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Genetic analysis for seed yield and its related attributes in Yellow Sarson (*Brassica rapa* var. Yellow Sarson)

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Abstract

Six generations (P_1, P_2, F_1, F_2, BC_1, BC_2) in each of three crosses were studied to estimate gene effects controlling yield and its related attributes by generation mean analysis and scaling test for ten physiological traits. These were evaluated in a compact family block design (CFBD) with three replications. Besides seed yield per plant, data also recorded for plant height, primary branches per plant, Days to 50% flowering, length of fruiting zone, siliqua per plant, siliqua length, Days of maturity, 1000-seed weight and oil content. The analysis of variance of three cross families revealed significant differences among the progenies (generations) within Family for most of the quantitative traits. Six parameters genetic model revealed the presence of additive (*d*), dominant (*h*) and epistasis (*i, j, l*) for most of the evaluated traits. Significant differences for two or more individual scaling tests (A, B, C, and D) in all three crosses were observed indicating the sight of non-allelic interactions. Further, it was confirmed by joint scaling test. All the crosses showed significant chi-square values for all the evaluated characters except for day to maturity in NDYS 427 x YST-151. Significant chi-square values indicated the presence of epistasis or inadequacy of additive-dominance model. The precise knowledge of nature of gene action for characters evaluated to productivity would aid in the choice of effective breeding methods to accelerate the pace of genetic improvement of seed yield.

***Key words**: Generation mean analysis, epistasis, gene interaction, Yellow Sarson*

Introduction

In India, rapeseed-mustard is the second most important edible oilseed after groundnut sharing 27.8% in the India's oilseed economy. The rapeseed-mustard group broadly includes Indian mustard, Yellow Sarson, Brown Sarson, Raya, and Toria crops. Yellow Sarson (*Brassica rapa* var. Yellow Sarson) is considered to be the most drought-tolerant and to have best oil quality among the three sub-species of *B. rapa* i.e. Yellow Sarson, Brown Sarson and Toria. It is mainly grown in Assam, Bihar, North-eastern States, Orissa, eastern Uttar Pradesh and West Bengal (Singh and Murty, 1980). The information about the nature and magnitude of gene effects involved in the expression of important characters is essential for formulation and execution of intensive breeding programme in any crop. Breeding in Yellow Sarson has primarily been confined to exploitation of available genetic variability resulting in establishment of homozygous lines. In order to determine genotypic values of the individuals and consequently mean genotypic values of families and generations, researchers use generation mean analysis to estimate the relative importance of average effects of the genes (additive effects), dominance deviations, and effects due to non-allelic genetic interactions (Viana, 2000). Generation mean analysis is one of the genetic models which is developed for the estimation of different genetic effects and used to partition the phenotypic variance to its components, *i.e.* genotyping, environmental, and genotype × environment components (Checa *et al.*, 2006; Tiruneh Mulugeta *et al.*, 2013). The simple scaling tests (Mather, 1949; Hayman and Mather, 1955) and joint scaling test (Cavalli, 1952) followed by generation mean analysis (Jinks and Jones, 1958) provide more precise assessment of additive, dominance and epistatic gene effects in respect of individual crosses. The genetic parameters facilitate in deciding the most appropriate methodology for further crop improvement. In present investigation, gene effects that governing seed yield and related yield components in three crosses of Yellow Sarson are discussed.

Material and Methods

The experimental material for the present investigation comprised 6 generations (P_1, P_2, F_1, F_2, BC_1, BC_2) of each of three crosses *viz*., Jagrati x YST-151, NDYS 427 x YST-151, Pusa Gold x Jagrati. All the four parents, Jagrati, YST-151, NDYS 427 and Pusa Gold were yellow seeded and belong to *Brassica rapa* L. var. Yellow Sarson. During 2009-2010 crop season, different crosses were performed and F_1 seeds harvested. In subsequent year (2010-11), F_1s were crossed with respective parents (P_1 and P_2) for developing back crosses (BC_1 and BC_2) population and also selfed to obtain F_2 seeds. Simultaneously, some fresh crosses were also attempted to produce F_1 seeds during same year.

Experimental material was evaluated Compact Family Block Design (CFBD) with three replications during *Rabi*, 2011-12 under timely sown condition at Research Farm, Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, India. Different generations were represented by 1 to 4 rows of 5m per replication depending upon the expected variance. Inter and intra- row-spacing was maintained at 30 x 10 cm. The number of competitive plants were randomly selected from each generation per replication (5 plants from P_1, P_2, F_1; 20 from F_2 and 10 from BC_1, BC_2). The observations were recorded on randomly selected plants for plant height (cm), primary branches/plant, Number of siliqua per plant, length of fruiting zone (cm), Seed yield per plant, 1000-seed weight and oil content (%) on plot basis. For each family, the plot means for each generation were averaged over the number of replications to get the generation means. These generation means formed the basis for calculation of various genetic parameters.

Statistical analysis

Analysis of variance was done following procedure of Singh and Chaudhary (1985) for all the crosses. The mean squares of treatments and replications were tested against corresponding mean square of error. The calculated '*F*' value was compared with table value of '*F*' at 5% and 1% level of significance. Six parameter model of generation mean analysis (Jinks and Jones, 1958) was used to study the nature and magnitude of gene effects for the tested characters as given below-

$$m = \bar{F}_1 - 4\bar{F}_2 - (1/2)\,\bar{P}_1 - (1/2)\,\bar{P}_2 + 2\overline{BC}_1 + 2\,\overline{BC}_2$$

$$d = \overline{BC}_1 - \overline{BC}_2$$

$$h = \bar{F}_1 - 4\bar{F}_2 - (1/2)\,\bar{P}_1 - (1/2)\,\bar{P}_2 + 2\overline{BC}_1 + 2\,\overline{BC}_2$$

$$i = 2\,\overline{BC}_1 + 2\,\overline{BC}_2 - 4\,\bar{F}_2$$

$$j = \overline{BC}_1 - ½\,\bar{P}_1 - \overline{BC}_2 + ½\,\bar{P}_2$$

$$l = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\,\bar{F}_2 - 4\overline{BC}_1 - 4\overline{BC}_2$$

Where, m (mean), d (additive effect), h (dominance effect), i (additive x additive gene interaction), j (additive x dominance gene interaction), *l* (dominance x dominance gene interaction). P_1, P_2, F_1, F_2, BC_1 and BC_2 are the mean values for different generation. The test for significance of gene effects was made by the 't' test. Further the analyses of data were performed by using simple scaling test based on formulas of Hayman and Mather (1955) for testing the validity of additive dominance model or for detecting non-allelic interactions. The joint scaling test (Cavalli, 1952) was also performed for detection and estimation of genic effects and testing the adequacy of model. All statistical analyses were carried out using Windostat software (V 8.6).

Results and Discussion

Analysis of variance (ANOVA) revealed significant differences among the progenies (generations) within sets of crosses (families) indicating the presence genetic variability (Table 1). The mean values and their standard errors for the analyzed characters are presented in Tables 2. The hybrids performed better than their respective parents in all crosses studied in regard to primary branches per

Table 1: Analysis of Variance for six generations of different agronomical traits (Mean squares)

Crosses	S.O.V.	*d.f.*	PH (cm)	PBPP	DF	LFZ (cm)	SPP	SL (cm)	DM	SYPP (g)	1000 SW (g)	OC (%)
Jagrati×YST-151	Replications	2	0.45	1.17	4.39	0.23	5.05	0.07	14.00	2.32	0.03	0.15
	Progenies	5	93.10**	1.57	22.59**	12.48**	16.46**	0.97**	14.53	15.79***	0.24*	1.48**
	Error	10	3.19	0.63	2.45	1.39	2.05	0.09	10.53	0.70	0.07	0.20
NDYS 427×YST-151	Replications	2	1.77	0.22	2.66	0.99	8.16	0.36	13.72	0.23	0.08	0.05
	Progenies	5	59.72***	0.99	21.17*	52.18***	8.00	0.40	20.99	23.12***	0.15	1.50***
	Error	10	2.16	0.96	4.53	1.06	3.97	0.27	8.79	0.72	0.09	0.04
Pusa Gold×Jagrati	Replications	2	0.89	0.22	4.39	0.90	6.06	0.20	0.17	0.30	0.06	0.01
	Progenies	5	79.28***	4.62**	17.39*	12.51***	6.09*	0.81	69.43***	17.54***	0.38*	0.86*
	Error	10	1.84	0.49	4.79	0.91	1.72	0.41	6.50	0.65	0.11	0.17

*, **, *** Significant at 5%, 1% and 0.1 % level of significance, respectively, S.O.V. (Sources of Variance), PH (Plant height), PBPP (Primary branches per plant), DF (Days to 50% flowering), LFZ (Length of fruiting zone), SPP (Siliqua per plant), SL (Siliqua length), DM (Days to maturity), SYPP (Seed yield per plant), TSW (Thousand grain weight), OC (Oil content)

Table 2. Means and their standard error of six generations for ten physiological traits

Generations	PH (cm)	PBPP	DF	LFZ (cm)	SPP	SL (cm)	DM	SYPP (g)	1000-SW (g)	OC (%)
Jagrati×YST-151										
P_1	116.53±0.35	5.00±0.22	44.67±0.55	51.05±0.23	45.33±0.45	5.33±0.07	113.33±0.45	15.71±0.21	3.97±0.05	44.35±0.08
P_2	115.80±0.25	6.00±0.22	47.00±0.44	54.83±0.24	40.33±0.13	4.50±0.08	118.33±0.45	16.71±0.34	3.80±0.02	43.30±0.02
F_1	101.77±0.31	6.33±0.13	39.00±0.22	50.17±0.26	46.00±0.58	5.93±0.03	112.33±0.54	21.53±0.17	4.20±0.06	43.63±0.13
F_2	115.00±0.18	4.33±0.06	41.67±0.06	50.33±0.12	46.33±0.16	5.57±0.02	113.67±0.50	16.75±0.12	3.60±0.02	45.20±0.01
BC_1	109.67±0.23	5.67±0.09	44.00±0.15	48.77±0.09	46.00±0.15	5.53±0.06	115.33±0.61	17.30±0.07	3.47±0.06	44.64±0.12
BC_2	110.50±0.36	5.67±0.18	44.00±0.30	50.90±0.21	46.33±0.09	5.20±0.05	113.00±0.55	14.98±0.10	3.53±0.04	44.62±0.01
NDYS 427×YST-151										
P_1	118.67±0.22	6.00±0.22	41.67±0.45	57.47±0.25	42.67±0.45	5.29±0.04	116.00±0.65	16.81±0.03	3.87±0.05	45.14±0.01
P_2	118.23±0.30	5.33±0.13	47.00±0.44	54.50±0.31	40.67±0.13	4.90±0.17	118.33±0.45	16.65±0.14	3.80±0.02	43.30±0.02
F_1	108.03±0.34	7.00±0.22	40.00±0.22	57.13±0.20	43.33±0.33	5.83±0.07	110.33±0.33	22.61±0.22	4.14±0.05	44.34±0.06
F_2	113.87±0.16	6.00±0.11	45.33±0.12	48.60±0.11	44.67±0.40	4.87±0.07	114.00±0.28	16.80±0.12	3.63±0.03	45.26±0.01
BC_1	111.02±0.25	5.67±0.09	43.33±0.32	49.60±0.12	43.33±0.23	5.17±0.10	114.00±0.66	14.84±0.16	3.53±0.06	44.33±0.04
BC_2	118.25±0.22	5.67±0.18	45.67±49	48.83±0.10	45.33±0.32	4.97±0.05	115.00±0.61	15.44±0.03	3.97±0.06	44.38±0.04
Pusa Gold×Jagrati										
P_1	120.57±24	5.67±0.13	42.67±0.67	51.67±0.18	44.67±0.25	4.98±0.08	120.00±0.22	15.55±0.03	4.10±0.02	44.29±0.07
P_2	116.97±0.25	4.33±0.13	44.67±0.55	51.11±0.21	44.33±0.50	5.97±0.18	133.33±0.45	15.53±0.14	3.97±0.05	44.35±0.08
F_1	116.75±0.43	7.67±0.13	40.67±0.13	51.22±0.20	47.33±0.25	5.52±0.20	105.67±0.13	21.20±0.21	4.50±0.08	44.50±0.08
F_2	110.53±0.05	5.33±0.06	44.00±0.11	49.73±0.13	46.33±0.16	4.41±0.02	110.33±0.06	16.09±0.11	3.90±0.06	45.33±0.03
BC_1	118.37±0.18	6.00±0.15	46.67±0.32	46.73±0.09	47.66±0.18	5.17±0.08	115.33±0.61	17.36±0.15	3.47±0.06	45.17±0.01
BC_2	107.07±0.22	4.33±0.09	47.00±0.40	47.73±0.17	45.00±0.26	5.23¡0.08	112.33±0.49	14.36±0.05	3.70±0.02	45.51±0.09

*, **, Significant at 5% and 1% level of significance, respectively, PH (Plant height), PBPP (Primary branches per plant), DF (Days to 50% flowering), LFZ (Length of fruiting zone), SPP (Siliqua per plant), SL (Siliqua length), DM (Days to maturity), SYPP (Seed yield per plant), TSW (Thousand grain weight), OC (Oil content)

Table 3: Estimates of components of generation means for different physiological traits, simple scaling test and type of epistasis in Jagrati×YST-151 cross

Characters	Gene effects						Scales				Type of epistasis
	m	d	h	i	j	*l*	A	B	C	D	
Plant height (cm)	115.00+0.18	-0.83**+0.42	-34.07**+1.16	-19.67**+1.10	-1.20*+0.47	15.20**+1.98	1.03+0.65	3.43**+0.82	24.13**+1.03	9.83**+0.55	D
Primary branches per plant	4.33+0.06	0.00+0.20	6.17**+0.50	5.33**+0.46	0.50*+0.25	-4.33**+0.91	0.00+0.31	-1.00*+0.43	-6.33**+0.47	-2.67**+0.23	D
Days to 50% flowering	41.67+0.06	0.00+0.34	2.50**+0.83	9.33**+0.72	1.17*+0.49	-15.67**+1.61	4.33**+0.66	2.00*+0.78	-3.00**+0.86	-4.67**+0.36	D
Length of fruiting zone (cm)	50.33+0.12	-2.13**+0.23	-2.77**+0.73	-2.0**0+0.66	-0.24+0.28	12.89**+1.19	-5.69**+0.39	-5.20**+0.55	-8.89**+0.78	1.00**+0.33	D
Siliqua per plant	46.33+0.16	-0.33+0.18	2.50**+0.97	-0.67+0.74	-2.83**+0.29	-6.33**+1.57	0.67+0.80	6.33**+0.62	7.67**+1.41	0.33+0.37	D
Siliqua length (cm)	5.57+0.03	-0.67**+0.08	-1.78**+0.20	-2.80**+0.17	-1.08**+0.09	5.03**+0.35	-2.20**+0.14	-0.03+0.12	0.57**+0.15	1.40**+0.09	D
Days to maturity	113.67+0.50	2.33**+0.82	-1.50+2.67	2.00+2.60	4.83**+0.88	-2.33+4.05	5.00**+1.42	-4.67**+1.31	-1.67+2.38	-1.00+1.30	-
Seed yield per plant (g)	16.75+0.12	2.33**+0.12	2.89**+0.59	-2.43**+0.53	2.83**+0.24	13.35**+0.86	-2.63**+0.31	-8.29**+0.43	-8.49**+0.74	1.21**+0.26	C
1000- grain weight (g)	3.60+0.02	-0.07+0.07	-0.08+0.18	-0.40*+0.17	-0.15*+0.08	2.57**+0.33	-1.23**+0.14	-0.93**+0.10	-1.77**+0.15	0.20+0.08	-
Oil content (%)	45.20+0.01	0.02+0.12	-2.48**+0.29	-2.29**+0.25	-0.51**+0.13	-1.31*+0.57	1.29**+0.29	2.30**+0.14	5.88**+0.28	1.14**+0.13	C

*, ** Significant at 5% and 1% level of probability, respectively; C = Complementary epistasis and D = Duplicate epistasis ,
m= mean, *d* = additive, *h* = dominance, *i*= additive x additive, j = additive x dominance, *l* = dominance x dominance

plant, siliqua per plant, seed yield per plant and 1000-seed weight, the most important physiological traits contributing to yield. It showed the possibility of exploiting heterosis existing in all crosses for those traits, through bi-parental or diallel method for improving the seed yield. However, for the traits plant height and days to maturity, the performance of $F_1$was inferior to their parents in Jagrati×YST-151 and NDYS 427×YST-151 crosses and in Pusa Gold x Jagrati cross, in regard of days to maturity only. For the other physiological traits, differences were not so conspicuous. These results were in concordance of Sharmila *et al.* (2007) who also reported the greater performance of hybrids over their respective parents in four crosses studied in sesame except in VS 9510 x Co1 cross for the number of seed capsules per plant and in NIC 7907 x TMV 3 cross in regard to capsule length. According to Khodambashi *et al.* (2012) the F_1 mean was greater than mean of both parents for the number of seeds per pod in lentil.

Information about the genetic components of variation helps the breeder in the selection of desirable parents for crossing programs and also in deciding a suitable breeding procedure for the genetic improvement of various quantitative traits (Singh and Narayanan, 2013; Meena *et al.*, 2015). Estimates of gene effects for digenetic epistasis interaction model or additive-dominance model and simple scaling test (A, B, C, D) for the evaluated traits of Jagrati x YST-151, NDYS 427 x YST-151 and Pusa Gold x Jagrati crosses are presented in Table 3, 4 and 5, respectively.

In our results, additive, dominance and epistatic types of gene interaction in each cross for different agronomical traits were found to differ from each other. The gene effects, dominance (*h*) and dominance x dominance (*l*), were in opposite direction for plant height, primary branches per plant, days to 50% flowering, length of fruiting zone, siliqua per plant and siliqua length in Jagrati xYST-151 cross (Table 3), suggesting the occurrence of duplicate epistasis. However, complementary type of gene interaction was pronounced for most of physiological traits in NDYS 427 x YST-151 cross as shown in Table 4. Duplicate-type epistasis played a greater role than complementary epistasis in expression of most of agronomical traits in Jagrati x YST-151 and Pusa Gold x Jagrati crosses. On the contrary, in NDYS 427 x YST-151 cross, complementary gene interaction was prominent for most of the agronomical traits. According to Singh *et al.* (2014) the dominance *(h)* and dominance x dominance *(l)* non-allelic interactions were most important for water use efficiency in BPR-543-2 x BPR-2 cross of Indian mustard. The estimates of six parameters from generation mean analysis showed that the additive (d) and dominance (h) were significant in all the crosses though the relative contribution of the dominance gene effect was higher that of additive gene effect. Akhshi *et al.* (2014) also reported that in comparison with the additive gene effects, dominance genes are the most important factors contributing to the genetic control of all traits except pod weight in DER × A1007 and seed number per pod in GOLI × D81 crosses in common bean. Generation mean analysis by using six parameters model and scaling test (simple and joint scaling test) suggested the presence of duplicate or complementary epistasis that indicates the inadequacy of additive-dominance model in all crosses for most of the traits studied.

Our results showed that both additive and non-additive type of gene action (epistasis) were significant in expression of agronomical traits. The significance of additive gene effects for the evaluated traits in the crosses studied indicating that feasibility of substantial improvement in yield through conventional breeding methods. The dominance and additive x dominance and dominance x dominance epistatic effects indicating non-fixable, non-additive gene action, were also significant for many traits. Importance of one or more types of non-additive components of genetic variance for most of the traits suggested the exploitation of heterosis in those traits for developing hybrid varieties. The application of methods like biparental mating and diallel selective mating system may be suggested for exploitation of dominance and epistatic effects for purpose of isolating transgressive segregants in advanced generations.

Table 4: Estimates of components of generation means for different physiological traits, simple scaling test and type of epistasis in NDYS427 x YST-151 cross

Characters	Gene effects						Scales				Type of
	m	d	h	i	j	*l*	A	B	C	D	epistasis
Plant height (cm)	113.87+0.16	-7.23**+0.34	-7.35**+1.01	3.07**+0.93	-7.45**+0.39	-8.63**+1.68	-4.67**+0.65	10.23**+0.64	2.50*+1.01	-1.53**+0.47	C
Primary branches per plant	6.00+0.11	0.00+0.20	0.00+0.63	-1.33*+0.58	-0.33+0.23	4.00**+1.02	-1.67**+0.36	-1.00*+0.43	-1.33*+0.66	0.67*+0.29	-
Days to 50% flowering	45.33+0.12	-2.33**+0.58	-7.67**+1.32	-3.33*+1.26	0.33+0.67	-6.00*+2.49	5.0**+ 0.81	4.33**+1.09	12.67**+0.91	1.67*+0.63	C
Length of fruiting zone (cm)	48.60+0.11	0.77**+0.16	3.62**+0.60	2.47**+0.53	-0.71*+0.25	26.89**+0.94	-15.39**+0.42	-13.97**+0.42	-31.83**+0.71	-1.24**+0.26	C
Siliqua per plant	44.67+0.40	-2.00**+0.40	0.33+1.84	-1.33+1.79	-3.00**+0.46	-6.00*+2.39	0.67+0.73	6.67**+0.73	8.67**+1.81	0.67+0.90	-
Siliqua length (cm)	4.87+0.07	0.20+0.11	1.54**+0.37	0.80*+0.36	0.01+0.14	0.79+0.57	-0.79**+0.21	-0.80**+0.21	-2.39**+0.36	-0.40*+0.18	-
Days to maturity	114.00+0.28	-1.00+0.90	-4.83*+2.18	2.00+2.12	0.17+ 0.98	-5.00+3.90	1.67+1.51	1.33+1.34	1.00+1.53	-1.00+1.06	-
Seed yield per plant (g)	16.80+0.12	-0.60**+0.16	-0.73+0.62	-6.61**+0.78	-0.68**+0.18	24.72**+0.92	-9.74**+0.39	-8.37**+0.27	-11.49**+0.66	3.31**+0.29	-
1000-grain weight (g)	3.63+0.03	-0.43**+0.08	0.77**+0.21	0.47+0.19	-0.46*+0.09	0.48**+0.37	-0.94**+0.14	-0.01+0.14	-1.41**+0.16	-0.23*+0.10	C
Oil content (%)	45.26+0.01	-0.05+0.06	-3.52**+0.14	-3.64**+0.12	-0.97**+0.06	3.34*+0,26	-0.82**+0.11	1.12**+0.09	3.94**+0.13	1.82**+0.06	D

*, ** Significant at 5% and 1% level of probability, respectively; C = Complementary epistasis and D = Duplicate epistasis ,
m= mean, *d* = additive, *h* = dominance, *i*= additive x additive, j = additive x dominance, *l* = dominance x dominance.

Table 5: Estimates of components of generation means for different physiological traits, simple scaling test and type of epistasis in Pusa Gold x Jagrati cross

Characters	Gene effects						Scales				Type of
	m	d	h	i	j	*l*	A	B	C	D	epistasis
Plant height (cm)	110.53+0.05	11.30**+0.28	6.72**+0.76	8.73**+0.61	9.50**+0.33	11.43**+1.47	-0.58+0.60	-19.58**+0.67	-28.90**+0.94	-4.37**+0.30	C
Primary branches per plant	5.33+0.06	1.67**+0.18	2.00**+0.46	-0.67+0.43	1.00**+0.20	5.33**+0.80	-1.33**+0.35	-3.33**+0.25	-4.00**+0.39	0.33+0.21	C
Days to 50% flowering	44.00+0.11	-0.33+0.51	8.33**+1.19	11.33**+1.11	0.67+0.67	-30.00**+2.27	10.00**+ 0.93	8.67**+0.98	7.33**+0.80	-5.67**+0.55	D
Length of fruiting zone (cm)	49.73+0.13	-1.00**+0.19	-10.17**+0.69	-10.00**+0.65	-1.28**+0.23	26.29**+1.04	-9.42**+0.32	-6.87**+0.44	-6.29**+0.71	5.00**+0.32	D
Siliqua per plant	46.33+0.16	2.67**+0.32	2.83*+0.98	0.00+0.91	2.50**+0.42	-1.67+1.61	3.33**+0.50	-1.67*+0.77	1.67+0.80	0.00+0.45	-
Siliqua length (cm)	4.41+0.02	-0.05+0.12	3.19**+0.33	3.15**+0.25	0.44*+0.15	-1.97**+0.65	-0.15+0.27	-1.03**+0.32	-4.33**+0.45	-1.57**+0.12	D
Days to maturity	110.33+0.06	3.00**+0.78	3.00+1.61	14.00**+1.59	-0.33+0.82	-24.67**+3.19	5.00**+1.25	5.67**+1.08	-3.33**+0.61	-7.00**+0.79	-
Seed yield per plant (g)	16.09+0.11	3.00**+0.16	4.72**+0.59	-0.94+0.54	2.99**+0.18	10.99**+0.90	-2.03**+0.37	-8.02**+0.27	-9.11**0.62	0.47+0.27	C
1000-grain weight (g)	3.90+0.06	-0.23**+0.06	-0.80*+0.27	-1.27**+0.26	-0.30**+0.07	4.01**+0.38	-1.68**+0.15	-1.07**+0.10	-1.48**+0.28	0.63**+0.13	D
Oil content (%)	45.33+0.03	0.66**+0.09	-0.77**+0.24	-1.95**+0.22	0.69**+0.11	2.22**+0.44	0.55**+0.11	-0.82**+0.22	1.68**+0.23	0.97**+0.12	D

*, ** Significant at 5% and 1% level of probability, respectively; C = Complementary epistasis and D = Duplicate epistasis, m= mean, *d* = additive, *h* = dominance, *i*= additive x additive, j = additive x dominance, *l* = dominance x dominance.

Table 6: The estimates of joint scaling test and Chi-square values for seed yield and its components

Characters	χ^2 values		
	Jagrati × YST-151	NDYS 427 × YST-151	Pusa Gold × Jagrati
Days to 50% flowering	242.91**	193.96**	193.66**
Days to maturity	30.54**	2.12	111.42**
Plant height (cm)	670.46**	413.32**	2048.80**
Length of fruiting zone (cm)	242.65**	2424.23**	1014.82**
Primary branches / plant	284.60**	24.90**	195.89**
Siliquae/plant	176.23**	99.06**	55.97**
Siliqua length (cm)	354.11**	52.25**	243.95**
Seed yield/plant (g)	388.02**	1162.35**	983.92**
1000-seed weight (g)	172.94**	105.49**	183.56**
Oil content (%)	568.28**	1793.21**	105.93**

*, ** Significant at 5% and 1% level of significance, respectively

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