



Original article

Line × Tester Analysis for Seed Yield and Its Related Traits in *Brassica napus* L.

Ali Hassan Khan ^{a,*} & Mariam Hassan ^b

^a University Of Agriculture Faisalabad, Pakistan

^b Oilseeds Research Institute, AARI Faisalabad, Pakistan

Abstract

The research was conducted in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. Experiment was conducted to evaluate the combining ability effects. Six lines viz. ZM-R-10, Chakwal Sarsoon, ZM-R-12, ZM-R-13, B-56 and ZM-R-11 and four testers viz. ZM-R-8, ZM-M-9, ZM-R-1, and ZMM-5 were crossed through line × tester breeding scheme. Twenty four crosses and their parents were evaluated using triplicate randomized complete block design. Data were recorded on yield and its related traits (plant height, primary branches per plant, secondary branches per plant, number of siliquae per plant, number of seeds per siliqua, 1000-seed weight, siliqua length, seed yield per plant). The recorded data were subjected to analysis of variance, and combining ability. Significant differences among entries for yield and its related traits indicated existence of genetic variability in breeding material. Lines Chakwal Sarsoon, ZM-R 12, ZM-R-13, B-56 and testers ZM-R-1, ZM-M-5, ZMM-9 were potential parents and good general combiners. Crosses Chakwal Sarsoon × ZM-R-1 Chakwal Sarsoon × ZM-M-5, ZM-R 12 × ZM-R-1 ZM-R 12 × ZM-R-8, ZM-R-11 × ZM-R-8, Chakwal Sarsoon × ZM-M-5, ZM-R-13 × ZM-R-8 and ZM-R-10 × ZM-R-8 were potential crosses and good specific combiners. The variances due to SCA were more than GCA which showed the role of non-additive gene action.

Keywords: *Brassica napus*, seed yield, combining ability analysis.

Received: 01 April 2019 * **Accepted:** 18 September 2019 * **DOI:** <https://doi.org/10.29329/ijjaar.2019.217.15>

* Corresponding author:

Ali Hassan Khan, University Of Agriculture Faisalabad, Pakistan.
Email: alihassanpbg@gmail.com

INTRODUCTION

Rapeseed (*Brassica napus*) is an important oilseed crop in Pakistan and all over the world. The high percentage of oil makes it the leading oil crop and it is a second chief source of protein meals (Azizinia, 2012). Because of its high percentage of good quality oil it is cultivated in large areas of Pakistan. During 2018-19 rapeseeds and mustard covered 2.64 million hectares area and its seed production was 1.42 million tonnes. Pakistan is still deficient in edible oil production. During 2018-19 total requirement of edible oil was 3.523 million tonnes while local production of edible oil contributed 0.507 million tonnes which is 15% of total requirement. To fulfill the gap between consumption and production 2.421 million tonnes oil was imported spending Rs.192.203 billion (Govt. of Pakistan, 2018-19). The edible oil situation in Pakistan needs improvement through different strategies. Lower edible oil production is partially due to non-availability of high yielding cultivars. One of the primary goals of any breeding program is to produce improved varieties with high yield. The prerequisite to attain this goal is to find adequate amount of variability. Yield is a complex character dependent on quantitative characters. Improvement for yield thus depends on the magnitude of genetic variability of different quantitative characters. Hence measurement and evaluation of genetic variability are needed for yield improvement (Bind et al., 2014). Line \times tester technique is efficient way to investigate the gene action and combining ability effects for yield contributing characters and selecting best combiner for successful hybridization (Singh and Chaudhary, 1979). General combining ability (GCA) is an average performance of a line in series of crosses while specific combining ability (SCA) average performance in hybrids (Rameeh, 2012). The objective of this study was therefore; to find out genetic variability for seed yield and its related traits. Combining ability effects and gene action were estimated for identification of potential parents and crosses

Material and Methods

Field experiment

The present study was conducted in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The experimental material consisted of ten accessions of *Brassica napus* L. collected and maintained by Oilseed Research Group., Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan. First year, 24 crosses of *Brassica napus* were developed by crossing of six lines and four testers. Crosses along with parents were sown in next year following a triplicate randomized complete block design. Spacing between plants and rows will be maintained as 30 and 60 cm, respectively. At maturity 10 guarded plants will be randomly taken from each entry per replication and data was recorded for the following traits plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, number of seeds per silique, 1000- seed weight (g), silique length (cm), seed yield per plant (g).

Statistical analysis

The data was subjected to analysis of variance following Steel et al. (1997). Data for the traits showing significant genotypic difference were further subjected to line \times tester analysis for estimation of combining ability effects according to Kempthorne (1957).

Results and Discussion

Analysis of variance

Results of analysis of variance for quantitative traits of *Brassica napus* L. are presented in Table 1.

Table 1. Mean square values for quantitative traits in *Brassica napus* L.

SOV	DF	PH	NPB	NSB	NSPP	SL	NSPS	SW	SYPP
Replications	2	17.4	0.013	0.82	421.32*	0.28	1.36	0.66*	6.39
Treatments	33	581.5*	2.80*	7.43*	3850.42*	0.46*	10.43*	4.22*	31.83*
Parents	9	630.69*	3.20*	9.06*	2848.20*	0.49*	15.57*	7.99*	37.27*
Parent vs Crosses	1	1.61	11.3*	21.1*	27287.59*	0.22	0.02	14.89*	44.44*
Crosses	23	587.56*	2.28*	6.19*	3223.59*	0.46*	8.87*	2.28*	29.15*
Lines (L)	5	718.18*	5.15*	6.84*	4091.41*	0.34*	5.48*	1.85*	27.86*
Testers (T)	3	208.11*	0.40*	1.43*	797.64*	0.60*	8.44*	3.51*	16.50*
L \times T	15	619.9*	1.70*	6.9*	3419.51*	0.48*	10.09*	2.18*	32.11*
Error	66	6.50	0.072	0.49	129.60	0.16	1.50	0.07	6.12

* = Significant at 0.05 probability level ** = significant at 0.01 probability level

Treatments, parents, crosses, lines, testers, and line \times tester were significant for all the traits. Parents vs crosses were significantly different for all traits except plant height, siliqua length and number of seed per siliqua. Result revealed that genetic variation is present among breeding material for yield and its related traits. So, these genotypes can be used for further breeding program. Hence later analysis of line \times tester for combining ability was possible.

Combining ability analysis

General combining ability effect

General combining ability (GCA) effects for lines and testers of *Brassica napus* L. are presented in Table 2.

Table 2. Estimation of GCA effects for yield and its related traits in *Brassica napus* L.

Parents	PH	NPB	NSB	NSPP	SL	NSPS	SW	SYPP
Lines								
ZM-R-11	-3.45	-0.88	-1	18.51*	0.17*	0.50*	-0.42	0.873*
Chakwal Sarson	11.9*	0.74*	-0.11	25.99*	0.24*	-1.0	-0.35	0.04
ZM-R-10	1.31*	0.75*	0.14	-3.96	-0.15	0.79*	0.19*	0.002
ZM.R 12	-8.76	0.001	1.14*	-18.28	-0.10	0.08	-0.01	0.071
ZM-R-13	-6.22	-0.15	0.40*	-4.50	-0.03	0.202	-0.04	1.77*
B-56	5.15*	-0.46	-0.57	-17.76	-0.12	-0.57	0.65*	-2.77
S.E	0.73	0.07	0.20	3.28	0.11	0.35	0.07	0.71
Testers								
ZM-R-1	-3.6	-0.16	0.14	-0.66	0.17*	0.66*	0.16*	-0.17
ZM-M-5	4.45*	0.19*	0.01	2.84*	-0.24	0.18	0.44*	1.39*
ZM-R-8	-1.04	-0.03	0.24*	-8.90	-0.02	-0.95	-0.01	-0.46
ZM-M-9	0.29	0.01	-0.39	6.72*	0.09*	0.09	-0.59	-0.75
SE	0.60	0.06	0.16	2.68	0.095	0.28	0.06	0.58

SE=Standard Error PH =Plant height NPB= primary branche NSB=No. of secondary

branches

NSPP=Number of siliqua per plant

SL=Siliqua length

NSPS=Number of seed per siliqua

SW=1000 seed weight

SYPP=Seed yield per plant

Among lines Chakwal sarson, ZM-R-10 and B-56 had positive and significant GCA effects and among tester ZM-M-5 best general combiners for plant height. Dar et al. (2011), Sincik et al. (2011) and Patel et al. (2012) also reported the positive and significant GCA effects for plant height in *Brassica napus* L. Among lines ZM-R-10 and Chakwal sarson and among testers ZM-M-5 had positive and significant GCA effects for number of primary branches per plant Akbar et al. (2008) and Singh et al. (2013) also reported the positive and significant GCA effects for number of primary branches per plant. Lines ZM-R-12 had positive and significant GCA effects followed by ZM-R-13 and among tester ZM-R-8 had positive and significant considered best general combiner for number of secondary branches per plant among lines Gupta et al. (2011) and Nigam and Alka (2008) also found the positive and significant GCA effects for number of secondary branches.

ZM-R-11 and Chakwal sarson had positive and significant GCA effects and were best general combiners for number of siliquae per plant among lines Dar et al. (2011) reported the positive and significant GCA effects for number of siliquae per plant. Akbar et al. (2008) and Rameeh (2012) reported the positive and significant GCA effects for siliqua length. Among testers ZM-M-9 and ZM-M-5 had positive and significant GCA effects. Accessions ZM-R-11 and Chakwal sarson among lines while among testers ZM-R-1 and ZM-M-9 showed positive and significant GCA effects and were best general combiners for siliquae length Akbar et al. (2008) and Rameeh (2012) reported the positive and

significant GCA effects for siliqua length. Line ZM-R-10 and tester ZM-R-1 had positive and significant GCA effects and were best general combiners for number of seed per siliqua Nassimi et al. (2006) and Rameeh (2012) reported the positive and significant GCA effects for number of seeds per siliqua.

Among lines ZM-R-1, B-56 and ZM-R-10 had positive and significant GCA effects and were best general combiners for 1000 seed weight. Among tester ZM-M-5 and ZM-R-1 had positive and highly GCA effects Dar et al. (2011), Gupta et al. (2011) and Turi et al. (2011) reported the positive and significant GCA effects for 1000 seed weight.. Accession ZM-R-13, ZM-R-11 (line) and ZMM-5 (tester) had positive and significant GCA effects and was best general combiners for seed yield per plant Akbar et al. (2008), Dar *et al.* (2011), Gupta *et al.* (2011), Rameeh et al. (2012), Turi et al. (2011) and Azizinia (2012) reported the positive and significant GCA effects for seed yield per plant.

Specific combining ability effect

Specific combining ability (SCA) effects for lines and tester of *Brassica napus* L. are presented in Table 3. Nine crosses had positive and significant SCA effects for plant height in *Brassica napus*. Cross B-56 × ZM-M-9 was the best specific combiner for plant height followed by Chakwal sarson × ZM-M-5.

Table 3. Estimation of specific combining Ability (SCA) effects for yield related traits in *Brassica napus* L.

Crosses	PH	NPB	NSB	NSPP	SL	NSPS	SW	SYPP
ZM-R-11 × ZM-R-1	-1.82	-0.60	-1.77	-63.68	0.04	1.39*	-0.69	-4.62
ZM-R-11 × ZM-M-5	-14.76	-0.13	-0.44	-22.32	0.47*	0.29	0.31*	0.87*
ZM-R-11 × ZM-R-8	17.78*	0.42*	0.25	55.15*	-0.02	0.20	-0.19	1.24*
ZM-R-11 × ZM-M-9	-1.19	0.31*	1.96*	30.86	-0.49	-1.90	0.57*	2.51*
Chakwal Sarson × ZM-R-1	5.61*	0.66*	-1.66	-12.43	-0.30	-0.53	0.22*	3.12*
Chakwal Sarson × ZM-M-5	19.97*	1.37*	2.63*	14.65*	0.20	1.87*	-0.87	1.45
Chakwal Sarson × ZM-R-8	-25.2*	-0.69	0.29	7.80*	0.14	-1.45	-0.52	-0.19
Chakwal Sarson × ZM-M-9	-0.33	-1.34	-1.26	-10.02	-0.04	0.12	1.1*	-4.38
ZM-R-10 × ZM-R-1	4.78*	-0.18	0.16	52.2*	-0.57	-2.65	0.8*	1.47*
ZM-R-10 × ZM-M-5	-0.27	-0.67	-1.20	-34.64	0.18	-0.14	-0.34	-2.43
ZM-R-10 × ZM-R-8	4.44*	0.3*	-0.03	-10.69	0.19	0.64	-0.13	1.70
ZM-R-10 × ZM-M-9	-8.94	0.4*	1.0*	-6.92	0.19	2.16*	-0.39	-0.74
ZM-R-12 × ZM-R-1	-2.17	0.3*	2.9*	13.7*	0.07	-0.65	0.07	3.75*
ZM-R-12 × ZM-M-5	7.08*	0.01	-0.79	-8.12	0.01	-0.38	-0.17	-1.25
ZM-R-12 × ZM-R-8	1.16	-0.49	-0.69	-21.51	-0.18	1.99*	0.54*	-0.79
ZM-R-12 × ZM-M-9	-6.07	0.16*	-1.45	15.86*	0.09	-0.96	-0.45	-1.70
ZM-R-13 × ZM-R-1	2.85*	-0.16	0.47*	-9.53	0.8*	-0.54	0.96*	-5.9
ZM-R-13 × ZM-M-5	-4.75	-0.49	0.007	31.08*	-0.41	1.33*	-0.19	2.29*
ZM-R-13 × ZM-R-8	12.40*	0.93*	0.36	-4.96	-0.33	-0.80	-0.46	1.42*
ZM-R-13 × ZM-M-9	-10.50	-0.27	-0.85	-16.58	-0.05	0.02	-0.30	2.17*
B-56 × ZM-R-1	-9.24	-0.02	-0.14	19.59*	-0.03	2.99*	-1.43	2.17*
B-56 × ZM-M-5	-7.26	-0.08	-0.20	19.35*	-0.47	-2.97	1.26*	-0.94
B-56 × ZM-R-8	-10.54	-0.55	-0.18	-25.76	0.20	-0.58	0.77*	-3.38
B-56 × ZM-M-9	27.05*	0.66*	0.53*	-13.18	0.30*	0.56	-0.59	2.15*
SE	1.49	0.15	0.40	6.19	0.2683	0.6517	0.16	0.31

SE=Standard Error PH=Plant height NPB= primary branche NSB=Number of secondary branches NSPP=Number of siliqua per plant SL=Siliqua length

NSPS=Number of seed per siliqua SW=1000 seed weight SYPP=Seed yield per plant

Dar et al. (2011), Gupta et al. (2010) and Sincik et al. (2011) reported the positive and significant SCA effects for plant height. So these crosses can be use for plant height trait. Ten crosses had positive and significant SCA effects. Chakwal sarson × ZM-M-5 was the best specific combiner for number of primary branches followed by ZM-R-13 × ZM-R-8. Six crosses had positive and significant SCA effects. ZM-R- 12 × ZM-R-1 was the best specific combiner for number of secondary branches followed by Chakwal sarson × ZM-M-5 Akbar et al. (2008), Gupta et al. (2010) and Singh et al. (2013) reported the positive and significant SCA effects for number of secondary branches per plant. Nine crosses had positive and significant SCA effects. ZM-R-11 × ZM-R-8 was the best specific combiner for number of siliquae per plant followed by ZM-R-10 × ZM-R-1 Dar et al. (2011) and Turi et al. (2011) reported the

positive and significant SCA effects for number of siliquae per plant. Three crosses had positive and significant SCA effects. ZM-R-11 × ZM-M-5, ZM-R-13 × ZM-R-1 and B-56 × ZM-M-9 was the best specific combiner for siliqua length Akbar et al. (2008) Turi et al. (2011) reported the positive and significant SCA effects for number of siliquae length..Six crosses had positive and significant SCA effects. B-56 × ZM-R-1 was the best specific combiner for number of seed per siliqua followed by ZM-R-10 × ZM-M-9 Dar et al. (2011) and Kang et al. (2013) reported the positive and significant SCA effects for number of seed per siliqua. Seven crosses had positive and significant SCA effects. B-56 × ZM-M-5 was the best specific combiner for 1000 seed weight followed by Chakwal sarson × ZM-M-9 Dar et al. (2011), Gupta et al. (2011) and Turi et al. (2011) reported the positive and significant SCA effects for 1000 seed weight. Two crosses had positive and significant SCA effects. ZM-R-12 × ZM-R-1 was the best specific combiner for seed yield per plant followed by Chakwal sarson × ZM-R-1. Akbar et al. (2008), Dar et al. (2011) and Turi et al. (2011) reported the positive and significant SCA effects for seed yield per plant.

Conclusions

Analysis of variance showed significant differences for all the traits in crosses parent, lines, testers. It indicated the existence of considerable genetic variability in breeding material. The variances due to specific combining ability (SCA) was more than general combining ability (GCA) which showed the role of non-additive gene action for these traits.

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