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QUANTITATIVE GENETIC EVALUATION OF PARENTAL LINES THROUGH COMBINING ABILITY AND HYBRID VIGOUR IN BRASSICA NAPUS

Original Article

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ABSTRACT

Background: Rapeseed (Brassica napus L.) remains a vital oilseed crop globally, yet local production in many regions, including Pakistan, falls short of rising edible oil demand. Hybrid breeding offers an effective pathway to improve yield and related agronomic traits, but its success relies on understanding the genetic contributions of parental lines. Combining ability and heterosis analyses provide essential insights into additive and non-additive genetic effects, enabling breeders to identify superior parents and productive cross combinations.

Objective: To evaluate the general combining ability (GCA), specific combining ability (SCA), and heterosis of Brassica napus genotypes for plant height, primary and secondary branches, 1000-seed weight, and seed yield per plant using a structured line × tester approach.

Methods: Five female lines and three male testers were crossed during the 2022–23 season to generate fifteen F_1 hybrids. These hybrids, along with their eight parents, were evaluated the following season under a randomized complete block design with three replications. Data from five quantitative traits were subjected to analysis of variance, followed by estimation of GCA and SCA based on established line × tester procedures. Mid-parent and better-parent heterosis were calculated to assess hybrid vigor.

Results: Highly significant differences were observed among treatments for all traits, confirming substantial genetic variability. Parent vs. cross differences were significant for all traits except plant height. The line × tester interaction was significant for all traits. Additive genetic effects predominated for plant height, branching traits, and 1000-seed weight, whereas seed yield was more strongly influenced by non-additive effects. Several hybrids displayed strong positive SCA and expressed significant positive heterosis over the better parent for seed yield, indicating strong hybrid potential.

Conclusion: The study identified valuable parental lines and promising hybrid combinations suitable for future rapeseed improvement. The results highlight the effectiveness of line × tester analysis in distinguishing superior combiners and support the development of high-yielding Brassica napus hybrids.

Keywords: Brassica napus L., Combining Ability, Heterosis, Hybridization, Line × Tester, Seed Yield, Yield Components.

INTRODUCTION

The economy of Pakistan remains deeply rooted in agriculture, with a substantial proportion of the population depending on this sector for livelihood and national food security. While major crops such as wheat, cotton, rice, maize, and sugarcane have received considerable attention over the decades, oilseed crops continue to be classified as minor commodities despite their high economic value (1,2). This persistent neglect has contributed to chronic deficits in edible oil production. During 2023–24, Pakistan required 3.18 million tons of edible oil to meet domestic demand, yet local production accounted for only 0.471 million tons—merely 23% of national availability—forcing the country to rely on imports for the remaining 77%. This heavy import dependence underscores the urgent need to strengthen domestic oilseed production systems (3,4). Among global oilseed crops, rapeseed (Brassica napus L.) holds a prominent position, ranking third after soybean and oil palm. Its versatility extends beyond food and feed applications to include widespread industrial use, particularly in bioenergy production. Rapeseed oil is the primary source of methyl ester, a critical constituent in biodiesel manufacturing (5,6). Given its broad utility, enhancing rapeseed productivity represents a strategic opportunity for improving national food security, reducing import reliance, and supporting sustainable industrial growth. Hybrid seed development has emerged as a cornerstone of modern rapeseed improvement programs, offering substantial yield gains over conventional cultivars. Evidence suggests that hybrid varieties exhibit an approximate 15% yield advantage, and the global adoption of rapeseed hybrids continues to rise, with China cultivating nearly 60% of its rapeseed area under hybrid varieties (7,8). The exploitation of heterosis depends largely on genetic diversity between parental lines, with broader divergence generally associated with stronger hybrid vigor (9).

Therefore, breeding programs oriented toward hybrid development require rigorous evaluation of parental performance to identify those combinations most capable of maximizing yield and oil content. Line × tester analysis provides a robust and efficient methodological framework for such evaluations, enabling breeders to differentiate the relative contributions of general combining ability (GCA) and specific combining ability (SCA). These parameters offer insight into the additive and non-additive genetic effects governing key agronomic traits and help determine the suitability of parental lines for hybridization. Previous work in oilseed Brassica spp. indicates that additive genetic effects predominate for yield-related traits, highlighting the importance of GCA in hybrid development (10-13). Despite these findings, studies on combining ability in Brassica napus remain limited in Pakistan, creating a critical knowledge gap that restricts efficient hybrid breeding. To address this gap, the present study evaluates five female lines and three male testers of Brassica napus to determine their genetic potential in diverse cross combinations. Through systematic assessment of GCA and SCA effects for yield and its related traits, the study aims to identify superior parental lines and promising hybrid combinations. The overarching objective is to pinpoint Brassica napus hybrids with enhanced seed yield and oil content, thereby contributing to stronger national oilseed productivity and reduced dependence on imported edible oils.

METHODS

The study was designed as an experimental line × tester breeding trial conducted to evaluate combining ability effects and heterosis expression in Brassica napus. The parental material consisted of eight genotypes—Golarchi, Star, Range, DGL, Ayub2000, Hybripol, Lagena, and BA0714—sourced from the germplasm maintained by the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad. Five genotypes (Golarchi, Star, Range, DGL, and Ayub2000) were designated as female lines, and three (Hybripol, Lagena, and BA0714) served as male testers. During the Rabi season of 2022–23, controlled hybridization was performed to develop fifteen F_1 combinations. Emasculation was conducted manually, after which racemes were immediately covered with butter paper bags to prevent unintended cross-pollination. Pollen from each male parent was collected separately during morning hours (7:00–9:00 AM), applied to the stigmas of individual female lines, and the bags were replaced after pollination to preserve isolation integrity. Standardized procedures for maintaining pollen viability, pollination timing, and isolation were followed to ensure uniformity and minimize environmental confounding. In the subsequent growing season, the fifteen F_1 hybrids along with the eight parental genotypes were evaluated in a randomized complete block design with three replications. Each experimental unit consisted of a 3 m × 9 m plot, maintaining a row spacing of 60 cm and plant spacing of 30 cm to ensure adequate growth conditions. All recommended agronomic practices for Brassica napus cultivation— including fertilization, irrigation scheduling, and pest management—were applied uniformly throughout the growing period. Data were collected from five key agronomic and yield-related traits, with mean values computed across replications for statistical evaluation. Inclusion criteria comprised genotypes with stable phenotypic expression and availability in sufficient seed quantity, while no explicit exclusion criteria were specified. Environmental conditions and management practices were kept consistent to prevent bias in phenotypic performance. The data were subjected to analysis of variance following the statistical procedures described by Steel. Components of variance attributable to general combining ability (GCA) and specific combining ability (SCA) were estimated in accordance with the methods established by Kempthorne. Heterosis over the mid-parent and better-parent values was quantified using the formulae proposed by Falconer and Mackay, enabling assessment of hybrid vigor for each cross (14-16). All statistical analyses were performed using standardized biometric protocols to ensure accuracy, reproducibility, and interpretability of genetic parameters. Ethical approval for the use of plant germplasm and field experimentation was obtained from the Institutional Biosafety and Research Ethics Committee of the University of Agriculture Faisalabad. As the study involved no human or animal subjects, informed consent was not applicable. All field activities were conducted in compliance with institutional and national biosafety guidelines.

RESULTS

Plant Height

Highly significant variation in plant height was observed among parents and their F_1 hybrids at both 5% and 1% probability levels, while the contrast between parents and hybrids was non-significant and the comparison between female and male parents was highly significant. General combining ability analysis showed that the female lines Star and Range expressed highly significant positive GCA effects (13.2 and 19.7, respectively), whereas Golarchi and Ayub2000 had highly significant negative GCA effects (−7.82 and −26.3, respectively). Among the male parents, Hybripol exhibited a highly significant positive GCA effect (10.8), while Lagena showed a significant negative GCA effect (−6.244), and BA0714 was negative but non-significant. For specific combining ability, several hybrids exhibited significant positive SCA effects, including DGL × Hybripol (11.0), Range × Lagena (12.6), and DGL × BA0714 (12.7), whereas Range × Hybripol (−11.0), DGL × Lagena (−24.0), and Ayub2000 × BA0714 (−12.0) showed significant negative SCA effects. Mid-parent heterosis for plant height ranged from −8.05% in Golarchi × Hybripol to 16.45% in DGL × BA0714. The most pronounced positive mid-parent heterosis was seen in DGL × BA0714 (16.452%), while several hybrids such as Golarchi × Hybripol and Golarchi × Lagena showed moderate, non-significant or negative values. No cross expressed significant positive heterosis over the better parent; however, nine hybrids exhibited highly significant negative better-parent heterosis, with values extending down to −60.41% in Range × BA0714.

Number of Primary Branches per Plant

For the number of primary branches per plant, parents, hybrids, the parent vs. hybrid comparison, and the partition into females, males, and female vs. male effects were all highly significant at both probability levels, indicating substantial genetic variability for this trait. Only one female line, Golarchi, showed a highly significant positive GCA effect (1.64), whereas Star and Range exhibited highly significant negative GCA effects (−0.518 and −1.302, respectively). DGL and Ayub2000 displayed small, non-significant GCA effects near zero. Among testers, Lagena had a significant positive GCA effect (0.505), while Hybripol (−0.326) and BA0714 (−0.179) showed significant negative GCA effects. In terms of SCA, the hybrids Star × Hybripol, DGL × Hybripol, Ayub2000 × Lagena, and Golarchi × BA0714 exhibited highly significant positive SCA effects (ranging approximately from 0.523 to 1.994), whereas Range × Hybripol and Golarchi × Lagena showed significant positive SCA effects of smaller magnitude. Conversely, Ayub2000 × Hybripol and DGL × Lagena showed highly significant negative SCA effects, and two additional crosses showed significant negative SCA effects, indicating unfavorable specific combinations for this trait. Mid-parent heterosis for primary branches ranged from −24.6% (Range × BA0714) to 24.36% (Ayub2000 × Lagena). Five hybrids displayed highly significant positive mid-parent heterosis, including DGL × Hybripol (24.35%) and Ayub2000 × Lagena (24.36%), while Golarchi × Lagena showed significant positive mid-parent heterosis (2.166%). A large number of hybrids expressed highly significant or significant negative mid-parent heterosis, reflecting reduced primary branching in several combinations. Better-parent heterosis was highly significant and positive in Ayub2000 × Lagena (9.166%) and Golarchi × BA0714 (4.17%), with Golarchi × Lagena showing significant positive better-parent heterosis. Eleven crosses expressed highly significant negative better-parent heterosis, spanning from approximately −3.33% to −29.4%.

Number of Secondary Branches per Plant

For secondary branches per plant, highly significant differences were detected among parents, hybrids, and their interactions, including male and female main effects and male × female effects at both probability levels. In GCA analysis, Star and DGL showed significant positive GCA effects (1.20 and 3.11, respectively), whereas Golarchi and Range had significant negative GCA effects (−0.63 and −3.49, respectively). Among testers, Hybripol and Lagena exhibited significant positive GCA effects (0.59 and 0.92), while BA0714 displayed a significant negative GCA effect (−1.19). For SCA, four hybrids—Range × Hybripol, Range × Lagena, Ayub2000 × Lagena, and DGL × BA0714—showed highly significant positive SCA effects, reflecting favorable specific combinations for enhanced secondary branching. Four crosses showed highly significant negative SCA effects, and Ayub2000 × Hybripol exhibited a significant negative SCA effect, indicating reduced secondary branches in these combinations, while the remaining hybrids were non-significant. Mid-parent heterosis for secondary branches ranged from pronounced negative values such as −61.0% in Range × BA0714 to strong positive values such as 41.69% in DGL × BA0714. DGL × Hybripol and DGL × BA0714 expressed highly significant positive mid-parent heterosis between 19.62% and 41.69%, whereas several hybrids, including Range × BA0714 and Ayub2000 × BA0714, displayed highly significant negative heterosis. Better-parent heterosis values ranged from −65.1% (Range × BA0714) to 37.40% (DGL × BA0714). Only DGL × Hybripol (17.14%) and DGL × BA0714 (37.40%) exhibited highly significant positive better-parent heterosis, while eight crosses showed highly significant negative better-parent heterosis and four displayed significant negative heterosis, indicating that most combinations did not surpass the better parent for this trait.

1000-Seed Weight

For 1000-seed weight, significant genetic variability was observed among parents and hybrids, with female parents and hybrids showing highly significant effects, whereas male parents were non-significant at both probability levels. The parent vs. hybrid comparison and female vs. male contrast were also significant or highly significant, and the interaction between parents and hybrids was significant, highlighting the role of both additive and non-additive effects. In GCA analysis, none of the female parents showed statistically significant effects for 1000-seed weight; their GCA estimates were close to zero and non-significant. Among testers, BA0714 exhibited a significant negative GCA effect (−1.3), while Hybripol and Lagena had non-significant GCA effects (−0.3 and 0.772). For SCA, only one hybrid, Ayub2000 × Hybripol, showed a significant positive SCA effect (2.99), indicating a specific favorable combination for 1000-seed weight; all other crosses were non-significant, suggesting limited specific combining ability variation for this trait. Mid-parent heterosis for 1000-seed weight ranged from negative, non-significant or modest values in several crosses to highly significant positive values up to 41.9847% in Ayub2000 × Hybripol. Golarchi × Hybripol, Golarchi × Lagena, Star × BA0714, and Ayub2000 × Hybripol all showed significant or highly significant positive mid-parent heterosis, with values between approximately 19.11% and 41.98%. Better-parent heterosis was highly significant and positive in three hybrids: Golarchi × Hybripol (17.384%), Ayub2000 × Hybripol (31.277%), and Golarchi × Lagena (15.359%). One cross, Range × Hybripol, expressed highly significant negative better-parent heterosis, whereas all remaining crosses were non-significant for better-parent heterosis in 1000-seed weight.

Seed Yield per Plant

For seed yield per plant, highly significant variation was recorded among parents, hybrids, parent vs. hybrid contrast, and male × female interaction, indicating strong genetic variability and substantial interaction between lines and testers for this key economic trait. In GCA analysis, the female parents Golarchi and Ayub2000 showed significant positive GCA effects (7.79 and 12.9, respectively), suggesting favorable general combining ability for increased seed yield. In contrast, Range (−12.0) and DGL (−4.63) exhibited significant negative GCA effects. Star had a negative but non-significant GCA effect (−3.514). All male parents—Hybripol (−0.49), Lagena (2.96), and BA0714 (−2.55)—showed non-significant GCA effects for seed yield per plant, indicating that the major additive contribution to yield came from the female side in this material set. Specific combining ability analysis identified several high-performing hybrid combinations. Range × Hybripol, Ayub2000 × Hybripol, Golarchi × Lagena, and Star × BA0714 showed highly significant positive SCA effects (e.g., 16.3, 21.2, 48.0, and 31.3, respectively), while DGL × Hybripol displayed a significant positive SCA effect (8.997). Several hybrids, including Golarchi × Hybripol and Star × Lagena, showed highly significant negative SCA effects, and five additional crosses had significant negative SCA values, indicating unfavorable specific combinations for seed yield. Mid-parent heterosis for seed yield per plant ranged widely, with highly significant positive values recorded in Golarchi × Lagena (110.77%) and Star × BA0714 (79.437%), and significant positive heterosis in Golarchi × BA0714. Numerous hybrids expressed highly significant negative mid-parent heterosis, such as Golarchi × Hybripol (−46.90%), Range × BA0714 (−42.58%), and Range × Lagena (−36.06%), while some had moderate or non-significant changes. Better-parent heterosis for seed yield per plant ranged from strongly negative values such as −60.41% in Range × BA0714 to highly positive values of 96.371% in Golarchi × Lagena and 60.966% in Star × BA0714. Overall, only Golarchi × Lagena and Star × BA0714 surpassed their better parent by a large margin, whereas most other crosses exhibited highly significant negative better-parent heterosis.

Table 1: Analysis of variance for five traits of Brassica napus L.

SOV	d.f	PH	PBPP	SBPP	SW	SY
Replication	2	17.93	0.0371	0.063	0.3578	17.62
Treatments	22	1655.20**	6.97**	25.1**	12.18**	2288**
Parents	7	2428.95**	10.3**	11.49**	12.33**	3580**
Crosses	14	1385.04**	5.75**	32.7**	9.27**	1701**
Parents vs Crosses	1	21.2	0.61**	13.7**	50.7**	1461**
Females	4	1960.23**	15.9**	5.39**	18.9**	4043**
Males	2	2135.11**	0.86**	28.4**	4.04	3003**
F Vs M	1	7279.4**	15.7**	380**	49.5**	1639**
Error	**44**	**54.47**	**0.0241**	**0.3477**	**1.9327**	**47.64**

Table 2: Analysis of variance for combining ability

Traits	d.f.	Plant Height	Primary Branches	Secondary Branches	1000-seed weight	Seed Yield per Plant
Replication	2	0.96	0.03	0.16	0.0317	3402
Lines (L)	4	2932.8**	10.6**	53.62**	14.64**	709944**
Testers (T)	2	1328**	2.97**	16.08**	3.57	737035**
L x T	8	625.4**	4.02**	26.50**	10.78**	262098**
Error	**28**	**64.88**	**0.03**	**0.3907**	**2.83**	**1216**

Table 3: General Combining Ability effects for Parents in respect to five Characters in Brassica napus

Character	Plant Height	Primary Branches	Secondary Branches	1000-seed weight	Seed Yield per Plant
Golarchi	-7.82*	1.64**	-0.63**	0.722	7.79**
Star	13.2**	-0.518**	1.20**	0.522	-3.514
Range	19.7**	-1.302**	-3.49**	-0.37	-12**
DGL	0.957	0.049	3.11**	-0. 088	-4.63*
Ayub2000	-26.3**	0.127	-0.186	-0.83	12.9**
Hybripol	10.8**	-0.326**	0.59**	-0.3	-0.49
Lagena	-6.244*	0.505**	0.92**	0.772	2.96
BA0714	**-4.576**	**-0.179****	**-1.19****	**-1.3***	**-2.55**

* Significant (α=0.05) ** Highly significant (α=0.01)

Table 4: Specific Combining Ability effects for Hybrids

	Crosses	Plant Height	Primary Branches	Secondary Branches	1000-seed weight	Seed Yield per Plant
1	Golarchi × Hybripol	-9.38	-0.193	0.278	-0.49	-37**
2	Star × Hybripol	7.29	0.523**	-0.555	-0.69	-8.7*
3	Range × Hybripol	-11*	0.260*	2.67**	-1.67	16.3**
4	DGL × Hybripol	11**	1.204**	-1.45**	-0.05	8.997*
5	Ayub2000×Hybrpol	1.513	-1.77**	-0.961*	2.99*	21.2**
6	Golarchi × Lagena	4.024	0.3653*	-2.45**	1.074	48**
7	Star × Lagena	-2.96	-0.327*	0.4514	-1.26	-22**
8	Range × Lagena	12.6*	-0.272*	2.18**	0.167	-6.366
9	DGL × Lagena	-24**	-1.08**	-2.09**	1.284	-6.846
10	Ayub2000 × Lagena	10.90	1.994**	1.84**	-1.25	-12.6*
11	Golarchi × BA0714	5.356	0.559**	2.137	-0.58	-10.4*
12	Star × BA0714	-4.31	-0.175	0.1036	1.960	31.3**
13	Range × BA0714	-1.20	0.026	-4.86**	1.516	-9.87*
14	DGL × BA0714	12.7*	-0.176	3.56**	-1.23	-2.150
15	**Ayub2000×BA0714**	**-12****	**-0.220***	**-0.9063**	**-1.66**	**-8.58***

Table 5: Heterosis for five traits

Sr.	Cross Name	Plant Height		Primary Branches		Secondary Branch		1000-seed weight		Seed yield per Plant	
		MP	BP	MP	BP	MP	BP	MP	BP	MP	BP
1	Golarchi × Hybripol	-8.05**	-8.7**	0.142	-3.33**	0.835	-5.94*	19.1104**	17.384**	-46.90**	-56.58**
2	Star × Hybripol	4.46	-1.14	-4.58**	-9.28**	3.903	-5.46*	10.4338	6.7221	-24.68**	-40.38**
3	Range × Hybripol	-1.72	-7.6**	-24.3**	-29.4**	-5.96*	-15.1**	-8.5637	-16.29**	-33.27**	-39.33**
4	DGL × Hybripol	8.45**	7.05**	24.35**	2.086*	19.62**	17.14**	31.5430**	14.635	-11.22*	-25.27**
5	Ayub200	-2.80	-10.91	-15.9**	-23.8**	-0.95	-4.90	41.9847*	31.277*	-9.837	-19.14**

Sr.	**Cross Name**	**Plant Height**		**Primary Branches**		**Secondary Branch**		**1000-seed weight**		**Seed yield per Plant**	
		MP	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**	**MP**	**BP**
	× Hybripol							*	*		
6	Golarchi × Lagena	-3.98	-10**	2.166*	2.166*	-27.4**	-32.5**	24.9122*	15.359*	110.77**	96.371**
7	Star × Lagena	-2.32	-12**	-8.16**	-15.5**	-4.85*	-9.25**	2.21031	-1.101	-11.13	-13.75
8	Range × Lagena	7.41**	-4.80	-24.4**	-27.1**	-21.0**	-23.9**	0.09484	-2.283	-36.06**	-53.68**
9	DGL × Lagena	-12.1**	-16**	4.346**	-16.6**	-1.34	-12.38*	35.2733**	11.471	2.8334	-7.296
10	Ayub2000 × Lagena	-0.18	-2.742	24.36**	9.166**	0.529	-9.10*	3.72300	-9.721	-18.08**	-41.20**
11	Golarchi × BA0714	5.02	-9.1**	8.695**	4.166**	2.197	-5.55**	7.86686	6.6566	20.849*	4.4457
12	Star × BA0714	4.90	-12**	-8.86**	-12.7**	-2.01	-11.6	19.4244*	15.038	79.437**	60.966**
13	Range × BA0714	8.96**	-9.8**	-24.6**	-30.2**	-61.0**	-65.1**	3.48326	-5.555	-42.58**	-60.41**
14	DGL × BA0714	16.452**	2.6392	11.92**	-7.57**	41.69**	37.40**	9.54214	-4.263	9.1993	-8.403
15	**Ayub2000 × BA0714**	**-4.884**	**-10****	**1.659**	**-7.27****	**-11.1****	**-15.5****	**-6.2096**	**-13.01**	**-15.56****	**-42.27****

* Significant (α=0.05)   ** Highly significant (α=0.01)

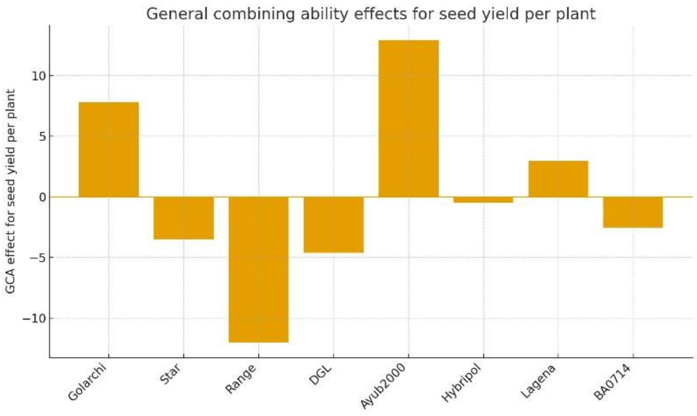

Figure 2 General Combining Ability Effects for Seed Yield per Plant

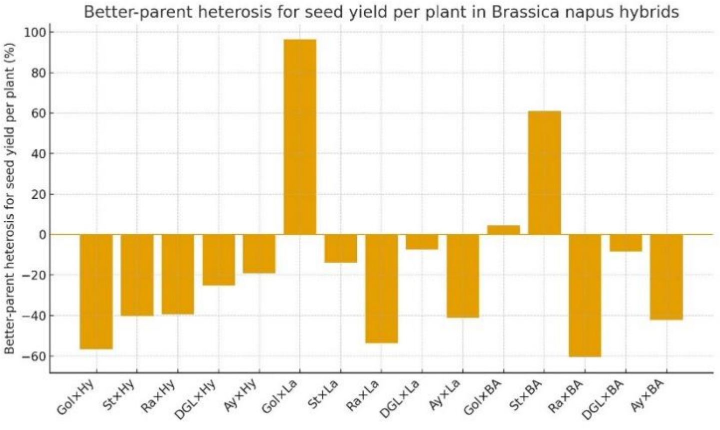

Figure 2 Better-parent Heterosis for Plant in Brassica Napus hybrids

DISCUSSION

The study demonstrated substantial genetic variability among Brassica napus parents and their F_1 hybrids for all evaluated traits, indicating that the selected material carried sufficient diversity to support meaningful progress through hybrid breeding. The consistent significance of treatment effects for plant height, branching traits, 1000-seed weight, and seed yield per plant aligned with previous reports in oilseed Brassica where wide phenotypic and genetic variability within breeding populations has been described. Earlier work on rapeseed has also emphasized that such variability provides a strong foundation for the identification of heterotic combinations and for the partitioning of additive and non-additive genetic components governing yield and its related traits. The current findings therefore reinforced the suitability of line × tester analysis as a practical tool for dissecting genetic control of complex traits in rapeseed breeding programs. Patterns of general combining ability across traits suggested that additive gene effects played an important role, particularly for branching and seed yield, which is consistent with previous evidence in oilseed Brassica that has frequently highlighted the predominance of additive variance for yield components (15,16). Female lines with favorable GCA for plant stature and yield-related traits emerged as valuable candidates for inclusion in future hybrid development pipelines, while testers with positive GCA for branching traits supported the notion that testers can be strategically chosen to improve plant architecture. At the same time, the presence of parents with negative GCA effects for certain traits reflected the inherent trade-offs that breeders encounter when attempting to combine favorable alleles for plant height, branching pattern, seed size, and yield within a single genotype. Such trade-offs are common in rapeseed and have been noted previously where increased vegetative growth did not always translate into higher seed yield, underscoring the need for balanced selection indices (17,18).

Specific combining ability patterns indicated that non-additive gene action also contributed meaningfully, especially for secondary branches and seed yield per plant. Several cross combinations expressed strong positive SCA effects for branching or yield traits, consistent with earlier studies where specific line × tester combinations in rapeseed outperformed expectations based on parental GCA alone (19,20). Hybrids that combined parents of contrasting GCA profiles for particular traits tended to show enhanced performance, supporting the concept that complementary gene action and overdominance can be effectively exploited through carefully planned crosses. At the same time, a considerable number of hybrids exhibited negative SCA effects for key traits, which mirrored previous observations that not all crosses between elite parents necessarily yield superior progeny. This dual behavior strengthened the rationale for systematic SCA-based screening rather than relying solely on the apparent superiority of individual parents. The heterosis patterns for plant height, branching, 1000-seed weight, and seed yield per plant further illustrated the complex interplay between genetic backgrounds. The presence of strong positive mid-parent and better-parent heterosis for seed yield in a limited number of hybrids echoed earlier reports in rapeseed where only a subset of cross combinations achieved substantial heterotic gains, while many showed neutral or negative heterosis. The occurrence of negative better-parent heterosis for certain traits, including seed yield, aligned with published findings that heterosis can manifest in either direction depending on the genetic constitution of the parents and the trait under consideration (21,22). In practical breeding terms, these results emphasized that a few promising hybrids with superior yield potential can be identified even within a relatively small set of line × tester combinations, but careful selection is required to avoid combinations that depress performance.

From an applied perspective, the identification of lines with favorable GCA for yield and yield components, together with hybrids exhibiting positive heterosis for seed yield, carried important implications for oilseed productivity enhancement in the context of Pakistan's edible oil deficit. Hybrids that combined desirable plant architecture, adequate seed size, and high seed yield per plant represented valuable starting points for further multilocation testing and possible commercial development. These findings were in agreement with previous breeding efforts where hybrid rapeseed cultivars consistently outperformed conventional varieties under diverse agro-climatic conditions (23,24). The present work therefore contributed additional evidence that hybrid development in Brassica napus remains a viable strategy for boosting local oilseed output and, indirectly, for reducing reliance on imported edible oils. The study had several strengths that enhanced its scientific value. The use of a structured line × tester design allowed simultaneous estimation of GCA and SCA effects and enabled a clear separation of additive and non-additive genetic components. The evaluation of multiple agronomic traits captured key determinants of productivity, and the inclusion of both parental lines and F_1 hybrids under uniform field conditions improved the reliability of comparisons across genotypes. The integration of combining ability analysis with heterosis assessment provided a comprehensive framework for identifying elite parents and cross combinations, which is particularly relevant for breeding programs operating under resource constraints.

However, some limitations needed to be acknowledged. The experiment was conducted at a single location and over a limited time frame, which restricted the ability to assess genotype × environment interactions and the stability of combining ability effects and heterosis across environments. The number of testers was relatively small, which may have constrained the breadth of genetic backgrounds sampled on the male side. Most notably, although one of the main objectives of the study was to identify hybrids with superior seed yield and higher oil content, empirical data on oil percentage and oil quality parameters were not reported. This omission limited the capacity to fully align the findings with the stated breeding goal of improving both yield and oil content. In addition, the absence of detailed descriptive statistics for each trait, such as means, ranges, and coefficients of variation for parents and hybrids, reduced the transparency of the phenotypic baseline. Future research would benefit from expanding the number of environments and years to capture G × E variability and to confirm the stability of promising hybrids. Inclusion of additional testers with diverse genetic backgrounds would broaden the scope for identifying novel heterotic patterns (25). Integrating seed oil content and quality traits, as well as molecular marker information, would strengthen the selection of parents and hybrids and would facilitate the mapping of loci contributing to additive and non-additive effects. Multi-environment testing of the most promising hybrids identified in this study, coupled with detailed oil profiling, would represent a logical next step toward the development of commercially viable Brassica napus hybrids tailored to the agro-ecological conditions and edible oil needs of Pakistan.

CONCLUSION

The study demonstrated meaningful genetic diversity among the evaluated Brassica napus lines and testers, confirming the potential of hybrid breeding to enhance seed yield and related agronomic traits. Strong general combiners and several promising hybrid combinations were identified, indicating that both additive and non-additive genetic effects contributed to performance. Golarchi, Ayub2000, Lagena, and Hybripol emerged as valuable parental resources, while specific hybrids showed superior potential for yield improvement and enhanced oil-related attributes. These findings reinforce the relevance of line × tester analysis in rapeseed breeding and provide a foundation for advancing high-yielding, stable hybrids. The identified crosses merit further multilocation testing to validate their consistency and suitability for large-scale cultivation.

AUTHOR CONTRIBUTIONS

Author	**Contribution**
Aziz Ullah*	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Misbah Zulfqar	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published
Maria Ghias	Substantial Contribution to acquisition and interpretation of Data Has given Final Approval of the version to be published
Sundus Shahzad	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Salsabeel Rauf	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Sajida Habib	Substantial Contribution to study design and Data Analysis Has given Final Approval of the version to be published
Muhammad Kashif Hanif	Contributed to study concept and Data collection Has given Final Approval of the version to be published
Safia Riaz	Writing - Review & Editing, Assistance with Data Curation

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