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## ESTIMATION OF COMBINING ABILITY EFFECTS FOR YIELD AND FATTY ACID-RELATED TRAITS IN *BRASSICA RAPA* USING LINE BY TESTER ANALYSIS

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### SUMMARY

*Brassica rapa* is an important oilseed crop in Pakistan. It is a rich source of oil and contains 40%–46% oil. In addition, its meal has 38%–40% protein. Given their high levels of erucic acid and glucosinolate, mustard and rapeseed oil is unhealthy as regular cooking oil. A dire need to exploit the genetic variability of rapeseed germplasm is necessary to improve the performance of cultivars. The line × tester analysis helped estimate various types of gene actions that are important to quantitative traits. The key to successful research is selecting suitable lines and testers and designing good mating patterns. Choosing and developing genotypes with high yield and fatty acid profiles are the major concern of rapeseed breeders. The current research on hybridization and evaluation of *Brassica rapa* accessions sought better harvest and its related traits from the selected germplasm. The combining ability effects determination used line × tester analysis in rapeseed. The accessions' variability analysis exhibited extremely significant differences in yield and related traits. Recorded data for different morphological and yield-related qualities provided days till 50% flowering, the number of major branches per plant, and the number of secondary branches per plant had positive and significant general combining ability estimates, and all yield-related variables had extremely notable specific combining ability estimates. All the yield-related characteristics displayed a favorable and substantial connection in the examined germplasm. Among the lines, 28244, 40980, and 40981 occurred to be the best general combiners showing the additive gene action. The cross combinations, 40977 × 26283, 40979 × 26283, and 40981 × 26283, indicated significant specific combining ability effects, which showed the non-additive genetic effects of total variance due to the dominance and/or epistasis. The results suggested that the research material used in the remarkable study can benefit by improving yield and fatty acids-related components and can further enhance upcoming breeding programs based on strong particular combining ability impacts.

**Keywords:** additive, non-additive, line × tester, glucosinolate, erucic acid, protein, rapeseed, analysis of variance

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**Key findings:** Among 150 accessions screened concerning yield and their related traits, the accessions 40977 × 26283, 40979 × 26283, and 40981 × 26283 were the best cross combinations for yield and fatty acids-related components. These accessions will benefit future breeding programs for harvest enhancement along with its quality components.

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## INTRODUCTION

*Brassica rapa* is an important oilseed crop in Pakistan. It is a rich source of oil, containing 40%–46% of it. In addition, its meal has 38%–40% protein. *Brassica rapa* is characteristic of high content of macro and microminerals, as well as, high glucosinolate contents. Glucosinolate has an anti-inflammatory activity linked to reducing several types of cancer. Inversely, the erucic acid is undesirable in edible oil, with the seed meal containing a high level of glucosinolate is undesirable for using this meal as a protein source in animal feed. Genetic variability is vital to develop cultivars with improved yields, wider adaptation, and desirable qualities. A dire need necessitates exploring the rapeseed germplasm's genetic variability to improve cultivar performance.

Plant breeders and geneticists use a variety of mating designs and arrangements to produce improved plants. The right mating design should be according to the research goals, time frame, space, cost, and related agricultural limitations for genetic variance estimation (Nduwumuremyi *et al.*, 2013; Verma *et al.*, 2016). Line × tester is the most basic mating design, which provides the GCA of the lines and also the testers. It is a requirement for the estimation of gene actions of quantitative traits. The line × tester design provides information regarding using female and male inbred lines as parents for hybridizing to produce segregating populations expected to yield prodigious selections.

The key to successful research is selecting suitable parents and designing good mating patterns (Singh *et al.*, 2012; Saha *et al.*, 2015). Canola, sunflower, cottonseed, and rapeseed-mustard are important oilseed crops

in Pakistan. *Brassica rapa* is an essential oilseed crop belonging to the Cruciferae family, known as rapeseed and mustard. It is the second most significant source of oil after cotton seed in Pakistan, growing different oilseed crops; however, *Brassica rapa* has great potential to improve the situation of edible oil in the country. The plant has produced 0.21 million t of edible oil, grown on 0.283 million ha. The total edible oil production from all the resources accounted for 0.460 million t, with the total demand at 3.214 million t. This huge gap has edible oil imports fulfilling it (Anonymous, 2021–2022).

Grain yield is always the primary objective of any breeder, along with yield, and a cultivar should also be responsive to certain quality factors like fatty acid profile (Singh *et al.*, 2013). An urgent need to develop high-yielding lines with better oil quality can be through conventional breeding (Teilep and AliAbdelsatar, 2021; Zada *et al.*, 2013). Thus, selection must be according to the combining ability and performance of the parents. For this purpose, the line × tester mating design provides enough genetic information (Kempthorne, 1957). For the parents' selection, combining ability effects and gene action for quantitative traits is helpful to use meticulously in future hybridization programs for successful results. With combining ability analysis, identifying better parents and cross combinations are easier. Considering these, the appropriate study to estimate general and specific combining ability effects of entries proceeded to benefit future breeding programs aimed at maximizing rapeseed yield through hybrid seed production or varietal development.

## MATERIALS AND METHODS

### Experimental layout

The progressive research was an offshoot from continued work on 150 *Brassica rapa* L. accessions screened for yield and quality-related traits. Among these accessions, 10 better performing lines and three testers stood out for hybridization. The study ensued at the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan. In the relevant investigation, the research materials used for the study comprised 10 genetically diverse lines, viz., 28244, 40961, 40970, 40975, 40977, 40978, 40979, 40980, 40981, and 40982, and three testers, namely, 26240, 26283, and 28215. Thirty hybrids (F<sub>1</sub>s) emerged, developing through line × tester mating design.

The material evaluation extended to 13 parents, 30 F<sub>1</sub>s hybrids, and one check cultivar in the line × tester mating design under RCB design using three replications. Maintaining the row-row and plant-plant distance ensured a good crop. Data recording from five randomly selected plants of each entry ran in each

duplication for 15 different yield and fatty acids-related characters.

### Data recorded

The data recorded on five randomly selected plants from each of the parents and crosses in each replication consisted of 15 characteristics (days-flower initiation, days-flower completion, days-silique formation, number of aborted silique/plant, plant height (cm), days-first harvest, number of branches/plant, number silique/plant, number of seed/silique, 100-seed weight, seed yield/plant (g), oil percentage, protein percentage, glucosinolate percentage, and erucic acid percentage in *Brassica rapa*).

### Statistical analysis

Means square of three replications with parents and crosses and statistical significance calculations employed Analysis of Variance using R-Software (Chambers, 2008) in line × tester mating design. Line × tester assessment also ran for combining ability analysis (Kempthorne, 1957) (Table 1).

**Table 1.** Mean square values from analysis of variances for yield and its related traits in *Brassica rapa*.

SOV	DF	DFI	DFC	DSF	ASPP	PH	NPBPP	NSBPP	NSPP	SS	HSW	YPP	OP	PP	Glu	EA
Rep	2	14.6**	16.05**	1.14	18.26**	44.52**	0.85	476.16**	0.84	1662.58**	0.00	12.33**	54.59**	40.13**	228.28**	84.41**
Treat	42	26.94**	18.64**	15.94**	2.05	3161.91**	33.523**	92.26**	33.52**	5728.21**	0.36	835.19**	22.04**	24.73**	319.89**	13.46**
Parents	12	27.23**	38.97**	15.31**	0.70	2388.33**	36.69**	65.80**	36.70**	5402.38**	0.49	748.28**	11.10**	61.21**	142.79**	16.62**
P Vs C	1	0.96	161.79	0.74	1.86	5782.29**	2.55	83.13**	2.55	479**	2.40	55.80**	158.25**	183.58**	0.25	73.69**
Crosses	29	27.71**	5.29*	16.72**	2.61	3391.65**	33.281**	103.51**	33.28**	6044.04**	0.23	898.03**	21.87**	4.15*	404.20**	10.07**
Lines	9	69.41**	3.02*	8.33**	1.55	3026.22**	31.98**	74.67**	31.98**	11716.69**	0.12	760.74**	10.45**	1.84	82.95**	13.52**
Testers	2	0.08	1.73	2.01	2.43	1047.14**	6.344*	195.48**	6.34*	33.64**	0.61	131.62**	74.15**	17.59**	3790.51**	15.04**
L × T	18	9.93**	6.82**	22.55**	3.16	3834.87**	36.92**	107.72**	36.93**	3875.53**	0.25	1051.83**	21.77**	3.81*	188.56**	7.80**
Error	84	19.23	23.78	5.81	0.88	118.87**	4.67	135.72	4.67	335.52	0.00	27.23	14.14	4.62	257.58	13.82
Total	128	2775.96	2812.24	1160.13	196.62	142874.25	1802.06	16227.49	1802.06	272093.3	15.37	37390.20	2222.24	1506.77	35528.45	1894.52

\*\*= Highly Significant at 0.01 level of probability,

DF = degrees of freedom, DFI = Days to flower initiation, DFC = Days to flower completion, DSF = Days to silique formation, ASPP = Aborted silique per plant, PH = Plant height, NPBPP = Number of primary branches per plant, NSBPP = Number of secondary branches per plant, NSPP = Number of silique per plant, SS = Seed per silique, HSW = hundred seed weight, YPP = Yield per plant, OC = Oil content, PC = Protein content, Glu = Glucosinolate content, and EAC= Erucic acid content.

## RESULTS AND DISCUSSION

Several techniques are now available with the advancement in biometrical genetics, which leads to the selection of promising parent crosses for further manipulation by quantitative genetic analysis. From the breeder's point of view, parents who produce good progenies on their crossing are of immense value. The success of any crop development program usually depends upon the isolation of valuable cross combinations with high combining ability. Combining ability analysis is a powerful tool for identifying the best cross combinations potential to transmit desirable traits to the progeny. Meanwhile, it benefits the estimation of gene action responsible for the inheritance of the attribute.

### Genetic variability

Analysis of variances for line  $\times$  tester progenies for 15 characteristics in *Brassica rapa* resulted in vast diversity that leads significantly to the development of various cross combinations. The ANOVA results exhibited significant variation within parents for all the qualities, which showed that the parents differ for these except the number of aborted siliques/plant, 100-seed weight for testers, number of aborted siliques/plant for parents, days-50% flower completion, 100-seed weight for parents vs. crosses, and number of aborted siliques/plant among crosses. Lines and line  $\times$  tester showed nonsignificant results that might be due to the use of diverse germplasm or environmental change. These results agree with Hassan *et al.* (2018), Ashish *et al.* (2019), Gul *et al.* (2019), Dezfouli *et al.* (2019), and Abdelsatar *et al.* (2020), who also reported similar findings. Ali *et al.* (2015) reported relevant results for the number of aborted leaves/plant and 100-seed weight. Sincik *et al.* (2011) also conveyed similar results for the days-50% flower completion, number of aborted leaves/plant, 100-seed weight, number of silique/plant, and number of branches/plant.

### General combining ability effects

The general combining effects for several quantitative traits of *Brassica rapa* under field conditions are in Table 2. Among lines, 28244 had negative and significant GCA effects for days-50% flower completion, days-50% silique formation, and the number of aborted silique/plant. The number of secondary branches/plant, weight of 100 seeds, and yield/plant showed positive and substantial GCA impacts. The numbers of seeds/silique, primary branches/plant, secondary branches/plant, yield/plant, and oil % exhibited positive and significant GCA estimates for line 40980. However, plant height, days-50% silique development, and glucosinolate, protein, and erucic acid percentages showed negative and substantial effects on combining ability.

Line 40981 exhibited significant but negative GCA effects for plant height, glucosinolate, protein, and erucic acid percentages. Positive, notable outcomes also showed for numbers of silique/plant, primary branches/plant, secondary branches/plant, yield/plant, and oil%. Rameeh (2017), Farshadfar *et al.* (2013), Kang *et al.* (2013), Meena *et al.* (2015), and Mahmud *et al.* (2009) also found positive and significant GCA effects for plant height, numbers of seeds/silique, primary branches/plant, secondary branches/plant, and yield-related traits in *Brassica rapa*. Shah *et al.* (2021) reported similar results for yield/plant, oil%, days-maturity, plant height, numbers of branches/plant, siliques on the main branch, total silique/plant, and seeds/silique. The parent GS 1 and PS66 were good general combiners. The parent GS 1 also showed good general combining ability for harvest index, days-50% flowering, 100-seed weight, and erucic acid and glucosinolate percentages.

Significant and negative combining ability estimates are ideal for days-50% flowering initiation, days-50% flower completion, days-50% silique formation, and plant height. These findings for yield-related components were also analogous to Qian *et al.* (2007), Sabaghnia *et al.* (2010), and Dar *et al.* (2011).

**Table 2.** General combining ability estimates for yield-related traits in parents and cross combinations.

Genotypes	DFI	DFC	DSF	ASPP	PH	NPBPP	NSBPP	NSPP	SS	HSW	YPP	OP	PP	Glu	EA
Lines															
28244	-0.44	-0.56	-2.41	-0.69	-0.33	10.42	3.05	0.17	1.07	37.03	3.83	13.69	0.14	0.19	0.01
40961	-1.33	-0.39	-4.91	0.15	-0.10	5.93	0.12	-1.21	-1.16	21.70	-2.50	-14.87	0.09	-0.54	0.23
40970	-1.11	-0.05	-3.20	-0.65	0.45	11.27	-0.14	2.17	2.73	-11.74	4.61	26.58	-0.58	-0.32	-0.12
40975	2.78	0.64	4.87	0.56	0.29	-2.16	0.03	-0.16	-0.60	-43.86	0.39	-17.64	-0.02	0.9	-0.54
40977	2.56	-2.52	1.40	0.27	-0.63	-10.53	0.15	-0.81	-0.82	-63.52	2.17	15.02	-0.13	-1.1	0.9
40978	-4.11	-1.30	-0.21	-0.34	1.20	0.83	0.02	2.23	2.73	28.19	1.61	-10.09	0.64	-0.46	0.23
40979	1.67	0.26	2.07	0.24	1.86	-5.85	0.09	-0.28	-0.82	-3.63	0.83	-24.31	0.09	0.68	-1.21
40980	-3.22	-0.67	0.15	-0.02	-0.70	9.53	-0.22	0.71	0.73	33.03	-3.72	23.13	-0.58	-0.46	-0.32
40981	-4.67	-1.64	-2.59	0.58	0.02	-4.24	-0.05	-0.3	-0.38	21.59	2.50	0.58	-0.02	0.68	0.12
40982	-0.33	1.18	-2.38	-0.12	-2.06	-15.19	0.05	-2.1	-3.49	37.59	-2.06	-12.09	-0.13	0.79	0.45
SE	0.49	0.54	0.27	0.10	1.21	1.29	2.04	0.24	0.20	0.52	0.01	0.95	0.23	0.56	0.33
Testers															
26240	0.53	12.38	0.79	-0.29	1.57	-0.107	0.28	0.11	0.64	-2.91	-1.72	0.3	-0.29	0.07	-0.01
26283	0.80	9.57	0.94	1.70	2.403	-0.051	0.34	0.18	0.68	1.86	-4.86	-1.03	0.18	1.27	1.056
28215	0.27	2.81	1.04	1.41	0.967	0.166	-0.52	0.34	-1.22	1.06	0.58	-0.27	0.21	0.2	-0.044
SE	0.17	0.44	0.89	0.80	0.95	0.01	0.41	-0.52	3.3	1.1	0.41	-0.32	0.34	1.13	1.99

DFI = Days to flower initiation, DFC = Days to flower completion, DSF = Days to silique formation, ASPP = Aborted silique per plant, PH = Plant height, NPBPP = Number of primary branches per plant, NSBPP = Number of secondary branches per plant, NSPP = Number of silique per plant, SS = Seed per silique, HSW = hundred seed weight, YPP = Yield per plant, OC = Oil content, PC = Protein content, Glu = Glucosinolate content, and EAC = Erucic acid content.

Among testers, 26283 had significant and positive combining ability effects for yield and fatty acids-related traits under study. Tester 28215 showed minor significant and positive GCA effects for plant height, number of primary branches/plant, and 100-seed weight. The tester, 26240 exhibited positive and meaningful GCA outcomes for the number of primary branches/plant. Testers 26240 (-0.53) and 28215 (-0.27) expressed the maximum negative GCA effects for the said trait.

### Specific combining ability effects

The specific combining ability (SCA) estimates ran through for yield and fatty acid-related traits of *Brassica rapa* under field conditions (Table 3). Among entries, crosses 40977 × 26283, 40979 × 26283, and 40981 × 26283 showed significant and positive SCA estimates for all yield and fatty acids-related traits. Crosses 40977 × 26283 and 40979 × 26283 marked positive and relevant SCA effects for the number of seeds/silique, primary and secondary branches/plant, yield/plant, and oil%. The highest negative and significant SCA estimates emerged in the cross 40977 × 26283 for the number of aborted silique/plant, plant height, glucosinolate, protein, and erucic acid percentages. In the cross, 40979 × 26283, positive and substantial SCA effects appeared for the number of silique/plant, primary and secondary branches/plant, yield/plant, and oil%. Except for days to maturity, the variance was higher due to SCA than GCA because of the non-additive type of gene action (Shah *et al.*, 2021). These findings concurred with those of Rahman *et al.* (2011), Dar *et al.* (2011), and Patel *et al.* (2013). Combining ability estimates showed that the traits 100-seed weight, number of silique/plant, and number of branches/plant were most efficient among the yield and fatty acid-related traits. Meanwhile, the maximum SCA value came from crosses 40981 × 26283, 40961 × 26240, and 40970 × 26240 for seed/silique. Singh *et al.* (2002) and Khan *et al.* (2008) found similar results for seed/silique.

In previous studies, Channa *et al.* (2018) and Oghan *et al.* (2018) reported that fatty acid-related traits are under control by non-additive genes. These include glucosinolate percentage and oil content. The F<sub>1</sub> cross combinations with parents of good GCA effects can serve effectively in any conventional breeding program as the pedigree method. Almost 50% of F<sub>1</sub> hybrids showed negative SCA effects and non-additive gene action types. These effects alone are of limited value for the choice of parents in the breeding programs; therefore, in combination with other parameters, these effects may be useful, such as, the GCA of the respective parents (Nassimi *et al.*, 2006). Rameeh (2012) revealed significant positive SCA effects for the number of silique/plant, seed/silique, thousand-seed weight, and erucic acid percentage. Arifullah *et al.* (2012) and Kumar *et al.* (2016) studied positive notable SCA effects for thousand-seed weights, oil percentage, and number of branches/plants. Mahmud *et al.* (2009), Viana and Matta (2003), and Farshadfar *et al.* (2013) studied the relevant and positive SCA effect on seed yield.

Significant SCA effects exhibited the predominance of non-additive gene action with maternal genetic effects. GCA and SCA effects showed both additive and non-additive gene actions controlling morphological, yield, and fatty acid-related characteristics of lines, testers, and F<sub>1</sub> crosses of rapeseed, respectively. Estimates of GCA and SCA gave a brief history of the genetic potential of the breeding material. Existing findings provided variable magnitude and direction of GCA in the parents. It proposes these lines can benefit for economically important characters in the hybridization scheme.

### CONCLUSIONS

This study evaluated the general combining ability of 10 superior lines and three testers and the specific combining ability of 30 crosses of rapeseed through line × tester analysis. The highest positive GCA value for seed yield pointed to the 28244 line. The GCA ranking of

**Table 3.** Specific combining ability estimates for yield-related traits in parents and cross combinations.

Cross Combinations	DFI	DFC	DSF	ASPP	PH	NPBPP	NSBPP	NSPP	SS	HSW	YPP	OP	PP	Glu	EA
28244 × 26240	-3.67	-3.67	-0.02	-12.31	-0.58	0.01	4.82	1.04	0.81	1.6	0.03	2.01	0.94	0.23	-1.58
40961 × 26240	16.32	15.32	0.25	28.70	12.43	0.10	-0.68	0.45	-0.18	1.48	-1.18	2.08	-1.44	1.70	-1.57
40970 × 26240	-1.67	-1.67	0.12	-7.15	2.06	0.26	-2.69	-0.39	-3.52	1.59	-0.29	-1.33	-2.07	1.85	1.30
40975 × 26240	2.54	2.54	-0.05	12.92	1.27	-0.14	-1.01	0.59	1.09	-1.96	-0.29	0.43	0.21	-0.09	-1.36
40977 × 26240	-0.34	-0.34	-0.15	6.84	2.92	0.32	8.18	-0.34	0.36	-0.96	0.36	-0.22	1.34	1.25	-1.47
40978 × 26240	-2.7	-2.7	0.03	-3.47	1.56	0.60	-9.78	1.93	-2.32	0.02	0.03	-0.09	0.48	0.58	1.01
40979 × 26240	1.52	1.52	-0.14	7.92	0.56	0.69	2.12	1.00	3.34	0.47	-1.41	-2.54	0.50	2.44	2.46
40980 × 26240	3.97	3.97	0.12	11.38	1.35	1.65	-4.35	0.67	-2.54	0.24	-0.96	-2.45	1.03	1.66	0.81
40981 × 26240	-0.7	-0.7	0.14	-5.29	0.57	0.11	0.67	1.38	0.23	1.24	0.14	-1.17	-0.37	4.38	-0.41
40982 × 26240	-2.58	-2.58	0.01	-7.22	-1.77	-1.47	15.01	1.04	-1.67	-1.2	-0.18	3.28	-0.61	-14.0	0.80
28244 × 26283	4.97	4.97	-0.34	30.49	0.66	-0.49	-5.40	-2.05	-3.76	-1.2	-0.63	-3.58	-1.53	9.54	-0.35
40961 × 26283	-2.81	-2.81	-0.40	-14.93	2.97	-0.60	-1.76	-2.91	-3.12	-1.76	-0.17	-2.64	0.76	-3.82	0.56
40970 × 26283	-1.47	-1.47	0.34	-7.71	0.39	-1.28	1.02	-0.42	2.34	-0.84	0.84	-0.02	0.42	2.50	-1.97
40975 × 26283	-2.36	-2.36	0.17	-10.74	-0.09	0.52	-3.36	-0.17	-2.54	-0.17	-3.04	-1.00	-0.32	-0.58	-0.03
40977 × 26283	-1.28	-1.24	-0.56	-0.42	-3.21	7.29	-5.82	6.76	4.09	10.24	11.28	8.99	-0.13	-16.3	-0.43
40978 × 26283	4.93	4.93	-0.08	13.37	2.01	0.94	0.23	-1.58	0.28	-0.84	-0.17	-0.58	0.01	4.82	1.04
40979 × 26283	-0.84	-0.59	-4.50	-11.46	-2.08	-1.44	3.89	7.98	6.90	4.76	10.21	9.43	-0.10	-0.68	0.45
40980 × 26283	-0.4	-0.4	-0.01	16.95	-1.33	-2.07	1.85	1.30	-3.62	0.71	-3.04	2.06	0.26	-2.69	-0.39
40981 × 26283	-2.40	-5.4	-0.18	-3.49	-0.43	10.21	6.09	5.36	7.37	6.04	14.28	10.27	-0.14	-1.01	0.59
40982 × 26283	-0.84	-0.84	-0.22	-15.62	-0.22	1.34	1.25	-1.47	-0.17	-0.17	0.39	2.92	0.32	8.18	-0.34
28244 × 28215	-1.4	-1.4	0.36	-18.17	-0.09	0.48	0.58	1.01	0.84	-0.4	-0.71	1.56	0.60	-9.78	1.93
40961 × 28215	-3.51	-3.51	0.15	-13.76	-2.54	0.50	2.44	2.46	-3.04	0.48	2.14	0.56	0.69	2.12	1.00
40970 × 28215	2.93	2.93	-0.46	14.86	-2.45	1.03	1.66	0.81	1.28	-2.51	-1.29	1.35	1.65	-4.35	0.67
40975 × 28215	-0.39	-0.39	-0.12	-2.17	-1.17	-0.37	-4.38	-0.41	0.39	0.71	-1.18	0.57	0.11	0.67	1.38
40977 × 28215	-1.51	-1.51	0.08	-6.42	3.28	-0.61	-14.0	0.80	-0.71	1.04	2.03	-1.77	-1.47	15.01	1.04
40978 × 28215	2.23	-2.23	0.06	9.90	3.58	-1.53	-9.54	-0.35	-2.14	-0.82	-1.63	0.66	-0.49	-5.40	-2.05
40979 × 28215	-2.01	-2.01	-0.36	-19.38	-2.64	0.76	-3.82	0.56	-1.29	-0.4	0.81	2.97	-0.60	-1.76	-2.91
40980 × 28215	-3.67	-3.67	-0.10	-28.33	-0.02	0.42	2.50	-1.97	-1.18	-0.96	-0.18	0.39	-1.28	1.02	-0.42
40981 × 28215	1.1	1.1	0.04	5.77	-1.00	-0.32	-0.58	-0.03	2.03	-2.39	-3.52	-0.09	0.52	-3.36	-0.17
40982 × 28215	3.32	3.32	0.20	22.84	1.99	0.13	-16.3	0.43	-1.63	1.37	1.09	-6.21	0.29	5.82	-0.46
SE	1.82	1.53	1.19	5.02	2.68	1.27	1.20	2.02	0.02	1.35	1.25	0.09	1.04	2.01	3.68

DFI = Days to flower initiation, DFC = Days to flower completion, DSF = Days to silique formation, ASPP = Aborted silique per plant, PH = Plant height, NPBPP = Number of primary branches per plant, NSBPP = Number of secondary branches per plant, NSPP = Number of silique per plant, SS = Seed per silique, HSW = hundred seed weight, YPP = Yield per plant, OC = Oil content, PC = Protein content, Glu = Glucosinolate content, and EAC = Erucic acid content.

the studied accessions for seed yield and fatty acids-related traits was 28244 > 40980 > 40981. The highest positive SCA value for seed yield came from 40977 × 26283 cross. The SCA ranking for seed yield was 40977 × 26283 > 40979 × 26283 > 40981 × 26283. Notably, 28244 and 40980 lines are the superior produced lines from their combination with other testers leading to F<sub>1</sub> hybrids with higher plant seed yield. On the specific combining ability indicator, the cross of 40977 × 26283 is the best cross for producing an F<sub>1</sub> hybrid with a higher seed yield and fatty acids-related traits. Genetic variability among sources of variations can further serve as yield improvement program in *Brassica rapa*. Mean values with the estimates of general and specific combining ability effects briefly described the genetic potential of the breeding germplasm. Existing findings showed variable magnitude and direction of GCA in the parents. It proposes that these lines can be helpful for economically important characters in the hybridization scheme.

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