



Genetic Analysis and Combining Ability Studies for Yield Related Characters in Rapeseed

Aamar Shehzad^{*1}, Hafeez Ahmad Sadaqat¹, Muhammad Asif¹, Muhammad Furqan Ashraf²

¹Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan

²College of Crop Science, Fujian Agriculture and Forestry University, Fuzhou-350002, China

ARTICLE INFO

Article history:

Received 08 May 2015

Accepted 26 August 2015

Available online, ISSN: 2148-127X

Keywords:

Rapeseed

Combining ability

Genetic effects

Yield related characters

*Corresponding Author:

E-mail: aamarshehzad1763@gmail.com

ABSTRACT

Combining ability analysis has a key position in rapeseed breeding. To estimate the combining ability effects for yield controlling traits in rapeseed, three testers and five lines were crossed using line \times tester design in randomized complete block design with three replications. Mean sum of squares of analysis of variances for genotypes were significant for all of the traits; indicating the presence of significant genetic variation. All the interactions between lines and testers exhibited significant results of mean sum of squares for combining ability. Line 'Duncled' was found good general combiner for decreased Plant height (PH:-2.0), Days taken to 50% flowering (DF: -15.8) and Days taken to maturity (DM:-3.4) while tester 'Punjab Sarson' for increased Number of seed/siliquea (SS: 2.2), Number of siliqueae/plant (SP: 2.2) and decreased DF (-3.0) traits. Significant general and specific combining ability effects were observed. The best hybrid combination on the basis of specific combining ability effects was "Durre-NIFA \times ZN-M-6" for Seed yield/plant (SY: 2.7), DF (-6.1) and DM (-3.5). PH (-0.2), Siliquea length (SL: -0.1), SS (-0.03) and SY (0.2) showed non-additive genetic effects. The half of the characters revealed additive and remaining half showed non-additive genetic effects. The present study unveiled the importance of both type of genetic effects demanding the application of integrated breeding approaches for exploiting the variability. 'Punjab Sarson \times ZN-M-6' exposed maximum SS (30) and SP (837). Maximum SY (75.9g) and minimum DF (64) were showed by 'Legend \times Duncled'. The present research delivers valuable information of genotypes for promoting yield by means of improving yield related characters.

Introduction

Rapeseed includes *Brassica napus* L. (AACC=38) and *Brassica rapa* (AA=10). Rapeseed has third rank in production and important source of vegetable oil for the world. It is also second leading source of protein meals for the world (Azizinia, 2012). The main rapeseed-producing countries of the world are Canada, China, India and France (FAOSTAT-2012).

The population of Pakistan is sixth in number in the world (188.02 million) and rising rapidly (1.9% growth rate) which is positively correlated with consumption of edible oil (Pak. Economic Survey, 2013-14). For that, the production of oilseed crops must be increased by giving high productive varieties to farmers.

Hybrid seed production at commercial level is an effective method to boost up production of rapeseed. Male sterility in rapeseed was found stable that is good for high seed fertility. But fertility restoration mechanism is not stable which hinder the CMS exploitation in hybrid seed production at commercial level (Akbar et al. 2008). Genetic variability can efficiently be used by gaining knowledge related to amount and type of genetic effects. Combining ability is useful to select superior lines for hybrid combination (Azizinia, 2012). The variances of general and specific combining abilities state the gene

action type in breeding material. Additive and non-additive genetic effects due to variance of GCA and SCA arise from dominance and epistatic deviations (Akbar et al. 2008)

Combining ability analysis provides information about desirable parents, nature and magnitude of gene action controlling polygenic traits (Ceyhan et al., 2008). Line \times tester analysis is an effective way to find out combining abilities i.e. GCA and SCA, of large number of crossed parents. Many researchers made use of line \times tester analysis for genetic analysis of agro-morphological traits as well as assessment of GCA and SCA effects in cotton, sunflower, soybean, wheat, pea and Brassica (Farshadfar et al., 2013). The present study is planned to evaluate the significance, GCA of lines and testers, SCA of hybrids for studied traits by using line \times tester method.

Materials and Methods

The experimental material consisted of eight *Brassica napus* L. genotypes named Duncled, K-258, ZN-R-1, ZN-R-8, ZN-M-6, Punjab Sarson, Legend and Durre-NIFA. These parental materials were obtained from germplasm collection of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. During

October, 2012-13, five lines and three testers were sown and crossed in line \times tester design to obtain cross seeds. Seeds of eight parents and 15 crosses were laid out in randomized complete block design (RCBD) with three replications during October, 2013-14. Each entry was sown in plot having dimension 3m \times 10m. The plant to plant (P \times P) distance was 30cm and row to row (R \times R) distance was 60 cm. Younger plants were thinned to maintain recommended P \times P distance. Optimum dose of NPK fertilizers were applied for healthy growth. Plant protection measures were utilized to maintain the experimental crop healthy. At the maturity stage, ten plants of each genotype from each plot were randomly chosen to record data of F1 plant for the 15 characters. Data were taken for characters i.e. plant height (cm), siliqua length (cm), number of siliquae/plant, number of seed/siliqua, 1000 seed weight, seed yield/plant (g), days taken to 50% flowering and days taken to maturity. Data were subjected to analysis of variance (Steel et al., 1997) to evaluate the significance of differences among F1 hybrids and their parents. Line \times tester analysis (Kempthorne, 1957) was used to estimate general combining ability (GCA) and specific combining ability effects (SCA).

Results and Discussion

Plant height (cm)

According to results of MSS (mean sum of squares) analysis of variance, parents, lines and testers showed non-significant ($P>0.05$) differences. Crosses and L \times T interactions showed significant results ($P<0.05$) for plant height. Female genotype Duncled revealed significant GCA (-2.0) for plant height (Table 1). All the remaining female genotypes (K-258, ZN-R-1, ZN-R-8 and ZN-M-6) and testers (Punjab Sarson, Legend and Durre-NIFA) showed non-significant results for GCA. Rameeh (2012b) conducted his studies in rapeseed and found that three lines revealed significant GCA effects; two lines in positive and one line in negative direction. The maximum negative GCA values (-5.93) showed by line RW. Azizinia (2012) also found the significant results in which parent (GA096) has significant negative GCA (-4.77). Lines Golarchi and Ayub2000 revealed significant and highly significant GCA effects (-7.82 and -26.3) for plant height.

According to the results of Table 2, out of fifteen crosses, one cross (Durre-NIFA \times Duncled) revealed significant SCA effects in positive direction. Taller plants in *Brassica napus* are susceptible to lodging, therefore short stature plants are required to gain maximum yield with negative SCA effects. Cross Punjab Sarsoon \times Duncled showed negative SCA trend (-1.4) for plant height. Significant GCA and SCA results were calculated by previous researchers. According to the study of Nassimi et al. (2006a), four parents exhibited negative effects of GCA for plant height. The maximum significant effect (-5.70) was found in NUR2 parent. Thirteen crosses out of 28 revealed SCA effect in negative direction. The maximum significant effect (-12.66) was found in NUR2 \times NUR4 cross which is higher than the present study. In

another study, Tester Lagena showed significant GCA (-6.244) and six hybrids out of 15 revealed significant ($P<0.05$) SCA results, three in negative and three in positive direction (Ahsan et al., 2013). Farshadfar et al. (2013) calculated the results in which five lines showed significant GCA values ($P<0.01$) while one line revealed GCA results ($P<0.05$) for plant height in both direction. Line Ceres showed maximum negative GCA (-17.98). Two crosses (Ryder \times Parade and Shiralee \times Parade) exhibited significant SCA results ($P<0.05$) in negative (-5.81) and positive (5.86) direction respectively. Muhammad et al. (2014) also calculated the similar results and found that line G2 showed minimum GCA (-4.98) effects followed by G4 (-1.92) and cross G2 \times G9 possessed minimum SCA values (-1.51) and proved best specific combiner.

Results of Table 4 exposed the mean values of plant height for fifteen crosses were 157.83 cm. The cross 'Legend \times K-258' showed maximum (172 cm) while 'Punjab Sarson \times Duncled' revealed minimum plant height (144 cm). Akbar et al. (2008) observed 167.5 cm average plant height in Rapeseed which is approximately close to present study. Noor-Ul-Abideen et al. (2013) determined plant height ranged from 156 to 180 cm with the mean value of 170 cm. Marjanovid-Jeromela et al. (2008) and Honsdorf et al. (2010) observed 132-193 cm and 142-181 cm plant height with mean 163 cm respectively. Girke et al. 2012 found supporting findings and calculated 146-177 cm plant height range in 44 resynthesized lines of rapeseed.

Siliqua length (cm)

In analysis of variance for siliqua length, parents, crosses and L \times T interactions revealed highly significant ($P\leq 0.01$) results. All the lines and testers showed non-significant results for GCA (Table 1). Siliqua length is directly correlated with number of seeds and ultimately yield, so positive SCA effects are beneficial. Hybrids (Legend \times K-258 and Durre-NIFA \times K-258) revealed highly significant (2.7) and significant SCA effects (-2.6) for siliqua length respectively. Other thirteen hybrids revealed non-significant results for SCA effects. Muhammad et al. (2014) concluded his studies where parent G6 possessed GCA values (0.89) and proved best general combiner for siliqua length. Cross G4 \times G6 proved best specific combiner as it revealed maximum SCA effects (0.93). Jia et al. (2013) also found similar results in which significant and highly significant GCA effects of eight rapeseed lines were calculated for siliqua length. Genotype ZAYOU66 revealed maximum GCA (3.52).

The siliqua length of the fifteen Brassica genotypes (Table 4) displayed that siliqua length present in 'Legend \times K-258' (8 cm) was the maximum and minimum in 'Durre-NIFA \times K-258' (5.4 cm) with the mean values (6.44 cm). Akbar et al. (2008) observed identical results and determined mean siliqua length of 6.87 cm. Rameeh (2012a) observed siliqua length range (4.40-6.25 cm) in six spring cultivars of rapeseed. Noor-Ul-Abideen et al. (2013) discover matching conclusions of siliqua length ranged from 6 to 8 cm with the mean value of 7 cm.

Table 1 General combining ability effects for eight characters in *Brassica napus* L.

Lines/characters	PH	SL	SS	SP	SW	SY	DF	DM
Duncled	-2.0*	1.6	1.1	0.9	-0.6	1.6	-15.8**	-3.4**
K-258	1.3	1.0	-2.1*	0.2	0.9	0.1	-1.9	-0.3
ZN-R-1	1.2	-0.5	1.2	-2.2	-1.0	-1.8	6.6**	3.2**
ZN-R-8	0.4	-2	-0.1	-0.8	-0.8	-1.3	3.3**	-4.3**
ZN-M-6	-1.0	-0.1	-0.2	1.9	1.5	1.4	7.8**	4.8**
Testers								
Punjab Sarson	0.1	-0.1	2.2*	2.2*	0.6	1	-3**	-1.6
Legend	0.7	1.5	-0.1	1.6	-1.8	2.3*	-6.4**	9.8**
Durre-NIFA	-0.9	-1.5	-2*	-3.8**	1.2	-3.4**	9.4**	-8.1**

* = Significant at level of P=0.05, ** = Significant at level of P = 0.01

Table 2 Specific combining ability effects for eight characters in *Brassica napus* L.

Hybrids/characters	PH	SL	SS	SP	SW	SY	DF	DM
Punjab Sarson × Duncled	-1.4	-0.1	-1.9	-2.4*	-1.9	-2.2*	1.3	-5.4**
Punjab Sarson × K-258	-0.3	-0.1	0.5	0.3	1.4	1.1	-8.6**	-3**
Punjab Sarson × ZN-R-1	-0.8	-0.9	-0.6	1.2	-0.4	1.1	7.8**	1.1
Punjab Sarson × ZN-R-8	1.4	0.2	0.4	0.6	0.1	0.5	0.0	5.9**
Punjab Sarson × ZN-M-6	1.2	0.9	1.7	0.3	0.8	-0.4	-0.6	1.4
Legend × Duncled	-0.7	-1.1	-0.8	0.2	0.4	1.6	-8.7**	3.8**
Legend × K-258	1.6	2.7**	1.3	1.0	-0.3	0.7	6.5**	2.7**
Legend × ZN-R-1	0.8	-0.5	0.8	-0.9	-0.7	-0.6	-4.2**	1.1
Legend × ZN-R-8	-0.3	-0.1	0.8	0.6	-1.1	0.7	-0.3	-9.7**
Legend × ZN-M-6	-1.4	-1.1	-2.2*	-0.9	1.7	-2.3*	6.8**	2.1*
Durre-NIFA × Duncled	2.1*	1.2	2.7**	2.2*	1.5	0.7	7.4**	1.7
Durre-NIFA × K-258	-1.3	-2.6*	-1.9	-1.3	-1.1	-1.8	2*	0.3
Durre-NIFA × ZN-R-1	0.0	1.4	-0.2	-0.2	1.1	-0.5	-3.5**	-2.2*
Durre-NIFA × ZN-R-8	-1.1	-0.1	-1.2	-1.2	1.0	-1.2	0.3	3.7**
Durre-NIFA × ZN-M-6	0.2	0.2	0.5	0.5	-2.5*	2.7**	-6.1**	-3.5**

* = Significant at level of P=0.05, ** = Significant at level of P = 0.01

Table 3 Variances due to GCA and SCA and their ratios for eight characters

Trait	PH	SL	SS	SP	SW	SY	DF	DM
Genetic effects	-0.2	-0.1	-0.03	1.2	2.6	0.2	1.1	1.4

Table 4 Range, Mean for eight characters in *Brassica napus* L.

Traits	PH _{cm}	SL _{cm}	SS	SP	SW _g	SY _g	DF	DM
Range	144-172	5.4-8	19-30	360-837	3.2-3.8	18-75.9	64-80	140-160
Mean	157.83	6.44	25.99	639.41	3.51	46.59	74.69	152.37

PH=Plant height SW=1000 seed weight SL=Siliqua length SP=Number of siliqua/plant SS=Number of seed/siliqua SY=Seed yield/plant DF=Days taken to 50% flowering DM=Days taken to maturity

Number of seeds/siliqua

Parents, crosses, testers and L x T interaction notified highly significant ($P \leq 0.01$) results. According to results of Table 1, only one line "K-258" showed significant ($P < 0.05$) GCA effects (-2.1). Testers (Punjab Sarson and Durre-NIFA) revealed significant effects of GCA (2.2 and -2.0) respectively for number of seeds/siliqua. According to the previous studies of Azizinia (2012), one parent (Zarfam) exposed significant GCA results (0.55). Farshadfar et al. (2013) predicted similar results in which four lines showed significant results of GCA at $P < 0.05$ or $P < 0.01$. Line 'Rgs003' revealed maximum GCA (6.24) tracked by line Duncled (3.24).

Two hybrids (Legend × ZN-M-6 and Durre-NIFA × Duncled) showed significant ($P < 0.05$) and highly significant ($P < 0.01$) effects of SCA (-2.2 and 2.7) respectively for number of seeds/siliqua (Table 2). Ahsan

et al. (2013) calculated similar effects where three lines showed GCA results at $P \leq 0.01$ (7.79, -12, 12.9) and one line at $P < 0.05$ (4.63). Twelve crosses expressed SCA results at $P < 0.05$ or $P < 0.01$, five in positive direction. Rameeh (2011) predicted significant effects of GCA (1.65) for line Modena. Four crosses exhibited significant ($P < 0.01$) results of SCA, two in positive and two in negative direction. Cross Zarfam x H1 showed maximum SCA effects (1.85). Rameeh (2012b) found highly significant GCA values (3.29) for line '19H'. Crosses 19H × R1 and RGS3006 × R2 possessed positive SCA effects and proved superior to others.

The number of seeds/siliqua was highest (30) in the genotype 'Punjab Sarson × ZN-M-6' and lowest (19) in 'Legend × ZN-M-6' with the mean values of 25.99 (Table 4).

Akbar et al. (2008) calculated 19.2 mean number of

seeds per siliqua in rapeseed. Rameeh 2012a observed range of number of seeds per siliqua (13-20) in six spring cultivars of rapeseed. Noor-Ul-Abideen et al. (2013) discovered close results to the present findings that number of seeds/ siliqua ranged from 19 to 25 with mean value of 22.

Number of siliquae/plant

The results of analysis of variance revealed that parents showed non-significant differences ($P>0.05$) and their crosses presented highly significant ($P<0.01$) results. Highly significant differences ($P<0.01$) were observed for genotypes. Table 1 exposed the results of GCA for lines and testers. All female lines showed non-significant ($P>0.05$) effects of GCA. Tester (Punjab Sarson) depicted significant result of GCA (2.2) while tester (Durre-NIFA) noticed highly significance GCA effects (-3.8) in negative direction for number of siliquae/plant. Azizinia (2012) found significant results in which two parents (Sunday and SW0756) revealed highly significant GCA (4.14 and 3.76) for number of siliqua per plant respectively. Farshadfar et al. (2013) disclosed the chosen results where four lines indicated highly significant results and one line exposed significant GCA effects. Line Duncled revealed maximum GCA (16.14).

More number of siliquae/plant, higher will be the yield of rapeseed/mustard plants so positive effects of GCA and SCA were desirable for this trait. Hybrid combinations (Punjab Sarson \times Duncled and Durre-NIFA \times Duncled) showed significant results ($P<0.05$) of SCA (-2.4 and 2.2) respectively. Significant results of GCA and SCA for number of siliquae/plant were also previously calculated. Farshadfar et al. (2013) found significant and highly significant SCA effects for five crosses. Cross Shiralee \times Parade unveiled maximum SCA (24.50) followed by Elect \times Option500 (20.19). Rameeh (2011) analyzed significant GCA effects. One line named Licord showed highly significant GCA effects (-11.13). Four crosses revealed significant SCA effects in both directions. Cross Licord \times H2 exhibited maximum SCA results (10.39). Rameeh (2012b) assessed favored effects in which six cross showed highly significant while one cross significant SCA effects in both direction. Cross Option \times R1 have maximum positive SCA values (15.06) for number of siliqua per plant.

According to the results (Table 4), number of siliquae/plant ranged from 360 (Durre-NIFA \times ZN-R-8) to 837 (Punjab Sarson \times ZN-M-6). The mean values of fifteen genotypes were 639.41 for number of siliquae/plant. Noor-Ul-Abideen et al. (2013) exposed that number of siliquae/plant ranged from 176 to 270 with mean value of 220.

1000 seed weight (g)

According to results of analysis of variance for 1000 seed weight, genotypes and crosses manifested significant ($P<0.05$) results while interactions (L \times T) showed highly significant ($P\leq 0.01$) results. None of the line/tester parent exhibited significant GCA effects (Table 1). Rameeh (2012b) calculated significant GCA (-0.30) for one line Sarigol that is not found in this study. Only one hybrid (Durre-NIFA \times ZN-M-6) out of fifteen showed significant

($P<0.05$) SCA result (-2.5) for 1000 seed weight. Similar results were also reported by Azizinia (2012) and Ahsan et al. (2013) in rapeseed and found highly significant SCA (0.589, 0.578 and 0.80) for three crosses and significant SCA (2.99) for one cross 'Ayub2000 \times Hybrpol' respectively. Farshadfar et al. (2013) estimated significant or highly significant GCA for six lines in both directions. Line 'Rgs003' and cross 'Magent \times Option500' possessed desirable GCA (0.21) and SCA (0.12) effects respectively. Rameeh (2011) found highly significant GCA results (0.26, -0.26) for both tester (H1, H2) respectively and significant GCA (0.20) for line Locord. Two crosses (Licord \times H1 and Licord \times H2) showed highly significant SCA (-0.36 and 0.36) respectively.

The range of 1000 seed weight in fifteen Brassica genotypes (Table 4) were from 3.2 g (Legend \times ZN-R-1) to 3.8 g (Punjab Sarson \times K-258) with the mean values of 3.51 g. Akbar et al. (2008) calculated mean 1000 seed weight of 3.16g in rapeseed genotypes. Rameeh 2012a determined 1000 seed weight in six spring cultivars of rapeseed ranged from 2.88 to 4.15 g. Noor-Ul-Abideen et al. (2013) found more variability and discovered the range of 1000 seed weight (3-5g) with the mean value of 4.0g.

Seed yield/plant (g)

In ANOVA, parents, genotypes, crosses, parents vs. crosses, testers and line \times tester interactions notified highly significant ($P\leq 0.01$) results. In Table 1, all female parents exhibited non-significant ($P>0.05$) results of GCA. Two testers (Legend and Durre-NIFA) revealed significant and highly significant GCA (2.3 and -3.4) results respectively for seed yield/plant. Amiri-Oghan et al. (2009) computed highly significant GCA values of four genotypes for grain yield. Rameeh (2012b) conducted his studies in rapeseed and found significant effects for four lines. The line 'RGS3006' exhibited maximum GCA values (375.38). The findings of Farshadfar et al. (2013) unveiled highly significant GCA for four lines and significant for one line. Line 'Rgs003' showed highest GCA effects (421.26).

According to results of Table 2, hybrids (Punjab Sarson \times Duncled and Legend \times ZN-M-6) revealed significant ($P<0.05$) results of SCA (-2.2 and -2.3) while hybrid "Durre-NIFA \times ZN-M-6" showed highly significant SCA effects (2.7). Seed yield/plant has positive effects on yield, so positive effects of GCA and SCA are desirable. Therefore, "Durre-NIFA \times ZN-M-6" cross showed highly significant SCA effects in positive direction and proved good specific combiner. Desirable results were also evaluated by different breeders in rapeseed germplasm and presented significant results for seed yield/plant. Azizinia (2012) assessed two crosses for highly significant SCA results. The maximum GCA effect (454.79) was shown by line Modena. Two crosses (Licord \times H1 and Licord \times H2) showed significant and other two (Zarfam \times H1 and Zarfam \times H2) highly significant SCA effects. The maximum positive effects (534.66) showed by cross Zarfam \times H1 (Rameeh, 2011). Rameeh (2012b) found positive effects of SCA for crosses (RW \times R1 and Sarigol \times R2) and proved good crosses to promote seed yield.

According to the results (Table 3) the mean values of seed yield/plant in fifteen crosses were 46.59 g. The cross 'Legend × Duncled' showed maximum (75.9 g) while 'Durre-NIFA × ZN-R-8' revealed minimum seed yield/plant (18 g). Akbar et al. (2008) described 23.2g average values of seed yield/plant which is lower than the present findings. Noor-Ul-Abideen et al. (2013) also discovered lower effects and calculated seed yield/plant ranged from 14 to 24g with the mean value of 18g.

Days taken to 50% flowering

In analysis of variance for days to 50% flowering, genotypes, parents, crosses, lines, testers and their interaction revealed highly significant ($P \leq 0.01$) differences. Early flowering enhances the length of seed filling period, so bold seed formation occurs due to the availability of enough time for seed filling. Therefore negative effects of GCA and SCA are desirable for rapeseed. Four female parents out of five (Table 1) revealed highly significant ($P \leq 0.01$) GCA effects. Testers (Punjab Sarson and Legend) showed desired significant GCA (-3 and -6.4) while Durre-NIFA revealed highly significant GCA results (9.4). Amiri-Oghan et al. (2009) estimated genotype 'Tower' as best general combiner and two genotypes (Regent and Tower) showed highly significant negative GCA for days to flowering.

According to the results of Table 2, nine hybrids showed highly significant SCA effects. Desirable negative effects of SCA were showed by hybrids (Punjab Sarson × K-258, Legend × Duncled, Legend × ZN-R-1, Durre-NIFA × ZN-R-1 and Durre-NIFA × ZN-M-6). The cross "Legend × Duncled" revealed highest SCA (-8.7) effects followed by Punjab Sarson × K-258 (-8.6). Significant effects of GCA and SCA for days to 50% flowering were determined by many researchers. Wang et al. (1997) found significant effects of GCA and SCA in Brassica plants. He recorded 14 crosses for early flowering. Nassimi et al. (2006a) predicted four parents that were showing negative effects of GCA and maximum negative effect exposed by parent NUR1 (-1.89). Seventeen crosses revealed SCA effect in negative direction. Cross NUR2 × NUR3 showed maximum SCA (-2.48). Similar results were also calculated by Muhammad et al. (2014) in *Brassica napus* and found genotype G2 as best general combiner and G4 × G9 and G6 × G9 proved best specific combinations.

The cross 'Punjab Sarson × ZN-R-1' showed highest (80) while 'Legend × Duncled' revealed minimum number of days (64) taken to 50% flowering. The mean values of fifteen genotypes were 74.69 days.

Days taken to maturity

The results of analysis of variance for days taken to maturity revealed that parents, crosses, genotypes, lines and testers showed highly significant ($P \leq 0.01$) results. Interactions (L × T) showed highly significant genetic differences. In Table 1, female genotypes (Duncled, ZN-R-1, K-258 and ZN-M-6) exhibited highly significant ($P \leq 0.01$) general combining ability effects. Females "Duncled" and "ZN-R-8" showed GCA effects in negative direction. Testers "Legend" and "Durre-NIFA" revealed highly significant effects of GCA (9.8, -8.1)

respectively for days taken to maturity.

According to the Table 2, crosses (Punjab Sarson × Duncled, Punjab Sarson × K-258, Punjab Sarson × ZN-R-8, Legend × Duncled, Legend × K-258, Legend × ZN-R-8, Durre-NIFA × ZN-R-8 and Durre-NIFA × ZN-M-6) revealed highly significant ($P \leq 0.01$) SCA (-5.4, -3.0, 5.9, 3.8, 2.7, -9.7, 3.7 and -3.5) while crosses "Legend × ZN-M-6 and Legend × ZN-M-6" manifested significant SCA (2.1 and -2.2) respectively. Early maturity crops are preferred to grow because these took less number of days for ripening so negative effects of SCA are beneficial. The hybrid "Legend × ZN-R-8" showed maximum negative effects of SCA (-9.7) followed by "Punjab Sarson × Duncled" (-5.4). Similar effects were also calculated by Amiri-Oghan et al. (2009) in rapeseed and found two parents (Regent and Tower) revealed highly significant and one parent (Cobra) showed significant negative results of GCA for days to maturity.

According to the results (Table 4) the mean number of days taken to maturity by fifteen crosses was 152.37. The cross 'Legend × ZN-M-6' showed highest (160) while 'Punjab Sarson × Duncled' revealed lowest number of days (140).

Variances due to GCA and SCA and their ratios

The variance owing to GCA and SCA were assessed to know the contribution of additive and dominance genetic effects involved in the inheritance of traits. Variances ratios between GCA and SCA less than unity specified the occurrence of non-additive genetic effects or vice versa to additive genetic effects. According to Table 3, Number of siliquae/plant, 1000 seed weight, days taken to flowering and days taken to maturity showed the occurrence of additive genetic effects while remaining four characters revealed non-additive genetic effects.

Rameeh (2011) and Rameeh (2012a) determined the similar results and described number of siliquae/plant, 1000 seed weight had additive and siliqua length, seed yield/plant, number of seeds/siliqua had non-additive gene actions respectively. Yadev et al. (2005) and Amiri-Oghan et al. (2009) evaluated the rapeseed genotypes and found additive as well as non-additive gene actions for seed yield and additive genetic effects for days taken to flowering and days taken to maturity respectively. Khan and Khan (2006) determined that number of seeds/siliqua, 1000 seed weight and seed yield/plot had non-additive effects while number of siliquae/plant had additive gene action that completely support the present study except 1000 seed weight. Akbar et al. (2008) evaluated *Brassica napus* germplasm and found non-additive genetic effects for plant height, siliqua length, number of siliquae/plant, number of seeds/siliqua, 1000 seed weight and seed yield. Singh et al. (2010) calculated the similar findings and exhibited additive effects in *Brassica juncea* for days taken to flowering, days taken to maturity, seed weight and non-additive for plant height and seed yield/plant. Saeed et al. (2013) predicted partially identical outcomes and evaluated additive effects in *Brassica juncea* for plant height, 1000 seed weight, number of seeds/siliqua, number of siliquae/plant, days taken to flowering, days taken to maturity while non-additive for seed yield/plant.

Conclusion

The present study assessed the importance of both types of gene actions i.e. additive and non-additive in controlling the yield related traits. The importance of additive gene action was computed by Cheema and Sadaqat (2004) and Rameah et al (2003) while Cheema and Sadaqat (2004) and Khan and Khan (2005) exposed the vital role of non-additive gene action for controlling yield related traits. Both effects for GCA and SCA were also important for controlling quantitative characters in rapeseed (Akbar et al., 2008). Cheema and Sadaqat (2004) recommended early generation selection for traits having additive genetic effects while selection in later generation was suggested for non-additive genetic effect.

This research leads to the identification of better combinations with greater improvement of traits. In a selection procedure, plant researchers put more stress to average performance of multiple characters (Azizinia, 2012). The cross 'Durre-NIFA × Duncled' revealed maximum number of seeds/siliqua and number of siliquae/plant. Amiri-Oghan et al. (2009) found positive effects of number of seeds/siliqua, 1000 seed weight and number of siliquae/plant on seed yield. Significant values of seed yield/plant, number of days to flowering and maturity were exhibited by the cross 'Durre-NIFA × ZN-M-6'. It is recommended to grow these crosses in different climatic zones of Pakistan to identify their potential and stability and recommended stable one for general cultivation.

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