



REGULAR ARTICLE

EVALUATION OF *BRASSICA JUNCEA* GERMPLASM THROUGH HERITABILITY ESTIMATION AND CORRELATION ANALYSIS

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ABSTRACT

The experiment was conducted to estimate genetic parameters of heritability and correlation for yield traits of indigenous *Brassica juncea* genotypes. RCB design with three replications was used to sow 20 Brassica genotypes. Highly significant genetic variations were obtained among studied parameters. Days to half flowering revealed positive associations with primary branches per plant ($r = 0.337^{**}$). Primary branches per plant was positively correlated with pod length ($r = 0.407^{**}$), seed per pod ($r = 0.418^{**}$) seed yield per plant ($r = 0.479^{**}$). Similarly, pod length showed positive correlation with seed per pod ($r = 0.324^{**}$) and seed yield per plant ($r = 0.331^{**}$), while seed per pod was positively correlated with seed yield per plant ($r = 0.878^{**}$). Highest broad-sense heritability was recorded for seed yield per plant (0.97), while lowest heritability was estimated for primary branches per plant (0.46).

Keywords: *Brassica*, Heritability, Correlation

INTRODUCTION

Edible oil is on the top in the imported bill of Pakistan mainly due to low local production. Brassica oilseed is the third edible oil source after Palm and Soybean world widely [1]. This high dependency on imported oil can be reasonably decreased by the development of oilseed genotypes having better adaptability into the cropping system of Pakistan [2]. Seed yield can be improved by improving parameters having high genetic divergence, heritability and selection response [3]. To run an effective breeding program, high heritability along with high selection response is desirable because a good understanding of selection response is helpful in the selection process [4]. It must be noted that high heritability with high selection response is an indication of additive genetic operation, while parameters with high heritability but low selection response is due to operations other than additive genes [5].

Evaluation of the variability among the genetic resources of the material is the top priority for the improvement because it generates necessary information which can speed up the breeding program [6, 7]. The necessary tools for the genetic improvement of crop plants in a breeding program are divergence among the material and parameters having high heritability with high selection response [8]. Selection response is a very useful tool which shows the extent of increment of a parameter under study and can be easily calculated with the help of heritability

estimates. It helps the breeder to proceed in a right way [9]. Correlation analysis is very helpful in understanding relationship between different sets of parameters [10].

MATERIALS AND METHODS

The planned study was conducted at the University of Agriculture, Peshawar during 2011-12 to estimate genetic parameters of heritability and correlation analysis among 20 Brassica genotypes. The research material was planted in RCB design with three replicates. Data were recorded on six agro-morphological and maturity parameters. Fifteen plants were selected for data recording in a single replication.

Statistical analysis

LSD test was used for means separation. Steel and Torrie [11] approach was used for the computation of analysis of variance. Broad-sense heritability estimates were recorded as a ratio of genotypic variance to the total phenotypic variance [12]. Selection response was calculated using Fehr [13] approach having selection intensity of 20%.

RESULTS AND DISCUSSION

Results and discussion describing heritability estimation and correlation analysis among 20 *Brassica juncea* genotypes are given below.

Days to half flowering

Days to half flowering showed significant ($P \leq 0.01$)

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differences among 20 genotypes (table 1). Our results are strongly supported by the previous findings [10, 14, 15]. Days to half flowering ranged from 58.00 to 89.00 d. Maximum days to half flowering (89.00 d) were observed in genotype J.600, whereas minimum days (58.00 d) were found in genotype J.617 (table 2). Genetic variance (40.02) was greater than environmental variance (37.53) for days to half flowering. Moderate broad-sense heritability (0.52) and high selection response (6.54) were recorded for the said trait (table 3). Our current findings are in contradiction with Mahto and Haider [16], who reported high broad-sense heritability which discourages our results but their findings agree with our results of obtaining moderate to high selection response for days to flowering. Highly significant and positive correlation were recorded between days to half flowering and primary branches per plant ($r = 0.337^{**}$) (table 4). Positive but non-significant associations between days to half flowering and primary branches per plant were noted by Nasim *et al.* [17] and strengthen our findings.

Primary branches plant⁻¹

For primary branches plant⁻¹, highly significant ($P \leq 0.01$) differences were computed from analysis of variance (table 1). Previous studies reported significant variation for the said trait and encourage our findings [18, 19, 20]. Primary branches plant⁻¹ ranged from 8.3 to 15.7. Maximum primary branch plant⁻¹ (15.7) was observed in genotype J.600, while genotype J.617 exhibited minimum number of primary branches (8.3) (table 2). Genetic variance (2.97) was lower in magnitude than environmental variance (3.53). Moderate broad-sense heritability (0.46) and low selection response (1.68) were recorded for the said trait (table 3). Our results are contradicted by the findings of Iqbal *et al.* [21] who observed high broad-sense heritability but are in agreement by reporting low selection response value. Low heritability estimates were obtained by Zhang and Zhou [1], for the said parameter. Primary branches plant⁻¹ showed significant and positive associations with pod length ($r = 0.407^{**}$), seed pod⁻¹ ($r = 0.418^{**}$) and seed yield ($r = 0.479^{**}$) (table 4). Positive and significant associations among primary branches plant⁻¹ with pod length, seed pod⁻¹ and seed yield were reported by Ali *et al.* [2] which confirmed our finding.

Main raceme length

Analysis of variance indicated significant ($P \leq 0.01$) differences for the said parameter (table 1). Zada *et al.* [7] observed significant differences in Ethiopian mustard. Our findings are also in similarity with the previous results [22, 14]. Main raceme length ranged from 40.1 to 77.8 cm. Maximum main raceme length (77.8 cm) was observed in genotype J.616, whereas minimum raceme length (40.1 cm) was found in genotype J.600 (table 2). Genetic variance (73.26) was greater in amount than environmental variance (53.86) for main raceme length. Moderate broad-sense heritability (0.58) and high selection response (9.36) were recorded for studied trait (table 3). Muhammad *et al.* [23] recorded moderate broad-sense heritability and extend our findings, while Nasim *et al.* [17] manifested low heritability estimates for the said parameter in *Brassica napus*. Main raceme length was negatively correlated with all the studied parameters. Our current results are discouraged by Choudhary *et al.* [24] who

reported positive associations for seed yield plant⁻¹ with the said parameter (table 4).

Seed pod⁻¹

There was significant ($P \leq 0.01$) variations for seed pod⁻¹ (table 1). Samad and Khaleque, [25] reported highly significant variation in *B. campestris* for the said parameter. However Bilgili *et al.* [26] observed non-significant differences for seed pod⁻¹ and discourage our findings. Seed pod⁻¹ ranged from 8 to 19. Maximum seed pod⁻¹ (19) was observed in genotype J.606, whereas minimum seed value (8) was found in genotype J.603. Genetic variance (10.28) was higher in magnitude than environmental variance (1.36) (table 2). High broad-sense heritability (0.88) and moderate selection response (4.34) were recorded for seed pod⁻¹ in current study, which suggested that the inheritance and improvement is under genetic control (table 3). High heritability with moderate selection response was resulted by Chaghakaboodi *et al.* [27] and confirm our result for the said trait.

Seed pod⁻¹ showed highly significant positive correlation with primary branches plant⁻¹ ($r = 0.418^{**}$), pod length ($r = 0.324^*$) and seed yield ($r = 0.878^{**}$) (table 4). Similar results of positive and significant correlations between seed pod⁻¹ with seed yield were supported by Akbar *et al.*, [28].

Pod length

Significant ($P \leq 0.01$) differences were exhibited for Pod length (table 1). Previous reports also showed significant values for pod length and encourage our results [10, 20, 22]. Pod length ranged from 1.9 to 4.3 cm. Genotype J.612 showed maximum pod length (4.3 cm), while minimum length (1.9 cm) was recorded in genotype J.616 (table 2). Genetic variance (0.34) was good enough in magnitude than environmental variance (0.11) for the said trait. Broad-sense heritability (0.76) was higher in amount however, low selection response (0.73) were recorded for pod length (table 3). Similar findings were obtained by previous studies [29, 30, 17].

Pod length showed significant and positive associations with primary branches per plant ($r = 0.407^{**}$), seed per pod ($r = 0.324^*$) and seed yield ($r = 0.331^{**}$) (table 4). Positive and significant associations between pod length with primary branches plant⁻¹ were reported by Ali *et al.* [2] which confirmed our finding.

Seed yield plant⁻¹

Seed yield plant⁻¹ indicated significant ($P \leq 0.01$) differences (table 1). These results are in agreement with earlier reports [22, 19]. Seed yield ranged from 6.17 to 33.83 g. Maximum seed yield (33.83 g) was observed in genotype J.606, whereas lowest seed yield (6.17 g) were found in genotype J.609 and J.618 (table 2). Genetic variance (51.62) was much greater than environmental variance (1.33). Highest broad-sense heritability (0.97) and selection response (10.22) were recorded for seed yield (table 3). Khan and Khan, [14] reported high heritability for the said trait and strengthen our results. Seed yield showed highly significant positive associations with primary branches plant⁻¹ ($r = 0.479^{**}$), pod length ($r = 0.331^{**}$) and seed pod⁻¹ ($r = 0.878^{**}$) (table 4). Positive and significant associations between seed yield and primary branches plant⁻¹ were observed by Akbar *et al.* [4] which supported our results.

Table 1: Mean squares for yield and maturity traits of 20 Brassica juncea germplasm

Traits	Replication	Genotype	Error	CV %
Days to half flowering	24.217	157.596**	37.532	8.390
Primary branches plant ⁻¹	1.017	12.431**	3.525	17.690
Main raceme length	23.195	273.625**	53.855	12.590
Pod length	0.101	1.138**	0.110	10.530
Seed pod ⁻¹	0.200	32.211**	1.358	9.710
Seed yield plant ⁻¹	8.020	156.178**	1.328	9.300

Table 2: Ranges with best genotype for yield and maturity traits of 20 Brassica juncea germplasm

Traits	Range	Best genotype
Days to half flowering (no)	58-89	J.617
Primary branches plant ⁻¹ (no)	8-16	J.600
Main Receme Length (cm)	40.10-77.80	J.616
Pod Length (cm)	1.90-4.30	J.612
Seed Pod ⁻¹ (no)	8-19	J.606
Seed Yield plant ⁻¹ (g)	6.17-33.83	J.606

Table 3: Environmental variances, genotypic variances, phenotypic variances, heritability and selection response for yield and maturity traits of 20 Brassica juncea germplasm

Trait	V _e	V _g	h ²	R _e
Days to half flowering (no)	37.53	40.02	0.52	6.54
Primary branches plant ⁻¹ (no)	3.53	2.97	0.46	1.68
Main Receme Length (cm)	53.86	73.26	0.58	9.36
Pod Length (cm)	0.11	0.34	0.76	0.73
Seed Pod ⁻¹ (no)	1.36	10.28	0.88	4.34
Seed Yield plant ⁻¹ (g)	1.33	51.62	0.97	10.22

Table 4: Correlation analysis for yield and maturity traits of 20 Brassica juncea germplasm

Traits	Primary branches plant ⁻¹	Main raceme length	Pod length	Seed pod ⁻¹	Seed yield ⁻¹
Days to half flowering	0.337**	-0.066	0.199	0.211	0.127
Primary branches plant ⁻¹		-0.124	0.407**	0.418**	0.479**
Main raceme length			-0.22	-0.152	-0.111
Pod length				0.324*	0.331**
Seed pod ⁻¹					0.878**

CONCLUSION

It is clear from the results that high genetic variability in the studied genotypes is great scope for selection. Traits like seed pod⁻¹ and seed yield plant⁻¹ has high heritability and selection can be based on these traits. Based on genetic parameters and mean performance, genotypes J.600, J.606 and J.616 were superior and hence can be recommended in breeding programs.

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