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#### Hari Ram

M.Sc. Research Scholar, Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur, Rajasthan, India

#### Hemlata Sharma

Associate Professor, Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur, Rajasthan, India

#### Amit Dadheech

Assistant Professor, Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur, Rajasthan, India

#### **DP** Singh

Assistant Professor, Department of Soil Science and Agriculture Chemistry, RCA, MPUAT, Udaipur, Rajasthan, India

#### MK Mahla

Professor, Department of Entomology, RCA, MPUAT, Udaipur, Rajasthan, India

#### Deepak Meena

Ph.D. Research Scholar, Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur, Rajasthan, India

Corresponding Author: Hari Ram M.Sc. Research Scholar, Department of Genetics and Plant Breeding, RCA, MPUAT, Udaipur, Rajasthan, India

## Studies on combining ability for yield and yield contributing traits in Indian mustard (*Brassica juncea* L.)

### Hari Ram, Hemlata Sharma, Amit Dadheech, DP Singh, MK Mahla and Deepak Meena

#### Abstract

The present study was carried out on 37 genotypes of Indian mustard, including 24  $F_{1s}$ , 11 parents, and 2 checks. Design used for this experiment was Line x Tester mating design and evaluated in Rabi 2022–2023 at the Instructional Farm at the Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur. According to the findings, general combining ability contributed more to the total mean squares for all traits than did specialised combining ability, indicating that additive gene activity was more important in the inheritance of these traits. The results of the analysis of variance showed that all of the traits had significant mean squares due to genotypes, parents, crosses, and parents v/s crosses, with the exception of the length of the main branch and the oil content due to parents, the length of the main branch due to crosses, and the length of the siliqua due to parents v/s crosses. Both additive and non-additive gene action were involved in the inheritance of the majority of the characteristics, as shown by the significance of General combining ability mean squares for lines and testers and Specific combining ability mean squares.

Keywords: Check, combining ability, gene action, heterosis, hybrids, line, tester

#### Introduction

One of the earliest plant groups to have been cultivated by humans is the rapeseed-mustard family of crops. Rapeseed and mustard are both members of the family Brassicaceae (Cruciferae) and the genus Brassica, both of which are widely cultivated in India. Brassica campestris (2n=20) and Brassica nigra (2n=16) were naturally crossed to create Indian mustard, a naturally occurring amphidiploid (2n=4x=36) (Nagaheru U, 1935)<sup>[4]</sup>. Its origins are in Asia, with China serving as the region with the most diversity (Vaughan, 1977)<sup>[9]</sup>. It began in China and extended from there to nations like India and Afghanistan, among others. Mustard is Temperate regions crop which cultivated during the Rabi season, requires relatively cool temperature. From 37 to 49% of the total weight is oil content is present in mustard (Bhowmik et al., 2014)<sup>[1]</sup>. Its seeds have 4.51 g of carbs, 1.40 g of sugar, 2 g of dietary fibre, 0.47 g of fat, and 2.56 g of protein per 100 g (Tyagi and Singh, 2016)<sup>[8]</sup>. The most affordable source of oil in our diets, edible oil is produced by crushing a lot of mustard seeds. Additionally, mustard seed is employed in pickling, medicine, and industry for things like softening leather. Young plants' green leaves are used as green vegetables because they provide adequate amounts of sulphur and minerals for the diet. India holds the top spot in terms of area and comes in second after China in terms of production. It is grown on an area of roughly 6.69 Mha in India, producing 10.11 Million tonnes annually at a productivity of 1511 kg/ha (Directorate of Economics and Statistics, 2021)<sup>[2]</sup>. The states of Rajasthan, Madhya Pradesh, Uttar Pradesh, Haryana, West Bengal, Gujarat, and Assam are the top producers of rapeseed-mustard. According to the Directorate of Economics and Statistics from 2021<sup>[2]</sup>, the area, production, and productivity of mustard in Rajasthan are 2.72 Mha, 4.51 MT, and 1659 Kg/ha, respectively. Alwar, Bharatpur, Jaipur, Dholpur, Sawai Madhopur, Jhunjhunu, Sikar, and Sriganganagar districts are where it is primarily grown. The creation of hybrids in mustard is necessary for the advancement of quality features and yield in general. One of the greatest methods for determining the worth of parental lines to develop superior hybrids and valuable recombinants is combining ability analysis (Singh et al., 2013)<sup>[5]</sup>.

#### Materials and Methods

Eight mustard lines were crossed during Rabi 2021-2022 with three testers, PM-26, RM-51, and Pusa Mahak, to produce twenty-four crosses; these twenty-four crosses, eleven parents, and two checks, RH-0749 and NRC-HB-101, were subsequently sown in a randomised block design with three replications while maintaining a crop geometry of 30 x 10 cm. During Rabi 2022-2023, the experiment was evaluated at the Rajasthan College of Agriculture's instructional farm at the Maharana Pratap University of Agriculture and Technology in Udaipur. The observations were recorded for fourteen characters, viz., days to 50 percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main branch (cm), number of siliqua per plant, length of siliqua (cm), number of seeds per siliqua, seed yield per plant (g), 1000-seed weight (g), biological yield per plant (g), harvest index, and oil content percent. Among them days to 50 percent flowering and days to maturity observations were recorded on whole plot basis. Oil content was estimated by using Soxhlet's method (Soxhlet 1879)<sup>[6]</sup>.

#### Statistical analysis

According to the procedure recommended by Kempthorne (1957), the combining ability analysis for the line x tester

mating design (L x T) was carried out. The following model was used to estimate general and specific combining ability effects of the ij<sup>th</sup> observations.

$$Y_{ijk} = \mu + G_i + G_j + S_{ij} + R_k + \Sigma e_{ijk}$$

Yijk	5 0 51	Ι	Varies from 1, 2, 3,l					
μ	replication Population mean,		Varies from 1, 2, 3,t					
$G_i$	GCA effects of i <sup>th</sup> line,	k	Varies from 1, 2, 3,r					
$G_j$	GCA effects of j <sup>th</sup> tester,	Rk	Effect of k <sup>th</sup> replication					
	SCA effects of cross		Uncontrolled variation/error					
Sij	between i <sup>th</sup> line and j <sup>th</sup>		associated with ij cross in kth					
	tester		replication					

#### **Result and Discussion**

Analysis of Variance for Combining Ability: The total variance was partitioned into components *viz.*, variance due to lines, testers and line x testers. The mean squares due to crosses, lines and testers were significant for all the traits, except for the length of main branch due to crosses, for oil content due to lines, for plant height, total number of secondary branches per plant, length of main branch, number of seeds per siliqua and 1000 seed weight due to testers.

Table 1: ANOVA for combining ability for fourteen traits in Indian mustard (Brassica juncea L.)

S.N.	Characters	Rep	Tester	Lines	Crosses	L vs T	Error	
		[2]	[2]	[7]	[23]	[14]	[72]	
1	Days to 50% flowering		4.72**	43.33**	15.31**	10.42**	0.94	
2	Days to maturity		145.47**	200.64**	92.30**	7.31**	2.74	
3	Plant height (cm)	78.54	2.39	292.33**	108.39**	62.51*	29.23	
4	Number of primary branches per plant	0.04	0.89**	1.07**	0.78**	0.74**	0.09	
5	Number of secondary branches per plant	0.00	0.14	1.31**	1.49**	1.44**	0.26	
6	Length of main branch (cm)	57.6	30.55	128.33	206.44	60.47	123.77	
7	Number of siliqua per plant		284.92**	1335.63**	1375.71**	331.62**	44.36	
8	Length of siliqua (cm)	0.12	0.50*	0.75**	0.51**	0.20*	0.11	
9	number of seeds per siliqua	0.91	0.00	5.85**	3.23**	0.83	0.55	
10	Seeed yield per plant (g)	1.13	8.60**	6.34**	5.88**	4.10**	0.83	
11	1000- seed weight (g)		0.03	0.96*	0.84**	0.25	0.35	
12	Biological yield per plant		122.60*	839.32**	937.45**	345.16**	28.24	
13	Harvest Index		11.15**	55.84**	66.05**	32.71**	1.34	
14	Oil content (%)		3.26**	1.07	1.29**	1.12*	0.52	

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

Estimation of General Combining Ability Effects: The estimates of general combining ability effects for lines and testers and specific combining ability effects of crosses for traits studied are presented in Table 2. Most of the traits showed significant GCA effects, while for testers the days to maturity, total number of primary branches per plant, seed yield per plant, harvest index and oil content showed significant GCA effects. Two lines, MAYA (-1.71) and PUSA JARAK (-2.67), showed significant negative gca effects for days to 50% flowering. Negative significant gca effects for days to maturity were expressed four lines (RGN-505, MAYA, PUSA JARAK and JM-1) with magnitudes ranging from -3.25 (JM-1) days to -4.94 (PUSA JARAK) days. These findings are in accordance with the results reported by Tomar et al. (2017)<sup>[7]</sup>. Only one line, RH-749, out of eight lines expressed negative significant gca effects for plant height with value of -10.71. Only one line expressed positive significant gca effects for the number of primary branches per plant that is 0.64 (PUSA JARAK). Two lines, out of the total

eight, showed significant positive gca effects for the number of secondary branches per plant, with magnitude ranging from 0.38 (JM-1) to 0.53 (MAYA). Only one line, out of the total eight, showed significant positive gca effects for the length of main branch, with the magnitude of 8.40 (PUSA JARAK). Four lines showed positive significant gca effects for the number of siliquae per plant, with the magnitude ranging from 7.61 (JM-1) to 23.71 (PUSA JARAK). Out of eight lines, two lines exhibited significant positive gca effects for siliqua length ranging from 0.39 (NRC-HB-101) to 0.59 (RH-749). Four lines expressed positive significant gca effects for number of seeds per siliqua with magnitude ranging from 0.64 (RGN-505) to 0.95 (JM-1). Only one line NRC -HB-101 (1.52) showed significant positive gca effects for seed yield per plant. Only one line, among the parents showed positive significant gca effects for 1000 seed weight with magnitude of 0.52 (JM-1). Two lines showed significant positive gca effects for biological yield with the magnitude ranging from 20.56 (PUSA JARAK) to 24.84 (NRC-HB-101).

3 lines expressed positive significant gca effects for harvest index with the magnitude ranged from 1.58 (RW-571-2) to 7.01 (RGN-73). Among the lines, none of the line showed significant positive gca effects for oil content.

Among the testers, 0.68 (RM-51) for seed yield per plant, 0.56 (Pusa Mahak) for harvest index, 0.40 (PM-26) for oil content, and 0.22 (PM-26) for number of primary branches per plant, exhibited positive significant *gca*. The tester Pusa Mahak showed negative significant *gca* effect for days to maturity (-2.71.)

According to the estimates of *GCA* effects, line PUSA JARAK is a very good general combiner for the majority of traits, including days to 50% flowering, days to maturity, number of primary branches per plant, length of main branch, number of siliqua per plant, and biological yield. The tester

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PM-26 was considered a good general combiner for the number of primary branches per plant and oil content.

#### **Estimation of Specific Combining Ability Effects**

Significant positive and negative *SCA* effects were recorded for all the observed traits (Table 2). Out of 33 crosses, only two crosses namely, RGN-505 x PM-26 and RH-749 x PUSA MAHAK exhibited positive significant *sca* effects for seed yield per plant. In addition to this, Cross RH-749 x PUSA MAHAK also showed highest positive significant *sca* effects for total number of primary branches per plant and total number of secondary branches per plant. None of the crosses exhibited positive significant *sca* effects for oil content. (Table 2).

Table 2: Estimates of General combining ability and Specific combining ability effects for fourteen characters in Indian mustard

S. No.	Genotype	DF 50%	DM	PH	NPB	NSB	LMB	NSP	LS	NSS	SYP	TW	BYP	HI	OC
1	PM-26	-0.31	0.63	-0.35	0.22**	-0.04	1.30	-3.74*	-0.01	0.00	-0.45*	-0.04	0.81	-0.76**	0.40*
2	RM-51	0.51*	2.09**	0.07	-0.12	0.09	-0.60	3.04	0.15	-0.01	0.68**	0.03	1.74	0.20	-0.34
3	PUSA MAHAK	-0.19	-2.71**	0.27	-0.10	-0.04	-0.70	0.70	-0.14	0.01	-0.23	0.01	-2.55*	0.56*	-0.06
4	RGN-73	-0.51	-0.72	4.38*	0.03	0.35	-0.94	-9.46**	-0.35**	0.91**	-0.15	-0.67**	-23.17**	7.01**	-0.19
5	RGN-505	-0.54	-3.72**	0.79	-0.11	-0.50**	7.25	22.00**	0.07	0.64*	0.57	-0.49*	-0.10	-0.06	-0.09
6	RW-571-2	0.18	7.80**	1.24	-0.02	-0.31	6.15	-20.62**	-0.24*	-1.42**	-0.68*	0.29	-9.53**	1.58**	0.08
7	MAYA	-1.71**	-3.57**	2.31	-0.08	0.53**	4.51	-6.56**	0.08	0.78**	0.30	0.26	-12.73**	3.42**	0.40
8	PUSA JARAK	-2.67**	-4.94**	5.59**	0.64**	0.18	8.40*	23.71**	-0.16	-0.13	0.33	0.33	20.56**	-4.89**	-0.23
9	JM-1	1.13**	-3.25**	-2.03	0.15	0.38*	-12.67**	7.61**	-0.38**	0.95**	-0.05	0.52*	1.03	-0.84*	0.09
10	NRC-HB-101	1.19**	0.08	-1.56	-0.42**	0.14	-7.61	15.49**	0.39**	-0.29	1.52**	-0.63**	24.84**	-5.13**	-0.55*
11	RH-749	2.93**	8.32**	-10.71**	-0.18	-0.76**	-5.09	-32.17**	0.59**	-1.45**	-1.85**	0.39	-0.90	-1.09**	0.49
12	RGN-73 x PM-26	-1.06	1.58	7.31	-0.07	0.23	-2.47	-2.28	-0.05	0.06	-0.26	0.09	9.60*	-3.81**	-0.39
13	RGN-505 x PM-26	0.06	-0.81	0.03	-0.09	-0.38	-5.04	1.66	0.03	-0.06	1.69*	0.12	4.05	0.32	0.28
14	RW-571-2 x PM-26	-1.69*	-1.05	-3.83	0.54*	-0.02	-1.81	2.49	-0.21	-0.18	0.74	0.02	0.71	0.52	0.10
15	MAYA x PM-26	-1.52*	2.17	-4.03	0.18	1.05**	-3.03	9.39	0.14	0.66	0.62	-0.22	-4.05	1.96*	0.77
16	PUSA JARAK x PM-26	0.73	-1.14	-0.95	0.06	-0.26	2.74	-10.20*	-0.39	-0.08	-0.35	0.10	-16.40**	3.54**	0.30
17	JM-1 x PM-26	1.30	0.97	3.42	-0.37	0.24	3.92	-13.60**	0.14	0.17	-0.11	0.01	-7.78*	2.24**	0.41
18	NRC-HB-101 x PM-26	0.24	-0.38	0.24	0.28	-0.47	6.19	16.33**	0.15	-0.17	-0.36	-0.22	-5.88	1.25	-0.72
19	RH-749 x PM-26	1.93**	-1.34	-2.18	-0.52*	-0.41	-0.50	-3.79	0.20	-0.41	-1.97**	0.10	19.73**	-6.02**	-0.76
20	RGN-73 x RM-51	1.54*	0.11	-6.60	0.51*	-0.06	-0.29	4.87	-0.05	0.29	-0.29	0.16	-13.69**	5.02**	-0.56
21	RGN-505 x RM-51	-0.32	1.85	-2.60	0.35	0.99**	-1.35	0.14	-0.04	0.81	-1.56*	0.14	1.86	-1.81*	-0.26
22	RW-571-2 x RM-51	-1.91**	0.78	3.95	-0.24	0.10	-3.33	-2.88	-0.09	0.27	-0.94	0.16	-2.62	-0.12	0.11
23	MAYA x RM-51	2.72**	-1.37	-0.92	-0.01	-1.02**	2.73	-14.00**	0.18	-0.69	0.24	0.28	3.29	-1.10	-0.33
24	PUSA JARAK x RM-51	-1.02	-1.36	2.95	-0.74**	0.45	1.91	14.58**	0.11	-0.64	0.46	0.03	6.41	-1.23	-0.13
25	JM-1 x RM-51	0.44	-0.68	3.28	0.29	-0.45	-1.07	-1.17	0.04	0.04	0.70	-0.49	5.71	-1.13	-0.24
26	NRC-HB-101 x RM-51	0.36	-0.34	-2.85	0.06	0.65	0.59	-5.25	0.17	-0.12	1.22	-0.18	2.66	0.11	0.96
27	RH-749 x RM-51	-1.81*	1.02	2.80	-0.21	-0.64	0.80	3.70	-0.32	0.05	0.17	-0.09	-3.63	0.27	0.44
28	RGN-73 x PUSA MAHAK	-0.49	-1.68	-0.71	-0.43*	-0.17	2.75	-2.60	0.10	-0.35	0.54	-0.25	4.09	-1.21	0.95
29	RGN-505 x PUSA MAHAK	0.26	-1.04	2.57	-0.26	-0.61	6.39	-1.80	0.01	-0.75	-0.12	-0.26	-5.91	1.50	-0.02
30	RW-571-2 x PUSA MAHAK	3.60**	0.27	-0.12	-0.30	-0.08	5.14	0.40	0.30	-0.09	0.20	-0.18	1.91	-0.40	-0.22
31	MAYA x PUSA MAHAK	-1.20	-0.80	4.95	-0.17	-0.03	0.30	4.61	-0.32	0.03	-0.86	-0.06	0.76	-0.86	-0.44
32	PUSA JARAK x PUSA MAHAK	0.29	2.51*	-2.00	0.68**	-0.19	-4.65	-4.38	0.28	0.72	-0.11	-0.13	9.99**	-2.31**	-0.17
33	JM-1 x PUSA MAHAK	-1.74*	-0.29	-6.70	0.08	0.21	-2.85	14.77**	-0.18	-0.21	-0.59	0.48	2.07	-1.11	-0.17
34	NRC-HB-101 x PUSA MAHAK	-0.60	0.72	2.62	-0.33	-0.18	-6.77	-11.09*	-0.32	0.29	-0.86	0.40	3.22	-1.36	-0.25
35	RH-749 x PUSA MAHAK	-0.12	0.32	-0.62	0.73**	1.05**	-0.30	0.09	0.13	0.36	1.81**	-0.00	-16.11**	5.75**	0.32

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

Days to 50% flowering (DF50%), Days to maturity (DM), Plant height (PH), Number of primary branches per plant (NPB), Number of secondary branches per plant (NSB), Length of main axis (LMA), Number of siliquae per plant (NSP), Length of siliqua (LS), Number of seeds per siliqua (NSS), Seed yield per plant (SYP), 1000-Seed weight (TW), Biological yield per plant (BYP), Harvest index (HI), Oil content (OC).

#### Conclusion

With the exception of length of the main branch and oil content due to parents, all genotypes showed significant variations, indicating the presence of high genetic variability among the parents, a requirement for the development of a successful breeding programme. The line x testers' significant mean squares demonstrated the hybrids' resilient contribution to specific combining ability variance components. According to the findings, the lines Pusa Jarak and JM-1 were good general combiners for the majority of traits, therefore both lines can be used in hybridization projects to create variety by

utilising non-additive gene action. The cross between RH-749 and PUSA MAHAK demonstrated the highest estimates of sca effects for NSB, NPB, and HI as well as the maximum positive significant specific combining ability effects for seed production per plant (1.81). As a result, employing this cross as a commercial hybrid may be suggested for utilising dominant gene effects.

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1213

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