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# Analysis of genetic basis of variations and combing ability for yield-related traits in *Brassica* lines by using line × tester analysis

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**Abstract**

Brassica is an important oilseed crop. The genetic basis of plant height, no. of primary branches, no. of pods per plant, no. of pods per raceme, pod length, beak length and 1000 grain weight in brassica lines was estimated through combining ability by using line × tester (5 × 3) analysis. The presence of a significant difference in the means squares of analysis of variance indicated that all the genotypes genetically differed from each other for investigated traits. The super value of $\sigma^2 sca$ over $\sigma^2 gca$ revealed the presence of non-additive gene action for all studied parameters. The results for the *gca* effect concluded that BN3, BN4, and BC27 had higher *gca* effect for many traits. Lines exhibited greater contribution then testers for every trait except beak length. The F1 hybrid of BN3 × BC27 was superiors in *sca* effect for many of the investigated traits. The other best performing hybrids were BN3 × BC7, BN4 × BC27, BCAC × BC7, BCAC × BC27, BCAA × BC7, BCAA× BC27, and BC44 × BC7. This research described the importance of the non-additive type of gene action in brassica and suggested its use in the breeding programs for evaluating genetic variations. The study presented useful information about gene action for various yield controlling traits. Thus, concluded that the use of lines having superior gca and sca in the yield improvement plans for brassica will help in obtaining improved cultivars.

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## Introduction

In Pakistan, the agriculture sector is the economic backbone of the country and impressively growing day-by-day. However, the edible oil scarcity is still alarming for this sector. Among oilseed crops, brassica is widely grown throughout the world. Although brassica is an oilseed crop it also has various uses such as industrial oil, vegetable, forage and fodder, 2nd chief protein source and for producing biodiesel (Kanwal *et al.*, 2014, Ahmad *et al.*, 2012, Azizina, 2012).

During cropping season 2016-17, the area and production for oilseed crops was 190 thousand hectare and 180.5 thousand tonnes in Pakistan. This production had contributed only 12% (0.4 MT) in the total oil (3.7 MT) available for the edible purpose in the country. The remaining 88% was obtained from other countries (Anonymous, 2017). Increase in population and per person consumption has enhanced the edible oil demand (Farhatullah *et al.*, 2004). After cotton, brassica was 2nd largest oil producing crop in Pakistan with 487 thousand acres total cultivation area and 61 thousand tones total production. (Anonymous, 2017-18). To overcome the national oil production and demand gape, it is needed to breed improved varieties (Azam *et al.*, 2013). To increase brassica production, at commercial levels production of hybrid seed has proved much effective. However, the hybrid production has slowed down by unstable fertility restoration system which exploited cytoplasmic male sterility of the hybrids (Akbar *et al.*, 2008). To develop high yield cultivars, identification of batter parents, their crosses abilities, their crossing combinations, and effective breeding method is very necessary (Acharya and Swain, 2004). Line × Tester is an effective mating design, used by the breeders to assess a large number of inbred lines for obtaining useful information on the GCA and SCA to find the genetic basis of useful traits (Farshadfar *et al.*, 2013). Useful information about the quantity and nature of genetic effect can be obtained from the presence of genetic variations. Combining ability provides knowledge about required parentage, type, and degree of gene action of those traits which are controlled by many genes (Ceyhen *et al.*, 2008). Thus it is an effective measure for selecting the best lines for making crossing combinations and (Azizina, 2012).

The presented research was conducted to find appropriate male and female parents with desirable GCA and SCA, hybrids with high SCA values, and to explain the nature of gene action tangled variations in the expressions of investigated traits.

## Material & methods

*Extermental Site*

The current experiment was conducted in the Department of Plant Breeding and Genetics, Faculty of Agricultural Sciences and Technology, Bahauddin Zakariya University, Multan.

*Experimental Material and Layout*

Eight genotypes were sown i.e. BN3, BN4, BCAC, BCAA, BC44 (lines) and BC27, BC7, BC5 (testers) during rabi season and crosses were made according to Line × Tester mating design. Seed obtained by these crosses and the parents were sown next year in randomized complete block design in three replications. Plant to plant distances was 30cm and row to row 60cm in a plot size of 3m x 9m. All the agronomic practices recommended for *Brassica* were followed throughout the growing season.

*Morphological Data*

At the maturity, data of F1 crosses and their parents were recorded for various plant parameters, i.e. plant height (PH, cm), primary branches/plant (NPB), number of siliqua/plant (NSP), main raceme length ( MRL, cm), number of siliquae/raceme (NPR), pod length (PL, cm), beak length (BL, cm), 1000- seed weight (1000SW, g) were measured.

*Statistical Analysis*

The data were subjected to analysis of variance according to (Steel *et al.*, 1997), general and specific combining ability was estimated by Line × Tester analysis described by Kempthorne (1957).

## Results

The current research was conducted to find appropriate parents for various traits in eight Brassica genotypes and to choice superior hybrids regarding their combining abilities for yield and its components. The analysis of variance for different characters is presented in (Table 1). Significant variances were observed between all genotypes for studied traits (Table 2). The mean sum of the square for both testers (males) and lines (females) was highly significant. For line x tester interaction plant height and a number of primary branches showed high significance, whereas the number of pods per raceme and beak length was significant. For studied parameters, the results of SCA were higher as compared GCA.

**Table 1.** Means squares from ANOVA of different traits in Brassica.

| Source | d.f | PH | NPB | MRL | NPR | NPP | PL | 1000GW | BL |
|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 36.900 | 0.86 | 15.47 | 12.88 | 1494.07 | 0.50 | 1.09 | 0.45 |
| Treatment | 22 | 415.95** | 9.18** | 200.89** | 192.96** | 18798.82** | 4.17** | 1.01** | 0.86** |
| Error | 44 | 14.980 | 2.35 | 44.86 | 23.86 | 2184.90 | 0.48 | 0.45 | 0.42 |

*, ** = Significant at 5% and 1% level of probability respectively, d.f = Degree of freedom, PH=Plant height, N.PB=No. of primary branches, MRL=Main raceme length, N.PR=No of pods per raceme, NPP=No of pods per plant, PL=Pod length, 1000GW=1000 grain weight, BL=Beak length.

**Table 2.** Analysis of variance for GCA of various parameters in Brassica.

| Source | d.f | PH | NPB | MRL | NPR | NPP | PL | 1000GW | BL |
|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 36.900 | 0.86 | 15.47 | 12.88 | 1494.07 | 0.50 | 1.09 | 0.45 |
| Lines | 4 | 425.550** | 5.01** | 82.47** | 44.89** | 5313.98** | 0.30** | 0.30** | 0.55** |
| Tester | 2 | 490.250** | 6.45** | 41.15** | 74.90** | 864.22** | 1.23** | 0.58** | 0.57** |
| L x T | 8 | 429.63** | 4.88** | 60.62 | 48.94* | 3504.81 | 0.87 | 0.30 | 0.52* |
| Error | 44 | 14.980 | 2.35 | 44.86 | 23.86 | 2184.90 | 0.48 | 0.45 | 0.42 |
| S²GCA | | 0.27 | 0.02 | 0.19 | 0.12 | 5.95 | 0.00 | 0.09 | 0.00 |
| S²SCA | | 139.84 | 1.70 | 6.02 | 9.55 | 442.24 | 0.07 | 4.54 | 0.05 |
| S²gca /S²sca | | 0.002 | 0.01 | 0.031 | 0.01 | 0.013 | 0.00 | 0.019 | 0.00 |
| Contribution (%) | | | | | | | | | |
| Lines | | 28.70 | 28.45 | 37.91 | 25.83 | 42.56 | 16.72 | 28.50 | 30.66 |
| Tester | | 17.10 | 19.50 | 10.09 | 21.90 | 4.42 | 29.10 | 20.89 | 17.32 |
| L x T | | 56.15 | 53.53 | 54.13 | 54.26 | 54.95 | 56.37 | 52.91 | 55.39 |

*, ** = Significant at 5% and 1% level of probability respectively,S²gca, variance of *gca*; S²sca, variance of *sca*, PH=Plant height, N.PB=No. of primary branches, MRL=Main raceme length, N.PR=No of pods per raceme, NPP=No of pods per plant, PL=Pod length, 1000GW=1000 grain weight, BL=Beak length

*Plant Height (cm)*

Plant height is one of the important yield-related components. In this study, the female (lines) genotypes BC44, BN3, and BN4, BCAA exhibited highly significant results in both positive and negative directions respectively. From the three testers, BC27 and BC7 showed significance in positive and negative GCA respectively (Table 3). The results of SCA presented in Table 4 demonstrated that all the F1 crosses showed better performance except BN3 X BC7. The F1 crosses BN3 X BC27, BN4 X BC5, BCAA X BC7 showed positive highly significant SCA, while BN4 X BC27, BN4 X BC7, BCAC X BC5, BC44 X BC7 showed highly significant results in a negative direction.

*A number of Primary Branches per Plant*

For a number of primary branches only three female parents BN3 exhibited positive significant and BC44, BN4 showed negative significant GCA. In male parents, BC27 and BC5 exhibited significant results in positive and negative direction correspondingly (Table 3). Out of 15 F1 crosses, the F1 crosses BCAC X BC27 and BCAA X BC7 responded positively significant, however, the crosses BCAA X BC27, BCAC X BC7, BN3 X BC27 showed negative but significant specific combining ability (Table 4).

*Main Raceme Length (cm)*

The GCA results presented in table 3 showed that out of 5 female parents (lines) only BCAC (-0.4*) showed negative but significance, whereas the results also revealed that none of the testers showed significant results for GCA. Table 4 presents that amongst 15 crosses combinations, the only F1 cross BC44 X BC7 showed the positive and significant result for SCA, while all other combinations were non-significant.

**Table 3.** Evaluations of GCA effect of male and female parentage.

| Parents | PH | NPB | MRL | NPR | NPP | PL | 1000GW | BL |
|---|---|---|---|---|---|---|---|---|
| Lines | | | | | | | | |
| BN3 | 6.3** | 1.0* | 3.6 | 4.90* | 39.95* | 0.09 | -0.20 | -0.17 |
| BN4 | -9.2** | -0.8* | 4.6 | -0.40 | 9.44 | 0.87 | 0.43 | 0.59* |
| BCAC | 3.0* | 0.8 | -5.1* | -2.32 | -12.10 | 0.14 | -0.54* | -0.42 |
| BCAA | -6.9** | 0.7 | -1.0 | -2.20 | -20.52 | -0.80 | 0.15 | -0.13 |
| BC44 | 8.0** | -0.9* | -2.1 | -0.10 | -18.80 | -0.69 | 0.20 | -0.15 |
| Tester | | | | | | | | |
| BC27 | 7.00** | 0.8* | -1.2 | -3.17* | 3.88 | -0.15 | 0.09 | 0.35* |
| BC7 | -6.5** | 0.7 | 2.5 | -0.46 | -9.70 | 0.48* | 0.43 | -0.23 |
| BC5 | -0.8 | -0.9* | -1.2 | 3.53* | 6.90 | -0.35 | -0.50 | -0.09 |

*, ** = Significant at 5% and 1% level of probability respectively, PH=Plant height, N.PB=No. of primary branches, MRL=Main raceme length, N.PR=No of pods per raceme, NPP=No of pods per plant, PL=Pod length, 1000GW=1000 grain weight, BL=Beak length.

**Table 4.** Effect of specific combining ability of hybrids for all traits in Brassica.

| Hybrids | PH | N.PB | MRL | N.PR | NPP | PL | 1000GW | BL |
|---|---|---|---|---|---|---|---|---|
| BN3 × BC27 | 8.07** | -1.8* | 3.2 | 6.7* | 8.8 | -0.32 | 0.09 | -0.19 |
| BN3 × BC7 | -1.5 | 0.9 | -5.2 | -5.85* | -35.1 | 0.60* | -0.35 | 0.09 |
| BN3 × BC5 | -4.9* | 1.0 | 3.0 | -0.18 | -12.1 | -0.25 | 0.22 | 0.09 |
| BN4×BC27 | -11.3** | 0.9 | 2.9 | -3.0 | 34.0 | 0.46 | -0.32 | 1.32** |
| BN4×BC7 | -9.5** | 0.6 | -5.2 | -1.5 | 2.5 | -0.008 | -0.12 | -0.42 |
| BN4 × BC5 | 19.9** | -1.0 | 3.3 | 4.2 | -34.9 | -0.46 | 0.45 | -0.50 |
| BCAC × BC27 | 4.5* | 1.8* | -4.3 | -1.0 | 11.0 | -0.32 | 0.09 | -0.24 |
| BCAC × BC7 | 10.8* | -1.9* | 2.0 | 0.08 | 18.1 | 0.30 | 0.06 | 0.22 |
| BCAC × BC5 | -12.4** | 0.5 | 1.8 | 1.0 | -32.2 | 0.05 | -0.14 | 0.020 |
| BCAA × BC27 | -4.0* | -1.9* | 1.0 | -2.0 | -37.1 | 0.10 | 0.06 | -0.20 |
| BCAA × BC7 | 9.7** | 1.15* | 1.8 | 3.1 | 4.01 | -0.43 | 0.20 | -0.07 |
| BCAA × BC5 | -2.5* | 0.6 | -3.5 | -1.0 | 36.0 | 0.31 | -0.22 | 0.25 |
| BC44 × BC27 | 5.6* | 1.0 | -2.1 | -0.7 | -38.5 | 0.23 | 0.12 | -0.30 |
| BC44 × BC7 | -9.0** | -0.9 | 7.3* | 4.3 | 10.2 | -0.50 | 0.23 | 0.072 |
| BC44 × BC5 | 4.6* | -0.5 | -5.2 | -4.0 | 31.5 | 0.6 | -0.35 | 0.22 |

*, ** = Significant at 5% and 1% level of probability respectively.

*Number of Pods per Raceme*

A number of pods per raceme play an important role in the Brassica seed yield. During this study, from lines, only BN3 showed positive and significant GCA effect. In three tester BC5 and BC27 showed significant GCA in positive and negative direction respectively (Table 3). Among fifteen hybrids, only two hybrids BN3 X BC27 and BN3 X BC7 exhibited significant SCA positively and negatively correspondingly (Table 4).

*Number of Pods per Plant*

The GCA results from table 3 showed that neither testers nor lines performed well except line BN3, which showed positive and significant general combining ability. In the case of SCA of crossing combinations, all the hybrids exhibited non-significant results.

*Pod Length (cm)*

In the current research, a non-significant GCA was observed for both testers and lines except BC7. The combining ability results for tester (male parent) BC7 were positive and significant (Table 3). The results of SCA presented in table 4 revealed that the performance of hybrids was non-significant except the performance of BN3 X BC7, which showed positive and significant specific combining ability.

*1000-Grain Weight (g)*

For 1000-grain weight the general combining ability of BCAC was significant but in a negative direction. All other lines demonstrated non-significant results. For GCA none of the testers had significant results (Table 3). In the case of SCA all the F1 cross combinations were non-significant (Table 4).

*Beak Length (cm)*

The results for GCA and SCA presented in (Table 3, 4) described that from lines only BN4, from testers BC27 added positive and significant results to GCA. Out of 15 f1 hybrids, only one F1 hybrid BN4 X BC27 revealed highly significant and positive specific combining ability.

## Discussion

To identify the genetic basis of various morphological traits i.e. plant height, main raceme length, beak length, pod length, number of pods per the main raceme, number of pods per plant and 1000 grain weight Line × Tester analysis was used. The significance in mean square values of hybrids and parents for investigated parameters showed the presence of desirable genetic variation among genotypes. The mean square values for parent vs crosses and line × tester were also significant for many of the traits. Thus the non-additive gene action and non-allelic interaction were found. (Akbar *et al*., 2008; Cheema and Sadaqat 2004; Rameah *et al*., 2003; Rao 2001; Sheikh 1998; Sheoran *et al*., 2000; Singh *et al*., 2010; Yadav *et al*., 2005) reported the presence of non-additive gene action in inheritance for various yield-related traits. The *σ2sca/σ2gca* ratio was higher than unity and the value of *σ2sca* was greater than *σ2gca* revealed that overdominance was present for all investigated traits. However, for 1000 grain weight in brassica presence of additive gene effect has also been reported previously by (Wu *et al.,* 2006b; Delourme *et al*., 2006; Sabaghnia *et al*., 2010; Shen *et al*., 2005; Singh *et al.,* 2010; Qian *et al.,* 2007), The *gca* effect of parent genotypes in mainly due to the accumulation of genes as a result of recurrent selection process and these can be transferred to the next generation.

The gene accumulates during recurrent selection results the genetic combining ability effect of parents. This effect can be transferred to the next generation (Hallauer and Miranda, 1988; Kang, 1994). The presence of positive *gca* effect for plant height, number of primary branches, no. of pods per raceme and per plant, pod length and beak length in various male and female parents showed that these genotypes can be helpful in contributing required alleles. Similar results for no. of pods per plant, plant height, beak length, and 1000 grain weight has been reported by Akbar *et al*., (2008). The maximum gca values of BC44, BN3 and BC27 for plant height, BC44, BN4, BCAC, BC27 and BC5 for no. of primary branches, BCAC, BN4, BC7 for main raceme length, BN3, BC27, BC5 for no. of pods/raceme, BN3, BCAA, BC7 and BC5 for pods/plant, BN4, BCAA, BC7 and BC5 for pod length, BCAC, BN4 and BC5 for 1000 grain weight, BN4, BCAC and BC27 for beak length showed that these genotypes can be effective for yield improvement in brassica. The results of this research suggested that the *gca* effect can be an effective method for identifying superior general combiners. The results were similar to the earlier findings of Rameeh *et al.,* (2012). Among crosses, the hybrids BN4 × BC5 and BCAA × BC7 with higher positive *sca* effect but negative *gca* effect proposed that best-combining parents with high *sca* can be obtained from the parents having negative *gca* effects. Azizina (2012) found a similar significant *sca* effect which included parents with negative *gca* values. The F1 cross obtained from parents containing negative *gca* effect shows that there is non-additive epistasis between them. The brassica hybrid between BN4 × BC27 with high gca effects of both parents and the highest *sca* value for beak length showed that the involvement of additive × additive gene action. Bhatt *et al.,* (2004) and Hariprasanna *et al.* (2006) stated that it is not necessary that the parental *gca* performance can influence the performance of hybrids. Differences in general combining ability effects have been attributed to additive, additive × additive, and higher-order additive interactions, whereas variances in *sca* have been attributed to non-additive genetic variance (Falconer, 1996). For hybrid breeding, it has been suggested that the consideration of the sum of gca values of both parents will be quite effective as compared to the individual gca value of each parent (shen *et al*., 2005).

## Conclusion

Breeding is an important application for improvement of the plant through this approach enhance the capability of plant and reshuffling of the gene by hybridization. Hybridization is the best way to develop good performing varieties. Among parents, BN3 and BC27 exhibited best performance for *gca* for various investigated traits such as plant height, no. of primary branches, no. of pods per raceme and number of pods per plant. The F1 hybrids of BN4 × BC5 for PH and 1000SW, BCAA × BC7 for NPB, BC44 × BC7 for MRL, BN4 × BC27 for NPP and BL, BN3 × BC27 for NPR and BN3 × BC7 for PL showed superior and significant *sca* performance and these genotypes has potential for being used in Brassica breeding programs for yield improvement. It is suggested that these hybrids should be cultivated in various areas of Pakistan to evaluate their effectiveness. The presence of non-additive gene action revealed that parents should be selected on the basis of performance will help in the improvement of various traits in Brassica.

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