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HAYMAN'S DIALLEL ANALYSIS FOR YIELD AND ATTRIBUTING TRAITS IN SESAME (*Sesamum indicum* L.)

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ABSTRACT

Eight genetically diverse parents of sesame were selected for crossing in diallel fashion to develop twenty-eight F_1 's excluding reciprocals. The F_1 's along with their parents were evaluated in randomized block design with three replications in two different environmental conditions created by two date of sowing i.e. normal sowing and late sowing during *kharif* 2024-25. Analysis of variance revealed significance genetic variation among parents and F_1 's for seed yield per plant and its attributes in both conditions. Additive-dominance model was fitted for plant height under the E_2 condition, branches per plant under both the conditions (E_1 and E_2), biological yield and chlorophyll content under the E_2 condition. These results revealed that the assumptions of diallel analysis were fulfilled for these traits only; therefore, the component analysis was carried out only for these traits. The evaluation of components of genetic variation confirmed that both additive (D) and dominance (H_1 and H_2) components were significant for those traits which fitted in additive-dominance model. The estimates of H_1 were higher than H_2 for plant height, branches per plant, biological yield and chlorophyll content under the E_2 condition. The estimation of 'F' value, which showed the relative frequency of dominant and recessive alleles in parents was found positive and highly significant for biological yield under the E_2 condition. The proportion $(H_1/D)^{1/2}$ signifying the degree of dominance as more than unity for plant height under the E_2 condition, branches per plant under both the conditions (E_1 and E_2), biological yield and chlorophyll content under the E_2 condition. The environmental component (E) was significant for branches per plant under both the E_1 and E_2 conditions and biological yield under the E_1 condition. The $H_2/4H_1$ ratio was less than 0.25 for plant height, branches per plant, biological yield and chlorophyll content under the E_2 condition. The ratio of dominant and recessive alleles $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was more than unity for all the traits which fitted in additive-dominance model except for branches per plant under the E_1 condition and chlorophyll content under the E_2 condition. The scattering of array points indicated the existence of genetic diversity among the parents for most of the characters.

Keywords : Sesame, diallel analysis, dominance and condition.

Introduction

Sesame (*Sesamum indicum* L.) is considered to be the oldest of the oilseed crops. The cultivated species of sesame is *Sesamum indicum* L. is proven to be domesticated in India around 5000 B.C. based on the archaeological evidence of charred sesame found in indus velly civilization (Bedigian, 2003 and Iqbal *et al.*, 2016). While many wild species of sesame are native to sub-Saharan Africa, the cultivated variety

originated in India. Sesame is known by various names such as gingelly, til, tal, benniseed, and simsin in different parts of the world (Sandhya *et al.*, 2021). It belongs to the Pedaliaceae family, is an annual plant, self-pollinated, and has a diploid chromosome number ($2n=26$).

Sesame is cultivated in tropical and subtropical regions up to an altitude of 1250 meters and is sensitive to low temperatures. Globally, sesame is the

sixth most important oilseed crop. Among the countries producing sesame, Myanmar is the largest producer. Other major sesame-producing countries include India, Sudan, China, Uganda, Nigeria, Pakistan, Mexico, Tanzania, and also Bangladesh, Somalia, Turkey, Thailand, Venezuela, Ethiopia, and Egypt. In India, the total area under sesame cultivation during 2025-26 was 15.76 lakh hectares with a production of 9.34 lakh tonnes and an average productivity of 613 kg per hectare (Anonymous, 2025a). In Rajasthan, the total area under sesame during the same period was 1.44 lakh hectares with a production of 0.46 lakh tonnes and an average productivity of 311 kg per hectare (Anonymous, 2025b). The major sesame-growing states in India are Gujarat, Rajasthan, Uttar Pradesh, Madhya Pradesh, Maharashtra, Andhra Pradesh, Orissa, Tamil Nadu, West Bengal, and Karnataka. In Rajasthan, the major sesame-producing districts include Pali, Nagaur, Jodhpur, Jalore, Bhilwara, Sirohi, Ajmer, and Alwar.

Sesame is referred to as the “Queen of oilseeds” for its high quality and stability of oil which is due to the presence of high polyunsaturated fatty acids such as oleic acid (43%), linoleic acid (35%), palmitic acid (11%), and stearic acid (7%) and antioxidants in the oil (Ashri, 1998). Apart from these, a group of special health-benefiting compounds called lignans that are antioxidants (sesamin, sesamol, sesaminol and sesamolol), tocopherol, phytosterols, phytates and some other micronutrients in the oil (Pathak *et al.*, 2014). Seeds are a rich source of linoleic acid, vitamins E, A, B1 and B2; and minerals including Ca and P. Seed coats are rich in calcium (1.3%) and provide a valuable source of minerals (Johnson *et al.*, 1979).

In sesame, component of genetic variation analysis is the primary step in the selection of an appropriate breeding methodology. Sesame is predominantly a self pollinated crop, therefore, breeders essentially will require a programme which is able to follow the accumulation of fixable genes in homozygous lines. Hence, the understanding of various kinds of gene action viz., additive, dominance and epistasis is pre-requisite to frame effective breeding programme. In this context, the study was undertaken to estimate the nature of gene action for various quantitative characters through genetic component analysis (Sapara *et al.*, 2019a). The diallel approach provides information on combining ability (GCA and SCA) variances and effects, as well as the genetic components of variances (additive and non-additive). This information is valuable for selecting ideal parents for hybridization, identifying superior cross combinations, and developing an effective

breeding program for sesame improvement. Hayman's diallel analysis is effective in providing insights into additive and dominance effects of genes, the proportion of dominance, the average degree of dominance, the direction of dominance, the distribution of genes among parents, maternal and reciprocal effects, and the ratio of dominant to recessive alleles in all parents (Ramya *et al.*, 2021).

Material and Method

The experimental material consisted of eight genetically diverse parents RT-346, RT-351, Pragati, RT-372, JLT-706, RT-127, RT-125, and TKG-22 were crossed in half diallel fashion excluding reciprocals in *kharif*, 2024. These eight parents along with their 28 F_1 progenies were evaluated in a randomized block design with three replications during *kharif*, 2025 at Instructional Farm, S.K.N. College of Agriculture, Jobner (Rajasthan). All the genotypes were sown under two different environments namely; normal and late condition. Rows were planted in 3m length spaced at 30 cm apart and 10 cm inter plant distance under both conditions. Observations were recorded on days to 50% flowering, days to maturity, plant height, branches per plant, capsules per plant, capsule length, seeds per capsule, 1000-seed weight, seed yield per plant, biological yield, harvest index, oil content and chlorophyll content on ten randomly plants taken in each of the F_1 's progenies along with each parent from each replication except days to 50% flower and days to maturity which were observed on plot basis. Genetic components of variance were computed by employing diallel cross method suggested by Hayman (1954) for the traits where additive – dominance model fitted well.

Results and Discussion

The mean sum of squares due to genotypes and various components (parents, F_1 's and parents vs. F_1 's) was found to be significant for all traits under both environmental conditions in the analysis of variance performed for individual environmental conditions, with the exception of 1000-seed weight and harvest index under the E_1 condition and capsule per plant under the E_2 condition due to parents, and 1000-seed weight under the E_1 condition and harvest index under the E_2 condition due to parents vs. F_1 's (Table 1). Pooled analysis of variance showed highly significant differences among the environments for all the traits studied. All traits were affected by the environments. The mean sum of squares for genotypes and their subdivisions due to parents (except days to maturity, seeds per capsule and seed yield per plant) F_1 's and parents vs F_1 's were significant for all traits. The mean

sum of squares due to the interaction between genotype and environment was significant for all traits, indicating that genotypes responded differently to changes in environmental conditions. Similarly, the mean sum of squares due to the interaction between parents and environment was significant except for

capsule per plant for all the traits. The mean sum of squares due to contrast (parents vs F_1 's) was significant for all traits (Table 2). Similar results finding by Vekaria *et al.* (2014), Hassan and Sedeck (2015), Raikwar *et al.* (2018), Sikarwar *et al.* (2021) Nehra *et al.* (2023).

Table 1: Mean square for parents and F_1 's for different characters under individual environment

Characters	Environment	Source of variation					
		Replication [2]	Genotypes [35]	Parents [7]	F_1 's [27]	P vs F_1 [1]	Error [70]
Days to 50% flowering	E ₁	5.16	32.28**	8.73**	38.56**	27.49**	2.37
	E ₂	0.28	35.76**	14.65**	40.83**	46.67**	1.93
Days to maturity	E ₁	0.49	45.94**	8.07*	46.75**	289.35**	3.65
	E ₂	3.86	53.42**	22.03**	59.00**	122.49**	3.47
Plant height (cm)	E ₁	1.25	1072.02**	280.92*	829.74**	13151.22**	100.78
	E ₂	3.10	644.61**	403.16**	389.96**	9210.29**	75.79
Branches per plant	E ₁	0.13	1.00**	0.96**	0.70**	9.49**	0.18
	E ₂	0.31	0.88**	0.70**	0.38**	15.46**	0.16
Capsules per plant	E ₁	54.77	477.84**	248.94**	349.64**	5541.47**	72.82
	E ₂	9.16	410.05**	37.82	366.86**	4181.69**	39.02
Capsule length	E ₁	0.00	0.10**	0.06*	0.08**	1.01**	0.02
	E ₂	0.06	0.10**	0.28**	0.04*	0.47**	0.02
Seeds per capsule	E ₁	1.38	134.04**	75.29*	111.68**	1148.89**	28.36
	E ₂	16.12	156.13**	159.48**	102.14**	1590.19**	29.66
1000-Seed weight (g)	E ₁	0.02	0.45**	0.16	0.54**	0.12	0.08
	E ₂	0.00	0.19**	0.34**	0.10**	1.42**	0.04
Seed yield per plant (g)	E ₁	1.02	3.34**	1.97**	3.14**	18.53**	0.65
	E ₂	0.17	1.74**	1.21**	1.13**	22.08**	0.28
Biological yield (g)	E ₁	4.97	32.80**	19.43**	33.81**	98.97**	3.36
	E ₂	0.85	23.51**	15.07**	9.25**	467.64**	3.17
Harvest index (%)	E ₁	11.47	11.50**	9.71	10.57*	49.31**	5.96
	E ₂	1.28	14.56**	18.31**	14.12**	0.37	4.05
Oil Content (%)	E ₁	4.07	30.03**	22.12**	21.29**	321.69**	6.94
	E ₂	2.36	39.81**	22.32**	28.19**	475.91**	5.18
Chlorophyll Content (SPAD)	E ₁	0.21	91.87**	69.39**	86.10**	405.07**	16.39
	E ₂	6.28	109.45**	85.04**	82.07**	1019.75**	9.25

*,** Significant at 5 and 1 percent respectively (Model I)

Table 2: Pooled analysis of variance showing mean sum of squares of parents and F_1 's for seed yield and its contributing characters

Characters	Source of variation						
	Environment	Rep/Env	Genotypes	Parents	F_1 's	P vs F_1	G x E
	[1]	[4]	[35]	[7]	[27]	[1]	[35]
Days to 50% flowering	1731.90**	2.72	45.90**	5.22*	55.45**	72.91**	22.14**
Days to maturity	8373.99**	2.18	44.14**	7.08	54.73**	17.66*	55.22**
Plant height (cm)	56331.85**	2.18	1386.71**	426.27**	865.35**	22186.50**	329.92**
Branches per plant	14.00**	0.22	1.33**	0.66**	0.65**	24.59**	0.55**
Capsules per plant	16328.17**	31.97	487.25**	184.01**	225.56**	9675.38**	400.64**

Capsule length	1.07**	0.03	0.13**	0.20**	0.06**	1.42**	0.08**	0.02
Seeds per capsule	2495.60**	8.75	174.15**	34.41	116.04**	2721.19**	116.02**	29.01
1000-Seed weight (g)	10.45**	0.01	0.32**	0.13*	0.33**	1.19**	0.32**	0.06
Seed yield per plant (g)	131.13**	0.60	2.42**	0.58	1.48**	40.53**	2.67**	0.46
Biological yield (g)	846.65**	2.91	29.03**	13.21**	15.74**	498.44**	27.28**	3.26
Harvest index (%)	294.37**	6.38	10.90**	11.41*	10.41**	20.56*	15.17**	5.00
Oil Content (%)	109.03**	3.21	48.43**	26.67**	26.60**	790.08**	21.42**	6.06
Chlorophyll Content (SPAD)	2128.74**	3.24	153.65**	104.67**	121.85**	1355.12**	47.67**	12.82

*, ** Significant at 5 and 1 percent respectively (Model I)

The additive–dominance model was adequate as obtained by significant differences of regression coefficient (b) W_r-V_r from zero but non-significant from unity (Hayman, 1954a). Additive-dominance model was fitted for different environments in different characters. Computation of components of genetic variances was done along with graphical analysis. But in some cases where additive-dominance model was not fitted, only graphical analysis was performed to obtain genetic information regarding parents.

The regression coefficient (b) exhibited significant from zero and non-significant from unity was observed for plant height under the E_2 condition, branches per plant under both the conditions (E_1 and E_2), biological yield and chlorophyll content under the E_2 condition. Additive-dominance model was fitted for these character (Table 3). These results revealed that the assumptions of diallel analysis were fulfilled for these characters only; therefore, the component analysis was carried out only for these characters. But where additive dominance model was inadequate, only graphical analysis was performed, which indicated the existence of epistatic interactions. This showed the importance of testing the genetic material in more than one environment in order to obtain unbiased estimates of various components. Similar results of adequacy of additive-dominance model in sesame were reported by Sedeck *et al.* (2013), Abd El-Kader *et al.* (2017), Suganthi *et al.* (2017), Abd Elaziz *et al.* (2018), Sapara *et al.* (2019), Gami *et al.* (2020), Kumar *et al.* (2021), Rathod *et al.* (2021), and Kabi *et al.* (2022).

The evaluation of components of genetic variation confirmed that both additive (D) and dominance (H_1 and H_2) components were significant for those traits which fitted in additive-dominance model; which indicated that both components were operating in the expression of the characters (Table 3-4). However, the

relative magnitude of dominance component was found to be higher than additive component. These consequences advocated the preponderance of dominance gene action. Sedeck *et al.* (2013), Kader *et al.* (2017), Suganthi *et al.* (2017), Ghada and Zeinab (2018), Sapara *et al.* (2019), Gami *et al.* (2020) and Kabi *et al.* (2022) also observed higher dominant component for different characters.

The estimates of H_1 were higher than H_2 except for branches per plant under the E_1 condition, suggesting unequal allelic distribution of frequencies at the appropriate locations in the populations. These findings showed that both additive and dominance gene action played an important role in the inheritance of these traits. The additive and dominant effects in sesame have been documented by Kader *et al.* (2017), Suganthi *et al.* (2017), Sapara *et al.* (2019a), Gami *et al.* (2020) and Rathod *et al.* (2021).

The estimation of 'F' value, which showed the relative frequency of dominant and recessive alleles in parents was found positive and highly significant for biological yield under the E_2 condition. These are in agreement with the results of Suganthi *et al.* (2017), Sapara *et al.* (2019a), Gami *et al.* (2020), Kumar *et al.* (2021) and Ramya *et al.* (2021).

The environmental component (E) was significant for branches per plant under both the E_1 and E_2 conditions and biological yield under the E_1 condition (Table 3 and 4), suggesting that the concerned characters were influenced by various environmental fluctuation. Abd Elaziz *et al.* (2018), Ghada and Zeinab (2018), Kumar *et al.* (2021) and Rathod *et al.* (2021) also reported same in sesame.

The proportion $(H_1/D)^{1/2}$ signifying the degree of dominance as more than unity for plant height under the E_2 condition, branches per plant under both the

conditions (E_1 and E_2), biological yield and chlorophyll content under the E_2 condition, which exhibited existence of over dominance. Degree of dominance in sesame was also reported by Sedeck *et al.* (2013), Kader *et al.* (2017), Sapara *et al.* (2019) and Kumar *et al.* (2021). Where additive-dominance model fitted showed unequal distributions of positive and negative alleles in parents as indicated by the $H_2/4H_1$ ratio which was less than 0.25 except for branches per plant under the E_1 condition. Similar results were reported by Sedeck *et al.* (2013), Abd Elaziz *et al.* (2018), and Gami *et al.* (2020) in sesame.

The ratio of dominant and recessive alleles $[(4DH_1)^{1/2} + F] / [(4DH_1)^{1/2} - F]$ was more than unity for all the traits which fitted in additive-dominance model except branches per plant under the E_1 condition and chlorophyll content under the E_2 condition, that displayed accumulation of dominant alleles (Table 3 and 4). Similar results finding by Kader *et al.* (2017), Suganthi *et al.* (2017), Sapara *et al.* (2019), Gami *et al.* (2020), Ramya *et al.* (2021) and Rathod *et al.* (2021) in sesame.

The narrow-sense heritability obtained in component analysis ranged from low to high for various traits. The lower value of heritability clearly showed that it was affected by environment. Similar findings have earlier been reported by Kader *et al.* (2017).

In the present investigation, both partial and over dominance was obtained for capsules per plant, capsule length, biological yield and chlorophyll content, whereas complete and partial dominance was observed for 1000-seed weight and seed yield per plant. Some traits namely day to 50% flowering, days to maturity,

plant height, branches per plant, harvest index and oil content exhibited only over dominance and seeds per capsule exhibited only partial dominance (Figure 1-13). Similar results for different features were obtained by Tripathy *et al.* (2016), Kader *et al.* (2017), Ghada and Zeinab (2018), Sapara *et al.* (2019), Ramya *et al.* (2021) and Rathod *et al.* (2021).

The scattering of array points indicated the existence of genetic diversity among the parents for most of the characters. Relative position of parental array points from origin shows relative proportion of dominant and recessive alleles in the parents. RT-346 for branches per plant, capsules per plant, 1000-seed weight, chlorophyll content under the E_1 condition; RT-127 for days to 50% flowering, days to maturity, oil content under the E_1 condition and seeds per capsule, harvest index under the E_2 condition; TKG for capsule length, seeds per capsule, biological yield under the E_1 condition and seed yield per plant under the E_2 condition; JLT-706 for plant height, seed yield per plant, harvest index, chlorophyll content under the E_1 condition and days to 50% flowering, plant height, capsule length under the E_2 condition; RT-351 for days to maturity, branches per plant, chlorophyll content under the E_2 condition; RT-372 for 1000-seed weight, biological yield under the E_2 condition; RT-125 for capsules per plant, biological yield under the E_2 condition, Pragati for oil content under the E_2 condition were closer to the point of origin, therefore, appeared to have the highest number of dominant alleles (Figure 1-13). Similar findings have earlier been reported in sesame by Kader *et al.* (2017), Ghada and Zeinab (2018), Sapara *et al.* (2019), Gami *et al.* (2020), Ramya *et al.* (2021) and Rathod *et al.* (2021).

Table 3 : Estimates of regression coefficient, standard errors, deviation from zero and unity for different characters in individual conditions

Character	Env.	Source of variation				
		T^2	b	$SE(b)$	$t(b-0)/SE(b)$	$t(1-b)/SE(b)$
Days to 50% flowering	E_1	1.81	0.18	0.24	0.78	3.47*
	E_2	2.24	-0.03	0.23	0.13	4.50**
Days to maturity	E_1	11.91*	0.06	0.13	0.46	7.25**
	E_2	2.27	0.51	0.18	2.80*	2.72*
Plant height (cm)	E_1	29.23**	0.22	0.08	2.67*	9.25**
	E_2	1.00	0.74	0.16	4.72**	1.69
Branches per plant	E_1	0.41	0.81	0.16	5.12**	1.23
	E_2	0.97	0.69	0.18	3.91**	1.79
Capsules per plant	E_1	1.09	0.08	0.27	0.30	3.42*
	E_2	10.29*	0.12	0.14	0.89	6.45**
Capsule length	E_1	11.19*	0.17	0.13	1.33	6.37**
	E_2	0.89	0.86	0.42	2.05	0.34
Seeds per capsule	E_1	26.03**	0.22	0.09	2.43	8.83**

1000-Seed weight (g)	E ₂	2.28	-0.22	0.22	1.01	5.57**
	E ₁	20.63**	0.29	0.10	3.00*	7.51**
Seed yield per plant (g)	E ₂	0.61	0.42	0.52	0.80	1.11
	E ₁	7.20*	0.23	0.15	1.55	5.08**
Biological yield (g)	E ₂	0.93	0.49	0.23	2.15	2.21
	E ₁	9.66*	0.20	0.14	1.45	5.87**
Harvest index (%)	E ₂	1.22	0.68	0.17	4.07**	1.91
	E ₁	0.39	0.45	0.27	1.65	2.00
Oil Content (%)	E ₂	0.01	0.20	0.39	0.53	2.07
	E ₁	0.29	0.51	0.27	1.86	1.80
Chlorophy Content (SPAD) value	E ₂	0.40	0.24	0.30	0.79	2.49*
	E ₁	3.59	0.52	0.15	3.36*	3.11*
	E ₂	1.70	0.58	0.18	3.26*	2.32

*, ** Significant at 5% and 1% respectively

Table 4: Estimates of components of genetic variances for plant height (cm) and branches per plant in sesame

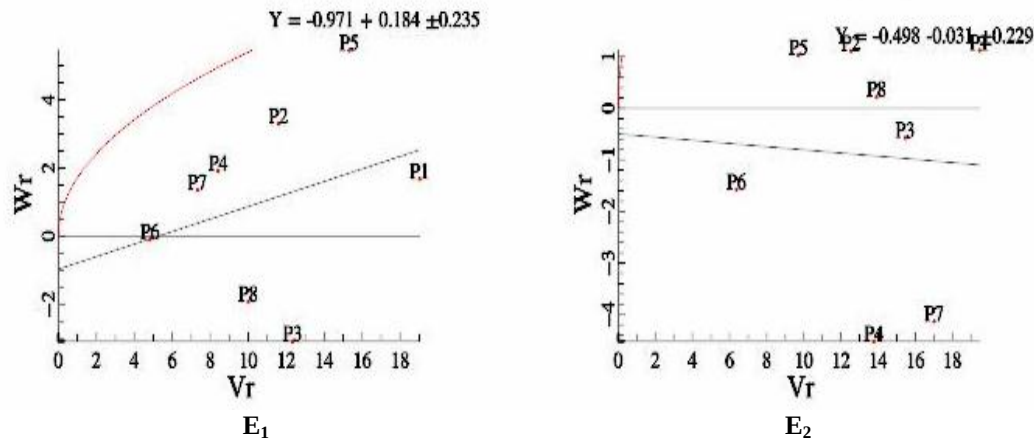
Characters	Plant height (cm)		Branches per plant			
Environments	E ₂		E ₁		E ₂	
Component	Estimates	SE	Estimates	SE	Estimates	SE
D	109.80*	40.15	0.26**	0.04	0.18**	0.04
H ₁	766.62**	92.29	0.44**	0.09	0.88**	0.09
H ₂	650.15**	80.29	0.47	0.08	0.82**	0.08
h ²	1500.30**	53.85	1.53**	0.05	2.51**	0.05
F	174.44	94.86	-0.11	0.09	0.2	0.09
E	24.59	13.38	0.06**	0.01	0.06**	0.01
(H ₁ /D) ^{1/2}	2.64		1.30		2.21	
H ₂ /4H ₁	0.22		0.27		0.24	
[(4DH ₁) ^{1/2} + F / [(4DH ₁) ^{1/2} - F	1.86		0.72		1.67	
h ² /H ₂	2.308		3.256		3.060	
h ² /(NS)	0.12		0.5		0.06	

*, ** Significant at 5% and 1% respectively

Table 5: Estimates of components of genetic variances for biological yield (g) and chlorophyll content (SPAD value) in sesame.

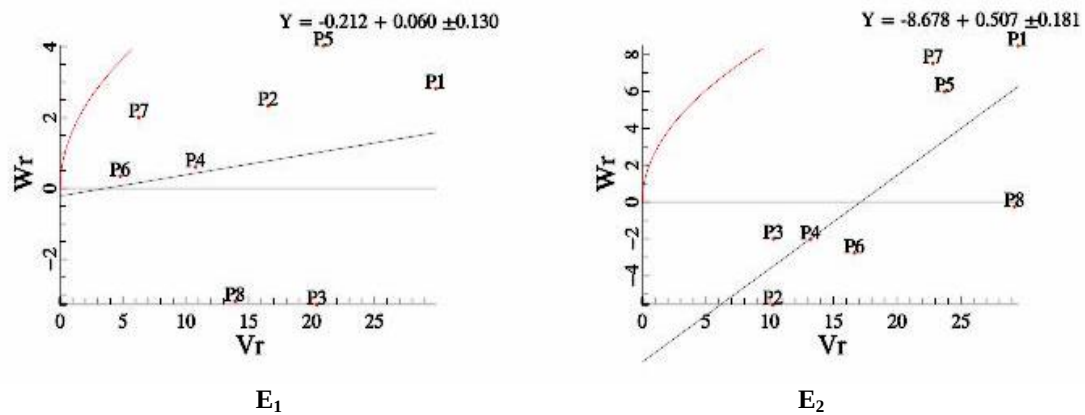
Characters	Biological yield (g)		Chlorophyll content (SPAD) value	
Environments	E ₂		E ₂	
Component	Estimates	SE	Estimates	SE
D	3.99**	1.15	25.29**	5.9
H ₁	25.49**	2.64	74.24**	13.56
H ₂	21.30**	2.30	61.28**	11.79
h ²	76.27**	1.54	165.97**	7.91
F	6.66*	2.72	-0.77	13.93
E	1.03*	0.38	3.06	1.97
(H ₁ /D) ^{1/2}	2.52			
H ₂ /4H ₁	0.21		0.21	
[(4DH ₁) ^{1/2} + F / [(4DH ₁) ^{1/2} - F	1.99		0.98	
h ² /H ₂	3.58		2.708	
h ² /(NS)	0.11		0.52	

*, ** Significant at 5% and 1% respectively



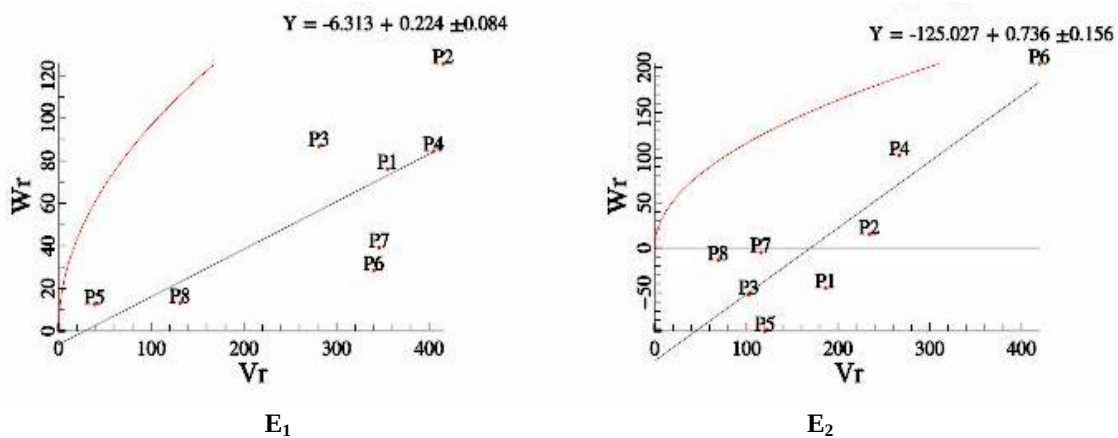
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 1: W_r - V_r graph for days to 50% flowering in E_1 and E_2 conditions



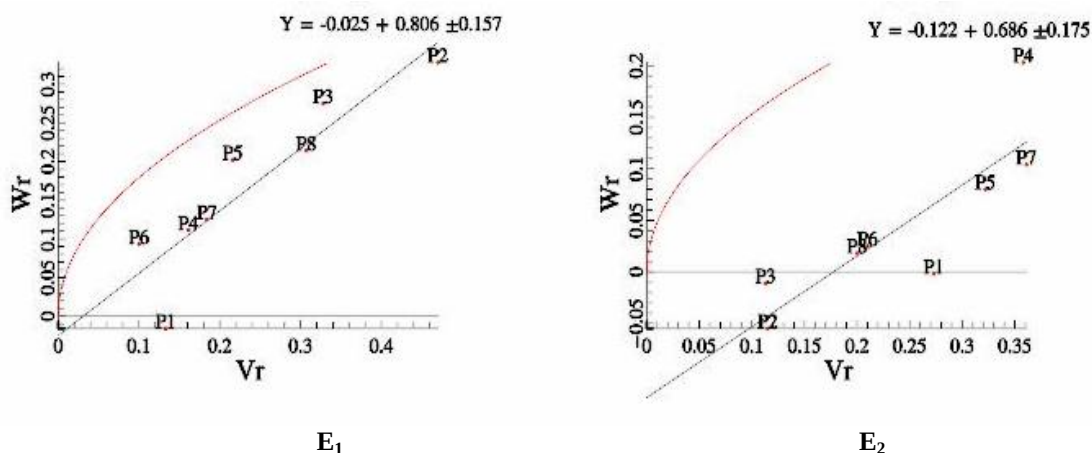
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 2: W_r - V_r graph for days to maturity in E_1 and E_2 conditions



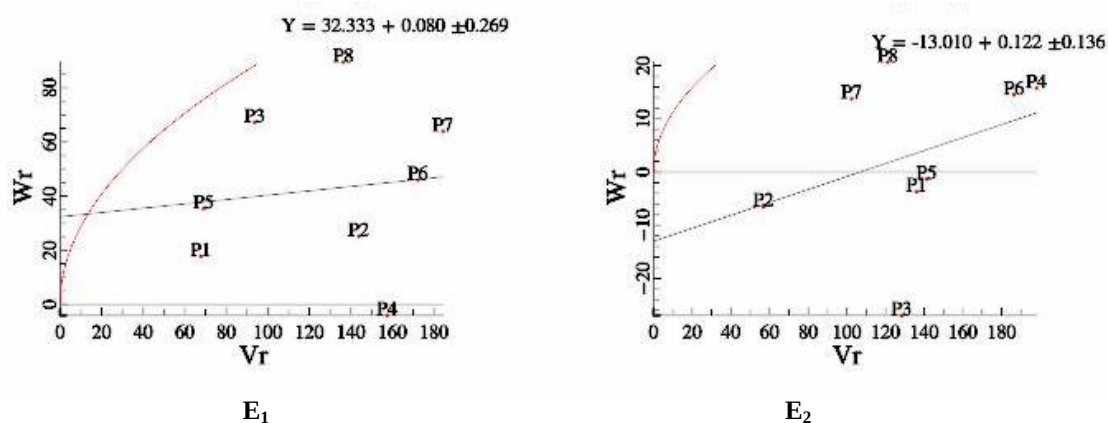
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 3: W_r - V_r graph for plant height (cm) in E_1 and E_2 conditions



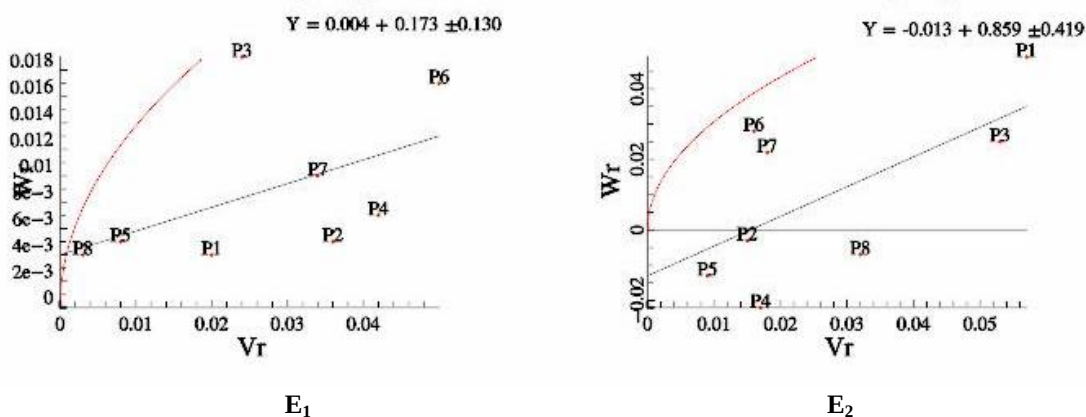
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 4: W_r - V_r graph for branches per plant in E₁ and E₂ conditions



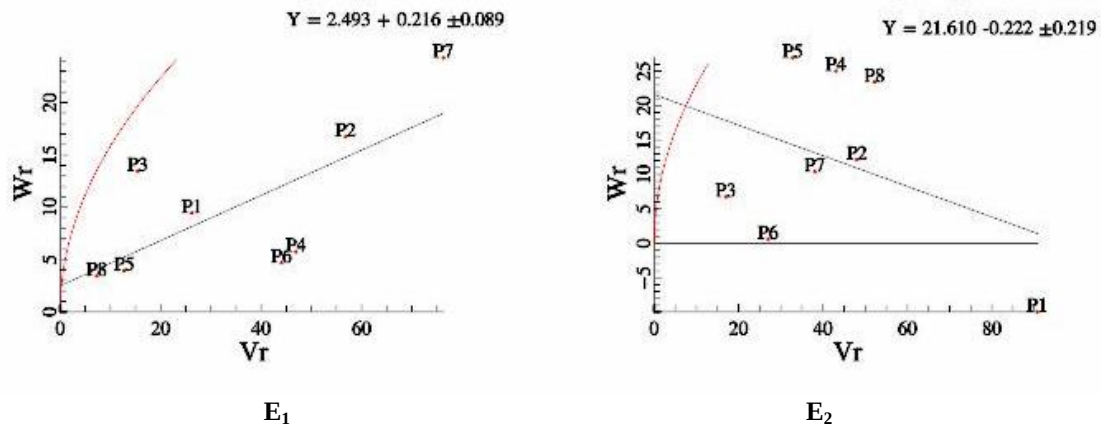
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 5: W_r - V_r graph for capsules per plant in E₁ and E₂ conditions



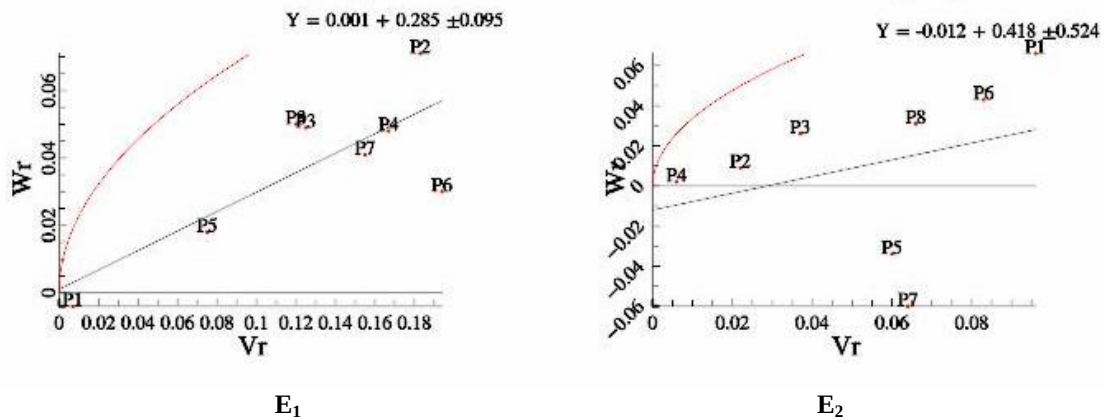
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 6: W_r - V_r graph for capsule length (cm) in E₁ and E₂ conditions



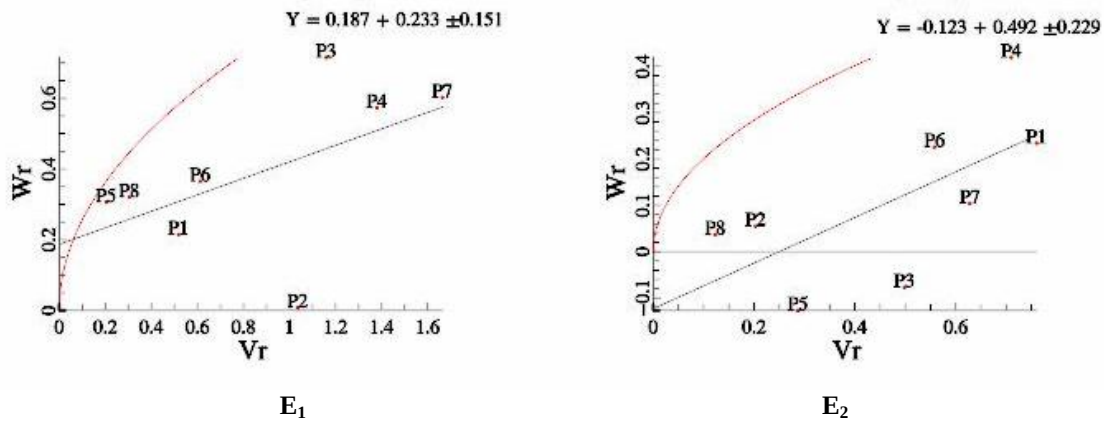
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 7: W_r - V_r graph for seeds per capsule in E_1 and E_2 conditions



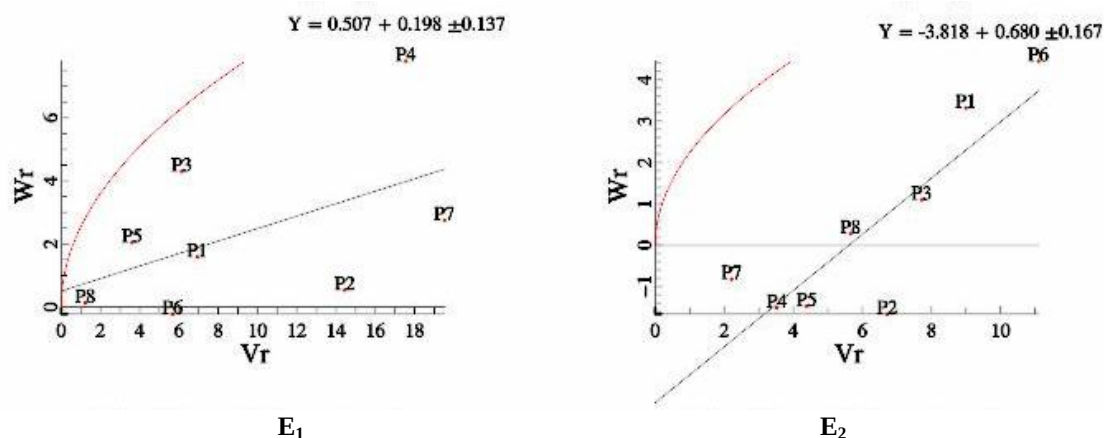
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 8: W_r - V_r graph for 1000-seed weight (g) in E_1 and E_2 conditions



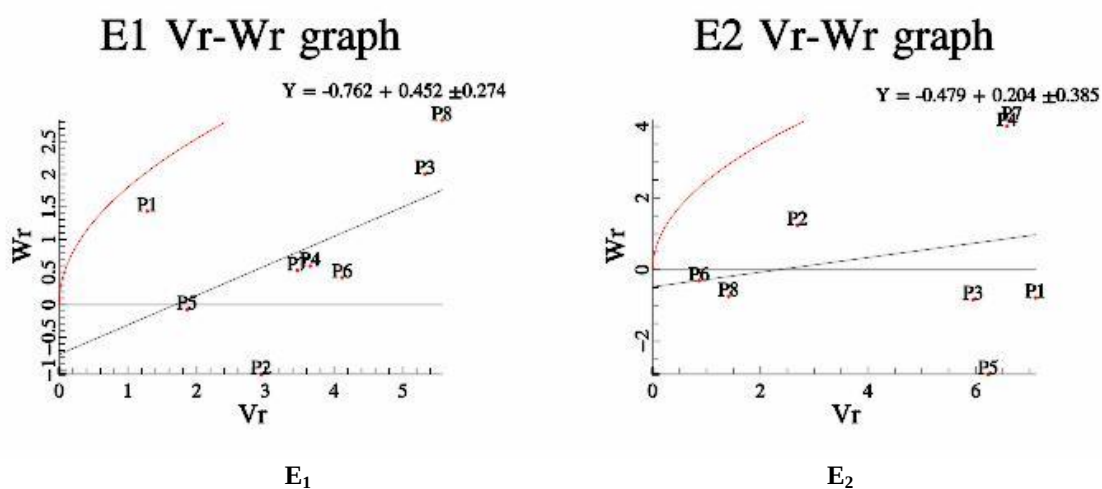
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 9: W_r - V_r graph for seed yield per plant (g) in E_1 and E_2 conditions



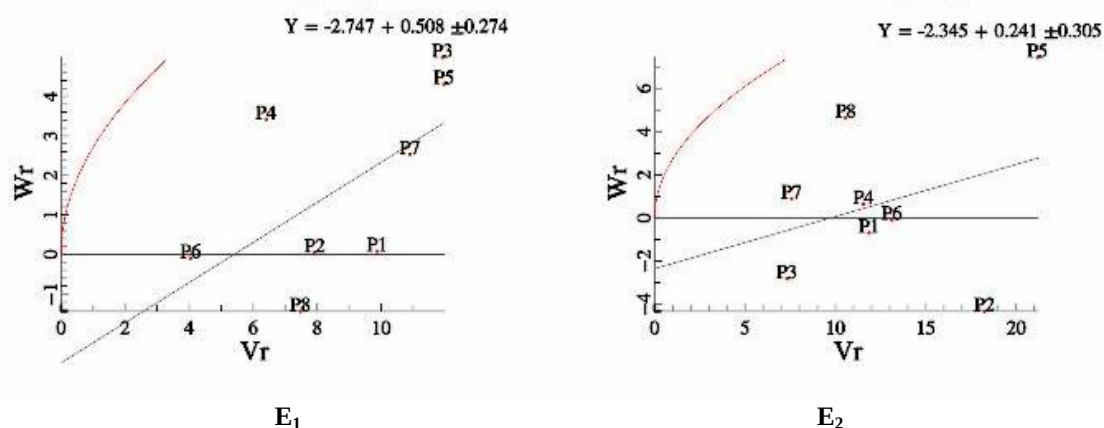
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4 = RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 10: W_r - V_r graph for biological yield (g) in E_1 and E_2 conditions



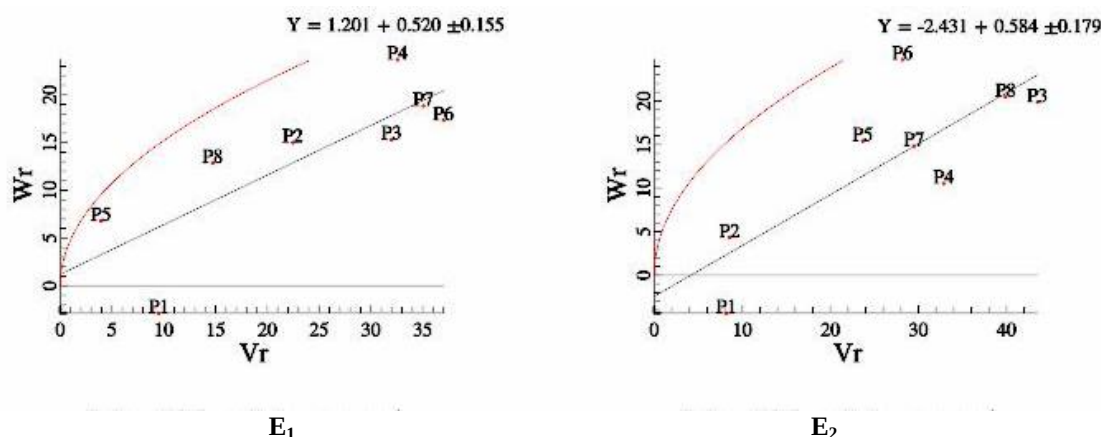
P1 = RT-346, P2 = RT-351, P3 = Pragati, P4 = RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 11: W_r - V_r graph for harvest index (%) in E_1 and E_2 conditions



P1 = RT-346, P2 = RT-351, P3 = Pragati, P4 = RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 12: W_r - V_r graph for oil content (%) in E_1 and E_2 conditions



P1 = RT-346, P2 = RT-351, P3 = Pragati, P4=RT-372, P5 = JLT-706, P6 = RT-127, P7 = RT-125, P8 = TKG-22

Fig. 13: Wr-Vr graph for chlorophyll content (SPAD value) in E₁ and E₂ conditions

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