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RESEARCH ARTICLE

Estimate the general and specific combining ability effects of yield components in Indian mustard {*Brassica juncea* (L.) Czern&Coss}

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ABSTRACT

Indian mustard (Brassica junceaL.)is the second most important group of oilseed crop in India after groundnut sharing 27.8% in the India's oilseed economy. Indian mustard originated through natural crossing between B. nigra and B. campestris and contributed more than 80% to the total rapeseedmustard production in the country. In order to break yield plateau, it is very important to study the genetic architecture of available material through the use of biometrical techniques, therefore, the present study was undertaken with the objectives to find out the nature and magnitude of gene action and to suggest an appropriate breeding methodology for further improvement in this crop.Diallel analysis was used to study the GCA and SCA effects using Method 2 Model I of [9]. The analysis of variance for combining ability indicated highly significant GCA and SCA variances for all the traits except seed weight per siliqua. RSPR-01 was found to be the best general combiner for days to reproductive phase, RSPR-03 for days to bloom, PM-21 for secondary branches per plant, PM-22 for pod intensity and plant height, PM-24 for harvest index, Varuna for primary branches per plant and seed yield per plant and Pusa-Karishma for seeds per sliqua, pod length and 1000 seed weight. The best crosses with high estimates of SCA were PM-21× PM-24, PM-21× PM-22, PM-24 × Pusa-Karishma and RSPR-01× Pusa-Karishma for secondary branches per plant, pod intensity, seed yield per plant and harvest index, respectively. The ratio of $\sigma_{2aca}^2/\sigma_{2sca}^2$ was smaller than unity for all the traits indicated the preponderance of dominance gene action. The degree of dominance was more than unity forall traits except days to bloom andplant height. The present investigation has demonstrated that immediate improvement in Brassica juncea(L)can be achieved through the exploitation of both the additive and nonadditive gene effects simultaneously.

Keywords: Brassica juncea, general combining ability, specific combining ability, additive, dominant

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INTRODUCTION

Rapeseed-mustard belongs to genus *Brassica* and family Brassicaceae. *Brassica* is economically most important genus consisting of oilseeds, vegetables and forage crops. *Brassica juncea*, L.commonly known as Indian mustard, is the second most important oilseed crops of India next to groundnut, sharing 27.8per cent in the India's oilseed economy [1]. Cytologically, Indian mustard is an amphidiploid (2n=36), derived from interspecific cross of *Brassica campestris*, L.(2n=20) and *Brassica nigra*, L. (2n=16) followed by natural chromosome doubling. These relationships have been confirmed by the artificial synthesis of amphidiploids species by hybridizing basic diploid species and also by analysis

of chloroplast and mitochondrial DNA restriction pattern of basic and amphidiploid species [23].

The crop along with rapeseed account for 22.7 per cent of the oilseed production and 19.2 per cent of the total cropped area in the country. At global level, it accounts for 23.5 per cent and 13.2 per cent of the total hectares and production respectively. There has been remarkable increase in the production, which was hovering around 2.68 m ton with productivity level of 650kg/ha until 1985-86 increased to 7.9 m ton in 2007-2008 while productivity increased to more than 1001kg/ha [8]. The mustard is predominantly self pollinated crop but to the extent of 5-18 % cross pollination occurs [17].The area, production and productivity of Indian mustard in India is 5.74 mha, 6.79 mt and 1.18 t ha⁻¹, respectively during 2015-16 [4].

The selection of available germplasm at Sher-e-Kashmir University of Agricultural Sciences and Technology led to the development of two varieties of *Brassica juncea*, L.namely; RSPR-01 and RSPR-03[4]. Future improvement in *Brassica juncea*, L. depends upon hybridization between the parents by assessing the genetic architecture of the available material through the use of biometrical technique.

The success of breeding programme depends upon the extent of genetic variation available and the ability of the parents that enters into hybridization to yield good recombinants. Therefore, choice of the parents for the hybridization is one of the critical and most difficult tasks of the plant breeder. The common approach of choosing parents on the basis of *per se* performance does not necessarily lead to the fruitful results [3].

Diallel analysis is one of the technique which was developed by [14] and [13] as a means of obtaining useful information on the differential parental combinations through an overall genetic architecture of the parental lines in relation to the character studied. [9] using diallel cross analysis has suggested a method for the precise measurement of general and specific combining ability which is very useful technique in selecting the parents for the hybridization programmes. The available information about the genetic architecture of seed yield, its component and some quality traits in Indian mustard (*Brassica juncea*, L.) is insufficient. Therefore, this investigation was undertaken on 7×7 diallelinvolving diverse parent.

More models were developed from time to time ([7]; [15]; [13]) which can be used for further subdivision of epistatic into digenic interactions of additive × additive, additive × dominance and dominance × dominance and their order of interaction.

MATERIAL AND METHODS

The present investigation was carried out in the Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology, Jammu, during the year 2013-2016. Seven diverse genotypes of *Brassica juncea*namely;RSPR-01, RSPR-03, PM-21, PM-22, PM-24, Varuna and Pusa Karishmawere crossed to produce F₁ half diallel set of crosses during 2013-14. Twenty-one crosses along with seven parents were sown in a randomized block design with three replications. Each entry was represented by three rows of 5 meter long, 30 cm apart with plant to plant distance being 15 cm. The nonexperimental rows were grown on both sides to avoid the border effect. Normal cultural practices were followed throughout the growing season. Data were recorded on five plants at random in each block for days to bloom, days to reproductive phase, primary branches per plant, secondary branches per plant, seeds per siliqua, seed weight per siliqua, pod length, 1000 seed weight, pod intensity, plant height, yield per plant and harvest index. The combining ability analysis was carried out in F₁ and parents following Method 2, Model I of [9] for the estimation of variances and combining ability effects, as the reciprocals were not included in the study and consisted of only parents and one set of F₁'s.

RESULTS

The analysis of variance for genotypes revealed significant differences among treatments, parents and hybrids were significant for almost all the traits except seed weight per siliqua. Mean squares due to parents vs hybrids were also significant for all the traits except days to reproductive phase, primary branches per plant and pod length (Table 1a &1b).

The analysis of variance for combining ability showed highly significant differences due to GCA and SCA effects for all the traits except seed weight per siliqua (Table 2a &2b). The

mean squares for days to bloom, days to reproductive phase, primary branches per plant, secondary branches per plant, seeds per siliqua, seed weight per siliqua, pod length, 1000 seed weight, pod intensity, plant height, yield per plant andindicated that both additive and non-additive types of gene actions were present in the genetic control of the character.

Sources	d.f.	Days to	Days to	Primary	Secondary	Seeds	Seed
		bloom	reproductive	branches	branches	persiliqua	weight per
			phase	per plant	per plant		siliqua
Replications	2	4.71	9.72	0.26	3.11	0.11	628.97
Treatments	27	69.03**	36.86**	1.70**	21.12**	1.48**	766.86
Parents	6	69.63**	34.65**	1.95**	9.17**	0.38	1976.00*
Hybrids	20	70.11**	39.30**	1.69**	12.98**	1.80**	206.45
Parent vs.	1	43.92**	1.40	0.28	255.61**	1.65*	4720.28**
Hybrids							
Error	54	1.70	3.60	0.17	1.47	0.34	627.14

Table 1a: Analysis of variance for different characters in a diallel cross

*,** significant at 0.05 and 0.01 level, respectively

Table 1b: Analysis of variance for different characters in a diallel cross

Sources	d.f.	Pod	1000 seed	Pod	Plant	yield per	Harvest		
		length	weight	intensity	height	plant	index		
Replications	2	0.20	0.04	0.01	0.10	2.93	26.91		
Treatments	27	0.39**	0.73**	0.02**	83.59**	40.56**	632.89**		
Parents	6	0.66**	0.23**	0.01*	62.63**	51.62**	913.22		
Hybrids	20	0.32**	0.82**	0.03**	92.08**	15.10**	549.53**		
Parent vs.	1	0.12	1.93**	0.02*	39.52*	483.57**	617.71**		
Hybrids									
Error	54	0.09	0.03	0.00	5.85	3.22	142.25		

*,** significant at 0.05 and 0.01 level, respectively

Table 2a: Analysis of variance for combining ability for different characters in a diallel cross

Cross											
Sources	d.f.	Days to bloom	Days to reproductive phase	Primary branches per plant	Secondary branches per plant	Seeds persiliqua	Seed weight per siliqua				
GCA	6	43.18**	7.72**	0.62**	10.47**	0.54**	235.65				
SCA	21	17.25**	13.59**	0.55**	6.06**	0.48**	261.33				
Error	54	0.57	1.20	0.06	0.49	0.11	209.05				

*,** significant at 0.05 and 0.01 level, respectively

Table 2b: Analysis of variance for combining ability for different characters in a diallel cross

Sources	d.f.	Pod	1000	Pod	Plant	yield	Harvest				
		length	seed	intensity	height	per	index				
		_	weight		_	plant					
GCA	6	0.11**	0.26**	0.02**	54.48**	14.33**	372.01**				
SCA	21	0.13**	0.24**	0.00**	20.26**	13.29**	164.95**				
Error	54	0.03	0.01	0.01	1.95	1.07	47.42				

*,** significant at 0.05 and 0.01 level, respectively

Estimates of Components of Variances: The variance due to general combining ability (σ^2_{gca}) was lower than specific combining ability variance (σ^2_{sca}) for all the traits studied(Table 3). The dominance genetic variance was larger than additive genetic variance for days to bloom, days to reproductive phase, primary branches per plant, secondary branches per plant, seeds per siliqua, seed weight per siliqua, pod length, 1000 seed weight, plant height, yield per plant and harvest index. The additive variance for pod intensity and plant height are more than dominance variance. The ratio of variance of general to specific combining ability ($\sigma^2_{gca}/\sigma^2_{sca}$) was smaller than unity for all the traits. The

degree of dominance $(\sigma_D^2/\sigma_A^2)^{1/2}$ is more than unity for almost all traits except days to bloom and plant height.

Characters	σ_{gca}^2	σ_{sca}^2	$\sigma^2_{ m gca} / \sigma^2_{ m sca}$	σ_D^2	σ_{H}^{2}	$\sqrt{(\sigma_H^2/\sigma_D^2)}$
Days to bloom	4.734	16.681	0.284	9.469	16.681	0.432
Days to reproductive phase	0.725	12.391	0.058	1.450	12.391	2.428
Primary branches per plant	0.062	0.495	0.126	0.124	0.495	5.674
Secondary branches per plant	1.108	5.570	0.199	2.217	5.570	1.065
Seeds per siliqua	0.047	0.364	0.129	0.094	0.364	6.419
Seed weight per siliqua	2.956	52.279	0.056	5.912	52.280	1.223
Pod length	0.009	0.104	0.086	0.018	0.104	17.917
1000 seed weight	0.027	0.229	0.120	0.055	0.229	8.701
Pod intensity	0.002	0.003	0.591	0.004	0.003	13.694
Plant height	5.837	18.309	0.319	11.674	18.309	0.367
yield per plant	1.473	12.216	0.121	2.947	12.216	1.186
Harvest index	36.066	117.534	0.307	72.132	117.537	0.151

Table 3: Estimates of components of variances for different characters

 σ^{2}_{D} : additive genetic variance, σ^{2}_{H} : dominance genetic variance, σ^{2}_{gca} : estimate of GCA variance, σ^{2}_{sca} : estimate of SCA variance and

 $\sigma^{2}_{\rm gca}$ / $\sigma^{2}_{\rm sca}$: average degree of dominance.

Estimates of Combining Ability Analysis: The analysis of variance for combining ability for various traits has been presented in Table 4a, 4b, 5a and 5b.

Table 4a: Estimates of general combining ability effects for different characters in a diallel cross

Parents	Days to	Days to	Primary	Secondar	Seeds	Seed					
	bloom	reproductive	branches	у	persiliqu	weight					
		phase	per plant	branches	а	per					
				per plant		siliqua					
RSPR-01	-1.96**	1.41**	-0.19*	-0.79**	-0.13	-8.35					
RSPR-03	-2.32**	-0.48	0.02	0.59**	-0.12	0.51					
PM-21	-1.00**	0.86*	-0.05	1.27**	-0.38**	-0.89					
PM-22	2.49**	0.23	0.23**	-0.09	0.02	-1.40					
PM-24	3.24**	-0.03	-0.36**	0.66**	0.36**	8.61					
Varuna	0.71**	-0.73*	0.43**	0.30	0.03	-1.39					
Pusa-Karishma	-1.16**	-1.26**	-0.08	-1.96**	0.22*	2.92					
SE(gi)	0.23	0.34	0.07	0.22	0.10	0.49					
SE(gi-gj)	0.36	0.52	0.11	0.33	0.16	0.75					

*,** significant at 0.05 and 0.01 level, respectively

Table 4b: Estimates of general combining ability effects for different characters in a diallel cross

Parents	Pod	1000	Pod	Plant	yield per	Harvest					
	length	seed	intensity	height	plant	index					
	_	weight	_	_	_						
RSPR-01	-0.22 **	-0.27 **	-0.03 *	-1.92 **	0.32	7.26**					
RSPR-03	0.01	0.03	-0.01	-0.27	0.87 **	-6.37 **					
PM-21	-0.05	0.03	0.04 **	0.52	-1.14 **	-2.99					
PM-22	0.09	-0.18 **	0.06 **	-3.47 **	-0.58	0.20					
PM-24	0.07	0.15 **	0.03 *	3.28 **	-1.52 **	8.67 **					
Varuna	-0.01	0.05	-0.03 **	-1.04 *	2.18 **	1.51					
Pusa-Karishma	0.11	0.19 **	-0.06 **	2.90 **	-0.11	-8.27 **					
SE _(gi)	0.05	0.03	0.01	0.43	0.32	0.57					
SE _(gi-gj)	0.08	0.05	0.02	0.66	0.49	0.85					

*,** significant at 0.05 and 0.01 level, respectively

dialier cross											
Crosses	Days	Days to	Primary	Secondary	Seeds	Seed					
	to	reproductiv	branche	branches	persili	weight					
	bloom	e phase	s per	per plant	qua	per					
			plant			siliqua					
RSPR-01× RSPR-03	-2.39**	7.63**	0.58*	0.21	0.09	0.74					
RSPR-01× PM-21	-2.71**	-0.51	0.12	1.26	0.29	1.65					
RSPR-01× PM-22	-3.94**	1.85	-0.37	0.75	0.82*	-0.06					
RSPR-01× PM-24	3.71**	-2.30*	0.29	0.01	-1.39**	-9.75					
RSPR-01× Varuna	3.31**	0.21	-0.89**	0.36	-0.12	-0.42					
RSPR-01× Pusa-	-1.69*	0.60	0.02	0.90	-0.31	-4.57					
Karishma											
RSPR-03× PM-21	-2.55**	-2.42*	-0.22	1.35*	-0.32	9.57					
RSPR-03× PM-22	-3.91**	0.41	0.29	-0.03	0.34	4.51					
RSPR-03× PM-24	3.74**	2.13*	-0.25	0.43	-0.40	-17.31					
RSPR-03× Varuna	3.88**	4.04**	-0.37	2.59**	0.73*	-7.64					
RSPR-03× Pusa-	-0.86	-2.43*	-0.26	2.05**	-0.72*	-13.16					
Karishma											
PM-21× PM-22	6.63**	-0.86	-0.63**	0.22	-0.73*	-6.27					
PM-21× PM-24	5.09**	-3.28**	-0.51*	3.55**	-0.60	-17.23					
PM-21× Varuna	-3.25**	-4.17**	-0.76**	2.77**	-0.27	10.70					
PM-21× Pusa-Karishma	0.15	6.23**	0.82**	0.31	0.41	11.10					
PM-22× PM-24	-6.07**	1.49	-0.20	-0.03	1.06**	-17.45					
PM-22× Varuna	0.33	1.73	0.82**	1.13	-1.41**	-1.03					
PM-22× Pusa-Karishma	3.60**	-4.41**	0.20	2.66**	-0.33	-10.82					
PM-24× Varuna	-0.95	-2.42*	-0.32	0.72	0.25	-16.71					
PM-24× Pusa-Karishma	-9.09**	-4.29**	0.32	2.45**	0.86**	-18.80					
Varuna× Pusa-	-1.82*	-0.78	2.00**	-2.52**	0.06	12.061					
Karishma											
SE _(sij)	0.68	0.98	0.22	0.63	0.30	1.44					
SE(Sij—Sik)	1.00	1.46	0.32	0.93	0.45	2.13					
SE(sij—skl)	0.94	1.37	0.30	0.87	0.42	2.00					

Table 5a: Estimates of specific combining ability effects for different characters in diallel cross

*,** significant at 0.05 and 0.01 level, respectively

Table 5b: Estimates of specific combining ability effects for different characters in diallel cross

ulanci cioss										
Crosses	Pod	1000	Pod	Plant	yield	Harvest				
	length	seed	intensit	height	per	index				
		weight	у		plant					
RSPR-01× RSPR-03	-0.18	0.15	0.04	-5.45**	0.78	4.00				
RSPR-01× PM-21	0.28	0.76**	-0.06	-2.18	2.53*	-5.58				
RSPR-01× PM-22	-0.23	0.06	0.04	-6.65**	0.87	5.97				
RSPR-01× PM-24	0.18	-1.12**	0.06	9.60**	1.58	-3.77				
RSPR-01× Varuna	0.40*	-0.33**	0.06	2.58	-1.23	-2.87				
RSPR-01× Pusa-	0.14	-0.05	-0.08*	1.71	1.84	20.70 **				
Karishma										
RSPR-03× PM-21	-0.19	-0.38**	-0.09*	-5.42**	1.14	-17.89				
						**				
RSPR-03× PM-22	0.00	-0.17	-0.01	0.44	1.03	4.15				
RSPR-03× PM-24	0.36*	0.62**	-0.04	-1.58	0.50	8.20				
RSPR-03× Varuna	0.91**	0.12	0.06	4.00**	0.90	6.29				
RSPR-03× Pusa-	-0.08	-0.38**	0.06	4.99**	2.20*	21.33 **				
Karishma										
PM-21× PM-22	0.14	0.57**	0.12**	-4.75**	2.68**	11.28				
PM-21× PM-24	0.09	0.21*	0.06	2.23	-4.04**	8.35				
PM-21× Varuna	-0.51**	-0.09	0.08*	-0.06	2.09*	-9.64				
PM-21× Pusa-Karishma	0.02	0.26**	0.04	-4.33**	4.79**	-15.18*				
PM-22× PM-24	-0.68**	0.19	0.07*	1.82	4.65**	-0.71				

PM-22× Varuna	-0.13	-0.09	-0.09*	-1.40	-0.58	4.52
PM-22× Pusa-Karishma	-0.15	0.05	-0.05	4.46**	4.02**	10.16
PM-24× Varuna	0.03	0.53**	-0.04	-4.28**	2.92**	2.05
PM-24× Pusa-Karishma	0.06	0.58**	-0.03	-2.35	2.79**	0.90
Varuna× Pusa-	0.03	0.36**	0.00	-1.71	-2.38*	-19.38
Karishma						**
SE _(sij)	0.16	0.09	0.03	1.25	0.93	1.62
SE(Sij—Sik)	0.23	0.14	0.05	1.86	1.38	2.40
SE(sij—skl)	0.22	0.13	0.05	1.74	1.29	2.25

*,** significant at 0.05 and 0.01 level, respectively

Days to bloom: Parents namely RSPR-01, RSPR-03, PM-21 and Pusa-Karishma showed negative and significant GCA effect. The cross combination*viz.*, RSPR-01 × RSPR-03, RSPR-01 × PM-21, RSPR-01 × PM-22, RSPR-01 × Pusa-Karishma, RSPR-03 × PM-21, RSPR-03 × PM-22, PM-21 × Varuna, PM-22 × PM-24, PM-24 × Pusa-Karishma followed by Varuna × Pusa-Karishma showed negative and significant SCA effects. RSPR-01 × RSPR-03, RSPR-01 × PM-21, RSPR-01 × Pusa-Karishma, RSPR-03 × PM-21, RSPR-03, RSPR-01 × PM-21, RSPR-01 × Pusa-Karishma, RSPR-03 × PM-21, showed desired SCA, involving both the best general combiner parents for days to bloom.

Days to reproductive phase: Two genotypes RSPR-01 and PM-21 showed positive and significant GCA effects.Estimates for specific combining ability indicated that four crosses exhibited positive SCA effects viz., RSPR-01 × RSPR-03, RSPR-03 × PM-24, RSPR-03 × Varuna and PM-21 × Pusa-Karishma, showed desired SCA effect.

Primary branches per plant: The positive general combining ability values for number of primary branches is desirable for increasing seed yield. PM-22 and Varuna were the two genotypes showed positive and significant GCA effects for primary branches per plant. SCA estimates revealed that combinations viz., , PM-24 × Varuna and Varuna × Pusa-Karishmashowed highly significant positive SCA involving at least one of the best general combiner parents (Varuna) for number of primary branches per plant whereas, RSPR-01 × RSPR-03 and PM-21 × Pusa-Karishma, also showed SCA effects but involved poor general combiners.

Secondary branches per plant: Parents namely RSPR-03, PM-21 and PM-24exhibited positive and significant general combining ability effects. Specific combining ability effects were positive and significant in seven crosses combinations. Positive and significant SCA effects were recorded for crosses combinations namely RSPR-03 × PM-21, RSPR-03 × Varuna, RSPR-03 × Pusa- Karishma, PM-21 × PM-24, PM-21 × Varuna, PM-22 × Pusa-Karishma followed by PM-24 × Pusa- Karishma. However, one cross combination viz., Varuna × Pusa- Karishma showed negative and significant SCA effects.

Seeds per siliqua: Two parents namely, PM-24 and Pusa- Karishma were showed positive and significant for general combining ability effects. Two crosses combinations*viz.*, RSPR-01 x PM-22 and PM-22 x PM-24 showed highly significant positive SCA, involving at least one of the best general combiner parent PM-24 for seeds per siliqua. PM-24 x Pusa-Karishma also showed SCA effects involving both the best general combiners parents whileRSPR-03 x Varuna showed SCA effects but involving both the poor general combiners.

Seed weight per siliqua: Both parents and crosses showed non-significant GCA and SCA effects respectively.

Pod length: Parent RSPR-01 recorded negative and significant general combining ability effects. Positive and significant SCA effects were recorded in three cross combinations *viz.*, RSPR-01 x Varuna, RSPR-03 x PM-24 and RSPR-03 x Varuna. Out of three crosses, the cross RSPR-01 x Varuna involved atleast one of the good combiner.

1000 seed weight: Two parents *viz.*, PM-24 and Pusa-Karishma exhibited highly significant general combining ability effects for 1000-seed weight. Estimates for specific combining ability indicated that eight crosses exhibited positive SCA effects while rest of the crosses either showed negative or non-significant SCA effects. Out of eight crosses, PM-24 x Pusa-Karishma involved both the good combiners and the five crosses *viz.*, RSPR-03 x PM-24, PM-21 x PM-24, PM-21 x Pusa-Karishma, PM-24 x Varuna and Varuna x Pusa-Karishma involved atleast one of the good combiners (PM-24 or Pusa-Karishma). Whereas, RSPR-01 x PM-21 and PM-21 x PM-22 involving both the poor combiners.

Pod intensity: The result of estimates for GCA revealed that three parents viz., PM-21, PM-22 and PM-24 exhibited highly significant general combining ability effects. Three cross combinations namely PM-21 x PM-22, PM-21 x Varuna and PM-22 x PM-24 exhibited positive SCA effects for pod intensity while rest of the crosses either showed negative or non-significant SCA effects. Out of these three crosses, two cross combinations viz., PM-21 x PM-22 and PM-22 x PM-24 involved both the good combiners. Whereas, PM-21 x Varuna involved atleast one (PM-21) of the good combiners.

Plant height: The general combining ability effects were positive and significant for parents PM-24 and Pusa-Karishma while RSPR-01, PM-22 and Varuna showed negative and significant and were detected as good general combiners for reducing plant height. Specific combining ability effects were observed significant and positive in 4 crosses namely RSPR-01 x PM-24, RSPR-03 x Varuna, RSPR-03 x Pusa- Karishma and PM-22 x Pusa-Karishma. However, six cross combinations exhibited negative and highly significant for plant height. Out of six cross combinations, RSPR-01 x PM-22, RSPR-01 x RSPR-03, PM-21 x PM-22, followed by PM-24 x Varuna involved atleast one of the good combiners. RSPR-03 x PM-21 and PM-21 x Pusa-Karishma involved both the poor combiners.

Yield per plant: ParentsRSPR-03 and Varuna showed positive and highly significant general combining ability effects. Nine cross combinations namely RSPR-01 x PM-21, RSPR-03 x Pusa-Karishma, PM-21 x PM-22, PM-21 x Varuna, PM-21 x Pusa-Karishma, PM-22 x PM-24, PM-22 x Pusa-Karishma, PM-24 x Varuna and PM-21 x Pusa-Karishma exhibited positive SCA effects for yield per plant. Out of these nine cross combinations, RSPR-03 x Pusa-Karishma, PM-21 x Varuna and PM-24 x Varuna involved atleast one (RSPR-03 or Varuna) of the good combiners. However, the remaining cross combinations involved both the poor combiners.

Harvest index: Two parents viz., RSPR-01 and PM-24 showed positive general combining ability effects for harvest index. Specific combining ability effects were observed significant and positive in two crosses namely RSPR-01 x Pusa-Karishma and RSPR-03 x Pusa-Karishma. Out of these two cross combinations, RSPR-01 x Pusa-Karishma involved atleast one (RSPR-01) of the good combiners while the remaining one involved both the poor combiners. However, the other cross combinations indicated negative and non-significant for SCA effects.

DISCUSSION

Brassica junce, L. is a predominantly self pollinated crop and the combining ability analysis in such crops has been frequently used to test the performance of parents in hybrid combinations and to determine the nature and magnitude of gene effects involved in the expression of the quantitative traits. The main objective of this analysis was to identify the best parent and the best cross on the basis of general and specific combining ability effects, respectively. The combining ability analysis clearly demonstrated the importance of both additive and dominance gene effects in the inheritance of all the traits under study except seed weight per siliqua. Similar results have been reported by [22]; [11]; [22]; [6]; [18]; [20]; [25]; [21]; [19] and [2]. The ratio of $\sigma_{\rm gca}^2/\sigma_{\rm sca}^2$ indicated the predominance of dominance component for most of the traits. The specific combining ability variances were nonsignificant for seed weight per siliqua thereby indicating the absence of dominance gene effects. In this situation, the additive component represents the true estimate of additive genetic variation. Therefore, this component can be exploited for the development of purelines. The estimates of general and specific combining ability effects enable the breeder to isolate good combining parents to be used in the breeding programme for the development of high yielding varieties in Indian mustard. The association between per se performance of parents and GCA effects have also been reported. The parent Varuna was found to be best for seeds per plant and primary branches per plant on the basis of both per se performance and GCA. For harvest index PM-24 was best, PM-22 was best for pod intensity and plant height. It was also observed that the best performing parent on the basis of GCA effects is in general involved in producing the crosses with superior SCA effects viz., PM-21 × PM-22, PM-21 × Pusa-Karishma, PM-22 × PM-24, PM-22 × Pusa-Karishma, PM-24 × Varuna, PM-24 × Pusa-Karishma for seed yield per plant. From this it becomes clear that the ranking of the parents on the basis of GCA and SCA effects is fairly good. It was also foundthat none of the parents was good combiner for all the traits. The

parent RSPR-01 was good combiner for seed yield per plant, harvest index, days to bloom, days to reproductive phase whereas the parent Pusa-Karishma was poor combiner for days to reproductive phase, primary branches per plant, secondary branches per plant, pod intensity, plant height, seed yield per plant and harvest index. The parent PM-24 is good combiner for most of the traits followed by PM-22. The parents which are good combiner for most of the traits can be exploited in hybridization with parents which are good combiners for those traits for which former are lacking. Because of high additive gene effects, such combinations are likely to throw transgressive segregates which can be identified and fixed.The best crosses for seeds per plant based on SCA effects were RSPR-01 ×RSPR-03, RSPR-01 ×PM-21, RSPR-01 ×PM-22, RSPR-01 ×Pusa-Karishma, RSPR-03 ×PM-21, RSPR-03 ×Pusa-Karishma, PM-21 ×PM-22, PM-21 ×Pusa-Karishma, PM-22 ×PM-24, PM-22 ×Varuna, PM-22 × Pusa-Karishma and PM-24 × Pusa-Karishma. Most of the crosses which exhibited good specific combining ability effects involved at least one parent as a good combiner. However, some of the crosses which exhibited high SCA effects had both or one of the parents with average combining ability. The superiority of average × average or average × low combination may be due to the presence of genetic diversity among the parents or there could be some complementation indicating the presence of non-additive gene effects. The variance due to GCA and SCA are estimated to assess the contribution of additive and nonadditive gene action involved in the inheritance of the traits. In most of the traits, the variances due to GCA were less than the unity which indicated the presence of dominance gene action. Similar results have also been reported by [16];[25] and [10]. Thus, both additive and non-additive gene actions were controlling the yield, yield contributing and quality traits.

CONCLUSION

The combining ability analysis was conducted to identify the best parent and the best cross for different traits. The ratio of $\sigma_{\text{gca}}^2 / \sigma_{\text{sca}}^2$ indicated the predominance of dominant component for all the traits. The genetic component analysis revealed that dominant component (H) was important in genetic manifestation of all the traits. In *Brassica juncea*, L. the additive gene effects can be effectively utilized by any conventional plant breeding program which involves hybridization. It mainly involves crossing of two or more diverse types and then selecting in the segregating generations to fix the additive genetic variance along with additive x additive (i) type of interaction. Biparental approach can also be useful in this crop. The advantage of this procedure is to captalize, both additive and non-additive variances simultaneously for effective improvement in the population.

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