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Research Article

Genetics of Seed Yield Attributes and Oil Contents in *Brassica rapa* L.

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ABSTRACT

Brassica rapa L. has become a promising crop to sustainable agricultural and industrial growth since reliance on imports goes up and biofuel is in demand. The current work dissected the variability in genetic aspects including ability, heterosis and heritability to seed yield and traits concerned with oil which provide new information in developing hybrids. Eleven high performing accessions were identified as female lines and three low yielding accessions were identified as testers and 33 F1 hybrids were produced in Line×Tester mating plan. The hybridization was controlled in 2022-23, and then the evaluation in the field was carried out in 2023-24 based on a randomized complete block design that had three replications. There was significant difference between parental lines and hybrids. Line 25052 showed high general combining ability (GCA) on average on various traits and the tester ORL1 had a positive effect in the branching, early flowering and seed productivity. Cross 25052×ORL1 was one of the best hybrids with high specific combining ability (SCA) and great level of heterosis, as it showed high levels of plant height, number of siliques, yield of seed per plant and oil content in both years of experimentation. In a similar manner, cross 25037×ORL3 and 25042×ORL3 were found to have significant SCA effects and heterotic expression, further supporting the fact of non-additive action of gene in hybrid vigor. Estimates of hereditability showed that quality-related traits (especially oil content and 100-seed weight) were largely under the influence of additive genetic effects, which ensured meritorious enhancement by means of breeding. Conversely, additive and dominance gene effects manifested in yield-related traits, thus explaining the relevance of the properties in breeding on heterosis. The results highly suggest a potential of cross 25052×ORL1 to improve yield and simultaneously enhance the quality of the oil in B. rapa. Its stability over the years of the experiments proves that it can be further developed into multi-location trials. This research, in addition to the direct implications of breeding, provides a set of breeding variances to be exploited in breeding breeds of B. rapa, which eventually result in the generation of high-yielding and high-oil content coupled with climate-tolerant crops to decrease dependence on imports and enhance the sustainability of agriculture.

Keywords: *Brassica rapa*, Combining ability, Crop breeding, Heterosis, Line×tester analysis, Oil content, Seed yield

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INTRODUCTION

Pakistan's annual fuel oil (furnace oil) requirement for 2024-25 is approximately 3-3.5 million tons, with local refineries producing 50-60% (1.5-2.1 million tons) from domestic crude oil production of 73,000 bpd, while the remaining 40-50% (1.2-1.7 million tons) is imported at an estimated cost of $0.9-1.3 billion annually, based on global oil prices averaging $80 per barrel. Local oil fields, including Toot, Lower Sindh, and Makori Deep-03, contribute to crude supply, but limited extraction capacity drives import reliance. Scaling biodiesel production and boosting local oil exploration could reduce import dependency. As per the 2024-25 agricultural survey of Pakistan, rapeseed and mustard were cultivated on 1.055 million hectares, producing approximately 0.470 million tons of seed, which yielded about 0.178 million tons of oil. (GOP, 2024-25). *Brassica rapa* L. possesses a high oil content potential, ranging from 35-45%. Its oil is used in medicine, food, massages, diabetes cure, chemical and engineering industries (Kaur *et al.*, 2021). Moreover, B. rapa oil has high medicinal value and is useful for cancer treatment due to its anticancer properties. Besides its uses in different fields, *Brassica rapa* L., oil is of high value due to presence of abundant unsaturated fatty acids which make the oil useful as source of lubricant, hydraulic fluids and biofuels (Raboanatahiry *et al.,* 2021). Moreover, rapa oil is used in different industries, which include pharmaceuticals, paints, and cosmetic products. Genetic variation is the crucial component for the determination of divergence among the individuals in the plant progeny. The heterogeneity among the species of a plant population allows a breeder to develop the varieties with desirable traits (Kaur *et al.*, 2007; Sikarwar *et al.*, 2017; Swarup *et al.,* 2021).

Breeders use different breeding techniques, which include conventional and non-conventional methods, to develop different high yielding varieties. Some of the breeding methods that are employed for enhancement of genetic makeup of resultant varieties are diallel, single cross, line tester, North Carolina, and pedigree method. Breeding methods other than the line × tester design generally require more time and resources. The line × tester mating design is widely used, as it provides comprehensive information about the combining ability of both female and male inbred lines (Muthoni & Shimelis, 2020). These inbred male and female lines are hybridized with each other to produce segregating populations. Inbred lines are those plants that are produced by a continuous process of selfing the plants to achieve homozygosity (Shuro, 2017). Line × Tester is a suitable and preferred method as it requires less area as compared to the North Carolina design because of a smaller number of crosses made. For measuring the combining ability of the yield contributing characters for good hybridization, the Line×Tester technique is useful (Singh & Chaudhary, 1979; Mustafa *et al.*, 2023).

To measure the suitability of the plants to be selected as female or male, combining ability analysis is a powerful tool. Combining ability analysis is used to test the superior parent lines and their combinations. General combining ability (GCA) provides the mean performance of crosses in the line parental combinations (Begna, 2021). By using line × tester method, the additive gene effects can be calculated through general combining ability. In contrast, specific combining ability determines which cross among the crosses achieved more success (Fasahat, 2016). Selection of parent plants must be based on the combining ability and performance of parents (Saha *et al.*, 2015). For the estimation of genetic variance mating designs should be according to the research time frame, goals, costs, and related agricultural limitations (Verma *et al.*, 2016).

Heterosis is the process where the offspring are considered superior to the parents (Nausheen *et al.*, 2015). The use of heterosis as a method helped scientists overcome rapeseed yield limitations while utilizing its genetic reserves. Phenotypic stability under stress can be achieved through heterosis (hybrid vigor) under stress and there is a balanced distribution of traits among the offspring from their parents (Nasim *et al.*, 2014;Tahir *et al.*, 2018). Heritability is an important genetic factor that is responsible for causing phenotypic variation in the offspring of the parents and is caused by genetic factors. Results of heritability offer a breeder benefit when selecting parents with desirable traits (Braun, 2011). Heritability is further classified into two types: broad-sense (BSH) and narrow-sense heritability (NSH). BSH measures both additive and gene's non-additive effects and contributes to the overall trait variation. Conversely, NSH estimates the distribution of phenotypic variability that is explained only by the additive genetic effects, which are directly inherited from parents to offspring through individual genes controlling the trait (Jahan *et al.*, 2014). The key objective of study is to figure out the heterogeneity for Seed yield attribute and oil content in *B. rapa* L. as well as to select the potential parents based on GCA and best cross combinations based on SCA, and heterosis.

MATERIALS AND METHODS

The study utilized locally adapted germplasm, and authorization for its use and for conducting field trials was obtained from the administration of the University of Agriculture Faisalabad, Pakistan. The study was restricted to a single location due to availability constraints, and multi-location trials will be considered in future research. A total of fourteen rapeseed (*Brassica rapa* L.) accessions were obtained from the Oilseeds Research Lab, Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. Based on two years (2022-23 & 2023-24) of seed and oil yield data, eleven high-performing accessions (25012, 25017, 25022, 25027, 25032, 25037, 25042, 25047, 25052, 25057, and 25067) were selected as female lines, whereas three low-yielding accessions (ORL1(Sandal Canola), ORL2 (Anmol Raya), and ORL3 (Nifa Sarson)) were chosen as testers (male parents).Crosses were developed using the Line × Tester mating design under controlled pollination conditions to ensure accuracy in hybridization. The resulting F_1 seeds were harvested separately, threshed with care, and stored under optimal conditions for subsequent field evaluation.

Experimental Design

In each of the two experimental years, the F 1 hybrids and the respective parents were replicated with three replicas in the experimental area in the RCB design. Fifteen seeds of the cross and parent were planted in each replication. The management of the experimental plots was maintained at the same level, i.e. Agronomic. The experimental units were 15 plants in a single row and 15 cm between plants and 45 cm between rows (row length of 2.25 m and the plot area in one replication about 1.0 m 2) to guarantee the adequate development of plants and to reduce the competition. All the suggested agronomic activities (fertilization, irrigation, and pest control) were closely observed.

Recording and Measurement of Phenotypic Data

To record data using the trait analysis method, based on ten healthy and representative plants of each entry per replication were randomly chosen to use in data recording. It assessed the following quantitative characteristics using standardized procedures. At maturity, the main shoot height was estimated in terms of length of main stem between the base to the apex of main stem by means of a meter rod. Time to half flowering was measured as the number of days between sowing and half flowering of the plants. The total number of primary and secondary branches in the plant was established by counting the number of branches between the base and the terminal one. Most of the siliques per plant were counted by hand to determine pod production. The number of seeds per plant was calculated with an automated seed counter to make it accurate. In the case of 100 seed weight, a 100 seed sample was randomly selected and weighed (g) on a precision balance. The yield of the seeds per plant was taken after the normal post-harvest practices. The amount of oil was measured using Soxhlet extraction method that gave a good estimate of the lipid content.

Statistical Analysis and Genetic Evaluation

Analysis of variance (ANOVA) was used to determine the level of significance and genotypic variation among the recorded data. The overall variability was also broken down into sources of variation (replication, treatment, and error) according to the steps outlined by Steel *et al.* (1997). Genetic analysis was done through measurement of general combining ability (GCA) and specific combining ability (SCA) with the use of line x tester analysis method as explained by Sprague and Tatum (1942) to explain additive and non-additive gene interactions. In addition, the measurement of hybrid vigor was done by estimating the heterosis on the basis of both, mid-parent value and better-parent value in all the quantitative traits by using the method of Kempthorne (1957).In addition, estimates of either broad-sense heritability or narrow-sense heritability were also calculated to measure the genetic control and the possible inheritance of the yield- and quality-related traits (Goldberger, 1979). These studies have been done individually in the years, the first year was spent in cross development and estimation of the genetic parameters and the second year was focusing on performance assessment in the field.

RESULTS AND DISCUSSION

Cross Development from Selected Parents

In the first year (2022-23) hybridization was performed based on a Line × Tester design to unravel genetic variation and approximate combining abilities between genotypes of *Brassica rapa* L. being selected. There was also a significant difference (Table 1), in plant height and the total primary branches per plant. Likewise, the yield levels of plants under treatments, parents, crosses and testers differed greatly. These results show that there is high genetic heterogeneity in the germplasm, which plays a vital role in successful selection and evolution of hybrids (Attri and Rahman, 2017). Lines 25027, 25047 and 25052 exhibited the largest general combining ability (GCA) effects relating to various yield and quality traits and are good choices to include them in breeding programs as shown in figure 1a (Nasim *et al.*, 2014; Rajkumar and Panjabi, 2022; Shelly, 2020). Particularly, GCA was significant in terms of line 25052 which represented plant height, number of primary and secondary branches, total amount of siliques and Number of seed per plant, hundred seed weight (grams), oil content, and single plant yield (grams). This indicates its constant additive effects on gene on agronomically significant characteristics (Tomar *et al.*, 2018; Zohora, 2022). The figure 1a line 25027 exhibited extremely strong values of GCA of plant height, number of primary branches per plant, number of secondary branches per plant, number of total seeds per plant, weight of hundred seeds, oil content and yield per plant (Farhana, 2012; Mustafa *et al.*, 2023).

Table 1. Analysis of variance of lines, testers, and Line×Tester of parents in *Brassica rapa* L (2022-23).

S.O.V.	D.F	PH	PBPP	SBPP	DFF	NSQPP	NSPP	HSW	OC	YPP
Replications	2	8.23*	4.21*	143.94*	61.12*	4.07*	155863.30*	6.29*	6187.58*	602.54*
Treatments	46	32.07*	5.87*	81.14*	22.56*	275.44*	84589.23*	0.29*	1646.06*	1394.58**
Parents	13	59.51	8.53*	114.52*	19.97*	295.26*	200260.08*	0.01*	9.08*	1042.92**
Parents vs Crosses	1	5.53*	11.30*	259.37*	19.13*	354.79*	93674.98*	13.94*	68799.06*	34909.73**
Crosses	32	21.63*	4.58*	61.19*	23.76*	264.51*	36412.13*	0.06*	7.81*	384.41*
Lines	10	7.27*	4.38*	70.69*	12.99*	348.96*	49411.44*	0.06*	9.17*	178.19*
Testers	2	6.29*	4.91*	21.59*	12.13*	77.83*	17639.84*	0.10*	15.24*	2552.44**
Line×Tester	20	30.52*	4.65*	60.84*	30.43*	243.02*	31998.28*	0.06*	6.31*	246.62*
Error	92	54.35	4.00	109.73	22.33	142.63	62245.10	0.10	139.57	237.10

**=Statistically very significant at @1%, *= Statistically significant at @5%, SOV= Source of variance, D. F= Degrees of Freedom, PH= Overall Plant Height, PBPP= Primary branching/ plant, SBPP= Secondary branching /plants, DFF= Days to fifty percent flowering, NSQPP= Number of silique/plant, NSPP= Number of seeds/plant, HSW= Hundred Seeds weight, YPP=Yield/plant, OC= Oil Contents.

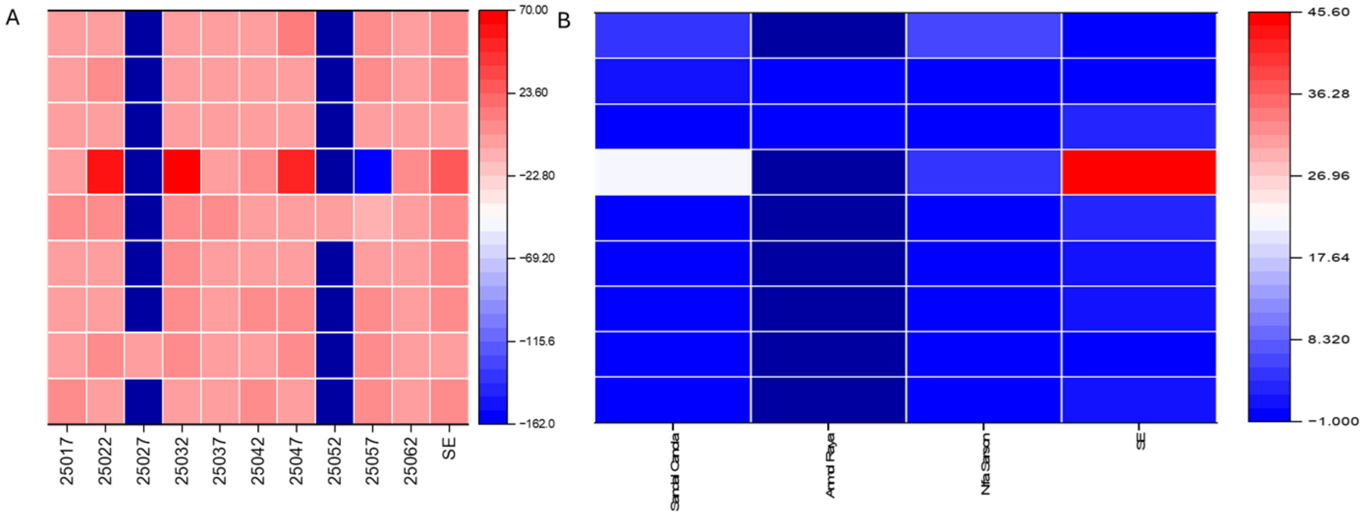

Figure 1. Heatmap showing the effects of general combining ability (GCA) of *Brassica rapa* lines (a) and testers (b). The red colours signify positive GCA values, which signify that parents are giving hybrids favorable alleles, and blue values. The analysis indicates that line 25052 and tester ORL1 are good general combiners that continuously enhance the characteristics such as yield, branching and oil content. The figure highlights the importance of having an appropriate selection of parents who have a stable additive genetic influence in breeding programs.

The parental line 25047 demonstrates GCA that are significant in terms of plant height, primary branches per plant, secondary branches per plant, and number of seeds per plant, number of hundred seed weight and yield per plant, which is another reason why it is useful in producing superior hybrids (Xie *et al.*, 2018). Based on GCA, the tester ORL1 (Figure 1b), was significantly high in primary and secondary branches in single plant, days to fifty percent flowering, number of siliques in single plant, and hundred seed weight, which showed that it can be used in hybrid combinations especially in the traits relating to architecture and early maturity.

In particular, specific combining ability (SCA) outcomes that were marked in figure 2, the crosses 25042×ORL3, and 25052×ORL1 were particularly promising (Gupta, 2021). These crosses showed significant SCA effects for primary and secondary branches per plant, days to fifty percent flowering, total siliques per plant, hundred seed weight, per plant productivity, and oil content. Such performance suggests a strong contribution from non-additive gene action, which is favorable for heterosis breeding in *Brassica rapa* L. (Begna, 2021; Rout *et al.*, 2025).

Heterobeltiosis was calculated for all yield and oil-related traits to evaluate hybrid vigor. Cross 25052×ORL1 (Figure 3) showed significant positive heterosis for overall height of plant, count of primary and secondary branches, seeds count in a single plant, hundred seeds weight, and oil content (Yue *et al.*, 2022), suggesting a strong synergistic effect between parental genotypes (Lyu *et al.*, 2024). Likewise, crosses 25032×ORL2, and 25032×ORL3 outperformed their better parent in the traits count of primary branches, days to fifty percent flowering, siliques number per plant, seeds count per plant, hundred seeds weight; and primary branching (per plant), number of siliques per plant, days to 50%

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flowering, number of seeds per plant, and yield per plant respectively (Das *et al.*, 2021). These findings underline the potential of specific crosses to deliver superior hybrids through both additive and dominance effects Gupta, 2021). The same results are supported by reported trait ranges in *Brassica rapa*, which exhibits considerable variability across germplasm. Plant height has been recorded to range from ~58 to 95 cm, thousand-seed weight (TSW) from ~2.7 to 4.4 g, seed yield per plant from ~3.8 to 20 g, and seed oil content from ~31% to 56% depending on genotype and growing environment (Jan *et al.*, 2017; Cartea *et al.*, 2019; Sultan *et al.*, 2017; Bassegio *et al.*, 2020).

Heritability estimates indicated significant positive values for narrow-sense heritability in quality-related traits shown in table 3, implying that additive genetic variance is substantial (GAIN, 2021). This suggests that traits like oil content and seed weight are heritable and can respond well to selection in early segregating generations, making them reliable targets for breeding programs focused on trait fixation (Shoily, 2021; Yan *et al.*, 2024).

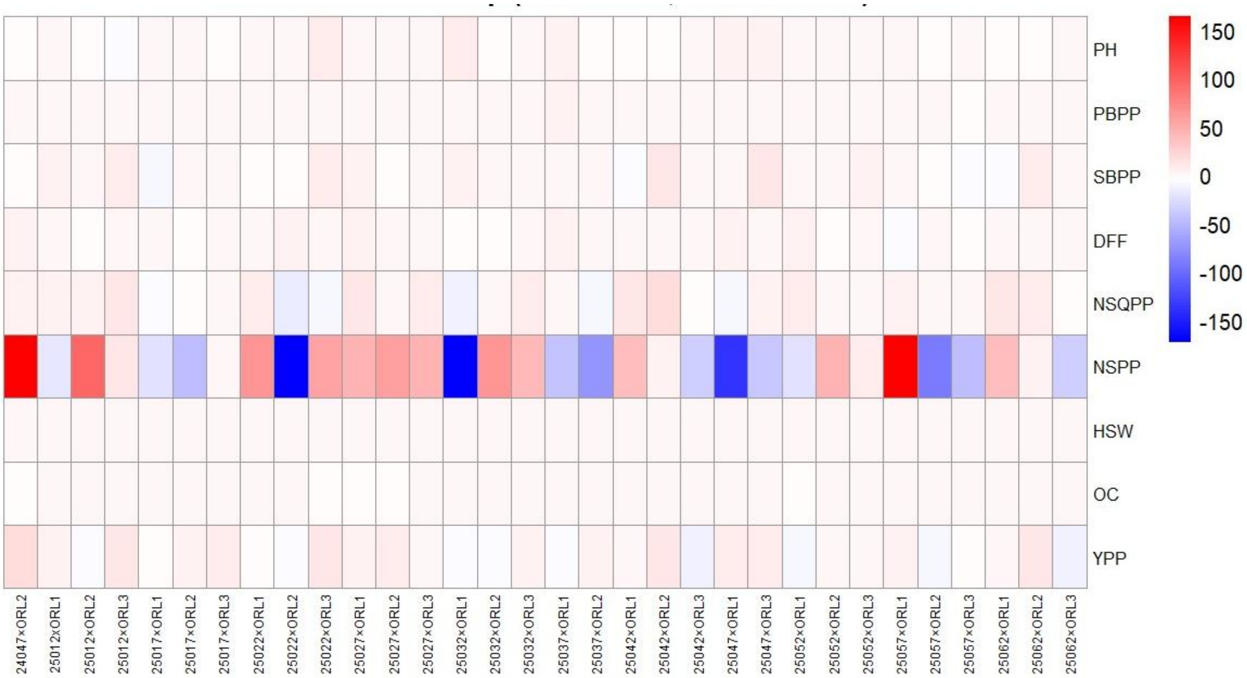

Figure 2. Heatmap representing SCA effects of Brassica rapa crosses, where red color indicates positive SCA values, suggesting crosses that outperform expectations due to non-additive genetic interactions, while blue represents weaker combinations. Notably, the cross 25052×ORL1 shows strong positive SCA across multiple yield and oil-related traits. Such findings confirm that certain hybrid combinations can exploit heterosis more effectively than others.

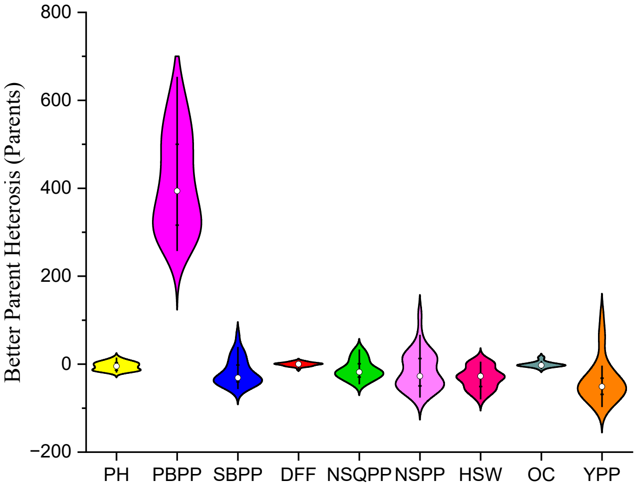

Figure 3. The violin graph depicts the mean values of better-parent heterosis for *Brassica rapa* hybrids concerning yield and oil-related attributes. The wider sections of the violins show higher density of hybrids exhibiting similar heterosis levels. Positive values reflect hybrids outperforming their better parent, particularly for traits like plant height, number of seeds, and oil content.

Evaluation of Developed Breeding Material (2023-24)

In the second year of experimentation, the evaluated hybrids developed from the initial *Brassica rapa* L., parental lines demonstrated notable variation in agronomic and quality-related traits. The variance analysis (ANOVA) revealed statistically significant variations among the genotypes for overall height of plant, count of primary and secondary branching in a single plant, days to fifty percent flowering, seed count, oil contents percentage, and seed yield per plant were shown in Table 2.

These findings indicate that most traits are genetically variable and responsive to selection, whereas silique number may be more influenced by environmental or non-genetic factors under the tested conditions. General combining ability for the lines and testers of *Brassica rapa* L., crosses were measured which showed that lines 25017, 25037, and 25052 exhibit significant values of GCA in terms of yield and oil content related traits. Line 25052 (Figure 4a) exhibits significant results for PBPP, SBPP, NSQPP, NSPP, HSW, OC and YPP, suggesting a consistent and strong additive genetic effect (So *et al.*, 2022; Yesmin, 2022). Similarly, the other two lines 25017 and 25037 recorded highly significant GCA for the primary and secondary branches per plant, days to 50% flowering, number of seeds per plant, hundred seeds weight, oil content, and yield per plant (Zohora, 2022). GCA for the tester ORL1 (Figure 4b), displayed significant GCA for the following traits, including plant height, primary branching/plant, count of siliques per plant, seeds count in single plant, oil contents, and yield per individual (Shelly, 2020), which highlighted its utility in contributing favorable alleles for multiple traits (Ali, 2014).

Table 2. Analysis of variance of lines, testers, and Line×Tester of *Brassica rapa* L. crosses (2023-24)

S.O. V	D.F	PH	PBPP	SBPP	DFF	NSQPP	NSPP	HSW	OC	YPP
Replications	2	2817.12*	10.53*	24.84*	42677.4*	14455.18*	920458.5**	1.55**	9083.96*	3849.6**
Treatments	46	780.67*	20.41**	222.65**	8928.61*	3276.41*	333271.30**	0.31**	1704.55*	1065.9**
Parents	13	522.3*	17.26*	384.23**	1534.88*	762.8*	121072.47*	0.09*	281*	370.41*
Parents vs Crosses	1	3492.04*	3.37*	531.28*	334146.3*	114528.8*	8395352.6**	10.15**	63538.04*	32568.8*
Crosses	32	800.91*	22.22*	147.36*	1769.3*	820.92*	167537.03*	0.10**	350.57*	363.98**
Lines	10	2470.8	56.27**	313.76*	5608.74*	2320.17*	292399.34*	0.19**	1109.34*	637.46*
Testers	2	20.01**	2.98**	30.44*	70.94*	236.96*	78784.77*	0.05*	7.1*	449.89*
Line×Tester	20	44.03	7.12*	75.85*	19.36*	129.7*	113981.1*	0.06*	5.52*	218.65*
Error	92	186.75	7.16	75.9	904.2	131.13	709238.9	0.02	187.93	296.94

**=Statistically very significant at @1%, *= Statistically significant at @5%, SOV= Source of variance, D. F= Degrees of Freedom, PH= Overall Plant Height, PBPP= Primary branching/ plant, SBPP= Secondary branching /plants, DFF= Days to fifty percent flowering, NSQPP= Number of silique/plant, NSPP= Number of seeds/plant, HSW= Hundred seeds weight, YPP=Yield/plant, OC= Oil contents.

Specific combining ability (SCA) analysis uncovered promising hybrid combinations (Ferdous, 2018; Liton, 2010). The cross 25052×ORL1 (Figure 5), exhibited superior SCA across maximum traits, which include plant height, primary branches per plant, secondary branches per plant, days to 50% flowering, number of siliques per plant, number of seeds per plant, hundred seeds weight, oil content, and yield per plant (Ara, 2022; Arif, 2020). Such broad-based SCA reflects favorable non-additive gene interactions, suggesting this cross could serve as a highly productive hybrid in commercial cultivation (Ferdous, 2018).

Likewise, the crosses 25037×ORL3 and 25062×ORL1 recorded significant SCA values for the plant height, count of main branches in single plant, count of siliques/plant, seeds count/plant, hundred seeds weight, oil content, and yield per individual, implying robust hybrid vigor and strong specific gene interactions (Chakraborty *et al.*, 2025; Habibi, 2018; Huq, 2007).

Heterotic performance over the better parent was also evaluated to identify crosses exhibiting hybrid superiority (Yue *et al.*, 2022). Cross 25052×ORL1 exhibited remarkable better parent heterosis (Figure 6) for most of the traits, which are plant height, primary branching, oil contents, and single plant yield (Chakraborty, 2020; Nasim *et al.*, 2014). The magnitude of heterosis in these traits underscores its breeding potential (Bisht *et al.*, 2024a). In addition, cross 25022×ORL3 exhibits significant values for hundred seeds weight, oil content and yield per plant and the cross 25032×ORL1 showed significant better parent values for seeds count in single plant, hundred seeds weight, and yield/plant (Bisht *et al.*, 2024b).

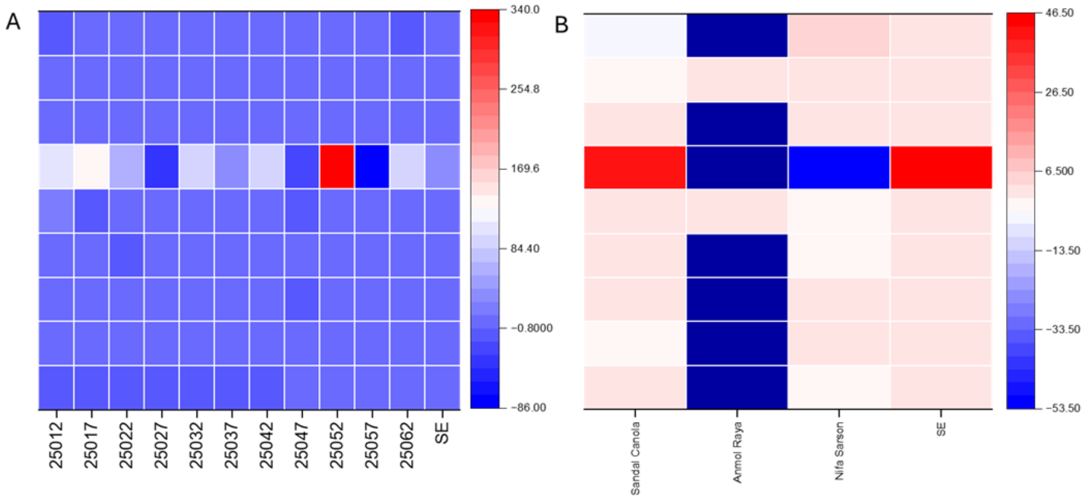

Figure 4. Heatmap displaying general combining ability (GCA) effects of *Brassica rapa* lines (A) and testers (B). The color scheme highlights positive contributions in red and negative in blue. Line 25052 and tester ORL1 again demonstrated consistently high GCA across key yield and oil-related traits. These results validate their stability as dependable general combiners across multiple environments.

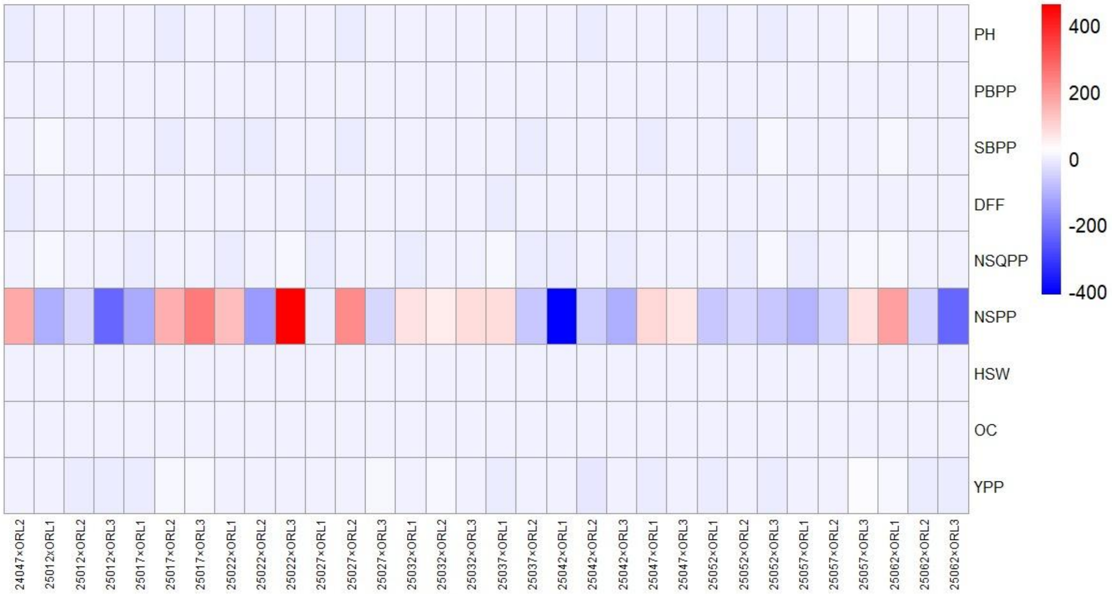

Figure 5. Heatmap illustrating the specific combining ability (SCA) effects for *Brassica rapa* hybrids evaluated in the second year. Red shading indicates superior crosses with high SCA values, while blue highlights less favorable combinations. Hybrids such as 25052×ORL1 and 25037×ORL3 showed strong positive SCA effects, underscoring their hybrid vigor. The findings reaffirm the role of non-additive gene action in achieving superior trait expression.

Broad- and narrow-sense heritability estimates revealed considerable genetic variation among the evaluated traits (Table 3). Broad-sense heritability (H^2)ranged from 0.18 for number of seeds per plant to 0.68 for plant height, indicating moderate to high genetic control for most traits. Relatively high H^2values for plant height, days to 50 % flowering, number of siliques per plant, and seed yield suggest that selection for these characters would be effective. Narrow-sense heritability (h^2)values were generally lower, reflecting the joint contribution of additive and non-additive gene effects. The highest h^2estimates for plant height and days to 50 % flowering indicates predominance of additive variance, while low $h^2$for oil content and seed number imply a stronger environmental influence. Heritability for hundred-seed weight was estimated as zero, showing no detectable genotypic variance in the present dataset. Overall, heritability analysis confirmed significant narrow-sense estimates for several yield- and quality-related traits, suggesting that these are primarily governed by additive effects and can be effectively improved through selection, supporting their inclusion in future breeding programs (Nasim *et al.*, 2014; Shelly, 2020; Rahman *et al.*, 2011; Wells, 2024).

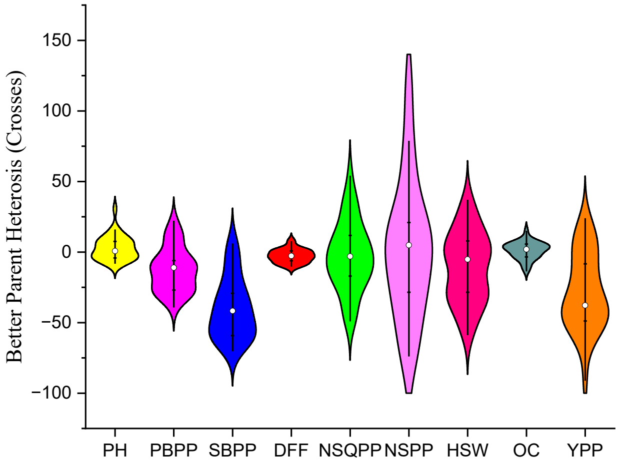

Figure 6. Violin graph representing the mean values of better parent heterosis for crosses regarding grain and oil yield-related attributes. The distribution shows that many hybrids surpassed their better parent in performance. PH= Overall Plant Height, PBPP= Primary branching/ plant, SBPP= Secondary branching /plants, DFF= Days to fifty percent flowering, NSQPP= Number of silique/plant, NSPP= Number of seeds/plant, HSW= Hundred seeds weight, YPP=Yield/plant, OC= Oil contents.

Table 3. Broad sense and Narrow sense heritability for yield and quality-related traits of parents in *Brassica rapa* L.

Character	NSH*	BSH**
PH	0.869	0.678
PBPP	0.568	0. 544
SBPP	0.578	0.661
DFF	0.741	0.619
NSQPP	0.609	0.648
NSPP	0.052	0.185
HSW	0.012	0.015
OC	0.055	0.459
YPP	0.565	0.640

*Narrow sense heritability, **Broad sense heritability, PH= Overall Plant Height, PBPP= Primary branching/ plant, SBPP= Secondary branching /plants, DFF= Days to fifty percent flowering, NSQPP= Number of silique/plant, NSPP= Number of seeds/plant, HSW= Hundred Seeds weight, YPP=Yield/plant, OC= Oil Contents

CONCLUSION

This study identified significant genetic variability in *Brassica rapa* L., with line 25052 and tester ORL1 emerging as superior general combiners. Cross 25052×ORL1 demonstrated exceptional specific combining ability and heterosis across both years, making it the most promising candidate for commercial development. The comprehensive genetic analysis framework successfully integrated combining abilities, heterosis, and heritability estimates. However, critical limitations constrain these findings: single-location evaluation limits understanding of genotype × environment interactions, the narrow tester base may have missed superior genetic combinations, and the absence of molecular validation restricts mechanistic insights. While these results provide a foundation for *Brassica rapa* improvement, translating findings into farmer-ready cultivars requires multi-location validation, expanded germplasm evaluation, and economic feasibility assessment. The identified crosses warrant immediate advancement to broader testing, but sustainable impact depends on addressing the methodological limitations highlighted.

AUTHOR CONTRIBUTIONS

Humera Razzaq: Writing – original draft. Laraib Chouhdary: Writing, editing, and statistical analysis. Waqar Ul Hassan: Statistical analysis and reviewing. Muhammad Ali Zia: r=Review & editing. Noreen Amjad: Writing–review & editing. Shamsa Kanwal: Proof reading and reviewing.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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