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Study on gene action involved in inheritance of yield and its contributing traits in brinjal (*Solanum melongena* L.)

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Abstract

The present investigation was carried out to evaluate the 45 F1 hybrids derived from half diallel fashion along with ten parents in randomized block design with three replications during Rabi season of 2018-19 (E_1) and 2019-20 (E_2) at the Main Experiment Station (MES) of the Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.). The genetic components of variation were determined for sixteen characters *viz*., days to 50 % flowering, leaf length (cm), leaf width, number of flower per inflorescence, days to first harvesting, plant height (cm), primary branches per plant, number of fruit per cluster, number of fruits per plant, average fruit weight (g), fruit length (cm), fruit circumference (cm), yield per plant (g), specific gravity, TSS (%) and dry weight/ 100g. The data were analyzed to fulfill the following objectives to estimates genes action for yield and its component traits analysis of variance revealed significant difference for the parents, F1 S and parent vs. F1s for all the characters indicating wide variation except fruit circumference in both years and fruit length inY1. Both additive and dominance variance were found important in the inheritance of most of the traits, whereas dominance showed over dominance for the most of the traits.

Keywords: *Solanum melongena*, gene action, yield parameters, diallel

Introduction

Brinjal belongs to the family Solanaceous and botanically known as *Solanum melongena* L. The family contains 75 genera and over 2000 species, out of which, about 150-200 are tuber bearing and belong to section Tuberarium. The majority of species (about 1800) are non-tuber bearing. Cytological studies have indicated that chromosome number 2n = 24 is same in almost all species. There are 3 main botanical varieties under the species melongena **(Choudhury, 1976a**). The common brinjal, to which large, round or egg-shaped fruited forms belong, are grouped under var. *esculentum*. The long, slender types are included under var. *serpentinum* and the dwarf brinjal plants are put under var. *depressum*. Brinjal is considered a native to India where the major domestication of large fruited cultivars occurred. In “Origin of cultivated plants” published in **1886 De Candolle**, stated that the species *S. melongena* has been known in India from ancient times and regarded it as a native of Asia. Vavilov (1928) was of the opinion that its center of origin was in the Indo-Burma region.

In brinjal, heterostyly is a common feature. Four types of flowers have been reported depending on the length of styles, viz. (i) long-styled with large ovary, (ii) medium-styled with medium size ovary, (iii) Pseudo short-styled with rudimentary ovary and (iv) true short-styled with very rudimentary ovary (Krishnamurthi and Subramaniam, 1954**).**

The de cholestrolizing action is attributed to the presence of polyunsaturated fatty acid (linoleic and linolenic) which are present in flesh and seed of the fruit in higher amount (65.1%). In addition, variation is also noticed for characters like vegetative growth, maturity and presence or absence of spines on leaves, stem and fruit calyx among the indigenous material. Among the various mating designs diallel cross techniques has been most frequently used to determine nature and magnitude of gene action through the estimate of genetic components, general and specific combining ability variances and their effects in many self, often-cross and cross-pollinated crops. In brinjal several workers have used this design for estimating component of variation and combining ability (Bavage *et al.*, 2005; Panda *et al.*, 2005; Suneetha *et al*., (2006a) and Hazra *et al*., 2010) [2, 13, 16, 9]. The high level of heterosis in desirable direction coupled with high sca variance and non-additive type of gene action have also been reported in several major economic traits of brinjal including yield

Materials and Methods

The present investigation entitled Study on gene action involved in inheritance of yield and its contributing traits in brinjal (*Solanum melongena* L.) was carried out at Main Experiment Station (Vegetable Research Farm), Narendra Nagar (Kumarganj), Ayodhya (U.P.) India, during *Rabi* season of 2018-19. Geographically the experimental site falls under humid subtropical climate and is located at 26.47° N latitude and 82.12° E longitude at an elevation of altitude of 113 meter above the mean sea level. Geographically it falls in north east genetic alluvial plains of eastern U.P. Ayodhya region. The experimental field had sandy loam soil, low in organic carbon, nitrogen, medium in phosphorous, potash and slightly alkaline (pH 8.0) in nature. The mechanical mixture of soil was 60.9 % sand, 27.8 % silt and 11.3 % clay. The climate of district Ayodhya is semi-arid with hot summer and cold winter. Maximum rains in this area are received from July to the end of September. The winter months are usually cool and dry but occasional light showers are also not uncommon whereas, summer months are extreme hot and dry. The data was recorded at meteorological observatory of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) The experiment was conducted in a Randomized Block Design (R.B.D.) with three replications to assess the performance of 45 F_1 hybrids and their 10 parents and one commercial check. The crop was planted in row length spaced 60 cm. apart where, 50 cm. plant to plant spacing was maintained. The ten pure lines of brinjal were provided by the Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) The selected parental lines namely NDB-51, Punjab Sadabahar, MK, KS-224, NDB-3, NDB-2, Pant Rituraj, Pant Smart and NDB- White were crossed in the all possible combinations, excluding reciprocals, during the *Rabi* season of 2018-19. These 45 F_1s along with their parents were evaluated for the study of heterosis, combining ability, gene action, heritability and genetic advance for 18 fruit yield and quality attributing traits. The ten diverse parental lines selected their characteristics and crossed in diallel mating design as suggested by **Griffing (1956 b) [7]** to produce 45 hybrids in *Rabi* season of 2018-19 and evaluated during *Rabi* season of 2018-19 and 2019-20. The experiment laid out in randomized block design with three replications and 55 treatment including 10 parents. The observation were recorded yield and its contributing traits in brinjal, Days to 50 per cent flowering days to 50 % flowering, leaf length (cm), leaf width, number of flower per inflorescence, days to first harvesting, plant height (cm), primary branches per plant, number of fruit per cluster, number of fruits per plant, average fruit weight (g), fruit length (cm), fruit circumference (cm), yield per plant (g), specific gravity, TSS (%) and dry weight/ 100g. The experimental data was compiled by taking the mean value of the 10 parents and 45 F_1's and one standard check for all the 16 characters from all the three replications. Then it was subjected to the following statistical analyses. Phenotypic and genotypic correlation coefficients were worked out to study the relationship of various pairs of characters as suggested by Al-Jibouri *et al*. (1958).

Result and Discussion

The estimates of the components of variation and their related statistics for different characters of brinjal have been presented in (Table- 1). Significant values of dominance components $\hat{H}_1$ and $\hat{H}_2$ for all the sixteen characters, except days to 50% flowering along with significant values of additive components $\hat{D}$ for most of the characters except for primary branches per plant and specific gravity indicated the importance of both additive and dominance gene action in expression of these characters which is in consonance with the finding of Hayward (1979) [8]; Vaghasiya *et al.* (2000) [18]; Chaudhary, D. R. (2001) [5]; Das *and Barua* (2001) [6]; and Singh *et al.* (2002) [14]. However, additive ($\hat{D}$) genetic variance components were generally lower in magnitude than dominant components of genetic variance most of the traits over both the seasons which showed preponderance of dominance components of variance in expression of yield per plant and its attributing traits in both the seasons. In brinjal similar findings was also recorded by Vaghasiya *et al.* (2000) [18], Chaudhary, D. R. (2001) [5], Das and Barua (2001) [6] and Singh *et al*. (2002) [14].

The positive values of $\hat{F}$ were found for all the traits except days to 50% flowering, leaf length and leaf width in both the seasons which indicated that there were excess of dominance gene in the inheritance of these traits among the parents. The average degree of dominance $(\hat{H}/\hat{D})^{1/2}$ involve in the action of genes was found as over dominance for all the traits except for days to 50% flowering, no. of flower per inflorescence, average fruit weight and fruit circumference in both the seasons. This suggested that heterosis breeding might be advantageous for improvement of yield and its component traits in brinjal. These findings are similar to that of Singh *et al*. (2002) [14]; Suneetha *et al*. (2008) [15]; Tha *et al*. (2006) [17]; Chaudhary and Kumar (1999) [4] and Patil *et al*. (2000) [12].

The estimates of components, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{E}$ were significant for number of flower per inflorescence during both the seasons (E_1, E_2). $\hat{F}$ and $\hat{h}^2$ were found non-significant and Environmental component $\hat{E}$ were found significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were less than one, which showed partial dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.19 and 0.19 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2} + \hat{F} / (4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ in the parents were more than one which indicated that the dominant genes were more frequent than recessive ones. The number of gene groups that control the character ($\hat{h}^2/\hat{H}_2$) and exhibit recessive was -0.01 and -0.01 in E_1 and E_2, respectively. The ‘r’ values were positive in both E_1 and E_2 which showed excess of dominant genes during both the seasons (E_1, E_2).

For days to first fruit harvest $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{F}$ and $\hat{E}$ in both season indicated that both additive as well as dominance variance were important in the expression of days to first fruit harvesting. The positive $\hat{F}$ value also suggested less frequency of dominant genes in the inheritance of this treat. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ was showed over dominance. The value of proportion of genes $(\hat{H}_2/4\hat{H}_1)^{1/2}$ ratio 0.08 and 0.11 indicated asymmetrical distribution of genes with positive and negative effect among the parents.

The values of t^2 and (1-b/SEb) for days to first fruit harvesting were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2).

The estimates of components, $\hat{D}$, $\hat{H}_1$ and $\hat{H}_2$ were significant for plant height during both the seasons (E_1,E_2). $\hat{F}$, $\hat{h}^2$ and $\hat{E}$ Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this trait character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.20 and 0.20 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2}+\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}-\hat{F}$ in the parents were more than one which indicated that the dominant genes were more frequent than recessive ones. The number of gene groups that control the character $(\hat{h}^2/\hat{H}_2)$ and exhibit recessive was -0.00 and -0.00 in E_1 and E_2, respectively. The ‘r’ values were positive in both E_1 and E_2 which showed excess of dominant genes during both the seasons (E_1, E_2). The values of t^2 and (1-b/SEb) for plant height per plant were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2).

$\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant for primary branches per plant during both the seasons (E_1, E_2). $\hat{D}$, $\hat{F}$, and Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1,E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.21 and 0.08 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2}+\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}-\hat{F}$ in the parents were more than one which indicated that the dominant genes were more frequent than recessive ones. The number of gene groups that control the character $(\hat{h}^2/\hat{H}_2)$ and exhibit dominance was 0.45 and 0.21 in E_1 and E_2, respectively. The ‘r’ values were positive in both E_1 and E_2 which showed excess of dominant genes during both the seasons (E_1, E_2).

For number of fruit per cluster

$\hat{H}_1$, $\hat{H}_2$ $\hat{F}$ and $\hat{h}^2$ were significant for number of fruits per cluster during both the seasons (E_1, E_2). $\hat{E}$ Environmental component was found non-significant for both the seasons (E_1,E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.18 and 0.18 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The above findings are in agreement with that of Arvindakshan *et al.* (2005) [1]; Bendale *et al.* (2005) [3]; Indiresh *et al.* (2005) [10] and Kaur and Thakur (2007) [11].

Table 1: Estimates of components of variation and their related statistics in 10 x 10 diallel crosses of brinjal over two seasons (E_1, E_2)

Components of variation and related statistics	**Seasons**	**Days to 50% flowering**	**Leaf length (cm)**	**Leaf width (cm)**	**Number of flower per inflorescence**	**Days to first harvesting**	**Plant height (cm)**	**Primary branches per plant**	**No. of fruit per cluster**
$\hat{D}$ (Additive effect)	E_1	9.12**±0.28	1.14*±0.56	0.75**±0.12	0.65**±0.05	8.15**±2.36	30.28**±7.38	0.20±0.21	0.14**±0.01
	E_2	10.65**±0.52	1.92**±0.52	1.06**±0.14	0.71**±0.05	12.48**±2.65	28.80**±8.85	0.23±0.27	0.56**±0.08
$\hat{H}_1$ (Dominance effect)	E_1	-5.56±0.59	3.58**±1.20	1.09**±0.21	0.65±.10	18.91**±5.02	104.52**±15.72	1.60**±0.46	0.15**±0.04
	E_2	-3.26±1.12	4.34**±1.12	1.39**±0.31	0.70**±0.11	30.90**±5.64	107.7**±18.84	1.78**±0.58	0.68**±0.18
$\hat{H}_2$ (Dominance	E_1	-3.55±0.50	3.05**±1.02	0.93**±0.23	0.51**±0.09	6.17±4.27	86.14**±13.36	1.40**±0.39	0.11**±0.03
	E_2	-1.76±0.95	3.64**±0.94	1.15**±0.26	0.55**±0.09	14.12**±4.80	86.22**±16.01	1.51**±0.49	0.51**±0.15

indicating asymmetry of +/- effect of genes)									
$\hat{F}$ (Mean Fr over arrays)	E_1	-3.78±0.64	-0.68±1.30	-0.21±0.29	0.05±0.11	12.54**±5.44	21.72±17.04	0.35±0.50	0.11**±0.04
	E_2	-1.84±1.21	-0.14±1.20	-.04±0.34	0.05±0.12	18.92**±6.12	20.71±20.42	0.43±0.63	0.48**±0.19
$\hat{h}^2$	E_1	-0.73±0.34	0.01±0.68	0.25±0.15	-0.08±0.06	-1.58±2.85	-0.81±8.94	0.64**±0.26	0.04*±0.02
	E_2	-.06±0.63	0.21±0.63	0.19±0.18	0.009±0.06	-0.48±3.21	-0.24±10.7	0.69*±0.33	0.20*±0.10
$\hat{E}$ (Environmental component)	E_1	2.58**±0.08	0.43**±0.17	0.17**±0.03	0.02*±0.01	4.39**±0.71	2.26±2.22	0.01±0.06	0.00
	E_2	2.21**±0.16	0.33**±0.15	0.15**±0.04	0.02*±0.01	1.33±0.80	3.95±2.66	0.022±0.08	0.01±0.02
$(\hat{H}_1/\hat{D})^{1/2}$ (Mean degree of dominance)	E_1	0.78	1.77	1.98	0.99	1.52	1.85	2.75	1.04
	E_2	0.55	1.50	1.15	0.99	1.57	1.93	0.02	1.09
$\hat{H}_2/4\hat{H}_1$ (Proportion of genes with +/- effects in parents)	E_1	0.16	0.21	0.21	0.19	0.08	0.20	0.21	0.18
	E_2	0.14	0.21	0.20	0.19	0.11	0.2	0.08	0.18
$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}$ $/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ (Proportion of dominant and recessive genes in parents)	E_1	0.58	0.70	0.78	1.09	3.04	1.47	1.89	2.25
	E_2	0.73	0.95	0.96	1.08	2.58	1.45	2.75	2.26
$\hat{h}^2/\hat{H}_2$ (Number of gene groups)	E_1	0.21	0.01	0.26	-0.01	-0.25	-0.00	0.45	0.41
	E_2	0.04	0.05	0.16	-0.01	-0.03	-0.00	0.21	0.07
R (Correlation coefficient)	E_1	0.89	0.78	0.84	0.83	0.47	0.78	0.15	0.82
	E_2	0.80	0.88	8.83	0.83	0.46	0.78	0.10	0.78
t^2	E_1	0.98	0.01	0.52	0.82	0.99	0.13	0.05	0.98
	E_2	0.6	0.00		0.82	0.98	0.00	0.01	0.99
1-b/SEb	E_1	0.93	0.37	0.71	0.73	0.51	0.55	0.08	0.87
	E_2	1.19	0.47	0.69	0.74	0.51	0.42	0.04	0.82

Components of variation and related statistics	**Seasons**	**No. of fruits per plant**	**Average fruit weight (g)**	**Fruit length (cm)**	**Fruit circumference**	**Yield per plant (g)**	**Specific gravity**	**TSS (%)**	**Dry weight/ 100g**
$\hat{D}$ (Additive effect)	E_1	29.49**±3.28	894.86**±18.97	7.61**±1.00	29.02**±2.89	2.30**±0.26	0.07±0.00	0.10**±0.03	0.37**±0.09
	E_2	32.15**±3.45	894.80**±19.02	8.08**±1.21	32.84**±3.23	2.44**±0.37	0.08±0.00	0.41**±0.04	0.41**±0.11
$\hat{H}_1$ (Dominance effect)	E_1	37.49**±6.99	178.97**±40.39	8.66**±2.14	12.02±6.15	4.90**±0.55	0.09**±0.01	0.08±0.31	0.89**±0.20
	E_2	40.41**±7.35	180.36**±40.49	9.76**±2.58	13.72*±6.89	5.78**±0.79	0.10**±0.02	0.47**±0.09	0.98**±0.23
$\hat{H}_2$ (Dominance indicating asymmetry of +/- effect of genes)	E_1	29.38**±5.94	160.44**±34.32	6.13**±1.82	10.18±5.23	3.82**±0.47	0.08**±0.01	0.06±0.11	0.61**±0.17
	E_2	31.94**±6.25	161.30**±34.41	6.92**±2.19	11.54±5.85	4.63**±0.67	0.08**±0.01	0.33**±0.08	0.66**±0.20
$\hat{F}$ (Mean Fr over arrays)	E_1	13.54±7.58	49.07±43.78	2.61±2.32	-0.83±6.67	2.30**±0.60	-0.01±0.02	0.08±0.00	0.49*±0.22
	E_2	14.32±7.97	46.21±43.89	2.53±2.79	0.38±7.46	2.39**±0.86	-0.01±0.02	0.13±0.10	0.55*±0.25
$\hat{h}^2$	E_1	0.33±3.98	203.44**±22.97	-0.07±1.22	-0.05±3.50	0.79**±0.31	0.09**±0.01	0.00±0.04	0.12±0.11
	E_2	0.38±4.18	205.59**±23.03	-0.07±1.46	-0.06±3.94	0.84±0.45	0.10**±0.01	-0.00±0.04	0.16±0.13
$\hat{E}$ (Environmental component)	E_1	0.09*±0.99	8.75±5.72	0.19±0.30	0.16±0.87	0.01±0.07	0.00	0.00±0.01	0.00±0.02
	E_2	0.11±1.04	8.65±5.73	0.22±0.36	0.18±0.97	0.01±0.11	0.00	0.00±0.01	0.00±0.03
$(\hat{H}_1/\hat{D})^{1/2}$ (Mean degree of	E_1	1.12	0.44	1.06	0.64	1.45	1.14	1.99	1.55
	E_2	1.12	0.44	1.11	0.64	1.53	1.14	2.05	1.54

dominance)									
$\hat{H}_2/4\hat{H}_1$ (Proportion of genes with +/- effects in parents)	E_1	0.19	0.22	0.17	0.21	0.19	0.21	0.18	0.17
	E_2	0.19	0.22	0.17	0.21	0.2	0.21	0.17	0.17
$(4\hat{D}\hat{H}_1)^{1/2}+\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}-\hat{F}$ (Proportion of dominant and recessive genes in parents)	E_1	1.51	1.13	1.38	0.95	2.03	0.84	1.75	2.49
	E_2	1.49	1.12	1.33	1.01	1.93	0.84	1.78	2.56
$\hat{h}^2/\hat{H}_2$ (Number of gene groups)	E_1	0.01	1.26	-0.01	-0.00	0.20	1.17	-0.00	0.20
	E_2	0.01	1.27	-0.01	-0.00	0.18	1.19	-0.00	0.24
R (Correlation coefficient)	E_1	0.94	0.97	0.83	0.53	0.49	0.86	0.31	0.10
	E_2	0.95	0.97	0.79	0.47	0.48	0.86	0.12	0.15
t^2	E_1	0.00	0.17	0.04	0.97	0.05	0.06	0.26	0.99
	E_2	0.00	0.15	0.06	0.98	0.01	0.07	0.12	0.92
(1-b/SEb)	E_1	0.41	0.87	0.56	0.48	0.28	0.62	0.21	0.11
	E_2	0.42	0.87	0.53	0.43	0.24	0.62	0.07	0.18

The components, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ were significant for number of fruits per plant during both the seasons (E_1,E_2). $\hat{F}$, $\hat{h}^2$ and Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.19 and 0.19 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2}+\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}-\hat{F}$ in the parents were more than one which indicated that the dominant genes were more frequent than recessive ones. The number of gene groups that control the character $(\hat{h}^2/\hat{H}_2)$ and exhibit dominance was 0.01 and 0.01 in E_1 and E_2, respectively. The 'r' values were positive in both E_1 and E_2 which showed excess of dominant genes during both the seasons (E_1, E_2). The values of t^2 and (1-b/SEb) for number of fruits per plant were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2).

$\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant for average fruit weight during both the seasons (E_1, E_2). $\hat{h}^2$ and Environmental component $\hat{E}$ were found significant for bo th the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were less than one, which showed partial dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.22 and 0.22 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2}+\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}-\hat{F}$ in the parents were more than one which indicated that the dominant genes were more frequent than recessive ones. R value found positive shows excess of dominant gene and t^2 and (1-b/SEb) was to be non-significant. The estimates of components, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ were significant for fruit length during both the seasons (E_1, E_2). $\hat{F}$, $\hat{h}^2$ and Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.17 and 0.17 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2}+\hat{F}/(4\hat{D}\hat{H}_1)^{1/2}-\hat{F}$ in the parents were more than one which indicated that the dominant genes were more frequent than recessive ones. The number of gene groups that control the character ($\hat{h}^2/\hat{H}_2$) and exhibit recessive was -0.01 and -0.01 in E_1 and E_2, respectively. The ‘r’ values were positive in both E_1 and E_2 which showed excess of dominant genes during both the seasons (E_1, E_2). The values of t^2 and (1-b/SEb) for fruit length were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2).

$\hat{D}$, $\hat{H}_1$, were significant for fruit circumference during both the seasons (E_1, E_2). $\hat{H}_2$, $\hat{F}$, $\hat{h}^2$ and Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1, E_2). The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were less than one, which showed partial dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.21 and 0.21 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ in the parents were less than one E_1 and more then one E_2 which indicated that the dominant genes were more frequent than dominance genes and recessive ones. The values of t^2 and (1-b/SEb) for fruit circumference were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2). The estimates of components, $\hat{D}$ $\hat{H}_1$, $\hat{H}_2$ and $\hat{h}^2$ were significant for Yield per plant during both the seasons (E_1, E_2). $\hat{h}^2$ and Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.19 and 0.20 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ in the parents were more than one which indicated that the dominant genes were more frequent than recessive ones. The number of gene groups that control the character ($\hat{h}^2/\hat{H}_2$) and exhibit dominance was 0.20 and 0.20 in E_1 and E_2, respectively. The ‘r’ values were positive in both E_1 and E_2 which showed excess of recessive genes during both the seasons (E_1, E_2). The values of t^2 and (1-b/SEb) for yield per plant were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2).

The value of $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$ were significant for specific gravity during both the seasons (E_1, E_2). $\hat{D}$ $\hat{F}$ were found non-significant Environmental component $\hat{E}$ were also found non-significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of recessive components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.21 and 0.21 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The values of t^2 and (1-b/SEb) for specific gravity were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2).

The estimates of components, $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ were significant for total soluble solid during both the seasons (E_1, E_2). $\hat{F}$, $\hat{h}^2$ and Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of dominance components for expression of this character. The mean degrees of dominance $(\hat{H}_1/\hat{D})^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- $(\hat{H}_2/4\hat{H}_1)^{1/2}$ were found 0.18 and 0.17 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ in the parents were more than one which indicated that the over dominant genes were more frequent than recessive ones. The number of gene groups that control the character ($\hat{h}^2/\hat{H}_2$) and exhibit not dominance and recessive was -0.00 and -0.00 in E_1 and E_2, respectively. The ‘r’ values were positive in both E_1 and E_2 which showed excess of dominance genes during both the seasons (E_1, E_2). The values of t^2 and (1-b/SEb) for total soluble solid were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2).

The value $\hat{D}$, $\hat{H}_1$, $\hat{H}_2$ and $\hat{F}$ were significant for dry weight/100g during both the seasons (E_1, E_2). However, $\hat{h}^2$ and Environmental component $\hat{E}$ were found non-significant for both the seasons (E_1, E_2). The significance of $\hat{H}_1$, H_2 values in both the seasons (E_1, E_2) suggested the role of recessive components for expression of this character.

The mean degrees of dominance ($\hat{H}_1/\hat{D}$)$^{1/2}$ were more than one, which showed over dominance during both the seasons (E_1, E_2). The value of proportion of genes +/- ($\hat{H}_2/4\hat{H}_1$)$^{1/2}$ were found 0.17 and 0.17 in E_1, and E_2 respectively indicating the asymmetrical distribution of genes with positive and negative effects among the parents. The proportions of dominant and recessive genes $(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$ in the parents were more than one which indicated that the over dominant genes were more frequent than recessive ones. The values of t^2 and (1-b/SEb) for dry weight/100g were found non-significant indicating the validity of the hypothesis of diallel cross analysis during both the seasons (E_1, E_2). similar findings was also recorded by Vaghasiya *et al.* (2000) [18], Chaudhary, D. R. (2001), (2005); Indiresh *et al.* (2005) [10] and Kaur and Thakur (2007) [11].

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