



Estimating combining ability of advanced rapeseed lines for seed yield and yield components

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<https://doi.org/10.56093/job.v17i2.9>

Received date : 14 June 2026; Revised date : 27 June 2026; Accepted date : 29 June 2026

Abstract

To estimate heritability and combining ability for yield components, seed yield, and related traits, a one-way diallel cross involving eight canola lines (G41, Zafar, G56, G31, G22, GF2, G204, and G104) and their parents was evaluated in a randomized complete block design with three replications. Diallel analysis revealed that the mean square for general combining ability (GCA) was significant for all traits, whereas specific combining ability (SCA) was significant for all traits except 1000-seed weight. Furthermore, the relatively high estimates of narrow-sense heritability for pod length (0.50), 1000-seed weight (0.69), seed yield (0.63), and harvest index (0.53) suggest that additive gene effects play a predominant role in the genetic control of these traits. The parental lines G41, Zafar, and G22 exhibited positive and significant GCA effects for seed yield and were identified as superior combiners. Moreover, hybrids with positive and significant SCA effects for seed yield generally included at least one parent with significant positive GCA for this trait. Among the evaluated hybrids, G41 × G22, G41 × GF2, Zafar × G22, and Zafar × G204 were identified as the most promising combinations, producing seed yields of 3422, 3400, 3348, and 3311 kg ha⁻¹, respectively.

Keywords: Additive effect of genes, diallele, degree of dominance, heritability

Introduction

Oilseed crops constitute the second largest source of food reserves worldwide after cereals (Azizinia 2012; Abbadi *et al.*, 2021). These crops contain approximately 20–50% oil, which generally has a balanced composition of saturated and unsaturated fatty acids. Among oilseed crops, species of the genus *Brassica* account for approximately 10% of global oilseed production and 14–15% of vegetable oil production (Rameeh 2014; Snowdon *et al.*, 2020). The existence of both spring and winter growth habits, together with adaptation to a wide range of climatic conditions, has contributed to the widespread cultivation of rapeseed worldwide (Sincik *et al.*, 2011; Raman *et al.*, 2016; Liu *et al.*, 2019). Improving seed yield remains a primary objective in rapeseed breeding programs. Therefore, understanding the genetic architecture of seed yield and its component traits is essential for developing ideotype cultivars with high genetic potential and superior productivity (Farshadfar 2013). In this context, estimation of heritability and combining ability provides valuable information for selecting suitable parental lines and designing effective breeding strategies (Nasrin 2011; Rameeh 2012; Rahman 2013; Wu *et al.*, 2019). Singh *et al.* (2012), using generation

mean analysis in Indian mustard, reported high narrow-sense heritability and consequently high expected genetic advance for plant height, number of pods on the main stem, and thousand-seed weight. Similarly, Qian *et al.* (2009) found that additive gene effects played the predominant role in the inheritance of biological yield. Sincik *et al.* (2011) reported that specific combining ability (SCA) was more important for seed yield, whereas both general combining ability (GCA) and SCA significantly influenced plant height, the number of primary and secondary branches, seeds per silique, and thousand-seed weight. They also observed that the number of secondary branches, siliques per secondary branch, and siliques per plant were mainly governed by GCA effects. Nasrin *et al.* (2011) found significant GCA and SCA effects for plant height, days to maturity, and thousand-seed weight in a one-way diallel population of seven Indian mustard genotypes. However, SCA effects were more important for the number of primary and secondary branches, pods per plant, and seed yield.

Azizinia (2012) investigated eight rapeseed genotypes in a complete diallel mating design and reported significant GCA and SCA effects for thousand-seed weight, oil content, and seed yield, indicating that both additive and

non-additive gene actions contributed to the inheritance of these traits. Rameeh (2012) estimated narrow-sense heritability values of 0.80, 0.90, and 0.81 for plant height, seeds per silique, and thousand-seed weight, respectively, in a line $\times$ tester analysis involving eight spring rapeseed lines. The additive gene effects were more important for the number of primary branches, suggesting that this trait can be effectively improved through early-generation selection (Farshadfar *et al.*, 2013). In contrast, non-additive gene effects predominated for plant height, pods per plant, and seed yield, indicating that hybrid breeding would be more effective for improving these traits. They further reported that both additive and non-additive gene effects contributed to the inheritance of seeds per silique and thousand-seed weight. Xing *et al.* (2014), using a diallel mating design involving 12 rapeseed genotypes evaluated across four environments, reported that the number of pods per plant, thousand-seed weight, and oil content were significantly influenced by both additive and dominance effects. In contrast, additive effects were more important for seeds per silique, whereas dominance effects played a greater role in the inheritance of seed yield. Moreover, additive $\times$ environment interactions significantly affected seed yield, pods per plant, and oil content, while dominance $\times$ environment interactions were significant for all evaluated traits. Because heritability estimates and other genetic parameters vary depending on the genetic background of the studied materials and environmental conditions, the present study was conducted to estimate the narrow-sense heritability of important agronomic traits and to evaluate the general and specific combining abilities of rapeseed lines in order to identify superior parents and promising hybrid combinations for breeding programs.

Materials and Methods

Seven advanced rapeseed lines (G41, G56, G31, G22, GF2, G204, and G104) together with the cultivar Zafar, comprising a total of eight parental genotypes, were crossed in a one-way diallel mating design during 2023–24 growing season. To obtain sufficient F_1 seed, 35 inflorescences from each female parent, each containing 12 emasculated flower buds, were manually crossed with each male parent. During 2024–25 growing season, 36 genotypes, including 28 F_1 hybrids and their eight parental lines, were evaluated at the Bayeh-Kola Agricultural Research Station, affiliated with the Mazandaran Agricultural and Natural Resources Research and Education Center, using a randomized complete block design (RCBD) with three replications. The experimental site is located at an altitude of 15 m above sea level (53°132 E, 36°432 N). Wheat was grown as the preceding crop.

Fertilizer application was based on soil test recommendations and consisted of 50 kg ha⁻¹ triple superphosphate, 100 kg ha⁻¹ potassium sulfate, and 150 kg N ha⁻¹ supplied through urea (46% N). Nitrogen fertilizer was applied in three equal splits: at planting, at the rosette stage, and at the budding stage.

Each experimental plot consisted of four rows, each 5 m long, with 30 cm spacing between rows and approximately 5 cm between plants within rows. Data were collected from the two central rows after excluding border plants at both ends of each plot to minimize border effects. The evaluated traits included pods per plant, pod length, seeds per pod, thousand-seed weight, seed yield, biological yield, and harvest index. Yield traits were determined using the middle five pods collected from 10 randomly selected plants in each plot. Seed yield was determined by harvesting the two central rows after excluding border effects and was expressed as kg ha⁻¹. Biological yield was measured from one representative row in each plot, and the harvest index was calculated as the ratio of seed yield to biological yield. Genetic analyses were performed using Griffing's (1956) diallel Method II, Model B (mixed model). General combining ability (GCA) and specific combining ability (SCA) effects were estimated, and their significance was assessed using Student's *t*-test. Before conducting the diallel analysis, the assumption of normality was verified using MSTAT-C software. Genetic parameter estimation and diallel analyses were performed using the DIALLEL program (Zhang and Kang 1997) implemented in SAS version 9.1.

Results and Discussion

The results of the analysis of genetic variance based on Griffing's (1956) Method II, Model B are presented in Table 1. The mean squares for general combining ability (GCA) were significant for all studied traits, including pods per plant, pod length, seeds per pod, thousand-seed weight, seed yield, biological yield, and harvest index, indicating the importance of additive gene effects in the inheritance of these traits. Likewise, specific combining ability (SCA) was significant for all traits except thousand-seed weight, demonstrating that non-additive gene effects also contributed substantially to the genetic control of most traits. The significant GCA/SCA variance ratio, together with the relatively high estimates of narrow-sense heritability for pod length, seeds per pod, thousand-seed weight, and seed yield, suggests that additive gene effects play a predominant role in the inheritance of these traits. Gupta and Kumar (2011), studying a one-way diallel cross among eight improved Indian mustard lines, similarly reported that GCA variance was more important for thousand-seed weight, whereas SCA variance

Table 1: Half diallel analysis of different traits for eight rapeseed genotypes

S.O.V	Mean squares							
	df	Pods per plant	Pod 's length	Seeds per pod	1000-seed weight	Seed yield	Biological yield	Harvest index
Rep	2	78.7	0.32	115.4**	0.14	1571000**	25240000**	6.7
Crosses	35	1417.3**	1.11**	18.9**	0.22**	387481**	7649000**	58.2**
GCA	7	1610.2**	2.43**	37.3**	0.75**	975122**	11020000**	76.2**
SCA	28	1369.1**	0.78**	14.3*	0.08	240570**	6807000**	53.8**
Error	70	103.8	0.33	8.4	0.08	64580	1795000	3.9
MS(GCA)/MS(SCA)		1.18	3.12*	2.61*	9.38**	4.05*	1.62	1.42
.h ² N		0.32	0.50	0.35	0.69	0.63	0.32	0.53

* and **: significant at 5% and 1% levels of probability, respectively.

Table 2: Mean comparison of yield components and seed yield of eight oil seed rape genotypes

Parents	Pods per plant (no.)	Pod 's length (cm)	Seeds per pod (no.)	1000-seed weight (g)	Seed yield (kg ha ⁻¹)	Biological yield(kg ha ⁻¹)	Harvest index(%)
G41	140 ^{ab}	7.13 ^a	27.57 ^{ab}	3.81 ^b	2929.2 ^a	13673.0 ^{ab}	21.62 ^b
Zafar	137 ^{ab}	7.47 ^a	26.50 ^{abc}	4.08 ^{ab}	2925.0 ^a	15022.2 ^a	19.88 ^b
G56	130 ^{bc}	7.60 ^a	20.93 ^{bc}	4.31 ^a	2866.7 ^a	13074.7 ^{abc}	21.95 ^b
G31	119 ^{bc}	6.37 ^{ab}	21.93 ^{bc}	3.96 ^b	2187.5 ^{bc}	11151.2 ^{bcd}	19.71 ^b
G22	158 ^a	7.23 ^a	24.53 ^{abc}	3.73 ^b	3120.8 ^a	10148.8 ^{cd}	30.81 ^a
GF2	112 ^{cd}	7.17 ^a	29.40 ^a	4.29 ^a	2737.5 ^{ab}	11880.7 ^{bc}	23.27 ^b
G204	130 ^{bc}	7.43 ^a	26.30 ^{abc}	3.94 ^b	2612.5 ^{abc}	11760.8 ^{bc}	22.22 ^b
G104	94 ^d	5.57 ^b	20.33 ^c	3.84 ^b	2083.3 ^c	8522.8 ^d	24.44 ^b

Mean, in each column, followed by at least one letter in common are not significantly different at the 1% level of probability- using Duncan's Multiple Range Test.

Table 3. General combining ability effects of yield components and seed yield in eight oil seed rape genotypes.

Parents	Pods per plant (no.)	Pod 's length (cm)	Seeds per pod (no.)	1000-seed weight (g)	Seed yield (kg ha ⁻¹)	Biological yield(kg ha ⁻¹)	Harvest index(%)
G41	10.72**	0.25**	1.56**	0.01	184.68**	477.01*	0.47
Zafar	9.31**	0.18*	0.52	0.06	147.26**	1086.89**	-0.50
G56	-8.78**	0.01	-1.12*	0.19**	27.47	274.56	-0.56
G31	0.33	-0.37**	-1.25*	-0.14**	-291.27**	-384.32	-2.03**
G22	3.59*	0.18*	0.44	-0.15**	187.30**	-736.26**	3.23**
GF2	-2.85	0.00	0.78	0.26**	9.99	27.13	-0.07
G204	-6.17**	0.26**	0.53	-0.05	-44.01	-616.22**	0.80*
G104	-6.16**	-0.50**	-1.45**	-0.15**	-221.41**	-128.79	-1.34**

* and **: Not -significant, significant at 5% and 1% levels of probability, respectively.

predominated for the remaining traits. Likewise, Xing *et al.* (2014) found that additive and dominance effects significantly influenced pods per plant, thousand-seed weight, and oil content in a diallel population of 12 rapeseed genotypes evaluated across four environments.

The number of pods per plant among the parental lines ranged from 94 to 158. The parental genotypes G22, G41, and Zafar produced the highest numbers of pods per

plant (158, 140, and 137, respectively) and were classified within the same statistical group according to Duncan's multiple range test (Table 2). Because pods per plant constitute a major component of seed yield, these parents, which also exhibited positive and significant GCA effects (Table 3), are considered valuable donors for improving this trait. However, the relatively low heritability estimate suggests that selection should be practiced in advanced generations, while hybrid breeding may also be effective

due to the contribution of non-additive gene effects.

Among the hybrids, pods per plant ranged from 96 (G56 × G104) to 177 (Zafar × G104). Hybrids G41 × GF2, G31 × GF2, Zafar × G204, and Zafar × G104 produced 172, 172, 173, and 177 pods per plant, respectively, and did not differ significantly (Table 4). Significant SCA effects were observed in 64% of the hybrid combinations, of which 29% were positive (Table 5). Most hybrids with significant positive SCA effects included at least one parent with significant positive GCA for this trait. Similar results were reported by Rameeh (2012), who observed significant GCA and SCA effects for pods per plant in spring rapeseed. Among the hybrids, pod length ranged from 5.47 cm (G31 × G104) to 7.73 cm (G41 × G22). Hybrids G41 × Zafar, G41 × G22, G41 × G204, G56 × G204, and GF2 × G204 produced the longest pods and did not differ significantly (Table 5). Significant SCA effects were detected in 14% of the

crosses, with G56 × G31 exhibiting the highest positive SCA effect (Table 5).

The number of seeds per pod among the parental lines ranged from 20.33 (G104) to 29.40 (GF2). Parents G41, Zafar, GF2, and G204 produced relatively high numbers of seeds per pod and belonged to the same statistical group (Table 2). Among these, G41 exhibited significant positive GCA effects and is therefore considered a superior parent for improving this trait (Table 3). In the hybrids, seeds per pod ranged from 20.27 to 29.07, with G41 × Zafar, G41 × G22, Zafar × G22, and G22 × G204 ranking among the best-performing combinations (Table 5). Significant SCA effects were detected in 14% of the crosses, with G41 × G104 showing the highest positive SCA effect (Table 5). Xing *et al.* (2014) likewise reported an important contribution of non-additive gene effects to the inheritance of seeds per pod.

Table 4. Mean comparison of yield components and seed yield of half diallel crosses of eight oil seed rape genotypes.

Crosses	Pods per plant (no.)	Pod 's length (cm)	Seeds per pod (no.)	1000-seed weight (g)	Seed yield (kg ha ⁻¹)	Biological yield (kg ha ⁻¹)	Harvest index (%)
G41 × Zafar	145 ^{c-g}	7.47 ^{ab}	28.07 ^a	4.22 ^{a-d}	2839.2 ^{a-i}	12416.3 ^{bcd}	22.84 ^{e-j}
G41 × G56	136 ^{e-h}	6.37 ^{a-d}	25.37 ^{ab}	4.30 ^{abc}	3180.8 ^{a-d}	11948.1 ^{b-e}	26.63 ^{c-f}
G41 × G31	138 ^{d-g}	6.23 ^{a-d}	25.93 ^{ab}	3.58 ^{cde}	2315.9 ^{hi}	11641.7 ^{b-e}	20.21 ^{hij}
G41 × G22	156 ^{a-e}	7.73 ^a	29.07 ^a	3.64 ^{b-e}	3412.7 ^a	12137.7 ^{bcd}	28.25 ^{bcd}
G41 × GF2	172 ^{ab}	7.00 ^{abc}	24.87 ^{ab}	4.44 ^a	3400.0 ^a	10698.4 ^{b-e}	31.57 ^{ab}
G41 × G204	162 ^{a-d}	7.40 ^{ab}	23.83 ^{ab}	3.95 ^{a-e}	3000.0 ^{a-g}	11023.6 ^{b-e}	27.15 ^{b-e}
G41 × G104	154 ^{a-f}	6.73 ^{a-d}	28.20 ^a	3.71 ^{a-e}	2908.3 ^{a-h}	13736.2 ^{ab}	21.35 ^{g-j}
Zafar × G56	139 ^{d-g}	6.83 ^{a-d}	27.37 ^{ab}	4.35 ^{ab}	3031.1 ^{a-f}	11829.8 ^{b-e}	25.68 ^{d-g}
Zafar × G31	129 ^{f-i}	6.97 ^{abc}	23.60 ^{ab}	3.75 ^{a-e}	2673.8 ^{c-i}	12611.0 ^{bcd}	21.27 ^{g-j}
Zafar × G22	145 ^{c-g}	6.87 ^{a-d}	28.60 ^a	3.81 ^{a-e}	3348.1 ^{ab}	10882.2 ^{b-e}	30.73 ^{abc}
Zafar × GF2	146 ^{c-g}	6.40 ^{a-d}	22.23 ^{ab}	4.22 ^{a-d}	2512.5 ^{e-i}	13159.9 ^{bcd}	19.10 ^{hij}
Zafar × G204	173 ^a	6.30 ^{a-d}	23.07 ^{ab}	3.91 ^{a-e}	3311.3 ^{abc}	9838.2 ^{de}	33.68 ^a
Zafar × G104	177 ^a	6.80 ^{a-d}	24.17 ^{ab}	3.72 ^{a-e}	2975.0 ^{a-g}	16265.0 ^a	18.48 ^j
G56 × G31	139 ^{d-g}	7.17 ^{abc}	24.00 ^{ab}	4.24 ^{a-d}	2302.5 ^{hi}	11806.9 ^{b-e}	19.52 ^{hij}
G56 × G22	148 ^{b-g}	5.73 ^{cd}	20.27 ^b	3.86 ^{a-e}	3287.4 ^{abc}	11691.1 ^{b-e}	28.12 ^{bcd}
G56 × GF2	124 ^{ghi}	6.43 ^{a-d}	27.60 ^{ab}	4.43 ^a	2915.4 ^{a-h}	13476.5 ^{abc}	21.89 ^{f-j}
G56 × G204	105 ^{ij}	7.23 ^{abc}	25.13 ^{ab}	3.74 ^{a-e}	2695.8 ^{c-i}	10054.1 ^{cde}	26.88 ^{b-e}
G56 × G104	96 ^j	5.80 ^{cd}	22.07 ^{ab}	3.85 ^{a-e}	2196.7 ⁱ	11967.6 ^{b-e}	18.34 ^j
G31 × G22	145 ^{c-g}	6.53 ^{a-d}	25.23 ^{ab}	3.53 ^{de}	2626.9 ^{d-i}	12026.0 ^{b-e}	21.85 ^{f-j}
G31 × GF2	172 ^{ab}	5.87 ^{cd}	22.37 ^{ab}	3.94 ^{a-e}	2511.7 ^{e-i}	10575.4 ^{b-e}	23.79 ^{d-i}
G31 × G204	112 ^{hij}	6.13 ^{bcd}	24.70 ^{ab}	3.67 ^{b-e}	2537.5 ^{d-i}	9691.5 ^{de}	26.13 ^{c-g}
G31 × G104	166 ^{abc}	5.47 ^d	22.73 ^{ab}	3.45 ^e	2812.5 ^{a-i}	11679.6 ^{b-e}	24.07 ^{d-h}
G22 × GF2	112 ^{hij}	7.07 ^{abc}	25.63 ^{ab}	4.13 ^{a-e}	2727.7 ^{b-i}	10729.2 ^{b-e}	25.40 ^{d-g}
G22 × G204	106 ^{ij}	7.20 ^{abc}	28.27 ^a	3.80 ^{a-e}	2413.7 ^{f-i}	12447.8 ^{bcd}	19.38 ^{hij}
G22 × G104	143 ^{c-g}	6.90 ^{a-d}	23.17 ^{ab}	3.75 ^{a-e}	2883.3 ^{a-h}	8603.6 ^e	33.51 ^a
GF2 × G204	131 ^{e-h}	7.43 ^{ab}	27.20 ^{ab}	4.25 ^{a-d}	3079.6 ^{a-e}	10947.5 ^{b-e}	27.98 ^{bcd}
GF2 × G104	125 ^{ghi}	6.23 ^{a-d}	24.00 ^{ab}	4.10 ^{a-e}	2546.4 ^{d-i}	13101.0 ^{bcd}	19.64 ^{hij}
G204 × G104	125 ^{ghi}	6.73 ^{a-d}	25.40 ^{ab}	3.75 ^{a-e}	2365.4 ^{ghi}	12491.3 ^{bcd}	18.93 ^{ij}

Mean, in each column, followed by at least one letter in common are not significantly different at the 1% level of probability- using Duncan's Multiple Range Test.

Table 5: Specific combining ability effects of yield components and seed yield in half diallel crosses of eight rapeseed genotypes

Crosses	Pods per plant (no.)	Pod 's length (cm)	Seeds per pod (no.)	1000-seed weight (g)	Seed yield (kg ha ⁻¹)	Biological yield (kg ha ⁻¹)	Harvest index (%)
G41 × Zafar	-12.08*	0.29	1.00	0.22	-278.1*	-945.1	-1.19
G41 × G56	-3.36	-0.63*	-0.05	0.17	183.2	-601.1	2.66*
G41 × G31	-9.84	-0.40	0.64	-0.22	-362.9**	-248.6	-2.29*
G41 × G22	4.51	0.56	2.08	-0.15	255.3	599.4	0.49
G41 × GF2	26.51**	0.00	-2.46	0.24	420.0**	-1603.3*	7.10**
G41 × G204	20.23**	0.15	-3.24*	0.07	74.0	-634.7	1.82
G41 × G104	11.79*	0.23	3.11*	-0.08	159.7	1590.4*	-1.84
Zafar × G56	0.84	-0.10	2.98	0.16	71.0	-1329.2	2.68*
Zafar × G31	-17.80**	0.40	-0.66	-0.12	32.4	110.9	-0.26
Zafar × G22	-4.69	-0.24	2.65	-0.05	228.1	-1266.0	3.94**
Zafar × GF2	2.35	-0.53	-4.05**	-0.04	-430.1**	248.3	-4.39**
Zafar × G204	32.37**	-0.89**	-2.97	-0.04	422.7**	-2430.0**	9.32**
Zafar × G104	36.22**	0.36	0.11	-0.14	263.8	3509.4**	-3.74**
G56 × G31	10.22	0.78*	1.38	0.25	-219.1	119.2	-1.95
G56 × G22	16.13**	-1.19**	-4.04**	-0.12	287.3*	355.3	1.39
G56 × GF2	-1.39	-0.32	2.96	0.04	92.6	1377.2	-1.55
G56 × G204	-17.27**	0.23	0.74	-0.34*	-73.0	-1401.8*	2.58*
G56 × G104	-26.12**	-0.46	-0.35	-0.13	-394.8**	24.3	-3.83**
G31 × G22	3.96	-0.03	1.05	-0.12	-54.5	1349.1	-3.41**
G31 × GF2	36.93**	-0.52	-2.15	-0.12	7.6	-864.9	1.82
G31 × G204	-19.75**	-0.51	0.43	-0.08	87.4	-1105.5	3.30**
G31 × G104	34.30**	-0.42	0.44	-0.20	539.8**	395.2	3.37**
G22 × GF2	-26.29**	0.14	-0.57	0.08	-255.0	-359.3	-1.83
G22 × G204	-28.14**	0.02	2.31	0.06	-515.0**	2002.8**	-8.72**
G22 × G104	8.11	0.47	-0.81	0.11	132.1	-2328.9**	7.56**
GF2 × G204	3.20	0.43	0.90	0.10	328.2*	-261.0	3.18**
GF2 × G104	-2.68	-0.02	-0.32	0.05	-27.5	1405.1*	-3.02**
G204 × G104	-0.23	0.22	1.33	0.01	-154.6	1438.8*	-4.60**

* and **: Not- significant, significant at 5% and 1% levels of probability, respectively

Among the major yield components, thousand-seed weight exhibited relatively high narrow-sense heritability, indicating that this trait is amenable to improvement through selection. Singh *et al.* (2012) similarly reported high narrow-sense heritability and substantial expected genetic advance for thousand-seed weight in Indian mustard.

The parental means ranged from 3.73 g (G22) to 4.31 g (G56), while Zafar, G56, and GF2 produced the highest values and formed the superior statistical group (Table 2). G56 and GF2 also exhibited significant positive GCA effects (Table 4). Among the hybrids, thousand-seed weight ranged from 3.45 g (G31 × G104) to 4.44 g (G41 × GF2), and 36% of the hybrids exceeded 4.0 g (Table 4). As expected from the predominance of additive gene effects, only one hybrid showed significant positive SCA effects for this trait (Table 5).

Seed yield among the parental genotypes ranged from 2083 kg ha⁻¹ (G104) to 3121 kg ha⁻¹ (G22). The parental lines G41, Zafar, and G22 produced the highest seed yields and did not differ significantly according to Duncan's test (Table 2). These three parents also exhibited significant positive GCA effects (Table 3), confirming their suitability for use in breeding programs aimed at increasing seed yield. Hybrid seed yield ranged from 2197 kg ha⁻¹ (G56 × G104) to 3413 kg ha⁻¹ (G41 × G22) (Table 4). Hybrids G41 × G56, G41 × G22, G41 × GF2, Zafar × G22, Zafar × G204, and G56 × G22 constituted the highest-yielding statistical group, producing between 3181 and 3413 kg ha⁻¹. Most high-yielding hybrids had at least one high-yielding parent. Significant positive SCA effects were observed for G41 × GF2, Zafar × G204, G56 × G22, G31 × G104, and GF2 × G204 (Table 5), demonstrating the importance of non-additive gene action for seed yield. Similar conclusions were reached by Farshadfar *et al.*

(2013), who reported that non-additive gene effects predominated for seed yield and recommended hybrid breeding for genetic improvement of this trait.

Biological yield among the parental lines ranged from 8523 to 15,023 kg ha⁻¹, with G41, Zafar, and G56 producing the highest values (Table 2). Because high biological yield, together with high seed yield and lodging resistance, enhances crop competitiveness, these genotypes represent valuable breeding materials. G41 and Zafar exhibited significant positive GCA effects, indicating the importance of additive gene action for this trait (Table 3). Among the hybrids, biological yield ranged from 8604 kg ha⁻¹ (G22 × G104) to 16,265 kg ha⁻¹ (Zafar × G104). Hybrids G41 × G104, Zafar × G104, G22 × G204, GF2 × G104, and G204 × G104 showed significant positive SCA effects and are promising combinations for improving biological yield (Table 5). The parental lines differed significantly in harvest index. G22 exhibited the highest harvest index (30.8%) and significant positive GCA effects, making it the most desirable parent for improving this trait (Tables 2 and 3). Harvest index among the hybrids ranged from 18.3% to 33.7%, with G41 × GF2, Zafar × G22, Zafar × G204, and G22 × G104 belonging to the highest statistical group (Table 4). Significant SCA effects were detected in 64% of the hybrids, with 32% showing positive significant values (Table 5). These findings indicate that both additive and non-additive gene effects contribute to harvest index. Similar observations have been reported by Qian *et al.* (2009), who found that additive gene effects played a major role in the inheritance of biological yield in rapeseed.

Conclusion

The present study showed that both additive and non-additive gene effects contributed to the inheritance of yield and its related traits in rapeseed, although additive effects predominated for pod length, seeds per pod, thousand-seed weight, and seed yield. The parents G41, Zafar, and G22 exhibited superior general combining ability for seed yield and several yield components, making them valuable donor parents for breeding programs. Several hybrids, particularly G41 × G22, G41 × GF2, Zafar × G204, and Zafar × G22, combined high mean performance with desirable specific combining ability effects, indicating their potential for hybrid development. The relatively high narrow-sense heritability of key yield components suggests that selection would be effective for their genetic improvement, however traits with greater non-additive effects may benefit from hybrid breeding strategies.

Acknowledgement

The author gratefully acknowledges the Mazandaran Agricultural and Natural Resources Research and Education Center for providing financial support, research facilities, and technical assistance for this study.

References

- Abbadi A, Leckband G, Obermeier C and Snowdon RJ. 2021. Advances in breeding winter oilseed rape for sustainable production. *Plant Breed* **140**: 487–505.
- Azizinia S. 2012. Combining ability analysis of yield component parameters in winter rapeseed genotypes (*Brassica napus* L.). *J Agric Sci* **4**: 87–94.
- Farshadfar E, Kazemi Z and Yaghotipoor A. 2013. Estimation of combining ability and gene action for agro-morphological characters of rapeseed (*Brassica napus* L.) using line × tester mating design. *Int J Adv Biol Biomed Res* **1**: 711–717.
- Griffing B. 1956. Concept of general combining ability in relation to diallel crossing system. *Aust J Biol Sci* **9**: 463–493.
- Gupta P and Kumar S. 2011. Heterosis and combining ability analysis for yield and its components in Indian mustard (*Brassica juncea* L.). *Acad J Plant Sci* **4**: 45–52.
- Liu S, Fan C, Li J, Cai G, Yang Q, Wu J, Yi X and Zhang C. 2019. Genetic architecture of important agronomic traits in rapeseed (*Brassica napus* L.). *Crop J* **7**: 485–496.
- Nasrin S, Nur F, Khurshida M, Shahidur NM, Bhuiyan R, Sarkar S and Islam MM. 2011. Heterosis and combining ability analysis in Indian mustard (*Brassica juncea* L.). *Bang Res Publ J* **6**: 65–71.
- Qian W, Li Q, Noack J, Sass O, Meng J, Frauen M and Jung C. 2009. Heterotic pattern in rapeseed (*Brassica napus* L.): II. Crosses between European winter and Chinese semi-winter lines. *Plant Breed* **128**: 466–470.
- Rahman H. 2013. Breeding spring canola (*Brassica napus* L.) by the use of exotic germplasm. *Can J Plant Sci* **93**: 363–373.
- Raman H, Raman R, Qiu Y, Yadav AS, Sureshkumar S, Borg L, Rohan M, Wheeler D, Owen O, Menz I and Balasubramanian S. 2016. Genetic and genomic resources for improving canola (*Brassica napus* L.) yield and adaptation. *Theor Appl Genet* **129**: 2187–2209.
- Rameeh V. 2012. Combining ability analysis of plant height and yield components in spring type of rapeseed varieties (*Brassica napus* L.) using line × tester analysis. *Int J Agric For* **2**: 58–62.

- Rameeh V. 2014. Cytoplasmic male sterility and inter and intra subgenomic heterosis studies in *Brassica* species: A review. *J Agric Sci* **59**: 207–226.
- Sincik M, Goksoy T and Turan ZM. 2011. The heterosis and combining ability of diallel crosses of rapeseed. *Not Bot Horti Agrobot Cluj Napoca* **39**: 242–248.
- Singh DK, Kumar K, Singh P, Singh VP and Solankey SS. 2012. Heritability and heterosis analysis for different crosses in *Brassica juncea* (L.) Czern. and Coss. with inheritance of white rust resistance. *New Agric* **23**: 1–8.
- Snowdon RJ, Lühs W and Friedt W. 2020. Oilseed rape. In: *Genetics, Genomics and Breeding of Oilseed Brassicas*. CRC Press.
- Wu D, Liang Z, Yan T, Xu Y, Xuan L, Tang J, Zhou G, Lohwasser U, Hua S, Wang H, Chen X, Wang Q, Zhu L, Maodzeka A, Hussain N, Li Z, Li X, Shamsi IH, Jilani G, Wu L, Zheng H, Zhang G, Chalhoub B, Shen L, Yu H and Jiang L. 2019. Whole-genome resequencing of diverse *Brassica napus* accessions reveals genetic basis of important agronomic traits. *Nat Commun* **10**: 1340.
- Xing N, Fan C and Zhou Y. 2014. Parental selection of hybrid breeding based on maternal and paternal inheritance of traits in rapeseed (*Brassica napus* L.). *PLoS ONE* **9**: 1–9.
- Zhang Z and Kang SK. 1997. A SAS program for Griffing's diallel analyses. *Agron J* **89**: 176–182.