

## GENETIC VARIABILITY AND HERITABILITY STUDIES IN INDIGENOUS BRASSICA RAPA ACCESSIONS

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### Abstract

Indigenous lines serves as an ideal germplasm for varietal development because of having broad genetic base. Current study was planned with an aim to check locally collected *Brassica rapa* (*B. campestris*, L.) accessions for genetic variability, heritability and genetic advance. The experiment was conducted at new development farm of The University of Agriculture, Peshawar during the main crop growing season of 2010-11. The experimental material consisted of ten locally collected *B. rapa* lines which were tested in randomized complete block design with three replications. Observations on eight quantitative parameters viz. primary branches, silique main raceme<sup>-1</sup>, main raceme length, silique length, silique width, plant height, seed silique<sup>-1</sup>, and 100 seed weight were made. Highly significant differences were observed in all traits except silique width, which showed significant variation. The highest heritability coupled with higher genetic advance was noticed in plant height which provided the evidence that this trait was under the control of additive genetic effects, while rest of the traits exhibited variable trends. Hence, it was observed that indigenous accessions have great proportion of genetic variability, which can be manipulated in future breeding programs to fully utilize their genetic potential.

### Introduction

Plant breeders always use their efforts in the development of new varieties. For this, knowledge of genetic variability and heritability present in available germplasm is a must. Locally collected accession and land races serves as a good source for initiating breeding program, because they have more variability present among them. This variability can be manipulated in breeding programs for the development of high yielding and promising varieties. Certain morphological parameters serve as tool for the estimation of genetic variability (Ali *et al.*, 2013) and heritability (Azam *et al.*, 2013). It is a common observation, that these parameters are influenced by the environment because of the polygenic inheritance of genes involved in their expression (Gaines *et al.*, 1996; Novoselovic *et al.*, 2004). The relative influence of effect of genes and environment can be measured by heritability, which indicates the extent to which a character would be transmitted to the succeeding generations. Hence behavior of the next generations may be predicted and process of selection may be authenticated (Khan *et al.*, 2003). Genetic progress expresses the direct relationship between heritability and response to selection. The expected response to selection is also known as genetic advance (GA). Heritability estimates therefore are used for calculation of GA, which measures extent of increase in any character under particular selection pressure. Thus, GA being a vital selection parameter helps breeder in selection of genotypes (Shukla *et al.*, 2004). High genetic advance along with high heritability estimates for a certain character is considered to be the most effective condition in selection programs. It has been stressed that heritability along with genetic advance should be considered in breeding programs. Present study was therefore conducted to estimate genetic variability, heritability and genetic advance in ten

indigenous accessions of *B. rapa*. It is normally believed that if a character is controlled by non-additive gene action, it may give high estimates for heritability but low genetic advance but if both heritability and genetic advance are high, then the character is considered to be under control of additive gene action.

### Materials and Methods

The present study was conducted in new development farm at The University of Agriculture, Peshawar, during main cropping season of 2010-11. The experimental material comprised of ten indigenous accessions of rapeseed (*Brassica rapa* L.) collected from different areas of Khyber Pakhtunkhwa and Punjab province having codes 118, 1800, 1900, 2300, 2706, 2712, 2713, 2723, 2724, 2729 (Table 2). These were sown in randomized complete block design with three replication having row spacing of 60 cm and plant to plant distance of 20 cm. Three rows of each accession were sown in each replication. Ten plants were selected at random from each replication and data on primary branches; silique main raceme<sup>-1</sup>, main raceme length, silique length and width, plant height and 100 seed weight were recorded at proper stage. Means were separated using Least Significant Difference test. The data recorded for these characters were subjected to analysis of variance (Steel & Torrie, 1980). Broad-sense heritability ( $h^2$ ) was calculated as the ratio of the genotypic variance to the phenotypic variance (Singh & Ceccarelli, 1996). Genetic advance was calculated following Allard (1960) using 10 % selection intensity.

### Results and Discussion

**Primary branches:** Primary branches refer to silique bearing branches and indirectly affects grain yield. More

and healthy branches are expected to bear more siliques. Highly significant results ( $p < 0.01$ ) were recorded for this trait (Table 1). The most primary branches (10) were recorded for the accessions 1900 and 2729, whereas the least number of primary branches (4) was recorded for the accessions 2706 and 2723 (Table 2). High heritability (0.76) coupled with genetic advance of 2.71 were exhibited by the studied genotypes for primary branches (Table 3). Ghosh & Gulati (2001) reported significant variation for primary branches in Indian mustard. The results of Samad & Khaleque (2000) and Dar *et al.*, (2010) also supported our findings who found high heritability in *B. campestris* L.

**Silique main raceme<sup>-1</sup>:** Productive siliques are considered to accommodate more seeds. Analysis of variance for this trait gave highly significant differences ( $p < 0.01$ ) among all the genotypes (Table 1). The genotype 2724 had maximum number of siliques (62), while the lowest number of silique (25) on main raceme was possessed by the genotype 2723 (Table 2). High heritability (0.87) coupled with high genetic advance (18.33) were recorded for this trait depicting the control of additive gene action for this trait (Table 3). Similar results were reported by Ghosh & Gulati (2001) in Indian mustard. Khan *et al.*, (2008) reported high heritability in  $F_{3:4}$  brassica populations for this trait.

**Table 1. Mean squares for certain morphological traits for 10 *B. rapa* accessions.**

Source of variation	df	Primary branches	Silique main raceme	Main raceme length (cm)	Silique length (cm)	Silique width (cm)	Plant height (cm)	Seeds silique <sup>-1</sup>	100 seed weight (g)
Replications	2	0.933	16.53	53.55	0.149	0.003	102.9	6.03	0.003
Genotypes	9	10.43**	397.51**	379.44**	1.85**	0.007*	2899.63**	20.55**	0.007**
Error	18	1.00	19.57	23.3	0.154	0.002	42.64	4.88	0.001
CV (%)	--	14.48	10.54	8.48	8.37	11.46	4.21	14.14	11.20

\* = Significant at 5% level of probability, \*\* = Significant at 1% level of probability

D.F. = Degrees of freedom, C.V. = Coefficient of variation

**Table 2. Collection sites and means for morphological traits for 10 *B. rapa* accession.**

Genotype	Site of collection	Primary branches	Silique main raceme <sup>-1</sup>	Main raceme length (cm)	Silique length (cm)	Silique width (cm)	Plant height (cm)	Seed silique <sup>-1</sup>	100 seed weight (g)
118	Rawalpindi	7	48	55.7	5.3	0.43	177.7	18	0.29
1800	Rustam (Mardan)	7	45	47.4	5.1	0.47	172.7	12	0.37
1900	Buner	10	31	46.9	4.5	0.47	152.3	12	0.25
2300	Hungu	6	55	56.1	5.9	0.47	151.7	16	0.33
2706	Fatah Jhang	4	42	64.1	4.9	0.40	163.3	15	0.32
2712	Lakki Marwat	7	32	63.6	6.3	0.37	162.3	16	0.32
2713	Shangla (Swat)	7	43	65.4	4.8	0.43	124.0	12	0.35
2723	Abbotabad	4	25	41.0	4.4	0.50	76.3	17	0.37
2724	Haripur	6	62	77.5	4.0	0.47	183.3	18	0.32
2729	Karak	10	43	59.6	4.8	0.43	166.0	19	0.31
<b>LSD (0.05)</b>		<b>1.72</b>	<b>7.58</b>	<b>8.28</b>	<b>0.67</b>	<b>0.08</b>	<b>11.20</b>	<b>3.79</b>	<b>0.06</b>

**Table 3. Estimation of heritability and genetic advance for morphological traits of 10 *B. rapa* accessions.**

Attribute	Primary branches	Silique main raceme <sup>-1</sup>	Main raceme length (cm)	Silique length (cm)	Silique width (cm)	Plant height (cm)	Seed silique <sup>-1</sup>	100 seed weight (g)
Vg	3.14	125.98	118.71	0.57	0.002	952.33	5.22	0.002
Vp	4.14	145.55	142.01	0.72	0.004	994.97	10.10	0.003
h <sup>2</sup>	0.76	0.87	0.84	0.79	0.45	0.96	0.52	0.67
G.A	2.71	18.33	17.48	1.17	0.05	52.99	2.88	0.06

Vg = Genotypic variance; Vp = Phenotypic variance

h<sup>2</sup> = Heritability; G.A. = Genetic advance

**Main raceme length:** Lengthier raceme is expected to have more number of silique. Data for main raceme length evinced highly significant differences ( $p < 0.01$ ) (Table 1). The genotype 2724 had lengthiest racemes (77.5 cm), while raceme of genotype 2723 was shortest of all (41 cm) (Table 2). Heritability (0.84) as well as genetic advance was high

for the said trait (17.48) (Table 3). Zada *et al.*, (2013) also reported presence of significant variation for this trait in Ethiopian mustard. The findings of Sadat *et al.*, (2010), Sheikh & Singh (1998), Choudhary *et al.*, (1999) supported our findings, while Zhang & Zhou (2006) reported moderate heritability for this trait.

**Siliqua length:** All genotypes presented highly significant results ( $p < 0.01$ ) for siliqua length (Table 1). Length of siliqua ranged from 4- 6cm. Length of siliqua was maximum in the genotype 2712, while siliques of genotype 2724 were less in length (Table 2). The trait was observed to be highly heritable (0.79) but genetic advance for siliqua length was low (1.17) (Table 3). The results are supported by the findings of Khan *et al.*, (2008) who reported high heritability for this trait in  $F_{3,4}$  brassica populations. The findings of Sheikh & Singh (1998) in *B. juncea* L., and Nasim *et al.*, (2013) in *B. napus* L., were also in agreement of our results.

**Siliqua width:** Significant differences ( $p < 0.05$ ) were observed among the genotypes for siliqua width (Table 1). Minimum siliqua width (0.37 cm) was recorded in the genotype 2712, whereas the siliques of genotype 2723 were the widest (0.50 cm) (Table 2). Low heritability (0.45) along with lowest genetic advance (0.05) confirmed the high impact of environment over the expression of this trait (Table 3). Hence it may be concluded that selection should be delayed to later generation.

**Plant height:** Analysis of variance revealed highly significant differences for this trait ( $p < 0.01$ ) (Table 1). The data for plant height fell in the range of 76.3-183.3 cm. The genotype 2724 had tallest plant while relatively short plants were observed in the genotype 2723 (Table 2). Of all the studied traits, plant height was exhibiting highest heritability value (0.96) coupled with highest genetic advance (52.99), hence it was confirmed that additive gene action was governing this trait in studied accessions (Table 3). Mahmood *et al.*, (2003) also reported the same results. The results are in conformity with that of Samad & Khaleque (2000) who recorded highly significant differences for plant height in *B. campestris* L. The results are also in line with findings of Emrani *et al.*, (2012) who reported highest estimates of heritability for plant height in  $M_3$  generation of canola. However the findings reported by Khan *et al.*, (2008) were in contrast to our results as they observed non-significant results for plant height. Our results are in agreement with Dar *et al.*, (2010) who reported high heritability and genetic advance as percent of mean in brown sarson (*B. rapa* L.).

**Seed siliqua<sup>-1</sup>:** Perusal of seed siliqua data elucidated highly considerable variations ( $p < 0.01$ ) (Table 1). More and healthy seeds enhance grain yield of crop. In the present study, highest number of seeds (19) was present in the accession 2729, while the minimum seeds (12) were possessed by three accession having codes 1800, 1900 and 2713 respectively (Table 2). This trait showed medium heritability (0.58) with genetic advance of 2.88 (Table 3). Samad & Khaleque (2000) also found highly significant differences in *B. campestris* L. However the findings of Bilgili *et al.*, (2002) were not in line with our results who reported non significant results for number of seeds per siliqua in *B. rapa* L. Choudhary *et al.*, (1999) found high heritability while Sadat *et al.*, (2010) reported low heritability and genetic advance in different brassica species.

**100 seed weight:** Scrutiny of data regarding maturity exhibited considerable variations ( $p < 0.01$ ) among *brassica Rapa* accessions (Table 2). Data recoded on accession for seed weight fell in the range of 0.25-0.37g. Accessions 2723 and 1900 defined the extremes of range (Table 2). Relatively high heritability (0.67) with low genetic advance (0.06) proved this trait to be under control of non additive gene effect for these accessions (Table 3). Results for this trait are in agreement with Akbar *et al.*, (2007), Aytaç & Kinacı (2009), Sadat *et al.*, (2010), Nasim *et al.*, (2013) who also reported highly significant differences and high heritability for this trait in mustard and rapeseed. Akbar *et al.*, (2003) reported same results in summer mustard. High heritability for seed weight was also reported in mustard by Akbar *et al.*, (2007), in winter rapeseed by Ali *et al.*, 2003; Aytaç & Kinaci, 2009, in brown sarson (Dar *et al.*, 2010) and in *B. napus* L. (Zhang & Zhou, 2006) for 1000-seed weight are same.

It is obvious that high proportion of genetic variability was found in the studied genotype reflecting great scope for selection.

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