

Short Communication

Line x Tester Analysis in Indian Mustard (*Brassica juncea* L. Czern & Coss)

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Oilseed brassicas are the most important rabi (winter) season oilseed crops of India. Amongst the different *Brassica* species cultivated in the country, Indian mustard (*Brassica juncea* (L.) Czern & Coss) is the dominant species covering major area under rapeseed-mustard. This species has better yielding ability under Indian conditions because of its suitability to drier conditions and early maturity (Kimber and McGregor, 1995). For yield improvement in *B. juncea* through hybridization, selection of desirable parents for specific traits is needed. The ability of the parents to combine well depends upon various complex genetic interactions. Combining ability analysis, the potential tool for the selection of suitable parents, provides information on nature and relative magnitude of fixable and non-fixable genetic variance and helps in planning a suitable breeding programme (Sheikh and Singh, 1998). Therefore, the present study was undertaken to identify the promising parents/crosses through line x tester analysis that can be involved in improvement of Indian mustard.

Thirteen genotypes viz., WFG, MN 9, MN 33, SKM 90-4, PYSR 1, CZM 2, WFM, LSBS, LSYS, YS 22, BS 6, HSG

and MN 22 (lines), and five promising cultivars/entries viz., Bio 902, Varuna, GM1, BTV and Bio-YSR (testers) of Indian mustard were crossed in line x tester fashion during rabi 1996-97 at Agricultural Research Station, Mandore. All the 65 crosses and their 18 parents were grown in a randomized block design replicated twice in the following season. Each genotype was planted in a single 3 m long row following 45 x 15 cm crop geometry. The observations recorded on five randomly selected plants from each plot for ten quantitative characters were subjected to analysis of combining ability as per standard method (Kempthorne, 1957).

The analysis of variance showed significant differences among genotypes for all the characters, indicating the existence of sufficient variability in the experimental material (Table 1). Significant variances were recorded for all the attributes due to crosses, depicting the presence of substantial heterosis in the hybrids. The value of variances, due to lines as well as testers, were significant for days to flowering, days to maturity and plant height indicating the importance of both additive

Table 1. Analysis of variances for combining ability in Indian mustard

Source	df	Days to flowering	Days to maturity	Plant height (cm)	Main receme length (cm)	Siliquae on main receme	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliqua length (cm)	Seeds siliqua ⁻¹	Seed yield (kg ha ⁻¹)
Replication	1	0.62	14.89**	782.78**	2.78	3.72	1.49	14.18	0.47	0.01	4.81
Crosses	64	12.90**	7.14**	385.03**	142.60**	63.78**	6.22**	29.94**	0.57**	4.36**	6515.71**
Lines	12	30.14**	12.56**	823.62**	176.26	70.11	4.89	31.36	1.39**	6.42	7858.34
Testers	4	43.09**	47.17**	1188.37**	35.34	17.18	24.81**	22.77	0.31	8.16	9734.13
Lines x Testers	48	6.07**	2.45**	208.44**	143.12**	66.08**	5.00**	23.51**	0.38*	3.53**	5911.85**
Error	64	1.76	1.39	47.95	33.09	24.94	0.98	4.24	0.24	1.11	740.23
σ^2_g		1.70	1.52	44.31	2.07	-1.25	0.55	0.20	0.03	0.21	160.24
σ^2_s		2.15	0.53	80.25	55.01	20.57	2.01	9.64	0.07	1.21	2585.81
σ^2_g/σ^2_s		0.79	2.86	0.55	0.04	-0.06	0.27	0.02	0.43	0.17	0.06

*, ** significant at 5 and 1%, respectively.

and nonadditive gene effects. The variances due to line x tester interactions were significant for all the characters under study, showing markedly different behavior of testers over different lines and vice-versa.

Combining ability analysis revealed that the variance of general combining ability (gca) was higher than specific combining ability (sca) for only days to maturity, indicating additive gene action for the trait. Non-additive type of gene action was observed to be predominant for all other characters, including seed yield, as also reported earlier in Indian mustard (Verma *et al.*, 1991; Chaudhary *et al.*, 1997; Singh *et al.*, 1996). The reason appears to be the narrow genetic base of the breeding material being used. As non-fixable component of variation was higher for seed yield and other related characters, the breeding programmes such as biparental mating (Singh and Murthy, 1980), recurrent

selection or diallel selective mating (Jenson, 1970) and interspecific hybridization (Choudhary, 1977) would be more useful than simple conventional pedigree or back cross techniques for genetic improvement and also to broaden genetic base of the crop (Sheikh and Singh, 1998).

The estimates of gca indicated that among the three released varieties used as tester, only Varuna was found to be good general combiner for seed yield (Table 2). These results are in close agreement with those reported by Sheikh and Singh (1998) and Chaudhary *et al.* (1997). Among the lines, CZM 2, YS 22, LSBS, SKM 90-4 and HSG showed significant gca for seed yield per plant. The genotypes WFG, MN 22, BTV and GM 1 exhibited significant negative gca for plant height, days to flowering and days to maturity and were considered as better general combiners for

Table 2. Estimates of general combining ability effects for various characters in Indian mustard

Source	Days to flowering	Days to maturity	Plant height (cm)	Main raceme length (cm)	Siliquae on main raceme	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Siliqua length (cm)	Seeds siliqua ⁻¹	Seed yield (kg/ha ⁻¹)
WFG	1.54**	-2.73**	-15.98**	-7.75**	0.42	0.25	-0.49	-0.53**	0.35	-0.82
MN 9	-1.72**	0.17	-1.98	3.15	-0.89	-0.86**	1.07	-0.14	-0.45	-17.42*
MN 33	0.88*	-0.53	9.22**	2.55	2.62	-0.01	3.07**	-0.33**	-0.95**	-21.42*
SKM 90-4	3.28	1.67**	18.82**	2.95	3.32*	-1.71**	-0.74	-0.16	0.05	26.18**
PYSR 1	0.68	0.17	-0.08	-2.45	0.12	0.25	0.37	-0.08	0.50	-0.72
CZM 2	0.38	0.27	2.42	4.85**	4.62**	0.70*	0.27	-0.25	-1.30**	98.42**
WFM	1.68**	-0.03	5.32*	1.45	-0.79	-0.11	-1.29	-0.13	0.45	-16.12
LSBS	1.98**	0.67	-6.28**	-1.85	-0.99	-0.31	-2.84**	0.48**	1.30**	27.18
LSYS	-1.32**	-0.33	-9.68**	-2.55	-5.09**	-0.01	-0.43	0.80**	1.00**	9.89
YS 22	-1.62	-0.43	5.72*	6.85**	0.32	0.35	2.02**	-0.03	-0.80*	49.18**
BS 6	1.22**	0.66	0.02	-2.85	1.32	1.10**	2.22**	0.52**	0.05	9.89
HSG	0.88*	1.47**	1.92	-5.35**	-1.39	-0.10	-0.59	-0.05	-0.80*	17.89*
MN 2	-2.32**	-1.03**	-9.78**	1.05	-3.59*	0.45	-2.64**	-0.07	0.60	-25.22**
SE (gi) ±	0.42	0.37	2.19	1.82	1.58	0.31	0.65	0.16	0.33	8.60
Testers										
Bio 902	-0.87**	0.58**	1.62	-1.17	-0.90	-1.22**	-0.17	-0.05	-0.94**	6.44
Varuna	0.17	1.31**	7.92**	0.14	0.18	-0.56**	-1.17**	0.12	0.32	18.25**
BTV	-0.91**	-1.08**	-8.54**	1.91	-0.48	0.84**	0.01	0.08	0.05	-31.60**
GM 1	-0.56*	-1.77**	-5.19**	-0.32	-0.05	1.13**	1.45**	-0.15	0.05	-3.64
Bio-YSR	2.17**	0.96**	4.19**	0.55	1.25	-0.19	-0.13	0.00	0.53*	10.55
SE (gi) ±	0.26	0.23	1.36	1.13	0.98	0.19	0.40	0.10	0.21	5.34

*, ** significant at 5 and 1%, respectively.

imparting dwarfness and earliness to their progenies. Significant and positive gca effects recorded in the genotypes CZM 2, BS 6, BTV and GM 1 for primary branches per plant, MN 33, YS 22, BS 6 and GM 1 for secondary branches per plant, CZM 2 and YS 22 for main raceme length, SKM 90-4 and CZM 2 for siliquae on main raceme, LSBS, LSYS and BS 6 for siliqua length, and LSBS, LSYS and Bio-YSR for seeds per siliqua, indicating a good

choice for improvement of these attributes. In all, CZM 2 and YS 22 genotypes were identified as better parents for improvement of seed yield and some other yield attributes.

Sixteen crosses out of 65, showed significant and positive sca for seed yield, of these three were between high x high, seven for high x low and six with low x low gca parents for seed yield. The crosses CZM 2 x Varuna, SKM 90-4 x Varuna and HSG x Varuna with high x high gca

parents and YS 22 x BTV, MN 22 x Varuna, SKM 90-4 x GM 1, CZM 2 x GM 1, CZM 2 x Bio-YSR and BS 6 x Varuna with high x low *gca* parents could be expected to generate positive heterosis in higher frequencies (Sheikh and Singh, 1998).

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