

Research Article



Genetic Variability and Heritability in F_4 Populations of *Brassica napus* L.

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Abstract | An experiment was conducted to estimate genetic variability, heritability and genetic advance for important attributes in *Brassica napus* using 10 parental lines and their 21 F_4 populations. Significant differences were observed among genotypes, parents, F_4 populations and parents versus F_4 populations for days to 50% flowering, days to maturity, plant height, primary branches plant⁻¹ and main raceme length. Among parents, CA2, DH8, DH4, CA4 and DH6 performed better for different traits. Whereas among F_4 populations, cross combinations CA5 × DH8, CA2 × DH7, CA2 × DH8, CA5 × DH7, CA4 × DH7 and CA4 × DH8 performed better. Plant height and main raceme length displayed moderate to high broad sense heritability and maximum genetic advance for most of the F_4 populations. Current results suggested the effectiveness of selection in early generations for the improvement of these traits.

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Introduction

Pakistan is chronically deficient in the production of edible oils and this deficit is continuously increasing due to the rapid rise in population and living standard of people. The local production of edible oil from all crops is only sufficient to meet one third of the domestic consumption while remaining being met through heavy imports by spending highly earned foreign exchange (FBS, 2014). Rapeseed and mustards share more than 20% in the domestic production which is the second largest share after cottonseed (FBS, 2014).

Rapeseed (mustards) is the second largest oilseed crop in the world providing 13% of the world's edible oil after soybean. During 2014, rapeseed/ mustard were globally grown on area of 36.5 million hectare with the total production of 72.7 million metric tons having

average yield of 1991.0 kg ha⁻¹ (FAO Statistics, 2014). European Union is the leading producer followed by Canada, China, India and France. In Pakistan, during 2013-14 rapeseed was grown on an area of 24.70 thousand hectare, which produced 232.0 thousand tons seed with an average yield of 901.3 kg ha⁻¹ (FAO Statistics, 2014). Due to increasing demand for rapeseed oil for food and non-food uses, the production of hybrid cultivars with higher seed and oil yields has become increasingly important (Ahmad et al., 2011). Rapeseed oil is used as food, as well as for industrial purposes including biodiesel production (Sabaghnia et al., 2010). A number of efforts have been undertaken to improve the rapeseed-canola cultivars for quality and production. Several genotypes/varieties have been developed and tested in different parts of Pakistan (Mahmood et al., 2011; Ahmad et al., 2012) but these varieties are not sufficient to fulfil domestic requirements. Furthermore, area under cultivation of

oilseed crops in the country is also decreasing with the passage of time showing the negligence of national policies. Non-availability of better-adapted genotypes is a reason for decreasing acreage of these crops (Khan et al., 2006). Oilseed brassica being well entrenched in the cropping system of Pakistan can potentially reduce consumption and production gap and decrease burden on exchequer (Syed et al., 1994).

Genetic variability, heritability as well as genetic gain in selection contribute to success of any crop improvement program (Khan et al., 2006). Genetic variability is the difference in plants on the basis of different characters. Plant breeders are trying to explore and induce diversity among the available genetic material. This helps in the selection of desirable line(s) and it also helps in developing a new cultivar which is adaptable to diverse agro-climatic conditions. Therefore, diversity of plant genetic resources is imperative for crop improvement (Jatoi et al., 2012).

Estimates of heritability help in predicting performance of genotypes in succeeding generations and thus provide a vital component of response to selection for successful breeding programs. Heritability is a key of transmissibility of traits and as such partition the total variance into genetic and environmental components (Falconer and Mackay, 1996; Marwede et al., 2004). Heritability can also help in determining the choice of breeding system. It plays a main role in bringing improvement in the crop plants. Genetic gain is the amount of increase in performance that is achieved through artificial genetic improvement. This term is usually used to refer to the increase after one generation has passed. Thus by estimating the genetic advance breeders can get clear idea that how much improvement is brought after passing one generation. Keeping in view the importance of rapeseed as an important oilseed crop an experiment was conducted to evaluate *Brassica napus* L. genotypes and their F_4 populations with the objectives to estimate genetic variability and broad sense heritability for important traits.

Materials and Methods

To study genetic variability, heritability and genetic advance in parents and F_4 populations of *Brassica napus*, an experiment was conducted during 2014-15 at The University of Agriculture, Peshawar - Pakistan.

Brassica napus germplasm comprised of ten parents (7

lines viz., DH-2, DH-3, DH-4, DH-5, DH-6, DH7 and 3 testers viz., CH-8, CA-2, CA-4 and CA-5) and their twenty-one F_4 populations. All genotypes were planted in randomized complete block design with three replications. Each genotype was planted in five rows replication⁻¹ with the row length of 5m. Row-to-Row and plant to plant distance was kept at 50 cm and 30 cm, respectively. All agronomic practices were performed uniformly for all genotypes.

Data were recorded on 10 randomly selected plants from each genotype at proper time for days to flowering, days to maturity, number of primary branches on main stem, plant height and main raceme length.

Statistical analysis

The data was statistically analysed according to the appropriate method recommended for randomized complete block design (Steel and Torrie, 1980). Mean separation was carried out following LSD test. Broad sense heritability for a particular trait was computed using parental and F_4 populations of each cross combination using the modified version of the formula suggested by Mahmud and Kramer (1951):

$$h^2 = \frac{VF_4 - \sqrt{VP_1 \times VP_2}}{VF_4}$$

Where,

VF_4 = Variance of F_4 population for a specific trait.

V_{P_1} and V_{P_2} = Variances of parent 1 and parent 2 of a specific F_4 population.

Genetic advance was computed by using following formula as suggested by Panse and Sukhatme (1965):

$$GA = k.(\sqrt{\sigma^2 P}).h^2$$

Where,

GA = Genetic advance, K = 1.76 for 10 % selection intensity, h^2 = Heritability coefficient (broad sense), $(\sqrt{\sigma^2 P})$ = Phenotypic standard deviation

Results and Discussion

The results of the experiment based on important characters are discussed below:

Days to 50% flowering

In rapeseed, early flowering generally results in early maturity which helps plants to escape heat stress therefore early flowering is considered favourable.

Table 1: Mean squares of parents and F_4 populations for various traits in *Brassica napus*

SOV	Rep (df=2)	Genotype (df=30)	Parents (df=9)	F_4 (df=20)	P vs F_4 (df=1)	Error	CV%
Days to 50% flowering	7.3	9.4**	14.0**	5.1*	51.7**	2.7	1.51
Days to maturity	17.8	56.5**	106.1**	26.2**	215.5**	12.5	2.14
Plant height	83.9	444.2**	160.7*	330.0**	5278**	77.0	5.13
Number of primary branches	0.3	2.7**	3.6**	2.2**	4.1**	0.8	0.8
Main raceme length	36.1	183.7**	166.7**	185.4**	302.8*	63.3	12.22

* and **: Significant and highly significant at 0.05 and 0.01 level of probability, respectively

In the current experiment, genotypes parents and parents versus F_4 showed highly significant difference ($p \leq 0.01$), whereas F_4 populations showed significant differences at ($p \leq 0.05$) (Table 1). The results indicated the presence of sufficient variability in the tested genotypes. Similar findings have been reported earlier by Nazeer et al. (2003), Azam et al. (2013), Nasim et al. (2013) and Muhammad et al. (2014) who observed significant differences for days to flowering in *Brassica napus* genotypes.

On overall basis, mean values for days to 50% flowering varied from 106 to 112 with an average value of 109 days. Data for parental genotypes ranged from 106 to 112 days with the mean of 108 days where earliest flowering was observed in DH2 whereas flowering in CA2 took maximum days. Mean values of F_4 population ranged from 108 to 112 days with mean of 110 days (Table 2). Earliest flowering was observed in CA2 \times DH3, CA2 \times DH7 and CA5 \times DH3. Overall variances vary between 2.3 for the genotype CA2 to 31.6 for cross CA2 \times DH4. Among parental genotypes, variance ranged between 2.3 for CA2 to 16.22 for DH4. In F_4 populations, variance varied from 6 to 31.6 for CA2 \times DH8 and CA2 \times DH4, respectively (Table 3). Heritability estimations exhibited that majority of the populations had moderate to low heritability. Broad sense heritability in the F_4 populations was lowest for CA2 \times DH7 (0.31) and highest for CA5 \times DH6 (0.63). Genetic advance was low for the cross CA4 \times DH3 (1.4) while it was highest for the cross CA2 \times DH4 (6.3). High heritability and genetic advance shows more genetic control and selection could be effective to bring improvement in days to flowering. Mahto and Haider (2002) and Chaghakaboodi et al. (2012) also reported similar results in rapeseed genotypes.

Days to maturity

Early maturity in rapeseed helps to escape heat

stress and some late coming diseases therefore early maturing genotypes are preferred by the farmers. In present study, highly significant differences ($P \leq 0.01$) were observed among genotypes, parents, F_4 populations and parents versus F_4 (Table 1). Zare and Sharafzadeh (2012) and Hasan et al. (2014) also reported significant differences for days to maturity among *Brassica napus* genotypes.

Mean data for days to maturity on overall basis showed that minimum days were taken by CA5 (153days) while the maximum days were taken by CA5 \times DH8 (175days). Among parental genotypes, maturity fluctuated from 153 to 172 days for CA5 and CA2 respectively with a mean of 163 days. Among F_4 populations, days taken to maturity were 162 to 175days for CA4 \times DH8 and CA5 \times DH8, respectively with the mean value of 166 days (Table 2).

On overall basis, variance for genotypes ranged between 2.17 to 19.10 for DH5 and CA2 \times DH7, respectively. Among parents, smallest variance (2.16) was recorded for DH5 while the highest (13.2) was recorded for DH2 whereas, in F_4 populations, the lowest variance (6.13) was displayed by CA4 \times DH5, while the highest variance (19.1) was recorded for CA2 \times DH7 (Table 3). Majority of the heritability estimates were moderate whereas few were low. The lowest value of heritability was recorded for CA5 \times DH7 (0.32) while highest value was displayed by CA2 \times DH8 (0.56). Lowest genetic advance was recorded for CA4 \times DH (1.6) while the highest for CA2 \times DH8 (4.1) (Table 3). Our results are partially in agreement with the earlier finding of Zare and Sharafzadeh (2012) and Rameeh (2014) who observed high heritability for days to maturity in *Brassica napus*.

Plant height (cm)

In brassica, medium sized plants are preferred because

Table 2: Means values of parents and F₄ populations of important traits in *Brassica napus*

Genotypes	Days to 50% flowering (days)	Days to maturity (days)	Plant height (cm)	No. Primary Branches (nos)	Main raceme length (cm)
CA2	112	172	185	8.6	81
CA4	111	168	186	5.4	64
CA5	107	153	188	6.9	80
DH2	106	162	172	5.3	65
DH3	109	156	188	6.0	68
DH4	106	163	186	5.5	69
DH5	108	168	178	6.1	62
DH6	108	162	179	5.3	68
DH7	107	160	168	5.3	61
DH8	107	168	190	7.2	59
Parents mean	108	163	182	6	68
CA2 × DH2	111	165	184	6.1	77
CA2 × DH3	108	164	175	4.2	75
CA2 × DH4	109	166	155	5.7	59
CA2 × DH5	109	166	143	4.6	50
CA2 × DH6	109	167	166	5.2	67
CA2 × DH7	108	166	165	5.2	74
CA2 × DH8	111	168	162	7.2	62
CA4 × DH2	109	170	162	5.7	55
CA4 × DH3	111	165	172	5.1	67
CA4 × DH4	112	172	183	7.7	71
CA4 × DH5	112	165	170	6.0	68
CA4 × DH6	112	166	164	6.1	63
CA4 × DH7	109	166	157	5.2	63
CA4 × DH8	109	162	169	5.3	59
CA5 × DH2	110	167	176	5.9	68
CA5 × DH3	108	166	157	4.9	63
CA5 × DH4	112	166	148	6.2	47
CA5 × DH5	109	165	163	5.7	69
CA5 × DH6	109	165	173	6.0	64
CA5 × DH7	110	163	176	4.8	64
CA5 × DH8	109	175	163	6.9	54
F ₄ mean	110	166	166	6	64
Genotypes mean	109	165.4	171	5.9	65
LSD _(0.05) Parents	0.58	1.26	3.13	0.31	2.84
LSD _(0.05) F ₄ 's	0.85	1.83	4.53	0.45	4.11
LSD _(0.05) Genotypes	2.69	5.77	14.33	1.44	13.00

medium plants can withstand against lodging therefore in breeding experiments plant height is given due importance. In current study, highly significant differences ($P \leq 0.01$) were observed for plant height among genotypes, parents versus F₄ and F₄ while significant differences ($P \leq 0.05$) existed among parents (Table 1). Azam et al. (2013) and Muhammad et al.

(2014) also reported significant differences for plant height in brassica genotypes.

On overall basis, plant height ranged from 143 to 190 cm for CA2 × DH5 and DH8, respectively. Plant height in the parents ranged between 168 to 190cm for DH7 and DH8 respectively with the average of 182 days

Table 3: Variances, heritability and genetic advance of days to 50% flowering, days to maturity and plant height in *Brassica napus* L

Genotypes	Days to flowering (days)			Days to maturity (days)			Plant height (cm)		
	Var.	H ² _(bs)	GA	Var.	h ² _(bs)	GA	Var.	h ² _(bs)	GA
CA2	2.3			7.4			54.8		
CA4	3.5			5.4			124.9		
CA5	2.6			4.9			34.7		
DH2	6.2			13.2			83.4		
DH3	5.1			6.1			157.2		
DH4	16.2			8.0			209.8		
DH5	3.6			2.2			116.9		
DH6	3.9			6.0			195.7		
DH7	3.4			8.6			159.9		
DH8	4.2			8.1			233.8		
CA2 × DH2	19.2	0.59	4.5	17.1	0.41	3.0	123.6	0.44	11.5
CA2 × DH3	6.1	0.34	1.5	10.9	0.36	2.1	447.2	0.60	12.8
CA2 × DH4	31.6	0.63	6.3	12.1	0.39	2.4	342.1	0.53	20.6
CA2 × DH5	7.2	0.53	2.5	11.1	0.55	3.2	213.1	0.57	13.6
CA2 × DH6	24.6	0.58	5.1	10.1	0.37	2.0	294.2	0.55	17.7
CA2 × DH7	10.3	0.41	2.3	19.1	0.50	3.9	294.8	0.59	12.4
CA2 × DH8	6.0	0.47	2.0	17.2	0.56	4.1	659.2	0.55	21.3
CA4 × DH2	8.3	0.44	2.2	14.8	0.42	2.8	359.6	0.56	14.5
CA4 × DH3	6.4	0.31	1.4	9.9	0.39	2.2	253.3	0.43	8.6
CA4 × DH4	16.4	0.33	2.4	14.1	0.41	2.7	528.2	0.45	13.4
CA4 × DH5	6.9	0.47	2.2	6.1	0.38	1.6	399.7	0.48	16.4
CA4 × DH6	6.6	0.37	1.7	10.2	0.36	2.1	237.3	0.32	10.1
CA4 × DH7	10.0	0.56	3.1	11.6	0.37	2.2	414.2	0.56	19.9
CA4 × DH8	9.0	0.46	2.4	10.9	0.38	2.2	374.2	0.48	15.5
CA5 × DH2	9.9	0.49	2.7	16.3	0.40	2.9	205.9	0.57	12.3
CA5 × DH3	6.6	0.31	1.4	9.2	0.40	2.1	227.4	0.56	8.1
CA5 × DH4	18.8	0.54	4.2	14.3	0.55	3.7	342.1	0.58	17.7
CA5 × DH5	9.4	0.59	3.2	6.7	0.47	2.1	566.0	0.52	24.8
CA5 × DH6	8.0	0.57	2.9	11.9	0.55	3.4	243.3	0.49	15.8
CA5 × DH7	9.9	0.62	3.4	9.9	0.32	1.7	289.6	0.54	18.6
CA5 × DH8	10.9	0.52	3.0	10.9	0.37	2.1	260.8	0.51	14.8

Among F₄ populations, plant height varied between 143 to 183cm for CA2 × DH5 and CA4 × DH4, respectively with the mean value of 166cm (Table 2).

Significant variations were observed for plant height among all genotypes. On overall basis, variance for plant height ranged from 34.7 to 659.2 for CA5 and CA2 × DH8, respectively. Variances among parents ranges from 34.7 to 233.8 for genotypes CA5 and DH8, respectively while variances among F₄ populations varied from 123.6 to 659.2 for CA2 × DH2 and CA2 × DH8, respectively. Moderate heritability in broad sense was observed for majority of the popula-

tions. The estimations of heritability ranged from 0.32 to 0.60 for CA4 × DH6 and CA2 × DH3, respectively. Genetic advance ranged from 8.6 to 25 for CA4 × DH6 and CA2 × DH8, respectively (Table 3). Most of the populations had moderate heritability coupled with high genetic advance, which shows that there is more genetic control over plant height therefore improvement in this character will be effective through selection. Our results are in line with the findings of Tariq et al. (2003) and Zhang and Zhou (2006) who reported high heritability and high genetic advance for plant height in *Brassica napus* and *Brassica juncea*, respectively.

Table 4: Variances, heritability and genetic advance of number of primary branches plant⁻¹ and main raceme length in *Brassica napus* L.

Genotypes	No. of Primary branches (nos)			Main raceme length (cm)		
	Var.	$h^2_{(bs)}$	GA	Var.	$h^2_{(bs)}$	GA
CA2	0.8			24.0		
CA4	0.4			88.1		
CA5	0.8			27.4		
DH2	1.9			81.7		
DH3	0.6			83.4		
DH4	0.7			204.1		
DH5	0.6			147.7		
DH6	1.3			21.5		
DH7	0.9			43.6		
DH8	1.6			87.5		
CA2 × DH2	4.0	0.57	2.0	82.0	0.26	4.1
CA2 × DH3	1.4	0.43	0.9	331.6	0.44	14.1
CA2 × DH4	5.6	0.54	2.2	316.3	0.58	18.1
CA2 × DH5	1.6	0.55	1.2	174.6	0.43	10.1
CA2 × DH6	2.9	0.58	1.7	48.2	0.45	5.5
CA2 × DH7	3.9	0.57	2.0	57.7	0.40	5.4
CA2 × DH8	3.4	0.47	1.5	119.6	0.53	10.2
CA4 × DH2	3.2	0.61	1.9	141.7	0.40	8.4
CA4 × DH3	1.3	0.57	1.1	216.1	0.59	15.1
CA4 × DH4	1.4	0.60	1.3	406.0	0.53	18.8
CA4 × DH5	7.2	0.57	2.7	461.0	0.55	20.9
CA4 × DH6	2.7	0.58	1.7	119.7	0.50	9.6
CA4 × DH7	1.6	0.49	1.1	168.3	0.50	11.4
CA4 × DH8	2.5	0.52	1.5	253.9	0.48	13.3
CA5 × DH2	3.4	0.54	1.8	125.4	0.53	10.4
CA5 × DH3	2.3	0.58	1.5	75.9	0.34	5.2
CA5 × DH4	2.0	0.47	1.2	428.4	0.59	21.5
CA5 × DH5	1.7	0.61	1.4	274.3	0.54	15.6
CA5 × DH6	2.9	0.54	1.6	64.2	0.41	5.8
CA5 × DH7	1.8	0.53	1.3	90.2	0.59	9.8
CA5 × DH8	2.5	0.48	1.3	106.5	0.45	8.3

Primary branches plant⁻¹

Number of primary branches is an important character of rapeseed and it is mainly related to the seed yield. Greater number of primary branches mostly produce greater number of pods that ultimately increase the seed yield in brassica. In current study, highly significant differences ($P \leq 0.01$) among genotypes, parents, F_4 populations and parents versus F_4 for number of primary branches (Table 1) were observed. Similar findings have been reported earlier by Azadgoleh et al. (2009), Gangapur et al. (2009), Khan

et al. (2013) and Ali et al. (2014). They also observed significant differences among brassica genotypes for number of primary branches.

Overall, mean value for primary branches plant⁻¹ varied from 4 to 9 for CA2 × DH3 and CA2, respectively with the average value of 5.9 (Table 4). Number of primary branches among parents ranged from 5 (DH7) to 8 (CA2) with mean of 6 branches. Among F_4 populations, primary branches plant⁻¹ ranged from 4 (CA2 × DH3) to 8 (CA4 × DH4) with an average value of 6 branches plant⁻¹ (Table 2).

Significant variations were observed among genotypes for primary branches indicating the presence of sufficient amount of variance among genotypes. Overall, variances among genotypes ranged from 0.4 to 7.2. Among parents, variances ranged from 0.4 to 1.9 for CA4 and DH2, respectively. Whereas among F_4 populations, variances varied between 1.2 to 7.2 for CA4 × DH3 and CA4 × DH5, respectively. Heritability estimates for F_4 populations exhibited moderate values for most of the populations. Heritability varied from 0.43 to 0.61 for cross combinations CA2 × DH3 and CA5 × DH5, respectively. Genetic advance ranged from 0.9 to 2.7, where minimum value was recorded for cross CA2 × DH3, while maximum value was noted for cross CA4 × DH5 (Table 4). Moderate heritability and genetic advance showed moderate genetic control suggesting that improvement in this trait possible through effective selection. Khan et al. (2013) and Ali et al. (2014) observed high heritability in *Brassica napus* genotypes. Similar results were earlier reported by Bozokalfa et al. (2010) in *Eruca* genotypes.

Main raceme length (cm)

Main raceme length is given due consideration in brassica breeding programs since longer racemes generally produce greater number of pods and ultimately enhancing seed yield. In the present study highly significant differences ($P \leq 0.01$) were observed for main raceme length among the genotypes, parents and F_4 populations whereas, significant differences ($P \leq 0.05$) were observed among parents versus F_4 (Table 1). Tahir et al. (2006) and Ali et al. (2014) also observed significant differences among brassica genotypes for main raceme length.

In the genotypes the minimum raceme length was noted for CA5×DH4 (47.1cm) while the maximum

length was recorded for CA2 (80.9cm). Parental mean data showed that minimum main raceme length was recorded for DH8 (59.1cm) while maximum main raceme length was displayed by CA2 (80.9cm). Considering the F_4 populations, the main raceme length ranged from 47.1cm to 77cm for CA5 \times DH4 and CA2 \times DH2, respectively. Average mean value of main raceme length was 65cm, 68cm and 64cm for genotypes, parents and F_4 populations, respectively (Table 2).

Variance on overall basis ranged from 21.15 to 461cm for DH6 and CA4 \times DH5, respectively. For parents, variance ranged from 21.5 to 204.07cm for DH6 and DH4, respectively. Among F_4 populations, variances ranged from 48.23 to 460.97 for CA2 \times DH6 and CA4 \times DH5, respectively (Table 4). Moderate to high heritability were noted for majority of the crosses for main raceme length. The range of heritability among F_4 population was 0.26 to 0.59 for CA2 \times DH2 and CA5 \times DH4, respectively. Genetic advance values ranged from 4.1 to 21.5 for CA2 \times DH2 and CA5 \times DH4, respectively (Table 4). Ali et al. (2014) also reported high heritability coupled with high genetic advance in *Brassica napus*. Zhang and Zhou (2006) reported similar results in *Brassica oleracea*.

Author's Contribution

Tahir khan was the main investigator of the research work, while Raziuddin was the supervisor. Muazam Jamal Razi helped in data collection. Fakharuddin helped in data collection, analysis and preparation of 1st draft of the paper.

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