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Gene Effects for Seed Yield and Yield Contributing Traits in Indian Mustard [*Brassica juncea* (L.) Czern & Coss.]

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ABSTRACT

Indian mustard (*Brassica juncea*) is an important *rabi* oilseed crop which has a distinctive role in human diet as well as in the economy of the country, however, the productivity of mustard is limited. This experiment was conducted to understand the gene effects governing various quantitative and qualitative traits utilizing generation mean analysis. Six generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) of four crosses each were evaluated to extract the information on gene effects. The results revealed that not a single model is adequate to explain the inheritance of traits rather traits are under the control of both fixable and non-fixable gene effects which are coupled with duplicate type of epistasis.

Keywords Scaling test, Gene effects, Additive, Dominance, Epistatsis.

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INTRODUCTION

Oilseed Brassica is the world's second-largest edible oil crop. In India, it is the most important oilseed crop contributing 35% production to primary sources and almost one-fourth to total domestic edible oil production (DAC and FW 2019). Of all the mustard varieties, *Brassica juncea* is the most important oilseed crop in India and it alone accounts for about 90% of the total area under Oilseed Brassica cultivation in India because of its high yield and oil content. Over the years, the total consumption of edible oil in the country has tremendously increased making Indiathe world's largest importer of edible oil. In order to meet the growing demand of the population, the production of oilseed crops needs to be increased. This can only be achieved through increasing the yield potential of newly developed varieties.

Seed yield is an important economic trait which results from the multiplicative interaction of component characters. For breeding high-yielding plant varieties, the selection of desirable parents is one of the most problematic tasks. To develop the high yielding cultivars, the selection of parents is one of the most important criterions but at the same time information regarding the effects of gene controlling the traits cannot be ignored. In most of the plant breeding experiments to determine the performance of parents and crosses scientists advocated the suitability of different mating designs viz., Diallel and Line × Tester. Information generated by these design

is incomplete and insufficient to explain the role of different gene effects as these designs do not partition genetic variance into its probable components i.e., additive, dominance and all types of epistasis. Generation mean analysis, developed by Hayman (1958) gives extensive information regarding all type of gene action along with the type of epistasis working in the family. The 'joint scaling test' proposed by Cavalli (1952) was applied to estimate the parameters of different models from means obtained from all the available generations. Considering all the above aspects the present investigation was conducted to determine the estimates of different gene actions operative for seed yield and also to detect the type of epistatsis present in different families for seed yield and component traits.

MATERIALS AND METHODS

Experimental material

The present investigation was carried out at Oilseed Breeding Block of Norman E. Borlaug Crop Research Center for field experiment and laboratory investigation was carried out in the Oilseeds Quality Laboratory (Genetics & Plant Breeding Dept.) of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand during *rabi* season of 2017-20. Four crosses viz; Donskaja × Varuna (Family A), PWR-13-8 × Vauna (Family B), PWR-13-8 × PRB-06-5 (Family C), and EC399301 × Vauna (Family D) and their generations (P_1, P_2, F_1, F_2, BC_1, and BC_2) were developed. In the next year (2019-20) the experimental material was evaluated in Compact Family Block Design (CFBD) with three replications. The row length for each plot was kept 3 m with inter row spacing of 30 cm and plant to plant distance of 15 cm was maintained. Observations were recorded on twelve important economic characters. For each family, the plot means for each generation were averaged over the number of replications to get the generation means.

Statistical analysis

Analysis of variance (ANOVA) was carried out for all the crosses following procedure prescribed by Singh and Chaudhary (1985) for the Compact Family Block Design to determine the significance of difference among various genotype means. The families showing significant differences among the progenies for the characters were subjected to simple scaling test (Mather, 1949, Hayman and Mather 1955) to determine the adequacy of additive dominance model for different characters 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. Adequacy of model was judged by non-significant value of $\chi 2$ and significant values of all the genetic parameters. For each character type of epistatic interaction, based on the direction of [h] and [l], was also determined according to Hayman and Mather (1955).

RESULTS AND DISCUSSION

Pooled analysis of variance (ANOVA) for various quantitative characters revealed that the progenies, within as well as between families were significantly different with respect to length of main raceme, number of siliquae on main raceme, siliqua length, number of seeds/siliqua, test weight, oil content, and glucosinolate content (Table 1).

Table 1. Pooled analysis of variance (Compact Family Block Design) of different families for various quantitative characters. *Significant at 5% probability level. **Significant at 1% probability level.

Source of variation	df	Mean sum of squares											
		PH	LMR	SMR	PB	SB	SL	S/S	SD	TW	Y/P	OC	GC
Replication	2	488.875	1.155	13.310	0.703	0.716	0.320	3.374	0.046	0.103	0.238	1.507	10.438
Families	3	1409.417	360.451**	326.534**	3.360	7.714	2.238**	22.607**	0.078	0.168**	38.702	17.953**	392.704**
Error(a)	6	720.153	34.556	13.978	0.498	1.683	0.094	1.947	0.025	0.018	5.666	1.121	26.238
Progenies	20	1267.046**	126.910**	126.187**	1.879**	10.726**	0.316**	3.214**	0.053**	0.210**	7.538**	11.505**	180.734**
Error(b)	40	178.305	24.912	9.158	0.254	1.942	0.078	0.455	0.009	0.032	1.339	0.763	18.676

Table 2. Adequacy of genetic models by χ^2 test for different characters.

Sl. No.	Chara-cters	Family A Adequate model	χ^2 value	Family B Adequate model	χ^2 value	Family C Adequate model	χ^2 value	Family D Adequate model	χ^2 value
1.	PH	AD; [m] [d] [h]	1.96^{ns}	AD; [m] [d] [h]	7.27^{ns}	AD; [m] [d] [h]	0.67^{ns}	AD; [m] [d] [h]	5.03^{ns}
2.	LMR	DI; [h] [i] [l]	7.48^{ns}	DI; [m] [h]	7.50^{ns}	DI; [h] [i] [j] [l]	0.78^{ns}	DI; [m] [d]	6.98^{ns}
3.	SMR	DI; [h] [i] [l]	5.40^{ns}	DI; [h] [i] [j] [l]	3.02^{ns}	DI; [m] [h] [i]	4.80^{ns}	DI; [m] [d] [h] [i] [l]	2.83^{ns}
4.	PB	DI; [m] [d] [j]	4.75^{ns}	DI; [m] [d] [j]	5.17^{ns}	DI; [m] [d] [j]	6.83^{ns}	DI; [m] [j]	8.96^{ns}
5.	SB	DI; [m] [d] [h] [i] [l]	0.35^{ns}	DI; [m] [h] [l]	6.41^{ns}	DI; [m] [d] [j]	7.32^{ns}	DI; [m] [h] [l]	3.15^{ns}
6.	SL	DI; [m] [d] [i] [j]	5.32^{ns}	DI; [m] [d]	2.08^{ns}	DI; [m] [d]	5.59^{ns}	DI; [m] [h] [i] [l]	3.89^{ns}
7.	SS	DI; [m] [h]	6.43^{ns}	DI; [m] [h] [j]	6.31^{ns}	DI; [m] [d] [h] [i] [j]	0.003^{ns}	DI; [m] [h]	3.28^{ns}
8.	SD	DI; [m] [d] [h]	4.21^{ns}	DI; [h] [i] [l]	7.79^{ns}	DI; [m] [h] [i] [j]	0.15^{ns}	DI; [m] [d]	5.40^{ns}
9.	TW	DI; [m] [h] [i] [j] [l]	2.65^{ns}	DI; [m] [d] [h] [i] [j] [l]	----	DI; [m] [j]	6.32^{ns}	DI; [m] [d] [h] [i] [l]	2.69^{ns}
10.	SY	DI; [m] [l]	3.82^{ns}	DI; [m] [h]	8.15^{ns}	DI; [m] [d] [j]	2.12^{ns}	DI; [d] [h] [i] [l]	3.81^{ns}
11.	OC	DI; [m] [d] [i]	6.22^{ns}	DI; [m] [h] [l]	7.71^{ns}	DI; [m] [i] [j]	6.53^{ns}	DI; [m] [d] [i] [j]	5.11^{ns}
12.	GC	DI; [m] [d] [h] [i] [l]	0.03^{ns}	DI; [m] [d] [j] [l]	3.38^{ns}	DI; [m] [d] [h] [j] [l]	0.20^{ns}	DI; [m] [h] [i] [l]	4.16^{ns}

Where, ns: non-significant χ^2 value. AD: additive dominance, DI: digenic interaction, PH: plant height, LMR: length of main raceme, SMR: siliquae on main raceme, PB: number of primary branches per plant, SB: number of secondary branches per plant, SL: siliqua length, SS: seeds per siliqua, SD: siliqua density, TW: test weight, SY: seed yield per plant, OC: oil content, GC: glucosinolate content.

Adequacy of model

The adequacies of different models are for all the families are given in Table 2. Two parameter model was found adequate for seed per siliqua and seed yield per plant in Family A; length of main raceme, siliqua length, and seed yield per plant in Family B; siliqua length and test weight in Family C; and length of main raceme, number of primary branches, seeds per siliqua, and siliqua density in Family D. Additive-dominance model with 3 parameters was found to be adequate for plant height in all the families and siliqua density in Family A. Digneic model with 3 parameters was adequate for length of main raceme, siliquae on main raceme, number of primary branches, and oil content in Family A; number of primary branches, number of secondary branches, number of seeds per siliqua, siliqua density, and oil content in Family B; siliquae on main raceme, number of primary branches, seed yield per plant, and oil content in Family C; and number of secondary branches in Family D. 6 parameter was found adequate for test weight in Family B and for the rest of the characters 4- or 5- parameter models were found adequate.

Detection of gene effects and the nature of epistasis

Significant values for all scaling tests (Table 3) indicated the presence of non-allelic interactions. Hence six parameter models were used to explain the nature of gene action and types of epistasis for the expression of characters. Significant values for almost all the simple scaling tests (Table 3) in all the families indicated the presence of non-allelic interactions. Thus, 6-parameter models were used to explain the nature of gene action and types of epistasis for the expression of characters. For different agronomic traits, additive, dominance and epistatic types of gene interaction were found in different cross which was presented in Table 4.

For plant height, all the families reported that dominance [h] effect had greater magnitude. But, the effect of [h] is not very important for breeder's point of view because its value in all the four families is positive. However, in Family C, additive [d] effect is the major contributor to the improvement of character in the desired direction (dwarfness). Involvement of additive and dominance gene effect was also observed in earlier reports (Meena *et al.* 2019, Liton *et al.* 2020). For length of main raceme, in Families A and C, dominance [h], additive x additive [i] and additive x dominance [j] gene effects played a major role in the inheritance of this character in the positive direction. The fixable as well as non-fixable gene effect was found important for the expression of length of the main raceme. For Family B, dominance [h] effect is predominant (Meena *et al*. 2015, Joshi 2015, Pathak, 2016 and Meena *et al.* 2019). In Family D, however, additive [d] gene effect was the major contributor

Table 3. The estimates of scaling tests for seed yield and component traits in Indian mustard.

Characters	Scales	Family A	Family B	Family C	Family D
Plant height	A	42.67±30.79	17.33±22.54	-7.03±12.45	19.60±9.50*
	B	10.93±17.77	25.07±12.36*	5.50±11.24	22.47±24.24
	C	52.67±75.97	-15.13±29.59	-8.40±45.76	23.27±26.79
	D	-0.47±34.81	-28.77±15.18	-3.43±23.33	-9.40±7.93
Length of main raceme	A	12.83±4.25**	16.67±7.23*	25.87±5.36**	3.80±8.37
	B	11.53±8.62	18.40±9.42	0.06±2.81	4.33±10.31
	C	-16.10±14.79*	23.27±12.81	-17.80±8.84*	-18.60±17.69
	D	-20.23±8.02	-5.90±6.73	-21.87±4.92**	-13.37±7.94
Siliqua on main raceme	A	-4.73±5.57	16.27±2.85**	-6.47±3.48	-2.53±2.45
	B	4.07±5.46	0.67±5.02	-12.60±5.62*	2.13±2.66
	C	-31.73±11.77**	-14.47±9.10	-43.47±4.96**	-20.80±5.43**
	D	-15.53±5.93**	-15.7±4.85**	-12.2±2.75**	-10.20±1.99**
Number of primary branches	A	3.80±0.81**	-0.13±0.57	-2.40±0.41**	-2.60±0.76**
	B	-1.13±0.61	1.07±0.30**	0.20±0.65	0.87±0.89
	C	2.73±1.94	3.07±1.60	-1.93±1.03	-1.13±1.70
	D	0.43±1.03	1.07±0.81	0.13±0.41	0.30+0.79
Number of secondary branches	A	2.33±2.26	3.67±1.12**	-9.53±2.01**	0.80±1.88
	B	1.00±0.61	7.17±1.73**	-0.93±2.85	5.07±2.37*
	C	-7.47±1.55**	10.17±3.60**	-3.73±4.39	7.93±4.94
	D	-5.40±1.29**	-0.33±1.77	3.37±1.74	1.03±2.52
Siliqua length	A	0.45±0.34	0.25±0.33	-0.61±0.37	1.57±0.30**
	B	-0.54±0.36	0.40±0.44	-0.59±0.44	0.77±0.47
	C	0.84±0.21**	1.15±1.21	-0.19±0.93	1.33±0.55*
	D	0.47±0.24*	0.25±0.60	0.51±0.34	-0.51±0.25*
Seeds per siliqua	A	-1.33±1.06	-1.93±0.50**	-0.93±0.72	3.53±2.15
	B	0.70±0.99	3.13±1.10**	-4.20±0.98**	1.27±1.55
	C	-2.97±2.48	-1.07±2.31	-10.13±1.25**	4.13±3.19
	D	-1.17±0.94	-1.13±1.11	-2.50±0.60**	-0.33±1.56
Siliqua density	A	0.15±0.23	-0.22±0.06**	0.02±0.02	-0.16±0.12
	B	-0.21±0.23	0.11±0.04**	0.54±0.08**	-0.07±0.15
	C	0.08±0.69	-0.03±0.13	-1.10±0.18**	0.17±0.32
	D	0.07±0.30	-0.18±0.07**	-0.29±0.09**	0.20±0.15
Test weight	A	-0.22±0.30	0.99±0.23**	-0.32±0.20	0.61±0.23**
	B	0.78±0.18**	0.22±0.23	0.43±0.26	0.25±0.26
	C	-1.49±0.37**	-0.14±0.26	-0.45±0.33	0.17±0.42
	D	-1.03±0.10**	-0.68±0.14**	-0.28±0.15	-0.34±0.08**
Seed yield per plant	A	-1.29±1.80	3.20±1.45*	-4.70±1.48**	3.91±1.60*
	B	-1.75±2.10	5.79±2.50*	5.57±3.26	1.79±1.42
	C	-2.25±3.44	5.85±3.27	0.65±4.34	-4.20±2.20
	D	0.39±1.19	-1.57±1.42	-0.11±2.60	-4.95±1.24**
Oil content	A	-1.40±1.82	-6.28±1.05**	3.89±1.43**	-2.46±0.79**
	B	0.60±1.25	-3.46±1.52*	-0.38±0.79	4.75±0.81**
	C	8.66±3.06**	-7.61±3.72*	10.09±1.05**	7.21±1.64**
	D	4.73±1.70**	1.06±1.85	3.10±0.88**	2.45±0.83**
Glucosinolate content	A	2.23±2.57	0.60±4.93	-2.81±7.80	13.40±2.95**
	B	2.87±3.67	23.93±5.69**	-37.98±7.55**	0.24±7.20
	C	70.66±5.45**	8.95±10.50	-36.59±16.35*	0.94±6.29
	D	32.78±1.66**	-7.79±5.22	2.10±4.67	-6.35±2.63*

*Significant at 5%probability level. **Significant at 1%probability level.

towards the inheritance of trait, albeit in negative direction. Inheritance of number of siliquae on main raceme was controlled by main effects and epistatic effects in Families A, B, C, and D. In Family A, C, and D, the significant role in positive direction was from dominance [h] and additive x additive [i] effects

Table 4. Estimates of genetic parameter under the adequate genetic model with respective value and type of epistasis.

Character	Family	m	d	h	i	j	l	χ^2	Epistasis
PH	A	159.20±7.10**	26.32±7.0*	40.12±12.45*				1.96	--
	B	143.43±3.75**	11.22±3.65*	63.42±7.56**				7.27	--
	C	163.64±3.15**	-10.12±3.09*	40.62±5.30**				0.67	--
	D	172.86±4.86**	13.22±4.45*	42.47±8.43**				5.03	--
LMR	A			90.32±4.96**	32.88±1.60**		-47.72±6.31**	7.48	Duplicate
	B	37.59±0.91**		13.37±2.99**				7.50	
	C			120.64±4.58**	42.66±1.46**	22.96±4.79**	-68.50±4.59**	0.78	Duplicate
	D	39.57±1.14**	-5.84±1.35**					6.98	
SMR	A			62.51±6.06**	17.90±0.90**		-16.11±7.78	5.40	Duplicate
	B			62.35±4.35**	23.03±1.50**	12.61±4.32*	-36.35±4.47**	3.02	Duplicate
	C	11.01±1.87**		35.03±3.42**	19.67±2.00**			4.80	--
	D	8.74±4.14	-2.79±0.65**	40.46±9.49**	20.49±3.99*		-19.46±6.25*	2.83	Duplicate
PB	A	5.49±0.06**	0.69±0.26			3.66±0.95**		4.76	--
	B	4.92±0.07**	0.63±0.14*			-1.61±0.49*		5.17	--
	C	5.20±0.08**	-0.41±0.13*			-2.94±0.41**		6.83	--
	D	5.87+0.12**				-1.46±0.51*		8.97	--
SB	A	-3.63±1.52	-0.60±0.09**	26.96±3.58**	9.57±1.52**		-11.66±2.26**	0.35	Duplicate
	B	6.08±0.28**		13.27±1.28**			-10.82±1.71**	6.41	Duplicate
	C	9.46±0.29**	1.12±0.32*			-11.4±0.29**		7.32	--
	D	8.11±0.47**		5.83±2.36*			-5.00±2.54	3.15	Duplicate
SL	A	4.10±0.01**	-0.41±0.06**		-0.28±0.06**	0.95±0.49		5.32	--
	B	3.82±0.07**	-0.58±0.11**					2.08	--
	C	4.39±0.04**	-0.39±0.08**					5.59	--
	D	2.22±0.51**		5.21±1.35**	1.03±0.50		-3.95±0.87**	3.89	Duplicate
SS	A	9.46±0.20**		2.62±0.46**				6.43	--
	B	11.12±0.21**		0.66±0.35		-3.23±0.70**		6.31	--
	C	8.67±0.60**	-1.27±0.11**	4.91±1.01**	5.06±0.61**	3.24±0.90*		0.003	--
	D	9.74±0.32**		1.37±0.80				3.29	--
SD	A	0.62±0.06**	0.17±0.03**	0.28±0.09*				4.21	--
	B			1.47±0.05**	0.56±0.01**		-0.84±0.05**	7.79	Duplicate
	C	-0.23±0.05**		0.51±0.05**	0.55±0.05**	0.58±0.05**		0.15	--
	D	0.68±0.02**	0.10±0.03*					5.40	--
TW	A	0.52±0.22		4.38±0.65**	2.06±0.20**	-1.38±0.18*	-2.43±0.49**	2.65	Duplicate
	B	1.04±0.29*	-0.27±0.01	3.84±0.83**	1.35±0.27**	0.77±0.31*	-2.56±0.55**	--	Duplicate
	C	2.56±0.03**				-0.80±0.23*		6.32	--
	D	1.57±0.18**	-0.36±0.05**	2.31±0.55**	0.68±0.16**		-1.67±0.51*	2.69	Duplicate
SY	A	4.36±0.31**					5.30±1.24**	3.82	--
	B	4.63±0.41**		3.69±0.90**				8.15	--
	C	8.89±0.34**	1.94±0.47**			-9.68±2.54**		0.21	--
	D		0.98±0.28*	17.16±1.40**	5.51±2.80**		-8.64±1.81**	3.81	Duplicate
OC	A	43.35±0.20**	2.67±0.47**		-4.58±0.55**			6.22	--
	B	41.65±0.39**		-10.79±1.38**			12.84±1.40**	7.71	--
	C	41.18±0.16**			-3.86±0.20**	4.46±1.25*		6.53	--
	D	42.48±0.17**	1.23±0.33*		-1.98±0.38**	-7.21±1.08**		5.11	--
GC	A	163.73±3.49**	-3.60±0.85**	-137.20±8.95**	-65.55±3.31**		60.80±6.60**	0.03	Duplicate
	B	102.07±1.34**	6.20±2.40			-21.46±7.19*	-12.86±2.15**	3.38	--
	C	110.54±1.10**	-7.60±1.10**	-56.04±8.52**		35.5±4.60**	39.97±14.51	0.20	Duplicate
	D	68.16±3.28**		57.63±9.04**	13.82±2.14**		-35.12±5.96**	4.16	Duplicate

Where *, ** significant at 5% and 1% level of significance respectively.

only. In Family B, in addition to [h] and [i], additive x dominance [j] effect also played a major role in controlling the trait. The results that [h] have major contribution to the inheritance of the trait was akin to the results concluded by Philanim *et al*. (2019), Meena *et al.* (2015), Pathak (2016), and Meena *et al.* (2019). For number of primary branches per plant, additive [i] and additive x dominance [j] effects played

a major role in controlling the trait. Pathak (2016) reported that the primary branches per plant was governed by additive and non-additive gene effects. Genetic control of number of secondary branches per plant was predominantly under dominance [h] effect for Families A, B, and D and this observation was similar to findings obtained by Liton *et al.* (2020). However, for Family C, additive [d] effect was found to be important. Joshi (2015), Meena *et al.* (2015), Pathak (2016), Manjunath *et al*. (2017), Raliya et al. (2018), Maurya *et al.* (2018), Meena *et al.* (2019), Tiwari (2019), and Kumar et al. (2020) also came to the same conclusion for this trait. The inheritance of siliqua length, was controlled by dominance [h] and additive x additive [i] effect in Family D. Meena *et al.* (2015), Pathak (2016), Meena *et al*. (2019), Liton *et al.* (2020) and Abdelsatar *et al.* (2021) also reported the importance of dominance effect in the inheritance of this trait. In Family A, additive x dominance [j] had positive contribution to the inheritance of the trait. However, in Families B and C, additive [d] effect was found to be as the major contributor to the trait but this effect was not important form breeder's point of view. Genetic control of number of seeds/siliqua was majorly under dominance [h] effect in Families A, B, and D this was also reported by Meena *et al*. 2019. In Family C, additive x additive [i] interaction was the major contributor and this was also confirmed by Joshi (2015) and Prajapati *et al.* (2014). For siliqua density, additive and non-additive effects were found to be important in improvement of the character in Families A, B, and C. This was reported by Philanim *et al.* (2019). However, in Family A, only additive [d] effect was found to be important. The inheritance of test weight was controlled by dominance [h] and additive x additive [i] effects in positive direction in Families A and D along with additive x dominance [j] gene interaction in Family B with [h] being the highest contributor to the trait in all the three families. Pathak (2016), and Philanim *et al.* (2019) also reported the importance of importance of dominance [h] effect for this trait. For inheritance of seed yield / plant dominance x dominance [l] gene interaction played a significant role in Family A and this result was similar to the results of Pathak (2016), and Meena *et al*. (2019). Philanim *et al.* (2019) reported the importance of additive [d] effect for this trait and this was also observed in Family C in our case. In Families B and D, however, dominance [h] effect is the most important and this was also reported Yadav *et al.* (2012), Meena *et al.* (2015), Meena *et al.* (2019), and Liton *et al.* (2020). Genetic control of oil content was mainly under the control of additive [d] gene effect for Families A and D which was in agreement with the findings of Yadav *et al.* (2012), Pathak (2016), Manjunath *et al*. (2017), Meena *et al.* (2019). However, for Family B and C, dominance x dominance [l] and additive x dominance [j] effect was found important. For glucosinolate content, both additive and non-additive gene effects were found to be important and this aligned with the findings of Pathak (2016). The highest contribution to the trait in the positive direction i.e., low glucosinolate content was from dominance [h] effect in Families A and C and from dominance × dominance [l] effect in Families B and D.

The result of A B C and D scaling test revealed that significant estimates of theses scale confirmed the presence of non allelic gene interaction working in expression of traits under study. Further the estimates of scaling test also suggested that only additive-dominance model will not be sufficient to explain the genetics of trait and also showed the preponderance of inter- allelic interactions. The mean parameter [m] for all, studied attributes indicated that the contribution due to the overall mean plus the locus effects and interaction of the fixed loci was significant. Significant additive gene action found for Length of main raceme in family D, Siliqua length in family B and C, Siliqua density in family D, was an indicative of potentiality of improving the performance of these character using the pedigree selection program on the other hand, the significance of dominance gene action [h] for rest of the traits suggested exploitation of heterosis breeding, line selection/family selection. Recurrent selection can be one of most important approaches through which desired improvement can be achieved. The significance of both [d] and [h] in the inheritance of Plant height, Secondary branches, test weight and glucosinloate content revealed that the both types of additive and dominance effects are involved in genetics of above trait. In case [d], [h] both are significant reciprocal recurrent selection is more effective. If [d]>[h]family selection with occasional intermating of in subsequent generations.

This will help in accumulating the favorable alleles/ chromosome blocks of favorable gene in superior line. The epistatic model was fitted for most of the characters involving additive, dominance and additive ×additive, dominance× dominance and additive ×dominance gene effects. It is therefore suggested that selection should be carried out in late generations and the interactions should be fixed by selection under selfing condition. The epistatic effects were also coupled with duplicate type epistasis. Due to presence of duplicate epistasis the variation increases between generations and in the segregating population so transgressive segregants can be obtained with high frequency. Importance of duplicate epistasis was also narrated by Abdelsatar *et al.* (2021) in Indian mustard for inheritance of seed yield traits.

CONCLUSION

The present study showed the importance of additive, dominance, and epistatic gene effects in the inheritance of yield and yield-related traits in *Brassica juncea.* The overall results proved that most of the characters in all the four families were under the control of both fixable, i.e., additive and additive × additive epistasis, and non-fixable, i.e., dominance, additive × dominance, and dominance × dominance, gene effects coupled with duplicate type of epistasis. Not a single model is sufficient to explain the inheritance of characters. Adequacy of model showed that there was involvement of different gene effects but the choice of breeding strategy will depend on estimates of gene effects. In general, the traits which are governed by fixable effects could be improved through pedigree selection method. Heterosis breeding would be most effective for traits controlled by non-additive gene action, i.e. dominance or epistasis; however, mode of crop reproduction and lack of a workable CGMS system would limit it; therefore, selection in later generations would be remunerative as time dominance could be reduced by selfing and/or inbreeding (Prajapati *et al.* 2014). For the traits which are governed by both additive and non-additive gene effects, population improvement through biparental mating and cyclic selection (such as reciprocal recurrent selection) would be most effective to stabilize the additive genes. Therefore, breeding strategies should be designed accordingly to get the desired results.

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