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Genetic variability and heritability for yield and yield associated traits among *Brassica napus* genotypes

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Abstract

An experiment was conducted to study genetic variability and heritability among ten *Brassica napus* L. genotypes for yield and yield associated traits. The genotypes (CA-2, CA-4, CA-5, DH-2, DH-3, DH-4, DH-5, DH-6, DH-8 and CA-20) were evaluated in randomized complete block design with three replications. Data were recorded on days to 50% flowering, primary branches plant⁻¹, plant height, pod main raceme⁻¹, main raceme length, pod length, 1000 seed weight, oil content, glucosinolate and erucic acid content. Results revealed significant differences ($p \leq 0.05$) for all studied traits except pod main raceme and oil content. *Brassica* genotype DH-7 exhibited minimum days to 50% flowering (109 days). Genotype CA-2 showed maximum 1000-seed weight (8.2g) and minimum erucic acid contents (29.2%) whereas genotype CA-5 exhibited maximum primary branches (9), plant height (224.5cm), glucosinolate (84.5 μ Mg), oil content (54.5%) and low erucic acid (36.3%). High broad sense heritability was observed for days to 50% flowering (0.70), primary branches (0.73), plant height (0.74), pod main raceme (0.84), main raceme length (0.92), pod length (0.68), 1000-seed weight (0.83), oil content (0.65), glucosinolate content (0.81) and erucic acid (0.98). Among the studied genotypes, CA-5 and DH-8 performed better for most of the traits therefore, these genotype could be used in the future brassica breeding programs.

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Introduction

The genus Brassica is one of the most economically important genera belonging to the family Brassicaceae (Rakow, 2004). Brassica genus consists of a diverse group of species including major oilseed crops and vegetables (Rich; 1991, Christopher *et al*, 2005). This family consists of 338 genera and 3709 species (Warwick *et al*, 2006). The genus Brassica has two major groups commonly known as rapeseed and mustard. In Pakistan, *Brassica campestris* “rapa”), Raya (*B. juncea*) and Taramira (*Eruca sativa*) are grown as oilseed crop for centuries (Turi *et al*, 2012). The oil import bill of Pakistan is the second largest after petroleum (Ahmad *et al*, 2013), so it is imperative to develop improved varieties of oilseed Brassica (Khatri *et al*, 2005).

Breeding programs have involved innovative techniques to assist the release of new cultivars. Success of any crop improvement depends upon the presence of substantial amount of genetic variability, heritability, as well as genetic gain in selection (Khan *et al*, 2006). Heritability of any traits depends upon genetics properties of breeding material and environmental conditions in which experiments are carried out (Falconer and Mackay, 1996). A character which have higher range of genetic variability, heritability and genetic advance would be an effective tool to improve seed yield (Aytac and Kinaci, 2009).

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 variance in plants on the basis of diverse types. Plant breeders are demanding to discover and induce diversity among the obtainable genetic material. This helps in the selection of desired line(s) and it also helps in emerging a new cultivar which is flexible to varied 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 F₄ populations with the objectives to estimate genetic variability and broad sense heritability for important traits.

Present study aimed to assess the genetic variability among *Brassica napus* L. genotypes. Estimates heritability for various morphological yield traits of *Brassica napus* genotypes and to select best genotypes for further breeding programmes.

Materials and methods

The experiment was conducted in the Plant breeding and Genetics research farm, The University of Agriculture, Peshawar Pakistan during brassica crop growing season 2017-18. Ten *Brassica napus* L. genotypes comprised (Chinese lines; CA-2, CA-4, CA-5) and (doubled haploids; DH-2, DH-3, DH-4, DH-5, DH-6, DH-7, DH-8) were evaluated in randomized complete block design with three replications. Three rows for each genotype, with row to row distance of 60cm and plant to plant distance of 20cm were maintained. Cultural practices such as hoeing, weeding were performed uniformly for all genotypes in order to reduce experimental error. Data were recorded for days to 50% flowering, primary branches, plant height, pod main raceme⁻¹, main raceme length, pod length, 1000 seed weight, oil content, glucosinolate content and erucic acid on 10 randomly selecting plants in Morphological traits: Days to 50% flowering were recorded in each plot from date of sowing to when 50% flowers emerged.

Primary branches are counted as number of branches arises from stem. Main raceme length was taken by measuring the upper most inflorescence arising from the main stem. Data on plant height (cm) was recorded through meter rod by measuring the distance from the soil to the tip of the plant at physiological maturity. Main raceme is the main stem that ends into inflorescence; pods located on main raceme were counted. Pod length (cm) was recorded by measuring the distance from base to tip of selected pods. Thousand seed was measured in grams by weighing a sample of 1000 healthy seeds through electrical balance. Biochemical analysis of seed samples for Oil content (%), Glucosinolate content (umol/g) and erucic acid contents (%) were scanned on Near Infrared Reflectance Spectroscopy (Font *et al*, 2006; Hom *et al*, 2006) at Nuclear Institute for Food and Agriculture (NIFA), Tarnab, Peshawar.

Statistical analysis

The data were properly compiled and subjected to analysis of variance appropriate for randomized complete block design using computer software MS Excel and least significant difference (LSD) test was applied to test the significance of treatment differences.

Genotypic and phenotypic variances and broad sense heritability were computed according to Burton and Devane (1953) and Singh and Chaudhary (1985):

$$\text{Genetic variance} = \frac{\text{Genotypes mean squares} - \text{Error mean square}}{\text{Number of replication}}$$

Environmental variance (Ve) = Error mean squares (EMS)

$$\text{Phenotypic variance (VP)} = Vg + Ve$$

$$\text{Heritability (BS)} = H^2 = \frac{Vg}{Vp}$$

Results and discussions

Days to 50% flowering

The analysis of variance showed significant differences ($p \leq 0.05$) among the brassica genotypes for days to 50% flowering (Table 1). Among genotypes minimum days to 50% flowering was observed in genotype DH-7 (109 days) whereas maximum days to

50% flowering was recorded for genotype CA-4 (120 days) (Table 2). Significant variation for days to flowering was also witnessed by (Khan and Khan 2003; Nazeer *et al*, 2003).

High broad sense heritability (0.70) was recorded for days to 50% flowering (Table 3) indicating more genetic control due to higher genetic variance (20.25) than environmental variance (8.76). Ali *et al*, (2003), Nazeer *et al*, (2003) and Bozokalfa *et al*, (2010) also reported high heritability for days to flowering.

Table 1. Mean squares for DF=days to 50% flowering, PB= primary branches, PH=plant height, PMR=pod main raceme⁻¹, PML=main raceme length, PL= pod length, TSw=1000 seed weight, OIL= oil content, GSL= glucosinolate content and EA=erucic acid.

Parameters	Mean Squares			
	Reps (df=2)	Genotype (df=9)	Error (df=18)	CV%
Days to 50% Flowering	2.84	23.17*	8.76	2.56
Primary Branches plant ⁻¹	6.26	4.94*	1.62	22.66
Plant height (cm)	1641.80	455.47*	143.26	6.15
Main raceme length	74.22	291.13**	25.08	6.73
Pods main raceme ⁻¹	372.27	398.81*	71.71	12.54
Pod length	0.23	1.15*	0.47	9.05
1000 seed weight (g)	1.73	0.78*	0.15	5.15
Oil content (%)	3.82	6.23ns	2.82	3.24
Glucosinolate (umol/g)	4.00	328.52*	69.52	11.45
Erucic acid (%)	0.79	179.73**	2.73	2.83

**= Highly significant, *= significant and ns= non-significant

Table 2. Means values for days for DF=days to 50% flowering, PB= primary branches, PH=plant height, PMR=pod main raceme⁻¹, PML=main raceme length, PL= pod length, TSw=1000 seed weight, OIL= oil content, GSL= glucosinolate content and EA=erucic acid of brassica genotypes.

Genotypes	DF	PB	PH	MRL	PMR	PL	TSW	OIL	GSL	EA
CA-2	117	6	182.1	76.5	77	8.1	8.2	50.5	59.2	29.2
CA-4	120	7	192.0	83.2	78	7.8	7.1	49.8	63.6	43.9
CA-5	117	9	224.5	92.7	90	7.1	8.2	54.5	84.5	36.3
DH-2	116	5	179.3	54.4	52	7.7	7.3	52.6	56.1	43.3
DH-3	115	6	197.9	75.6	63	6.6	7.1	51.1	76.2	53.8
DH-4	114	5	194.9	70.5	71	6.8	7.2	52.6	80.9	56.2
DH-5	117	5	200.6	74.8	63	7.5	7.3	51.2	82.1	43.0
DH-6	115	5	193.5	73.5	67	7.4	7.2	53.4	69.7	46.8
DH-7	109	4	193.3	74.3	56	8.2	6.6	51.0	84.0	46.8
DH-8	115	5	189.4	68.3	59	8.5	7.7	51.6	71.7	45.9
LSD ^{0.05}	5.07	2.18	20.53	8.59	14.52	1.17	0.65	2.87	14.30	2.83

Table 3. Variances components and heritability for days to 50% flowering, primary branches, plant height, pod main raceme, main raceme length, pod length, 1000 seed weight, oil content, glucosinolate content and erucic acid

Parameters	Vg	Ve	hbs
Days to 50% flowering	20.25	8.76	0.70
Primary branches	4.40	1.62	0.73
Plant height	407.71	143.26	0.74
Main raceme length	282.77	25.08	0.92
Pods main raceme ⁻¹	374.91	71.71	0.84
Pod length	0.99	0.47	0.68
1000 seed wt.	0.73	0.15	0.83
Oil content	5.29	2.82	0.65
Glucosinolate	305.35	69.52	0.81
Erucic acid	178.82	2.73	0.98

Primary branches plants⁻¹

Significant differences ($p \leq 0.05$) were found among the brassica genotypes for primary branches plant⁻¹ (Table 1). Among genotypes maximum primary branches plant⁻¹ (9) was recorded for CA-5 while minimum value for primary branches plant⁻¹ (4) was recorded for DH-7 (Table 2).

Perusal of primary branches plant⁻¹ data highly exhibited significant differences among *Brassica napus* genotypes. These results are supported by Gangapur *et al.* (2009) and Azadgoleh *et al.* (2009) who found significant differences among Brassica genotypes.

Higher Broad sense heritability was recorded for primary branches plant⁻¹ (0.73) (Table 3) Genetic variance (4.40) was found higher than environmental variance (1.62). High magnitude of heritability was observed for primary branches plant⁻¹ indicating that this trait is more genetically controlled and could be used as potential selection criteria for the improvement in rapeseed (Fehr, 1987).

Plant height

The analysis of variance observed significant differences ($p \leq 0.05$) among the brassica genotypes for plant height (Table 1). Moreover, CA-5 showed maximum plant height (224.5cm), whereas DH-2 exhibited minimum plant height (179.3cm) (Table 2).

Maximum plant height is an important characteristic of brassica genotypes due to it is related to flowering

time because as more time passes before flowering, more height is obtained through vegetative growth of the primary stem and primary branches are also dependent on plant height that contributes towards yield by providing base for secondary branches, main raceme length and pods plant⁻¹. Ali *et al.* (2003) and Ali *et al.* (2002) also reported significant differences among brassica genotypes for plant height.

Broad sense heritability for plant height (0.74) depicted high heritability indicating more genetic control due to higher genetic variance (407.71) than environmental variance (143.26) (Table 3). Our result for heritability is close agreement with the result of Mahmood *et al.* (2003), Zhang and Zhou (2006) and Tariq *et al.* (2003).

Main raceme length

The analysis of variance manifested highly significant differences ($p \leq 0.01$) among the brassica genotypes for main raceme length (Table 1). Data regarding main raceme length genotype CA-5 showed maximum main raceme length (92.7cm) whereas minimum value (54.4cm) was observed for DH-2 (Table 2). Analysis of variance for main raceme length exhibited highly significant differences among *Brassica napus* genotypes indicating the existence of huge variability. These results are in agreement with those of Tahir *et al.* (2006) and Khan and Khan (2003), who also reported significant differences among all the genotypes for main raceme length.

Broad sense heritability for primary branches was high (0.92) (Table 3). High heritability for main raceme length is the result of more genetic variance (282.77) or less influence of the environment variance (25.08). The present findings are in close conformity with the research work of Ghosh and Gulati (2001), Tariq *et al.* (2003), and Zhang and Zhou (2006), who also observed high magnitude of heritability for main raceme length.

Pods main raceme⁻¹

Analysis of variance for pods main raceme⁻¹ exhibited highly significant differences ($P \leq 0.01$) among brassica genotypes (Table 1).

Maximum pods main raceme⁻¹ was observed for CA-5 (90cm) whereas minimum value for pods main raceme⁻¹ was recorded for DH-2 (52cm), (Table 2). Analysis of variance for pods main raceme⁻¹ revealed highly significant differences in *Brassica napus* genotypes showing that there is sufficient variability to have an effective selection. The obtained results are in line with those of Aytac and Kinaci (2009), Nazeer *et al.* (2003), and Tahir *et al.* (2006), who also reported significant differences among Brassica genotypes for pods main raceme⁻¹.

Maximum broad sense heritability for pods main raceme⁻¹ was observed for populations (0.84) (Table 3). Genetic variance for pods main raceme⁻¹ was observed (374.91) and environmental variance was (71.71). High heritability for pods main raceme⁻¹ indicating that this trait is more genetically controlled and early generation selection based on this trait will be effective (Fehr, 1987).

Pod length

Analysis of variance for pods length indicated significant differences ($P \leq 0.01$) among brassica genotypes (Table 1). Data regarding for pods length maximum (8.5cm) was observed for DH-8 (8.5cm) whereas minimum value for pods length (6.6cm) was recorded for DH-3 (Table 2).

Pod length is an important yield contributing trait having direct association with seeds pod⁻¹ and ultimately to seed yield. Pod length data exhibited significant differences among *Brassica napus* genotypes showing the presence of sufficient variability to have an effective selection. Our findings are in close agreement with those of Ayatic and Kinaci (2009), Azadgoleh *et al.* (2009), and Tahir *et al.* (2006), who also reported significant variation for pod length.

Broad sense heritability for pods length was high (0.68) (Table 3). Genetic variance for pod length was (0.99) whereas environmental variance was (0.47) with high heritability indicating that this trait is more genetically controlled and early generation selection will be effective (Fehr, 1987). These results are in close conformity with the previous observations of Zhang and Zhou (2006), Bozokalfa *et al.* (2010) and Mahmood *et al.* (2003).

1000 seed weight

The analysis of variance showed significant differences ($p \leq 0.01$) among the brassica genotypes for 1000 seed weight (Table 1). Data regarding 1000 seeds weight maximum (8.2g) was observed for CA-5 whereas minimum value for 1000 seed weight (6.6g) was recorded for DH-7 (Table 2).

Thousand seed weight revealed highly significant differences among the tested *Brassica napus* genotypes showing the presence of genetic variation among the genotypes to have an effective selection. Our findings are in close agreement with those of Nazeer *et al.* (2003), Azadgoleh *et al.* (2009) and Tahir *et al.* (2006) also reported significant variation for 1000-grain weight among brassica genotypes.

Broad sense heritability for 1000 seeds weight was (0.83%) (Table 3). Genetic variance for 1000 seeds weight observed (0.73) which is higher than environmental variance (0.15). Heritability for 1000-seed weight was high indicating that more genetic control results in high heritability for this trait (Fehr, 1987). The present findings are in close conformity with the research work of Zhang and Zhou (2006), Ali *et al.* (2003) and Nazeer *et al.* (2003), who also observed moderate to high magnitude of heritability for 1000-seed weight.

Oil content

Analysis of variance for oil content showed non-significant differences ($p \geq 0.05$) among brassica genotypes (Table 1). Data regarding oil content maximum (54.5%) was observed for CA-5 whereas minimum value for oil (49.8%) was recorded for CA-4 (Table 2).

Analysis of variance for oil content manifested significant result for *Brassica napus* genotypes. Similar results are also finding by Tuncturk and Ciftci (2007) and Rameeh (2010) they obtained non-significant results for oil content in *brassica napus*. Turi *et al.* (2010) obtained significant results for oil content in *brassica juncea*.

Broad sense heritability for oil content (0.65%) (Table 3). Genetic variance for oil content was recorded (5.29) whereas environmental variance was recorded

(2.82). High magnitude of broad sense heritability was also observed by Rameeh (2012) in rapeseed.

Glucosinolate (μMg)

The analysis of variance showed significant differences ($p \leq 0.01$) among the brassica genotypes for glucosinolate (Table 1). Data regarding glucosinolate (GSL) maximum (84.5 μMg) was observed for CA-5 whereas minimum glucosinolate (56.1 μMg) was recorded for DH-2 (Table 2). Based on preferable lower glucosinolate content, in the next coming generations selection for reduce GSL in rapeseed will be effective. These results are fully in conformity to the work of Bhardwaj and Hamama (2000) Rahman *et al*, (2009) reported significant differences in *Brassica napus*. Turi *et al*, (2010) reported significant differences for GSL in *Brassica juncea*.

Broad sense heritability estimates for glucosinolate was high for genotypes (0.81) (Table 3). Genetic variance for glucosinolate was (305.35) which is higher than environmental variance (69.52). Our heritability (bs) for glucosinolate was an agreement with the result of Khan *et al*, (2008) and Hu *et al*, (1988) in brassica genotypes.

Erucic acid

The analysis of variance showed highly-significant differences ($p \leq 0.01$) among the brassica genotypes for erucic acid (Table 1). Data regarding erucic acid, maximum (56.2%) was observed for DH-4 minimum value for CA-2 (29.2%) (Table 2).

For erucic acid analysis of variance shows significant differences similar to the results of Ahmad *et al*, (2013) and Khan *et al*, (2008) and Turi *et al*, (2010). Our results are in line with the earlier work of Patel and Vyas (2011).

Broad sense heritability for erucic acid was high (0.98) (Table 3). The genetic variance for erucic acid was observed (178.82) and environmental variance was (2.73). Similar heritability and genetic variance was also reported by Bashir *et al*, (2013).

Conclusions

Brassica napus L. commonly used as oilseed rape, canola or rapeseed is widely used as main vegetable oil source and 2nd most important crop that can be used as a source of protein. Edible oil is an essential component of regular diet. Edible oil can be obtained from brassica seeds. Breeding programs have involved innovative methods to support the release of new cultivars. Success of any crop improvement depends upon the presence of substantial quantity of genetic variability, heritability as well as genetic gain in selection. In breeding programs oilseed breeders mostly focus on improvement of qualitative and quantitative traits such as yield, oil, protein content, erucic acid and reduce level of glucosinolate. The application of genetic variation can also be manipulated either for selecting superior genotypes or to be utilized as parents for the development of future cultivars through hybridization.

Highly-significant differences were recorded for main raceme length and erucic acid while significant for days to 50% flowering, primary branches, plant height, pod main raceme, pod length, 1000 seed weight, glucosinolate content, and non-significant for oil content.

Broad sense heritability estimates were high and ranged from 0.65 to 0.98%. Genotype CA-2 showed maximum 1000 seed weight and minimum erucic acid contents whereas CA-4 had maximum days to 50% flowering and minimum oil content, CA-5 showed maximum primary branches, plant height, pod main raceme, main raceme length, oil content, 1000 seed weight, glucosinolate content. DH-2 showed minimum plant height, pod main raceme and glucosinolate. DH-3 minimum pod length, DH-4 showed maximum erucic acid, DH-5 and DH-6 showed average performance in all traits, DH-7 showed minimum days to 50% flowering and maximum pod length and DH-8 showed maximum performance in pod length.

From the present study, Genotypes CA-5 and DH-7 was found superior therefore could be used in future breeding program. The overall study showed that the genotypes are highly heritable.

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