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Decoding Gene Activity and Heterosis: Line × Tester Analysis for Yield Traits in Rapeseed (*Brassica napus* L.)

Rashma Afrose[1], Thashin Tabassum[1], Fatamatul Mohosina[2]
Habiba Zannat Meem[3], Md. Mahmud Al Noor[4], Md. Nazmul Hasan Mehedi[3]

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ABSTRACT

Background: The study aimed to assess five female lines and eight male testers using a line × tester mating design at Sher-e-Bangla Agricultural University in Bangladesh over two consecutive years during the winter season (from November to April). The objective of this study is to investigate the genetic basis of heterosis and gene activity for yield and related traits in rapeseed (*Brassica napus* L.) genotypes using line × tester analysis, with the aim of identifying superior parental lines and hybrids for enhanced productivity and breeding efficiency.

Methods: Data collected from 40 F1 hybrids and their parental lines revealed significant general combining ability (GCA) effects for traits such plant height, days to 50% flowering, number of silique/plant, seeds/siliqua, thousand seed weight and seed yield/plant.

Result: A high ratio of GCA to specific combining ability (SCA) variance suggested that non-additive gene effects play a significant role in the inheritance of these yield traits. Lines Nap 9908 and Nap 94006 were identified as strong general combiners, while 16 of the hybrids were recognized as good specific combiners for yield and associated traits. Various types of heterosis- over mid parent (Hm), better parent (Hb) and a standard check (Hc)- were measured for the forty hybrids. The average heterosis for seed yield over the mid parent was 3.27%, while it was -9.72% over the better parent and 5.60% over the standard check. Lines Nap 9908 and Nap 94006, along with 16 high-performing hybrids, are acclaimed for enhancing rapeseed productivity, emphasizing hybrid breeding to exploit non-additive gene effects and heterosis.

Key words: Cross breeding, Gene action, Heterosis, Mustard, Trait improvement.

INTRODUCTION

Rapeseed (*Brassica napus* L.) is a significant oilseed crop in Bangladesh. Rapeseed and mustard are both self-pollinated and cross-pollinated plants, typically categorized as largely self-pollinating (Shimpy *et al.,* 2024). This plant, known for its bright yellow flowers, belongs to the Brassicaceae (Cruciferae) family and is an amphidiploid with 2n = 38 chromosomes, combining genomes from *Brassica rapa* (2n=20) and *Brassica oleracea* (2n=18). Rapeseed and mustard seeds contain about 42% oil and 25% protein (Khaleque, 1985). The oil serves mainly as a dietary product, providing a rich energy source (9 kcal/g) along with fat-soluble vitamins A, D, E and K. According to Mondal *et al.* (2001), oilseed crops produce approximately 0.16 million tons of edible oil annually, compared to the 0.5 million tons needed to meet the demands of Bangladesh's 130 million population, resulting in a persistent edible oil deficit. Mustard seed yields/hectare in Bangladesh are significantly lower than yields achieved in developed nations (BBS, 2022), primarily due to the reliance on low-yield local cultivars, limited availability of locally developed hybrids and suboptimal crop management practices. To increase productivity, a combination of molecular markers and morphological features is advised to boost yield attributes (Saha *et al.,* 2024). Additionally, rapeseed is mostly grown in winter under residual soil moisture and managed with minimal care, contributing to its lower average yield compared to developed countries (Hasanuzzaman and Karim, 2007).

[1]Department of Agricultural Extension, Ministry of Agriculture, Dhaka-1215, Bangladesh.
[2]Department of Genetics and Plant Breeding, Patuakhali Science and Technology University, Bangladesh.
[3]Department of Horticulture, Patuakhali Science and Technology University, Bangladesh.
[4]Department of Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture, Bangladesh.

Corresponding Author: Md. Nazmul Hasan Mehedi, Department of Horticulture, Patuakhali Science and Technology University, Bangladesh. Email: nazmul02348@gmail.com
ORCID: 0000-0002-0526-7164

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Yield improvements in rapeseed can be achieved by expanding cultivation, developing high-yielding, resistant varieties, protecting plants, promoting multiple cropping and reducing both quantitative and qualitative post-harvest losses. Developing varieties that are high-yielding and resistant is key to boosting production. Breeding goals focus on creating varieties with early to medium maturity, non-shattering traits, shorter, high harvest index, responiveness

to optimal management, resistance to diseases and pests and better oil and meal quality.

For oilseed crops, commercial hybrid varieties are gaining importance, as mutation breeding, marker-assisted selection, genetic engineering and protoplast fusion have so far made limited contributions to disease and pest resistance. In mustard hybrid breeding, a cytoplasmic male sterile line (A), a maintainer line (B) and a restorer line (R) are essential for successful commercial hybridization. In breeding programs for both hybrid and open-pollinated rapeseed varieties, general combining ability (GCA) and specific combining ability (SCA) are critical indicators of inbred line potential within hybrid combinations. Line × tester analysis is an effective method for assessing a large number of inbreds, providing insights into the relative importance of GCA and SCA effects among parental lines and tester pairs, thus helping to understand the genetic basis of key plant traits (Mather and Jinks, 1982). Many researchers have reported GCA and SCA effects for yield and its components in various crops (Muraya *et al.,* 2006; Jan *et al.,* 2005), though studies on gene action in *Brassica* yield traits remain limited. Therefore, understanding combining ability and heterosis is vital for selecting parent plants for hybridization, understanding the inheritance of quantitative traits and identifying promising crosses for further breeding. This study aimed to evaluate combining ability, gene action and heterosis effects to provide insights for guiding future hybrid development breeding programs of *Brassica*.

MATERIALS AND METHODS

The experiment was carried out at the research farm of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh, during the winter season over two consecutive years (2020-21 and 2021-22). The location had an annual rainfall of 2152 mm, with an average maximum temperature of 30.34°C and a minimum of 21.21°C. The experimental soil was a deep red-brown terrace type with a silty clay loam texture, low organic matter (0.82%) and a pH range of 5.47 to 5.63. Five lines-Nap94006, Nap9908, Nap2037, BARI Sarisha7 and BARI Sarisha13-and eight testers-Nap248, Nap179, Nap206, Nap2001, Nap2057, Nap2012, Nap2013 and Nap2022-were used to produce F_1 test cross progenies for assessing combining ability and heterosis.

Seeds from 40 F_1 crosses were sown in separate lines, with parental genotypes planted in alternate rows. Rows were spaced 30 cm × 15 cm and seedlings emerged within four days. The five seed parental lines (Nap94006, Nap9908, Nap2037, BARI Sarisha7 and BARI Sarisha13) were crossed with the eight pollen parent testers in a one-way cross. Sepals and petals from the upper portion of the CMS Brassica genotype buds were removed in the evening to expose the stigma for pollination and hand pollination was performed the next morning using pollen from fertile *Brassica napus* genotypes. The cross-pollinated buds were bagged and tagged for 3-4 days to prevent unwanted pollination, producing 40 F_1 test crosses. After maturity, siliquae were harvested individually, threshed, dried and F_1 and parental seeds were stored in cold storage for the following year's study.

In the next season, the test cross progenies were evaluated alongside thirteen parent lines, 40 F_1 hybrids and BARI Sarisha13 (used as a check variety) in a randomized complete block design (RCBD) with three replications. Ten randomly selected competitive plants from each parent and F_1 cross were evaluated for traits including plant height, days to 50% flowering, siliquae/plant, seeds/silique and seed yield/plant. Hybrid performance for the five lines and eight testers was assessed using variance analysis for hybrids, line, tester, line × tester interactions, combining ability and other components *via* the line × tester method as outlined by Kempthorne (1957).

RESULTS AND DISCUSSION

Combining ability analysis for different characters in lines, testers and crosses

The treatment mean sum of squares was further divided into variances due to lines (female parents), testers (male

Table 1: ANOVA for combining ability in *Brassica napus* genotypes.

Source of variation	Degree of freedom	Plant height	Days to 50% flowering	Number of siliqua/plant	Number of seeds/siliqua	Seed yield/ plant (g)
Treat	52	168.247	6.793	1753.164	10.830	15.586
Rep	2	270.578	1.491	27143.280	3.886	250.619
Hybrid	39	192.94**	8.340**	1706.895	10.367**	17.699**
Line (female)	4	348.71*	9.179	3627.433**	25.582*	72.920**
Tester (male)	7	188.370	7.189	1931.501	2.706	12.962
L vs T	28	171.83**	8.508**	1376.381	10.109	10.995**
Error	104	57.259	1.523	1086.410	1.891	4.802
			Component of variance			
σ^2gca		0.330	-0.003	5.162	0.004	0.105
σ^2sca		38.191	2.328	96.657	2.739	2.064
σ^2GCA/σ^2SCA		0.009	-0.001	0.053	0.001	0.051
CV%		7.180	4.222	20.947	8.534	10.847

σ^2gca: Variance of general combining ability; σ^2sca: Variance of specific combining ability **and* Significance at 1% and 5% level.

parents) and their interaction (line × tester). Variance attributed to lines was highly significant at the 1% level for seed yield/plant (g) (Table 1 and 2). For plant height and number of seeds/siliqua, line variance was significant at the 5% level. The line × tester interaction variance was highly significant for all traits except for seeds/siliqua and number of siliquae/plant. The high magnitudes of SCA variance across all traits indicate a predominance of non-additive gene action. This predominance of non-additive gene action suggests that these traits may be useful for heterosis breeding.

Mean performance and combining ability effects

Results revealed that there was a wide range of variation in combining ability estimates and means. Forty cross combinations were categorized in two groups considering all characters. Sixteen crosses were found under high (H) SCA group and 24 crosses were under low (L) SCA group (Table 7).

Plant height

Mean performance

The tallest plant (127.20 cm) was found from the cross Nap 9908×Nap 206 and followed by Nap 2037×Nap 2012 (121.60 cm) and Nap 9908×Nap 2013 (116.50 cm). The shortest plant (88.37 cm) was found from the BS-7×Nap 2057 which was followed by Nap 94006×Nap2022 (91.83 cm), Nap 2037 × Nap 206 (93.43 cm) (Table 3 and 4).

General combining ability (GCA) effects on plant height

GCA varied from -5.77 to 3.86 for lines and from-5.73 to 4.42 for testers. Among lines Nap 9908 exhibited the highest positive significant GCA effect (3.86) followed by Nap 94006 (2.91). BS-7 had the highly significant negative GCA effects (-5.77). Among *Brassica napus* testers Nap 2012 exhibited the highest positive highly significant GCA effect (4.42) followed by Nap 2013 (3.83) and Nap 206 (3.28). Nap 2057 had the highly significant negative GCA effects (-5.73) (Table 5 and 6). Those effects indicated that lines and testers having positive values of GCA effects possessed more positive alleles and those having negative values possessed more negative alleles for the tallness.

Specific combining ability (SCA) effects

The cross Nap9908×Nap206 (15.93) showed the highest positive SCA effects and it was followed by Nap2037× Nap2012 (12.94), Nap2037×Nap2022 (7.25). Good specific combiner for tallness was evolved from low × low, high × high general combiner parents. So additive × additive gene effects were observed in good specific cross combinations. The promising hybrids with negative significant SCA effects were considered as good specific combiner for dwarfness. The crosses Nap9908×Nap2012 (-14.11) Nap94006× Nap2022 (-13.47) and Nap9908× Nap179 (-10.69) had high negative significant SCA effect (Table 7). Sheoran *et al.* (2000) observed similar result for this trait in brown sarson (*Brassica campesties* L.).

Days to 50% flowering

Mean performance

The earliest (flowering) three hybrids were BS-13 × Nap 2012 (31.67days), BS-13× Nap 248(32 days) and Nap 2037× Nap 2012 (32 days). The three crosses Nap 9908 × Nap 179 (38 days), BS-7 × Nap2012 (37.67days) and Nap 94006 × Nap 2022 (37.67 days) were take highest time to 50% flowering (Table 3 and 4).

General combining ability effects

Among five (5) lines, two (2) showed significant GCA effect for days to 50% flowering, among them one was negative and one was positive. Parents with negative GCA effects were good general combiner earliness. BS-13 showed the lowest (-0.81) and Nap 94006 showed the highest GCA effects (0.76) (Table 5 and 6). In case of eight testers four showed significant GCA effect for days to 50% flowering, among them two were positive and two were negative, those are Nap 179 (0.67), Nap 2057 (-0.52), Nap 2012 (-1.05), Nap 2013 (1.14).

Specific combining ability effects

The cross BS-13 × Nap 248, Nap 2037 × Nap 2012 (-2.58) showed the highest (-2.58) negative SCA effect whereas, BS-7 × Nap 2012 (2.89), showed the highest positive SCA value (Table 7). It indicated that the first two combinations were the best for earliness. The best specific combination evolved from low × low general combiners. It indicated that additive × additive gene action existed in this specific cross. A similar result was found by Singh *et al.* (2005).

Number of Siliqua per plant

Mean performance

The highest three cross combinations for number of silique/plant were Nap 9908 × Nap 206 (175), Nap 94006 × Nap 2001(161.20) and Nap 94006 × Nap 179 (146.60); all of which exceeded their estimated parental means. The lowest three cross combinations were Nap2037×Nap248 (71.73), BS-7×Nap2057 (75.73) and BS-13×Nap2001 (79.45) (Table 3 and 4).

Table 2: Proportional contribution of line testers and their interactions to the total variance.

Source	Plant height	Days to 50% flowering	Number of siliqua/plant	Number of seeds/siliqua	Seed yield/plant (g)
Due to lines	18.537	11.288	21.797	25.309	42.256
Due to testers	17.523	15.472	20.311	4.684	13.145
Lines × testers	63.940	73.239	57.893	70.007	44.599

General combining ability effects

Nap2012 had highest positive GCA effects (18.36). Nap 248, showed negative GCA effect *viz*. -13.27. Nap 94006 showed highest positive GCA effects (14.25) (Table 5 and 6). These facts indicated that among the testers Nap 2012 with significant positive GCA values are good general combiner for the trait and possessed more positive alleles for the trait. These materials could be utilized for evolving more silique/plant. On the other hand, the genotype showing a negative GCA effect considered as poor general

Table 3: Per *se* performance (mean) of forty crosses in *Brassica napus* L.

Cross	Plant height	Days to 50% flowering	Number of siliqua/plant	Number of seeds/siliqua	Seed yield/plant (g)
1 × 11	105.10	37.00	121.10	23.83	11.47
1 × 12	112.40	35.00	146.60	22.80	9.10
1 × 13	110.90	35.00	115.70	23.43	9.47
1 × 14	108.20	36.33	161.20	24.60	9.27
1 × 15	106.70	35.33	111.90	24.57	7.40
1 × 16	109.20	37.00	123.90	23.33	8.87
1 × 17	111.60	37.00	146.60	22.67	11.50
1 × 18	91.83	37.67	87.20	25.80	10.27
2 × 11	105.10	37.00	121.10	23.83	11.47
2 × 12	95.83	38.00	98.80	20.27	9.13
2 × 13	127.20	37.33	175.40	23.53	10.83
2 × 14	108.50	36.00	123.30	22.47	16.87
2 × 15	100.00	35.00	129.80	20.33	14.73
2 × 16	118.50	34.00	143.70	21.10	14.83
2 × 17	116.50	35.00	105.70	22.50	15.07
2 × 18	98.33	33.00	100.10	24.43	8.43
3 × 11	100.50	36.00	71.73	19.57	10.73
3 × 12	99.30	36.33	90.51	23.40	12.13
3 × 13	93.43	32.67	120.90	20.73	8.10
3 × 14	104.50	35.33	116.90	23.83	9.40
3 × 15	99.98	35.67	79.53	21.13	7.47
3 × 16	121.60	32.00	139.60	20.47	10.93
3 × 17	105.00	37.00	126.00	18.23	10.07
3 × 18	109.80	36.00	128.80	20.70	8.33
4 × 11	97.40	35.00	82.67	23.20	6.07
4 × 12	98.07	36.67	87.27	23.83	8.17
4 × 13	94.20	35.33	87.83	23.20	6.37
4 × 14	101.60	36.67	107.30	20.33	9.17
4 × 15	88.37	35.00	75.73	21.90	7.90
4 × 16	102.30	37.67	142.30	24.10	11.00
4 × 17	103.30	37.00	113.00	20.37	8.73
4 × 18	101.30	33.33	113.40	19.63	8.73
5 × 11	101.10	32.00	99.70	20.30	9.27
5 × 12	107.70	35.00	96.70	21.27	8.86
5 × 13	111.10	37.00	99.93	20.50	10.30
5 × 14	95.37	34.67	79.45	19.10	8.50
5 × 15	96.73	34.00	100.30	23.27	10.37
5 × 16	97.20	31.67	104.80	23.27	10.33
5 × 17	103.20	37.33	125.70	24.00	8.23
5 × 18	110.70	36.00	116.80	24.83	8.70
Mean	104.20	35.53	112.97	22.27	9.91
Maximum	127.20	38.00	175.40	25.80	16.87
Minimum	88.37	31.67	71.73	18.23	6.07

[1=Nap 94006; 2=Nap 9908; 3=Nap 2037; 4= BARI Sarisha-7; 5=BARI Sarisha-13; 11=Nap 248; 12=Nap 179; 13=Nap 206; 14=Nap 2001; 15=Nap 2057; 16=Nap 2012; 17=Nap 2013; 18=Nap 2022].

combiner and possesses more negative alleles for the trait. Singh *et al.* (2005) found good general combiners in their experiments in Indian mustard and cited similar interpretations.

Specific combining ability effects

The cross combination Nap9908×Nap2057 (43.30) followed by Nap94006 × Nap2001 (29.29) and Nap94006× Nap179 (28.34) showed the highest value (Table 7). The above-said hybrids were considered the best specific combiners for the trait number of silique/plant. The best specific combination evolved from low × low general combiners for the trait. It revealed that additive × additive type of gene action governed this trait. Chaudhary *et al.* (1997) suggested that both additive and non-additive type of gene action were present in the expression of the trait.

Number of seeds per siliqua

Mean performance

The highest mean for number of seeds per siliqua (25.80) was observed in the cross Nap94006×Nap2022 and it was followed by BS-13×Nap2022 (24.83), Nap94006×Nap2001 (24.60) where the range was 18.70 to 25.80 (Table 3 and 4).

General combining ability effects

Nap94006 was the best combiner due to highest significant positive GCA value (1.61) for no. of seeds/siliqua. Nap2037 had the lowest significant GCA value (-1.26) hence, it was a poor general combiner. Among eight (8) pollen parents, two (2) showed a significant GCA effect. Of them, one (1) showed positive and one showed negative GCA effects. Nap2013 had significant positive GCA value (0.81) and Nap2022 (-0.71) had significant negative GCA value (Table 5 and 6). It indicated that good general combiners possessed more positive alleles but poor general combiners possessed less positive alleles. Ghosh *et al.* (2002) agreed with these findings.

Specific combining ability effects

The cross combination Nap9908×Nap2013 showed the highest SCA effect (3.02). Other two cross combinations closer to this value were BS-13×Nap2013 (2.65) and Nap2037×Nap179 (2.35). The cross BS-7×Nap2022 showed the lowest SCA effect (-3.25) for number of seeds/ silique (Table 7). In this experiment, high x low and high × high general combiner parents produced best specific combination of crosses with positive SCA effects for this character. It indicated that additive × dominance and additive × additive type of gene action are exhibited here. Yadav *et al.* (2004) observed the best specific cross combination from high × low, low × low and high × high general combiner parents.

Seed yield/plant

Mean performance

The highest mean seed yield/plant (16.87) was observed in the hybrid Nap9908×Nap2001 and it was followed by Nap9908×Nap2013 (15.07) and Nap9908×Nap2012 (14.83) (Table 3 and 4). The seed yields/plant of the above crosses were higher than both of their parents. Seed yield/ plant (6.07) was produced by the cross BS-7×Nap248 which was lower than both female and male.

General combining ability effects

Among the five female parents two were with significant GCA effects, of them one was positive and one was negative. Nap 9908 had highly significant highest positive GCA effect (2.95). On the contrary, BS-7 had the lowest GCA

Table 4: Inter se (estimated) mean of thirteen genotypes.

Parents	Plant height	Days to 50% flowering	Number of siliqua/plant	Number of seeds/siliqua	Seed yield/plant (g)
1	105.80	36.00	89.30	19.40	8.10
2	106.80	36.00	113.10	18.70	7.06
3	106.30	36.33	160.40	24.10	10.40
4	111.40	35.33	118.70	21.87	7.33
5	103.30	35.33	130.00	22.20	9.43
11	104.60	36.33	105.20	23.67	11.03
12	98.90	35.67	101.40	20.33	11.50
13	109.90	36.00	120.70	23.23	8.13
14	99.63	37.00	122.20	22.17	11.00
15	109.20	36.67	153.50	21.57	10.43
16	101.10	35.33	138.10	22.83	12.40
17	113.40	36.00	156.30	22.50	12.00
18	92.53	35.00	99.90	24.20	11.23
Mean	104.80	35.92	124.29	22.26	10.00
Maximum	113.40	37.00	160.40	24.20	12.40
Minimum	92.53	35.00	89.30	18.70	7.06

[1=Nap 94006; 2=Nap 9908; 3=Nap 2037; 4= BARI Sarisha-7; 5=BARI Sarisha-13; 11=Nap 248; 12=Nap 179; 13=Nap 206; 14=Nap 2001; 15=Nap 2057; 16=Nap 2012; 17=Nap 2013; 18=Nap 2022].

value (-1.70). Goswami *et al.* (2005) reported good and well general combiner parents in rape seed for yield. Both significant positive and negative GCA effects were observed in pollen parents. The positive GCA effect was observed in Nap 2012 (1.59) and the negative GCA effect was observed in Nap2022 (-1.07) followed by Nap 206 (-0.95) (Table 5 and 6).

Specific combining ability effects

The cross combination, Nap9908×Nap2001 had the highest SCA value (3.28) and two of its closest values were 2.97 and 2.13 for cross combination Nap2037×Nap179 and Nap9908×Nap2012 respectively. The cross combinations with positive significant SCA value were good specific cross for the trait and it was produced by poor × good, good × good and good × poor general combiner parents. The lowest SCA value (-3.41) was observed in the cross combination Nap9908×Nap2022 and it was followed by Nap9908×Nap179 (-3.29) and Nap94006×Nap2012 (-2.39) (Table 7). Ghosh *et al.* (2002) supported this finding in their reports.

Heterosis for different characters

Plant height

Twenty eight hybrids exhibited significant heterosis over mid (Hm) parent. The range of the heterosis was -19.89% to 17.38% with a mean of-1.00%. It indicated that some hybrids were smaller and some were taller (plant height) than their mid parental value about -0.41% to 17.38%. The hybrids Nap9908×Nap206 (15.75%) had the highest significant estimate over better (Hb) parent and it was followed by Nap2037×Nap2012 (14.39%). The hybrid BS-7×Nap2057 showed significant negative estimate. It indicated that this hybrid was shorter than its better parent. In case of heterosis over check variety (Hc) BARI Sharisha-13, 50% hybrids exhibited significant positive heterosis and 50% hybrids negative. The hybrid Nap9908×Nap206 possessed the highest estimate (23.14%) and the hybrid

Table 5: GCA effects of testers for different characters.

Parents	Plant height	Days to 50% flowering	Number of siliqua/plant	Number of seeds/siliqua	Seed yield/plant (g)	GCA group
11	-2.24	-0.12	-13.27*	-0.12	-0.16	L
12	-1.42	0.67*	-8.55	0.05	-0.48	L
13	3.28*	-0.05	7.38	0.01	-0.95*	H
14	-0.45	0.27	5.12	-0.20	0.68	H
15	-5.73**	-0.52*	-13.06*	-0.03	-0.39	L
16	4.42**	-1.05**	18.36**	0.19	1.59**	H
17	3.83*	1.14**	7.28	0.81 **	0.78	H
18	-1.69	-0.32	-3.26	-0.71*	-1.07*	L
SE (±)	1.95	0.31	8.51	0.35	0.56	
SE(gi-gj)T	2.76	0.45	12.03	0.50	0.80	
MAX	4.42	1.14	18.36	0.81	1.59	
MIN	-5.73	-1.05	-13.27	-0.71	-1.07	

[11=Nap 248; 12=Nap 179; 13=Nap 206; 14=Nap 2001; 15=Nap 2057; 16=Nap 2012; 17=Nap 2013; 18=Nap 2022].

*and**Significance at 5% level and 1% level, SE: Standard error, SE(gi-gj): Standard error difference between GCA effect of two testers, H: High, L: low.

Table 6: GCA effects along with their combining ability status in five lines.

Parents	Plant height	Days to 50% flowering	No. of siliqua/plant	No. of seeds/siliqua	Seed yield plant (g)	GCA group
1	2.91	0.76**	14.25*	1.61**	-0.30	H
2	3.86*	0.14	12.22	0.04	2.95**	H
3	0.18	-0.40	-5.52	-1.26**	-0.32	L
4	-5.77**	0.30	-11.37	-0.20	-1.70**	L
5	-1.20	-0.81**	-9.59	-0.20	-0.64	L
SE (±)	1.54	0.25	6.72	0.28	0.44	
SE (gi-gj) L	2.18	0.35	9.51	0.39	0.63	
MAX	3.86	0.76	14.25	1.61	2.95	
MIN	-5.77	-0.81	-11.37	-1.26	-1.7	

1=Nap 94006; 2=Nap 9908; 3=Nap 2037; 4= BARI Sarisha-7; 5=BARI Sarisha-13.

*and**Significance at 5% level and 1% level, SE: Standard error, SE(gi-gj): Standard error difference between GCA effect of two lines; H: High, L: low.

BS-7×Nap2057 had the lowest (-14.43%). It indicated the hybrid Nap9908×Nap206 was the tallest among the hybrids and the hybrid BS-7×Nap2057 was the shortest one and it was a dwarf hybrid in respect of standard check variety

Table 7: SCA effects along with their combining ability status.

Hybrids (cross)	Plant height	Days to 50% flowering	Number of siliqua/plant	Number of seeds/siliqua	Seed yield/plant (g)	SCA group
1 × 11	0.34	0.83**	7.56	0.07	1.96**	H
1 × 12	6.82**	-1.96**	28.34**	-1.13**	-0.08	H
1 × 13	0.65	-1.23**	-18.42**	-0.46*	0.75*	L
1 × 14	1.68	-0.23	29.29**	0.92**	-1.08**	H
1 × 15	5.43**	-0.43*	-1.78	0.71**	-1.88**	L
1 × 16	-2.24	1.76**	-21.23**	-0.73**	-2.39**	L
1 × 17	0.77	-0.43*	12.57*	-0.50*	1.06**	H
1 × 18	-13.47**	1.70**	-36.31**	1.11**	1.67**	L
2 × 11	-0.60	1.45**	9.59	1.65**	-1.28**	H
2 × 12	-10.69**	1.65**	-17.39**	-2.09**	-3.29**	L
2 × 13	15.93**	1.72**	18.11**	1.21**	-1.13**	H
2 × 14	1.00	0.05	-6.57	0.36	3.28**	L
2 × 15	-2.21	-0.14	43.30**	-1.95	2.21**	H
2 × 16	-14.11**	-0.60**	0.62	-1.40**	2.13**	L
2 × 17	4.69**	-1.80**	-26.32**	3.02**	1.48**	H
2 × 18	-7.92**	-2.34**	-21.35**	1.31**	-3.41**	L
3 × 11	-1.55	1.00**	-21.98**	-1.32**	1.25**	L
3 × 12	-3.54**	0.53**	-7.94	2.35**	2.97**	L
3 × 13	-0.19	-2.40**	6.52	-0.29	-0.60	L
3 × 14	0.64	-0.06	4.81	0.90**	-0.92**	L
3 × 15	1.42	1.06**	-14.40**	0.15	-1.79**	L
3 × 16	12.94**	-2.58**	14.24**	-0.73**	-0.30	H
3 × 17	-3.06*	0.73**	-6.27	-2.06**	-0.36	L
3 × 18	7.25**	1.20**	25.03**	-1.12**	-0.24	H
4 × 11	1.32	-0.70**	-5.21	1.25**	-2.04**	L
4 × 12	1.17	0.15	-5.33	1.72**	0.38	L
4 × 13	-7.40**	-0.44*	-21.03**	1.12**	-0.95**	L
4 × 14	3.73**	0.55**	1.05	-1.54**	0.22	L
4 × 15	-4.22**	-0.30	-12.35*	-0.14	0.02	L
4 × 16	-0.40	2.89**	22.82**	1.84**	1.14**	H
4 × 17	1.15	0.02	4.57	-0.99**	-0.31	L
4 × 18	4.63**	-2.17**	15.47**	-3.25**	1.54**	H
5 × 11	0.48	-2.58**	10.04*	-1.65**	0.11	H
5 × 12	6.23**	-0.38*	2.32	-0.85**	0.03	H
5 × 13	4.92**	2.35**	-10.37*	-1.58**	1.93**	L
5 × 14	-7.07**	-0.31	-28.58**	-2.77**	-1.50**	L
5 × 15	-0.42	-0.18	10.43*	1.23**	1.43**	H
5 × 16	-10.10**	-1.98**	-16.45**	1.01**	-0.58	L
5 × 17	-3.55**	1.48**	15.45**	2.65**	-1.87**	H
5 × 18	9.50**	1.61**	17.16**	1.95**	0.45	H
SE (±)	1.19	0.19	5.21	0.21	0.34	
SE (sij-kl)	6.18	1.00	26.91	1.12	1.78	
Max	15.93	2.89	43.30	3.02	3.28	
Min	-14.11	-2.58	-36.31	-3.25	-3.41	

[1=Nap 94006; 2=Nap 9908; 3=Nap 2037; 4= BARI Sarisha-7; 5=BARI Sarisha-13; 11=Nap 248; 12=Nap 179; 13=Nap 206; 14=Nap 2001; 15=Nap 2057; 16=Nap 2012; 17=Nap 2013; 18=Nap 2022].

*and**Significance at 5% level and 1% level, SE: Standard error; SE (sij-kl): Standard error of the difference between for any two SCA effect of hybrids; H: High L: Low.

Table 8: Estimation of heterosis over mid parents, better parents and standard check for different characters.

Hybrids	Plant height			Number of siliqua/plant			No. of seeds/siliqua			Seed yield (g)/Plant		
	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)	H(m)	H(b)	H(c)
1 × 11	-0.41	-1.28	1.78	24.47***	35.57***	-6.87	10.77	0.70	7.36	18.01	0.88	21.55
1 × 12	9.52***	5.57*	8.84	53.74***	64.13***	12.74**	14.86	12.13	2.70	-6.98	-20.87	-3.53
1 × 13	2.56	0.97	7.42	10.20***	-4.14*	-10.97*	10.02	0.86	5.56	16.87	16.39	0.35
1 × 14	5.03*	1.66	4.81	52.46***	80.52***	34.95***	18.46	10.98	10.81	-2.80	-15.76	-1.77
1 × 15	-1.04	-2.26	3.32	-7.79***	-27.06***	-13.90**	20.03	13.91	10.66	-20.00	-29.07	-21.55
1 × 16	5.20*	2.54	5.71	8.96***	38.75***	-4.69	10.58	2.19	5.11	-13.21	-28.30	-6.01
1 × 17	1.50	-1.62	8.07	19.41***	-6.18***	12.79**	8.37	0.89	2.10	14.62	-4.17	21.91
1 × 18	-7.71***	-13.74***	-11.07	-7.84***	-2.35	-32.92***	11.77	-3.73	16.22***	6.39	-8.61	8.83
2 × 11	-0.57	-1.59	1.78	10.90***	7.04**	-6.87	12.60	0.70	7.36	24.64	0.88	21.55
2 × 12	-6.78**	-10.27***	-7.20	-7.86***	-12.64***	-24.00***	3.93	-0.33	-8.71	-1.44	-20.58	-3.18
2 × 13	17.38***	15.75***	23.14***	50.05***	45.31***	24.00***	12.33	1.29	6.01	42.86	33.20	14.84
2 × 14	5.12*	1.59	5.07	4.82**	9.02***	-5.15	10.04	1.35	1.20	87.06***	53.33*	78.80**
2 × 15	-7.39***	-8.40***	-3.16	-2.61	-15.42***	-0.15	1.08	-5.72	-8.41	68.70**	41.21	56.18
2 × 16	7.92***	5.02*	8.62	14.42***	27.09***	10.56*	1.69	-7.59	-4.95	71.48**	34.50	76.33**
2 × 17	5.77**	2.67	12.78*	-21.53***	-32.37***	-18.69***	-21.69*	-24.34*	-17.87*	59.37**	26.39	60.78**
2 × 18	-1.34	-7.93***	-4.78	-5.99**	-11.46***	-22.97***	-18.66*	-22.76*	-6.76	-7.66	-24.93	-10.60
3 × 11	-4.74*	-5.52*	-2.71	-47.38***	-57.15***	-44.82***	1.90	-1.97	4.50	-1.38	-5.57	13.78
3 × 12	-3.18	-6.61**	-3.84	-32.66***	-45.94***	-30.38***	12.95	8.99	7.36	10.81	5.51	28.62
3 × 13	-13.57***	-14.96***	-9.52	-16.08***	0.14	-7.00	2.88	-0.14	4.50	-12.59	-22.12	-14.13
3 × 14	1.44	-1.76	1.16	-19.24***	-30.15***	-10.05*	-7.65	-8.27	-8.41	-12.15	-14.55	-0.35
3 × 15	-7.22***	-8.43***	-3.20	-50.43***	-48.18***	-38.82***	0.84	0.15	-1.35	-28.32	-28.43	-20.85
3 × 16	17.29***	14.39***	17.79**	-8.62***	-16.61***	7.38	7.83	5.55	8.56	-3.95	-11.59	15.90
3 × 17	-4.41*	-7.41***	1.71	-33.27	-35.48	-16.92	-8.12	-9.35	-8.26	-10.12	-16.11	6.71
3 × 18	10.46***	3.29	6.36	-3.67*	-23.08***	-0.95	-19.32*	-26.74**	-11.56	-22.96	-25.82	-11.66
4 × 11	-9.83***	-12.59***	-5.68	-26.16***	-30.34***	-36.41***	-11.48	-14.23	-8.56	-35.12	-46.63	-35.69
4 × 12	-6.71**	-12.00***	-5.04	-20.68***	-26.46***	-32.87***	0.00	-4.20	-4.20	-13.27	28.99	-13.43
4 × 13	-14.87***	-15.47***	-8.78	-26.90***	-27.53***	-32.69***	-9.76	-11.76	-7.66	-17.67	-21.72	-32.51
4 × 14	-3.73	-8.82***	-1.61	-10.87***	-12.14***	-17.44***	-13.90	-13.96	-13.96	0.00	-16.67	-2.83
4 × 15	-19.89***	-20.70***	-14.43*	-44.34***	-50.65***	-41.74***	6.32	4.80	4.80	-11.07	-24.28	-16.25
4 × 16	-3.69	-8.17***	-0.90	10.85***	3.04	9.49*	3.33	1.90	4.80	11.68	-11.05	16.61
4 × 17	-8.12***	-8.93***	0.03	-17.81***	-27.70***	-13.08**	7.46	6.82	8.11	-9.66	-27.22	-7.42
4 × 18	-0.70	-9.12***	-1.94	3.72	-4.47*	-12.79**	1.36	-7.34	11.86	-5.92	-22.26	-7.42
5 × 11	-2.69	-3.31	-2.07	-15.23***	-23.31**	-23.31***	1.38	-4.05	0.30	-10.90	-18.48	-1.77
5 × 12	6.60**	4.29	4.29	-16.41***	-25.62***	-25.62***	20.03	13.91	16.22	-15.29	-22.90	-6.01

Table 8: Continue...

Table 8: Continue...

5 × 13	4.25*	1.12	7.59	-20.29***	-23.13***	-23.13***	-21.69	-26.74	-17.87	17.27	9.19	9.19
5 × 14	-6.00**	-7.65**	-7.65	-36.97***	-38.87***	-38.87***	-21.69*	-24.34*	-17.87*	-16.80	-22.73	-9.89
5 × 15	-8.93***	-11.39***	-6.33	-29.23***	-34.64***	-22.85***	-18.66*	-22.76*	-6.76	4.36	-0.64	9.89
5 × 16	-4.86*	-5.87*	-5.87	-21.81***	-24.11***	-19.36***	1.90	-1.97	4.50	-5.20	-16.44	9.54
5 × 17	-4.78*	-9.05***	-0.10	-12.21***	-19.60***	-3.33	12.95	8.99	7.36	-23.17	-31.39	-12.72
5 × 18	13.07***	7.20**	7.20	1.62	-10.13***	-10.13*	2.88	-0.14	4.50	-15.81	-22.55	-7.77
Mean	-1.00	-3.97	0.79	-7.46	-16.19	-13.45	-7.65	-8.27	-8.41	3.27	-9.72	5.60
Maximum	17.38	15.75	23.14	53.74	45.31	34.95	0.84	0.15	-1.35	87.06	53.33	78.80
Minimum	-19.89	-20.70	-14.43	-50.43	-57.15	-44.82	7.83	5.55	8.56	-35.12	-46.63	-35.69

[1=Nap 94006; 2=Nap 9908; 3=Nap 2037; 4= BARI Sarisha-7; 5=BARI Sarisha-13; 11=Nap 248; 12=Nap 179; 13=Nap 206; 14=Nap 2001; 15=Nap 2057; 16=Nap 2012; 17=Nap 2013; 18=Nap 2022].

(Table 8). Saurabh *et al.* (2005) observed positive heterosis for plant height over parents in *Brassica juncea* they mentioned that heterosis for plant height did not change the plant type as in their experiment both parents had semi dwarf gene.

Number of silique/plant

The hybrid Nap94006×Nap179 had the highest value of heterosis over mid parent (53.74%) and followed by the hybrid Nap94006×Nap2001 (52.46%).The hybrid Nap9908 × Nap206 (45.31%) had the highest value over the better parent. On the other hand, when compared the heterosis with standard check six hybrids exhibited significant positive heterosis. The hybrid Nap94006× Nap2001 had the highest (34.95%) estimate but BS-7×Nap2012 exhibited the lowest (9.49%) significant estimate. It indicated that the hybrid Nap94006×Nap2001 produced the highest number of silique/plant and the hybrid BS-7×Nap2012 produced the lowest (Table 8). Shen *et al.* (2005) also observed positive heterosis for the number of silique/plant.

Number of seeds/siliqua

The hybrids showed mid parent heterosis with the range -21.69% to 20.03% and mean 1.38%. In case of better parent heterosis the hybrid Nap94006×Nap2057 also showed maximum significant +ve heterosis (13.91%). The range of better parent heterosis was -26.74% to 13.91% with a mean of -4.05%. On the other hand, one hybrids exhibited significant positive and one significant negative standard heterosis for the trait. The hybrid Nap94006×Nap2022 exhibited the highest (16.22%) standard heterosis which was followed by BS-13×Nap2022 (11.86%), Nap94006× Nap2001 (10.81%) (Table 8). The result revealed that most of the hybrids exhibited significant positive heterosis for the trait.

Seed yield/plant

Out of forty hybrids, four exhibited significant positive mid parent heterosis for seed yield/plant. One exhibited significant zero heterosis and others were non-significant negative. For better parent heterosis, two hybrids exhibited significant positive values with a range of -46.63% to 53.33%, where mean heterosis was -9.72%. The hybrid Nap9908×Nap2001 showed the highest (53.33%) better parent heterosis for seed yield/plant. The hybrid Nap9908× Nap2001 showed the highest (78.80%) significant positive standard heterosis (Table 8). In India, Katiyar *et al.* (2004) observed standard heterosis of 43.38% and best parent heterosis of 150.33% for yield yellow sarson (*Brassica campestris*). In India, Chander and Verma (2004) found heterosis over both better parent and mid parent for seed yield/plant in cabbage. Moreover, Aditi *et al.* (2022) reported that, genotypes such as BPR 541-4 was found to be tolerant to heat stress at terminal stage and crosses such as Vardan × PM 30, Kranti × RH 406 and Kranti × Urvashi were found to be tolerant to heat stress for

seed yield per plant at terminal stage. In the present study most of the hybrids showed positive heterosis for seed yield/plant. It might be due to selection of good specific cross combinations for yield and yield-related characters as promising hybrids.

CONCLUSION

The estimates of general combining ability (GCA) effects for various traits indicated that among the lines, Nap9908 was the best general combiner for the number of primary and secondary branches per plant and seed yield per plant. Line Nap94006 was the top general combiner for the number of siliquae/plant and seeds/siliqua. Among the testers, Nap2057 was the best general combiner for plant height. Tester Nap2012 showed strong GCA for number of siliquae/plant and seed yield/plant. Tester Nap2013 was the best for the number of seeds/silique. The specific combining ability (SCA) estimates showed that the cross Nap9908 × Nap2012 was the best specific combiner for plant height, while Nap9908 × Nap2001 had the highest SCA effect for seed yield/plant. The cross Nap9908 × Nap2013 performed best in terms of seeds/siliqua, whereas Nap9908 × Nap2057 showed the best SCA effect for the number of siliquae/plant. On average, heterosis for seed yield over the mid-parent was 3.27%, while it was -9.72% over the better parent and 5.60% compared to the standard check. Based on the study findings, the lines Nap 9908 and Nap 94006 are recommended as promising general combiners for use in rapeseed breeding programs due to their strong general combining ability (GCA) effects across key yield-related traits. Additionally, the 16 hybrids identified as good specific combiners should be prioritized for further evaluation and potential commercial utilization to enhance productivity. Given the significant role of non-additive gene effects in trait inheritance, hybrid breeding strategies should focus on exploiting heterosis, particularly hybrids with positive heterosis over the mid-parent and standard check. Future breeding efforts should aim to refine hybrid development while leveraging identified parental lines to achieve improved yield and breeding efficiency.

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Disclaimers

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Conflict of interest

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