HETEROTIC AND GENETIC EFFECTS IN INTRA-SPECIFIC POPULATIONS OF *BRASSICA NAPUS* L.

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Abstract

Eight parents viz., Rustam Canola, Abasin-95, NIFA Gold, Durr-e-NIFA, Punjab Sarsoon, Faisal Canola, Rainbow and Dunkled were crossed in a complete diallel fashion in rapeseed (*Brassica napus* L.). The resultant 56 F$_1$ hybrids along with eight parental genotypes were grown in a randomized block design with two replications and evaluated for genetic variability, heterosis and combining ability through earliness, morphological and yield traits. The F$_1$ hybrids and their parental cultivars revealed highly significant differences for all the traits which revealed that breeding material has greater genetic variability and scope for further improvement through intensive selection. Mean squares due to general combining ability (GCA), specific combining ability (SCA) and reciprocal combining ability (RCA) were found highly significant ($p \leq 0.01$) for days to maturity, secondary branches per plant, pods per plant, seeds per pod and seed yield per plant which signifying the equal shares of both additive and dominance genetic effects. However, the variances due to σ^2SCA were higher in magnitude than σ^2GCA, and the ratios of σ^2GCA/σ^2SCA were also below than unity which revealed the predominance of non-additive gene action for inheritance of all the traits. Parental cultivars Punjab Sarsoon and Dunkled were identified as best general combiners and performed better for the majority of the traits. Therefore, these general combiners produced some best specific cross combinations with the promising mean performance which involve high × high, low × high and high × low GCA parental genotypes. The F$_1$ hybrids Dunkled × Rainbow, Abasin-95 × NIFA Gold, Durr-e-NIFA × Punjab Sarsoon, Rustam Canola × Punjab Sarsoon and Punjab Sarsoon × Abasin-95 revealed best mean performance for earliness, morphological and yield traits hence these genotypes could be used in the future breeding programs.

Key words: Genetic variability, Heterosis, Combining ability, Additive and nonadditive gene action, General and specific combiners, *B. napus* L.

Introduction

Rapeseed (*Brassica rapa* L. and *B. napus* L.) and mustard (*B. juncea* L.) are the important crops grown in Pakistan (Nasim *et al.*, 2014). *Brassica napus* is originated naturally by a cross between *B. campestris* and *B. oleracea* and is an amphidiploids with chromosome number of 38 (2n = 4x = 38) (Zhou *et al.*, 2006). Rapeseed is known as the third largest source of vegetable oil after soybean and palm (40-46%) in the world. In addition to edible purposes, its oil is preferably used as hair oil. It is being extensively used in cattle feed, lubricants and in fertilizer industry (Abbas *et al.*, 2008).

Rapeseed being traditional oilseed crop of Pakistan is grown over a larger area in all four provinces under both irrigated and rainfed conditions. In Pakistan rapeseed/mustard was cultivated on an area of 0.193 million hectares with average seed and oil production of 0.179 and 0.061 million tons, respectively which is very low as compared to other countries (Anon., 2016-2017). Pakistan is facing a persistent shortage of edible oil because edible oil production from all traditional and non-traditional oilseed crops is only enough to meet about one-fourth of local demand while the remaining requirement is met through imports (Nausheen *et al.*, 2015). There are many causes of low yield but one of most important among them is the non-availability of high yielding cultivars. To bridge the gap between local production and import of edible oil in the country, it is imperative to develop improved cultivars of Brassica with higher seed and oil yields (Abbas *et al.*, 2008).

In the development of hybrids, the genetic components of variance studied through combining ability are important indicators to determine the potential of inbred lines to be used in hybrid combinations (Mohammed, 2011). Combining ability is a statistical procedure used for analysis of diallel crosses in a universal statistical technique (Griffing, 1956). The diallel analysis provides a mating design where the selected parents are crossed in all possible combinations; the mean values are used for predicting combining ability of the parental genotypes and their hybrids to enlighten the nature of gene action involved in the inheritance of different traits. Combining ability can be delineated as the ability of genotypes to combine with each other during hybridization and transfer the desirable characters to the next generation (Prasad *et al.*, 2002). Sincik *et al.*, (2014) depicted that GCA as an average performance of a genotype in a series of crosses while SCA is the performance of inbreds in specific hybrid combinations. In crosses, the genotypes revealing higher values for average combining ability are regarded as good general combiners while if its performance is good in particular crosses, they are deemed to have good specific combining ability. In quantitative genetics, the genetic components of variance and their estimation in form of expression are very important to understand the inheritance pattern of different traits.

Hybrid crop production is used as a principal technique for enhancement of crops yield. Hybrid cultivars can bring an increase of 15% or even more in the yield than other conventional cultivars (Khan *et al.*, 2006). Heterosis is the superiority in the performance of F_1 hybrids relative to the mid-parent (MP) or better parent (BP) values. While the practical application of heterosis in plant breeding is quite successful in many crops through the development of hybrid cultivars. Goodnight (1999) explained the three main genetic bases and hypotheses which might be responsible for heterosis i.e., dominance, overdominance, and epistasis. The dominance hypothesis supposes that deleterious recessive alleles of one of the parents are complemented in the F_1 hybrid by the dominant alleles of the other parent (Radoev *et al.*, 2008). The overdominance hypothesis states that the heterozygous combination of the alleles at a locus is superior to either of the two possible homozygous combinations. Epistasis assumes that epistatic interactions between different loci is the cause of heterosis. The utilization of heterosis has become a major strategy to increase the productivity of plants and animals (Stuber, 1994). Despite successful utilization of heterosis in many crops, there still exists a contradiction between heterosis utilization and understanding of the genetic basis of heterosis which hampers the effective exploitation of this biological phenomenon.

The diallel mating design is extensively used to investigate the combining ability, heterosis and genetic mechanisms controlling a particular trait (Mohammed, 2011). For improvement of a particular trait, it is imperative to obtain genetic information related to that character. For the development of hybrids, it is crucial to know combining ability of a genotype as it result in heterosis. Many studies have been performed to tackle the results of GCA and SCA for yield and its components. Past studies on combining ability in relation to other yield-related traits of Brassica species have been reported the preponderance of both additive and non-additive gene action in the inheritance of earliness and yield contributing traits (Nausheen *et al.*, 2015; Sincik *et al.*, 2014; Mohammed, 2011; Abbas *et al.*, 2008; Khan *et al.*, 2006; Prasad *et al.*, 2002). Keeping in view its economic importance, a research program was undertaken to assess the genetic potential and heterotic effects, genetic components of variance and effects due to GCA, SCA and RCA in 8 × 8 F_1 diallel crosses and their parental cultivars for earliness and yield contributing traits in *Brassica napus* L.

Materials and Methods

Plant material and procedure: Breeding material comprising eight *Brassica napus* L. genotypes i.e., Rustam Canola (R.C), Abasin-95 (A-95), NIFA Gold (N.G), Durr-e-NIFA (D.N), Punjab Sarsoon (P.S), Faisal Canola (F.C), Rainbow (R.B) and Dunkled (D.K) collected from Oilseed Division, National Agriculture Research Center (NARC), Islamabad, Pakistan. These eight genotypes were crossed in an 8 × 8 complete diallel fashion during 2014-2015 at The University of Agriculture, Peshawar, Pakistan. During 2015-2016, the

seeds of 56 F_1 hybrids and their parental lines were sown in a randomized complete block design (RCBD) with two replications. Each genotype was grown with plants and rows spacing of 40 and 50 cm, respectively with row length of 10 m. Recommended and uniform cultural practices were applied to all the genotypes to avoid field variations and environmental influences.

Traits measurement and statistical analysis: Data were recorded on 10 randomly selected plants on the single plant basis and then averaged for earliness and yield traits i.e., days to maturity, secondary branches per plant, pods per plant, seeds per pod, and seed yield per plant. All the data were subjected to analysis of variance according to Steel *et al.*, (1997). After getting the significant differences among the parental genotypes and their F_1 hybrids for various traits, the heterosis and combining ability analyses were carried out as follows.

Heterosis: Heterosis over mid-parent was calculated in terms of percent increase (+) or decrease (-) of the F_1 hybrids over its mid-parent value (Fehr, 1987).

$$Heterosis \quad (\%) = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

Heterobeltiosis: Heterobeltiosis as coined by Fonseca (1965), was estimated in terms of percent increase or decrease of the F_1 hybrid over its better parent.

$$Heterobelt \quad iosis \quad (\%) = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Heterotic values for above two categories were further subjected to "t" test to determine whether F_1 hybrid means were statistically different from their mid and better parents. The "t" values were computed according to Wynne *et al.*, (1970) as follows.

't' for mid-parent heterosis

$$t = \frac{F_1 - MP}{\sqrt{\frac{3}{2r}(EMS)}}$$

't' for better parent heterosis

$$t = \frac{F_1 - BP}{\sqrt{\frac{2}{r}(EMS)}}$$

where
MP = Mid parent value of the particular F_1 cross
BP = Better parent value in the particular F_1 cross
r = Number of Replications
EMS = Error mean square
t = Obtained value was tested against the tabulated t-value at error degree of freedom

Combining ability analysis: The data were 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.

Results and Discussion

Genetic variability and heterotic effects: Parental genotypes and their F_1 hybrids showed significant ($p \leq 0.01$) differences for days to maturity, secondary branches per plant, pods per plant, seeds per pod and seed yield per plant which revealed that breeding material had greater genetic variability (Table 1). Past findings also reported significant mean differences among different populations of *B. napus* and *B. juncea* for earliness and yield traits (Synrem *et al.*, 2015; Meena *et al.*, 2014). Significant variations were reported in intra-specific crosses of *B. juncea* for days to flowering and maturity, morphological and yield traits (Maurya *et al.*, 2012; Singh *et al.*, 2010). The trait-wise results about genetic variability, heterosis and combining ability are presented herein.

Days to maturity: Days to maturity ranged from 168.3 to 183.6 days among parental genotypes with a mean value of 176.2 days, where the minimum and maximum days to maturity were taken by parental genotypes Dunkled and Rainbow, respectively (Table 2). In F_1 hybrids, days to maturity ranged from 158.3 to 189 days with a mean value of 176.8 days. By comparing the mean performance of the parental genotypes and their F_1 populations, the F_1 hybrids (176.2 days) took less days to maturity than their parental genotypes (176.8 days). The F_1 hybrid Dunkled × Rustam Canola (158.3 days) was noted with less days to maturity followed by other hybrid Dunkled × Punjab Sarsoon (162.0 days), and it was found at par with two other F_1 hybrids i.e., Dunkled × NIFA Gold (162.1 days) and NIFA Gold × Dunkled (162.5 days). However, the F_1 hybrid Faisal Canola × Durr-e-NIFA (189.0 days) manifested maximum days to maturity followed by F_1 hybrids like Rainbow × Abassin-95 (188.7 days), Rainbow × Dunkled (188.7 days), Rainbow × Rustam Canola (187.5 days) and Faisal Canola × NIFA Gold (187.9 days). Days to maturity is a useful criterion for selection of genotypes with earliness which provides sufficient time for genotypes to avoid approaching heat stress and helps to vacate the land for the following crop. Present results are in close agreement with the finding of Jahan *et al.*, (2014), Oghan *et al.*, (2009) and Khan *et al.*, (2006) who also reported significant differences for days to flowering in *Brassica napus* genotypes. Significant variations were reported between parents and F_1 populations for flowering in *B. juncea* L. (Singh *et al.*, 2010; Maurya *et al.*, 2012).

In case of earliness, the negative heterosis is always desirable for early maturity as late maturity cause losses to seed yield and oil quality traits. In case of mid-parent heterosis, 24 out 56 F_1 hybrids showed negative heterosis ranging from -0.14 to -8.73% (Table 4). Of these crosses, 21 F_1 hybrids exhibited significant negative heterosis where the maximum negative heterotic value was recorded in F_1 hybrid Dunkled × Rustam Canola (-8.73). Negative heterosis over better-parent was exhibited by 31 F_1 hybrids ranging from -0.44 to -11.37%. Maximum significant negative and desirable heterotic effects over better parent were observed in F_1 hybrid Dunkled × Rustam Canola (-

11.37%). In rapeseed, the early maturity is also desirable, therefore, the F_1 hybrids with negative heterotic effects could be used in the development of early maturing genotypes. Kang *et al.*, (2014) also reported significant negative mid and better parent heterosis for earliness and maturity traits in *B. napus*. In *B. juncea,* the negative heterotic effects for days to maturity have also been reported (Turi *et al.*, 2006). Significant negative mid-parent and better-parent heterosis were also found for day to flowering in various populations of *B. napus* L. (Abbas *et al.*, 2008). Significant negative commercial heterosis was also reported for days to maturity in Indian mustard (Synrem *et al.*, 2015; Meena *et al.*, 2014).

Secondary branches per plant: Secondary branches per plant is an important trait because more secondary branches produce more flowers with seeds which ultimately results in greater seed yield. Secondary branches per plant ranged from 17.5 to 36.5 among parental genotypes with a mean value of 27.4 nonetheless cultivar Abasin-95 produced maximum while genotype Rainbow produced minimum secondary branches (Table 2). Among F_1 hybrids, the mean values ranged from 14.2 to 47.9 with a mean value of 30.1 branches. In comparison, F_1 populations (30.1) showed more secondary branches per plant than their parental genotypes (27.4). Overall, maximum primary branches per plant were observed in F_1 hybrid Faisal Canola × Rustam Canola (47.9) and it was found at par with two other F_1 hybrids viz., Punjab Sarsoon × Dunkled (47.0) and Punjab Sarsoon × Durr-e-NIFA (47.0) followed by Punjab Sarsoon × Rustam Canola (44.5). The minimum number of secondary branches per plant was noted in F_1 hybrid Rainbow × NIFA Gold (14.2) followed by two other F_1 hybrids i.e., Faisal Canola × NIFA Gold (16.1) and NIFA Gold × Punjab Sarsoon (16.2). The moderate number of secondary branches per plant was observed in all other parental genotypes and F_1 hybrids. Present results indicated that parental genotypes and F_1 hybrids had sufficient genetic variability for secondary branches per plant which could be exploited in the future breeding program. Highly significant variations were reported among populations of various species of Brassica for secondary branches per plant (Jahan *et al.*, 2014; Muhammad *et al.,* 2014).

Heterosis over mid-parent showed that 35 F_1 hybrids revealed positive heterotic effects ranging from 1.87 to 111.31% (Table 4). Of these, 29 F_1 hybrids revealed significant positive heterotic effects over mid parent while maximum heterosis was recorded for F_1 hybrid Dunkled × Rainbow (111.31%). Regarding best parent heterosis, 23 F_1 hybrids revealed positive heterotic effects ranging from 1.11 to 92.06%. The 19 F_1 hybrids showed significant positive heterotic values over best parent, and maximum significant positive value was observed in F_1 hybrid Dunkled × Rainbow. Current results are in line with earlier findings of Akabari & Sasidharan (2016) and Singh *et al.*, (2005) who have also reported significant positive mid and better parent heterotic effects for secondary branches in Indian mustard. Present findings are also in agreement with earlier findings of Sabaghnia *et al.*, (2010) who has also found significant positive mid, better and commercial parent heterosis for secondary branches in rapeseed.

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

Traits	Mean Squares			CV (%)
	Replications (d.f. = 1)	Genotypes (d.f. = 63)	Error (d.f. = 63)	
Days to maturity	61.05	120.80**	0.75	0.49
Secondary branches plant⁻¹	116.47	136.90**	1.53	4.16
Pods plant⁻¹	696.577	15213.23**	10.28	0.81
Seeds pod⁻¹	25.02	9.01**	0.14	1.49
Seed yield plant⁻¹	91.33	247.71**	0.72	1.90

** Significant at $p \leq 0.01$, d.f. = degree of freedom

Table 2. Mean performance of 8 × 8 F₁ diallel hybrids of *B. napus* for various traits.

Parents & F₁ hybrids	Days to maturity	Secondary branches plant⁻¹	Pods plant⁻¹	Parents & F₁ hybrids	Days to maturity	Secondary branches plant⁻¹	Pods plant⁻¹
Rustam Canola (R.C)	178.6	26.0	321.7	D.N × R.B	182.8	23.7	387.7
Abasin-95 (A-95)	175.7	36.5	363.5	D.N × D.K	165.6	36.3	448.5
NIFA Gold (N.G)	177.5	36.1	304.6	P.S × R.C	186.7	44.5	504.2
Durr-e-NIFA (D.N)	170.0	20.2	294.6	P.S × A-95	175.9	41.6	485.4
Punjab Sarsoon (P.S)	175.3	26.0	296.9	P.S × N.G	178.2	36.5	416.1
Faisal Canola (F.C)	181.0	35.6	321.8	P.S × D.N	164.1	47.0	519.7
Rainbow (R.B)	183.6	17.5	327.7	P.S × F.C	185.7	32.3	323.0
Dunkled (D.K)	168.3	21.4	303.5	P.S × R.B	186.1	28.7	405.5
R.C × A-95	168.5	25.7	254.3	P.S × D.K	165.3	47.0	564.6
R.C × N.G	173.3	29.8	339.3	F.C × R.C	182.4	47.9	610.1
R.C × D.N	181.6	31.9	380.4	F.C × A-95	173.3	17.1	313.7
R.C × P.S	172.7	44.1	564.8	F.C × N.G	187.9	16.1	355.6
R.C × F.C	180.3	27.4	389.0	F.C × D.N	189.0	20.8	504.8
R.C × R.B	179.2	34.3	413.8	F.C × P.S	172.6	23.7	535.9
R.C × D.K	175.4	40.4	440.6	F.C × R.B	174.1	36.2	449.3
A-95 × R.C	175.8	35.1	421.3	F.C × D.K	165.7	24.5	320.9
A-95 × N.G	177.8	24.6	465.8	R.B × R.C	187.5	27.5	319.0
A-95 × D.N	176.9	17.8	363.2	R.B × A-95	188.7	26.1	419.9
A-95 × P.S	177.8	35.7	405.6	R.B × N.G	180.3	14.2	322.9
A-95 × F.C	180.0	33.0	560.6	R.B × D.N	183.6	22.0	399.9
A-95 × R.B	182.0	20.3	354.6	R.B × P.S	184.7	32.9	316.8
A-95 × D.K	163.4	36.3	472.1	R.B × F.C	183.6	27.3	384.1
N.G × R.C	174.1	33.1	365.5	R.B × D.K	188.7	25.2	420.0
N.G × A-95	182.9	21.6	547.2	D.K × R.C	158.3	31.6	361.0
N.G × D.N	172.1	34.8	446.6	D.K × A-95	173.7	34.6	326.6
N.G × P.S	169.3	16.2	386.0	D.K × N.G	162.1	30.7	230.6
N.G × F.C	176.7	24.4	390.2	D.K × D.N	170.7	31.0	320.9
N.G × R.B	183.8	27.3	344.4	D.K × P.S	162.0	34.7	315.8
N.G × D.K	162.5	24.3	432.1	D.K × F.C	182.3	34.2	347.8
D.N × R.C	185.6	23.8	484.7	D.K × R.B	185.1	41.1	524.5
D.N × A-95	171.9	26.5	481.0	Parental means	176.2	27.4	316.8
D.N × N.G	184.6	17.7	231.6	F₁ means	176.8	30.1	407.1
D.N × P.S	170.6	36.3	335.9	LSD₀.₀₅	1.73	1.82	6.4
D.N × F.C	178.9	25.5	418.4				

Pods per plant: Pods per plant is the major yield contributing factor and play an important role towards final seed yield in rapeseed. Among parental genotypes, the pods per plant varied from 294.6 (Durr-e-NIFA) to 363.5 (Abasin-95) with a mean value of 316.8 pods per plant (Table 2). In F₁ hybrids, the mean values ranged from 230.6 to 610.1 with a mean value of 407.1 pods per plant. By comparing the means of parental cultivars and F₁ hybrids, F₁ populations (407.1) showed more pods per plant than their parental genotypes (316.8). In overall mean performance, F₁ hybrid Faisal Canola × Rustam Canola (610.1) recorded with maximum pods per plant followed by at par performance of two other F₁ hybrids i.e., Rustam Canola × Punjab Sarsoon (564.8) and Punjab Sarsoon × Dunkled (564.6). However, minimum pods per plant were observed in F₁ hybrid Dunkled × NIFA Gold (230.6) and it was found at par with one other F₁ hybrid Durr-e-NIFA × NIFA Gold (231.6) followed by Rustam Canola × Abasin-95 (254.3) and parental genotype Durr-e-NIFA (294.6). In rapeseed, seed yield is dependent on pods per plant and seeds per pod, therefore, plant breeders prefer the greater number of pods and seeds in development of high yielding genotypes. Significant differences were observed among various genotypes of *B. napus* for pods per plant (Farshadfar *et al.*, 2013). Past studies reported that various populations of Brassica showed significant difference for yield traits including pods per plant, and F₁ hybrids produced more pods per plant than parental genotypes in *B. juncea* L. (Arifullah *et al.*, 2012; Turi, 2011).

Table 3. Mean performance of 8 × 8 F₁ diallel hybrids of *B. napus* for various traits.

Parents & F$_1$ hybrids	Seeds pod^{-1}	Seed yield plant^{-1}	Parents & F$_1$ hybrids	Seeds Pod^{-1}	Seed yield plant^{-1}
Rustam Canola (R.C)	24.0	35.27	D.N × R.B	26.6	46.52
Abasin-95 (A-95)	27.7	48.16	D.N × D.K	24.8	50.70
NIFA Gold (N.G)	26.4	36.51	P.S × R.C	26.6	60.30
Durr-e-NIFA (D.N)	25.5	34.27	P.S × A-95	27.4	57.85
Punjab Sarsoon (P.S)	22.6	31.91	P.S × N.G	27.4	49.52
Faisal Canola (F.C)	23.9	35.59	P.S × D.N	25.2	56.46
Rainbow (R.B)	22.1	32.82	P.S × F.C	25.1	34.50
Dunkled (D.K)	23.3	32.03	P.S × R.B	20.2	34.18
R.C × A-95	25.5	29.83	P.S × D.K	28.1	66.86
R.C × N.G	24.4	38.30	F.C × R.C	28.4	82.76
R.C × D.N	20.1	34.11	F.C × A-95	27.2	38.26
R.C × P.S	23.4	61.31	F.C × N.G	26.4	39.60
R.C × F.C	21.5	33.20	F.C × D.N	23.9	53.30
R.C × R.B	23.7	44.48	F.C × P.S	25.8	61.32
R.C × D.K	25.7	52.06	F.C × R.B	25.4	51.08
A-95 × R.C	20.9	40.59	F.C × D.K	26.8	31.32
A-95 × N.G	24.6	52.02	R.B × R.C	24.0	31.57
A-95 × D.N	22.1	37.60	R.B × A-95	25.7	47.38
A-95 × P.S	25.9	48.05	R.B × N.G	27.0	36.56
A-95 × F.C	18.8	45.07	R.B × D.N	25.0	44.56
A-95 × R.B	21.8	34.23	R.B × P.S	27.6	40.53
A-95 × D.K	24.7	51.96	R.B × F.C	26.3	46.46
N.G × R.C	25.4	40.36	R.B × D.K	27.5	50.77
N.G × A-95	23.9	58.23	D.K × R.C	27.0	45.09
N.G × D.N	24.4	50.43	D.K × A-95	23.5	35.73
N.G × P.S	26.8	47.26	D.K × N.G	25.7	25.51
N.G × F.C	24.9	44.96	D.K × D.N	26.6	38.53
N.G × R.B	26.0	41.63	D.K × P.S	26.2	36.68
N.G × D.K	27.2	54.73	D.K × F.C	27.3	41.81
D.N × R.C	28.0	61.69	D.K × R.B	27.6	64.97
D.N × A-95	24.8	55.60	Parental means	24.4	35.82
D.N × N.G	23.3	25.30	F$_1$ means	25.1	45.82
D.N × P.S	26.6	39.48	LSD$_{0.05}$	0.74	1.70
D.N × F.C	22.7	42.94			

For pods plant, the heterotic effects over mid-parent demonstrated that 49 F₁ hybrids had significant positive effects ranging from 2.14 to 89.62% (Table 4). Of these crosses, maximum significant heterosis over mid parent was observed for F₁ hybrids Faisal Canola × Rustam Canola (89.62%) and Punjab Sarsoon × Dunkled (88.07%). Regarding best parent heterosis, 44 F₁ hybrids revealed significant positive heterotic effects ranging from 4.05 to 89.59%. Among F₁ hybrids, the highest value over better parent was observed for F₁ hybrids Faisal Canola × Rustam Canola (89.59%) and Punjab Sarsoon × Dunkled (86.03%). In Brassica, the pods per plant is also an important component of grain yield and maximum pods on plant result in higher seed yield, therefore, positive heterosis is desired to develop high yielding genotypes. Significant positive heterotic values were recorded among various populations of Indian mustard for pods per plant and other yield contributing traits (Akabari & Sasidharan, 2016; Singh *et al*., 2005). Significant positive mid-parent, better-parent and commercial heterosis were reported for pods per plant in *B. napus* L. (Sabaghnia *et al*., 2010).

Seeds per pod: Seeds per pod is an important yield contributing parameter and have a direct effect on seed yield. Therefore, seeds per pod are always an important

objective of the plant breeders for producing high yielding genotypes. In parental genotypes, the mean values ranged from 22.1 (Rainbow) to 27.7 (Abasin-95) with a mean value of 24.4 seeds per pod (Table 3). The F₁ hybrids varied from 18.8 (Abasin-95 × Faisal Canola) to 28.4 (Faisal Canola × Rustam Canola) with a mean value of 25.1 seeds per pod. On average, the F₁ populations (25.1) showed more seeds per pod than their parental genotypes (24.4). In the comparison of parental genotypes and F₁ hybrids, the highest number of seeds per pod were observed in F₁ hybrid Faisal Canola × Rustam Canola (28.4) and it was found at par with one other F₁ hybrid Punjab Sarsoon × Dunkled (28.1) followed by Durr-e-NIFA × Rustam Canola (28.0). A minimum number of seeds per pod was noted in F₁ hybrid Abasin-95 × Faisal Canola (18.8) followed by at par performance of two other F₁ hybrids i.e., Rustam Canola × Durr-e-NIFA (20.1) and Rustam Canola × Faisal Canola (21.5). A moderate number of seeds per pod were observed in all other parental genotypes and F₁ hybrids. Present findings suggested the existence of enough genetic variability in the tested material which is in close agreement with the findings of Rameeh (2013). Significant differences were reported among the various populations of *B. napus* for yield contributing traits including seeds per pod (Gangapur *et al*., 2009; Khan & Khan, 2003; Ghosh & Gulati, 2002).

Table 4. Heterosis in 8 × 8 F₁ diallel hybrids of *B. napus* for various traits.

F₁ Hybrids	Days to maturity		Secondary branches plant⁻¹		Pods plant⁻¹	
	MPH (%)	BPH (%)	MPH (%)	BPH (%)	MPH (%)	BPH (%)
R.C × A-95	-4.88**	-5.66**	-17.76**	-29.59**	-25.77**	-30.04**
R.C × N.G	-2.67**	-2.97**	-4.03	-17.45**	8.35**	5.47**
R.C × D.N	4.19**	1.68**	38.10**	22.69**	23.45**	18.25**
R.C × P.S	-2.40**	-3.30**	69.62**	69.62**	82.61**	75.57**
R.C × F.C	0.28	-0.39	-11.04**	-23.03**	20.90**	20.88**
R.C × R.B	-1.05*	-2.40**	57.70**	31.92**	27.44**	26.27**
R.C × D.K	1.12**	-1.79**	70.46**	55.38**	40.95**	36.96**
A-95 × R.C	-0.76	-1.57**	12.32**	-3.84	22.97**	15.90**
A-95 × N.G	0.68	0.17	-32.23**	-32.60**	39.44**	28.14**
A-95 × D.N	2.34**	0.68	-37.21**	-51.23**	10.38**	-0.08
A-95 × P.S	1.31**	1.20**	14.24**	-2.19	22.83**	11.58**
A-95 × F.C	0.93	-0.55	-8.46**	-9.59**	63.61**	54.22**
A-95 × R.B	1.31**	-0.87*	-24.81**	-44.38**	2.60**	-2.45**
A-95 × D.K	-5.00**	-7.00**	25.39**	-0.55	41.56**	29.88**
N.G × R.C	-2.22**	-2.52**	6.60	-8.31**	16.72**	13.62**
N.G × A-95	3.57**	3.04**	-40.50**	-40.82**	63.81**	50.54**
N.G × D.N	-0.95*	-3.04**	23.62**	-3.60	49.07**	46.62**
N.G × P.S	-4.02**	-4.62**	-47.83**	-55.12**	28.35**	26.72**
N.G × F.C	-1.42**	-2.38**	-31.94**	-32.41**	24.58**	21.26**
N.G × R.B	1.80**	0.11	1.87	-24.38**	8.94**	5.10**
N.G × D.K	-6.02**	-8.45**	-15.48**	-32.69**	42.11**	41.86**
D.N × R.C	6.48**	3.92**	3.03	-8.46*	57.29**	50.67**
D.N × A-95	-0.55	-2.16**	-6.53	-27.40**	46.18**	32.32**
D.N × N.G	6.24**	4.00**	-37.12**	-50.97**	-22.70**	-23.97**
D.N × P.S	-1.19**	-2.68**	57.14**	39.62**	13.58**	13.14**
D.N × F.C	1.94**	-1.16**	-8.60*	-28.37**	35.76**	30.02**
D.N × R.B	3.39**	-0.44	25.73**	17.33**	24.60**	18.31**
D.N × D.K	-2.10**	-2.59**	74.52**	69.63**	49.97**	47.78**
P.S × R.C	5.51**	4.54**	71.15**	71.15**	63.01**	56.73**
P.S × A-95	0.23	0.11	33.12**	13.97**	47.00**	33.54**
P.S × N.G	1.02**	0.39	17.55**	1.11	38.35**	36.61**
P.S × D.N	-4.95**	-6.39**	103.46**	80.77**	75.72**	75.04**
P.S × F.C	4.24**	2.60**	4.87	-9.27**	4.41**	0.37
P.S × R.B	3.71**	1.36**	31.95**	10.38*	29.84**	23.74**
P.S × D.K	-3.78**	-5.70**	98.31**	80.77**	88.07**	86.03**
F.C × R.C	1.45**	0.77	55.52**	34.55**	89.62**	89.59**
F.C × A-95	-2.83**	-4.25**	-52.57**	-53.15**	-8.45**	-13.70**
F.C × N.G	4.83**	3.81**	-55.09**	-55.40**	13.54**	10.50**
F.C× D.N	7.69**	4.42**	-25.45**	-41.57**	63.79**	56.87**
F.C × P.S	-3.12**	-4.64**	-23.05**	-33.43**	73.23**	66.53**
F.C × R.B	-4.50**	-5.17**	36.35**	1.69	38.35**	37.11**
F.C × D.K	-5.12**	-8.45**	-14.04**	-31.18**	2.64**	-0.28
R.B × R.C	3.53**	2.12**	26.44**	5.77	-1.76*	-2.65**
R.B × A-95	5.04**	2.78**	-3.33	-28.49**	21.50**	15.52**
R.B × N.G	-0.14	-1.80**	-47.01**	-60.66**	2.14*	-1.46
R.B × D.N	3.85**	0.00	16.71**	8.91	28.52**	22.03**
R.B × P.S	2.93**	0.60*	51.26**	26.54**	1.44	-3.33**
R.B × F.C	0.71	0.00	2.82	-23.31**	18.28**	17.21**
R.B × D.K	7.25**	2.78**	29.56**	17.76**	33.08**	28.17**
D.K × R.C	-8.73**	-11.37**	33.33**	21.54**	15.48**	12.22**
D.K × A-95	0.99*	-1.14**	19.52**	-5.21	-2.07*	-10.15**
D.K × N.G	-6.25**	-8.68**	6.78	-14.96**	-24.16**	-24.29**
D.K × D.N	0.92*	0.41	49.04**	44.86**	7.31**	5.73**
D.K × P.S	-5.70**	-7.59**	46.41**	33.46**	5.20**	4.05**
D.K × F.C	4.38**	0.72	20.00**	-3.93	11.24**	8.08**
D.K × R.B	5.20**	0.82*	111.31**	92.06**	66.19**	60.05**

Regarding mid-parent heterosis, 37 F_1 hybrids showed positive heterotic effects ranging from 0.43 to 23.49% (Table 5). However, 34 F_1 hybrids revealed significant positive heterotic values. Maximum significant heterosis over mid parent was found in F_1 hybrid Rainbow × Punjab Sarsoon (23.49%) followed by Punjab Sarsoon × Dunkled (22.44%). According to best parent heterosis, 23 F_1 hybrid showed positive heterotic effects ranging from 1.52 to 22.12%, and 21 F_1 hybrids showed significant positive heterotic values. Maximum significant heterosis over best parent was presented by F_1 hybrids Rainbow × Punjab Sarsoon (22.12%) and Punjab Sarsoon × Dunkled (20.60%). Seeds per pod is major seed yield contributing trait in rapeseed, therefore, positive heterosis for the said trait is valuable to develop the high yielding genotypes. Kang *et al*., (2014) reported significant positive heterosis in various populations of *B. napus* for seeds per pod. Significant positive mid and better heterotic values were recorded in various populations of Indian mustard for seeds per pod and other yield contributing traits (Meena *et al*., 2014; Synrem *et al*., 2015).

Seed yield per plant: Majority of the rapeseed breeding programs aims to increase the seed yield, whereas seed yield is dependent on different morphological and yield-related traits. Seed yield per plant ranged from 31.91 to 48.16 g for parental genotypes, while in F_1 hybrids the said range was 25.30 to 82.76 g (Table 3). By comparing the parental cultivars and F_1 hybrids, the parental genotypes (35.82 g) produced less seed yield per plant than their F_1 populations (45.82 g). Overall, the mean values revealed that maximum seed yield was produced by F_1 hybrid Faisal Canola × Rustam Canola (82.76 g) and was identified as the best specific cross among all other F_1 hybrids followed by Punjab Sarsoon × Dunkled (66.86 g) and Dunkled × Rainbow (64.97 g). Poor performance and least seed yield per plant were observed in F_1 hybrid Durr-e-NIFA × NIFA Gold (25.30 g) followed by Dunkled × NIFA Gold (25.51 g). Other parental genotypes and F_1 hybrids revealed medium seed yield per plant. Highly significant differences with larger genetic variability were observed in different rapeseed populations for seed yield and yield-related traits (Synrem *et al.,* 2015; Nasim *et al*., 2014; Kang *et al*., 2014).

Enhanced seed yield is an ultimate goal of the majority of rapeseed breeding programs, therefore, positive heterosis is desirable for developing high yielding genotypes. Heterosis estimates over mid-parent for seed yield per plant revealed that 44 crosses had positive heterotic effects ranging from 2.22 to 133.59% (Table 5). In these F_1 populations, 43 F_1 hybrids exhibited significant positive heterotic effects over mid parent. Maximum significant heterosis over mid parent was noted for F_1 hybrid P Faisal Canola × Rustam Canola (133.59%). Regarding the best parent heterosis, 37 F_1 hybrids exhibited significant positive heterotic effects ranging from 7.89 to 132.54%. Maximum significant heterosis over best parent was observed in F_1 hybrid Faisal Canola × Rustam Canola (132.54%). Khan *et al*., (2006) also reported significant positive mid and better parent heterotic values for seed yield in various populations of *B. napus* L. In Indian mustard, Akabari & Sasidharan (2016) also observed significant positive mid and better parent heterosis for seed yield and other yield components. Present results are in

accordance with Liton *et al*., (2017) who reported significant positive heterosis over mid and better parents for seed yield per plant in various populations of rapeseed.

Combining ability analysis: Analysis of variance for combining ability revealed that mean squares due to general combining ability (GCA), specific combining ability (SCA) and reciprocal combining ability (RCA) were found highly significant ($p{\leq}0.01$) for days to maturity, secondary branches per plant, pods per plant, seeds per pod and seed yield per plant in evaluation of parental genotypes and their F_1 hybrids signifying the role of both additive and non-additive gene effects (Table 6). However, GCA mean squares were leading and greater in magnitude than SCA and RCA for traits i.e., days to maturity, secondary branches per plant and seeds per pod. For pods per plant and seed yield per plant, the mean squares due to SCA and RCA, respectively were greater in magnitude than GCA. Combining ability effects due to GCA, SCA and RCA are used as main indicators for the identification and selection of potential inbred lines in most of the crops and in Brassica species for the development of hybrids and open-pollinated cultivars (Akbar *et al*., 2008). Combining ability effects have been successfully used for the selection of parental genotypes and crosses in rapeseed (Khalil & Raziuddin, 2017; Muhammad *et al*., 2014; Sabaghnia *et al*., 2010) and Indian mustard (Shrimali *et al*., 2016; De at al., 2009; Prasad *et al*., 2002). Highly significant mean squares were observed for GCA, SCA and RCA among various populations of rapeseed for earliness, morphological and yield traits (Arifullah *et al*., 2012; Naheed *et al*., 2017a, b). However, Farshadfar *et al*., (2013) and Azizinia *et al*., (2012) reported nonsignificant mean squares due to GCA and SCA for seeds per pod. Highly significant mean squares due to GCA, SCA and RCA were reported for different morpho-yield traits in various species of Brassica (Suchindra & Singh, 2006; Ali *et al*., 2014, 2015).

Variances due to GCA, SCA, and RCA: For days to maturity, the variances due to σ^2GCA, σ^2SCA, and σ^2RCA were 15.25, 39.13, and 17.67, respectively (Table 6). The ratio of σ^2GCA/σ^2SCA (0.38) was less than unity and showing the predominance of non-additive gene action for days to maturity in rapeseed genotypes. Nasim *et al*., (2014) and Vaghela *et al*., (2011) also reported predominant role of non-additive genetic effects in inheritance of earliness traits in various populations of *B. napus* L. and *B. Juncea* L. However, in other studies of *B. juncea*, the days to maturity were controlled by additive gene effects (Parmar *et al*., 2011; Gupta *et al.,* 2011). For secondary branches per plant, the variance due to σ^2SCA (34.39) was higher than σ^2GCA (6.18) and σ^2RCA (26.06), and the ratio σ^2GCA/σ^2SCA (0.18) depicted the importance of non-additive gene action for secondary branches per plant. Present results also got support from the previous findings of Mohammed (2011) and Sabaghnia *et al.,* (2010) who also reported nonadditive gene action for secondary branches. However, Shrimali *et al.,* (2016) mentioned an important role of additive gene action in the inheritance of secondary branches in Indian mustard.

Table 5. Heterosis in 8 × 8 F₁ diallel hybrids of *B. napus* for various traits.

F₁ Hybrids	Seeds pod⁻¹		Seed yield plant⁻¹	
	MPH (%)	BPH (%)	MPH (%)	BPH (%)
R.C × A-95	-1.35	-7.94**	-28.49**	-38.06**
R.C × N.G	-3.17*	-7.58**	6.71**	4.90
R.C × D.N	-18.79**	-21.18**	-1.90	-3.29
R.C × P.S	0.43	-2.50	82.52**	73.83**
R.C × F.C	-10.23**	-10.42**	-6.29**	-6.72**
R.C × R.B	2.82*	-1.25	30.65**	26.11**
R.C × D.K	8.67**	7.08**	54.71**	47.60**
A-95 × R.C	-19.15**	-24.55**	-2.70	-15.72**
A-95 × N.G	-9.06**	-11.19**	22.88**	8.01**
A-95 × D.N	-16.92**	-20.22**	-8.77**	-21.93**
A-95 × P.S	2.98*	-6.50**	20.02**	-0.23
A-95 × F.C	-27.13**	-32.13**	7.63**	-6.42**
A-95 × R.B	-12.45**	-21.30**	-15.46**	-28.92**
A-95 × D.K	-3.14*	-10.83**	29.59**	7.89**
N.G × R.C	0.79	-3.79**	12.45**	10.55**
N.G × A-95	-11.65**	-13.72**	37.55**	20.91**
N.G × D.N	-5.97**	-7.58**	42.50**	38.13**
N.G × P.S	9.39**	1.52	38.15**	29.44**
N.G × F.C	-0.99	-5.68**	24.72**	23.14**
N.G × R.B	7.22**	-1.52*	20.09**	14.02**
N.G × D.K	9.46**	3.03*	59.70**	49.90**
D.N × R.C	13.13**	9.80**	77.42**	74.91**
D.N × A-95	-6.77**	-10.47**	34.90**	15.45**
D.N × N.G	-10.21**	-11.74**	-28.51**	-30.70**
D.N × P.S	10.60**	4.31**	19.31**	15.20**
D.N × F.C	-8.10**	-10.98**	22.93**	20.65**
D.N × R.B	11.76**	4.31**	38.68**	35.75**
D.N × D.K	1.64	-2.75*	52.94**	47.94**
P.S × R.C	14.16**	10.83**	79.52**	70.97**
P.S × A-95	8.95**	-1.08	44.50**	20.12**
P.S × N.G	11.84**	3.79**	44.75**	35.63**
P.S × D.N	4.78**	-1.18	70.63**	64.75**
P.S × F.C	7.96**	5.02**	2.22	-3.06
P.S × R.B	-9.62**	-10.62**	5.61*	4.14
P.S × D.K	22.44**	20.60**	109.13**	108.74**
F.C × R.C	18.58**	18.33**	133.59**	132.54**
F.C × A-95	5.43**	-1.81	-8.63**	-20.56**
F.C × N.G	4.97**	0.00	9.85**	8.46**
F.C × D.N	-3.24*	-6.27**	52.59**	49.76**
F.C × P.S	10.97**	7.95**	81.69**	72.30**
F.C × R.B	10.43**	6.28**	49.33**	43.52**
F.C × D.K	13.56**	12.13**	-7.36**	-12.00**
R.B × R.C	4.12**	0.00	-7.27**	-10.49**
R.B × A-95	3.21*	-7.22**	17.02**	-1.62
R.B × N.G	11.34**	2.27	5.47*	0.14
R.B × D.N	5.04**	-1.96	32.84**	30.03**
R.B × P.S	23.49**	22.12**	25.23**	23.49**
R.B × F.C	14.35**	10.04**	35.83**	30.54**
R.B × D.K	21.15**	18.03**	56.58**	54.69**
D.K × R.C	14.16**	12.50**	34.00**	27.84**
D.K × A-95	-7.84**	-15.16**	-10.89**	-25.81**
D.K × N.G	3.42*	-2.65	-25.56**	-30.13**
D.K × D.N	9.02**	4.31**	16.23**	12.43**
D.K × P.S	14.16**	12.45**	14.73**	14.52**
D.K × F.C	15.68**	14.23**	23.66**	17.48**
D.K × R.B	21.59**	18.45**	100.37**	97.96**

MPH (%) = Mid-parent heterosis, BPH (%) = Better-parent heterosis

Table 6. Analysis of variance of combining ability, estimates of components of variance and their ratio for various traits in *B. napus* L.

Traits	Mean Squares				σ^2GCA	σ^2SCA	σ^2RCA	σ^2GCA/σ^2SCA
	GCA (df = 7)	SCA (df = 28)	RCA (df = 28)	Error (df = 63)				
Days to maturity	244.21**	39.32**	35.53**	0.06	15.25	39.13	17.67	0.38
Sec. branches plant[-1]	159.52**	61.63**	52.50**	0.38	6.18	34.39	26.06	0.18
Pods plant[-1]	4874.78**	7017.69**	8878.49**	2.57	126.24	3938.15	2437.96	0.04
Seeds pod[-1]	4.09**	3.50**	5.61**	0.03	0.25	3.45	2.79	0.07
Seed yield plant[-1]	43.34**	114.44**	153.40**	0.18	2.69	114.26	76.61	0.02

Table 7. General combining ability effects in eight parental genotypes of *B. napus* for various traits.

Genotypes	Days to maturity	Sec. branches plant[-1]	Pods plant[-1]	Seeds pod[-1]	Seed yield plant[-1]
Rustam Canola	0.63**	3.31**	9.92**	-0.51**	0.81**
Abasin-95	-0.54**	-0.44**	16.60**	-0.54**	0.97**
NIFA Gold	-0.50**	-3.29**	-28.10**	0.59**	-2.23**
Durr-e-NIFA	-0.66**	-2.54**	-1.26**	-0.35**	-0.46**
Punjab Sarsoon	-1.64**	4.82**	20.65**	0.31**	2.81**
Faisal Canola	2.87**	-0.90**	11.06**	-0.15**	0.29*
Rainbow	6.80**	-3.39**	-13.43**	-0.14**	-2.04**
Dunkled	-6.95**	2.41**	-15.44**	0.80**	-0.15
S.E.(gi)	0.10	0.14	0.37	0.04	0.09

For pods per plant, the variances owing to σ^2GCA (126.24), σ^2SCA (3938.15), and σ^2RCA (2437.96) depicted the ratio of 0.04 which also revealed the predominance of non-additive gene action (Table 6). Prevalence of non-additive genetic control for pods per plant in *B. juncea* was also reported in the earlier studies (Ali *et al.*, 2015). Similarly, Acharya and Swain (2004) also reported non-additive genetic effects for pods per plant in different populations of *B. juncea.* The preponderance of non-additive gene action was confirmed by the relative magnitude of variances due to σ^2GCA (0.25), σ^2SCA (3.45), σ^2RCA (2.79) and their ratio of σ^2GCA/σ^2SCA (0.07) for seeds per pod. Present results are in conformity to the earlier findings of Azizinia (2011) and Singh *et al.,* (2005) who reported the outstanding role of nonadditive gene action for controlling the seeds per pod in winter rapeseed and Indian mustard, respectively. A higher magnitude of σ^2SCA (114.26) than σ^2GCA (2.69) and σ^2RCA (76.61) and the ratio of σ^2GCA/σ^2SCA (0.02) revealed that inheritance in seed yield per plant was managed by non-additive gene action. In past studies, the prevalence of non-additive gene action for seed yield was also reported in different populations of *B. juncea* L. (Shrimali *et al.*, 2016; Singh *et al.*, 2010). Overall, the ratios of σ^2GCA/σ^2SCA were below unity which revealed the predominance of non-additive gene action for the inheritance of all the traits. The effects due to various components of combining ability i.e., GCA, SCA and RCA for parental genotypes, direct and reciprocal crosses are discussed as follows.

General combining ability: Earlier maturity is desirable, therefore, negative combining ability effects are useful in the development of rapeseed populations with early maturity. In present studies, five out of eight parental genotypes such as Dunkled (-6.95), Punjab Sarsoon (-

1.64), Durr-e-NIFA (-0.66), Abasin-95 (-0.54) and NIFA Gold (-0.50) exhibited negative GCA effects (Table 7). However, genotype Rainbow (6.80) exhibited maximum positive GCA effects followed by Faisal Canola (2.87) and Rustam Canola (0.63) for days to maturity. Secondary branches per plant is an important yield contributing traits in Brassica crops. Among the parental genotypes, the maximum positive GCA effects were recorded in genotype i.e., Punjab Sarsoon (4.82) followed by Rustam Canola (3.31) and Dunkled (2.41) for secondary branches per plant. However, other five genotypes revealed negative GCA effects ranging from -0.44 to -3.39, while maximum negative GCA effects were observed in genotype Rainbow (-3.39). For pods per plant, the positive GCA effects were observed in four parental genotypes ranging from 9.92 to 20.65 while maximum GCA effects were observed in Punjab Sarsoon (20.65) followed by Abasin-95 (16.60). The other four genotypes exhibited negative GCA effects ranging from -1.26 to -28.10 while maximum negative GCA effects were recorded by the genotype NIFA Gold (-28.10) followed by Dunkled (-15.44). Highest and desirable GCA effects with promising general combiners were reported among different populations of *B. juncea* for earliness, morphological and yield traits (Arifullah *et al.*, 2012; Shrimali *et al.*, 2016; Naheed *et al.*, 2017a, b).

The greater number of seeds per pod is one of the prime objectives in rapeseed breeding because it directly contributes to seed yield. Three out of eight parental genotypes showed positive GCA effects for seeds per pod (Table 7). Genotype Dunkled (0.80) showed maximum positive GCA effects followed by NIFA Gold (0.59) and Punjab Sarsoon (0.31) while maximum negative GCA effects were observed in parental genotype Abasin-95 (-0.54) for seeds per pod. In seed yield per plant, four out of eight parental genotypes revealed positive GCA effects ranging from 0.29 to 2.81, whereas maximum positive

GCA effects were recorded in parental genotype Punjab Sarsoon (2.81). The other four genotypes revealed negative GCA effects ranging from -0.15 to -2.23 while NIFA Gold showed maximum negative GCA effects (-2.23). The genotype Punjab Sarsoon was identified as best general combiner for seed yield and yield contributing traits with earliness followed by parental cultivar Abasin-95. For yield components and seed yield, the desirable positive GCA effects were reported in different populations of Indian mustard (Vaghela *et al.*, 2011; De *et al.*, 2009). Highest and desirable GCA effects with prominent general combiners were reported in various populations of *B. juncea* for earliness, morphological and yield traits (Gupta *et al.*, 2011; Parmar *et al.*, 2011).

Specific combining ability: For days to maturity, 14 each F_1 hybrids out of 28 showed negative and positive SCA effects, respectively (Table 8). However, the highest negative SCA effects were observed for F_1 hybrid Faisal Canola × Rainbow (-7.61) followed by Durr-e-NIFA × Punjab Sarsoon (-7.13) and identified as best specific combiners. In these promising F_1 hybrids, the low × low and high × high GCA parents were involved in the presentation of prominent SCA. The F_1 hybrid Dunkled × Rainbow revealed highest positive SCA effect (10.26) for earliness. For secondary branches per plant, 13 F_1 hybrids showed positive SCA effects, and highest positive SCA effects (9.61) were expressed by F_1 hybrid Durr-e-NIFA × Punjab Sarsoon followed by Faisal Canola × Rainbow (6.29) (Table 8). Hence, these F_1 hybrids involve low × high and low × low general combiners and could be considered as best specific combiners for secondary branches per plant. For secondary branches per plant, 15 F_1 hybrids revealed negative SCA effects while highest negative SCA values were observed in F_1 hybrid Punjab Sarsoon× Faisal Canola (-5.67). For pods per plant, 18 F_1 hybrids showed positive SCA effects where the highest positive SCA effects were observed for F_1 hybrid Abasin-95 × NIFA Gold (122.20) which involve high × low GCA parents. The negative SCA effects were noted in 10 F_1 hybrids while maximum negative SCA effects were observed in F_1 hybrid Rustam Canola × Abasin-95 (-84.51) for pods per plant. Nasim *et al.,* (2014) also observed significant and desirable SCA effects with low × low, low × high and high × high general combiners in the inheritance of earliness and yield traits in *B. napus* L. Similarly, Ali *et al.,* (2015) also reported prominent SCA effects for earliness, morphological and yield traits in *B. carinata* L.

For seeds per pod, 16 F_1 hybrids showed positive SCA effects whereas maximum positive SCA effects were recorded for F_1 hybrid Dunkled × Rainbow (1.84) followed by Abasin-95 × Punjab Sarsoon (1.83), and these F_1 hybrids involve high × low and low × high GCA parents, respectively (Table 8). The genotype NIFA Gold × Durr-e-NIFA (-1.43) exhibited maximum negative SCA effects for seeds per pod. For seed yield per plant, 16 out of 28 F_1 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 × Punjab Sarsoon (12.61) for seed yield. However, maximum negative SCA effects were expressed by F_1 hybrid Rustam Canola × Abasin-95

(-11.15) for seed yield per plant. The F_1 hybrids i.e., Dunkled × Rainbow and Rustam Canola × Punjab Sarsoon were considered as best specific cross combinations with promising mean performance and involve low × low and high × high GCA parents for seed yield. Current results are in agreement with the earlier findings of Shrimali *et al.,* (2016), Sincik *et al.,* (2014) and Suchindra and Singh (2006) who also found significant SCA effects for various morphological and yield traits in rapeseed. However, Singh *et al.,* (2010) and Acharya and Swain (2004) noted the equal importance of both GCA and SCA for morphological and yield traits in *B. juncea* genotypes. In Ethiopian mustard, the GCA effects were prominent for morphological and yield traits (Mohammad *et al.*, 2011).

Reciprocal combining ability: For days to maturity, 17 out of 28 F_1 reciprocal hybrids showed negative maternal effects whereas maximum negative effects were recorded for F_1 reciprocal hybrid Dunkled × Faisal Canola (-8.30) followed by Punjab Sarsoon × Rustam Canola (-7.00) (Table 9). These promising F_1 reciprocal hybrids involve high × low GCA parents in the presentation of promising RCA effects for earliness. For secondary branches per plant, 15 F_1 reciprocal hybrids revealed positive RCA effects, whereas the highest positive reciprocal effects were recorded in F_1 reciprocal hybrid Durr-e-NIFA × NIFA Gold (8.55) followed by Faisal Canola × Abasin-95 (7.95). These reciprocal F_1 hybrids were considered as best specific cross combinations which involved low × low general combiners for secondary branches per plant. Significant and desirable reciprocal effects were reported in F_1 reciprocal hybrids of rapeseed for various morphological and yield traits (Naheed *et al.*, 2017a, b).

For pods per plant, 13 F_1 reciprocal hybrids showed positive RCA effects whereas F_1 reciprocal hybrid Faisal Canola × Abasin-95 showed highest positive RCA effects (123.45) which involved high × high GCA parents (Table 9). However, maximum negative RCA effects were recorded in F_1 reciprocal hybrid Faisal Canola × Rustam Canola (-110.55) for pods per plant. The eight reciprocal F_1 hybrids showed positive RCA effects for seeds per pod. The maximum maternal effects were observed in F_1 reciprocal hybrid Abasin-95 × Rustam Canola (2.30) followed by F_1 reciprocal hybrid Rainbow × Durr-e-NIFA (0.80). Hence, these F_1 hybrids were considered as best specific combiners for seeds per pod which involved low × low and low × high general combiners (Table 8). For seed yield per plant, 13 reciprocal F_1 hybrids noted with positive RCA effects. However, the highest positive maternal effects were recorded in F_1 reciprocal hybrid Dunkled × Punjab Sarsoon (15.09) followed by F_1 hybrid Dunkled × NIFA Gold (14.61) and were considered as best specific combiners. These promising F_1 hybrids involve low × high and low × low GCA parents showed the best performance in the presentation of desirable RCA effects for seed yield per plant. However, maximum negative RCA effects were recorded for F_1 hybrid Faisal Canola × Rustam Canola (-24.79). Highly significant reciprocal effects were reported in various populations of *B. napus* and *B. Juncea* for morphological and yield traits (Akbar *et al.*, 2008; Arifullah *et al.*, 2012).

Table 8. Specific combining ability effects in 8 × 8 F₁ diallel hybrids of *B. napus* for various traits.

F₁ Hybrids	Days to maturity	Secondary branches plant⁻¹	Pods plant⁻¹	Seeds pod⁻¹	Seed yield plant⁻¹
R.C × A-95	-4.73**	-2.23**	-84.51**	-0.80**	-11.15
R.C × N.G	-3.21**	1.67**	-25.21**	-0.23	-3.82**
R.C × D.N	6.85**	-2.68**	28.10**	-0.13	2.98**
R.C × P.S	3.93**	6.41**	108.14**	0.15	12.61**
R.C × F.C	1.07**	5.49**	82.78**	0.57**	12.31**
R.C × R.B	-0.86**	1.22**	-25.88**	-0.55**	-5.33**
R.C × D.K	-3.61**	0.52	10.53**	1.02**	3.34**
A-95 × N.G	4.60**	-2.93**	122.20**	-0.85**	11.81**
A-95 × D.N	-1.19**	-4.63**	10.97**	-0.71**	1.53**
A-95 × P.S	2.24**	4.51**	12.45**	1.83**	4.60**
A-95 × F.C	-2.47**	-3.36**	13.70**	-1.36**	-4.17**
A-95 × R.B	2.30**	-2.73**	-11.71**	-0.63**	-2.70**
A-95 × D.K	-0.75*	3.72**	2.40	-1.21**	-1.55**
N.G × D.N	2.72**	2.32**	-27.33**	-1.43**	-4.01**
N.G × P.S	-0.89**	-4.94**	12.70**	1.15**	3.24**
N.G × F.C	3.14**	-5.31**	-5.85**	0.17	-0.34
N.G × R.B	-1.04**	-2.33**	-20.61**	1.00**	-1.21**
N.G × D.K	-7.04**	-1.38**	-20.90**	0.02	-2.07**
D.N × P.S	-7.13**	9.61**	12.62**	0.90**	1.05**
D.N × F.C	4.96**	-3.16**	56.01**	-1.24**	3.72**
D.N × R.B	0.28	-0.98	12.70**	1.24**	3.46**
D.N × D.K	-1.03**	4.02**	5.61**	0.21	0.66
P.S × F.C	1.14**	-5.67**	1.95	0.25	0.24
P.S × R.B	3.46**	-0.38	-41.86**	-1.32	-7.98**
P.S × D.K	-4.54**	3.86**	34.20**	0.10	4.54**
F.C × R.B	-7.61**	6.29**	23.28**	1.09**	5.95**
F.C × D.K	1.29**	-1.91**	-75.76**	1.36**	-8.15**
D.K × R.B	10.26**	4.37**	105.33**	1.84**	15.48**
SE₍ₛᵢⱼ₎	0.27	0.39	1.00	0.12	0.26

Table 9. Reciprocal combining ability effects in 8 × 8 F₁ diallel hybrids of *B. napus* for various traits.

F₁ Hybrids	Days to maturity	Sec. branches plant⁻¹	Pods plant⁻¹	Seeds pod⁻¹	Seed yield plant⁻¹
A-95 × R.C	-3.65**	-4.70**	-83.50**	2.30**	-5.38**
N.G × R.C	-0.40	-1.65**	-13.10**	-0.50**	-1.03**
N.G × A-95	-2.55**	1.50**	-40.70**	0.35*	-3.11**
D.N × P.S	-2.00**	4.05**	-52.15**	-3.95**	-13.79**
D.F × A-95	2.50**	-4.35**	-58.90**	-1.35**	-9.00**
D.N × N.G	-6.25**	8.55**	107.50**	0.55**	12.57**
P.S × R.C	-7.00**	-0.20	30.30**	-1.60**	0.51
P.S × A-95	0.95	-2.95**	-39.90**	-0.75**	-4.90**
P.S × N.G	-4.45**	-10.15**	-15.05**	-0.30*	-1.13**
P.S × D.N	3.25**	-5.35**	-91.90**	0.70**	-8.49**
F.C × R.C	-1.05*	-10.25**	-110.55**	-3.45**	-24.79**
F.C × A-95	3.35**	7.95**	123.45**	-4.20**	3.40**
F.C × N.G	-5.60**	4.15**	17.30**	-0.75**	2.68**
F.C × D.N	-5.05**	2.35**	-43.20**	-0.60**	-5.18**
F.C × P.S	6.55**	4.30**	-106.45**	-0.35**	-13.41**
R.B × R.C	-4.15**	3.40**	47.40**	-0.15	6.46**
R.B × A-95	-3.35**	-2.90**	-32.65**	-1.95**	-6.58**
R.B × N.G	1.75**	6.55**	10.75**	-0.50**	2.54**
R.B × D.N	-0.40	0.85	-6.10**	0.80**	0.98**
R.B × P.S	0.70	-2.10**	44.35**	-3.70**	-3.17**
R.B × F.C	-4.75**	4.45**	32.60**	-0.45**	2.31**
D.K × R.C	8.55**	4.40**	39.80**	-0.65**	3.48**
D.K × A-95	-5.15**	0.85	72.75**	0.60**	8.12**
D.K × N.G	0.20	-3.20**	100.75**	0.75**	14.61**
D.K × D.N	-2.55**	2.65**	63.80**	-0.90**	6.08**
D.K × P.S	1.65**	6.15**	119.40**	0.05	15.09**
D.K × F.C	-8.30**	-4.85**	-32.15**	-0.25	-5.24**
D.K × R.B	1.80**	-7.95**	-52.25**	-0.05	-7.10**
S.E₍ᵣᵢⱼ₎	0.43	0.62	1.13	0.13	0.30

Conclusion

Comparatively, the variances of SCA were higher in magnitude than GCA which revealed the predominance of non-additive gene action for the inheritance of all the traits studied. Parental cultivars Punjab Sarsoon and Dunkled were identified as best general combiners and performed better for the majority of the traits. Therefore, the F_1 progenies of these general combiners i.e., Dunkled × Rainbow, Abasin-95 × NIFA Gold, Durr-e-NIFA × Punjab Sarsoon, Rustam Canola × Punjab Sarsoon and Punjab Sarsoon × Abasin-95 revealed best mean performance for earliness, morphological and yield traits and these genotypes could be used in future breeding programs.

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