



## Combining ability analysis for seed yield and its components over environments in Indian mustard (*Brassica juncea* L.)

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### Abstract

Combining ability was analyzed using a Line x tester of ten lines and five testers in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. Combining ability analysis, on pooled basis, revealed the importance of both additive as well as non-additive genetic variances for control of various traits. However, the ratio of  $\sigma^2_{gca}/\sigma^2_{sca}$  revealed the preponderance of non-additive gene action for all the traits except for days to maturity where the additive gene action was predominant. The parents, GM 3, RSK 28 and SKM 0149 were the good general combiners, whereas, hybrids RH 819 x RSK 28, NDR 8501 x NUDH YJ-3 and SKM 0149 x RSK 28 were found to be best specific combiners for seed yield per plant and some of the yield contributing traits. However, on the basis of *per se* performance and significant sca effects for seed yield per plant and some of its important components, hybrids RH 819 x RSK 28, SKM 0149 x RSK 28 and NDR 8501 x NUDH YJ-3 were considered to be most promising for further exploitation in breeding programmes.

**Key words:** Indian mustard, Combining ability, Environment effect, Yield components

### Introduction

Rapeseed-mustard is the second important oilseed crop of the country after soybean and plays a significant role in the Indian oil economy by contributing about 27% to the total oilseed production. Indian mustard or raya or laha is covering more than 80% of the total rapeseed and mustard area and contributes to production in same proportion. It is because of its wider adaptability and comparative tolerance to biotic and abiotic stresses as compared to other *Brassica* species grown as oilseeds (Yadava *et al.*, 2010). In order to incorporate desirable characters to maximize economic yields, the knowledge of combining ability is useful to get information on selection of parents and nature of gene actions involved. Since, very little information is available on the inheritance of the yield and yield component traits in this crop. Hence, the present study has been carried out over environments to obtain more precise estimates for seed yield and related characters in Indian mustard.

### Materials and methods

Ten female lines of Indian mustard viz. GM 1, GM 2, GM 3, CS 52, NDR 8501, DIR 337, RH 819, SKM 0139, SKM 0125 and SKM 0149 were crossed with five tester NUDH YJ-3, TM 40, EC 287711, RSK 28 and ZEM 2 during *rabi*-2004-05. A set of 65 genotypes consisting of ten female lines, five testers and their 50 resultant  $F_1$  crosses were evaluated following randomized block design with three replications in four different environments [ $E_1$ : Sardarkrushinagar 15.10.2005 normal sown,  $E_2$ : Sardarkrushinagar 16.11.2005 late sown,  $E_3$ : Deesa 16.10.2005 normal sown and  $E_4$ : Deesa 7.11.2005 late sown] during *rabi* 2005-06. Each plot consisted of single row of five meter length. Row to row and plant to plant distance were kept 45 cm and 15 cm, respectively. All recommended agronomical practices and plant protection measures were adopted for raising the good crop. Observations were recorded on five randomly selected plants in each replication for every entry for all the characters

except days to 50 percent flowering and days to maturity where, the observations were recorded on the plot basis. The mean of each plot was used for statistical analysis. The data were first subjected to the usual analysis followed for a randomized block design for individual environment as suggested by Panse and Sukhatme (1967). Line x tester analysis was done environment-wise and also on pooled basis Kempthorne (1957).

## Results and discussion

The analysis of variance for combining ability (table 1) revealed that mean squares due to females were found to be significant for all the character in individual environments and also on pooled basis except 1000-seed weight in  $E_1$ ,  $E_2$ ,  $E_3$  and  $E_4$ . However, the ratio of  $\sigma^2_{gca}/\sigma^2_{sca}$  indicated the preponderance of non-additive type of gene action for all the characters in individual environments as well as pooled basis except for days to maturity, seeds per siliqua in  $E_3$  and days to 50 percent flowering in  $E_4$ , where the additive type of gene action was predominant.

The parents classified as good, average and poor combiners on the basis of estimates of general combining ability effects on pooled basis for various characters are listed in Table 1 and 2. It was observed that none of the parents was good general combiner for all the characters. However, the parents GM 1, GM 3, RSK 28 and SKM 0149 were found to be good general combiners for seed yield per plant; RH 819, SKM 0139, SKM 0125, SKM 0149, NUDH YJ-3, TM 40, EC 287711 and RSK 28 for days to 50 percent flowering; RH 819, SKM 0139, SKM 0125, SKM 0149 and TM 40 for days to maturity; GM 2, GM 3, RSK 28 and ZEM 2 for siliquae per plant; GM 2, DIR 337 and RSK 28 for seeds per siliqua; GM 1, GM 2, CS 52, NDR 8501, NUDH YJ-3 and ZEM 2 for 1000-seed weight were found to be good general combiners. In general, it is evident from the data on pooled basis that the parents which were good general combiners for seed yield per plant, were also good general combiners for some of its yield contributing traits like days to 50 percent flowering, days to maturity and siliquae per plant. From the results, it is observed that the

use of parents, GM 3, RSK 28 and SKM 0149 in future breeding programme would be more useful for augmenting genes for high seed yield as they were found to be good general combiners for seed yield per plant and some of the important yield components, It was interesting to note that all these parental lines exhibited superior *per se* performance for seed yield per plant and involvement of these parents had resulted into hybrids expressing useful heterosis for various characters. These results pointed out that selection of parents for hybridization programme based on *per se* performance may be reliable and such parents generally turn out to be good combiners as well. The results obtained in the present study are in conformity with Singh *et al.* (2000), Rao *et al.* (2001), Singh *et al.* (2002), Singh *et al.* (2003), Solanki *et al.* (2009), Srivastava *et al.* (2009), and Tripathy and Lenka (2010).

The variance due to sca was greater than gca, which indicated the preponderance of non-additive gene action for plant height, primary and secondary branches, mature pods, immature pods and pod yield per plant (Mothilal *et al.*, 2007). The parents *viz.*, CO3, TNAU 325, TNAU 387 and M13 can be considered as superior parents in the present study as they recorded high *per se* with positive significance gca effect for seed yield per plant. Among the 36 hybrids, evaluated, crosses *viz.*, CO3 X M13, TNAU 387X M13, CO3 X ICGV 93260, TNAU 325 X M13 and CO2X GG2 were considered as superior hybrids as they observed high *per se* and non- significant sca effect for seed yield per plant. These superior crosses involved parents with significant positive gca effects which in turn suggested the possible role of additive gene action in these crosses.

The best three hybrids on the basis of *per se* performance *viz.*, RH 819 x RSK 28 (good x good), SKM 0149 x RSK 28 (good x good) and NDR 8501 x NUDH YJ-3 (good x average) had significant desired sca effects, significant heterotic response over mid and better parent for seed yield per plants. High yielding hybrids also possessed desirable sca effects, high heterosis as well as high *per se* performance for some of its important yield

**Table 1: Estimates of general combining ability effects of parents for various characters of mustard over environments**

Genotype	Seed yield per plant(g)				Days to 50 percent flowering				Days to maturity						
	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	Pooled	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	Pooled	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	Pooled
GM 1	-0.497	0.158	0.763*	1.310**	0.434*	1.380**	2.373**	4.427**	2.307**	2.622**	1.567	1.133	6.707**	2.047**	2.863**
GM 2	-0.665	-0.837**	-0.075	0.521	-0.264	0.180	-0.427	3.493**	2.640**	1.472**	1.567	3.000**	4.907**	3.647**	3.280**
GM 3	1.602**	0.806**	1.816**	0.953**	1.294**	4.913**	1.707**	8.627**	4.973**	5.055**	3.900**	5.867**	8.907**	4.847**	5.880**
CS 52	0.103	0.126	0.000	-0.857**	-0.157	0.847*	0.107	2.027**	1.840**	1.205**	2.500**	-1.600	2.840	-2.620**	0.280
NDR 8501	-0.974*	-0.401	-1.600**	0.411	-0.641**	-0.887*	-1.160**	1.693**	1.440**	0.272	0.700	0.533	-0.893	0.847	0.297
DIR 337	1.224**	-1.232**	-0.451	-1.447**	-0.476*	-0.753	0.507	-1.107*	-0.160	-0.378	-0.367	2.200*	-6.960**	0.980	-1.037
RH 819	-0.233	0.613*	1.471**	0.343	0.548**	-0.887*	-1.427**	-2.907**	1.240**	-0.995**	-3.233**	-1.867	-3.027	0.580	-1.887**
SKM 0139	-0.773	0.086	-0.800*	-0.903**	-0.597**	-2.021**	-1.360**	-5.107**	-6.027**	-3.628**	-2.967**	-1.800	-5.893**	-1.687*	-3.087**
SKM 0125	-0.653	0.627*	-1.742**	-1.435**	-0.801**	-0.753	0.507	-5.773**	-3.560**	-2.395**	-1.967*	-4.800**	-3.893*	-6.687**	-4.337**
SKM 0149	0.865	0.053	0.619	1.103**	0.660**	-2.020**	-0.827*	-5.373**	-4.693**	-3.228**	-1.700	-2.667*	-2.693	-1.953**	-2.253**
S.Em.±	0.446	0.286	0.314	0.309	0.172	0.421	0.336	0.504	0.429	0.213	0.940	1.093	1.571	0.718	0.562
<b>Testers</b>															
NUDH-YJ	3-0.694**	-0.029	0.398*	-0.077	-0.100	0.180	-0.293	-0.273	-1.427**	-0.453**	-2.167**	0.667	-1.260	0.613	-0.537
TM 40	0.239	-0.786**	-0.121	0.040	-0.157	-0.720**	-0.527**	-1.640**	-0.193	-0.770**	-1.633**	-0.667	0.673	-3.353**	-1.245**
EC 287711	-0.868**	-0.237	-0.931**	-0.058	-0.523**	-1.287**	-0.860**	-0.240	0.973**	-0.353*	4.867**	-0.167	-0.360	-2.620**	0.430
RSK 28	1.271**	1.204**	1.065**	0.907**	1.112**	-1.253**	-1.227**	-1.340**	-2.060**	-1.470**	-0.867	-0.100	1.807*	-1.053**	-0.053
ZEM 2	0.052	-0.152	-0.412*	-0.812**	-0.331**	3.080**	2.907**	3.493**	2.707**	3.047**	-0.200	0.267	-0.860	6.413**	1.405**
S.Em.±	0.316	0.202	0.222	0.218	0.122	0.297	0.238	0.356	0.304	0.151	0.664	0.773	1.111	0.508	0.398

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

**Table 2: Estimates of general combining ability effects of parents for various characters of mustard over environments**

Genotype	Number of siliquae per plant				Number of seeds per siliqua				1000-seed weight (g)							
	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	Pooled	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	Pooled	E <sub>1</sub>	E <sub>2</sub>	E <sub>3</sub>	E <sub>4</sub>	Pooled	
GM1	2.301	0.598	-10.016	-11.288*	-4.601	0.087	-0.887**	0.053	-0.233	-0.245	-0.120	0.028	0.871**	0.450**	0.307**	
GM2	-0.962	12.531**	11.150	15.241**	9.490*	-0.580*	1.247**	0.320	0.500	0.372*	0.226	-0.120	0.486	0.003	0.149**	
GM3	43.298**	31.141**	73.384**	19.584**	41.851**	-0.780**	-1.153**	-0.413	-0.033	-0.595**	-0.404**	-0.114	-0.311**	-0.712**	-0.386**	
CS 52	1.083	6.992	13.322	2.158	5.889	1.020**	-0.353	0.053	0.321	0.038	0.252*	-0.132	0.252**	0.013	0.096*	
NDR 8501	-15.243*	3.736	-18.152*	-7.224	-9.221*	0.553*	0.513	-0.213	-0.033	0.205	0.276*	0.083	0.036	0.147**	0.135**	
DIR 337	-10.496	-4.829	17.358*	5.306	1.835	-0.180	1.580**	0.187	0.700**	0.572**	-0.100	0.061	-1.109**	0.245**	-0.226**	
RH819	-0.264	-11.443**	13.372	4.742	1.602	0.420	-0.287	-0.680*	0.833**	0.072	0.188	0.159	0.107	0.077	0.133	
SKM0139	-25.544**	-19.328**	-55.216**	-10.740*	-27.707**	-0.647*	-0.553	0.587	-0.433	-0.262	-0.234*	-0.192*	-0.615**	-0.287**	-0.332**	
SKM0125	-5.035	-5.482	-29.346**	-1.804	-10.417**	-0.180	0.047	0.187	-1.100**	-0.262	0.119	0.078	0.196**	-0.239**	0.038	
SKM0149	10.862	-13.916**	-15.854*	-15.974**	-8.721*	0.287	-0.153	-0.080	0.367	0.105	-0.204	0.152	0.086	0.304**	0.084	
S.Em.±	7.615	4.083	7.605	5.122	3.150	0.255	0.318	0.319	0.262	0.145	0.117	0.094	0.059	0.055	0.043	
<b>Testers</b>																
NUDH-Y13	-12.666**	-6.248**	-32.796**	-7.944**	-14.914**	0.320*	0.413*	0.387*	0.100	0.012	-0.004	0.040	0.123**	0.284**	0.305**	
TM 40	-3.638	2.210	-13.511**	-2.890	-4.457*	0.087	-0.120	0.287	-0.133	0.081**	0.167*	-0.002	0.080*	-0.009	0.030	
EC287711	2.924	-6.138**	19.360**	-7.632**	2.128	-0.847**	-0.053	-0.580**	-0.600**	-0.057**	0.213**	0.025	0.347**	-0.026	-0.520**	
RSK28	17.635**	5.513*	6.510	8.118**	9.444**	-0.480**	-0.720**	-0.580**	0.100	-0.024	-0.077	0.109*	-0.010	0.007	-0.420**	
ZEM 2	-4.254	4.664*	20.438**	10.350**	7.799**	0.920**	0.480**	0.487**	0.533**	0.511**	-0.299**	-0.172**	-0.541**	-0.256**	0.605**	
S.Em.±	5.385	2.887	5.377	3.622	2.227	0.180	0.225	0.226	0.185	0.103	0.083	0.066	0.042	0.039	0.030	

contributing characters. This appeared appropriate as yield being a complex character depends on number of traits. Considering the *per se* performance of hybrid SKM 0149 x RSK 28 was found to be superior for days to 50 percent flowering (table 1). Significant positive sca effects for seed yield and its important yield component traits have also been reported by Bhatia *et al.*, (1995); Patel *et al.*, (1996); Varshney and Rao, (1997); Singh *et al.*, (2000); Rao and Gulati, (2001); Singh *et al.*, (2002); Singh *et al.*, (2003), Srivastava *et al.*, (2009), and Tripathy and Lenka (2010).

The information regarding three best performing parents, best general combiners, best performing hybrids alongwith their per cent heterosis over mid parent as well as better parent and sca effects for different traits based on pooled analysis (table 1 and 2) revealed that parents with good *per se* performance were in general, good combiners. However, good general combiners may not necessarily always produce good specific combinations for different traits. In many cases, it was observed that at least one good general combining parent was involved in heterotic hybrids having desirable sca effects. This was true for most of the traits studied. This suggested that information on gca effects of the parents should be considered alongwith sca effect and *per se* performance of hybrid for predicting the value of any hybrid. It is desirable to search out parental lines with high gca effects and low sensitivity to environmental variation in a crop improvement programme with respect to combining ability effects.

It is clear from the above discussion that hybrids RH 819 x RSK 28, SKM 0149 x RSK 28 and NDR 8501 x NUDH YJ-3 having high mean values and desirable sca effects for seed yield per plant and some of its components traits could be exploited in practical plant breeding. It is also cleared that high magnitude of non-additive type of gene action for seed yield per plant and some of its important component traits observed in the present study favours hybrid breeding programme. The evaluation of hybrid has suggested that a substantial degree of heterosis was available in some

crosses in respect of seed yield and majority of its component traits. Looking to the significance of both GCA and SCA variances for all the characters in the present materials, it is also suggested that reciprocal recurrent selection should be employed so that additive as well as non-additive gene action could be exploited simultaneously for further improvement in Indian mustard.

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