

GENETIC VARIABILITY AND HERITABILITY STUDIES IN RELATION TO SEED YIELD AND IT'S COMPONENTS TRAITS IN MUSTARD (*BRASSICA JUNCEA L.*)

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ABSTRACT: *In crop improvement and varietal improvement programme, diversity is the pre-requisite to obtain the desirable recombinants in separating generations. The purpose of Fresh study was to check Brassica juncea L. sequences for genetic variability, heritability and genetic advance (G.A). The experiment was implemented at Oilseeds Research Institute of Faisalabad during zaid kharif season of 2013-14. In this experiment ten Brassica juncea genotypes which were used randomized with (RCBD) complete block design with triplicate. In this research there are eight quantitative parameters were observed viz. Days to 50% flowering, Days to 70% maturity, Plant height, Number of primary branches, Silique length, Number of seeds silique⁻¹, 1000 seed weight and Seed yield were noted. Extremely substantial changes ($p < 0.05$) remained taken in all characters which demonstrated substantial difference. The high heritability in aggregation with high genetic development was noted in plant height, silique length and seed yield which gave the indication that these traits were under the control of additive gene which will be more useful in expecting the gain under collection than heritability alone, while days taken to flowering, days taken to maturity, number of branches per plant, number of seeds per silique and 1000 seed weight revealed capricious trends. Hence, it was observed that adequate scope of genetic variability is present for selection of superior genotypes, which can be exploited in future breeding programs.*

Key words: *Brassica juncea L., genetic advance, gene action, heritability.*

INTRODUCTION

Brassica juncea L. is a very important oilseed crop. The demand of oilseed crops increasing rapidly, so it is necessary to increase the yield of the crops. Yield is a complex trait, polygenic in inheritance, more prone to environmental fluctuations [1,2]. The relative impact of genes and environment can be restrained by heritability, which shows a good index of transmission from parents to their offsprings [3,4]. It displays an important role in predicting the behavior of the next generations and selection process in plant breeding may be valid [5]. Genetic advance is measure of genetic gain under selection which shows the strong association between heritability and response to selection [6]. Understanding of heritability and genetic advance is a pre-requisite for making effective selection [7-13]. In research programs high genetic advance and heritability are very important tools for selection. [14] Communicated that maximum heritability along with maximum genetic advance was shown additive gene action [13,15,16] and high heritability associated with low genetic advance was indication of dominance and epistatic effects

MATERIAL AND METHODS

The recent studies were performed at the research area of Oilseeds Research institute, AARI, Faisalabad during zaid-kharif season during 2013-14. The Experiment was laid out in a randomized complete block design (RCBD) with triplicate. Ten genotypes of *Brassica juncea* were used. The plot size of 6 × 1.8 m was used, plant to plant and row to row distance was 15 cm and 45 cm respectively. Four rows of every genotype were seeded in respectively replication. Ten plants were chosen at haphazardly from each replication.

Observations on eight quantitative parameters viz. Days taken to 50% flowering, Days taken to 70% maturity, Plant height, Number of primary branches, Silique length, Number of seeds per silique, 1000 seed weight and Seed yield were noted. Recommended cultural practices like weeding and hoeing were performed during the growing season when required. The differences among the cultivars for the above mentioned parameters were tested for significance using ANOVA technique with the help of Statistix 8.1 program. LSD test was used to test the differences among mean values. [17].

Heritability Estimates

Broad-sense heritability (h^2) was estimated by the ratio of the genotypic variance to the phenotypic variance. The heritability gives information on transmission of traits from parents to offsprings hence aiding in selection.

$$h^2 = \sigma_g^2 / \sigma_p^2$$

Where, h^2 is broad sense heritability, σ_g^2 is genotypic variance and σ_p^2 is phenotypic variance

Genetic Advance

Evaluation of heritability can also be used to predict genetic advance below assortment, so that the plant breeder can be hopeful of progress from various types and intensities of selection. Predictable genetic advance under selection (G.A) was computed according to the formula given by [18].

$$GA = (\sigma_g^2 / \sigma_p) \times K$$

Where,

σ_g^2 is genotypic variance

σ_p is phenotypic standard deviation of the original population

K is selection differential at a particular level of selection intensity

Genetic Advance as Percentage of Mean

GAM expressed in percentage was computed by the formula given by [19].

$$GAM = (G.A/\text{mean}) \times 100$$

Where,

G.A= Genetic advance

RESULT AND DISCUSSION

Improvement in genetic architecture of crop plants is essential to improve the agricultural foodstuffs in order to meet the basic requirement of quickly increasing population. So, a successful breeding programme and to achieve its desirable objective the selection of appropriate parents is one of the crucial aspects. The information on the nature of genetic control of yields and its components helps the breeder in selecting suitable parents and determining the appropriate selection strategies in successive breeding generations. A close observation of Table 1 shows that genotypes were highly significant ($p \leq 0.01$) for all the traits i.e. DOF, DM, PH, BR/Plant, SL, Seed/Sil, 1000SW and Y. This shows the existence of significant variability among the genotypes under this study. This suggested that satisfactory range is open for assortment of best genotypes expected at increasing heritable yield prospective of *Brassica juncea* L. Inherited characters (Table 2) were studied to scrutinize the genetics of yield related traits, centered on genetic variability estimates viz., mean, heritability (h^2), genetic advance (GA) and (GAM). The coefficient of variation does not offer the full scope of heritable variation. With the help of more accuracy it can be measure when heritability and genetics advance were studying together. Hence, h^2 and G.A are key parameters to study the range of development in numerous characters through selection. High heritability and genetic advance are more useful in expecting the increase in assortment than heritability estimations alone.

Days taken to flowering:

For this character Table 1 shows maximum variation ($p < 0.05$). Similar findings have been reported by [20]. Mean values of the data showed a range of 52 (Toria) to 65 (ZBJ-09007) with an average of 59.63 days (Table 2). Genetic variance was 34.42. Heritability (0.97) coupled with genetic advance of 19.96 were exhibited by the tested genotypes (Table 3). Maximum heritability with great genetic advance exposes that this trait is governed by additive genetic effects.

Days taken to maturity:

For this character Table 1 showed maximum differences ($p < 0.05$). Mean values of the data showed a range of 132 (Toria) to 153 (ZBJ-11030) with an average of 149.53 days (Table 2). Genetic variance was 128.68. The character showed high heritability (0.99) but genetic advance was moderate (15.59) (Table 3).

No. of primary branches per plant:

The no. of primary branches per plant is the mutual effect of the $G \times E$ interaction and indirectly affects grain yield. In Table 1 significant differences ($p < 0.05$) were observed for this character [16]. Mean values showed a range of 7.07 (ZBJ-06012) to 9.67 (ZBJ-09007) for primary branches per plant with an average of 8.673 (Table 2). Genetic variance was 1.68. Heritability (0.46) coupled with genetic advance of 20.91 were exhibited by the tested genotypes (Table 3). Low heritability accompanied with high genetic advance reveals that this trait is governed by additive genetic effects. The low heritability is being revealed due to high environmental effects [21]. Selection may be effective for this character. Our results are in contrast with the findings of [22,23].

Plant height:

The plant height exposed the growth demonstration of a crop. Ecofriendly dynamics similarly play an energetic character in determining the height of the plant. Table 1 shown maximum variation for this trait ($p < 0.01$). However [20] reported non-significant results for plant height. Mean values displayed a range of 160.3 (Toria) to 214.2 cm (ZBJ-09007) for primary branches plant⁻¹ with an average of 8.673 (Table 2). Plant height displayed indication of high heritability value (0.70) composed with high genetic advance (22.67) was a sign of additive gene action (Table 3). The similar effects are described by [12,24,25,26-27]. Our results are opposed by the result of [28] who perceived effect of atmosphere on the presence of genes regulatory plant height.

1000 seed weight:

Seed heaviness is an imperious yield factor as it shows a crucial part in defining the yield prospective of a genotype. The analysis of variance for 100 seed weight exposed extremely significant variances (Table 1). Data recorded for seed weight was in the range of 3.16 - 3.57 g. Genotypes ZBJ-11002 and ZBJ- 08051 exhibited supreme collection (Table 2). High heritability (0.53) laterally with minimum genetic development (8.19) delivered evidence that this quality is under control of non-additive gene action (Table 3). Hence the selection should be delayed to later generation. Results for this trait are in conformity with [13,14,29,30-31]

Seed yield:

Seed yield is the ultimate goal of plant breeder. Table: 1 shows the data of seed yield elucidated extremely considerable variations ($p < 0.01$). In the present study, maximum yield of seed (3344 kg/ha) was shown by ZBJ-10021, while the minimum yield of seed (1607 kg/ha) was possessed by ZBJ-08051 (Table 2). This character revealed high heritability (0.76) with highest genetic advance of 64.76 (Table 3) indicating additive gene actions.

Table 1: Mean square values for different morphological, yield and yield related traits of 10 *B. juncea* L. genotypes

	DF	DOF	DM	PH	BR/Pl	SL	Seed/Sil	1000 SW	Y	DOF
R	2	0.43	0.533	653.77	1.31	0.75	29.97	0.01	1018228	0.43
G	9	34.77*	128.90*	828.01*	2.32*	0.69*	2.90**	0.04*	981730**	34.77*
E	18	1.06	0.68	311.14	1.94	0.13	0.79	0.03	287194	1.06
CV		1.73	0.55	8.62	16.09	8.09	5.66	5.14	20.59	1.73

* = Significant at 0.05 probability level ** = Significant at 0.01 probability level

DF = Degrees of freedom, CV = Coefficient of variation, DOF = Days taken to flowering, DM= Days taken to maturity, PH = Plant Height, BR/Plant= Number of Branches per Plant, SL= Silique length, Seed/Sil = No of seeds / silique, 1000SW = 1000 Seed Weight, Y= Yield.

Table 2: Means values for different morphological traits of 10 *B. juncea* L. genotypes.

Genotype	DOF	DM	PH (cm)	BR/Pl	SL (cm)	Seed/Sil	1000 SW (g)	Y (kg ha ⁻¹)
ZBJ-10020	61	150	213	8.8	4.39	15.49	3.3	2972
ZBJ-10021	58	148	213	7.9	4.47	16.38	3.4	3344
ZBJ-08047	60	149	209	8.3	4.1	15.76	3.5	2773
ZBJ-09007	65	152	214	9.6	4.93	16.13	3.5	2934
ZBJ-11030	62	153	208	9.2	4.57	15.97	3.5	2935
ZBJ-11002	59	154	205	7.8	4.69	14.89	3.1	2502
ZBJ-06012	58	155	198	7	4.04	14.97	3.5	2065
RAYA ANMOL	61	151	218	9.6	4.66	15.61	3.4	3025
TORIA	52	132	160	8.6	5.68	18.12	3.5	1868
ZBJ-08051	59	149	203	9.6	4.18	14.69	3.5	1607

DOF = Days taken to flowering, DM= Days taken to maturity, PH = Plant Height, BR/Plant= Number of Branches per Plant, SL= Silique length, Seed/Sil = No of seeds / silique, 1000SW = 1000 Seed Weight, Y= Yield

Table 3: Estimation of Heritability and Genetic Advance for Morphological Traits in 10 genotypes of *B. Juncea* L

Traits	V _g	h ²	GA (as % of mean)
Days to flowering	34.42	1	19.96
Days to maturity	128.68	1	15.59
Plant height	724.3	0.7	22.67
No. of Branches	1.68	0.5	20.91
Silique length	0.65	0.8	32.87
No. of seeds /silique	2.64	0.8	18.57
Yield	885998	0.8	64.74
1000 Seed Weight	0.04	0.5	8.19

V_g = Genotypic variance, h² = Heritability; G.A. = Genetic advance

Seed yield:

Seed yield is the ultimate goal of plant breeder. Table: 1 shows the data of seed yield elucidated extremely considerable variations ($p < 0.01$). In the present study, maximum yield of seed (3344 kg/ha) was shown by ZBJ-10021, while the minimum yield of seed (1607 kg/ha) was possessed by ZBJ-08051 (Table 2). This character revealed high heritability (0.76) with highest genetic advance of 64.76 (Table 3) indicating additive gene actions.

CONCLUSION:

It is conclusion that high percentage of genomic multiplicity was establish in the considered genotypes reproducing prodigious scope for assortment nature and designing the selection methodology. High heritability was found for silique length followed by number of seeds silique⁻¹ indicating that phenotypic assortment for these characters would be operational. High heritability accompanied with

high genetic advance was found for silique length indicating additive gene action which should be given due consideration for effective selection in earlier generation for future hybridization programs of *Brassica juncea*.

REFERENCES:

- [1] Gaines C.S, P.L. Finney, G. Rubenthaler. "Milling and baking qualities of some wheats developed for eastern or northwestern regions of the United States and grown at both locations". *C. Chem*, **73**: 521-525 (1996).
- [2] Novoselovic D, M. Baric, G. Drezner, J. Gunjaca and A. Lalic. "Quantitative inheritance of some wheat plant traits". *Genet & Mol Bio.*, **27**: 92-98 (2004).
- [3] Marwede V, A. Schierholt, C. Möllers and H. C. Becker. "Genotype× environment interactions and heritability of tocopherol contents in canola". *Crop Sci.*, **44**: 728-731 (2004).

- [4] Falconer D. S and T. F. Mackay. "Introduction to quantitative genetics". Harlow, UK: Longman, (1996).
- [5] Khan R and F. A. Khan. "Evaluation of genetic potential of some Brassica germplasm collections". *Int J Agri Biol.*, **5**: 630-631 (2003).
- [6] Shukla S, A. Bhargava, A. Chatterjee and S. Singh. "Estimates of genetic parameters to determine variability for foliage yield and its different quantitative and qualitative traits in vegetable amaranth (*A. tricolor*)[India]". *J Gen & Breed (Italy)*, **58**: 169-176 (2004).
- [7] Khan A. H, M. Tariq and S. A. H. Shah. "Path-coefficient analysis of morphological traits with seed yield in Raya". *Pak J Agric Res.*, **13**: 334-337 (1992).
- [8] Sarawgi A, N. Rastogi and D. Soni. "Correlation and path analysis in rice accessions from Madhya Pradesh". *Field Crops Res.*, **52**: 161-167 (1997).
- [9] Chaudhry A, P. Barua and P. Duara. "Siliques traits for determining seed yield in Indian rapeseed". *J Agric Sci Soc North East India.*, **12**: 60-63 (1999).
- [10] Kakroo P and S. Kumar. "Genetic determination of seed yield through it's components in Indian mustard. *Ind J Genet Pl Breed.*, **51**: 82-87 (1991).
- [11] Pant S. C and P. Singh. "Genetic variability in Indian mustard". *Agric Sci Digest.*, **21**: 28-30 (2001).
- [12] Mahmood T, M. Ali, S. Iqbal and M. Anwar. "Genetic Variability and Heritability estimates in summer Mustard (*Brassica juncea*). *Asian J Pl Sci.*, **2**(1): 77-79 (2003).
- [13] Akbar M, T. Mahmood, M. Yaqub, M. Anwar and M. Ali. "Variability, correlation and path coefficient studies in summer mustard (*Brassica juncea* L.). *Asian J Pl Sci.*, **2**: 696-698 (2003).
- [14] Aytac Z. and G. Kınacı. "Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.)". *Afric J Biotech.*, **8**: 3547-3554 (2009).
- [15] Khulbe R., D. Pant and N. Saxena. "Variability, heritability and genetic advance in Indian mustard [*Brassica juncea* (L.) Czern & Coss]". *Crop Res (Hisar)*, **20**: 551-552 (2000).
- [16] Ghosk S. and S. Gulati. "Genetic variability and association of yield components in Indian mustard". *Crop Res.*, **21**: 245-249 (2001).
- [17] Steel R. G. D. and J. H. Torrie. *Principles and Procedures of Statistics.* McGraw Hill Book Co., Inc. New York, USA. (1980).
- [18] Johnson H. W., H. Robinson and R. Comstock. "Estimates of genetic and environmental variability in soybeans". *Agron J.*, **47**: 314-318 (1955).
- [19] Mehdi SS, Khan IA. *Experimental design and analysis.* In: Plant Breedin. E. Bashir and R. Bantel Editors. National book foundation, Islamabad. (1994).
- [20] Khan S., R. Farhatullah, I. Khalil, M. Khan and N. Ali. "Genetic variability, heritability and correlation for some quality traits in F_{3,4} Brassica populations". *Sarhad J Agric.*, **24**: 223-231 (2008).
- [21] Afrin S. K., M. Firoz, B. Rahid, S Muahammad and M. Rahim. "Assessment of genetic variation among advanced lines of *Brassica napus* L". *Agron Glas.*, **73**: 201-226 (2012).
- [22] Dar Z., S. Wani, G. Zaffar, M. Habib and M. Wani. "Variability studies in brown sarson (*Brassica rapa* L.)". *Res J Agric Sci.*, **1**: 273-274 (2010).
- [23] Samad A. and M. Khaleque. "Diversity estimates of yield and some of the agronomical characters in rapeseed (*Brassica campestris* L.)". *Ban J Sci & Ind Res.*, **35**: 20-26 (2000).
- [24] Basalma D. "The correlation and path analysis of yield and yield components of different winter rapeseed (*Brassica napus ssp. oleifera* L.) cultivars". *Res J Agric Biol Sci*, **4**: 120-125 (2008).
- [25] Yadava D, S. Giri, M. Vignesh, S. Vasudev, Kumar and A. Yadav. "Genetic variability and trait association studies in Indian mustard (*Brassica juncea*)". *Ind J Agric Sci.*, **81**: 712-716 (2011).
- [26] Emrani S. N., A. Arzani, G. Saeidi, M. Abtahi and M. Banifateme. "Evaluation of induced genetic variability in agronomic traits by gamma irradiation in canola (*Brassica napus* L.)". *Pak J Bot.*, **44**: 1281-1288 (2012).
- [27] Belete Y. S., B. Yohannes and T. D. Wami. "Analysis of genetic parameters for some agronomic traits of introduced Ethiopian mustard (*Brassica carinata* A. Brun) genotypes". *Int J Agric Res.*, **7**: 160-165 (2012).
- [28] Huang L., J. Cao, W. Ye, T. Liu and L. Jiang. "Transcriptional differences between the male-sterile mutant bcms and wild-type *Brassica campestris* ssp. chinensis reveal genes related to pollen development". *Pl Bio.*, **10**: 342-355 (2008).
- [29] Nasim A., S. I. Farahtullah, S. Shah and S. M. Azam. "Genetic variability and correlation studies for morpho-physiological traits in *B. napus* L". *Pak J Bot.*, **45**: 1229-1234 (2013).
- [30] Sadat H. A., G. A. Nematzadeh, N. B. Jelodar and O. G. Chapi. "Genetic evaluation of yield and yield components at advanced generations in rapeseed (*Brassica napus* L.)". *Afric J Agric Res.*, **5**: 1958-1964 (2010).
- [31] Zhang G and W. Zhou. "Genetic analyses of agronomic and seed quality traits of synthetic oilseed *Brassica napus* produced from interspecific hybridization of *B. campestris* and *B. oleracea*". *J Genetic.*, **85**: 45-51 (2006).