

Research Article



Combining Ability Analysis for Maturity and Plant Architecture Traits in Intra-Specific Crosses of Rapeseed (*Brassica napus* L.)

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Abstract | Combining ability was determined in an 8×8 diallel intra specific F_1 crosses in rapeseed (*Brassica napus* L.) during 2011-2013 to scrutinized potential lines, hybrids, and nature of gene action involved in the inheritance of maturity and plant architecture traits. Analyzed data revealed highly significant differences among the genotypes for days to flowering, maturity, plant height, primary branches plant⁻¹ and main raceme length. Analysis of combining ability revealed highly significant GCA (general combining ability), SCA (specific combining ability) and RCA (reciprocal combining ability) effects for the studied traits. Based on GCA, best general combiners were AUP-7 for earlier flowering and maturity, AUP-2 for plant height, AUP-14 for primary branches plant⁻¹ and AUP-9 for main raceme length. Based on SCA effects, best F_1 hybrids were AUP-7 \times AUP-14 (days to flowering), AUP-8 \times AUP-9 (days to maturity), AUP-17 \times AUP-18 (plant height), AUP-14 \times AUP-20 (primary branches plant⁻¹) and AUP-14 \times AUP-20 (main raceme length) and could be utilize in future rapeseed breeding programs. The estimates of variances of combining ability (σ^2 GCA, σ^2 SCA) and predictability ratio (σ^2 GCA/ σ^2 SCA>1.00) indicated that gene action was predominantly additive for days to flowering while, for the rest of the traits non additive gene action was responsible as the predictability ratio was less than unity which was further confirmed by higher values of variances of SCA than GCA. In present study for all the traits except days to flowering, non-additive gene action was prominent therefore selection should be delayed to late segregation generation.

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Introduction

Rapeseed and mustard belong to brassicaceae family and is considered as the most important oil seed crop. Worldwide it ranks third with an annual growth rate of the soybean and palm. It is the second leading source of protein meals around the globe. China, Canada, India and Northern Europe are mustard leading producing regions of the world. Rapeseed oil is used for various purposes i.e. food, industrial and biodiesel production (Sabaghnia et al., 2010). In Pakistan, rapeseed and mustard are major oil seed crops. In

Pakistan edible oil demand is increasing each year and domestic production cannot met the consumption requirements, therefore, huge amount of edible oil is imported each year (Fayaz et al., 2014). The domestic production of oilseed crops per unit area is quite lower due to the decrease in cultivatable lands, less access to quality seeds, poor socioeconomic condition of the farmers and sudden climatic changes.

To feed the ever-increasing population development of new varieties with early maturity and high yield are prerequisites. Hybridization is one of the technique

through which superior germplasm could be developed by combining genes from suitable parents of diverse origin. Selection of the parents based on diversity and hybridizing them, is necessary to know about the nature and magnitude of gene actions responsible for controlling the inheritance of various attributes along with combining ability of the parents and their cross combinations. In the current scenario of climatic change, development of new lines with early maturity and short stature plants are desirable in rapeseed. Early maturity escapes plant from environmental stresses, incidence of insects' pest and diseases that generally coincides with flowering and maturity. Dwarf plants are resistance to lodging and more fertilizer responsive as compared to taller plants.

The yield advancement and development of new lines in brassica requires information regarding the nature of combining abilities of parents and gene actions involved in expression of maturity and plant phenological traits. Diallel mating is one of the methods used by rapeseed breeder to identify superior lines and their best promising hybrids through general combining ability (GCA) and specific combining ability (SCA) effects. Griffing (1956) approach of diallel analysis has been used widely for combining ability analysis. This technique elucidates the nature and magnitude of various types of gene actions involved in the expression of the studied traits. The variance for GCA includes the additive portion of the total variance, whereas for SCA includes the non-additive portion of the total variance, arising largely from dominance and epistatic deviations (Malik et al., 2004). The present study was undertaken to; 1) identify promising parents and their F₁ hybrids 2) determine the inheritance pattern (nature of gene action) responsible for maturity and plant architecture traits and 3) utilize the potential parents as a source of germplasm in future rapeseed breeding programs to develop early maturing and lodging resistant (short stature) plants.

Materials and Methods

The research was conducted at Research Farm, Department of Plant Breeding and Genetics, The University of Agriculture Peshawar Pakistan. Breeding material consisted of eight *Brassica napus* L. lines viz., AUP-2, AUP-7, AUP-8, AUP-9, AUP-14, AUP-17, AUP-18 and AUP-20. These lines were of diverse origin and were crossed in complete diallel fashion during 2011-12. A set of eight parents and their 56

F₁ hybrids (both direct and reciprocal crosses) were evaluated during 2012-13 in randomized complete block design (RCBD) with three replications. Each entry was grown in two rows with row length of five meter. Plant to plant and row to row distances were 25 and 50 cm, respectively. Standard cultural practices were adopted throughout the crop season. To minimize environmental effects to the maximum possible extent crop was grown under uniform conditions. In F₁ generation data on days to flowering and maturity were recorded on plot basis while, for plant architecture traits data was recorded on ten randomly selected plants in each entry during crop season. The data were subjected to analysis of variance (ANOVA) technique according to Steel & Torrie (1980) to test the null hypothesis of no differences among the parental lines and their F₁ hybrids. After analysis of variance, significant data were further subjected to combining ability analysis according to Griffing (1956).

Results and Discussion

Analysis of Variance

Analyzed data revealed highly significant differences (P<0.01) among the parents and their F₁ hybrids for flowering, maturity and plant architecture traits (Table 1). Current results revealed that parental genotypes and F₁ hybrids were genetically diverse and produced flowers in wide span of time. Significant genotypic differences for days to 50% flowering have been reported by Oghan et al. (2009), Singh et al. (2010), Vaghela et al. (2011), Rameeh (2011), Maurya et al. (2012) and Nasim et al. (2013) in rapeseed. Similarly, for days to maturity, considerable genetic variability have been reported by Singh et al. (2010), Maurya et al. (2012) and Meena et al. (2014) in *Brassica juncea*. In the current study plant height also varied significantly among the parents and their crosses (Table 1).

Table 1: Mean squares for different traits in an 8 × 8 F₁ diallel cross of *Brassica napus* conducted during 2012-13

Traits	Mean squares			
	Genotype	Replication	Error	CV(%)
Days to 50 % flowering	106.55**	14.474	4.00	1.69
Days to maturity	35.76**	8.521	3.40	1.03
Plant height	119.0**	50.07	18.99	2.47
Primary branches plant ⁻¹	4.820**	0.775	0.46	6.66
Main raceme length	37.08**	12.30	2.13	2.12

Sincik et al. (2011) and Rameeh (2012) found significant differences for plant height among rapeseed genotypes. Among the rapeseed parental lines and cross combinations, primary branches plant⁻¹ and main raceme length also varied significantly indicating presence of diversity among the rapeseed genotypes. Highly significant variations among rapeseed genotypes for primary branches plant⁻¹ and main raceme length were reported by Ali et al. (2014) and Iqbal et al. (2014).

Combining Ability Analysis

Combining ability analysis revealed highly significant (P≤0.01) general, specific and reciprocals combining ability effects for all the studied parameters (Table 2). Various effects and predominant mode of genetic effects are discussed as follows.

Table 2: Analysis of combining ability for different traits in *B. napus*

Traits	Mean squares			
	GCA	SCA	RCA	Error
Days to 50 % flowering	127.42**	12.28**	35.770**	0.58
Days to maturity	44.46**	12.57**	3.129**	1.13
Plant height	132.13**	28.27**	27.93**	6.33
Primary branches plant ⁻¹	1.46**	2.28**	1.07**	0.14
Main raceme length	35.53**	12.43**	6.498**	0.71

** Significant at 1% level of probability

Days to 50% Flowering

Early flowering is one of the important traits in majority of the crop plants as it offers adequate time for grain development and can result in early maturity. In

rapeseed breeding programs, genotypes started flowering earlier are preferred therefore, negative combining ability effects are desirable for days to flowering (Table 2). Five out of eight parental lines exhibited negative GCA effects viz., AUP-7 (-3.27), AUP-17 (-2.24), AUP-14 (-2.11), AUP-2 (-1.71) and AUP-18 (-0.49). The maximum positive GCA effect of 3.65 was recorded for genotype AUP-20 followed by AUP-8 (3.09) (Table 3) and were poor combiners for flowering. The best general combiner, AUP-7 (-3.27), also thrived best on mean performance and flowered earlier. Among the direct crosses, 10 out of 28 crosses showed negative SCA effects. The highest negative SCA effect (-4.29) was observed for the cross AUP-7 x AUP-14 followed by AUP-8 x AUP-17 (-3.43) and therefore could be considered as the best crosses. The highest positive SCA effect (5.52) expressed by AUP-7 x AUP-9 followed by AUP-8 x AUP-14 (3.01) declared as poor combiners for days to flowering (Table 4). RCA effects for 12 out of 28 crosses were negative, the highest being -8.67 (AUP-20 x AUP-18) followed by -4.67 (AUP-20 x AUP-17). Maximum positive RCA of magnitude 7.33 was noted for AUP-18 x AUP-8 (Table 5). Hybrid combinations with negative SCA and RCA effects were best and could be given due importance in rapeseed breeding programs to develop new lines that start earlier flowering. Variances due to GCA (σ^2GCA), SCA (σ^2SCA) and RCA (σ^2RCA) were 7.21, 6.57 and 17.60, respectively. Comparatively higher value of GCA than SCA and predictability ratio σ^2GCA/σ^2SCA (1.10) showed the predominance of additive gene action (Table 6). Our results are in conformity with Gupta et al. (2011), who reported additive genetic effects for days to 50% flowering. However, Vaghela et al. (2011) and

Table 3: Estimates of general combining ability effects for days to 50% flowering, days to maturity, plant height, primary branches plant⁻¹ and main raceme length in an 8x8 diallel cross of *B. napus*

Genotypes	Days to 50% flowering	Days to maturity	Plant height	Primary branches plant ⁻¹	Main raceme length
AUP-2	-1.71	-2.18	-4.77	0.04	-1.07
AUP-7	-3.27	-2.26	-0.65	-0.63	-1.14
AUP-8	3.09	0.68	0.73	-0.18	-0.87
AUP-9	3.08	1.41	1.02	0.15	2.88
AUP-14	-2.11	-1.05	-3.75	0.35	-0.46
AUP-17	-2.24	-0.07	2.18	-0.01	0.72
AUP-18	-0.49	1.76	2.15	0.24	1.27
AUP-20	3.65	1.72	3.09	0.04	-1.32
S.E(gi)±	0.18	0.25	0.59	0.09	0.20
S.E (gi-gj)±	0.27	0.38	0.89	0.13	0.30

Table 4: Estimates of specific combining ability effects for days to 50 % flowering, days to maturity, plant height, primary branches plant⁻¹ and main raceme length of 28 F₁'s derived from an 8 parents of diallel cross in *B. napus*

Hybrid Combination	Days to 50% flowering	Days to maturity	Plant height	Primary branches plant ⁻¹	Main raceme length
AUP-2 × AUP-7	1.65	1.28	1.35	0.62	3.10
AUP-2 × AUP-8	1.28	-0.32	1.40	0.63	2.29
AUP-2 × AUP-9	-3.54	0.61	2.74	0.51	3.96
AUP-2 × AUP-14	1.32	1.74	6.02	-0.53	-2.52
AUP-2 × AUP-17	0.95	1.26	-2.26	-0.17	1.10
AUP-2 × AUP-18	-1.13	0.09	4.69	0.05	-2.65
AUP-2 × AUP-20	0.72	0.80	-2.38	1.08	0.73
AUP-7 × AUP-8	1.76	0.76	-1.53	0.40	-1.15
AUP-7 × AUP-9	5.52	0.20	3.58	0.35	1.05
AUP-7 × AUP-14	-4.29	1.99	1.04	-0.07	-4.01
AUP-7 × AUP-17	2.68	0.84	4.03	0.20	1.51
AUP-7 × AUP-18	-2.07	0.18	-2.45	0.35	2.31
AUP-7 × AUP-20	1.20	0.39	-2.54	-1.15	-2.85
AUP-8 × AUP-9	-0.26	-2.07	-2.18	0.62	1.34
AUP-8 × AUP-14	3.01	0.39	2.29	0.82	-0.03
AUP-8 × AUP-17	-3.43	0.91	-3.85	0.28	-1.05
AUP-8 × AUP-18	-2.27	-0.76	-1.13	0.10	1.05
AUP-8 × AUP-20	0.42	-0.39	-0.48	0.03	-3.62
AUP-9 × AUP-14	1.69	-0.51	-1.88	0.36	-0.67
AUP-9 × AUP-17	-0.34	1.18	-0.29	0.72	0.85
AUP-9 × AUP-18	-1.17	-0.32	0.56	0.04	1.30
AUP-9 × AUP-20	0.60	-1.78	-2.39	-1.66	-1.22
AUP-14 × AUP-17	1.18	3.14	1.47	0.42	1.29
AUP-14 × AUP-18	0.93	1.30	-2.84	0.17	1.04
AUP-14 × AUP-20	0.28	1.01	-2.00	1.30	2.25
AUP-17 × AUP-18	1.23	2.32	-4.92	0.69	-0.89
AUP-17 × AUP-20	-3.08	0.70	-0.98	1.09	1.39
AUP-18 × AUP-20	1.17	-0.14	0.04	0.78	1.14
SE(sij)	0.47	0.67	1.57	0.24	0.53
SE(sij-ski)	0.66	0.92	2.35	0.33	0.73

Nasim et al. (2014) reported predominant role of non-additive genetic effects in inheritance of days to 50% flowering. Huang et al. (2010) reported the role of both additive and non-additive control, but additive genetic control was more prevalent for days to flowering.

Days to Maturity

Most of the rapeseed breeding programs primarily focused on development of new lines with early maturity, as it escape genotypes form environmental stresses (drought and heat etc). Thus negative combining abil-

ity effects are desirable for days to maturity in rapeseed. Analysis of variance (ANOVA) pertaining to combining ability revealed highly significant (P≤0.01) GCA, SCA and RCA effects for days to maturity (Table 2) Results were in conformity with Suchindra and Singh (2006), who reported highly significant GCA, SCA and RCA effects for days to maturity. Four out of eight parental lines exhibited negative GCA effects viz., AUP-7 (-2.26), AUP-2 (-2.18), AUP-14 (-1.05) and AUP-17 (-0.07). The maximum positive GCA effect of 1.76 was recorded for genotype AUP-18 followed by AUP-20 (1.72) (Table 3). The parental line

Table 5: Estimates of reciprocal combining ability effects for days to 50% flowering, days to maturity, plant height, primary branches plant⁻¹ and main raceme length of 28 F₁'s derived from an 8 parents of diallel cross in *B. napus*

Hybrid Combination	Days to 50 % flowering	Days to maturity	Plant height	Primary branches plant ⁻¹	Main raceme length
AUP-7 × AUP-2	-4.33	-1.00	6.47	-0.60	1.35
AUP-8 × AUP-2	4.00	-0.67	5.30	0.80	1.70
AUP-8 × AUP-7	0.08	0.33	2.40	-0.83	-1.50
AUP-9 × AUP-2	5.83	-2.00	6.67	-0.53	-0.88
AUP-9 × AUP-7	-0.67	-0.83	-0.27	-0.77	-1.75
AUP-9 × AUP-8	5.25	-1.50	-2.32	-0.63	-1.70
AUP-14 × AUP-2	-2.83	0.67	-5.57	-0.03	-1.40
AUP-14 × AUP-7	-4.33	-0.83	-4.25	-1.98	-1.45
AUP-14 × AUP-8	8.67	0.17	0.62	-0.50	-3.90
AUP-14 × AUP-9	2.67	1.00	-0.83	-0.17	1.50
AUP-17 × AUP-2	-0.33	-0.50	-0.22	0.23	-0.50
AUP-17 × AUP-7	2.83	-0.33	0.30	0.07	1.65
AUP-17 × AUP-8	3.75	-0.67	-1.83	0.67	0.35
AUP-17 × AUP-9	-0.17	0.67	0.65	0.97	1.00
AUP-17 × AUP-14	-2.50	-0.17	-1.67	0.53	-1.50
AUP-18 × AUP-2	0.67	-0.50	-6.15	0.17	1.80
AUP-18 × AUP-7	0.50	-0.17	-2.70	-0.80	-0.50
AUP-18 × AUP-8	7.33	-1.83	3.80	0.67	-2.00
AUP-18 × AUP-9	7.08	-1.67	-7.88	0.60	-1.40
AUP-18 × AUP-14	-1.33	-2.17	-0.80	0.87	0.10
AUP-18 × AUP-17	3.83	-0.50	5.15	-0.50	-1.25
AUP-20 × AUP-2	-2.67	-0.17	2.55	-0.13	3.50
AUP-20 × AUP-7	-2.25	-1.67	-3.32	0.17	-1.35
AUP-20 × AUP-8	3.50	0.83	-5.58	1.60	4.15
AUP-20 × AUP-9	4.67	-2.17	-0.67	-0.57	-0.90
AUP-20 × AUP-14	1.50	-3.17	0.92	0.33	-0.97
AUP-20 × AUP-17	-4.67	0.17	2.93	-0.43	-1.95
AUP-20 × AUP-18	-8.67	1.50	-1.10	-0.63	-1.25
S.E(r _{ij}) ±	0.54	0.75	1.78	0.27	0.60
S.E(r _{ij} -r _{kl}) ±	0.76	1.06	2.52	0.38	0.84

Table 6: Estimates of variances due to general combining ability (σ^2GCA), specific combining ability (σ^2SCA) and reciprocal combining ability (σ^2RCA) and error variance (σ^2e) and ratio of σ^2GCA/σ^2SCA for studied traits in *B. napus*

Traits	σ^2GCA	σ^2SCA	σ^2RCA	σ^2e	$\sigma^2GCA / \sigma^2SCA$
Days to 50 % flowering	7.21	6.57	17.60	0.58	1.10
Days to maturity	2.01	6.42	1.00	1.13	0.31
Plant height	6.515	12.319	10.800	6.330	0.529
Primary branches plant ⁻¹	-0.049	1.203	0.465	0.142	-0.041
Main raceme length	1.46	6.58	2.89	0.71	0.22

AUP-7 was found best general combiner and could be utilized in rapeseed breeding programs for the development of new lines for early maturity. Among the direct crosses, eight out of 28 crosses showed negative SCA effects. The highest negative SCA effect (-2.07) were observed for the cross AUP-8 × AUP-9 followed by AUP-9 × AUP-20 (-1.78). The highest positive SCA effect (3.14) expressed by AUP-14 × AUP-17 followed by AUP-17 × AUP-18 (2.32) (Table 4). RCA effects for 20 out of 28 crosses were negative, the highest being -3.17 (AUP-20 × AUP-14) followed by -2.17 (AUP-18 × AUP-14). Maximum positive RCA of magnitude 1.50 was noted for AUP-20 × AUP-18 (Table 5). Variances due to GCA (σ^2 GCA), SCA (σ^2 SCA) and RCA (σ^2 RCA) were 2.01, 6.42 and 1.00, respectively. Comparatively higher value of σ^2 GCA than σ^2 SCA and predictability ratio σ^2 GCA/ σ^2 SCA (0.31) showed the predominance of non-additive gene action (Table 6). The gene action in current study is in conformity with Nasim et al. (2014) and Vaghela et al. (2011), who reported predominant role of non-additive genetic effects in inheritance of days to maturity. However, Parmar et al. (2011), Gupta et al. (2011) and Gupta et al. (2006) reported the effectiveness of additive genetic effects for managing days to maturity in rapeseed.

Plant Height

Plant height is an important trait and has been given due importance in rapeseed breeding programs. Rapeseed breeders are interested in development of new *Brassica napus* lines having short stature and are less likely to lodge. Therefore, negative combining ability effects are desirable for plant height in rapeseed. In the current study an attempt has been made to identify best lines and cross combinations based on combining ability for the said trait. ANOVA of combining ability revealed highly significant ($P \leq 0.01$) GCA, SCA and RCA effects for plant height (Table 2). Sincik et al. (2011) found highly significant GCA, SCA and RCA for plant height in rapeseed. The present results are in contrast to Aghao et al. (2010), who revealed non-significant GCA and significant SCA effects for plant height. Three out of eight parental lines exhibited negative GCA effects viz., AUP-2 (-4.77), AUP-14 (-3.75), and AUP-7 (-0.65). The maximum positive GCA effect of 3.09 was recorded for genotype AUP-20 followed by AUP-17 (2.18) (Table 3). Among the direct crosses, 16 out of 28 crosses showed negative SCA effects. The highest negative SCA effect (-4.92) was observed for the cross AUP-17 × AUP-

18 followed by AUP-8 × AUP-17 (-3.85). The highest positive SCA effect (6.02) expressed by AUP-2 × AUP-14 followed by AUP-2 × AUP-18 (4.69) (Table 4). Reciprocal effects for 15 out of 28 crosses were negative, ranging from -7.88 to -0.22. The desirable highest being -7.88 (AUP-18 × AUP-9) followed by -6.15 (AUP-18 × AUP-2). Maximum positive RCA of 6.47 was noted for F_1 hybrid AUP-7 × AUP-2 (Table 5). Parental lines and hybrid combinations with negative GCA, SCA and RCA effects could be exploited in rapeseed improvement programs to develop short stature breeding lines. σ^2 GCA, σ^2 SCA and σ^2 RCA which represent variances due to general, specific and reciprocal combining ability were 6.515, 12.319 and 10.800, respectively. Higher value of σ^2 GCA than σ^2 SCA and predictability ratio (σ^2 GCA/ σ^2 SCA) (0.529) showed the predominance of non-additive gene action (Table 6). Akbar et al. (2008) and Parmar et al. (2005) reported importance of non-additive genetic control for plant height. Acharya and Swain (2004) found additive and non-additive genetic effects for plant height. Singh et al. (2008) and Noshin et al. (2008) detected the presence of additive type of gene action for plant height.

Primary Branches Plant⁻¹

Rapeseed breeder's primary focused on development of new breeding lines with more no of primary branches per plant. As more numbers of healthier primary branches per plant with more number of pods are the major yield contributing traits therefore, positive combining ability effects are desirable for number of branches in *Brassica napus*. Analysis of combining ability (Table 2) revealed highly significant ($P \leq 0.01$) GCA, SCA and RCA effects for primary branches plant⁻¹. Gupta et al. (2011) and Akbar et al. (2008) reported highly significant GCA and SCA effects in rapeseed. Teklewold and Becker (2005) reported significant GCA and non-significant SCA in Ethiopian mustard. Parental lines AUP-2, AUP-9, AUP-14, AUP-18 and AUP-20 exhibited positive GCA effects of 0.04, 0.15, 0.35, 0.24 and 0.04, respectively. The maximum positive GCA effect of 0.35 was recorded for genotype AUP-14 followed by AUP-18 (0.24) (Table 3). Maximum negative GCA effect of -0.63 was recorded for genotype AUP-7 followed by AUP-8 (-0.18). AUP-14 with maximum positive combining ability value appeared to be the best general combiner. Among the direct crosses, 23 out of 28 crosses showed positive SCA effects. The highest positive SCA effect (1.30) was observed for the cross AUP-14 × AUP-20

followed by AUP-17 × AUP-20 (1.09). The highest negative SCA effect (-1.66) expressed by AUP-9 × AUP-20 followed by AUP-7 × AUP-20 (-1.15) (Table 4). RCA effects for 14 crosses were positive, the highest being 1.60 (AUP-20 × AUP-8) followed by 0.97 (AUP-17 × AUP-9). Maximum negative RCA of magnitude -1.98 was noted for AUP-14 × AUP-7 (Table 5). Variances due to GCA (σ^2 GCA), SCA (σ^2 SCA) and RCA (σ^2 RCA) were -0.049, 1.203 and 0.465, respectively. Comparatively higher value of σ^2 SCA variance than σ^2 GCA and predictability ratio (σ^2 GCA/ σ^2 SCA) (-0.041) showed the predominance of non-additive gene action (Table 6). Gupta et al. (2011) also reported prevalence of non-additive genetic control. Acharya and Swain (2004) revealed equal importance of additive and non-additive control. Aher et al. (2009) reported preponderance of additive genetic effects; whereas, Singh and Dixit (2007) revealed equal importance of additive and non-additive control for number of primary branches plant⁻¹ in *B. juncea*. Larik and Rajput (2000) and Yadav et al. (2005) reported additive gene action in controlling number of primary branches in *B. napus* and *B. juncea*, respectively.

Main Raceme Length

In rapeseed, development of new lines with longer racemes is one of the major objectives of rapeseed improvement programs. Genotypes with longer racemes are expected to have more number of seed bearing pods and results into greater seed yield. Therefore, positive combining ability effects are desirable for main raceme length in rapeseed. The combining ability ANOVA (Table 2) showed significant GCA, SCA and RCA effects for main raceme length indicating the importance of both additive and non-additive gene effects. Parental lines AUP-9, AUP-18 and AUP-17 exhibited positive GCA effects of 2.88, 1.27 and 0.72, respectively (Table 3). Maximum negative GCA effect of -1.14 was recorded for genotype AUP-7 followed by AUP-20 (-1.32). AUP-9 was best general combiner while, AUP-7 was poorest combiner among the parents for the said trait (Table 3). Among the direct crosses, 17 out of 28 crosses showed positive SCA effects. The highest positive SCA effect (3.96) was observed for the cross AUP-2 × AUP-9 followed by AUP-2 × AUP-7 (3.10). The highest negative SCA effect (-4.01) expressed by AUP-7 × AUP-14 followed by AUP-8 × AUP-20 (-3.62) (Table 4). RCA effects for 10 crosses were positive, the highest being 4.15 (AUP-20 × AUP-8) followed by

3.50 (AUP-20 × AUP-2). Maximum negative RCA of magnitude -3.90 was noted for AUP-14 × AUP-8 (Table 5). Parental lines and crosses having positive combining ability effects were best and could be exploited in future breeding programs. Variances due to GCA (σ^2 GCA), SCA (σ^2 SCA) and RCA (σ^2 RCA) were 1.46, 6.58 and 2.89, respectively. Comparatively higher value of variances of σ^2 SCA than σ^2 GCA and predictability ratio (σ^2 GCA/ σ^2 SCA) (0.22) showed the predominance of non-additive gene action (Table 6). Singh et al. (2010) also observed significant GCA and SCA effects for main raceme length in *Brassica juncea*. Ali et al. (2014) and Upadhyay and Kumar (2014) found both additive and non-additive gene actions in *B. napus* and *B. juncea*, respectively.

Conclusions

Analysis of combining ability revealed that AUP-7 was best general combiner for flowering and maturity, AUP-2 for plant height and AUP-14 for no of primary branches. AUP-9 was potential good general combiners for main raceme length and could be used in future rapeseed breeding programs. Genetic effects regarding maturity and plant architecture traits revealed the preponderance of non-additive type of gene action for majority of the parameters. Therefore selection in later segregating generations could be fruitful to develop early maturing lines with modified plant architecture in *B. napus*.

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Author's Contribution

Muhammad Ishaq designed, conducted research, collected, analyzed data and prepared rough draft of the manuscript. Raziuddin supervised all the research activities and made final draft and reviewed it.

Conflict of Interest

The author(s) declare(s) that there is no conflict of interest regarding publication of this research article.

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