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INHERITANCE STUDIES THROUGH COMBINING ABILITY FOR MORPHOLOGICAL AND YIELD TRAITS IN F_1 POPULATIONS OF *BRASSICA NAPUS* L.

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ABSTRACT

Inheritance study was carried out through combining ability for identification of potential parental cultivars, F_1 hybrids, and nature of gene action involved in morphological and yield traits in 8 × 8 diallel crosses of *Brassica napus* L. Genotypes revealed highly significant differences for all the traits i.e., days to 50% flowering, primary branches per plant, pods per main raceme, pod length and seed yield per plant. Mean squares due to general (GCA), specific (SCA) and reciprocal combining ability (RCA) were highly significant for all the studied traits, which revealed imperative role of dominance, additive, and maternal effects. Comparatively higher values of σ^2SCA than σ^2GCA and σ^2RCA with less than unity ratios of σ^2GCA/σ^2SCA showed the predominance of non-additive gene action for the inheritance of the studied traits followed by maternal effects. Parental cultivars, Abassin-95 and Punjab Sarsoon were identified as best general combiners and in combination with other genotypes performed better for majority of the traits. The F_1 hybrids i.e., Rustam Canola × Faisal Canola, Punjab Sarsoon × Dunkled and Dunkled × Rainbow showed prominent SCA and best mean performance for studied traits. Therefore, the involvement of high and low general combiners performed well in the synthesis of superior F_1 populations of rapeseed.

Key words: Diallel crosses; GCA and SCA; Additive and non-additive gene action; Morphological and yield traits; *Brassica napus* L.

INTRODUCTION

Rapeseed (*Brassica napus* L.) is an important oilseed crop of the world and belongs to family *Cruicifereae.* This family contains 375 genera and 3200 species. The species of genus Brassica are classified into two major groups commonly known as rapeseed and mustard. Rapeseed mainly includes *B. napus* L.*, B. rapa* L.*, B. nappobrassica* L. while, mustard includes *B. nigra* L.*, B. carinata* L.*, B. juncea* L.*, B. hirta* L. and *B. arvensis* L. (Zhou *et al*., 2006). Rapeseed and mustard being traditional oilseed crops of Pakistan are grown over a large area under both irrigated and rain-fed conditions (Khan *et al*., 2004). *Brassica napus* L. is the most important species, its cultivation as a seed crop is limited to Khyber Pakhtunkhwa province and some areas of Punjab province of Pakistan (Saleem *et al*., 2015)

In Pakistan, during 2016, rapeseed and mustard were grown on an area of 24.7 thousand hectares and production was 23.2 thousand tons with average yield of 939.27 kg ha^{-1} (FAO Statistics, 2016). The national average yield of this crop is quite lower than its potential yield. Many factors responsible for its low yield include non-availability of high yielding cultivars, water scarcity, ignorance of modern technology, extreme weather conditions, climatic change, and increasing population, etc. To bridge the gap between local production and import of edible oil, it is imperative to develop improved cultivars of oilseed crops, especially in Brassica (Ghosh and Gulati*,* 2002).

Combining ability is a biometrical procedure used for analysis of diallel crosses in a universal theoretical form (Griffing, 1956) in which an individual genotype transmit its performance to the offspring (Sincik *et al.,* 2015). Success of plant breeding programs for development of high yielding cultivars requires the knowledge about genetic potential of different genotypes, types of gene action, their relative contribution to the genetic variance and estimation of general (GCA) and specific combining ability (SCA) effects. Combining ability determine the ability of the genotypes to be included or not in a future breeding program on the basis of their GCA and SCA effects (Zhou *et al*., 2006).

Many researchers reported highly significant mean squares due to GCA, SCA and RCA effects for yield and its components, signifying the preponderance of both additive and non-additive gene action in the inheritance of morphological and yield traits (Dholu *et al.,* 2014; Nasim *et al*., 2014). Other studies showed significant GCA and SCA effects with additive and non-additive gene action for yield traits in different species of Brassica (Muhammad *et al.,* 2014; Ali *et al.,* 2015). Keeping in view its economic importance, a research program was undertaken to evaluate the genetic variances and effects due to GCA, SCA and RCA through combining ability analysis for morphological and yield traits in a set of 8 × 8 diallel crosses of *B. napus* L.

MATERIALS AND METHODS

Breeding material and procedure: Breeding material comprised of a set of eight diverse *Brassica napus* L. genotypes i.e., Rustam Canola (R.C), Abassin-95 (A-95), NIFA Gold (N.G), Dure-NIFA (D.N), Punjab Sarsoon (P.S), Faisal Canola (F.C), Rainbow (R.B) and Dunkled (D.K) which were 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, 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 in two rows, with a row length of 10 m, and rows' and plants' spacing of 5 m and 30 cm, respectively. Recommended and uniform cultural practices were applied to all the genotypes to avoid field variations and environmental influences.

Ten randomly selected plants were used for recording the data on single plant basis for studied traits i.e., days to 50% flowering, primary branches per plant, pods per main raceme, pod length and seed yield per plant. All the data were analyzed using 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 combining ability analysis was carried out to determine the various genetic effects due to GCA, SCA and RCA (Griffing, 1956).

RESULTS AND DISCUSSION

Highly significant differences were observed among parental genotypes and their F_1 hybrids for all the studied traits (Table 1). Genotypes showed the existence of greater genetic variability which confirmed to be further studied through combining ability analysis for selection of promising parental genotypes and their F_1 hybrids. Significant differences were reported among the different populations of *B. napus* L. (Khan *et al*., 2006; Amiri-Oghan *et al.,* 2009) and *B. rapa* (Jahan *et al*., 2014) for morphological and yield traits. Similarly, significant variation was observed among parental genotypes and their F_1 populations for days to flowering, morphological and yield related traits in *B. juncea* L. (Singh *et al*., 2005; Singh and Singh, 2008).

Mean performance of parental genotypes and F_1 hybrids: Days to 50% flowering varied from 135.3 to 119.3 days among parents, while in F_1 hybrids the said range was 110.3 to 141.3 days (Table 2). By comparing the means of the parents and their hybrids, the parental genotypes (127.8 days) took fewer days to flowering than their F_1 populations (128.8 days). However, F_1 hybrid D.K × R.C (110.3 days) was noted with fewer days to flowering, and it was found at par with two other hybrid combinations i.e., D.K × N.G (113.7 days) and D.K × P.S (114.2 days). The F_1 hybrid F.C × D.N (141.3 days) manifested maximum days to 50% flowering and was found at par with two other F_1 hybrids viz., R.B × A-95 (140.6 days) and R.B × D.K (140.6 days) followed by F.C × N.G (139.9 days) and R.B × R.C (139.6 days). Early flowering is one of the most important traits for selecting early maturing and high yielding genotypes in majority of crop plants. Early flowering provides sufficient time for grain filling which results into bolder/heavier seed and ultimately higher seed yield. Previous studies also reported highly significant mean squares and greater genetic variability among various populations of rapeseed for days to flowering (Acharya and Swain, 2004; Akbar *et al.,* 2008; Amiri-Oghan *et al.,* 2009; Ali *et al*., 2015).

Primary branches per plant varied from 3.6 to 6.9 and 3.7 to 10 among parental genotypes and F_1 hybrids, respectively (Table 2). By comparing the overall means, F_1 populations (6.0) showed more primary branches per plant than their parental genotypes (5.1). In overall means of parental genotypes and F_1 hybrids, a greater number of primary branches per plant were observed in F_1 hybrid F.C × R.C and it was found at par with two other F_1 hybrids P.S × D.K (8.6) and D.K × R.B (8.5). A minimum number of primary branches per plant was noted in parental genotype Punjab Sarsoon (3.6) and was found similar with two other F_1 hybrids F.C × A-95 (3.7) and R.B × N.G (3.8). Primary branches per plant is an important trait and play an imperative role in seed yield in Brassica species. More primary branches coupled with pods may lead to ultimately increased seed yield. Highly significant differences with greater genetic variability were observed among Brassica genotypes for primary branches per plant (Azadgoleh *et al.*, 2009; Gangapur *et al.*, 2009).

Mean values for pods per main raceme ranged from 42.0 to 65.3 in parental genotypes, while in F_1 hybrids the said range was 33.3 to 80.8 (Table 2). By comparing the overall means, F_1 populations showed more pods per main raceme (59.4) than their parental genotypes (51.2). Overall mean performance showed that F_1 hybrid F.C × R.C (80.8) revealed higher number of pods per main raceme followed by P.S × D.K (78.8) and it was found same with three other F_1 hybrids P.S × A-95 (77.5), R.C × D.K (75.5) and R.C × F.C (75.2). However, the minimum number of pods per main raceme was revealed by F_1 hybrid D.N × N.G (33.3) and a parental genotype Faisal Canola (42.0). Pods per main raceme is one of the major seed yield contributing factor, therefore, for increased seed yield, the plants with greater number of pods on main raceme are preferred.

Table 1. Analysis of variance for the studied traits in an 8 × 8 diallel cross of *B. napus* L.

Traits	Mean Squares			CV (%)
	Replication (d.f. = 1)	Genotype (d.f. = 63)	Error (d.f. = 63)	
Days to 50% flowering	22.445	123.267**	0.236	0.378
Primary branches plant^{-1}	1.112	3.609**	0.210	7.793
Pods main raceme^{-1}	92.480	261.374**	7.338	4.639
Pod length	0.002	0.729**	0.133	4.884
Seed yield plant^{-1}	91.333	247.716**	0.721	1.906

** Significant at P≤0.01, d.f. = degree of freedom

Table 2. Mean performance of parents and hybrids in an 8 × 8 diallel cross of *B. napus* L. for the studied traits.

Parental genotypes & F_1 hybrids	Days to 50% flowering	Primary branches plant^{-1}	Pods main raceme^{-1}	F_1 hybrids	Days to 50% flowering	Primary branches plant^{-1}	Pods main raceme^{-1}
Rustam Canola (R.C)	130.9	4.7	44.0	D.N × R.B	134.8	7.5	44.9
Abassin-95 (A-95)	127.5	6.9	65.3	D.N × D.K	117.6	6.5	54.0
NIFA Gold (N.G)	129.5	5.5	61.2	P.S × R.C	138.9	6.4	45.9
Durr-e-NIFA (D.N)	121.1	5.1	43.9	P.S × A-95	127.9	6.5	77.5
Punjab Sarsoon (P.S)	126.1	3.6	55.4	P.S × N.G	130.5	7.8	56.6
Faisal Canola (F.C)	132.8	5.6	42.0	P.S × D.N	116.6	8.1	43.7
Rainbow (R.B)	135.3	4.5	54.4	P.S × F.C	136.6	7.0	47.9
Dunkled (D.K)	119.3	4.7	44.1	P.S × R.B	138	7.8	56.4
R.C × A-95	119.6	6.9	52.7	P.S × D.K	117.5	8.6	78.8
R.C × N.G	120.0	6.7	64.6	F.C × R.C	135.3	10.0	80.8
R.C × D.N	132.5	6.3	63.7	F.C × A-95	125.4	3.7	58.4
R.C × P.S	124.0	7.2	45.5	F.C × N.G	139.9	6.2	45.8
R.C × F.C	131.2	5.5	75.2	F.C × D.N	141.3	4.4	73.9
R.C × R.B	130.8	5.4	65.3	F.C × P.S	124.3	4.7	56.2
R.C × D.K	127.2	5.6	75.5	F.C × R.B	125.9	5.3	72.7
A-95 × R.C	127.8	5.7	54.8	F.C × D.K	118.1	6.3	43.9
A-95 × N.G	129.5	6.4	70.6	R.B × R.C	139.6	4.6	51.3
A-95 × D.N	129.1	4.9	57.5	R.B × A-95	140.6	4.5	65.9
A-95 × P.S	130.3	6.5	62.2	R.B × N.G	132.5	3.8	65.9
A-95 × F.C	133.1	5.4	74.5	R.B × D.N	135.3	4.5	74.3
A-95 × R.B	134.0	4.8	66.7	R.B × P.S	136.7	7.7	54.7
A-95 × D.K	115.6	7.4	66.5	R.B × F.C	136	4.5	49.5
N.G × R.C	126.5	4.7	68.2	R.B × D.K	140.6	5.6	43.6
N.G × A-95	135.2	5.8	55.1	D.K × R.C	110.3	5.2	74.7
N.G × D.N	124.1	6.3	57.8	D.K × A-95	126.1	4.9	53.9
N.G × P.S	121.5	8.3	49.1	D.K × N.G	113.7	4.5	44.4
N.G × F.C	129.0	7.5	53.6	D.K × D.N	122.5	5.6	47.9
N.G × R.B	136.0	5.4	49.8	D.K × P.S	114.2	5.1	46.3
N.G × D.K	115.5	5.0	65.0	D.K × F.C	134.4	5.5	54.1
D.N × R.C	137.6	5.2	69.8	D.K × R.B	137.8	8.5	76.3
D.N × A-95	124.1	6.4	64.0	Parental means	127.8	5.1	51.2
D.N × N.G	136.7	6.1	33.3	F_1 hybrid means	128.8	6.0	59.4
D.N × P.S	122.8	4.7	65.2	$LSD_{0.05}$	0.972	0.84	0.73
D.N × F.C	131.1	4.5	61.3				

Highly significant variations were reported among F_1 populations and their parental genotypes of rapeseed for pods per main raceme (Hamid, 2007; Rameah *et al.*, 2003).

Mean values of pod length ranged from 6.05 to 8.47 cm and 6.50 to 8.87 cm in the parental genotypes and their F_1 hybrids, respectively (Table 3). Overall, F_1 population (7.58 cm) revealed longer pods than their parental cultivars (6.82 cm). The overall performance showed that F_1 hybrid F.C × R.C (8.87 cm) revealed highest pod length and it was found similar in performance with two other hybrids P.S × D.K (8.55 cm) and D.K × R.B (8.54 cm) followed by parental genotype Abassin-95 (8.47 cm). Minimum pod length was observed in the parental cultivar Dunkled (6.05) followed by F_1 hybrid D.K × D.N (6.50 cm) and exposed as poor hybrid followed by R.C × A-95 (7.02 cm). Pod length is an important yield contributing trait having the direct association with seeds per pod. Longer pods can produce more seeds, thus, result in greater seed yield. Significant variation was observed among *B. napus* L. populations for pod length (Firoz *et al.*, 2008).

Seed yield per plant ranged from 31.9 to 48.2 g for parental genotypes, while in F_1 hybrids the said range was 25.3 to 82.8 g (Table 3). Overall comparison showed that parental genotypes produced less seed yield per plant (35.8 g) than their F_1 populations (45.8 g). Overall mean values revealed that higher seed yield was produced by F_1 hybrid F.C × R.C (82.8 g) and it was identified as the best cross among all the cross combinations followed by two other F_1 hybrids i.e., P.S × D.K (66.9 g) and D.K × R.B (64.9 g). Poor performance and least seed yield per plant was shown by F_1 hybrid D.N × N.G (25.3 g) followed by D.K × N.G (25.5 g). Majority of the rapeseed breeding programs are focused to increase seed yield, whereas seed yield is dependent on different morphological and yield related traits. Highly significant differences with sufficient genetic variability were reported in parental genotypes and their F_1 populations of rapeseed for seed yield (Nasim *et al.*, 2014).

Combining ability analysis: Analysis of variance for combining ability revealed that mean squares due to GCA, SCA and RCA were highly significant for all the studied traits in the tested genotypes indicating the important role of additive, nonadditive and maternal gene effects (Table 4). However, SCA mean squares were greater in magnitude than GCA and RCA for primary branches per plant, pods per main raceme and pod length. The magnitude of GCA effect was found greater than SCA and RCA for days to 50% flowering. In the case of seed yield per plant, mean squares due to RCA were greater than GCA and SCA which being influenced by maternal effects. Results further enunciated that due to the preponderance of SCA and RCA effects, the non-additive and maternal effects were more important in the inheritance of these traits. In previous studies, mean squares due to GCA and SCA were significant for morphological and yield traits in parental genotypes and F_1 populations of rapeseed (Singh and Singh, 2008; Singh *et al.*, 2005). Highly significant mean squares were observed due to GCA and SCA while non-significant for RCA for various morphological and yield traits in F_1 populations of *B. napus* (Sincik *et al.,* 2015). Trait and genotype-wise genetic effects due to GCA, SCA and RCA are discussed as follows.

Early flowering is prime objective of the rapeseed breeding program, therefore, negative GCA and SCA effects are found desirable for days to 50% flowering. In eight parental genotypes, the GCA effects ranged from -6.88 to +6.83 (Table 5). Among parents, five out of eight genotypes viz., Dunkled (-6.83), Punjab Sarsoon (-1.69), Durr-e-NIFA (-0.67), NIFA Gold (-0.59) and Abassin-95 (-0.36), revealed desirable negative GCA effects indicating less days to 50% flowering. However, higher positive GCA effect of was recorded for parental genotype Rainbow (6.88) followed by Faisal Canola (3.01) and Rustam Canola (0.25). The cultivar Dunkled was found to be the best general combiner for days to 50% flowering which was also confirmed by its mean performance, and took fewer days to 50% flowering. Earlier studies also reported highly significant negative GCA effects for days to flowering and identified early maturing parental genotypes in different rapeseed populations (Acharya and Swain, 2004; Akbar *et al.,* 2008; Ali *et al*., 2015).

For SCA effects, the 28 F_1 hybrids were ranging from -0.41 to 10.46 for days to 50% flowering (Table 6). Highest negative SCA effects were observed for the F_1 hybrid F.C × R.B (-7.63) followed by N.G × D.K (-6.67), and hence, proved as best specific cross combinations for days to 50% flowering. These two promising F_1 hybrids involve low × low and high × high GCA parental genotypes, produced F_1 populations with less days to 50% flowering. For RCA effects, the reciprocal crosses ranged from -2.05 to 8.45 (Table 7). The 17 out of 28 F_1 reciprocal hybrids showed negative RCA effects whereas maximum negative RCA effect was recorded for reciprocal hybrid D.K × F.C (-8.15) followed by P.S × R.C (-7.45). For days to flowering, variances due to general, specific and reciprocal combining ability were 15.28, 40.07 and 18.67, respectively in this set of rapeseed genotypes (Table 8). Comparatively higher value of σ^2SCA than σ^2GCA with a ratio of σ^2GCA/σ^2SCA (0.38) showed the predominance of non-additive gene action. In earlier studies, the predominant role of non-additive gene effects was reported in the inheritance of days to 50% flowering in hybrid populations of *B. napus* which also involve high × high and low × high GCA parents (Nasim *et al*., 2014). However, an important role of additive gene effects was also mentioned for days to 50% flowering in F_1 populations of *B. napus* (Amiri-Oghan *et al*., 2009; Ishaq and Raziuddin, 2016). The possible reason for the discrepancies between the present and past findings could be the varied genetic makeup of Brassica genotypes environments and genotype by environment interaction effects.

For primary branches per plant, the GCA effects for parental genotypes ranged from -0.03 to +0.60 (Table

5). Three parental genotypes showed positive GCA effects in which higher GCA value was recorded for parental genotype Punjab Sarsoon (0.60) followed by NIFA Gold (0.08) and Rustam Canola (0.04). These parental genotypes were considered as best general combiners for primary branches per plant, as also confirmed by their mean performance for the said trait. Remaining five genotypes had negative GCA effects i.e., Rainbow (-0.33), Durr-e-NIFA (-0.18), Faisal Canola (-0.15), Abassin-95 and Dunkled (-0.03). Earlier findings also revealed significant and desirable GCA effects of parental genotypes in *B. napus* L. for primary branches per plant (Suchindra and Singh, 2006).

Table 3. Mean performance of parents and hybrids in an 8 × 8 diallel cross of *B. napus* L. for the studied traits.

Parental genotypes & F_1 hybrids	Pod length (cm)	Seed yield plant^{-1} (g)	F_1 hybrids	Pod length (cm)	Seed yield plant^{-1} (g)
Rustam Canola (R.C)	5.99	35.3	D.N × R.B	7.20	46.5
Abassin-95 (A-95)	8.47	48.2	D.N × D.K	7.12	50.7
NIFA Gold (N.G)	8.14	36.5	P.S × R.C	7.51	60.3
Durr-e-NIFA (D.N)	5.68	34.3	P.S × A-95	7.46	57.8
Punjab Sarsoon (P.S)	6.70	31.9	P.S × N.G	7.82	49.5
Faisal Canola (F.C)	5.75	35.6	P.S × D.N	7.05	56.5
Rainbow (R.B)	7.80	32.8	P.S × F.C	7.38	34.5
Dunkled (D.K)	6.05	32.0	P.S × R.B	7.75	34.2
R.C × A-95	7.02	29.8	P.S × D.K	8.55	66.9
R.C × N.G	7.35	38.3	F.C × R.C	8.87	82.8
R.C × D.N	7.70	34.1	F.C × A-95	7.68	38.3
R.C × P.S	8.37	61.3	F.C × N.G	7.46	39.6
R.C × F.C	7.30	33.2	F.C × D.N	7.69	53.3
R.C × R.B	7.04	44.5	F.C × P.S	7.57	61.3
R.C × D.K	7.03	52.1	F.C × R.B	7.87	51.1
A-95 × R.C	7.53	40.6	F.C × D.K	7.56	31.3
A-95 × N.G	7.40	52.0	R.B × R.C	7.34	31.6
A-95 × D.N	8.25	37.6	R.B × A-95	7.64	47.4
A-95 × P.S	7.67	48.0	R.B × N.G	7.59	36.6
A-95 × F.C	7.77	45.1	R.B × D.N	7.72	44.6
A-95 × R.B	7.19	34.2	R.B × P.S	7.51	40.5
A-95 × D.K	7.39	51.9	R.B × F.C	7.77	46.5
N.G × R.C	7.57	40.4	R.B × D.K	7.91	50.8
N.G × A-95	7.09	58.2	D.K × R.C	7.42	45.1
N.G × D.N	7.75	50.4	D.K × A-95	7.85	35.7
N.G × P.S	7.30	47.3	D.K × N.G	7.60	25.5
N.G × F.C	7.65	44.9	D.K × D.N	6.50	38.5
N.G × R.B	7.60	41.6	D.K × P.S	8.42	36.7
N.G × D.K	7.58	54.7	D.K × F.C	7.50	41.8
D.N × R.C	7.77	61.7	D.K × R.B	8.54	64.9
D.N × A-95	7.42	55.6	Parental means	6.82	35.8
D.N × N.G	7.69	25.3	F_1 hybrid means	7.58	45.8
D.N × P.S	7.09	39.5	$LSD_{0.05}$	0.16	1.7
D.N × F.C	7.62	42.9			

Table 4. Analysis of variance of combining ability for the studied traits in *B. napus* L.

Traits	Mean Squares			
	GCA (d.f. = 7)	SCA (d.f. = 28)	RCA (d.f. = 28)	Error (d.f. = 126)
Days to 50% flowering	244.59**	40.13**	37.39**	0.06
Primary branches plant^{-1}	1.21**	2.07**	1.68**	0.05
Pods main raceme^{-1}	103.18**	137.55**	130.69**	1.83
Pod length	0.33**	0.62**	0.11**	0.03
Seed yield plant^{-1}	43.34**	114.44**	153.40**	0.18

** Significant at $P \leq 0.01$ d.f. = degree of freedoms

For primary branches per plant, the SCA effects ranged from -0.02 to 1.97 (Table 6). Highest positive SCA effects were observed in F_1 hybrid R.C × F.C (1.97) followed by P.S × R.B (1.62). These two F_1 populations also showed best mean performance, and proved as best specific combinations which involve high × low GCA parental genotypes. However, the highest negative SCA effects were expressed by F_1 hybrid N.G × D.K (-1.19).

RCA effects ranged from -0.75 to 1.75 and highest positive RCA values were recorded for reciprocal hybrid D.K × P.S (1.75) which showing the involvement of maternal effects in the inheritance of said trait (Table 7). Variances due to GCA, SCA and RCA were 0.05, 1.13 and 0.81, respectively (Table 8). The comparatively higher value of σ^2SCA than σ^2GCA predicted the predominance of non-additive gene action as confirmed by the ratio of σ^2GCA/σ^2SCA (0.04). Equal share and importance of additive and non-additive gene control were reported for primary branches in *B. juncea* L. (Acharya and Swain, 2004). However, some studies revealed equal importance of additive and non-additive control for primary branches per plant in *B. juncea* (Singh and Dixit, 2007). The contradiction in the findings might be due to varied genetic makeup of Brassica genotypes and the environment where grown.

For pods per main raceme, the GCA effects ranged from 42.00 to 65.30 (Table 5). Parental genotype Abassin-95 with higher positive GCA effects (65.30) appeared to be the best general combiner followed by NIFA Gold (61.20) and Punjab Sarsoon (55.40). Highly significant GCA, SCA and reciprocal effects were reported with desirable GCA effects for pods per main raceme in parental genotypes and F_1 populations of *B. napus* L. (Suchindra and Singh, 2006; Sincik *et al*., 2015).

The SCA effects ranged from 43.65 to 78.81 for pods per main raceme (Table 6). Highest positive SCA effects were observed for cross P.S × D.K (78.81) followed by R.C × D.K (75.54) and R.C × F.C (75.20). Therefore, these F_1 hybrids could be considered as the best specific cross combinations with promising mean performance which involve high × high GCA parents. For RCA effects, the 28 F_1 reciprocal hybrids ranged from -15.9 to 15.0 (Table 7). Highest positive RCA effects were recorded for F_1 hybrid D.K × R.B (80.81). Variances due to GCA, SCA and RCA were 1.99, 76.19 and 64.43, respectively (Table 8). The comparatively higher value of σ^2SCA than σ^2GCA with a σ^2GCA/σ^2SCA ratio of 0.03 showed the preponderance of non-additive gene action for pods per main raceme. Non-additive control of morphological traits including pods per main raceme was reported in various hybrid populations of Brassica species (Acharya and Swain, 2004; Ali *et al*., 2015). Non-additive genetic control was also reported in F_1 populations of *B. napus* L. (Sabaghnia *et al*., 2010).

Parental genotypes GCA ranged from 5.68 to 8.47 for pod length (Table 5). Higher GCA effects were recorded for genotype Abassin-95 (8.47) followed by NIFA Gold (8.14) while, minimum GCA values were noticed for parental cultivar Durr-e-NIFA (5.68) followed by Rustam Canola (5.99). Genotype Abassin-95 with greater GCA values appeared as good general combiner, while Durr-e-NIFA appeared as poor general combiner among the tested parental genotypes for pod length. Highly significant positive GCA, SCA and RCA effects were reported for pod length in rapeseed genotypes (Singh *et al.,* 2005).

For pod length, the SCA values for F_1 hybrids were ranged from 7.02 to 8.55 (Table 6). The highest positive SCA effects were observed in F_1 hybrid P.S × D.K (8.55) followed by R.C × P.S (8.37) and A-95 × D.K (8.25). Hence, these F_1 hybrids were considered as best specific cross combinations with a remarkable mean performance for pod length and involve high × high GCA parents. For pod length, the RCA effects were ranging from -0.8 to 0.4 (Table 7). Among reciprocal hybrids, the highest RCA effects attained by reciprocal hybrid F.C × R.C (8.87) followed by D.K × R.B (8.54) and D.K × P.S (8.42). Variances due to σ^2GCA, σ^2SCA and σ^2RCA were 0.02, 0.33 and 0.04, respectively (Table 8). Higher SCA variance than GCA and ratio of σ^2GCA/σ^2SCA (0.06) showed the predominance of non-additive gene action for pod length. Prevalence of non-additive gene action was reported for pod length and other morphological traits in different rapeseed populations (Singh *et al*., 2005; Akbar *et al*., 2008).

For seed yield per plant, the parental genotypes GCA ranged from -2.23 to +2.81 (Table 5). Four out of eight parental genotypes revealed positive GCA effects whereas greater positive GCA effects were recorded in Punjab Sarsoon (2.81) and was identified as the best general combiner for seed yield. However, NIFA Gold (-2.23) showed maximum negative GCA effects and was considered as the poorest general combiner for seed yield per plant. For seed yield per plant, the desirable positive GCA effects were reported in different populations of Indian mustard (De *et al*., 2009).

For seed yield, the hybrids SCA effects were ranging from -11.15 to +15.48 (Table 6). Among F_1 hybrids, 16 out of 28 F_1 cross combinations revealed positive SCA effects for seed yield per plant. The highest positive SCA effects were observed in F_1 hybrid D.K × R.B (15.48) followed by R.C × P.S (12.61). The F_1 hybrids i.e., D.K × R.B and R.C × P.S were considered as best specific cross combinations with promising mean performance and involve low × low and high × high GCA parents for seed yield per plant. However, maximum negative SCA effects were expressed by F_1 hybrid R.C × A-95 (-11.15). In reciprocal F_1 hybrids, the RCA effects were ranging from -24.79 to +15.09 (Table 7).

Table 5. General combining ability (GCA) effects of parental genotypes of *B. napus* L. for the studied traits.

Genotypes	Days to 50% flowering	Primary Branches plant^{-1}	Pods Main raceme^{-1}	Pod Length	Seed yield plant^{-1}
Rustam Canola	0.25**	0.04	44.00**	5.99**	0.81**
Abassin-95	-0.36**	-0.03	65.30**	8.47**	0.97**
NIFA Gold	-0.59**	0.08	61.20**	8.14**	-2.23**
Durr-e-NIFA	-0.67**	-0.18**	43.90**	5.68**	-0.46**
Punjab Sarsoon	-1.69**	0.60**	55.40**	6.70**	2.81**
Faisal Canola	3.01**	-0.15*	42.00**	5.75**	0.29*
Rainbow	6.88**	-0.33**	54.40**	7.80**	-2.04**
Dunkled	-6.83**	-0.03	44.10**	6.05**	-0.15
S.E (gi)	0.05	0.05	0.32	0.01	0.09

*, ** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 6. Specific combining ability (SCA) effects of hybrids in an 8 × 8 diallel cross of *B. napus* L. for the studied traits.

F$_1$ Hybrids	Days to 50% Flowering	Primary branches plant^{-1}	Pods main raceme^{-1}	Pod length	Seed yield plant^{-1}
R.C × A-95	-4.88**	0.40**	52.71**	7.02**	-11.15**
R.C × N.G	-5.10**	-0.31	64.62**	7.36**	-3.82**
R.C × D.N	6.78**	0.00	63.73**	7.70**	2.98**
R.C × P.S	4.20**	0.30*	45.51**	8.37**	12.61**
R.C × F.C	1.30**	1.97**	75.20**	7.30**	12.31**
R.C × R.B	-0.63**	-0.60**	65.33**	7.04**	-5.33**
R.C × D.K	-3.36**	-0.50**	75.54**	7.03**	3.34**
A-95 × N.G	4.61**	0.17	70.64**	7.40**	11.81**
A-95 × D.N	-1.06**	-0.02	57.55**	8.25**	1.53**
A-95 × P.S	2.46**	0.07	62.22**	7.67**	4.60**
A-95 × F.C	-2.09**	-1.15**	74.53**	7.77**	-4.17**
A-95 × R.B	2.08**	-0.88**	66.72**	7.19**	-2.70**
A-95 × D.K	-0.65**	0.32*	66.50**	7.39**	-1.55**
N.G × D.N	2.97**	0.44**	57.80**	7.75**	-4.01**
N.G × P.S	-0.41**	1.49**	49.12**	7.30**	3.24**
N.G × F.C	3.34**	1.04*	53.63**	7.65**	-0.34
N.G × R.B	-0.73**	-1.09*	49.82**	7.60**	-1.21**
N.G × D.K	-6.67**	-1.19*	65.00**	7.58**	-2.07**
D.N × P.S	-6.63**	0.10	65.20**	7.09**	1.05**
D.N × F.C	5.17**	-1.10**	61.33**	7.62**	3.72**
D.N × R.B	0.15	0.62*	44.00**	7.20**	3.46**
D.N × D.K	-1.13**	0.37*	54.00**	7.12**	0.66
P.S × F.C	0.44**	-0.48**	47.91**	7.38**	0.24
P.S × R.B	3.47**	1.62**	56.43**	7.75**	-7.98**
P.S × D.K	-4.32**	0.39*	78.81**	8.55**	4.54**
F.C × R.B	-7.63**	-0.51**	72.73**	7.87**	5.95**
F.C × D.K	1.38**	0.22	43.94**	7.56**	-8.15**
D.K × R.B	10.46**	1.52**	43.65**	7.91**	15.48**
S.E (sij)	0.15	0.14	0.85	0.11	0.26

*, ** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

For RCA effects, 13 out of 28 hybrids were positive and the highest RCA values were recorded in F$_1$ hybrid D.K × P.S (15.09) followed by D.K × N.G (14.61). 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) depicted that the inheritance in seed yield per plant was managed by non-additive gene action (Table 8). In earlier studies, the prevalence of non-additive gene action was also reported for seed yield in F$_1$ populations of *B. juncea* L. (Singh *et al.*, 2005; Singh and Singh, 2008).

Table 7. Reciprocal combining ability (RCA) effects of hybrids in an 8 × 8 diallel cross of *B. napus* L. for the studied traits.

F_1 Hybrids	Days to 50% Flowering	Primary branches plant^{-1}	Pods main raceme^{-1}	Pod length	Seed yield plant^{-1}
A-95 × R.C	-4.10**	0.60*	54.81**	7.53	-5.38**
N.G × R.C	-3.25**	1.00**	68.22**	7.57	-1.03**
N.G × A-95	-2.85**	0.30	55.13**	7.09	-3.11**
D.N × P.S	-2.55**	0.55	69.81**	7.77	-13.79**
D.F × A-95	2.50**	-0.75**	64.00**	7.42	-9.00**
D.N × N.G	-6.30**	0.08	33.33**	7.69	12.57**
P.S × R.C	-7.45**	0.43	45.94**	7.51	0.51
P.S × A-95	1.20**	0.03	77.52**	7.46	-4.90**
P.S × N.G	-4.50**	0.25	56.63**	7.82	-1.13**
P.S × D.N	3.10**	-1.70**	43.74**	7.05	-8.49**
F.C × R.C	-2.05**	-2.25**	76.32**	8.87	-24.79**
F.C × A-95	3.85**	0.85**	58.41**	7.68	3.40**
F.C × N.G	-5.45**	0.65**	45.81**	7.46	2.68**
F.C × D.N	-5.10**	0.05	73.94**	7.69	-5.18**
F.C × P.S	6.15**	1.15**	56.25**	7.57	-13.41**
R.B × R.C	-4.40**	0.40	51.33**	7.34	6.46**
R.B × A-95	-3.30**	0.15	65.92**	7.64	-6.58**
R.B × N.G	1.75**	0.85**	65.94**	7.59	2.54**
R.B × D.N	-0.25	1.50**	74.35**	7.72	0.98**
R.B × P.S	0.65**	0.02	54.71**	7.51	-3.17**
R.B × F.C	-5.05**	0.40	49.53**	7.77	2.31**
D.K × R.C	8.45**	0.20	74.75**	7.42	3.48**
D.K × A-95	-5.25**	1.25	53.96**	7.85	8.12**
D.K × N.G	0.90**	0.25	44.41**	7.60	14.61**
D.K × D.N	-2.45**	0.45	47.91**	6.50	6.08**
D.K × P.S	1.65**	1.75	46.32**	8.42	15.09**
D.K × F.C	-8.15**	0.43	54.11**	7.50	-5.24**
D.K × R.B	1.40**	-1.45**	80.81**	8.54	-7.10**
S.E (rij)	0.17	0.23	1.35	0.18	0.30

*, ** Significant at $P \leq 0.05$ and $P \leq 0.01$, respectively

Table 8. Variances due to general (σ^2GCA), specific (σ^2SCA), reciprocal (σ^2RCA) combining ability, and ratio of σ^2GCA/σ^2SCA for the studied traits in *B. napus* L.

Traits	Σ^2GCA	σ^2SCA	σ^2RCA	σ^2GCA/σ^2SCA
Days to 50% flowering	15.28	40.07	18.67	0.38
Primary branches plant^{-1}	0.05	1.13	0.81	0.04
Pods main raceme^{-1}	1.99	76.19	64.43	0.03
Pod length	0.02	0.33	0.04	0.06
Seed yield plant^{-1}	2.69	114.26	76.61	0.02

Conclusion: Comparatively higher variances of SCA than GCA revealed the predominance of non-additive gene action for the inheritance of all the studied traits. Parental cultivars Abassin-95 and Punjab Sarsoon were identified as best general combiners and performed better for majority of the traits. However, F_1 hybrids i.e., Rustam Canola × Faisal Canola, Punjab Sarsoon × Dunkled and Dunkled × Rainbow revealed prominent SCA and best mean performance for yield traits. Therefore, the said breeding material can be safely used for further improvement of yield related traits in rapeseed (*B. napus* L.).

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