



Research Article

Combining Ability, Heritability and Gene Action Assessment in Rapeseed (*Brassica napus* L.) for Yield and Yield Attributes

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Abstract | An F1 hybrid of *Brassica napus* L., derived from 5 × 5 diallel, was studied to estimate combining ability, heritability and gene action of morphological and yield associated traits, utilizing randomized complete block design (RCBD) with two replications, at Bacha Khan Agricultural Research Farm (BARF), Charsadda, Khyber Pakhtunkhwa, Pakistan during the growing season of 2017-18. The data were collected for pods related traits and total yield. The results of the study showed significant differences among parents and F1's for all the studied traits. General and specific combining ability analysis revealed non-significant results for the traits under consideration, suggesting the involvement of non-additive type of gene action. A higher broad sense heritability estimate was evident. It was concluded from the combining ability analysis of the present study that genotype 2702 was best general as well as a specific combiner for pod length (PL), seeds pod⁻¹ (SPP), total yield (TY), and 1000 seed weight (SW). In addition, maximum pod length, seeds pod⁻¹, total yield, 1000 seed weight and pods plant⁻¹ (PPP) were observed for those F1 hybrids where genotype 2702 was used as seed setter, i.e. 2702 × P1-119 and 2702 × DUNCLED. Higher broad-sense heritability and non-additive type of genetic variability indicated that it could be integrated as a valuable tool in breeding strategies to choose genotypes of *B. napus* L. for high yielding traits.

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Introduction

Brassica napus L. is a particular canola cultivar, having a bright yellow flowering of the family Cruciferae, cultivated widely for the rich source of oil. Rapeseed and mustard are two main key groups used to categorize the species of *Brassica* genus. *Brassica rapa* L., *B. napus* L., and *B. nappobrassica* L., are generally considered as rapeseed (Zhou *et al.*, 2006). *Brassica* genus had vast economic importance on the base of oilseed crop throughout the world. In the South East of Asia, it was cultivated since 4000

BC (Snowdown *et al.*, 2007). *Brassica* species are believed to be originated at Mediterranean, Canada and Europe (Rakow, 2004). In *Brassica* species the most promising species is *Brassica napus* L., an amphidiploid having AACC genome (2n=38), is one of the most promising brassica species developed by a cross between *B. rapa* L. (2n=20, AA genome) and *B. oleracea* L. (2n=18, CC genome) (Iniguez and Federico, 2010).

In Pakistan, the total area of 24.7 thousand hectares was planted by rapeseed and mustard with a per

hectare production of 939.27 kg (FAO Statistics, 2016). *Brassica napus* L., was generally grown for seed and oil purpose. The limited cultivation of rapeseed in Khyber Pakhtunkhwa and some areas of Punjab province are the main reasons for low production (Saleem *et al.*, 2015). The factors responsible for this, lower than the world average, production scarcity of quality varietal seeds, limitation of irrigational water, unavailability of modern technologies, unexpected weather conditions, climate change and growing population. It is need of the time to develop high yielding cultivars especially in *B. napus* L., to fill up the gap of local requirements and ultimately reduce the import of edible oil (Ghosh and Gulati, 2002).

Diallel crosses were analyzed in theoretical practices utilizing a biometrical program specified for combining ability (Griffing, 1956). Combining ability helped us to determine the performance of individual genotypes by observing its combination in offsprings (Sincik *et al.*, 2015). Based on general and specific combining ability effects, it could be determined whether an individual be involved or not in advanced breeding practices (Zhou *et al.*, 2006). Combining ability provides information about the desirable genotype, nature and magnitude of gene action. The GCA represents the additive type of gene action, while the SCA represents the non-additive gene action (Malik *et al.*, 2004; Akbar *et al.*, 2008). The genetic diversity among the genotypes is evident from combining ability, gene action and heritability studies, as they all are linked together, thus used in the selection procedure of superior genotypes. Narrow sense heritability is generally related to the GCA and additive gene action, whereas SCA and non-additive gene action is correlated with broad-sense heritability (Marwede *et al.*, 2004). The existence of genetic variability can be calculated using heritability estimates, thus helped in bringing improvement in the crop performance (Khan *et al.*, 2006).

Keeping in view the significance of edible oil and its scarcity in the country, the present research was designed to determine the effect of combining ability, heritability and gene action on the yield performance of different diallel crosses in *B. napus* developed for high yielding traits.

Materials and Methods

The field experiments related to oil crop research

were carried out at the Bacha Khan Agriculture Research Farm (BARF) Charsadda during 2017-2019. The experimental material consisted of five rapeseed varieties. Parental material sowed under field condition during December, 2017. During February, 2018 at the time of flowering hybridization through emasculation and controlled pollination was carried out in 5×5 diallel fashion. Sowing of the investigational material included of F1 hybrid seed resulting from intercrosses among these five varieties, including self, direct and reciprocals were carried out in randomized complete block design (RCBD) having two replications during 2018-2019 sowing season at BARF Charsadda. Each entry comprised of a single row of 1 m length. Rows were kept at 60 cm apart whereas the standard distance of 25 cm was maintained by thinning out additional plants at an early four-leaf stage in each experimental plot. Standard agricultural practices were adopted during the vegetative and reproductive phases. At maturity data was collected for days to 50% flowering, days to 50% maturity, plant height, primary branches plant⁻¹, pods plant⁻¹, pod length, seed pod⁻¹, seed yield plant⁻¹, total yield and 1000 seed weight. Traits revealing significant differences were analyzed according to Griffing (1956) method (fixed effect) for combining ability analysis; heritability estimates and gene action.

Statistical analysis

$$Y_{ij} = m + g_i + g_j + s_{ij} + r_{ij} + 1/bc \sum e_{ijkl}$$

Y_{ij} = mean of $i \times j$ th genotype over k and l

g_i = GCA of i th parent

g_j = GCA effect of j th parent

s_{ij} = SCA effect

$1/bc \sum e_{ijkl}$ = mean error effect

Estimation of heritability was studied according to Weber and Moorthy (1952).

Results and Discussion

The average performance of various genotypes and their crosses revealed significant and highly significant differences for different traits, i.e., pods plant⁻¹ (Ali *et al.*, 2015), pod length (Sincik *et al.*, 2011), seed pod⁻¹ (Ali *et al.*, 2015), total yield (Ali *et al.*, 2015) and 1000 seed weight (Junaid *et al.*, 2014) (Table 1). Mean value of pods plant⁻¹ revealed that parental genotype P1-801 attained the maximum value of 192, while genotype 2702 revealed minimum mean value 157 pods in each plant, the maximum

value of 222 pods plant⁻¹ among cross combinations were exhibited by 2702 × DUNCLED, while P1-801 × P1-119 attained minimum 172 pods plant⁻¹. It is cleared from Table 2 that maximum and minimum mean pod length among parental lines were evident for genotype 2702 (7.5 cm) and genotype P1-801 (6.4), respectively whereas maximum and minimum mean value among cross combination varied between 7.1 cm and 5.9 cm attained by P1-119×2702 (F1) and 2722×P1-801(F1). Parental genotype P1-119 and 2722 attained maximum (26.1) and minimum (24.6) values, respectively when seeds pod⁻¹ was taken into consideration, however for cross combinations, the maximum number of 27.4 seed pod⁻¹ were reported for 2702×2722, while the minimum value for seeds pod⁻¹ (14) was recorded in P1-801×2722 (F1). Maximum mean total yield for parental and F1 genotypes was attained by 2722 (109g) and P1-119×2722 (114g) while minimum mean total yield was observed for parental genotype DUNCLED (82.9 g) and DUNCLED×27012 (74 g), respectively. Parental genotypes 2702 and P1-119 revealed maximum (6.1g) and minimum (4.0g) mean values for 1000 seed weight, respectively. Whereas P1-801×P1-119 (F1) and P1-119×P1-801 (F1) attained highest (6.4 g) and lowest (4.09 g) seed weight among the cross combinations, respectively. Pod length, pods plant⁻¹, Seeds pod⁻¹ and seed yield plant⁻¹ are the major yield contributing traits.

Table 1: Analysis of variance for combining ability in *Brassica napus*. L.

SOV	D.F	PPP	PL (cm)	SPP	TY(g)	1000 SW(g)
Reps	1	1551.2	8.703	14.15	264.04	1.613
Crosses	24	512.9*	0.319*	16.62*	235.24**	0.882**
Error	24	220.3	0.160	6.61	61.41	0.31
CV (%)	...	7.9	6	11.2	9	10.5

*, ** probability levels at 0.05 and 0.01, respectively.

Variation among genotypes for combining ability analysis, to identify the best-performing parents for yield attributes, was carried out for those traits which showed significant differences. The results for general combining ability were shown in Table 3. General combining ability is useful to figure out a good combiner, which ultimately helps in developing cultivars having wider adaptability and resistance. Now a days the breeders are struggling to produce the short duration genotype having high

yield and quality through combining ability studies. It was revealed from Table 3 that pods plant⁻¹, pod length, seed pod⁻¹, total yield and 1000 grain weight exhibited significant differences among the genotypes studied. Parental genotype 2722 (10.1) exhibited good general combining ability for pods plants⁻¹ performance among the genotypes studied, whereas parental genotype P1-119 (-6.45) revealed poor combining ability for the said trait. The range of GCA effects for pod length varied between 0.22 (2702) and -0.25 (2722). The analyzed data for seeds pod⁻¹ revealed that parental genotype 2702 (1.62) was significantly different for general combining ability compared to other parental genotypes hence proved to be a finest general combiner for this trait followed by P1-119 (0.15), the rest of genotypes showed relatively less general combining ability. Total yield, the most looked-for trait, revealed that the genotypes 2702 (5.76) and DUNCLED (-5.91) bare significant differences and were found to be best and worst general combiners for this trait. The better combining ability performance of parental genotype 2702 (0.37) for 1000 seed weight was evident from Table 3. On the other hand, parental genotype P1-119 (-0.51) revealed a significantly low general combining ability was. The contradiction in the conclusions must be due to diversified genotypes and environment. Highly significant GCA were reported with desirable GCA effects for relevant traits among parents of *B. napus* L. (Gul *et al.*, 2018; Suchindra and Singh, 2006; Sincik *et al.*, 2015).

The best cross combinations were identified by subjecting the significantly different traits to analysis for specific combining ability (Table 4). High significant and superior specific combining ability for pods plant⁻¹ was evident for a cross combination of 2702×DUNCLED (34.9), whereas DUNCLED×P1-119 (-7.63) revealed poor specific combining ability for this trait. Similarly, P1-801×P1-119 cross combination revealed the maximum value of SCA (0.46) for pod length, likely followed by 2702×P1-119 (-0.05), besides P1-119×2722 determined the minimum SCA (-0.44) for pod length. Variance due to SCA for seeds pod⁻¹ revealed that cross combination 2702×DUNCLED (1.89) attained maximum value followed by P1-801×P1-119 (1.71), similarly significantly different and minimum SCA value was observed for DUNCLED×P1-119 (-7.14). When total yield was taken into consideration, it was cleared from SCA values that a cross combination

of genotype 2702×2722 attained significantly high value (18.7) for this trait followed by 2702×P1-119 (10), whereas minimum significant different SCA values were evident for a cross between genotype 2702×DUNCLED and 2702×P1-801 (-10.8). The analysis of data for 1000 seed weight revealed the positively high value of variance due to SCA for P1-119×2722 (0.51), whereas minimum negative SCA (-0.68) value was reported for P1-801×P1-119. [Yadava et al. \(2012\)](#) also elaborated significant negative results for specific combining ability. It is evident from the above discussion that the performance of those crosses where genotype 2702 was used as seed setter or donor parent was better as compared to others. This affirmed our general combining ability results which revealed genotype 2702 as a good general combiner.

Table 2: Mean performance for pods plant⁻¹, pod length (cm), Seeds pod⁻¹ (g), total yield (g) and 1000 seed weight (g) of five parents and diallel crosses.

S. No	Parents and crosses	PPP	PL (cm)	SPP	TY (g)	1000 SW (g)
1	2702	156.6	7.5	25.3	93.3	6.1
2	DUNCLED	158.8	7.1	24.7	82.9	5.2
3	P1-801	192	6.4	26	84.1	5.9
4	P1-119	179.9	6.7	26.1	96.0	4.0
5	2722	178.1	6.6	24.6	109	4.9
6	2702×DUNCLED	222	6.7	24.5	74.4	5.4
7	2702×P1-801	186.3	7	21.9	75.2	5.7
8	2702×P1-119	216.9	7	23	76.4	5.6
9	2702×2722	213.0	6.8	27.4	80.8	5.6
10	DUNCLED×2702	200.3	6.5	24.6	74.0	5.2
11	DUNCLED×P1-801	187.6	6.5	23.4	78.0	5.6
12	DUNCLED×P1-119	184.1	6.5	21.6	87.1	5.6
13	DUNCLED×2722	178.9	7	20.43	83.0	5.6
14	P1-801×2702	185.5	6.4	24.6	93.0	5.8
15	P1-801×DUNCLED	178.5	6.6	17.5	87.4	5.7
16	P1-801×P1-119	172	6.8	25.3	99.6	6.4
17	P1-801×2722	178.1	6.2	14	79.7	6.2
18	P1-119×2702	184.5	7.1	23.7	79.8	4.9
19	P1-119×DUNCLED	175.8	7	24.3	78.0	4.6
20	P1-119×P1-801	181.5	6.2	21.55	104.9	4.1
21	P1-119×2722	194.7	6.2	21.6	114	4.1
22	2722×2702	200.9	6.1	20.7	79.0	4.7
23	2722×DUNCLED	196.6	6	21	85.2	4.7
24	2722×P1-801	196.0	5.9	23.5	86.5	4.8
25	2722×P1-119	205.2	6.9	23.9	87.5	4.8

Table 3: General combining ability (GCA) effects of

parents for different yield related traits in *Brassica napus* L.

Parents	PPP	PL (cm)	SPP	TY (g)	1000 SW (g)
2702	-5.46	0.22	1.62*	5.76*	0.37
DUNCLED	4.23	-0.03	-1.35	-5.91*	0.06
P1-801	-2.44	0.04	-0.50	-2.29	0.30
P1-119	-6.45	0.02	0.15	-1.48	-0.51*
2722	10.12*	-0.25	0.08	3.91	-0.21

* and ** probability levels at 0.05 and 0.01, respectively.

Table 4: Specific combining ability effects (SCA) of the crosses for different yield related traits in *Brassica napus* L.

Crosses	PPP	PL (cm)	SPP	TY (g)	1000 SW (g)
2702×DUNCLED	34.98**	-0.08	1.89	-10.8*	-0.31
2702×P1-801	7.56	-0.41	-0.06	-10.8*	0.08
2702×P1-119	-3.73	-0.05	1.19	10.0	0.04
2702×2722	2.05	-0.41	-2.44	18.7**	-0.53
DUNCLED×P1-801	-5.68	-0.16	1.11	9.9	0.31
DUNCLED×P1-119	-7.63	-0.45	-7.14**	1.8	0.03
DUNCLED×2722	-1.45	-0.23	-0.37	-4.4	-0.17
P1-801×P1-119	5.45	0.46	1.71	-1.8	-0.68
P1-801×2722	0.98	-0.40	-0.92	-1.8	-0.33
P1-119×2722	4.39	-0.49	0.93	-1.3	0.51

* and ** probability levels at 0.05 and 0.01, respectively.

The heritability analysis and gene action were shown in [Table 5](#). The higher value of phenotypic variance than genetic variance indicated that the environment has a profound effect on the phenotypic expression of these traits. Broad sense heritability and non-additive type of gene action were observed for the traits under study (PPP, PL, SPP, TY and 1000 SW). These findings are in agreement with [Khan et al. \(2013\)](#) and [Aytac and Kinaci \(2009\)](#) who reported high broad-sense heritability. Contrary to our finding [Afrin et al. \(2012\)](#), [Zare and Sharafzadeh \(2012\)](#) and [Rameeh \(2015\)](#) reported narrow sense heritability in *B. napus* L.

Table 5: Heritability estimates and gene action of different yield related traits.

Attributes	h ² B	h ² N	σ ² A	σ ² D	σ ² P
PPP	0.14	0.14	58.8	0	412.5
PL	0.30	0.04	0.01	0.06	0.24
SPP	0.14	0.12	1.53	0.31	12.5
TY	0.56	0.28	45.3	46.7	162.1
1000 SW	0.27	0.27	0.20	0	0.75

Conclusions and Recommendations

Relatively higher values for variances due to SCA than GCA confirmed the occurrence of Broad sense heritability, whereas gene action for the traits under study was found to be of non-additive type. Genotype 2702 performed better for pod length, seed pod⁻¹, total yield and 1000 seed weight and was identified as a best general combiner. Similarly, among a cross combination of parental genotypes, 2702 × P1-119 attained prominent SCA for all the traits except pods plant⁻¹ and showed better average performance. Thus it could be evident from the above combining ability and genetic studies that genotypes 2702 and P1-119 could be further exploited for future breeding programs and could be securely used for the betterment of related traits in Rapeseed canola.

Novelty Statement

Identify the variation in the existing germplasm to get promising lines for future breeding program of the department.

Author's Contribution

Muhammad Ali Shah: Data analysis and write up

Faiz ur Rehman: Helped in data collection..

Abbas Mehmood: Performed field work.

Fareed Ullah: Field work.

Sayed Irfan Shah: Helped in data entry and compiling.

Syed Majid Rasheed: Supervised the research.

Conflict of interest

The authors have declared no conflict of interest.

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