HETEROTIC RESPONSE AND COMBINING ABILITY ANALYSIS IN F₁ DIALLEL POPULATIONS OF *BRASSICA NAPUS* L.

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Abstract

Eight Brassica napus L. genotypes including Rainbow, Rustam Canola, Dunkled, Abasin-95, NIFA Gold, Durr-e-NIFA, Punjab Sarsoon and Faisal Canola, varied by genetic makeup and yield traits were crossed during 2014-15 in a 8 × 8 complete diallel fashion at the University of Agriculture, Peshawar, Pakistan. Parental genotypes and their 56 F1 hybrids were sown during 2015-16 in a randomized complete block design to evaluate through mean performance, heterosis and combining ability effects. Significant ($p \le 0.01$) differences were observed among the parental genotypes and their F₁ hybrids for all the studied traits. The F1 hybrids NIFA Gold × Rustam Canola, Rustam Canola × Punjab Sarsoon and Punjab Sarsoon × Abasin-95 exhibited best mean performance and maximum mid- and better-parent heterosis for plant height, 1000-seed weight and seed yield per plant. Combining ability analysis revealed significant ($p \le 0.01$) mean squares due to general (GCA), specific (SCA) and reciprocal combining ability (RCA) for all the traits indicating the importance of additive, non-additive and maternal effects. For plant height and main raceme length, the mean squares due to GCA were greater in magnitude than SCA and RCA. However, for 1000-seed weight and seed yield per plant, the mean squares due to RCA were found greater followed by SCA and GCA. Results further enunciated that due to the preponderance of GCA and RCA effects, the contribution of additive and maternal effects was more important in the expression of these traits. Parental genotypes Abasin-95 and Punjab Sarsoon were found as best general combiners and performed better in combination with other genotypes for the majority of the traits. The F1 hybrids NIFA Gold × Rustam Canola, Rustam Canola × Punjab Sarsoon, Punjab Sarsoon × Abasin-95 and Dunkled × Rainbow exhibited best mean performance and renowned SCA for yield traits. The variances due to σ^2 SCA were higher than σ^2 GCA and σ^2 RCA. The ratios of σ^2 GCA/ σ^2 SCA were noted to be less than unity which revealed that all the traits were controlled nonadditively and hence, the delayed selection in later segregating generations might be more effective. Based on the GCA and SCA effects and mean performance, the promising parental genotypes and F1 hybrids could be further utilized in future breeding programs to develop the rapeseed genotypes with good yield potential and oil quality traits.

Key words: Heterotic effects, Diallel analysis, Additive and non-additive gene action, Brassica napus L.

Introduction

Pakistan's economy is mainly dependent on agriculture, however, due to scarcity of edible oil, an enormous amount of foreign exchange is spent on its import (Ahmadi et al., 2002; Gul et al., 2018a). The scarcity of edible oil in the country is attributed mainly to the population growth, increase in the per capita income and consumption, and non-availability of high yielding oilseed cultivars. Expanding urbanization and stagnant local production of oilseeds and meager availability of animal fats have concomitantly signified the problem (Abbas & Ali, 2015). Oilseeds are mainly produced for vegetable oil and increasingly for making bio-diesel, and also their meal for animal feed. They are grown widely across the world in both temperate, sub-tropical and tropical regions (Ahmadi et al., 2002). In Pakistan, rapeseed and mustard were grown on an area of 0.199 million hectares with average seed and oil production of 0.225 and 0.072 million tons, respectively (PBS, 2017-18).

China, India, Canada, Japan and Germany are the leading rapeseed-mustard growing countries. *Brassica napus* L. belongs to family Brassicaceae / Cruciferae which contains about 372 genera and 4060 accepted species (Brassicaceae, 2017). Rapeseed is a natural amphidiploids (AACC genome 2n = 38) between *Brassica campestris* and *Brassica oleracea* (Afrin *et al.*, 2011; Chai *et al.*, 2019). It has high quality seed production and oil characters so found superior over other *Brassica* species. Hence, it is considered to be the best future oilseed crop in the world (Akbar *et al.*, 2008; Gul *et al.*, 2018b).

Edible oil is extracted from conventional and nonconventional oilseed crops. Conventional oilseeds contain cotton, rapeseed, mustard, groundnut and sesame while non-conventional includes sunflower, canola, soybean and safflower (Afrin *et al.*, 2011). Rapeseed (*Brassica napus* L.) is the most important oilseed crop and ranked third position in the world behind soybean and oil palm (Chai *et al.*, 2019), while in Pakistan it ranks second behind cottonseed (Nausheen *et al.*, 2015). Seed yield and other yield related parameters of Brassica crop has been tried to improve by several researchers (Ahmadi *et al.*, 2002; Akbar *et al.*, 2008; Abbas & Ali, 2015; Nausheen *et al.*, 2015).

The aim of the hybrid seed production is to increase the yield and improve the quality of oil in oilseed crops. Heterosis is the interpretation of increased vigor, size, fruitfulness, development speed, resistance to disease and insect pests or climatic vigor, manifested by cross-bred organisms as compared with corresponding inbreds (Shull, 1952). Heterosis has been widely exploited and utilized in rapeseed breeding (Wang *et al.*, 2017; Xie *et al.*, 2018). Reliable and precise prediction techniques of heterosis contributed in accelerating the crossbreeding and reducing the cost of large-scale field evaluation. In past studies, marked heterotic effects were reported in oilseed rape for seed yield ranging from 4.56 to 90.17% more than that of the better parent. However, the yield of the best hybrid amounted to 108.6% of the seed yield of the open-pollinated cultivar (94.4%) of that of the hybrid cultivar (Szała *et al.*, 2019).

For studying the inheritance of quantitative characters and evaluation of various possible breeding procedures in heterosis phenomena, the comprehensive study of combining ability is immensely essential (Vaghela *et al.*, 2011; Kaur *et al.*, 2019). Combining ability defined as the ability of parental genotypes to combine among each other during hybridization with the aim to transmit desirable genes to their offspring, and it classified into general combining ability (GCA) and specific combining ability (SCA) (Sprague & Tatum, 1942). GCA is the average performance of a genotype in a series of hybrid combinations and SCA as those cases in which certain hybrid combinations perform better or poorer than expected, based on average performance of the parental inbred lines.

ability studies Combining emphasized the preponderance effects of GCA on yield and most of the vield components, indicating the importance of additive gene action (Ali et al., 2015; Xie et al., 2018). On the other hand, Akbar et al. (2008) reviewed evidences for the presence of significant SCA effects for yield and yield components, indicating the importance of non-additive gene action. Singh (2005) reported that non-additive genetic effects in addition to additive effects accounted for yield heterosis. Diallel mating design has been extensively used to analyze the combining ability effects of B. napus L. genotypes and to provide information regarding genetic mechanisms controlling the seed yield and other traits. This technique can be exploited for hybrids development and populations can be studied through intensive selection in segregating generations.

In the perception of aforementioned and elucidated condition of rapeseed in Pakistan, the present study was planned to evaluate a) mean performance of parental genotypes and their F_1 hybrids, b) heterosis in F_1 hybrids, and c) to study the general and specific combining ability effects in parental genotypes and their specific F_1 hybrids, respectively.

Materials and Methods

Breeding material comprised of 8 diverse *Brassica* napus genotypes i.e., Rainbow (R.B), Rustam Canola (R.C), Dunkled (D.K), Abasin-95 (A-95), NIFA Gold (N.G), Durr-e-NIFA (D.N), Punjab Sarsoon (P.S) and Faisal Canola (F.C) was collected from Oilseed Division, National Agriculture Research Center (NARC), Islamabad - Pakistan. These eight genotypes were crossed in a 8×8 complete diallel fashion during 2014-2015 at the University of Agriculture, Peshawar - Pakistan. During 2015-2016, the seeds of parental genotypes and their 56 F₁ hybrids were sown in a randomized complete block design (RCBD) with 2 replications. Each plot comprised of four rows with row length of 5 meter while inter-row and intra-row spacing were kept 50 and 30 cm, respectively. Recommended and uniform cultural practices were applied throughout the growing season to all the genotypes to avoid field variations and environmental influences.

Traits measurement and statistical analysis: Data were recorded on 10 randomly selected plants from central two rows on single plant basis for plant height and yield traits i.e., main raceme length, 1000-seed weight and seed yield per plant. All recorded data were subjected to analysis of variance (ANOVA) technique to test the null hypothesis of no differences between parental means and their F₁ populations (Steel et al., 1997). After getting the significant differences among the parental genotypes and their F₁ hybrids for various traits, the data were further subjected to combining ability analysis as outlined by Griffing (1956) Method-I, based on Eisenhart's Model-II to assess the genetic variances due to GCA and SCA and maternal effects. Heterosis (mid- and better-parent, commercial) analysis was carried out according to Matzingar et al., (1962) while its significance was assessed by 't-test' (Wynne et al., 1970).

Results and Discussion

Analysis of variance exhibited significant $(p \le 0.01)$ differences among parental genotypes and their F₁ hybrids for plant height, main raceme length, 1000-seed weight and seed yield per plant (Table 1). Genotypes revealed existence of greater genetic variability which was further used for heterosis and combining ability analyses. Significant differences were reported among parental genotypes and F₁ hybrid combinations of *Brassica napus* L. (Poonam & Singh, 2004; Tuncturk & Ciftci, 2007; Ahmad et al., 2009; Ali & Pant, 2013; Kang et al., 2014) and Brassica juncea L. (Kumari & Kumari, 2018; Raliya, 2018) for earliness and yield related traits. Greater genetic variability and positive correlation among yield related traits were reported in Indian mustard genotypes (Dawar et al., 2018; Kaur et al., 2019). Similarly, significant differences were revealed by different brassicas for plant height, main raceme length, pods per main raceme, pod length, pod width, seeds per pod, 100-seed weight and seed yield per plant (Sohail et al., 2018).

Table 1. Mean squares for various traits in 8 × 8 F₁ diallel cross of *B. napus* L.

Traits		CV (0/)		
	Replications (d.f. = 1)	Genotypes (d.f. = 63)	Error (d.f. = 63)	CV (70)
Plant height	0.661	482.936**	3.135	1.484
Main raceme length	83.205	243.665**	0.656	1.614
1000-seed weight	0.063	0.049**	0.002	1.107
Seed yield per plant	91.333	247.716**	0.721	1.906

** Significant at $p \le 0.01$, d.f. = Degree of freedom

Mean performance and heterotic studies

Plant height: Plant height is an important characteristic of brassica which directly proportional to flowering time as more time passes before flowering, plant becomes more taller through vegetative growth of the primary stem. Mean values for plant height among the parents varied from 84.2 to 108.8 cm with an average value of 95.18 cm (Table 2). Minimum plant height was recorded for parental line Abasin-95 while Rainbow attained maximum plant height. In F₁ hybrids, plant height ranged from 85.4 to 145 cm with mean value of 122.73 cm. Minimum plant stature was recorded for F1 hybrid Rustam Canola × Durr-e-NIFA which was found at par with two parental genotypes i.e., Durr-e-NIFA (85.1 cm) and Abasin-95 (84.2 cm). The F_1 hybrid Faisal Canola \times Rustam Canola attained maximum plant height and found at par with two other F1 hybrids viz., Faisal Canola \times Durr-e-NIFA (143) and Rainbow \times Durr-e-NIFA (142.4). Present results about plant height were in agreement with the past findings as mentioned that highly significant genotypic differences were observed among parental genotypes and F_1 populations of B. juncea for plant height (Tuncturk & Ciftci, 2007; Poonam & Singh, 2004; Chaurasiya et al., 2018).

Heterotic studies regarding plant height revealed that 55 F_1 hybrids showed significant positive effects for mid parent heterosis ranging from 5.12 (Abasin-95 \times NIFA Gold) to 55.10% (NIFA Gold \times Rustam Canola) (Table 2). Heterosis over better parent identified 54 F1 hybrids having significant positive effects and the values ranged from 3.71 (Rustam Canola \times NIFA Gold) to 49.78% (NIFA Gold \times Rustam Canola). Commercial heterosis showed three F₁ hybrids with significant positive values i.e., Rainbow \times NIFA Gold (1.71%), Faisal Canola \times Rustam Canola (2.14%) and Punjab Sarsoon × Abasin-95 (3.57%). Plant height is a vital agronomic trait for crops, including oilseed crops such as rapeseed (Brassica napus L.). It affects the crop yield, oil content, and lodging resistance in rapeseed (Chai et al., 2019). Medium to tall plant height is considered desirable in rapeseed therefore, F₁ hybrids having medium effects shall be an asset for future breeding programs. Past studied reported significant positive mid- and better-parent heterosis for plant height in F1 populations of Brassica napus genotypes (Abbas et al., 2008). Similarly, Meena et al., (2014) and Synrem et (2015) also reported significant positive al., commercial heterotic effects in F1 populations of Indian mustard for plant height.

Main raceme length: Main raceme length is responsible for greater seed yield because genotypes with longer main racemes produce more flowers, fruits and seeds, and thus results in greater seed yield. The mean values for main raceme length among parental genotypes ranged from 52 cm (Rustam Canola) to 66.3 cm (Punjab Sarsoon) with a mean value of 58.5 cm (Table 3). Data for F_1 populations varied from 22.3 cm (Durr-e-NIFA × Punjab Sarsoon) to 74.3 cm (Rustam Canola × Rainbow) with a mean value of 48.98 cm. The F_1 hybrid Rustam Canola × Rainbow exhibited maximum main raceme length (74.3 cm), and it was found at par with a parental genotype Punjab Sarsoon (66.3 cm) and a hybrid Dunkled × Rainbow (66.1 cm). However, minimum main raceme length was observed in F_1 hybrid Durr-e-NIFA × Punjab Sarsoon and was also found same in performance with two other F_1 hybrids i.e., Durr-e-NIFA × Rainbow (33.1 cm) and Dunkled × Punjab Sarsoon (34.1 cm). Significant variations were reported among parental genotypes and their F_1 hybrids of rapeseed for main raceme length (Ahmad *et al.*, 2009; Ali & Pant, 2013).

Heterotic effects for main raceme length identified 21 F₁ hybrids with significant positive effects for mid parent varied from 11.24 to 61.67% (Table 3). Concerning better parent heterosis, 13 F₁ hybrids revealed significant positive values ranging from 10.61 to 49.80%. In both mid and better parent heterosis, maximum values were observed in F1 hybrid Rustam Canola \times Punjab Sarsoon. The commercial heterotic estimates for main raceme length revealed that 35 F₁ hybrids with significant positive effects where data ranged from 6.00 to 91.60%. Maximum commercial heterosis was recorded in F_1 hybrid Punjab Sarsoon \times Abasin-95. In rapeseed, primary and secondary branches appear on main racemes therefore, longer main racemes are considered valuable for seed yield. Current results found several F1 hybrids showing positive heterosis for main raceme length. Sabaghnia et al., (2010) also reported significant positive mid and better parent heterosis in B. napus F1 populations for main raceme length, while Meena et al., (2014) reported commercial heterotic effects in different F₁ hybrids for said trait in Indian mustard.

1000-seed weight: Thousand seed weight manage the seed yield because genotypes with heavier seeds can result in greater seed yield. Among parental genotypes, the mean values for 1000-seed weight ranged from 4.51 to 4.78 g with a mean value of 4.60 g (Table 4). Overall, the parental genotype Abasin-95 exhibited maximum value for 1000-seed weight (4.78 g) while minimum and same value (4.51 g) for said trait revealed by two genotypes i.e., Dunkled and Durr-e-NIFA. Means for F₁ hybrids varied from 4.00 (Rustam Canola × Faisal Canola) to 4.73 g (Faisal Canola × Rustam Canola) with mean value of 4.47 g. The later promising hybrid was followed by F_1 hybrids Abasin-95 × Durr-e-NIFA and Dunkled × Abasin-95 with same value for 1000-grain weight (4.70 g). Minimum 1000-grain weight exhibited by F_1 hybrid Rustam Canola × Faisal Canola (4.00 g) followed by Rainbow \times Rustam Canola (4.09 g). Past studies revealed that highly significant genotypic differences were observed among rapeseed lines and their F₁ populations for 1000-seed weight and other yield related (Ahmad et al., 2009; Kang et al., 2014).

Plant height (cm)						
Parental genotypes	Means	Parental genotypes	Means	Parental genotypes	Means	
Rustam Canola (R.C)	93.5	Durr-e-NIFA (D.N)	85.1	Rainbow (R.B)	108.8	
Abssin-95 (A-95)	84.2	Punjab Sarsoon (P.S)	90.4	Dunkled (D.K)	97.8	
NIFA Gold (N.G)	99.6	Faisal Canola (F.C)	102.1	Parent means (cm)	95.18	
F1 Hybrids		Means (cm)	MP	BP	СН	
$RC \times A-95$		97.2	9 40**	3.96*	-30 57**	
$R C \times N G$		103.3	6 99**	3 71*	-26 21**	
$RC \times DN$		85.4	-4 37	-8 66**	-39 00**	
$RC \times PS$		97.9	6 47**	4 71**	-30.07**	
$R C \times FC$		109.3	11 76**	7.05**	-21 93**	
$\mathbf{R} \mathbf{C} \times \mathbf{R} \mathbf{B}$		113 7	12 41**	4 50**	-18 79**	
$R C \times D K$		103.2	7 89**	5 52**	-26 29**	
$A-95 \times B C$		93.4	35 83**	33 58**	-10 79**	
$A-95 \times NG$		113.7	5 12**	-0.11	-33 29**	
$A-95 \times D N$		117.1	23 72**	14 16**	-18 79**	
$\Delta_{-95} \times PS$		118.2	38 33**	37 60**	-16 36**	
$A-95 \times FC$		126.3	35 /0**	30.75**	-15 57**	
$A = 75 \times 1.0$ A = 95 × P B		120.5	35 50**	23 70**	0 70**	
$A = 55 \times R.D$ A = 95 × D K		117.2	35 73**	10 0/**	6 70**	
$\mathbf{N}\mathbf{G} \times \mathbf{P}\mathbf{C}$		126.0	55 10**	10.74	3 70**	
$N.G \times A.95$		120.0	24 95**	10 18**	-5.29	
$N.G \times D.N$		137.8	24.95 28 70**	10.10	16 20**	
$N.G \times PS$		113.6	30 50**	26 51**	-10.00**	
$N.G \times FC$		117.8	16 1/1**	3/ 8/**	-/ 07**	
$N.G \times R.B$		117.0	40.14	38 35**	-1.57**	
$N.G \times D.K$		108.1	10 58**	14 06**	-1.57	
$N.0 \times D.K$		124.6	50 20**	15.00	5 86**	
$D.N \times A.95$		124.0	29 56**	-5.00 22 1/**	-10.00	
$D N \times N G$		114.2	40.46**	22.14	-0.07	
$D N \times PS$		121.6	16 81**	15 38**	-15 86**	
$D.N \times FC$		121.0	10.01	6.07**	-17 57**	
$D N \times R B$		126.6	9 52**	8 53**	-77 79**	
$D N \times D K$		114 5	30 53**	33 26**	-11 00**	
$PS \times RC$		124.9	33 58**	28 53**	-10.21**	
$PS \times A-95$		135.4	48 26**	42 02**	3 57**	
$PS \times NG$		118 7	51.05**	37 81**	0.50	
$PS \times DN$		131.8	23 85**	22 33**	-10 79**	
$PS \times FC$		124 7	47 08**	46 30**	-11.07**	
$PS \times RB$		139.9	23 66**	14 66**	-18 43**	
$PS \times D.K$		125.7	38.58**	34.51**	-13.14**	
$EC \times R.C$		145.0	52.78**	40.06**	2.14**	
$F.C \times A-95$		140.7	38.70**	30.75**	-4.64**	
$F.C \times N.G$		124.9	11.62**	8.18**	-15.93**	
$F.C \times D.N$		143.0	24.86**	22.23**	-10.86**	
$F.C \times P.S$		133.5	33.86**	24.45**	-3.29**	
$F.C \times R.B$		117.7	39.64**	28.01**	-6.64**	
$F.C \times D.K$		124.8	30.58**	16.36**	-9.57**	
$R.B \times R.C$		135.4	19.59**	6.07**	-17.57**	
$R.B \times A-95$		115.4	22.07**	16.91**	-9.14**	
$R.B \times N.G$		127.2	46.88**	30.88**	1.71**	
$R.B \times D.N$		142.4	40.26**	28.40**	-0.21	
$R.B \times P.S$		139.7	26.88**	22.98**	-4.43**	
$R.B \times F.C$		133.8	30.20**	23.62**	-3.93**	
R.B imes D.K		134.5	25.21**	17.08**	-18.21**	
$D.K \times R.C$		135.6	41.77**	38.65**	-3.14**	
$D.K \times A-95$		133.4	46.59**	36.40**	-4.71**	
$D.K \times N.G$		129.3	31.00**	29.82**	-7.64**	
$D.K \times D.N$		120.5	31.77**	23.21**	-13.93**	
$D.K \times P.S$		128.4	36.45**	31.29**	-8.29**	
$D.K \times F.C$		110.4	10.46**	8.13**	-21.14**	
$D.K \times R.B$		120.1	16.26**	10.39**	-14.21**	
F ₁ population means (cm	n)	122.73	$LSD_{0.05} = 3.53$			

 Table 2. Means, mid (MP), better parent (BP) and commercial heterosis (CH) in parental genotypes and their

 F1diallel populations of B. napus L. for plant height.

Main raceme length (cm)						
Parental genotypes	Means Parental genoty	pes Means	Parental genotypes	Means		
Rustam Canola (R.C)	52.0 Durr-e-NIFA (D.)	N) 61.7	Rainbow (R.B)	61.0		
Abssin-95 (A-95)	64.1 Puniab Sarsoon (P.S) 66.3	Dunkled (D.K)	58.0		
NIFA Gold (N.G)	41.3 Faisal Canola (F)	C) 63.6	Parent means (cm)	58.5		
F ₁ Hybrids	Means (cm)	MP	BP	СН		
$R C \times A-95$	47.8	-15 47**	-25 43**	2.80		
$R C \times N G$	61.9	37 10**	25.15	19 20**		
$R C \times D N$	39.2	_22.01**	_25.55	27 60**		
$R C \times PS$	12 1	61 67**	/9 80**	27.00 76.40**		
$R.C \times F.C$	56.0	22 80**	16 12**	9 60**		
$\mathbf{R} \cdot \mathbf{C} \times \mathbf{R} \cdot \mathbf{R}$	74.3	35.00**	21.80**	37 20**		
$\mathbf{R} \cdot \mathbf{C} \times \mathbf{D} \cdot \mathbf{K}$	56.1	1.86	3 28	61 60**		
$A 05 \times P C$	13 7	10 35	-5.20	78 00**		
$A - 95 \times N.C$	43.7 60.9	-10.33	-10.94 31.83**	/0.00		
$A - 75 \times N.O$	50.1	15 56**	-51.65	1.60		
$A - 75 \times D.$	36.0	14.21**	-4.22	-1.00		
$A - 75 \times FC$	62.2	-14.21	-21.04	-20.00**		
$A -93 \times \Gamma.C$	03.5	-22.37**	-30.04	42.00**		
$A - 7J \times R.D$	62 1	17.55	-1.25	10 00**		
$A-93 \times D.K$	03.1 54.2	-2.52	-4.00 10.91**	-18.80***		
$N.G \times K.C$	54.2 46 1	-2.95	-19.01	46.00**		
$N.G \times A-95$	40.1	0.50	J.74 1 56	40.00**		
$N.G \times D.N$	45.8	3.30 20.04**	-1.30 10 61**	43.20***		
$N.G \times P.S$	40.7	20.04***	20.01***	52.40*** 12.40**		
$N.G \times P.P$	40.0	-12.32**	-20.00***	-15.00**		
$N.G \times R.B$	4/.1	-1.49	-12.14**	39.20*** 25.20**		
$N.G \times D.K$	55.2 57.9	24.45***	20.17**	-35.20**		
$D.N \times R.C$	57.8	-22.12**	-30.17**	88.00**		
$D.N \times A-95$	59.0 54.5	10.10*	13.70**	29.20**		
$D.N \times N.G$	54.5	-9.14	-23.44***	14.80**		
$D.N \times P.5$	22.3	30.03***	33.U3*** 22.70**	-2.40		
$D.N \times F.C$	33.9 22.1	-7.92	-22.19***	9.20**		
$D.N \times K.B$	51.2	23.20***	5.52	-2.80		
$D.N \times D.K$	51.2 40.7	22 46**	9.00	-4.00		
$P.S \times K.C$	40.7	52.40*** 42.20**	13.9/**	72.00**		
$P.S \times A-93$	42.4	45.20***	20.51***	91.00*** 21.60**		
$P.S \times N.G$	44.2	-14.93**	-28.33***	-51.00**		
$F.S \times D.N$	50.8 27.1	20.01	7.02	-55.00**		
$\Gamma.S \times \Gamma.C$	57.1	2.03	-7.02	0.00*		
$P.S \times R.D$	40.7	-33.32**	-00.13**	-29.20**		
$F.S \times D.K$	61.2	-47.31**	-32.94	45.20**		
$F.C \times K.C$	01.5	12.30°	2.83 10 5 0**	-10.80**		
$F.C \times A-93$	45.0	10.60**	19.30	-3.20*		
F.C × N.G EC× D N	30.2	17.09**	2.02	2.00		
$F.C \times D.N$	58.2 47 1	-17.52**	-27.70**	-2.00		
$\Gamma.C \times \Gamma.S$	47.1	-10.91	-23.00**	2.00		
$F.C \times K.B$	02.0	-23.44	-51.00**	2.00		
$\Gamma.C \times D.K$	54.9 45 7	-19./9	-23.23	-3.20**		
\mathbf{K} . $\mathbf{D} \times \mathbf{K}$. \mathbf{C}	43.7	-0.08	-2.30	4.40		
\mathbf{R} . $\mathbf{D} \times \mathbf{A}$ -95 $\mathbf{D} \mathbf{D} \times \mathbf{N} \mathbf{C}$	02.5 56 0	6 77	-0.72	-43.20**		
\mathbf{K} . $\mathbf{D} \times \mathbf{N}$. \mathbf{U}	50.9	0.77	-0.49	-12.00***		
$\mathbf{R} \cdot \mathbf{D} \times \mathbf{D} \cdot \mathbf{N}$	54.4	12 42*	-10.82*	0.20**		
$\mathbf{R} \cdot \mathbf{D} \times \mathbf{F} \cdot \mathbf{C}$	54.4 45 9	-12.45	-24.72	9.20		
$\mathbf{R} = \mathbf{D} \mathbf{K}$	4J.0 20 9	-24./1	-20.30**	0.00 15 20**		
\mathbf{X} . $\mathbf{D} \times \mathbf{D}$. \mathbf{X}	37.0 64 2	1.J4 20 10**	-3.10	4J.20*** 26 40**		
D.K \times K.C D K \times A 05	04.5	20.19*** 11 55**	10.00**	∠0.40*** 28 40**		
$D.\mathbf{K} \times \mathbf{A} - \mathbf{y}\mathbf{J}$	40.U 24.0	-11.33*** 1/ 60**	-13.70***	20.40*** 22 00**		
$\mathbf{D}.\mathbf{K} \times \mathbf{N}.\mathbf{U}$	54.9 24.9	14.00 ^{***} 22 5 9**	-1.90 27.07**	22.00***		
$\mathbf{D}.\mathbf{K} \times \mathbf{D}.\mathbf{N}$	54.8 24.1	-23.38** 12 42*	-2/.0/**	24.00*** 20 00**		
$D.K \times F.S$	54.1 47.2	13.45*	-2.41 19 45**	38.8U** 26 90**		
$\mathbf{D}.\mathbf{K} \times \mathbf{\Gamma}.\mathbf{C}$	4/.3	-0.89	-18.45**	30.80** 64.40**		
	00.1	0.00	3.93	04.40***		
r_1 population means (cm)	48.98	$LSD_{0.05} = 1.01$				

 Table 3. Means, mid (MP), better parent (BP) and commercial heterosis (CH) in parental genotypes and their

 F1diallel populations of *B. napus* L. for main raceme length.

1000-seed weight (g)						
Parental genotypes	Means	Parental genoty	pes Means	Parental genotypes	Means	
Rustam Canola (R.C)	4.55	Durr-e-NIFA (D.1	N) 4.51	Rainbow (R.B)	4.63	
Abssin-95 (A-95)	4.78	Puniab Sarsoon (P.S) 4.69	Dunkled (D.K)	4.51	
NIFA Gold (N G)	4 59	Faisal Canola (F)	C) 4 61	Parent means (g)	5 60	
F1 Hybrids		Means (g)	MP	BP	СН	
$\mathbf{P} \mathbf{C} \times \mathbf{A}$ 05		4.60	16 21**	2.12	0.52 **	
$R.C \times A-93$		4.00	10.31**	-2.15	9.52 ***	
$\mathbf{K}.\mathbf{C} \times \mathbf{N}.\mathbf{G}$		4.00	21.21***	5.02	9.52**	
$R.C \times D.N$		4.39	32.03**	27.62**	4.52*	
$R.C \times P.S$		4.62	31.66**	25.35**	10.00**	
$R.C \times F.C$		4.00	22.27**	5.94	-4.76*	
$R.C \times R.B$		4.55	20.53**	4.84	8.33**	
$R.C \times D.K$		4.58	36.31**	30.48**	9.05**	
$A-95 \times R.C$		4.61	33.73**	27.32**	7.62**	
$A-95 \times N.G$		4.51	16.56**	-1.91	9.76**	
$A-95 \times D.N$		4.70	-0.66	-4.04	7.38**	
$A-95 \times P.S$		4.52	15.48**	0.00	11.90**	
$A-95 \times FC$		4 32	9 58*	-3.83	7 62**	
$A-95 \times RB$		4 4 5	0.66	-2 77	2.86	
$\Lambda 95 \times DK$		1.13	1.55	5 32	5.05**	
$A-95 \times D.K$		4.42	-1.55	-5.52	1 20	
$N.O \times R.C$		4.54	0.10	-0.81	4.29	
$N.G \times A-93$		4.40	8.93*	-1.57	2.80	
$N.G \times D.N$		4.66	/.0/	-5.96	5.24*	
$N.G \times P.S$		4.57	14.36**	-0.91	3.33	
$N.G \times F.C$		4.56	-1.76	-5.11	6.19*	
$N.G \times R.B$		4.67	19.18**	6.39*	10.95**	
$N.G \times D.K$		4.60	15.26**	4.34	8.81*	
$D.N \times R.C$		4.53	26.18**	24.23	5.00**	
$D.N \times A-95$		4.59	8.95*	-1.37	2.86	
$D.N \times N.G$		4.55	15.84**	5.30	-0.24	
$D.N \times P.S$		4.49	4.11	4.11	8.57*	
$DN \times FC$		4 55	7 11	6.62*	11 19**	
$DN \times RB$		4 46	16 60**	5.02	9 52**	
$D N \times D K$		4.51	36 24**	31 69**	7.86**	
$D.N \wedge D.K$		4.51	22 00**	22 24**	7.00 9.22**	
$P.S \times R.C$		4.32	33.99 ⁴⁴	0.12*	0.00***	
$P.5 \times A-95$		4.58	25.90***	9.13*	12.02*	
$P.S \times N.G$		4.32	-0.22	-3.62	/.86**	
$P.S \times D.N$		4.41	-4.11	-4.11	0.00	
$P.S \times F.C$		4.32	12.78**	-2.34	9.29**	
$P.S \times R.B$		4.19	5.88	-5.48	8.33**	
$P.S \times D.K$		4.55	28.47**	26.48**	6.90**	
$F.C \times R.C$		4.73	13.81**	1.60	5.95**	
$F.C \times A-95$		4.53	11.48*	0.91	5.24**	
$F.C \times N.G$		4.20	2.52	2.05	6.43**	
$F.C \times D.N$		4.45	16.86**	5.25	-1.43	
$F.C \times P.S$		4.42	8.34	-5.76	-2.62**	
$FC \times RB$		4 47	16 37**	3 88	8 33**	
$FC \times DK$		4 14	14 65**	2.76	6 19*	
$\mathbf{R} \mathbf{B} \times \mathbf{R} \mathbf{C}$		4.09	-3.54	_7 23**	3.81	
$R.D \land R.C$ $P P \lor A 05$		4.36	-3.34	4 70	0.62	
$R.D \land A-9J$		4.30	-4.30	-4.79	-0.02	
\mathbf{K} . \mathbf{D} × \mathbf{N} . \mathbf{U}		4.17	10.43***	4.38	/.00**	
$\mathbf{K}.\mathbf{B} \times \mathbf{D}.\mathbf{N}$		4.55	1/.11***	0.45*	10.00**	
$R.B \times P.S$		4.62	6.65	6.16*	10./1**	
$\mathbf{R}.\mathbf{B} \times \mathbf{F.C}$		4.65	12.36**	1.61	5.00*	
$R.B \times D.K$		4.41	29.78**	28.49**	7.38**	
$D.K \times R.C$		4.61	37.20**	31.34**	9.76**	
$D.K \times A-95$		4.70	14.49**	0.00	11.90*	
$D.K \times N.G$		4.34	10.01*	-0.91	3.33	
$D.K \times D.N$		4.49	29.21**	27.92**	6.90**	
DK×PS		4 44	25 78**	25 07**	5 71*	
$DK \times FC$		 1 12	12 0/**	0.01	5 7/*	
		4.42	14.04	2 40	J.24 7 1/**	
		4.50	14.03**	3.09	/.14**	
F ₁ population means (g)		4.47	$LSD_{0.05} = 0.09$			

Table 4. Means, mid (MP), better parent (BP) and commercial heterosis (CH) in parental genotypes and theirF1 diallel populations of B. napus L. for 1000-seed weight.

Heterosis estimations over mid-parent revealed that 40 F1 hybrids had significant positive effects for 1000-seed weight ranging from 9.58 to 37.20% (Table 4). However, maximum significant heterosis over mid parent was noticed for F_1 hybrid Dunkled × Rustam Canola (37.20%). Regarding best parent heterosis, 16 F1 hybrids exhibited significant positive heterotic values ranging from 6.16 to 33.24% whereas maximum value was noticed for F1 hybrid Punjab Sarsoon × Rustam Canola (33.24%). In case of commercial heterosis, 43 F₁ hybrids were identified with significant positive effects ranging from 4.52 to 12.62 whereas maximum value was noted for F1 hybrid Punjab Sarsoon × Abasin-95 (12.62%) for 1000-seed weight. Heavier seeds are given due consideration in rapeseed breeding because they contain greater amount of oil therefore, positive heterotic effects are desirable for 1000seed weight. Current studies identified several F1 hybrids with positive heterotic effects for 1000-seed weight which were in conformity with the earlier findings of Rameah et al., (2003), Singh (2005), Gul et al., (2018b) and Szała et al., (2019) who reported significant positive mid and better parent heterosis for 1000-seed weight in Brassica napus L. and B. juncea L, respectively. Meena et al., (2014) also reported significant positive commercial heterosisin Indian mustard for 1000-seed weight.

Seed yield per plant: Majority of the rapeseed breeding programs aims to increase the seed yield, whereas seed yield is dependent on different yield contributing traits. Seed yield per plant ranged from 31.91 g (Punjab Sarsoon) to 48.16 g (Abasin-95) for parental genotypes (Table 5). Mean values among F1 hybrids for seed yield per plant varied from 25.30 g (Durr-e-NIFA \times NIFA Gold) to 82.76 g (Faisal Canola \times Rustam Canola). Overall, the F_1 hybrid Faisal Canola × Rustam Canola (82.76) was found as best cross combination followed by two other F1 hybrids viz., Punjab Sarsoon \times Dunkled (66.86 g) and Dunkled \times Rainbow (64.97 g). However, poorest performance was shown by F_1 hybrid Durr-e-NIFA × NIFA Gold (25.30 g) followed by Dunkled \times NIFA gold (25.51 g). In previous studies, highly significant differences with larger genetic variability were reported among F1 populations and their parental genotypes of rapeseed for seed yield and yield attributing traits (Kang et al., 2014; Nasim et al., 2014; Synrem et al., 2015; Chaurasiya et al., 2018).

Heterosis estimates over mid-parent for seed yield per plant revealed that 43 F1 hybrids were noted with significant positive heterotic effects ranging from 5.47 to 133.59% (Table 5). Maximum significant heterosis over mid parent was recorded in F_1 hybrid Punjab Sarsoon \times Abasin-95 (133.59%). Regarding best parent heterosis, 37 F1 hybrids exhibited significant positive effects ranging from 8.01 to 132.54% whereas F1 hybrid Punjab Sarsoon × Abasin-95 (132.54%) revealed maximum positive effects. Commercial heterosis revealed that 32 out of 56 F1 hybrids were with significant and positive heterotic values ranging from 2.23 to 97.05%. However, maximum commercial heterosis was noted for F1 hybrid Punjab Sarsoon × Abasin-95 (97.05%). Enhanced seed yield is an ultimate goal of the majority of the rapeseed breeding programs therefore, positive heterosis is desirable for improving the seed yield in rapeseed genotypes. Present

results identified several F_1 hybrids with positive heterotic effects over mid, better and commercial variety and these promising population could be utilized in future breeding program to develop high yielding rapeseed genotypes. Significant positive heterosis was reported in F_1 populations as compared to their parental genotypes of rapeseed for seed yield (Khan *et al.*, 2006; Liton *et al.*, 2017). Similarly, Akabari and Sasidharan (2016) and Kaur *et al.*, (2019) also reported significant mid and betterparent heterosis in F_1 populations of Indian mustards for seed yield and other yield components. Positive commercial heterotic effects were observed among F_1 hybrids of Indian mustard and rapeseed for yield related traits and seed yield (Lalji and Zehr, 1999; Synrem *et al.*, 2015; Szała *et al.*, 2019).

Combining ability analysis: Analysis of variance for combining ability revealed that GCA, SCA and RCA mean squares were found significant ($p \le 0.01$) for plant height, main raceme length, 1000-seed weight and seed yield per plant in the tested F_1 populations and their parental genotypes indicating the important role of both additive and non-additive gene effects (Table 6). However, contribution of GCA mean squares were leading and greater in magnitude than SCA and RCA for plant height and main raceme length. For 1000-seed weight and seed yield per plant, the contribution of RCA mean squares were found greater than SCA and GCA. Results further enunciated the preponderance of GCA and RCA effects which revealed that additive and maternal effects were more important in expression of these traits. Significant mean squares due to GCA SCA and RCA were observed among F₁ populations and their parental genotypes for yield related traits in B. napus (De et al., 2009; Aghao et al., 2010; Vaghela et al., 2011; Ali et al., 2014; Shrimali et al., 2016). In previous studies, mean squares due to GCA and SCA were significant for plant height and yield related traits in parental genotypes and F₁ populations of rapeseed (Singh et al., 2005; Singh & Singh, 2008; Gul et al., 2018a). The components of variance and effects due to GCA, SCA and RCA for plant height, main raceme length, 1000-seed weight and seed yield per plant are discussed herein.

Variances due to GCA, SCA, and RCA: Variances due to σ^2 SCA (291.77) were found higher than σ^2 GCA (19.85) and σ^2 RCA (85.19). The ratio of σ^2 GCA/ σ^2 SCA (0.07) was also less than unity which depicted the importance of nonadditive gene action for plant height in current set of genotypes (Table 7). Non-additive type of gene action was involved for controlling plant height in various populations of Brassica species (Akbar et al., 2008; Ali et al., 2015). For main raceme length, preponderance of non-additive gene action was confirmed by relative magnitude of variances due to σ^2 GCA (12.27), σ^2 SCA (111.74) and σ^2 RCA (56.46) and less than unity ratio of σ^2 GCA/ σ^2 SCA (0.11). Present results also got support from the past findings of Sabaghnia et al., (2010) and Mohammed (2011) who also reported non-additive gene action for main raceme length. However, Shrimali et al., (2016) mentioned an important role of additive gene action in the inheritance of main raceme length in Indian mustard.

Seed yield per plant (g)					
Parental genotypes	Means Parental genoty	oes Means	Parental genotypes	Means	
Rustam Canola (R.C)	35.27 Durr-e-NIFA (D.N	N) 34.27	Rainbow (R.B)	32.82	
Abssin-95 (A-95)	48.16 Punjab Sarsoon (I	P(S) 31.91	Dunkled (D.K)	32.03	
NIFA Gold (N.G)	36.51 Faisal Canola (F.	C) 35.59	Parent means (g)	35.82	
F1 Hybrids	Means (g)	MP	BP	СН	
$R.C \times A-95$	29.83	-28.49**	-38.06**	-28.98**	
$R C \times N G$	38 30	671**	4 90	-8 81**	
$RC \times DN$	34.11	-1.90	-3 29	-18 79**	
$RC \times PS$	61 31	82 52**	73 83**	45 98**	
$R C \times FC$	33.20	-6 29**	-6 72**	-20.95**	
$\mathbf{R} \cdot \mathbf{C} \times \mathbf{R} \cdot \mathbf{B}$	11 18	30.65**	26.11**	5 91**	
$\mathbf{R} \cdot \mathbf{C} \times \mathbf{D} \cdot \mathbf{K}$	52.06	54 71**	47 60**	23 06**	
$A 05 \times P C$	40.59	70 52**	70.07**	23.90 13 56**	
$A - 95 \times N.C$	52.02	2 70	15 72**	3 35**	
$A - 95 \times N.O$	37.60	-2.70	-13.72 8 01**	-3.35	
$A - 5J \times D.$	48.05	22.00**	21.02**	10.48**	
$A - 75 \times FC$	48.03	-0.77**	-21.95	-10.40**	
$A-93 \times \Gamma.C$	45.07	20.02***	-0.23	14.42*** 7.20**	
$A-93 \times K.D$	54.25	1.03***	-0.42***	19 51**	
$A-93 \times D.K$	10.26	-13.40**	-20.92**	-10.31	
$N.G \times R.C$	40.30	44.50***	20.12**	5/./5**	
$N.G \times A-95$	58.25	44./5***	33.03**	17.89**	
N.G × D.N	50.43	29.59**	/.89**	23.71**	
N.G × P.S	47.26	12.45**	10.55**	-3.90**	
$N.G \times F.C$	44.96	37.55**	20.91**	38.64**	
$N.G \times R.B$	41.63	42.50**	38.13**	20.07**	
$N.G \times D.K$	54.73	38.15**	29.44**	12.51**	
$D.N \times R.C$	61.69	70.63**	64./5**	34.42**	
$D.N \times A-95$	55.60	2.22	-3.06	-17.86**	
$D.N \times N.G$	25.30	5.61*	4.14	-18.61**	
$D.N \times P.S$	39.48	24.72**	23.14**	7.06**	
$D.N \times F.C$	42.94	20.09**	14.02**	-0.88	
$D.N \times R.B$	46.52	59.70**	49.90**	30.31**	
$D.N \times D.K$	50.70	77.42**	74.91**	46.89**	
$P.S \times R.C$	60.30	109.13**	108.74**	59.19**	
$P.S \times A-95$	57.85	133.59**	132.54**	97.05**	
$P.S \times N.G$	49.52	-8.63**	-20.56**	-8.90**	
$P.S \times D.N$	56.46	9.85**	8.46**	-5.71**	
$P.S \times F.C$	34.50	34.90**	15.45**	32.37**	
$P.S \times R.B$	34.18	-28.51**	-30.70**	-39.77**	
$P.S \times D.K$	66.86	19.31**	15.20**	-5.99**	
$F.C \times R.C$	82.76	52.59**	49.76**	26.89**	
$F.C \times A-95$	38.26	81.69**	72.30**	45.99**	
$F.C \times N.G$	39.60	49.33**	43.52**	21.61**	
$F.C \times D.N$	53.30	-7.36**	-12.00**	-25.43**	
$F.C \times P.S$	61.32	-7.27**	-10.49**	-24.84**	
$F.C \times R.B$	51.08	22.93**	20.65**	2.23*	
$F.C \times D.K$	31.32	38.68**	35.75**	10.75**	
$R.B \times R.C$	31.57	17.02**	-1.62	12.80**	
$R.B \times A-95$	47.38	5.47*	0.14	-12.96**	
$R.B \times N.G$	36.56	32.84**	30.03**	6.09**	
$R.B \times D.N$	44.56	25.23**	23.49**	-3.49**	
$R.B \times P.S$	40.53	35.83**	30.54**	10.63**	
$R.B \times F.C$	46.46	56.58**	54.69**	20.89**	
R.B imes D.K	50.77	52.94**	47.94**	20.71**	
$D.K \times R.C$	45.09	34.00**	27.84**	7.37**	
$D.K \times A-95$	35.73	-10.89**	-25.81**	-14.94**	
$D.K \times N.G$	25.51	-25.56**	-30.13**	-39.25**	
$D.K \times D.N$	38.53	16.23**	12.43**	-8.26**	
$D.K \times P.S$	36.68	14.73**	14.52**	-12.67**	
$D.K \times F.C$	41.81	23.66**	17.48**	-0.46	
$D.K \times R.B$	64.97	100.37**	97.96**	54.69**	
F_1 population means (g)	45.82		$LSD_{0.05} = 1.70$		

 Table 5. Means, mid (MP), better parent (BP) and commercial heterosis (CH) in parental genotypes and their

 F1 diallel populations of *B. napus* L. for seed yield per plant.

	Mean squares					
Traits	GCA	SCA	RCA	Error		
	(d.f. = 7)	(d.f. = 28)	(d.f. = 28)	(d.f. = 126)		
Plant height	318.34**	292.56**	171.16**	0.78		
Main raceme length	196.54**	111.90**	113.08**	0.16		
1000-seed weight	0.02**	0.02**	0.03**	0.07		
Seed yield per plant	43.34**	114.44**	153.40**	0.18		

Table 6. Analysis of variance of combining ability for various traits in B. napus L.

d.f. = degree of freedom

Table 7. Variances due to general (σ^2 GCA), specific (σ^2 SCA), reciprocal combining ability (σ^2 RCA) and ratio of
σ^2 GCA/ σ^2 SCA for various traits in <i>B. napus</i> L.

Traits	σ ² GCA	Σ ² SCA	σ²RCA	σ ² GCA / σ ² SCA		
Plant height	19.85	291.77	85.19	0.07		
Main raceme length	12.27	111.74	56.46	0.11		
1000-seed weight	0.001	0.02	0.02	0.06		
Seed yield per plant	2.69	114.26	76.61	0.02		

Table 8. General combining ability effects of parental genotypes for various traits in B. napus L.

Parental genotypes	Plant height	Main raceme length	1000-seed weight	Seed yield plant ⁻¹
Rustam Canola	93.50*	2.97*	0.00	0.81*
Abasin-95	84.20*	3.49*	0.06*	0.97*
NIFA Gold	99.60*	-1.97*	0.00	-2.23*
Durr-e-NIFA	85.10*	-3.83*	0.03*	-0.46*
Punjab Sarsoon	90.40*	-4.74*	0.00	2.81*
Faisal Canola	102.10*	-1.07*	-0.05*	0.29*
Rainbow	108.80*	4.75*	-0.04	-2.04*
Dunkled	97.80*	0.40*	-0.01*	-0.15
S.E (gi)+	0.21	0.09	0.01	0.09
CD _{0.05} (gi)	0.41	0.18	0.01	0.19

Significant at CD_{0.05} (gi)

For 1000-seed weight, prevalence of non-additive gene action could be evident from the relative values of variances i.e., 0.001, 0.02, 0.02 due to σ^2 GCA, σ^2 SCA, and $\sigma^2 RCA$, respectively and ratio of $\sigma^2 GCA/\sigma^2 SCA$ (0.06). Non-additive type of gene action was reported in F1 populations and their parental genotypes of rapeseed for 1000-grain weight and other yield related traits (Rameah et al., 2003; Parmar et al., 2011). Higher variances of σ^2 SCA (114.26) than σ^2 GCA (2.69) and σ^2 RCA (76.61) and ratio of σ^2 GCA/ σ^2 SCA (0.02) which was also less than unity, depicted that inheritance in seed yield was managed by non-additive type of gene action (Table 7). In earlier studies, the prevalence of nonadditive gene action was also reported for seed yield in B. juncea L. populations (Singh et al., 2005; Singh & Singh, 2008; Kaur et al., 2019). Contradiction in the present and past findings might be due to varied genetic makeup of brassica genotypes, environments and genotype by environment interaction effects. The variance due to GCA, SCA and RCA revealed that all the traits were controlled non-additively and hence, selection in later segregating generations will be might more effective.

Effects due GCA, SCA and RCA in parents and F1 hybrids: In *Brassica napus*, the moderate plant height is

preferred to avoid lodging and efficient nutrients uptake, therefore, minimum combining ability effects are desirable for plant height. For plant height, the minimum GCA effects were recorded in parental genotype Durr-e-NIFA (85.10) followed by Abasin-95 (84.20) and were considered as best general combiners. However, maximum GCA effects were recorded for genotypes Rainbow (108.80) and Faisal Canola (102.10) (Table 8). Among the direct F_1 hybrids, lowest SCA effect was observed for the F_1 hybrids Rustam Canola \times Abasin-95 (97.20) and Rustam Canola × Durr-e-NIFA (85.40) hence, these F₁ hybrids could be considered as the best specific combiners for average plant height (Table 9). These two promising F_1 hybrids which involve low \times low GCA parental genotypes, produced F₁ populations with reduced plant height. The highest SCA effects were expressed by F_1 hybrid Punjab Sarsoon × Rainbow (139.90) followed by NIFA Gold \times Durr-e-NIFA (137.80). In reciprocal effects, lowest RCA effects were observed for F1 hybrid Abasin-95 \times Rustam Canola (93.40) followed by Dunkled × Faisal Canola (110.40) (Table 10). Earlier studies also reported significant ($p \le 0.01$) GCA, SCA and RCA effects in different rapeseed populations for plant height and yield traits and identified desirable populations (Acharya & Swain, 2004; Akbar et al., 2008; Ali et al., 2015).

Table 9. Spec	Table 9. Specific combining ability effects in 8×8 F initiallel hybrids for various traits in <i>B</i> . <i>napus</i> L.					
F1 Hybrids	Plant height	Main raceme length	1000-seedweight	Seed yield plant ⁻¹		
$R.C \times A-95$	97.2*	-10.88*	0.06*	-11.15*		
R.C imes N.G	103.3*	6.88*	-0.02	-3.82*		
$\textbf{R.C} \times \textbf{D.N}$	85.4*	-0.81*	-0.06*	2.98*		
$R.C \times P.S$	97.9*	-6.85*	0.08*	12.61*		
$R.C \times F.C$	109.3*	7.03*	-0.07*	12.31*		
R.C imes R.B	113.7*	2.10*	-0.15*	-5.33*		
R.C imes D.K	103.2*	6.65*	0.11*	3.34*		
$A\text{-}95 \times N.G$	113.7*	1.81*	-0.05*	11.81*		
$A\text{-}95 \times D.N$	117.1*	5.02*	0.07*	1.53*		
$A-95 \times P.S$	118.2*	-9.72*	-0.09*	4.60*		
$A-95 \times F.C$	126.3*	1.96*	-0.07*	-4.17*		
$A-95 \times R.B$	130.5*	3.38*	-0.11*	-2.70*		
$A\text{-}95 \times D.K$	117.2*	1.48*	0.02	-1.55*		
$\text{N.G}\times\text{D.N}$	137.8*	4.78*	0.09*	-4.01*		
$N.G \times P.S$	113.6*	1.99*	-0.03*	3.24*		
$N.G \times F.C$	117.8*	-6.03*	-0.05*	-0.34		
N.G imes R.B	115.4*	-0.95*	-0.03*	-1.21*		
$\text{N.G}\times\text{D.K}$	108.1*	-3.55*	-0.01	-2.07*		
$D.N \times P.S$	121.6*	-12.05*	-0.07*	1.05*		
$D.N \times F.C$	130.7*	-8.22*	0.03*	3.72*		
$\mathrm{D.N} imes \mathrm{R.B}$	126.6*	-4.19*	0.00	3.46*		
$\mathrm{D.N} imes \mathrm{D.K}$	114.5*	-3.74*	-0.02	0.66*		
$P.S \times F.C$	124.7*	-2.26*	-0.06*	0.24		
$P.S \times R.B$	139.9*	0.37*	-0.05*	-7.98*		
P.S imes D.K	125.7*	2.92*	0.02	4.54*		
$F.C \times R.B$	117.7*	0.35*	0.15*	5.95*		
$F.C \times D.K$	124.8*	-8.40*	-0.15*	-8.15*		
$D.K \times R.B$	134.5*	-2.38*	0.00	15.48*		
SE (sij)+	0.55	0.25	0.02	0.26		
CD _{0.05} (Sij)	1.15	0.5	0.03	0.52		

Among parental genotypes, the Rainbow (4.75) showed maximum positive GCA effects while maximum negative GCA effects were recorded in genotype Punjab Sarsoon (-4.74) for main raceme length (Table 8). Parental genotype Rainbow with maximum positive GCA effects appeared to be the best general combiner for main raceme length. Among the direct F₁ hybrids, 14 out of 28 F1 hybrids showed positive SCA effects. The maximum positive SCA effects were observed for F1 hybrid Rustam Canola \times Faisal Canola (7.03) and was considered to be the best specific combination for raceme length (Table 9). The above promising F₁ hybrid also showed best mean performance, and proved to be the best specific combination which involved high \times low GCA parental genotypes. For RCA effects, 13 of 28 F₁ hybrids were noted with positive RCA effects, and the highest positive RCA effects were observed in F_1 hybrid Dunkled \times Punjab Sarsoon (14.65) while maximum negative RCA effects were noted for Rainbow \times Durr-e-NIFA (-13.80) (Table 10). In parental genotypes and their F_1 populations of Indian mustard, desirable general and specific combiners were identified for main raceme length and yield contributing traits (De et al., 2009; Shrimali et al.,

2016). Earlier findings also revealed significant and desirable GCA, SCA and RCA effects in parental genotypes and F1 populations for main raceme length in B. napus L. (Suchindra & Singh, 2006).

Five out of eight parental lines exhibited positive GCA effects for 1000-seed weight whereas the highest positive GCA effects were observed in Abasin-95 (0.06) and was considered as best general combiner. However, maximum negative GCA effects were recorded in genotype Faisal Canola (-0.05) (Table 8). Among direct F₁ hybrids, 11 F₁ hybrids showed positive SCA effects for 1000-seed weight (Table 9). The highest positive SCA effects were observed for F_1 hybrid Faisal Canola \times Rainbow (0.15) followed by Rustam Canola \times Dunkled (0.11). Therefore, these F₁ hybrids could be considered as the best specific cross combinations with promising mean performance which involve low \times low GCA parents. The highest negative SCA effects were recorded for Faisal Canola \times Dunkled (-0.15). Among reciprocal F₁ hybrids, RCA effects for 16 F1 hybrids were positive, and the highest RCA values were observed in F1 reciprocal Rainbow \times NIFA Gold being (0.25) followed by Rainbow \times Rustam Canola (0.23) (Table 10). Genotypes and F₁

hybrids having maximum positive GCA, SCA and RCA effects could be considered as best for 1000-seed weight. Highly significant GCA, SCA and reciprocal effects were reported in parental genotypes and F_1 populations for 1000-seed weight in *B. napus* L. (Suchindra & Singh, 2006; Sincik *et al.*, 2015).

For seed yield per plant, the GCA effects of parental genotypes ranged from -2.23 to +2.81 (Table 8). Four out of eight parental genotypes revealed positive GCA effects whereas maximum positive GCA effects were recorded in Punjab Sarsoon (2.81), and was identified as best general combiner for seed yield. However, NIFA Gold (-2.23) showed maximum negative GCA effects, and was considered as poorest general combiner for seed yield per plant. For seed yield, the SCA effects were ranging from -11.15 to +15.48 among F₁ hybrids (Table 9). In F₁ hybrid, 16 out of 28 F1 hybrids revealed positive SCA effects for seed yield per plant. The highest positive SCA effects were observed in F_1 hybrid Dunkled × Rainbow (15.48) followed by Rustam Canola \times Punjab Sarsoon (12.61). Hence, these F₁ hybrids were considered as best specific cross combinations with a remarkable mean performance for seed yield and involve low \times low and high \times high

GCA parents. However, maximum negative SCA effects were expressed by F_1 hybrid Rustam Canola × Abasin-95 (-11.15). In reciprocal F₁ hybrids, the RCA effects were ranged from -24.79 to +15.09 (Table 10). In reciprocals, 13 out of 28 F₁ hybrids revealed positive RCA effects whereas the highest values were recorded in F₁ hybrid Dunkled \times Punjab Sarsoon (15.09) followed by Dunkled \times NIFA Gold (14.61) (Table 10). However, maximum negative RCA effects were recorded for F₁ hybrid Faisal Canola \times Rustam Canola (-24.79). For seed yield and yield components, the desirable positive GCA, SCA and RCA effects were reported in parental genotypes and F₁ populations of B. napus L. (Sabaghnia et al., 2010), Indian mustard (De et al., 2009) and brassica species (Acharya & Swain, 2004; Ali et al., 2015). In present studies, the F_1 hybrids i.e., Dunkled \times Rainbow and Rustam Canola × Punjab Sarsoon were considered as best F₁ hybrids with promising mean performance and involved low \times low and high \times high GCA parents for seed yield per plant. In the past studies, prevalence of nonadditive type of gene action was reported in various populations of B. juncea for seed yield and yield components (Singh et al., 2010; Shrimali et al., 2016).

Table 10. Reciprocal combining ability effects in 8 × 8 F₁diallel hybrids for various traits in *B. napus* L.

F1 Hybrids	Plant height	Main raceme length	1000-seed weight	Seed yield plant ⁻¹
$A-95 \times R.C$	93.4*	2.05*	-0.01	-5.38*
N.G imes R.C	126.0*	3.85*	0.13*	-1.03*
$N.G \times A-95$	134.3*	7.40*	0.03*	-3.11*
$D.N \times P.S$	124.6*	-9.30*	-0.07*	-13.79*
$D.N \times A-95$	124.5*	-4.75*	0.05*	-9.00*
$D.N \times N.G$	114.2*	-5.35*	0.06*	12.57*
$P.S \times R.C$	124.9*	0.85*	0.05*	0.51
$P.S \times A-95$	135.4*	-3.21*	0.07*	-4.90*
$P.S \times N.G$	118.7*	1.25*	0.13*	-1.13*
$P.S \times D.N$	131.8*	-7.25*	0.04*	-8.49*
$F.C \times R.C$	145.0*	-2.20*	-0.37*	-24.79
$F.C \times A-95$	140.7*	8.75*	-0.11*	3.40*
$F.C \times N.G$	124.9*	4.90*	0.18*	2.68*
$F.C \times D.N$	143.0*	-1.15*	0.05*	-5.18*
$F.C \times P.S$	133.5*	-5.00*	-0.05*	-13.41*
$R.B \times R.C$	135.4*	14.30*	0.23*	6.46*
$R.B \times A-95$	115.4*	-0.70*	0.05*	-6.58*
R.B imes N.G	127.2*	-4.90*	0.25*	2.54*
R.B imes D.N	142.4*	-13.80*	-0.04*	0.98*
$R.B \times P.S$	139.7*	-3.85*	-0.22*	-3.17*
$R.B \times F.C$	133.8*	8.41*	-0.09*	2.31*
$D.K \times R.C$	135.6*	-4.10*	-0.01	3.48*
$D.K \times A-95$	133.4*	7.55*	-0.14*	8.12*
$D.K \times N.G$	129.3*	10.15*	0.13*	14.61*
D.K imes D.N	120.5*	8.20*	0.01	6.08*
$D.K \times P.S$	128.4*	14.65*	0.06*	15.09*
$D.K \times F.C$	110.4*	-6.20*	-0.14*	-5.24*
$D.K \times R.B$	120.1*	-13.15*	-0.04*	-7.10*
S.E (rij)+	0.61	0.29	0.02	0.3
CD _{0.05} (rij)	1.23	0.56	0.03	0.59

Conclusion

Highly significant differences were observed among the parental genotypes and F1 populations for all the studies traits. Parental genotypes Abasin-95 and Punjab Sarsoon were identified as best general combiners for seed yield. The F_1 hybrids NIFA Gold \times Rustam Canola, Rustam Canola \times Punjab Sarsoon and Punjab Sarsoon \times Abasin-95 exhibited maximum mid- and better-parent heterosis, respectively for 1000-seed weight and seed yield per plant. The F1 hybrids Punjab Sarsoon × Abasin-95 exhibited highest commercial heterosis for all the traits. Based on SCA effects, the F_1 hybrids Dunkled \times Rainbow and Rustam Canola × Punjab Sarsoon were found to be the best specific combiners for seed yield per plant. Results further revealed that all the traits were controlled non-additively and hence, selection in later segregating generations might be more effective.

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