

## Genetic Variability Studies Of Some Quantitative Traits In Advancemutant Lines Of Winter Rapeseed (*Brassica Napus L.*)

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**ABSTRACT:** Information about the genetic variability and the extent and type of relationship of some quantitative characters in rapeseed is important for an efficient breeding program. Thirty five advance brassica mutant lines and one check were evaluated for genetic variability between days to 50% flowering, plant height (cm), 1000 seed weight (g), seed yield (kg ha<sup>-1</sup>) and oil yield (kg ha<sup>-1</sup>) during 2008-09. The mutant lines and the check were sown in four replications using Randomized Complete Block Design (RCBD). The research experiment was conducted during 2008-09 at Nuclear Institute for Food and Agriculture (NIFA) Peshawar. High genetic variability were recorded for oil yield, seed yield and number of days to flowering which demonstrated the effect of environment for the inheritance of these characters. Heritability and genetic advance were recorded high for oil yield and seed yield showing the existence of additive gene action for the expression of these traits. In order to increase oil yield selection based on seed yield would be more effective. More over all the traits showed sufficient variability in the tested mutant lines however, the mutant lines OA5, G1 and O6 were superior having high seed yield, oil yield and 1000 seed weight and also early in flowering.

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**Key words:** *Brassica napus L.*, phenotypic variance, genotypic variance, seed yield, oil yield, plant height.

### INTRODUCTION

Rapeseed (*Brassica napus L.*) is an important source of edible oil in many countries including Pakistan and producing about 21 percent of the total edible oil production all over the world (PARC, 1991 and Downey et al., 1987). In Pakistan, *brassica* ranked second in edible oil production covering an area of 307,000 hectares with 233,000 tones of annual production. But this fulfills only 17% of our domestic edible oil requirement (PARC, 2006). The main species of brassica group cultivated in Pakistan are mustard "rapeseed" (*B. napus*), "sarson" (*B. campestris*) "raya" (*B. juncea*), and "taramira" (*Eruca sativa*). *Brassica campestris* is also one of the major oil seed crop in the Indian subcontinent. In Khyber pakhtunkhwa (KPK) almost 3% of total cropped area is covered with rapeseed. The average yield of rapeseed in KPK is 472 kg ha<sup>-1</sup>. This yield is even less than our national average yield (Sajid et al., 2008). Besides increasing yield, improving quality of the oil seed crop is also very essential. The oil seed will be considered to be of good quality if it has high protein, oil, oleic acid and low linolenic acid, glucosinolates and erucic acid (CFIA 1999).

There is enormous scarcity of edible oil in Pakistan mainly due to rapid increase in population. This increases the demand for oil in the country by 3-4% per year (AOCS, 2006 and Anonymous, 2002-03).

The oil content in cottonseed ranged from 10-12 percent, canola 42, rape and mustard 36-41, groundnut 48-50, sunflower 32-36, safflower 17-32, linseed 35-45, sesame 46-48, and in coconut the oil content ranged from 47-50 percent (Nasr et al., 2006). The oil contents in these plants are under the control of multiple genes and can be altered through induces mutation. About twenty-two hundred different mutant varieties with improved quality and other morphological characters in various crops have been established and distributed to the farmers (Abdullah et al., 2005 and Maluszynski et al., 2010). Knowledge of the relative level of various genetic parameters of oil yield, seed yield and quality characters are important for an excellent breeding program. A trait having the wider range of genetic variability, relatively high heritability and moderate to high genetic advance would be an effective mean to get better seed yield (Aytaç et al., 2009). Efforts are in progress to create rapeseed genotypes with improved quality characters. Genetic variability was estimated in some studies (Giessen et al., 2003 and Akbar et al., 2007). In order to make the selection more effective, both heritability and genetic advance will be considered instead of heritability alone (Johnson et al., 2003).

The present research work was designed to find out the extent of genetic variability, heritability and genetic advance between days to flowering, plant

height, 1000 seed weight, seed yield and oil yield in thirty five advanced mutant lines of winter rapeseed.

## MATERIALS AND METHODS

Thirty five advance mutant lines were selected due to their best yield and quality performance during 2007-08. The check used in this experiment was Abasin-95. The mutant lines and the check were evaluated in four replications according to the design described in RCBD. The research experiment was conducted during 2008-09 at NIFA, Peshawar. The materials were sown on a well-prepared seed bed in October 2008, using 10 kg/ha seed. The sowing plot consists of 6 rows each 5m long with 30 cm distance between the rows and 5-10 cm distance between the plants. The experimental plot was irrigated three times during the entire period, first time after 29 days of sowing, second time when the flowering arises and third time during the grain filling period. The thinning was performed once to retain 10 cm space among the plants. At maturity, yield components such as number of days to 50% flowering of the plot and plant height in centimeters were measured. Approximately, three months after harvesting as international seed testing association (ISTA) suggests, 1000 seeds weight was calculated by taking 8 replicated 100 seeds from each plot and was weighted in grams and the mean was multiplied with 10. Seed yield was calculated in kg/ha by taking the plants from the central three rows of the plot. Crude oil yield was calculated from crude oil content and seed yield. Crude oil content was measured by Near Infra red Reflectance (NIR) Spectroscopy System (FOSS 6500 equipped with ISI version 1.02, Infra Soft International) through non destructive technique (Perez-Vich et al., 1998 and Hom et al., 2007). Genetic parameters were determined in accordance with Singh and Chaudhry (1979) method and were statistically analyzed for variability and heritability of different traits (Singh et al., 1979).

### Heritability estimates

Heritability estimates were calculated by using the following formulae (Khan et al., 1992).

$$V_p = V_g + V_e$$

$$h^2_{(BS)} = V_g / V_p$$

### Analysis of variance

The data obtained were processed with Microsoft excel 2007 software and statistically analyzed by MSTATC program for Randomized Complete Block Design (RCBD). The LSD (0.05) was used for mean comparisons (Steel and Torri, 1980).

## RESULTS

### Days to flowering (DF)

The results obtained from the analysis of variance (ANOVA) for all traits are presented in (Table-2). According to this table significant differences were observed for number of days to flowering among 35 tested genotypes against the

check. The early flowering was recorded in 25 mutant lines. However, OA5 (68.75), OA6 (68.75), G8 (69.0) and G1 (69.25) flowered earliest compared to check (Table-1). Delayed flowering was observed in one mutant line i.e. O9 (91.50) compared to check. On average, the tested genotypes were earlier in flowering than the check. The phenotypic variance ( $\sigma^2_p$ ) was 50.54 and genotypic variance ( $\sigma^2_g$ ) was 45.65 and the phenotypic coefficient of variations (PCV) and the genotypic coefficient of variations (GCV) were 9.06 and 8.61 respectively (Table 3). Estimates of heritability (broad sense) and genetic advance as percent of means were presented in Table 5. High value of heritability (90.3) and moderate value of genetic advance (16.88) were observed for days to flowering (Table 3) suggesting non-additive (dominance or epistatic) gene effect.

### Plant height (PH)

The final plant height reflects the growth behavior of a crop. Both genetic and environmental factors play a vital role in determining the plant height of a plant. The data revealed that the plant height of different brassica genotypes under study was significant (Table-2). Five mutant lines O3 (145.5), O5 (149.9), O6 (157.3), O8 (157.3) and G8 (153.8) were shorter than the check while two mutant lines O6 (197.9) and O9 (199.0) were taller than the check (Table-1). For Plant height  $\sigma^2_p$  (137.19) was slightly higher than the  $\sigma^2_g$  (106.98) and similarly PCV (9.90) was higher compared to GCV (6.10) and (Table 3) while the said trait according to Table-3 exhibited high heritability (78.0) and moderate genetic advance (11.11). This suggests the involvement of non-additive (dominance or epistatic) gene effect for this trait.

### 1000 seed weight (SW)

The data revealed that significant differences were observed for 1000 seed weight among 35 tested genotypes against the check (Table-2). Thirty mutant lines showed low 1000 seed weight compared to check (table-1). However EA3 (4.1), EA2 (4.2), G6 (4.3), O4 (4.3), O6 (4.4) and G7 (4.5) shows the lowest values for 1000 seed weight. Only two mutant lines OA5 (5.65) and G1 (5.60) showed a higher value for 1000 seed weight compare to check. For this trait phenotypic variance was 0.14 and genotypic variance was 0.12 and the phenotypic and the genotypic coefficient of variations were 7.88 and 7.43 respectively (Table 3). On average the check showed higher value of 1000 seed weight than the mutant line. Moreover the trait 1000 seed weight (Table 3) exhibited high heritability (88.9) and moderate genetic advance (14.46).

### Seed yield (SY)

The data revealed that significant differences were observed for seed yield among 35 tested genotypes against the check (Table-2). Nineteen mutant lines showed low values for seed yield

compared to check and four mutant lines produced higher values. However G9 (1083), O7 (1333), O3 (1417), EA5 (1417) and EA6 (1417) showed the lowest values and OA5 (2708) showed the highest value for seed yield. High phenotypic variance (144969.56) and high genotypic variance (123563.75) were observed for seed yield. The phenotypic and the genotypic coefficient of variations for seed yield were 20.59 and 19.01 respectively, while the seed yield displayed high heritability (85.2) and high genetic advance (36.20) for the tested genotypes (Table 3).

#### Oil Yield (OY)

Significant differences were observed for oil yield among thirty five tested genotypes against the

check (Table-2). Twelve mutant lines give low oil yield while six mutant lines give higher oil yield compared to check. However G9 (570.2), O7 (690.9), EA7 (702.3), EA5 (720.3), EA6 (730.5) and EA8 (757.6) showed the lowest values and OA5 (1410) and G1 (1299) showed the highest values for oil yield compared to check. The phenotypic variance for oil yield was 41123.48 and genotypic variance was 40550.88 and the phenotypic and the genotypic coefficient of variations were 20.91 and 20.76 respectively (Table 3). The oil yield (Table 3) gives highest heritability (98.6) and highest genetic advance (42.54).

**Table1. Mean values of some quantitative traits of advance brassica mutant lines.**

S.No	Genotype	Days to flowering	Plant height (cm)	1000 seed weight	Seed yield (kg ha <sup>-1</sup> )	Oil yield (kg ha <sup>-1</sup> )
1	O1	83.25 <sup>BCDEFG</sup>	164.2 <sup>DEFGH</sup>	4.550 <sup>GHIJKL</sup>	1750 <sup>FGHIJKL</sup>	953.9 <sup>EFGHIJKL</sup>
2	O2	83.00 <sup>BCDEFG</sup>	188.6 <sup>AB</sup>	4.900 <sup>CDEFGH</sup>	2250 <sup>ABCDE</sup>	1177 <sup>ABCDEF</sup>
3	O3	72.25 <sup>KLM</sup>	145.5 <sup>I</sup>	4.650 <sup>FGHIJK</sup>	1417 <sup>JKLM</sup>	749.8 <sup>JKLMN</sup>
4	O4	83.50 <sup>BCDEFG</sup>	188.8 <sup>AB</sup>	4.300 <sup>KLM</sup>	2417 <sup>ABC</sup>	1288 <sup>ABC</sup>
5	O5	71.00 <sup>LM</sup>	149.9 <sup>HI</sup>	5.300 <sup>ABC</sup>	1708 <sup>FGHIJKL</sup>	915.9 <sup>GHIJKLM</sup>
6	O6	88.75 <sup>ABCD</sup>	197.9 <sup>A</sup>	4.400 <sup>JKLM</sup>	2500 <sup>AB</sup>	1327 <sup>AB</sup>
7	O7	88.00 <sup>ABCD</sup>	157.3 <sup>FGHI</sup>	4.800 <sup>DEFGHIJ</sup>	1333 <sup>LM</sup>	690.9 <sup>MN</sup>
8	O8	78.50 <sup>EFGHIJK</sup>	157.3 <sup>FGHI</sup>	5.000 <sup>CDEF</sup>	1750 <sup>FGHIJKL</sup>	908.8 <sup>GHIJKLM</sup>
9	O9	91.50 <sup>A</sup>	199.0 <sup>A</sup>	4.500 <sup>HJKLM</sup>	2333 <sup>ABCD</sup>	1230 <sup>ABCD</sup>
10	G1	69.25 <sup>M</sup>	168.1 <sup>CDEFGH</sup>	5.600 <sup>A</sup>	2500 <sup>AB</sup>	1299 <sup>AB</sup>
11	G2	72.00 <sup>KLM</sup>	169.1 <sup>CDEFG</sup>	5.100 <sup>BCDE</sup>	1708 <sup>FGHIJKL</sup>	919.8 <sup>GHIJKLM</sup>
12	G3	79.75 <sup>EFGHIJ</sup>	172.9 <sup>BCDEFG</sup>	4.700 <sup>EFGHIJK</sup>	1875 <sup>DEFGHIJ</sup>	1002 <sup>DEFGHIJ</sup>
13	G4	76.25 <sup>GHIJKLM</sup>	169.4 <sup>CDEFG</sup>	4.850 <sup>DEFGHI</sup>	2042 <sup>BCDEFG</sup>	1103 <sup>BCDEFGH</sup>
14	G5	71.75 <sup>KLM</sup>	166.4 <sup>CDEFGH</sup>	4.650 <sup>FGHIJK</sup>	1917 <sup>DEFGHI</sup>	1007 <sup>DEFGHIJ</sup>
15	G6	71.50 <sup>KLM</sup>	164.0 <sup>DEFGH</sup>	4.300 <sup>KLM</sup>	1958 <sup>CDEFGH</sup>	1018 <sup>DEFGHI</sup>
16	G7	71.50 <sup>KLM</sup>	164.6 <sup>DEFGH</sup>	4.550 <sup>GHIJKL</sup>	1833 <sup>EFGHIJK</sup>	967.9 <sup>EFGHIJK</sup>
17	G8	69.00 <sup>M</sup>	153.8 <sup>GHI</sup>	4.950 <sup>CDEFG</sup>	2000 <sup>CDEFGH</sup>	1046 <sup>CDEFGHI</sup>
18	G9	73.25 <sup>IKLM</sup>	159.3 <sup>EFGHI</sup>	4.950 <sup>CDEFG</sup>	1083 <sup>M</sup>	570.2 <sup>N</sup>
19	OA1	77.75 <sup>FGHIJKL</sup>	169.4 <sup>CDEFG</sup>	4.800 <sup>DEFGHIJ</sup>	1583 <sup>GHIJKL</sup>	838.8 <sup>IKLM</sup>
20	OA2	69.50 <sup>M</sup>	171.4 <sup>BCDEFG</sup>	4.800 <sup>DEFGHIJ</sup>	1917 <sup>DEFGHI</sup>	1003 <sup>DEFGHIJ</sup>
21	OA3	80.00 <sup>EFGHIJ</sup>	160.4 <sup>DEFGHI</sup>	4.550 <sup>GHIJKL</sup>	1542 <sup>HJKLM</sup>	815.1 <sup>IKLMN</sup>
22	OA4	89.50 <sup>ABC</sup>	168.1 <sup>CDEFGH</sup>	4.700 <sup>EFGHIJK</sup>	1583 <sup>GHIJKL</sup>	814.9 <sup>IKLMN</sup>
23	OA5	68.75 <sup>M</sup>	171.4 <sup>BCDEFG</sup>	5.650 <sup>A</sup>	2708 <sup>A</sup>	1410 <sup>A</sup>
24	OA6	68.75 <sup>M</sup>	164.9 <sup>CDEFGH</sup>	4.950 <sup>CDEFG</sup>	2167 <sup>BCDEF</sup>	1138 <sup>BCDEFG</sup>
25	OA7	72.75 <sup>JKLM</sup>	179.4 <sup>BCD</sup>	5.150 <sup>BCD</sup>	1750 <sup>FGHIJKL</sup>	923.5 <sup>FGHIJKLM</sup>
26	OA8	82.00 <sup>DEFGH</sup>	184.0 <sup>ABC</sup>	4.550 <sup>GHIJKL</sup>	1708 <sup>FGHIJKL</sup>	882.0 <sup>HJKLM</sup>
27	OA9	80.25 <sup>EFGHI</sup>	168.2 <sup>CDEFGH</sup>	4.750 <sup>DEFGHIJ</sup>	2292 <sup>ABCDE</sup>	1205 <sup>ABCDE</sup>
28	EA1	82.25 <sup>CDEFGH</sup>	173.1 <sup>BCDEF</sup>	4.650 <sup>FGHIJK</sup>	1833 <sup>EFGHIJK</sup>	937.0 <sup>FGHIJKLM</sup>
29	EA2	73.25 <sup>IKLM</sup>	173.3 <sup>BCDEF</sup>	4.200 <sup>LM</sup>	1667 <sup>GHIJKL</sup>	877.8 <sup>HJKLM</sup>
30	EA3	85.75 <sup>ABCDE</sup>	171.4 <sup>BCDEFG</sup>	4.100 <sup>M</sup>	1958 <sup>CDEFGH</sup>	1031 <sup>DEFGHI</sup>
31	EA4	84.75 <sup>ABCDEF</sup>	175.4 <sup>BCDEF</sup>	5.050 <sup>CDEF</sup>	1583 <sup>GHIJKL</sup>	796.5 <sup>IKLMN</sup>
32	EA5	80.25 <sup>EFGHI</sup>	165.8 <sup>CDEFGH</sup>	4.400 <sup>JKLM</sup>	1417 <sup>JKLM</sup>	720.3 <sup>JKLMN</sup>
33	EA6	75.50 <sup>HJKLM</sup>	159.9 <sup>EFGHI</sup>	4.300 <sup>KLM</sup>	1417 <sup>JKLM</sup>	730.5 <sup>JKLMN</sup>
34	EA7	80.50 <sup>EFGHI</sup>	170.8 <sup>BCDEFG</sup>	4.500 <sup>HJKLM</sup>	1375 <sup>KLM</sup>	702.3 <sup>LMN</sup>
35	EA8	89.75 <sup>AB</sup>	166.3 <sup>CDEFGH</sup>	4.450 <sup>IKLM</sup>	1458 <sup>IKLM</sup>	757.6 <sup>JKLMN</sup>
36	Control	89.75 <sup>AB</sup>	177.6 <sup>BCDE</sup>	5.450 <sup>AB</sup>	2250 <sup>ABCDE</sup>	1157 <sup>BCDEFG</sup>

DMR test (0.05): Means followed by same letters are not significantly different from each other.

S.No	Parameters	Mean squares
1	Days to flowering	202.2**
2	Plant height (cm)	548.8**
3	1000 seed weight	0.6**
4	Seed yield (kg/ha <sup>-1</sup> )	579878.2**
5	Oil yield (kg ha <sup>-1</sup> )	164493.9**

\*\*Significant at 1% level

**Table 3. Genetic parameters of some quantitative traits of advance brassica mutant lines**

Parameter	$\sigma^2_p$	$\sigma^2_g$	PCV	GCV	h <sup>2</sup> (%)	GA (%)
Days to flowering	50.54	45.65	9.06	8.61	90.3	16.88
Plant height (cm)	137.19	106.98	6.90	6.10	78.0	11.11
1000 seed weight (g)	0.14	0.12	7.88	7.43	88.9	14.46
Seed yield kg ha <sup>-1</sup> )	144969.56	123563.75	20.59	19.01	85.2	36.20
Oil yield (kg ha <sup>-1</sup> )	41123.48	40550.88	20.91	20.76	98.6	42.54

$\sigma^2_p$  (phenotypic variance),  $\sigma^2_g$  (genotypic variance), PCV (phenotypic coefficient of variation), GCV (genotypic coefficient of variation), h<sup>2</sup> (heritability), GA (genetic advance)

## DISCUSSIONS

### Days to flowering (DF)

Flowering is the most critical stage having great influence on the yield of oilseed *Brassica*. The onset of flower initiation can have strong influence on flower, siliquae and seed related parameters (Campbell and Kondra, 1978). Various studies on oilseed rape (*Brassica napus* L) have shown flowering period to be a highly heritable character. In the present project the advance mutant lines took less days on average (84) for the 50% flowering period than that of parental lines (89.75). Our results are in conformity with the findings of some already reported research regarding the said parameter (Olivieri and Parrini, 1979, Singh et al., 2007c, Lefort-Buson and Dattee, 1982a.) which strengthened our results. On the other hand there are some reverse results are also reported (Sajid et al., 2008 and Ghosh and Gulati 2001) who reported in their studies that the hybrids F<sub>2</sub> population took more days on average for the flowering period than that of parental lines.

Similarly  $\sigma^2_p$  and the PCV give larger values than the  $\sigma^2_g$  and the GCV for this trait. Kashif *et al.* (2003) also indicated same results. Slightly higher value of PCV than GCV and similarly higher value of  $\sigma^2_p$  compared to  $\sigma^2_g$  shows environmental effect on this character. The coefficient of variation shows only the extent of total variability and does not separate the variability into heritable and non-heritable portion. High value of heritability (90.3) and moderate value of genetic advance (16.88) were observed for days to flowering (Table 3) suggesting non-additive (dominance or epistatic) gene effect. Kumar and Misra (2007) also reported high heritability for days to flowering. This indicated that a trait having high

heritability did not essentially produce high genetic advance. Thus only heritability did not give the indication for genetic advancement that could be maintained through selection.

### Plant height (PH)

The plant height (PH) reflects the growth pattern of a crop. Genetic characteristics as well as environmental condition play vital role in the determination of PH of any individual plant. In this study, parental line was observed to be taller than the observed material. Our results are confirmed by various early reports (Aytac and Kinaci 2009, Khan et al., 2006a).

Similarly plant height also produced same trend of higher  $\sigma^2_p$  (137.19) than the  $\sigma^2_g$  (106.98) and similarly higher PCV (9.90) compared to GCV (6.10). Ali (1985) also found high genotypic and phenotypic variances for plant height and pods per plant in *Brassica juncea*. Which indicated the environmental effects? High value of heritability and moderate value of genetic advance were observed for plant height. Slightly higher phenotypic variance than the genotypic variance and high heritability along with moderate genetic advance for this trait was probably due to non-additive (dominance or epistatic) gene effects. Ali (1985) also found high genotypic and phenotypic variances for plant height and pods per plant in *Brassica juncea*. This indicated that a trait having high heritability did not essentially produce high genetic advance. Thus only heritability did not give the indication for genetic advancement that could be maintained through selection.

### 1000 seed weight (SW)

The weight of seed depicts the magnitude of seed development that determines seed yield of any

variety. There was not any major difference among the seed weight (SW) of parent and the mutant population. On average, 1000-SW of parental line was 5.45gm while the mean of the mutant populations for 1000-SW was 4.56gm. Similar finding for the said trait were already reported (Aytac and Kinaci 2009). For 1000 SW phenotypic variance was higher than genotypic variance and the phenotypic coefficient of variations was higher than the genotypic coefficient of variations respectively. Our results are similar with some already reported results (Akbar et al., 2007a, Kumar and Misra 2007).

#### Seed yield (SY)

High phenotypic variance (144969.56) and high genotypic variance (123563.75) were observed for seed yield. The phenotypic and the genotypic coefficient of variations for seed yield were also high (20.59 and 19.01) respectively. High GCV, PCV were stated for seed yield and number of pods per plant (Giessen *et al.*, 2003; Akbar *et al.*, 2007; Akbar *et al.*, 2003). Higher  $\sigma^2_g$  and  $\sigma^2_p$  were recorded for seed yield (Aytac *et al.*, 2008). The seed yield (Table 3) displayed high heritability (85.2) and high genetic advance (36.20). Both heritability and genetic advance showed higher values for this trait which suggests the effect of additive gene for the inheritance and selection in the early generation in this trait could be productive in improving this character.

#### Oil yield (OY)

Most of the mutant lines give low oil yield while some mutant lines give higher oil yield compared to check. The value of  $\sigma^2_p$  was high compared to  $\sigma^2_g$  and the value of PCV was recorded higher compared to GCV for oil yield. This suggests the effect of environment for the inheritance of this character. The coefficient of variation shows only the extent of total variability present for specific characters and does not demarcate the variability into heritable and non-heritable portion. The oil yield (Table 3) gives highest heritability (98.6) and highest genetic advance (42.54). A trait having high heritability and high genetic advance is considered under the control of additive genes for inheritance which highlights the usefulness of plant selection based on phenotypic performance and selection in the early generation could be fruitful in improving this character (Giessen *et al.*, 2003; Akbar *et al.*, 2007).

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