

HERITABILITY AND COMBINING ABILITY OF VEGETATIVE GROWTH AND PHENOLOGICAL DEVELOPMENT OF DIALLEL CROSSES OF RAPESEED

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To estimate combining ability and heritability of F₂ populations of 4 x 4 full diallel crosses and parents, an experiment was carried out at The University of Agriculture, during 2012-2013. Four parental lines and F₂ populations of six direct and six reciprocal crosses were planted in the experiment using RCB design. Data were recorded on phenological and vegetative growth traits: Days to flowering, plant height, main stem length, main raceme length, primary branches, and days to maturity. Analysis of variance revealed significant variation among genotypes for all the parameters studied. The results of combining ability analysis showed that general combining ability (GCA) was highly significant for primary branches plant⁻¹, significant for plant height and days to physiological maturity and non-significant for the remaining traits. Specific combining ability (SCA) and reciprocal effects (RE) were significant for plant height, days to flowering, main raceme length and days to physiological maturity. Genotype AUP-401 was best general combiner for main raceme length, primary branches plant⁻¹ and days to physiological maturity. Among the crosses, AUP-404 x AUP-402 was best specific combiner for plant height, days to flowering and main stem length. Broad sense heritability was high (>70%) for plant height, main stem length and primary branches. Moderate heritability was observed for main raceme length, days to 50% flowering and days to physiological maturity. The variance components of SCA were greater than respective GCA components of all the characters signifying the presence of non-

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additive genetic effects in transfer of these traits and selection in the later generations should be practiced for improvement of these traits.

Keywords: combining ability, heritability, phenological development, rapeseed, vegetative growth

INTRODUCTION

Rapeseed (*Brassica napus* L.) is an important oil seed crop widely grown in many countries particularly in Asia. The crop is also planted for forage purpose; generally mixed with legumes such as Egyptian clover (*Trifolium alexandrinum* L.) and Persian clover (*Trifolium resupinatum* L.). The young inflorescences before the flowering stage, known as rapeseed tops, are cooked and eaten as vegetable. Crop growth and balanced phenological development are important for biological and economic yields. Vegetative growth is important because photosynthetic machinery is developed during vegetative phase before flowering and it affects reproductive sink capacity and seed yield. Raceme length is one of the criteria for reproductive growth. Change from vegetative to reproductive phase and flower initiation affects seed yield through its effects on number of pods and number of seeds per pod and per unit area (DIEPENBROCK, 2000). Balanced phenological development with enough vegetative growth to produce optimum leaf area as source of assimilates and proper length of reproductive phase for seed formation are important for economic yield. Crop modeling work by (HABEKOTTE, 1997) shows that early flowering and late maturity is most promising plant type for higher seed yield because it increase seed fill duration. Quick weather change in spring initiate rapid maturity in autumn planted rapeseed thus comparatively early flowering is needed for longer seed fill duration.

The breeding processes mainly rely upon the selection of superior genotypes from base population. Selection is done on the basis of phenotype but in cases where phenotypic superiority is more due to environment and less due to genotype, selection process is not very effective (MARJANOVIC *et al.*, 2011). Therefore knowledge of genetic mechanism of crop plants involved in expression of traits is essential for the success of any breeding program. Determination of combining ability is important for selection of parents in hybridization program to evolve new high yielding varieties, the type of gene action involved in transmission of a trait and to select an appropriate breeding method for improvement of traits. Some of the previous studies (FARSHADFAR *et al.*, 2013; AZIZINIA, 2012; SAEED *et al.*, 2013) reported additive gene action while other studies (ARIFULLAH *et al.*, 2012; DAR *et al.*, 2013; GUPTA and LAL, 2011) reported non additive genetic effects for number of branches. GUPTA and LAL (2011) and SAEED *et al.* (2013) reported additive gene action for days to flowering and plant height. Non-additive gene action was observed for days to flowering by RAMEEH (2012) and for plant height by FARSHADFAR *et al.* (2013) and SINCIK (2011). Heritability estimate determines the degree of transmission of a particular genetic character to the successive generations which in turn helps in selection. ZARE and SHARAFZADEH, (2012) and OGHANA *et al.* (2009) reported high heritability for flowering and maturity time. MARJANOVIC *et al.* (2011) observed moderate heritability for days to flowering. For plant height and days to maturity low heritability was reported by MARJANOVIC *et al.* (2011) and SADAT *et al.* (2010). AYTAC *et al.* (2008) and ZARE and SHARAFZADEH (2012) reported high heritability for plant height.

MATERIALS AND METHODS

Four *Brassica napus* L. genotypes AUP-401, AUP-402, AUP-403, and AUP-404, introduced from China and F₂ generations of their 12 possible crosses (six direct crosses and six reciprocal crosses) were used in this experiment to evaluate combining ability and heritability of vegetative growth and phenological traits. All the 16 genotypes of rapeseed were sown on October 18, 2012 using a randomized complete block design with three replications at Agriculture Research Farm of The University of Agriculture, Peshawar, during 2012-13. Each experimental unit had three rows, 5 meters long with 60 cm row to row distance and 30 cm plant to plant distance. Recommended doses of fertilizers were applied and uniform standard cultural practices were followed to raise the crop.

Ten guarded plants were randomly selected in each experimental unit and tagged for recording data on days to 50% flowering (calculated as the difference between date of sowing and date at which 50% plants bloomed flowers in each plot), plant height (measured in centimeters ground level to the tip of plant), main stem length (measured in centimeters from ground level to the base of main raceme), main raceme length (measured in centimeters from base to the tip of upper most inflorescence, raceme of the main shoot), primary branches (counted as the number of branches arising from main stem), and days to maturity (calculated from date of sowing and date when majority of the plants reached physiological maturity).

Analysis of variance (ANOVA) technique appropriate for randomized complete block design was used to test the null hypothesis of no significant differences among the genotypes. GRIFFING (1956) numerical approach Method 1, Model 1 (fixed effect) as explained by SINGH and CHAUDHRY (1985) was used for combining ability analysis using mean values of the four parents and the 12 F₂ generations of both direct and reciprocal crosses for the traits. Broad-sense heritability was calculated for each trait.

RESULTS AND DISCUSSION

The mean squares for the genotypes (Table 1) show highly significant ($p \leq 0.01$) differences among genotypes for days to 50 % flowering, plant height, main stem length, main raceme length, primary branches, and days to maturity. Similar results of highly significant differences among genotypes of rapeseed for these traits were reported by OGHANA *et al.* (2009), and NASSIMI *et al.* (2006). RAMEAH (2003) reported significant differences ($p < 0.05$) among genotypes for agronomic traits of rape seed genotypes.

Table 1. Mean squares for replications, genotypes and error from the preliminary ANOVA for various traits of 4x4 diallel crosses of rapeseed

Parameter	Replications (df=2)	Genotypes (df=15)	Error (df=30)	CV (%)
Days to 50% flowering	50.02	16.20 **	5.488	2.262
Plant height (cm)	305.5	348.7 **	81.77	4.913
Main stem length (cm)	204.7	238.0 **	41.86	6.289
Raceme length (cm)	124.0	228.1 **	77.93	10.90
Primary branches	0.991	1.424 **	0.312	13.61
Days to maturity	16.14	5.189 **	1.816	0.772

** = significant at 0.01

Combining ability**Days to 50% flowering**

Days to flowering is an important phenological events and it determine the length of reproductive period from flowering to maturity; length of reproductive period or seed fill duration is important because it affects seed yield. Combining ability analysis (Table 2) revealed that mean squares for GCA were not significant, mean squares for SCA were significant and mean squares for RCA were highly significant for days to flowering. AGHAO *et al.* (2010), OGHANA *et al.* (2009) and NASRIN *et al.* (2011) reported significant GCA and SCA for days to flowering. SAEED *et al.* (2013) reported significant mean squares of GCA, SCA and RCA for this trait.

Table 2. Mean squares for GCA, SCA, RCA, and error from combining ability analysis for various traits of F_2 diallel population in rapeseed

Parameter	GCA (df=3)	SCA (df=6)	RCA (df=6)	Error (df=30)
Days to 50% Flowering	2.28	5.12 *	7.24**	1.83
Plant height (cm)	85.55 *	98.80 **	149.0 **	27.26
Main stem Length (cm)	1.10	187.7 **	10.14	13.95
Main Raceme length (cm)	53.79	77.79 *	85.42 *	25.98
Primary branches	0.61 **	0.23	0.65**	0.10
Days to maturity	2.09 *	1.49 *	1.79 *	0.61

* = significant at 0.05 and ** = significant at 0.01

Table 3. Estimates of GCA of parents, and SCA and RCA of F_2 population of rapeseed crosses

Genotype/ Cross	Days to 50 % flowering	Plant heigh (cm)	Main stem length (cm)	Main Raceme length (cm)	Primary branches plant ⁻¹	Days to maturity
AUP-401	0.46	4.70 **	-0.16	3.60	0.29 **	-0.56 **
AUP-402	- 0.54	-1.61 *	-0.37	-0.68	0.16 **	-0.29 *
AUP-403	0.46	- 0.41	0.50	-0.35	-0.13 *	0.55 **
AUP-404	- 0.37	- 2.69 **	0.03	-2.57	-0.32 **	0.30 *
AUP-401xAUP-402	0.3	10.2 **	6.3 **	4.8 **	0.2	-0.5 **
AUP-401xAUP-403	0.2	1.1	5.6 **	-3.7 **	-0.1	0.0
AUP-401xAUP-404	1.0 **	- 0.2	4.4 **	-3.3 **	-0.3	0.2
AUP-402xAUP-403	- 0.2	4.7 **	8.5 **	-3.1 **	0.1	0.5 **
AUP-402xAUP-404	- 2.0 **	-2.7 **	-0.3	-3.0 **	-0.4	0.8 **
AUP-403xAUP-404	- 0.8 **	-2.2 *	2.5 **	-5.2 **	-0.1	0.8 **
AUP-402xAUP-401	- 1.5	-5.2	-0.8	-4.4	-0.5	-1.3
AUP-403xAUP-401	- 1.0	-1.8	0.8	-2.6	0.5	-0.7
AUP-404xAUP-401	3.3 *	7.8	0.0	7.9	0.0	-0.3
AUP-403xAUP-402	0.0	13.6 *	4.9	7.0	0.9 *	-0.6
AUP-404xAUP-402	2.0	13.0 *	2.2	10.8 *	0.8 *	-0.9
AUP-404xAUP-403	1.8	0.6	-0.3	0.9	0.3	-1.4 *

* = significant at 0.05 and ** = significant at 0.01

The ratio of GCA variance to SCA variance was less than unity for this trait indicating the presence of non-additive type of gene action (Table 4). Similar results of non-additive gene effects were observed by RAMEEH (2012), whereas, NASRIN *et al.* (2011), GUPTA and LAL (2011) and SAEED *et al.* (2013) reported additive gene effect for days to flowering.

Table 4. Estimates of components of variance due to GCA, SCA and RCA of various traits of rapeseed

Components of variance	GCA	SCA	RE	Error	Total
Days to 50% flowering	0.06	3.29	2.71	1.83	7.88
Plant height	7.29	71.54	60.87	27.26	166.96
Main stem length	-1.61	173.71	-1.91	13.95	184.15
Main raceme length	3.48	51.81	29.72	25.98	110.98
Primary branches	0.06	0.13	0.27	0.10	0.57
Days to maturity	0.19	0.88	0.59	0.61	2.27

Plant height

Plant height is one of the non-destructive criteria for vegetative growth especially in case of data on individual plants in segregating generations where destructive sampling is not possible. The results of combining ability analysis revealed that mean squares due to SCA and RCA were highly significant while mean squares due to GCA were significant for plant height (Table 2). Similar results of significant GCA and SCA mean squares were reported by AZIZINIA (2012) and DAR *et al.* (2013). Significant reciprocal effects were observed for this trait by SINCIK *et al.* (2011) and NASSIMI *et al.* (2006).

Combining ability for plant height ranged from -2.7 to 4.70 in the present study (Table 3). Reduced plant height is a preferred character in rapeseed to avoid lodging of the plants. Two parents were identified as good general combiners for plant height. Highest significant negative GCA was observed for AUP-404 followed by AUP-402. Among the direct F_2 crosses, the SCA values ranged from -2.7 to 10.2. As shorter plant height is desirable, cross AUP-402 x AUP-404 with lowest SCA was the best specific combiners followed by AUP-403 x AUP-404. Both of the good specific combiners have at least one parent with significant negative general combining ability. Reciprocal effect of AUP-403 x AUP-402 was highest which was closely followed by reciprocal effect of AUP-404 x AUP-402; both the effects were significant showing that these reciprocal crosses had shorter plants than their direct crosses. The use of AUP-402 as male parent decreased plant height as compared to its use as female parent with AUP-403 and AUP-404.

Pre-dominance of non-additive gene action was observed for plant height from the perusal of general and specific combining abilities variances (Table 4). The present results are in conformity with the results of SINCIK *et al.* (2011) and FARSHADFAR *et al.* (2013). However, GUPTA and LAL (2011), RAMEEH (2012), and SAEED *et al.* (2013) found additive affects for plant height.

Main stem length

Analyses given in Table 2. showed that mean squares for general and reciprocal combining abilities were not significant for main stem length, whereas highly significant mean squares of specific combining ability were found for main stem length. GUPTA and LAL (2011)

reported highly significant mean squares for GCA and SCA; these results are in conformity for SCA and in contrast for GCA effects.

A range of 8.8 was found in SCA estimates of the crosses for main stem length with lowest value of -0.3 and a highest value of 8.5 (Table 3). The GCA estimates of parents and reciprocal effects of the reciprocal crosses though not-significant, ranged from -0.37 to 0.50 and -0.8 to 4.9 respectively. The SCA values of five out six crosses were significant. None of the crosses exhibited significant desirable negative SCA. The highest positive and significant SCA of 8.5 was noted for cross AUP-402 x AUP-403 followed by SCA of 6.3 for cross AUP-401 x AUP-402.

Lower variance of GCA than SCA signified that main stem length is controlled by non-additive gene action (Table 4). SABAGHNIA *et al.* (2010) and GUPTA and LAL (2011) observed similar results.

Main raceme length

Analysis of combining ability for main raceme length showed significant means squares due to SCA and reciprocal effects while mean squares due to GCA was not significant (Table 2). These results are partially similar to NOSHIN *et al.* (2007), who reported significant GCA and SCA mean squares while not significant RCA mean squares.

Increase in length of raceme generally increase number of pods raceme⁻¹ and plant⁻¹ and thus affect one of the seed yield component. General combining ability estimates showed that only one parent (AUP-401) showed positive GCA value (3.60) for main raceme length (Table 3). Results of SCA estimates showed positive specific combining ability value for only one cross, AUP-401 x AUP-402 and negative SCA value for rest of the crosses. Estimates of RCA revealed positive RCA value for AUP-404 x AUP-402 and non-significant RCA values for rest of the reciprocal crosses. The female parents of the cross with maximum positive specific combining ability value exhibited positive GCA while the male parent had negative GCA values. The greater reciprocal effect of the cross AUP-404 x AUP-402 shows that use of AUP-402 as female parent with AUP-404 as male parent produced longer main racemes than when AUP-402 was used as male with AUP-404 as female parent.

Specific combining ability variance was of greater magnitude than general combining ability variance suggesting the importance of non-additive gene action for main raceme length (Table 4). The observations of NOSHIN *et al.* (2007) showing the pre-dominance of non-additive genetic effects are similar to the results of present study.

Primary branches plant⁻¹

Number of branches is also one of the non-destructive criteria for vegetative growth especially in case of data on individual plants. The results of combining ability analysis showed no significant specific combining ability mean squares and highly significant general and reciprocal combining ability mean squares for primary branches plant⁻¹ (Table 2). Significant GCA and RCA mean squares were previously reported by SAEED *et al.* (2013) and NASSIMI *et al.* (2006) for this plant character. Similar results of not significant SCA for primary branches plant⁻¹ mean squares were also reported by AGHAO *et al.* (2010)

In the present study combining ability estimates ranged from -0.5 to 0.9 for primary branches (Table 3). Significant GCA estimates were observed for all the parents. Two genotypes were found to be good general combiners for increasing branches per plant. Highest GCA was

observed for AUP-401 followed by AUP-402 and lowest GCA was observed for AUP-404. Positive SCA value was observed for cross AUP-401 x AUP-402 and AUP-402 x AUP-403 while rest of the crosses showed negative SCA value. Maximum RCA value was recorded for AUP-403 x AUP-402 closely followed by AUP-404 x AUP-402; significantly higher reciprocal effects for these crosses show that their direct crosses are better than the reciprocal crosses. The negative reciprocal effect for cross AUP-402 x AUP-401 show that the use of AUP-402 as female and AUP-401 as male was better than vice versa. The crosses with desired combining ability for primary branches involve at least one good general combiner.

The ratio of GCA variance to SCA variance was less than unity for number of primary branches plant⁻¹ indicating the presence of non-additive gene action for controlling this trait (Table 4). ARIFULLAH *et al.* (2012), GUPTA and LAL (2011) and DAR *et al.* (2013) observed similar effects. Whereas FARSHADFAR *et al.* (2013), SAEED *et al.* (2013) and AZIZINIA (2012) observed additive genetic control for this trait.

Days to maturity

Maturity time in relation to flowering time determine length of reproductive period which affect yield; early maturity may avoid late drought when crop is grown without irrigation but under irrigation and in areas with mild terminal temperature late maturity may be desirable to increase seed fill duration. GCA, SCA and RCA mean squares were significant ($p < 0.05$) for days to maturity (Table 2). Results of OGHANA *et al.* (2009), RAMEEH (2012), SAEED *et al.* (2013) and NASRIN *et al.* (2011) are similar to the present results. However, AGHAO *et al.* (2010) observed contrary results of not significant GCA and SCA mean squares.

For development of early maturing genotypes for dry land crop production with terminal high temperature, parents with negative GCA are required to be used in hybridization programs. For rapeseed production in areas with irrigation facilities and mild summer, parents with positive GCA may be better to develop high yielding varieties of rapeseed. Combining ability for days to maturity ranged from -0.56 to 0.8 in the present study (Table 3). Lowest significant GCA was observed for AUP-401 followed by AUP-402 and these parents may be better for hybridization program to develop early maturity rapeseed varieties for rain-fed areas with terminal drought. Parent AUP-403 had the highest positive GCA followed by parent AUP-404 and these parents may be used in hybridization program to develop varieties with greater yield potential for irrigated areas having mild summer temperature regimes. Among the F₂ populations, only one cross, AUP-401 x AUP-402, had significant negative specific combining ability; this cross may be used to develop early maturing varieties of rapeseed for dry land condition with terminal moisture stress. AUP-402 x AUP-401 and AUP-404 x AUP-403 had the lowest reciprocal effects, thus they were late in term of maturity than their direct crosses and thus AUP-401 and AUP-403 in the said crosses should be used as female parents.

The ratio of GCA variance to SCA variance suggested the presence non-additive gene action for the inheritance of days to physiological maturity (Table 4). Results of genetic effects for days to maturity in current study are in contrast to the results observed by RAMEEH (2012), OGHANA *et al.* (2009) and GUPTA and LAL (2011).

Heritability

Broad sense heritability values for phenological traits like days to 50% flowering and days to maturity were 66.1% and 65.0% respectively. The results are in contrast with the results

of MARJANOVIC *et al.* (2011) who reported low heritability for phonological traits. High heritability value of 76.5%, 82.4%, and 78.1% was observed for plant height, main stem length and primary branches respectively. These results are supported by the findings of AYTAC *et al.* (2008), SADAT *et al.* (2010) and ZARE and SHARAFZADEH (2012). Moderate heritability was observed for main raceme length (65.8%). For most of the traits in this study heritability estimates were moderate or high as a result of high genetic variance, signifying less environmental influence. For such traits selection is effective and gain from selection is more.

Table 5. Variance components and heritability estimates of various traits of parents and F_2 population of rapeseed

Parameters	Vg	Ve	Vp	H
Days to 50% Flowering	3.571	1.829	5.400	66.1
Plant height	88.97	27.26	116.2	76.5
Main stem Length	65.39	13.95	79.34	82.4
Main Raceme length	50.06	25.98	76.04	65.8
Primary branches	0.371	0.104	0.475	78.1
Days to maturity	1.124	0.605	1.730	65.0

Vg is genetic variance, Ve is environmental variance, Vp is phenotypic variance and H is broad sense heritability

CONCLUSION

The SCA variance of all traits was more than the respective GCA variance signifying the presence of non-additive gene effects in the transmission of these traits. And so selection should be delayed to later generations for improvement of these traits. Parent AUP-402 and crosses AUP-402 x AUP-401 and AUP-403 x AUP-401 should be used in hybridization program to develop early maturing varieties for avoiding terminal drought and produce comparatively high yielding varieties for dry land conditions. Parent AUP-404 and crosses AUP-402 x AUP-404 and AUP-403 x AUP-404 should be used in hybridization program to develop high yielding varieties for more favorable conditions.

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**HERITABILNOST I KOMBINACIONA SPOSOBNOST VEGETATIVNOG
PORASTA I FENOLOŠKOG RAZVOJA DIALELNIH UKRŠTANJA
ULJANE REPICE**

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Izvod

Za procenu kombinacione sposobnosti i heritabilnosti kod F₂ populacija 4 x 4 dialelnog ukrštanja i roditelja, postavljen je eksperiment na Univerzitetu za poljoprivredu, tokom 2012-2013. Četiri roditeljske linije i F₂ populacije od šest direktnih i šest recipročnih ukrštanja, činilo je eksperiment postavljen po RCB dizajnu. Ocenjivana su sledeća fenološka i vegetativna svojstva: broj dana do cvetanja, visina biljke, visina glavnog stabla, dužina glavnog grozda, primarne grančice i broj dana do pune zrelosti. Analizom varijanse utvrđene su značajne varijacije između genotipova za sva izučavana svojstva. Rezultati za kombinacionu sposobnost, pokazali su da je opšta kombinaciona sposobnost (GCA) visoko značajna za broj primarnih grana biljka⁻¹, značajna za visinu biljke i broj dana do fiziološke zrelosti i nesigifikantna za ostale osobine. Specifična kombinaciona sposobnost (SCA) i recipročni efekat (RE) su bili značajni za visinu biljke, broj dana do cvetanja, dužinu glavnog grozda i broj dana do fiziološke zrelosti. Genotip AUP-401 je bio najbolji kombinatorka za dužinu glavnog grozda, broj primarnih grančica⁻¹ i broj dana do fiziološke zrelosti. Ukrštanje AUP-404 x AUP-402 je imalo najbolju specifičnu kombinacionu sposobnost za visinu biljke, broj dana do cvetanja i dužinu glavnog stabla. Heritabilnost u širem smislu je bila visoka (>70%) za visinu biljke, dužinu glavnog stabla i broj primarnih grančica. Srednja heritabilnost je utvrđena za dužinu glavnog grozda, broj dana do 50% cvetanja i broj dana do fiziološke zrelosti. Komponente varijanse za specifičnu kombinacionu sposobnost bile su veće u odnosu na odgovarajuće komponente za opštu kombinacionu sposobnost za sve osobine, ukazujući na prisustvo ne-aditivnog genetičkog efekta u nasleđivanju ovih osobina, kao i na moguću primenu selekcije u kasnijim generacijama za popravku ovih svojstava.

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