

Research Article

Combining ability analysis of yield and yield components in second filial (F₂) generation of mustard (*Brassica juncea*)

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Abstract

This study was conducted at The University of Agriculture, Peshawar in 2006-07 to evaluate the performance of eight Mustard genotypes and their 56 combinations in F₂ population. The Mustard genotypes (NUMYT-009, NUMYT-103, NUMYT-105, NUMYT-113, NUMYT-117, NUMYT-120, NUMYT-123, and NUMYT-124) were crossed in a complete diallel fashion. All the F₂ recombinants along with parental lines were sown in RCB design. Data were collected for plant height, primary branches plant⁻¹, pods main raceme⁻¹, pod length, seeds pod⁻¹, and seed yield plant⁻¹. Mean values for all the genotypes showed highly significant ($P \leq 0.01$) differences for all the traits except primary branches plant⁻¹. Combining ability studies revealed that all the traits showed significant general combining ability (GCA) effects. Most of the traits also gave significant specific combining ability SCA effects except seed yield plant⁻¹ for which non-significant SCA effects were observed. Reciprocal effects for all the traits were significant. The genotype NUMYT-103 and NUMYT-123 proved to be the best general combiner among all the cultivars because they showed desirable positive GCA effects for two traits (pods main raceme⁻¹ and pod length) and desirable negative GCA effect for plant height. F₂ specific cross combination, NUMYT-103 × NUMYT-117 showed highest desirable positive SCA effects for seed yield plant⁻¹. The best reciprocal cross for pod length was NUMYT-117 × NUMYT-103. These genotypes may prove to be effective for improvement of the important traits in future breeding program.

Keywords: *Brassica juncea*; Combining abilities; Yield

Introduction

Indian mustard also known as *Brassica juncea* is one of the most important oil seed crop grown in the Indian subcontinent during winter season [1]. In Pakistan the yield of the *B. juncea* is low, although it has the great potential for high production. In low rainfall areas, *B. juncea* cultivars perform better and are more heat, drought and shattering resistant as compare to *B.*

napus [2]. Under semi-arid condition of Pakistan, *B. juncea* matures earlier than *B. napus* and subsequently easily escape the attack of hairy caterpillars and aphid [3]. In order to develop a high yielding varieties in mustard it is necessary to identify the parents having desirable combining ability for different characteristics. Combining ability analysis helps to identify the promising lines that can be used to develop

hybrids [4]. It can also help elucidating the nature of gene action responsible for the expression of yield and its component that could be further used to select parents for hybridization program [5].

In mustard the yield advancement needs the information about the nature of gene action and different combining abilities of parental lines involved in expression of different desirable characters that are responsible for increase in yield [6]. Diallel analysis has widely been used to explore the inheritance of important traits where the selected parents are crossed in all the possible combinations [6, 7]. Diallel crossing are specifically used to find out the combining ability of parental lines in order to identify the superior parent which will be further used in the hybrid development program [7]. Diallel analysis partitioned the total genetic variability in to general combining ability (GCA), which enlighten the combining ability of parents as well as indicating the importance of additive type of gene action [8]. Whereas specific combining ability (SCA) includes the nature of gene action involved in inheritance of characters among the hybrid arising mainly from non-additive type of gene action [8, 9]. Most of the past studies indicated significant GCA, SCA and maternal effects for yield and yield related traits [6, 10]. Correspondingly both additive as well as non-additive type of genetic pattern were found important for inheritance of different yield related traits [11, 12]. Therefore the present study is designed to investigate the genetic potential and gene action of eight genotypes of mustard (*B. juncea*) and their F₂ recombinants for yield traits and to identify the best general and specific combiners which could be used as a source material for future breeding program.

Material and methods

Genetic material and field procedure

The research work on combining ability analysis of yield and yield components in F₂ generation of mustard crossed in an 8×8 diallel fashion was conducted at The

University of Agriculture, Peshawar. Seeds for the experiment were obtained from the pool of National Uniform Mustard yield Trial (NUMYT). All the 56 Second filial generation (F₂) populations along with eight parents were sown with hand drill in a randomized complete block (RCB) design with three replications during mid of September in three rows of five-meter length with plants and rows spacing of 05 and 30 cm, respectively. Data were recorded on selected F₂ plants and single plant selection was carried out in this generation. Selection in F₂ was carried out on basis of phenotypic performance of the plants. The data were recorded on;

1. Genetic Variability

The genetic variability obtained in F₂ generation was further partitioned in to General and specific combining ability, as defined by Spargue and Tatum 1942 and the reciprocal effect as outlined by Griffing 1956 Method I, Model II.

2. Plant Height (cm)

Five plant in each experimental unit were randomly selected and with the help of meter rod plant height (cm) was recorded from base to tip of the plant.

3. Pods Receme⁻¹

Randomly several receme were collected from various plant in each experimental treatment, counted manually number of pods per receme and then average were calculated accordingly.

4. Pod Length (cm)

Randomly 25 pods were selected in every experimental unit and their length (cm) were recorded through measuring tap and the average pod length (cm) was worked out.

5. Seed Pod⁻¹

Some 25 number of pods were chosen randomly in every experimental unit, counted number of seeds per pod in each pod and then average seed per pod was recorded.

6. Seed yield (g)

Randomly ten plants were selected in every experimental treatment for manual threshing separately, weighted the seed in (g) through electronic balance and the average seed yield per plant (g) was calculated and recorded.

All the recommended cultural practices and inputs were applied uniformly to all the entries from sowing till harvesting.

Results and discussion

Genetic variability

The data (Table 1) revealed highly significant ($P \leq 0.01$) differences among genotypes for plant height, pods main raceme⁻¹, pod length, seeds pod⁻¹ and seed yield plant⁻¹. However, the primary branches plant⁻¹ was found non-significant. The total genetic variability obtained in F₂ generation was further partitioned into General and specific combining ability, as defined by Spargue and Tatum 1942 and the reciprocal effect as outlined by Griffing 1956 Method I, Model II.

Plant height

The mean square (Table 2) for combining ability indicated that the effect due to GCA, SCA and RCA were highly significant ($P \leq 0.01$) for plant height. In *Brassica* taller plants are not desirable, therefore six out of eight parents exhibited negative GCA for plant height. The desirable maximum negative GCA (Table 3) was shown by NUMYT-123 (-6.56) followed by five other genotypes having also negative GCA effects for plant height ranged from -0.05 to -4.70. The two genotypes out of eight parents showed positive GCA NUMYT-103 (11.89) followed by NUMYT-105 (7.40).

According to SCA (Table 4) in plant height 11 out of 28 F₂ specific combinations showed negative SCA effects, whereas the best specific combination was NUMYT-105 × NUMYT-123 with maximum negative value (-26.58) followed by NUMYT-103 × NUMYT-120 (-19.59). For plant height, the maximum positive SCA effects (21.93) were found in the cross NUMYT-103 × NUMYT-123. The reciprocal effects (Table 5) also showed that twelve crosses showed negative maternal effects for plant height. The cross combination NUMYT-123 × NUMYT-105 exhibited maximum desirable negative reciprocal effects for plant height (-31.44).

From breeding point of view in *B. juncea*, the taller plants are susceptible to lodging

thus medium or short stature plants are desirable. Hence negative combining ability for plant height is required for better yield. In our experiment, the significantly negative GCA and SCA (Table 2) effects were recorded both for parents and crosses for plant height thus indicating that these parents and crosses could be used for developing short stature plants with higher yield. Parents and crosses having negative general, specific and reciprocal combining ability effects could be used to develop short stature lines in mustard breeding program. Our results are in agreement with the earlier reports of Kumar *et al.* [17] who observed that the GCA and SCA variances for plant height were highly significant which directed the importance of both additive and non-additive type of gene action. They observed additive type of gene action involved in the expression of plant height, as the GCA values for plant are comparatively higher than the SCA values. Similar results were also observed by Singh *et al.* [21] who observed the importance of additive genetic effect for plant height.

Pods main raceme⁻¹

For pods main raceme⁻¹, the mean square values (Table 2) for GCA were significant ($P \leq 0.05$) and were found highly significant ($P \leq 0.01$) for SCA and RCA. For pods main raceme⁻¹, out of eight parents five showed positive GCA values with the range of 0.83 to 4.42 (Table 3). The maximum GCA effects were observed in NUMYT-103 (4.42) found to be best general combiner for pods main raceme⁻¹ followed by NUMYT-117 (4.11). The NUMYT-123 was a poor general combiner by exhibiting the minimum negative GCA value (-7.31).

Similarly the SCA (Table 4) effect for pod main raceme⁻¹ indicated that 11 out of 28 F₂ hybrid showed positive SCA positive effects, where the maximum values were exhibited by F₂ population NUMYT-105 × NUMYT-124 (14.07). However, the poor specific cross was NUMYT-113 × NUMYT-117 (-10.72) by having least SCA value. Further examination for RCA (Table 5) revealed that among 28 crosses, the eight

crosses showed positive value for pods main raceme⁻¹, while the best reciprocal cross was NUMYT-113 × NUMYT-103 (14.25). For pods main raceme⁻¹ significant GCA was reported by Singh and Sachan [23]. Similar results were also presented by Iqbal *et al.* [16] and Khan *et al.* [6].

Pod length

According to combining ability ANOVA (Table 2), the effects due to GCA, SCA and RCA for pod length was found highly significant ($P \leq 0.01$). In Mustard, plants with long pod length are contributing to the higher yield therefore positive GCA and SCA effects are desirable. In case of pod length, the three parents (NUMYT-103, NUMYT-120 and NUMYT-123) manifested maximum positive GCA effect (0.25, 0.15 and 0.06), respectively. Minimum GCA effects for pod length were exhibited by NUMYT-009 (-0.20).

For SCA effect (Table 4), 15 crosses out of 28 exhibited positive effects, while the best specific performance was observed in the F₂ cross NUMYT105 × NUMYT-120 with the maximum positive SCA value 0.35. The minimum SCA effects were recorded in crosses NUMYT-105 × NUMYT-113 and NUMYT-103 × NUMYT-124 (-0.27, -0.24) for pod length. The reciprocal effects (Table 5) also showed that 9 reciprocal crosses showed positive maternal effects for pod length. Maximum RCA effects for pods length was recorded in NUMYT-117 × NUMYT-103 (0.43) followed by NUMYT-124 × NUMYT-105 (0.33). Parents and hybrid combination having positive general, specific and reciprocal combining ability effects for pod length could be utilized in future breeding program to produce longer pods. Higher values of GCA effect the SCA and RCA effect showed that the character is under the control of additive type of gene action (Khan *et al.* [6] and Nassimi *et al.* [10]. Hu *et al.* [15] and Singh *et al.* [22] reported significant GCA and SCA effects for pod length in mustard. Both additive and non-additive type of genetic control were observed by Muhammad *et al.* [18] and

Upadhyay and Kumar [24] in mustard and rapeseed.

Seeds pod⁻¹

Mean square values (Table 2) for seeds pod⁻¹ showed highly significant ($P \leq 0.01$) differences for GCA, SCA and RCA representing the importance of both additive and non-additive type of gene action as reported by Muhammad and Raziuddin [9]. Seeds pod⁻¹ is considered one of the major yield-contributing factor, hence positive combining ability effect is desirable for this trait. For seeds pod⁻¹, the maximum GCA (Table 3) values were owned by parent NUMYT-120 (1.40) followed by NUMYT-117 (0.14). The minimum GCA effects for said trait were given by four genotypes i.e. NUMYT-009, NUMYT-123, NUMYT-124, and NUMYT-105 with range of -0.66 to -0.10. According to seeds pod⁻¹ (Table 4) the cross combination NUMYT117 × NUMYT-120 was on the top among 13 good specific combinations and revealed maximum positive values (1.84), while NUMYT-120 × NUMYT-124 showed the worst performance (-1.22) for SCA determination. In reciprocal effect, 14 combination exhibited positive effect with the maximum RCA exhibited by combination NUMYT-123 × NUMYT-120 (2.18) (Table 5). In Brassica significant GCA, SCA and RCA effect were observed by Nassimi *et al.* [10]. Similar results were also discussed by Hu *et al.* [15] Whereas Khan *et al.* [6] observed the non-significant effect due to GCA and SCA for seed pod⁻¹ in *B. juncea*.

Seed yield

In (Table 2) indicated that the mean square values for seed yield were found highly significant ($P \leq 0.01$) for GCA and RCA effects whereas for SCA effects non-significant differences were observed. For seed yield plant⁻¹ two out of eight parents showed positive GCA effect (Table 3) in which the maximum GCA effect (4.07) was recorded for parent NUMYT-124 followed by NUMYT-120 (3.63). Low GCA effect for seed yield was observed in NUMYT-

123 (-3.86). It is evident from Table 5.4.1 for seed yield plant⁻¹ that the maximum positive SCA was shown by cross combination NUMYT-105 × NUMYT-124 (4.47) followed by 12 other genotypes showing positive SCA effects for seed yield plant⁻¹ ranged from 0.71 to 4.46, while minimum value (-6.54) was observed in NUMYT-117 × NUMYT-124 (Table 4). Similarly positive RCA (Table 5) was recorded in 11 crosses where highest RCA effects were given by cross NUMYT-105 × NUMYT-103 (3.98) followed by NUMYT-113 × NUMYT-105 (3.48).

The analysis of variance indicated highly significant differences for seed yield plant⁻¹ (Table 1). Our results are further supported by the findings of Nassimi *et al.* [10] who studied variability for seed yield and yield components in *B. napus*. They found significant differences among genotypes for most of the traits. The maximum genotypic and phenotypic variations were available for yield plant⁻¹.

The higher yield in *Brassica* is the major goal of majority of the breeding programs; therefore improvement in the yield and its components is necessary. Hence, positive combining ability is considered desirable for yield and yield contributing traits. In our

studies, significantly positive GCA, SCA and RCA effects were recorded for majority of the parents, crosses and their reciprocals, respectively. In present study, seed yield was governed by additive portion of gene action. Ali *et al.* [3] reported significant GCA and non-significant SCA effect for seed yield and suggested additive genetic portion for inheritance of seed yield in *B. juncea*.

Fray *et al.* [14] found that in *B.napus* and *Arabidopsis*, mean squares due to GC were significant for yield and its components. Our results are further supported by the earlier findings of Youping and Peng [25] who reported significant GCA for seed yield and 1000 seed weight. The results are further strengthened by Hu *et al.* [15] who reported that GCA was significant for seed yield plant⁻¹, pod length and 1000 seed weight. Qian *et al.* [20] also reported significant GCA effects for seed yield in inter-specific cross of *B.napus* and *rapa*. However, Zhou *et al.* [26] developed hybrids in *B.napus*, which were morphologically intermediate between their parents and had a significantly higher GCA for 1000 seed weight.

Table 1. Analysis of variance for various traits in an 8×8 F₂ diallel population of *B.juncea*

Parameters	Mean square		
	Reps	Genotypes	Error
Plant height	1297.88**	1288.32**	266.42
Pods main receme ⁻¹	0.01 ^{ns}	273.06**	86.24
Pod length	0.006 ^{ns}	0.42**	0.07
Seeds pod ⁻¹	2.69 ^{ns}	9.36**	1.39
Seed yield	1261.43**	131.09**	43.92
Primary branches	19.83 ^{ns}	7.67 ^{ns}	10.48

**= Highly significant, *= Significant, ns = Non-significant,

Table 2. Analysis of variance for combining ability in 8×8 F₂ diallel hybrids in *B.juncea*

Parameters	Mean squares			
	GCA	SCA	RCA	Error
Plant height	655.04**	332.62**	469.85**	16.76
Pods raceme ⁻¹	251.44*	65.56**	76.36**	28.74
Pod length	0.36**	0.07**	0.15**	0.02
Seeds pod ⁻¹	6.66**	1.36**	4.24**	0.46
Seed yield	130.28**	22.30 ^{ns}	43.44**	14.63

**= Highly significant (P≤0.01), *= Significant (P≤0.05), ns = Nonsignificant

Table 3. General combining ability effects for all the 8 genotypes in *B.juncea*

Parameters	NUMYT-009	NUMYT-103	NUMYT-105	NUMYT-113	NUMYT-117	NUMYT-120	NUMYT-123	NUMYT-124
Plant height	-4.7	11.9	7.40	-1.24	-3.94	-2.79	-6.56	-0.05
Pods raceme ⁻¹	0.83	4.42	-3.67	0.93	4.11	1.88	-7.31	-1.20
Pod length	-0.20	0.24	-0.05	-0.003	-0.14	0.15	0.063	-0.063
Seeds pod ⁻¹	-0.66	0.12	-0.11	.004	0.14	1.40	-0.62	-0.28
Seed yield	-1.32	0.34	-2.30	-1.84	1.27	3.63	-3.86	4.07

Table 4. Estimates of specific combining ability effects for various traits in an 8×8 F₂ population of *B. juncea*

Genotype	Plant Height	Pods raceme ⁻¹	Pod length	Seeds pod ⁻¹	Seed yield
NUMYT-009 × NUMYT-103	-5.62	6.74	-0.12	0.56	3.31
NUMYT-009 × NUMYT-105	16.00	-2.83	-0.03	-0.59	-1.19
NUMYT-009 × NUMYT-113	1.02	4.86	0.24	0.55	1.61
NUMYT-009 × NUMYT-117	1.16	-0.81	-0.10	-0.15	2.14
NUMYT-009 × NUMYT-120	4.27	0.91	0.23	0.21	4.46
NUMYT-009 × NUMYT-123	2.16	-2.45	-0.04	0.31	-1.54
NUMYT-009 × NUMYT-124	-14.98	0.49	-0.02	-0.28	-3.12
NUMYT-103 × NUMYT-105	8.15	-1.11	0.18	0.25	-0.08
NUMYT-103 × NUMYT-113	9.42	-0.22	-0.07	-0.23	-3.83
NUMYT-103 × NUMYT-117	1.25	6.03	0.10	-1.18	4.47
NUMYT-103 × NUMYT-120	-19.59	-4.79	-0.14	-0.19	-6.41
NUMYT-103 × NUMYT-123	21.93	-0.85	-0.20	-0.79	3.25
NUMYT-103 × NUMYT-124	-0.58	-0.96	-0.24	0.74	1.77
NUMYT-105 × NUMYT-113	-5.90	-1.93	-0.27	-0.25	2.21
NUMYT-105 × NUMYT-117	4.93	-1.23	0.11	-0.33	0.71
NUMYT-105 × NUMYT-120	-14.85	-0.57	0.35	1.66	-0.57
NUMYT-105 × NUMYT-123	-26.58	-2.25	-0.12	-0.44	-0.53
NUMYT-105 × NUMYT-124	16.49	14.70	0.05	0.28	4.73
NUMYT-113 × NUMYT-117	-0.67	-10.72	-0.02	-0.31	0.75
NUMYT-113 × NUMYT-120	-22.19	1.25	0.004	-0.44	1.77
NUMYT-113 × NUMYT-123	11.63	2.32	0.21	0.38	1.05
NUMYT-113 × NUMYT-124	8.25	-4.09	0.03	0.73	-1.52
NUMYT-117 × NUMYT-120	1.70	-3.92	0.02	1.84	5.04
NUMYT-117 × NUMYT-123	-3.04	7.45	0.06	0.05	-2.02
NUMYT-117 × NUMYT-124	0.45	0.03	-0.06	-0.21	-6.54
NUMYT-120 × NUMYT-123	19.31	12.06	0.13	0.98	-1.53
NUMYT-120 × NUMYT-124	5.05	-2.79	0.03	-1.22	-1.08
NUMYT-123 × NUMYT-124	-12.99	-5.54	0.04	-0.19	2.61

Table 5. Estimates of reciprocal combining ability effects for various traits in an 8×8 F₂ population of *B. juncea*

Genotypes	Plant height	Pods raceme ⁻¹	Pod length	Seeds pod ⁻¹	Seed yield
NUMYT103 × NUMYT-009	2.75	-5.37	-0.39	-0.56	-1.79
NUMYT-105 × NUMYT-009	-3.88	-1.43	0.22	0.56	0.74
NUMYT-105 × NUMYT-103	-24.50	7.12	0.22	0.81	3.98
NUMYT-113 × NUMYT-009	3.38	6.25	-0.01	0.56	2.54
NUMYT-113 × NUMYT-103	6.25	14.25	-0.05	0.43	1.13
NUMYT-113 × NUMYT-105	4.19	-2.56	-0.36	0.81	3.48
NUMYT-117 × NUMYT-009	-5.94	-2.62	-0.18	1.00	-3.27
NUMYT-117 × NUMYT-103	9.00	-4.93	0.43	1.00	-9.79
NUMYT-117 × NUMYT-105	-10.19	-8.31	0.24	0.62	1.29
NUMYT-117 × NUMYT-113	7.19	-2.68	-0.02	-1.25	-5.35
NUMYT-120 × NUMYT-009	-16.56	-2.62	-1.01	-2.25	-4.13
NUMYT-120 × NUMYT-103	4.31	-0.75	-0.20	-2.12	-5.87
NUMYT-120 × NUMYT-105	8.06	-8.5	-0.28	-4.25	-1.46
NUMYT-120 × NUMYT-113	-6.19	3.18	-0.01	-1.25	-7.09
NUMYT-120 × NUMYT-117	4.50	-4.56	0.03	-1.43	5.17
NUMYT-123 × NUMYT-009	-22.94	-7.56	-0.20	-1.31	-1.60
NUMYT-123 × NUMYT-103	-5.31	6.75	-0.02	1.00	-0.59
NUMYT-123 × NUMYT-105	-31.44	-8.25	-0.09	-1.12	-1.48
NUMYT-123 × NUMYT-113	35.00	10.68	-0.23	1.43	1.03
NUMYT-123 × NUMYT-117	24.88	-3.25	0.13	1.25	2.55
NUMYT-123 × NUMYT-120	0.50	-1.5	-0.20	2.18	4.88
NUMYT-124 × NUMYT-009	-11.94	-6.00	0.10	-1.18	-3.67
NUMYT-124 × NUMYT-103	-6.81	9.25	0.15	-0.50	-6.94
NUMYT-124 × NUMYT-105	5.23	-1.93	0.33	-2.31	-9.05
NUMYT-124 × NUMYT-113	10.00	-1.5	0.27	-0.75	-7.42
NUMYT-124 × NUMYT-117	27.88	1.43	-0.05	1.31	-0.88
NUMYT-124 × NUMYT-120	26.00	-2.5	-0.04	0.18	0.74
NUMYT-124 × NUMYT-123	-6.56	-9.31	-0.14	-0.06	1.60

Conclusion

On the basis of combining ability ANOVA, it is concluded that all the traits were governed by additive type of gene action and intensive selection in the said breeding material will provide the basis for further improvement and to boost up the seed yield of the mustard. However SCA and RCA effects of the hybrids were also significant hence it necessitates the use of further integrated breeding strategies to efficiently utilize the present genetic material in the future breeding programs.

Authors' contributions

Conceived and designed the experiments: S Inayat & M Zakirullah, Performed the experiments: S Inayat, M Zakirullah & L Naz, Analyzed the data: A Shafi & S Akbar,

Contributed materials/ analysis/ tools: M Ali & S Khan, Wrote the paper: S Inayat & M Zakirullah.

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