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Heterosis and combining ability analysis for yield and its component traits in Indian mustard (*Brassica juncea*)

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ABSTRACT

Ten diverse lines of Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] were crossed in diallel mating design excluding reciprocals during winter (*rabi)* season 2014–15 to study heterosis and combining ability. The mean squares due to genotypes including parents, crosses and parents vs. crosses were significant for all the traits. The analysis of variance revealed significant mean sum of squares of general combining ability (GCA) and specific combining ability (SCA) for most of the characters at all three environments, except mean sum of squares due to GCA for length of siliqua in E_3 environment and mean sum of squares due to SCA for plant height in E_1 and for number of secondary branches per plant in E_3 environment. In pooled analysis, mean squares due to GCA, SCA, GCA × E and SCA × E were significant for all the eight characters except SCA × E for plant height and GCA × E for protein content. The estimates of GCA effects revealed that parents, viz. Pusa Vijay, PM-30 and Bio-902 were good general combiners for yield contributing traits and the best specific cross combinations for yield and its attributing traits were PM-27 × RGN-229, PM-27 × RGN-73, Pusa Vijay × Laxmi, Pusa Vijay × DRMR-IJ-31 and Pusa Vijay × RGN-73 on the basis of pooled analysis. The crosses Bio-902 × RGN-48, PM-30 × Bio-902 and Bio-902 × RGN-73 exhibited highest and positive significant heterotic effects for seed yield per plant and its important component traits. These F_1s may be exploited for obtaining transgressive segregants for development of hybrid varieties in Indian mustard.

Keywords: *Brassica juncea*, Diallel analysis, GCA, Heterosis, SCA, Yield components

Brassica crops are highly diverse and second most important source of edible oil in India. Indian mustard [*Brassica juncea* (L.) Czern. & Coss.] is predominantly cultivated and accounts more than 70% of the area under the rapeseed-mustard crops. The area, production and productivity of rapeseed-mustard in India are 6.0 million hectares and 7.98 million tonnes and 1324.0 kg/ha, respectively (Anonymous 2018). India holds third position in area and production after Canada and China (Jat *et. al.* 2019). In India, Rajasthan is the largest producer of rapeseed-mustard followed by Uttar Pradesh, Haryana, Madhya Pradesh, West Bengal, Gujarat and Assam. It is mostly grown in Alwar, Bharatpur, Sri Ganganagar, Kota, Bikaner and Jaipur districts of Rajasthan. Indian mustard is a natural amphidiploid, derived from cross of *B. rapa* and *B. nigra* (Banuelos *et al.* 2013). Seed oil ranges from 38–40% which is an cooking and frying medium throughout the north India.

The meal cake after extraction of oil is important source of cattle feed protein. The information on magnitude and nature of genetic variations is necessary to judge genetic potential of available genetic resources. Evaluation of parental lines for heterotic effects and combining ability facilitates the selection of desirable parents for further hybridization programs. Therefore, the present study was carried out to know high heterotic crosses and more precise estimates of general combining ability and specific combining ability over the environments.

MATERIALS AND METHODS

The experimental material comprised 10 parents, viz. PM-27, Pusa Vijay, PM-30, Bio-902, Laxmi, RGN-229, RB-50, DRMR-IJ-31, RGN-48, RGN-73 and their 45 half diallel crosses. The seeds of 45 crosses and ten parents were produced by hand emasculation-hand pollination and selfing, respectively, during winter (*rabi*) season 2014–15. These 45 crosses along with 10 parents and two checks, viz. NRCHB-506 and DMH-1 were evaluated in randomized block design with three replications at three locations, viz. RCA, MPUAT, Udaipur (E_1), Instructional Farm, CTAE, MPUAT, Udaipur (E_2) and KVK, MPUAT, Chittorgarh (E_3). Inter and intra row spacing was kept 30 and 15 cm, respectively. All the recommended package of practices were adopted to raise a good crop. Observations on five

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randomly selected competitive plants in each replication for each genotype were recorded for days to 50% 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 siliquae per plant, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g), seed yield per plant (g), oil content (%) and protein content (%). Analysis of variance suggested by Panse and Sukhatme (1967) was used to test the significance. Heterosis expressed as per cent increase or decrease in F_1 over its better parent value in the desirable direction was estimated for various traits. Data were subjected to combining ability analysis as per Griffing (1956) model-I and method-II.

RESULTS AND DISCUSSION

The pooled analysis revealed significant differences between the environments for all the characters except days to 50% flowering, seed yield per plant and protein content. The mean squares due to genotypes including parents, crosses and parents vs. crosses were also significant for all the characters. Mean squares due to genotypes × environment interactions were significant for all these characters, indicating influence of environment on the expression of these eight characters. The partitioning of mean squares due to parents × environments were significant for all the characters except plant height and protein content while mean squares due to crosses × environments interaction were significant for all the characters. The mean squares due to parent v/s crosses × environments interaction were significant only for length of main branch and harvest index while for other characters, viz. days to 50% flowering, plant height, number of primary branches per plant, seed yield per plant, 1000 seed weight and protein content were non-significant.

Considerable amount of heterobeltiosis and standard heterosis were observed for yield and most of other related traits studied, however the degree of heterosis varied from cross to cross. On overall basis, three crosses, viz. Bio-902 × RGN-48, PM-30 × Bio-902 and Bio-902 × RGN-73 expressed economic heterosis and heterobeltiosis for seed yield per plant. These crosses were also found promising as they exhibited higher seed yield over best check NRCHB-506 along with higher per se performance for 1000 seed weight and number of siliquae per plant. The cross Bio-902 × RGN-73 also showed higher estimates of significant positive economic heterosis for biological yield per plant in E_2 and E_3 environments. While Bio-902 × RGN-48 for seed yield per plant, crosses PM-30 × Bio-902 and Bio-902 × RGN-48 for protein content also exhibited positive significant economic heterosis on pooled basis. Earlier studies by Narsin *et al.* (2011), Lal *et al.* (2012), Niranjana *et al.* (2014) and Chaurasiya *et al.* (2018) also revealed heterosis in desirable direction for various characters in Indian mustard.

The analysis of variance for combining ability revealed significant effects due to GCA and SCA for all the traits except effects due to GCA for length of siliqua in E_3 environment, effects due to SCA for plant height in E_1 and for number of secondary branches per plant in E_3 environment (Table 1). These results suggest the existence of additive and non-additive gene actions for various traits in the material studied. The magnitude of effects due to GCA was higher than SCA for most of the characters except number of seeds per siliqua in E_3 and biological yield per plant in E_2 where effects due to SCA were higher. In pooled analysis, effects due to environments were significant for number of primary branches per plant and length of main branch, while effects due to GCA, SCA, GCA × E and SCA × E were significant for all the eight characters except SCA × E for plant height and GCA × E for protein content (Table 2). The interaction effect of variance due to general combining ability with environments (σ^2GCA × e) were higher than interaction effect of variance due to general combining ability with environments (σ^2SCA × e) for all the eight characters. These results are in accordance with the findings of Singh *et al.* (2010), Tele *et al.* (2014), Vaghela *et al.* (2014) and Kumar *et al.* (2015).

The estimates of GCA effects revealed that parents, viz. Pusa Vijay, PM-30 and Bio-902 were good general combiner parents for seed yield per plant and 1000 seed weight on pooled basis. These parents were also good general combiners for majority of yield and yield contributing traits, viz. Bio-902 in E_1, E_2 and E_3 environment and Pusa Vijay in E_3 for number of seeds per siliqua; PM-30 and Bio-902 in E_1, E_2 and E_3 environments for number of siliquae per plant; Pusa Vijay and Bio-902 in E_1 environment for biological yield per plant. The parent Bio-902 was found good general combiner for all the eight traits studied on pooled basis. Singh *et al.* (2010), Turi *et al.* (2011), Niranjana *et al.* (2014) and Patel *et al.* (2015) were also found good general combiners for seed yield per plant, number of seeds per siliqua, number of siliquae per plant and biological yield per plant. A perusal of SCA effects revealed that positive significant SCA effects for seed yield per plant were observed in fourteen crosses, viz. PM-27 × RGN-229, PM-27 × RGN-73, Pusa Vijay × Laxmi, Pusa Vijay × DRMR-IJ-31, Pusa Vijay × RGN-73, PM-30 × Bio-902, PM-30 × Laxmi, Bio-902 × RGN-48, Bio-902 × RGN-73, Laxmi × RGN-229, RGN-229 × RGN-48, RB-50 × DRMR-IJ-31, RB-50 × RGN-48 and RB-50 × RGN-73 on pooled basis. The cross Bio-902 × Laxmi also exhibited positive significant SCA effects for number of siliquae per plant in E_1 environment. Another cross PM-27 × Bio-902 showed positive significant SCA effects for days to maturity, number of siliqua per plant and oil content in E_3 environment. Vaghela *et al.* (2014), Kumar *et al.* (2015), Patel *et al.* (2015) and Kaur *et al.* (2019) also reported significant SCA effects for seed yield per plant. Significant SCA effects for number of siliquae per plant and number of seeds per silique was observed by Tele *et al.* (2014).

The analysis of variance for combining ability in each environment indicated that GCA effects were significant for all characters except effects due to GCA for length of siliqua in E_3 environment, while SCA effects were significant for all

Table 1 Combining ability mean square and EMS for different characters in E_1, E_2 and E_3 environments

Character	Env	Source			Var Model I		
		GCA	SCA	Error	GCA	SCA	Error
		[9]	[45]	[108]			
Days to 50% flowering	E_1	77.74**	3.81**	1.10	19.15	40.48	1.10
	E_2	70.55**	5.71**	0.82	17.43	73.28	0.82
	E_3	96.44**	5.19**	1.00	23.85	62.85	1.01
Days to maturity	E_1	76.30**	4.77**	1.86	18.61	43.66	1.85
	E_2	94.7**	9.19**	1.15	23.38	120.44	1.15
	E_3	80.65**	11.31**	1.44	19.80	147.99	1.43
Plant height	E_1	324.89**	27.50	22.38	75.63	76.84	22.38
	E_2	176.05**	46.97**	24.09	37.98	343.18	24.09
	E_3	159.61**	56.89**	30.56	32.26	394.98	30.56
No. of primary branches/plant	E_1	1.92**	0.43**	0.14	0.44	4.24	0.14
	E_2	0.73**	0.46**	0.14	0.14	4.77	0.14
	E_3	0.25*	0.39**	0.11	0.03	4.03	0.11
No. of secondary branches/plant	E_1	10.02**	2.59**	0.35	2.41	33.53	0.35
	E_2	3.41**	1.29**	0.44	0.74	12.71	0.44
	E_3	3.82**	0.92	0.66	0.78	3.86	0.66
Length of main branch	E_1	153.56**	29.34**	5.11	37.11	363.31	5.11
	E_2	100.12**	30.77**	4.58	23.88	392.74	4.58
	E_3	88.43*	35.35**	4.04	21.09	469.52	4.04
No. of siliquae/plant	E_1	24413.6**	3588.83**	352.39	6015.3	48546.6	352.39
	E_2	24814.6**	2947.7**	312.07	6125.63	39534.5	312.07
	E_3	19410.6**	3732.7**	547.44	4715.8	47778.8	547.45
Length of siliqua	E_1	0.21**	0.11**	0.038	0.05	1.08	0.04
	E_2	0.16**	0.12**	0.033	0.04	1.39	0.04
	E_3	0.07	0.09*	0.07	0.01	0.55	0.06
No. of seeds/siliqua	E_1	2.29**	0.69**	0.13	0.54	8.52	0.13
	E_2	2.08**	0.78**	0.12	0.49	9.96	0.12
	E_3	1.16**	1.41**	0.22	0.23	18.01	0.22
Biological yield/plant	E_1	298.36**	143.33**	7.31	72.76	2040.39	7.30
	E_2	61.56**	123.92**	15.67	11.47	1623.77	15.66
	E_3	237.97**	112.09**	7.62	57.59	1567.02	7.61
Seed yield/plant	E_1	104.43**	14.24**	2.82	25.39	171.15	2.82
	E_2	60.60**	22.95**	2.87	14.43	301.07	2.87
	E_3	50.68**	17.37**	3.25	11.86	211.87	3.25
1000-seed weight	E_1	1.23**	0.21**	0.03	0.29	2.50	0.03
	E_2	0.46**	0.28**	0.03	0.10	3.72	0.04
	E_3	0.56**	0.29**	0.02	0.13	4.00	0.02
Harvest index	E_1	42.52**	29.95**	6.24	9.06	355.69	6.24
	E_2	117.26**	61.62**	7.87	27.34	806.18	7.87
	E_3	75.5**	38.18**	8.05	16.86	451.99	8.05
Oil content	E_1	4.56**	1.20**	0.04	1.12	17.30	0.07
	E_2	4.34**	1.97**	0.07	1.06	28.54	0.08
	E_3	4.58**	1.81**	0.09	1.11	25.74	0.09
Protein content	E_1	7.94**	2.10**	0.46	1.87	24.66	0.40
	E_2	3.94**	2.70**	0.31	0.90	35.83	0.32
	E_3	2.98**	2.77**	0.42	0.63	35.25	0.43

*,**Significant at 5% and 1% level of significance, respectively (Model I).

Table 2 Combining ability mean square and EMS for different characters over the environments

Character	Source						Bartlet	Variance Model I				
	Env	GCA	SCA	GCA × E	SCA × E	Pool Error		GCA	SCA	GCA × E	SCA × E	Error
	[2]	[9]	[45]	[18]	[90]	[324]	[2]					
Days to 50% flowering	0.95	222.46**	7.19**	11.13**	3.754**	0.97	2.40	-0.00	55.37	93.32	15.23	0.97
Days to maturity	11.28**	202.78**	10.18**	24.44**	7.533**	1.48	6.11*	0.36	50.32	130.59	34.42	1.48
Plant height	35.02	536.54**	69.57**	62.01**	30.897	25.67	2.93	0.34	127.71	658.45	54.49	25.67
No. of primary branches/plant	1.88**	1.52**	0.43**	0.69**	0.424**	0.13	1.44	0.06	0.35	4.44	0.8343	0.14
No. of secondary branches/plant	1.88*	14.17**	3.48**	1.54**	0.660*	0.48	10.76**	0.05	3.42	44.96	1.57	0.48
Length of main branch	17.68*	289.56**	45.05**	26.27**	25.196**	4.57	1.47	0.48	71.25	607.05	32.53	4.57
No. of siliquae/ plant	299.98	68026.5**	8366.34**	306.15	951.448**	403.97	9.80**	-3.78	16905.6	11943	-146.73	403.97
Length of siliqua	0.19*	0.26**	0.132**	0.1**	0.101**	0.04	10.97**	0.00	0.05	1.321	0.082	0.04
No. of seeds/ siliqua	0.28	4.85**	1.79**	0.34**	0.545**	0.15	12.69**	0.00	1.17	24.69	0.28	0.15
Biological yield/ plant	28.52	281.75**	201.57**	158.07**	88.88**	10.19	21.13**	0.67	67.89	2870.66	221.80	10.19
Seed yield/plant	1.94	196.72**	35.10**	9.5**	9.729**	2.98	0.63	-0.03	48.43	481.75	9.77	2.98
1000-seed weight	0.04	1.80**	0.44**	0.22**	0.16**	0.03	2.80	0.00	0.44	6.14	0.28	0.03
Harvest index	21.78	126.24**	44.90**	54.51**	42.42**	7.39	2.08	0.52	29.71	562.76	70.69	7.39
Oil content	0.76**	13.15**	3.88**	0.17**	0.55**	0.07	12.69**	0.02	3.27	57.16	0.13	0.07
Protein content	0.21	13.23**	6.65**	0.81**	0.46	0.39	4.31	-0.00	3.21	93.76	0.62	0.39

*,** Significant at 5% and 1% level of significance, respectively (Model I).

the characters except for plant height in E_1 and for number of secondary branches per plant in E_3 environment. The ratio of GCA/SCA variances was less than unity which expressed the preponderance of non- additive gene inheritance for all the traits in all the environments. The estimates of GCA effects revealed that parents Bio-902, Pusa Vijay and PM-30 and were good general combiner parents for seed yield and its attributing characters on pooled basis.

Promising cross combinations identified on the basis of heterotic effects (economic heterosis) for various traits are PM-27 × Bio-902 for days to 50% flowering, Pusa Vijay × Bio-902 for days to maturity, PM-30 × Laxmi for plant height, PM-30 × Bio-902 for number of primary and secondary branches per plant, Bio-902 × RB-50 for length of main branch, RB-50 × RGN-73 for number of siliquae per plant, Laxmi × DRMR-IJ-31 for length of siliqua, PM-30 × Bio-902 for number of seeds per siliqua and PM-30 × Bio-902 for seed yield per plant and 1000-seed weight.

It is concluded that the higher order of SCA effect for seed yield per plant over the environment was shown by crosses Bio-902 × RGN-48 (5.42**), PM-30 × Bio-902 (3.33**) and Bio-902 × RGN-73 (4.07**). These three crosses, viz. Bio-902 × RGN-48 (43.64 g), PM-30 × Bio-902 (42.78 g) and Bio-902 × RGN-73 (41.63 g) were also performed best on the basis of per se performance for seed yield per plant. Therefore, these above new cross combinations are useful populations for obtaining transgressive sergeants and heterotic hybrids.

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