate of heritability in narrow sense indicates the presence of medium degree of non-additive gene action while, low narrow sense heritability estimates for most of the traits indicated that in the present set of material, the genes were showing non-additive gene action and isolation of high yielding purelines/inbreds would not be feasible unless the non-allelic interactions and/or linkage are not dissipated through a selection procedure, which can slow down the rate of homozygosity in the segregating generation (Dutta *et al.*, 2013). Diallel selective mating design proposed by Jenson (1970) would be appropriate for the present set of material to increase chances of isolation of good recombination and often fixation of alleles. The non-significant deviation of regression coefficient from unity along with the non-significant value of t^2 for all the traits in both the environments revealed the absence of epistasis for all the traits. Similar findings have also been reported by Gaikwad *et al.* (2009), Akhtar and Hazra (2013), Dutta *et al.* (2013), Amin *et al.* (2017) and Ibirinde *et al.* (2022) for different quality traits in tomato.

CONCLUSION

The analysis of variance revealed significant mean squares for all the traits under both the environments. The additive variance was found higher than the dominance variance for most of the quality traits among all the crosses in both the environments. The gene action studies revealed greater magnitude of dominance component than its corresponding additive component demonstrated greater role of dominance component in the inheritance of traits studied. The net dominance effect component (h^2) showed absence of significantly high dominance effect in heterozygote and absence of directional dominance for all such traits. However, for TS and Lyc in both environments; Caro and Pro in E_1, significantly high dominance effect in heterozygote and presence of directional dominance was observe. The F value indicated higher frequency of dominant alleles in the parents for traits *viz.,* AA, Lyc and Caro in both the environments; TS and TA in E_2. The $[(H_1/D)^{1/2}]$ revealed over dominance range for all the traits under study in both the environments. The $H_2/4H_1$ indicated the asymmetrical distribution of alleles with positive and negative effect in the parents for all the traits KD/KR revealed excess of dominant genes in parents as compared to the recessive genes The h^2/H_2 depicted the less proportion of dominance gene groups for major traits however, for TS and Lyc in E_2 it indicated higher proportion of dominance gene groups. The estimates of h^2 (n.s.) revealed that the genes were showing non-additive gene action for most of the traits in present set of material.

CONFLIT OF INTEREST

All the authors affirm that there is no conflict of interest among them. All research activities comply with relevant legal, institutional and ethical standards.

AUTHOR CONTRIBUTION

All the authors contributed equally in the present study.

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