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Studies on combining ability effect on seed yield and it's components in Indian mustard (*Brassica juncea* L.)

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Abstract
Combining ability analysis of 10 x 10 diallel set of crosses in Indian mustard for eleven quantitative traits revealed preponderance of non-additive gene effects for all the eleven characters whereas additive gene effect was found to be predominant for the inheritance of most of the characters. Significant differences were observed for both general combining ability and specific combining ability for almost all the traits studied. The high magnitude of general combining ability and specific combining ability effects indicated the presence of both additive and non-additive gene interactions for the inheritance of different traits. Parents, CSR1020, CSR1027, CSR1066 and CSR1118 were exhibited to be good general combiners for seed yield per plant, as well as on the basis of specific combining ability effects out of forty five crosses twenty one crosses were observed better for seed yield per plant. In view of preponderance of non-additive gene action for seed yield per plant, hybrid breeding would be the most appropriate breeding methodology. However, to exploit both additive and non-additive gene actions as observed under the present investigation, biparental mating and inter se crossing between suitable lines following reciprocal recurrent selection may be employed. Most of the crosses involving high x low general combining parents exhibited high specific combining ability effects for various traits.

Keywords: *Brassica juncea*, combining ability

Introduction
Brassica juncea is an important oilseed crop plays a crucial role in edible oil economy of India and occupies premier position in Indian agriculture. It is major *rabi* oilseed crop of the Indian subcontinent occupies more than 80% of the total rapeseed mustard cultivated area. Contributes nearly 27% of edible oil pool in India and accounts for more than 13% of the global edible oil production (6). Mustard seed contains about 38 to 43 percent oil which is considered to be the healthiest and nutritious cooking medium. It is a plant of Asiatic origin with major center of diversity in china and it was introduced in India from China. Indian mustard (Brassica juncea (L.) Czern and Coss) is a natural amphidiploids (2n=36) of Brassica campestris (2n=20) and Brassica nigra (2n=16). It is (85 to 90%) self pollinated crop and 4 to 15% cross pollinated by honey bees. These occupied almost 6.28 tonne million ha during 2014-15 (1) with the production and productivity of 7.46 million tonnes and 1168 kg/ha, respectively (1). Where as in Uttar Pradesh mustard is most important *rabi* oilseed crop, it occupies 0.63 million hectares of total cropped area with production of 0.58 million tonnes and productivity of 930 kg/ha during the year 2014-15 (2). Heterosis breeding could be used for enhancing crop productivity in Brassica juncea, a major oilseed crop of the Indian subcontinent. It is an important tool to overcome the existing yield barriers. Comprehensive analysis of the combining ability involved in the inheritance of quantitative characters and in the phenomenon of heterosis is necessary for the evaluation of various possible breeding procedures (1). For developing promising varieties through hybridization a careful choice of parents and breeding methodology are matters of great concern to a plant breeder. Therefore, the effort has been made to assess the genetic worth of parents and hybrids by using diallel mating design involving ten lines of Indian mustard.

Material and Method
The experimental material comprised total ten promising genotypes of mustard *i.e.* CSR1020, CSR1088, CSR1027, CSR1014, CSR1082, CSR1025, CSR1066, CSR1118, CSR1104 and CSR1102 obtained from C.S. Azad University of Agriculture and Technology, Kanpur for 5m long rows of the research trail Indian mustard genotypes were sown in the agriculture research farm, Brahamanand Post graduate College, Rath (Hamirpur) maintaining plant to plant and row to row distances of 30 cm and 90 cm, respectively. At the flowering, these ten genotypes were crossed in all possible combinations under complete diallel system through hand

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emasculations and controlled pollinations. Kraft paper bags were used for avoiding the out crossing. Pollinations to emasculated florets were repeated once after two days for maximum seed setting. The seeds of F_1 cross, reciprocal and selfed parents were sown under a Randomized Complete Block Design with three replications in the field. Row to row distance of 75 cm and plant to plant distance of 25 cm were maintained, respectively. Each 5m long row was accommodating about 15 plants. All standard agronomic practices were carried out as mentioned earlier days to flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per main raceme, number of seeds per siliqua, siliqua length, days to maturity, 1000 seed weight, oil content and seed yield per plant. The data was recorded on five randomly selected plants of each genotype per replication and then average was calculated. The data collected from 55 genotypes (ten parents and 45 F_1 crosses) for 1 yield related traits were subjected to analysis of variance (11) to determine the significance of difference among various genotype means. The combining ability analysis was carried out for all the parents and F_1 genotypes according to procedure outlined by (5). Total variability was partitioned into component like general combining ability (GCA), specific combining ability (SCA) and error. Information was derived regarding the type of gene action controlling different traits and pattern of selection for improvement of the Indian mustard genotypes.

Result and Discussion
Analysis of variance
The analysis of variance revealed considerable genetic variation among parents and hybrids for almost all the traits under study (Table-1). The average performance of hybrids differed significantly from the average performance of parents indicating the presence of overall combining ability effects, which was also evident from the significance of parents vs. hybrids comparison for all the traits except for day to flowering (6 & 7). The analysis of variance for combining ability showed that general and specific combining ability variance were highly significant for almost all the characters indicating the importance of both additive and non-additive gene actions in the expression of seed yield and its component traits. The variance ratio was less than one for seed yield per plant (0.179).

Combining ability
Estimates of components of variance and their magnitude
The analysis of variance for combining ability was carried out separately for all the eleven characters are given in Table-2. The general combining ability was found highly significant for all the characters namely, days to flowering (25.740), plant height (1594.39),number of primary branches per plant (0.60), number of secondary branches per plant (6.50), number of siliquae per main raceme (2256.35), number of seeds per siliqua (4.34), siliqua length (0.34), days to maturity (1521.59), 1000 seed weight (0.97), oil content (12.30) and seed yield per plant (22.53). The specific combining ability was also observed highly significant for all the characters. The values of general combining ability variances were found higher than the specific combining ability variance for all the characters except number of siliquae per main raceme. The estimates of component of variance *i.e.* σ^2g and σ^2s had been worked out through combining ability variance for all the eleven characters. The σ^2g were partitioned into σ^2g due to males σ^2s and due to females (Table-2). The ratio between σ^2g

pooled and σ^2s and average degree of dominance expressed as (σ^2g/σ^2s) have been worked out. A ratio of 1:1 σ^2g/σ^2s indicates the equal important of σ^2g and σ^2g expression of particular characters while deviation between from 1:1 exhibited the relative importance of σ^2g or σ^2s depending on the value. The estimates of components of variance, their ratio and degree of dominance for different attributes are presented in table-2. The estimates of σ^2s due to female were found to be higher than σ^2g due to male for all the characters except number of siliques per main raceme. A comparison of relative magnitude of these observed to focus that additive gene action. However, the σ^2g due to male showed higher than the σ^2s due to female only one attribute number of siliques per main raceme (1868.80) indicated pre-dominance role of additive gene action. The ratio between estimated variance owing σ^2g/σ^2s was less than one unity for days to flowering, plant height, number of primary branches per plant, number of secondary branches per plant, number of siliquae per main raceme, number of seeds per siliqua, siliqua length, days to maturity, 1000 seed weight, oil content and seed yield per plant.

General combining ability effect (GCA)
This indicated the predominant role of non-additive gene action in the inheritance of seed yield per plant was observed by (3 and 9). The estimates of GCA effects (Table-3) revealed that the parent, CSR1020, CSR1027, CSR1066 and CSR1118 possessed highly significant and positive GCA effects for seed yield per plant indicating the presence of additive gene action or additive × additive interaction effects, (5 and 10), reported that when general combining ability effects are significant additive or additive x additive gene effects are responsible for the inheritance of that particular trait. However, it is evident from results that high general combining ability effects for seed yield per plant in the parents *viz.*, CSR1020, CSR1027, CSR1066 and CSR1118 were found to be good general combiners for this trait. The general combining ability is due to the additive and additive x additive gene effects which are fixable components of genetic variation Therefore, it would be worthwhile to use above parent lines in hybridization programme.

Specific combining ability effect (SCA)
The results of specific combining ability effects of hybrids expressed that none of the hybrids were consistently superior for all the characters are presented in table-3. The estimates of specific combining ability effects revealed that twenty one cross combinations *i.e.*, CSR1020 x CSR 1027, CSR1020 x CSR1014, CSR1020 x CSR 1066, CSR1020 x CSR 1102, CSR1088 x CSR1082, CSR1088 x CSR1025, CSR1027 x CSR1014, CSR1027 x CSR1082, CSR1027 x CSR1066, CSR1027 x CSR1102, CSR1014 x CSR1025, CSR1014 x CSR1066, CSR1014 x CSR1118, CSR1014 x CSR1102, CSR1082 x CSR1025, CSR1082 x CSR1102, CSR1025 x CSR1104, CSR1066 x CSR1118, CSR1066 x CSR1104, CSR1118 x CSR1104 and CSR1118 x CSR1102 exhibited significant and positive specific combining ability effects for seed yield per plant (Table-3). The cross with highest specific combining ability effects for seed yield per plant was CSR1066 x CSR1118; this cross had also found significant and positive specific combining ability effects in the desired directions for all the characters except 1000-seed weight, number of primary branches per plant and oil content. The result was also observed by (8). The cross CSR1020 x

CSR1027 has also exhibited significant and positive sca effect for number of secondary branches per plant, number of siliquae per main raceme and number of seeds per siliqua, CSR1020 x CSR1014 for days to maturity and 1000 seed weight, CSR1020 x CSR 1066 had only 1000 seed weight, CSR1020 x CSR 1102 for plant height, number of secondary branches per plant and number of siliquae per main raceme, CSR1088 x CSR1082 had plant height, CSR1088 x CSR1025 for plant height and 1000 seed weight, CSR1027 x CSR1014 had days to flowering and days to maturity, CSR1027 x CSR1082 number of seeds per siliqua, siliqua length and 1000 seed weight, CSR1027 x CSR1066 had number of siliquae per main raceme and number of seeds per siliqua, CSR1027 x CSR1102 for plant height, number of siliquae per main raceme and 1000 seed weight, CSR1014 x CSR1025 had number of seeds per siliqua, CSR1014 x CSR1066 for plant height, number of secondary branches per plant, number of siliquae per main raceme, number of seeds per siliqua, siliqua length and days to maturity, CSR1014 x CSR1118 had number of secondary branches per plant, number of siliquae per main raceme and 1000 seed weight, CSR1014 x CSR1102 for plant height, number of secondary branches per plant, number of siliquae per main raceme, number of seeds per siliqua, days to maturity and 1000 seed weight, CSR1082 x CSR1025 had number of siliquae per main raceme and 1000

seed weight, CSR1082 x CSR1102 for plant height, number of secondary branches per plant, number of siliquae per main raceme and number of seeds per siliqua, CSR1025 x CSR1104 had days to flowering, number of secondary branches per plant, number of siliquae per main raceme and 1000 seed weight, CSR1066 x CSR1118 for days to flowering, plant height, number of secondary branches per plant, number of siliquae per main raceme, number of seeds per siliqua, siliqua length and days to maturity, CSR1066 x CSR1104 had number of secondary branches per plant and number of siliquae per main raceme, CSR1118 x CSR1104 for days to flowering, plant height, number of siliquae per main raceme and number of seeds per siliqua and hybrid CSR1118 x CSR1102 exhibited significant and positive specific combining ability effect for plant height, number of seeds per siliqua, days to maturity and 1000 seed weight. However, none of the hybrid revealed significant positive SCA effect for oil content and number of primary branches. The outcomes clearly indicated that the parents involved in these crosses are good specific combiners; however, the relative contribution of the parents to specific combining ability effect for seed yield is through various yield attributing traits in different hybrids. Hence, the crosses are expected to through transgressive segregants with later generations (6).

Table 1: Analysis of variance for parents and F_1's for yield and its component characters in Indian mustard

Source of variation	d. f.	Days to flowering	Plant height (cm)	No. of Branches per plant		Number of siliquae per main raceme	Number of seed per siliqua	Siliquae length	Days to maturity	1000-seed weight (g)	Oil content (%)	Seed yield per plant (g)
				Primary	Secondary							
Replication	2	2.567	3.512	1.615	7.824	232.462	0.205	1.128	37.010	0.0034	0.031	0.075
Parents	9	44.900**	3562.476**	1.060**	8.250**	7519.936**	6.902**	0.887**	1105.818**	O.907**	11.612**	14.752**
F_1's	44	20.293**	735.202**	0.613	9.109**	3105.942**	3.827**	0.418**	1671.151**	0.712**	5.324**	34.564**
PvF1s	1	2.966	227.928**	2.150**	127.290**	31768.646**	11.898**	0.204**	1472.315**	0.925**	0.612**	377.736**
Error	108	1.949	1.949	0.178	1.108	414.185	0.207	0.097	36.062	0.010	0.233	0.424

Table 2: Analysis of variance for combining ability for 11 different traits in Indian mustard

Source of variation	d. f.	Days to flowering	Plant height (cm)	No. of Branches per plant		Number of siliquae per main raceme	Number of seed per siliqua	Siliquae length	Days to maturity	1000-seed weight (g)	Oil content (%)	Seed yield per plant (g)
				Primary	Secondary							
GCA	9	25.740**	1594.39**	0.60**	6.50**	2256.35**	4.34**	0.34**	1521.59**	0.97**	12.30**	22.53**
SCA	44	4.48**	175.10**	0.16**	3.01**	8447.55**	0.92**	0.12**	324.98**	0.14**	0.52**	10.54**
Error	108	0.64	1.63	0.59	0.37	137.92	0.69	0.32	12.02	0.03	2.37	0..14
σ^2_g		2.09	132.72	0.04	3.06	1868.80	0.35	0.02	125.80	0.08	0.82	1.86
σ^2_S		3.83	173.46	0.10	3.23	839.62	0.85	0.09	199.17	0.10	2.32	1.40
σ^2_g / σ^2_S		0.52	0.74	0.46	0.65	0.310	0.45	0.25	0.63	0.80	0.35	0.17

Table 3: Top ranking crosses for seed yield per plant in Indian mustard.

S. No.	Crosses	SCA effects	Per se performance	Magnitude of GCA effect	
				P_1	P_2
1	CSR1020 x CSR 1027	3.11**	25.97	2.78**	1.49**
2	CSR1020 x CSR1014	1.23**	22.97	2.78**	-0.63**
3	CSR1020 x CSR 1066	2.18**	25.34	2.78**	0.80**
4	CSR1020 x CSR 1102	3.93**	26.54	2.78**	0.24
5	CSR1088 x CSR1082	1.75**	19.62	-1.12**	-0.60**
6	CSR1088 x CSR1025	1.81**	20.54	-1.12**	-0.29**
7	CSR1027 x CSR1014	2.17**	17.28	1.49**	-0.63**
8	CSR1027 x CSR1082	2.38**	21.85	1.49**	-0.60**
9	CSR1027 x CSR1066	1.56**	22.44	1.49**	0.80**
10	CSR1027 x CSR1102	5.29**	27.38	1.49**	0.24
11	CSR1014 x CSR1025	1.59**	20.81	-0.63**	-0.29**
12	CSR1014 x CSR1066	3.21**	22.97	-0.63**	0.80**
13	CSR1014 x CSR1118	1.50**	20.71	-0.63**	1.25**

14	CSR1014 x CSR1102	3.04**	22.24	-0.63**	0.24
15	CSR1082 x CSR1025	3.88**	23.12	-0.60**	-0.29**
16	CSR1082 x CSR1102	3.28**	22.50	-0.60**	0.24
17	CSR1025 x CSR1104	2.74**	20.12	-0.29**	-2.47**
18	CSR1066 x CSR1118	7.06**	25.93	0.80**	1.25**
19	CSR1066 x CSR1104	2.99**	20.90	0.80**	-2.47**
20	CSR1118 x CSR1104	3.95**	21.32	1.25**	-2.47**
21	CSR1118 x CSR1102	1.77**	21.85	1.25**	0.24

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