ISSN 0258-7122
Bangladesh J. Agril. Res. 39(2): 227-241, June 2014

VARIABILITY AND HERITABILITY ANALYSIS IN F_4 GENOTYPES OF *Brassica rapa L.*

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Abstract

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Department, Sher-e Bangla Agricultural University, Dhaka, Bangladesh to study variability in 10 F_4 lines obtained through intervarietal crosses along with 8 released varieties of *Brassica rapa*. Significant variation was observed among all the genotypes for all the characters studied. Considering genetic parameters high genotypic co-efficient of variation (GCV) was observed for number of secondary branches per plant, siliquae per plant, yield per plant, whereas days to maturity showed very low GCV. High heritability with low genetic advance in percent of mean was observed for days to maturity which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height and days to 50% flowering indicating that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Considering, inter genotypic variability, heritability, and genetic advance, % co-efficient of variation and other agronomic performance G_2, G_{14}, G_{18}, G_1, G_9, G_{12}, G_{16}, G_{17} may be considered to be better parents for future uses in hybridization programme.

Keywords: Variability, heritability, *Brassica rapa* L.

Introduction

The oleiferous *Brassica* symbolized by rapeseed mustard is one of the leading oilseed crops in our country. It is used as a condiment, salad, green, manure and fodder crop and as a leaf and stem vegetable in various mustard growing countries of the world. It is mainly cross-pollinating crop, although on an average 7.5 to 30% out-crossing does occur under natural field conditions (Abraham, 1994; Rakow and Woods, 1987).

From nutritional point of view, fats and oils in our diets are mostly needed for calories and vitamin absorbent. It produces highest amount of calories per unit in comparison with carbohydrate and protein diets. For human health, in a balanced diet 20-25% of calories should come from fats and oils. Although, oilseed crops play a vital role in human diet, the consumption rate of oil in our country is far below than that of balanced diet (6 g oil per day per capita against

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the optimum requirement of 37g per head per day (Rahman, 1981). The genus *Brassica* has generally been divided into three groups, namely (i) the mustard (ii) the rapeseed and (iii) the cole. The genomic constitutions of the three elemental species of *Brassica* are as follows: 'AA' for *B. rapa*, 'BB' for *B. nigra* and 'CC' for *B. oleracea* having haploid chromosome number 10, 8, and 9, respectively. The species *B. juncea* (AABB), *B. carinata* (BBCC), and *B. napus* (AACC) are the amphidiploids and originated by combinations of the diploid elemental species. All these species have many cultivated varieties suited to different agro-climatic conditions. These varieties did not fit to the existing T.Aman-Mustard-Boro cropping pattern. Farmers are cultivating short duration Tori 7 variety though the yield of this variety is very low. This variety fits very well in the existing cropping pattern but we are deficient in short duration high yielding varieties. It is, therefore, needed to develop improved mustard and rapeseed varieties with high yield potential, shorter growth duration which could be fit into cropping pattern T.Aman–Mustard-Boro. There is plenty of scope to increase yield per unit of area through breeding superior varieties. The production potential of rapeseed and mustard may be well exploited if the varieties can be identified with early maturity, rapid response to high fertility, large seed size, and high oil content. The oil content of mustard in Bangladesh varies from 30 to 40 percent depending on the variety, climate and production condition (Rahman *et al.*,1993).

This experiment was done to analyze the genetic variability of the genotypes in respect of different morphological characters and to screen out the suitable genotypes for future use. Precise information about the extent of genetic divergence and on characters used for discrimination among the population is crucial in any crop improvement programme, because selection of parents based on genetic divergence has become successful in several crops (Ashana and Pandey, 1980; Ananda and Rawat, 1984; De *et al.*,1988).

Materials and Method

A field experiment was conducted in the experimental field of Genetics and Plant Breeding Field Laboratory of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period from November 2007 to March 2008 to study genetic variability in *Brassica rapa*. The soil of the experimental area was loamy belonging to the Madhupur Tract under AEZ 28.The soil of the experimental plots were clay loam, land was medium high with medium fertility level. Eighteen genotypes were used in the study. Description of the 18 genotypes is given in Table 1.

During the rabi season the rainfall generally is scanty and temperature (10.8ºC-30.6ºC) moderate with short day length. Meteorological data on rainfall, temperature, relative humidity from November 2007 to March 2008 were

obtained from the Department of Meteorological centre, Dhaka-1207, Bangladesh. The experiment was conducted using ten F_4 lines along with their five parental materials and three check varieties. The fertilizers N, P, K, S, and B in the form of Urea (250kg/ha), TSP (170 kg/ha), MoP (85 kg/ha), Gypsum (150

Table 1. Sources of 18 *Brassica rapa* genotypes.

Designation	Genotypes	Sources
	Parents	
G_1	BARI Sarisha-6	BARI
G_2	SS-75	BARI
G_3	F_6	SAU
G_4	Tori-7	BARI
G_5	BARI Sarisha-9	BARI
	F_4 lines	
G_6	F_6 × BARI Sarisha-9	SAU
G_7	BARI Sarisha-9 × F_6	SAU
G_8	Tori-7 × BARI Sarisha-6	SAU
G_9	BARI Sarisha-6 × Tori-7	SAU
G_{10}	Tori-7× F_6	SAU
G_{11}	F_6 × Tori-7	SAU
G_{12}	Tori-7× SS-75	SAU
G_{13}	SS-75 × Tori-7	SAU
G_{14}	BARI Sarisha-9×BARI Sarisha-6	SAU
G_{15}	BARI Sarisha-6×BARI Sarisha-9	SAU
	Checks	
G_{16}	BARI Sarisha-15	BARI
G_{17}	Real Tori-7	Farmer's Field
G_{18}	SAU sarisha-1	SAU

kg/ha), and Borax (60 kg/ha), respectively, were applied. The entire amount of TSP, MP, Gypsum, Zinc sulphate, and borax was applied during the final preparation of land. Urea was applied in two equal installments before sowing and flowering. Field lay out was done after final land preparation. The seeds of parents and F_4 materials were laid out in a Randomized Complete Block Design (RCBD) with three replications. The size of the plot was 5m×25m. A distance of 1.5 m from block to block, 30 cm from row to row, and 10 cm from plant to plant was maintained. Seeds were sown in lines in the experimental plots on 11th November 2007 by hand uniformly. The seeds were placed at about 1.5 cm depth in the soil. After sowing, the seeds were covered with soil carefully so that no

clods were on the seeds. Seed germination started after 3 days of sowing on 14th November 2007. Treatment was distributed in the operations which were accomplished for better growth and development of the *Brassica* seedlings. Malathion 57 EC insecticide was applied after one month of seeds sowing at 12 days interval for 3 times with 1 ml in 2.5 liters water for protecting the crop from the attack of aphids and Rovral-50 WP was sprayed @ 20g/10L water first one at the time of siliquae setting of fruiting and second one after 15 days of 1st spraying to control *Alternaria* leaf spot. No remarkable disease attack was observed. Harvesting was started from 5 February 2008 depending upon the maturity of the plants. When 80% of the plants showed symptoms of maturity i.e; straw colour of siliquae, leaves, stem, and desirable seed colour in the matured siliquae, the crop was assessed to attain maturity. Ten plants were selected at random from each plot in each replication. The sample plants were harvested by uprooting and then they were tagged properly. Data were recorded from these plants. The data were analyzed for different components. Phenotypic and genotypic variance were estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Genotypic and phenotypic variances were estimated according to the formula of Johnson et al. (1955).

Results and Discussion

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for plant height (555.475**) indicating the presence of genotypic differences present among the genotypes used in the present study (Table 2). Among the genotypes, mean value G1 was the tallest (125.23 cm), which was statistically different from other genotypes except G3 (119.06 cm) while, the shortest genotype was G17 (65.367 cm), which was followed by G8 (88.4 cm) (Table 3).The phenotypic variance (216.72) was considerably higher than the genotypic variance (169.38) and the phenotypic and genotypic co-efficient of variations were 14.49 % and 12.81 %, respectively, for plant height (Table 4). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for plant height were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al*. (2001) in their studies. Analysis of variance of the data for number of primary branches/plant showed statistically highly significant difference among the genotype (Table 2). Maximum number of primary branches per plant was recorded in genotype G1 (8.07) which was significantly different from other genotypes and the genotypes G2 and G16 were statistically similar (both are 7.10) (Table 3).On the other hand, the minimum number of primary branches/

plant was recorded in the genotypes G17 (4.17), which was followed by G18 (4.20).The phenotypic variance (1.54) was slightly higher than the genotypic variance (1.09) indicating less environmental influence on this characters (Table 4) and relatively moderate genotypic co-efficient (18.53%) and phenotypic co-efficient of variation (21.97%) which indicate that the genotype has high variability (Table 4). Chawdhury *et al.* (1987) found significant differences for number of primary branches per plant. Kuriakose and Joseph (1986), Alam *et al.* (1985) and Uddin *et al.* (1995) reported similar results earlier.

In the present experiment, analysis of variance of the data for number of secondary branches per plant showed highly significant difference among the genotypes included in the present experiment. The mean square value, (16.426**) regarding number of secondary branches per plant (Table 2) indicated the presence of variability among the genotypes.

Highest number of secondary branches per plant was recorded in genotype G9 (9.40) (Table 3), which was statistically similar with G7, G11, G12, G13.The lowest mean was observed in G18 (1.73), which was statistically different with 16 genotypes except G16 (Table 3). Number of secondary branches per plant showed low values and little differences between genotypic (5.13) and phenotypic (6.16) variance indicating that they had some short of interaction with environment and relatively high GCV (35.65%) and PCV (39.07%) which indicated that the genotype had high variability (Table 3). Lekh *et al.* (1998) reported similar results in their study.

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From the (Table 2) there were highly significant variations among the genotypes (61.020**) for days to 50% flowering. The days to 50% flowering was observed highest (41.33) in G18 which was statistically similar with G1 was G2. and G16, but significantly different from other genotypes. The lowest value found in G17 (25.333) which was followed by that ofG8 (Table 3).

Genotypic and phenotypic variance of days to 50% flowering was observed 18.66 and 23.71, respectively, with high differences between them indicating large environmental influences on these characters for their phenotypic expression, and values of GCV and PCV were 12.75% and 14.37%, respectively, which indicate moderate variability present among the genotypes for this character (Table 5). Lekh *et al.* (1998) recorded highest GCV and PCV for days to 50% flowering.

Table 2. Analysis of variance of the data of 10 important characters in respect of 18 *Brassica rapa* genotypes.

Sources of variation	D.F	Mean Sum of Squares of characters									
		Plant height (cm)	No. of primary branches / plant	No. of secondary branches /plant	Days to 50% flowering	Days to maturity	No. of siliquae/ plant	Length of siliqua (cm)	No. of seeds/ siliqua	1000-seed wt (g)	Seed yield/plant (g)
Replication	2	30.525	0.020	1.074	7.167	6.907	565.729	0.151	3.245	0.095	1.404
Genotype	17	**	**	**	**	**	**	**	**	**	**
		555.475	3.721	16.426	61.020	32.153	6302.133	0.584	26.070	0.422	5.876
Error	34	47.34	0.444	1.032	5.049	5.300	658.212	0.087	3.898	0.122	0.451
CV(%)		6.77	11.81	15.99	6.63	2.49	13.51	7.62	11.74	11.56	10.39

** Denote significant at 1% level of probability

Table 3. Mean performance of ten different characters of 18 genotypes of *Brassica rapa.*

Designation	Plant height (cm)	No. of primary branches/plant	No. of secondary branches/plant	Days to 50% flowering	Days to maturity	No. of siliquae /plant	Siliquae length (cm)	No. of seeds/pod	1000-seed wt (g)	Yield (g)
G1	125.23a	8.07a	3.43fg	40.33a	92.00c-e	235.73a-c	4.13bc	21.61ab	2.93bc	8.97a
G2	115.97a-c	7.10ab	5.80c-e	40.00a	99.00a	201.20b-f	3.36ef	17.29cd	3.79a	8.06ab
G3	119.60ab	6.07b-e	8.17ab	35.67bc	90.67ef	244.40ab	3.46d-f	12.99ef	2.94bc	6.44c-e
G4	92.00gh	5.47c-g	6.03c-e	31.33de	99.00a	143.07gh	3.88b-e	15.26c-f	2.63cd	6.00c-f
G5	95.03f-h	4.60gh	4.60ef	34.33b-d	91.00d-f	133.27h	3.73b-f	14.74d-f	3.01bc	4.22g
G6	102.77d-g	5.03e-h	6.67b-d	33.33c-e	95.33a-d	186.13d-g	4.00b-d	18.86bc	3.50ab	5.52ef
G7	99.13f-h	6.63bc	8.50a	32.00c-e	90.00ef	211.63a-e	3.90b-e	16.61c-e	3.06bc	8.66a
G8	88.4h	4.37gh	5.60de	29.00ef	96.67ab	172.03e-h	3.96b-d	16.58c-e	2.59cd	5.70d-f
G9	100.17e-h	5.87b-f	9.40a	30.00de	93.00b-e	228.77a-d	3.96b-d	15.17c-f	2.99bc	7.00bc
G10	105.30c-g	5.47c-g	6.17c-e	31.33c-e	92.67b-e	231.43a-d	3.68b-f	14.40d-f	2.98bc	6.92b-d
G11	96.30f-h	5.93b-e	8.77a	32.67c-e	91.67c-e	197.43b-f	3.84b-f	16.26c-e	2.63cd	5.94c-f
G12	107.53b-f	5.27d-h	9.13a	34.00b-e	91.33c-e	259.57a	3.30f	12.05f	2.70cd	5.40e-g
G13	99.97e-h	5.10e-h	8.77a	30.00de	90.33ef	220.40a-e	3.70b-f	18.03cd	2.82cd	8.24a
G14	112.57b-e	6.50b-d	6.13c-e	37.67ab	90.33ef	187.33c-g	4.26b	17.68cd	2.29d	5.01fg
G15	95.47f-h	4.60f-h	5.93c-e	31.33de	95.67ac	155.90f-h	3.75b-f	15.25e-f	3.00bc	5.59ef
G16	113.37a-d	7.10ab	1.83g	40.33a	86.67f	146.87gh	3.87b-f	22.89a	2.21d	8.01ab
G17	65.37 i	4.17h	7.70a-c	25.33f	91.33c-e	182.80d-g	3.64cf	15.40c-f	3.08bc	5.30e-g
G18	94.47f-h	4.20gh	1.73g	41.33a	90.67ef	79.60i	5.33a	21.70ab	2.98bc	5.34e-g
LSD (0.05)	11.42	1.106	1.686	3.728	3.82	42.57	0.489	3.276	0.555	1.114

Note: Means separated by uncommon letters in order of alphabetic preferences are significantly different from each other at p = 0.05.

Table 4. Estimation of genetic parameters for yield and yield contributing characters of 18 genotypes of *Brassica rapa.*

Genetic parameters → / Characters ↓	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	ECV (%)
Plant height	169.38	216.72	47.34	12.81	14.49	6.77
No. of Primary branches/plant	1.09	1.54	0.44	18.53	21.97	11.81
No. of secondary branches/ plant	5.13	6.16	1.03	35.65	39.07	15.99
Days to 50% flowering	18.66	23.71	5.05	12.75	14.37	6.63
Days to maturity	8.95	14.25	5.30	3.23	4.08	2.49
Siliquae/plant	1881.31	2539.52	658.21	22.84	26.54	13.51
Siliqua length	0.17	0.25	0.09	10.51	12.98	7.61
No. of seeds/pod	7.39	11.29	3.90	16.16	19.98	11.74
1000-seed wt	0.103	0.215	0.112	11.10	16.02	11.56
Yield/plant	1.81	2.26	0.45	20.81	23.26	10.39

Table 5. Grand mean and range of yield and yield contributing characters of 18 genotypes of *Brassica rapa.*

Identifier	Minimum	Maximum	Mean
Plant height	65.4	125.2	101.6
No. of primary branches/plant	4.167	8.067	5.641
No. of secondary branches/plant	1.733	9.400	6.354
Days to 50% flowering	25.33	41.33	33.89
Days to maturity	86.67	99.00	92.63
Siliquae/plant	79.6	259.6	189.9
Siliqua length	3.296	5.333	3.874
seeds/pod	12.05	22.89	16.82
1000-seed wt	2.213	3.787	2.896
Yield/plant	4.218	8.967	6.462
Identifier	Minimum	Maximum	Mean

Significant difference was observed among all the genotypes (32.153**) studied for this character (Table 2).The days to maturity was observed lowest in G16 (86.667) which was statistically significant and different from those of 17 other genotypes. The highest value was in G2 and G4, which was statistically significant and different from those of 16 other genotypes.

Genotypic and phenotypic variance of days to maturity was observed 8.95 and 14.25, respectively. with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of GCV and PCV were 3.23% and 4.08%, respectively which indicated that the genotype has relatively less variation (Table 4). Higher genotypic variances indicate the better transmissibility of a character from parent to the offspring (Ushakumari *et al.,* 1991).

The mean square value due to genotype from the analysis of variance was found statistically significant differences at 1% level of probability for number of siliquae per plant among the genotypes used as experimental material under the present experiment (Table 2). From the mean value, it was found that the highest number of siliquae per plant was recorded for the genotype G12 (259.57) which were closely followed by the genotype G3 (244.4), while the minimum number (79.60) was recorded for the genotype G18.

The phenotypic variance (2539.52) was considerably higher than the genotypic variance (1881.31) and the phenotypic and genotypic co-efficient of variations were 26.54% and 22.84%, respectively (Table 4). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for number of siliquae per plant were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

A significant variation was recorded among the genotypes in consideration of length of siliquae (Table 2). Maximum length of siliquae were recorded in G18 (5.33cm) genotypes followed by G14 (4.263cm). Minimum length of siliquae (3.30 cm) was recorded for the genotype G12 (Table 3).

Length of siliquae showed minimum amount of genotypic and phenotypic variance (0.17 and 0.25, respectively) with minimum difference between them indicating that they were less responsive to environmental factors for their phenotypic expression. According to Table 4, GCV (10.51%) and PCV (12.98%) for length of siliquae indicated the existence of sufficient variation among different genotypes. Deshmukh *et al*. (1986) also reported phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation.

The value of the analysis of variance of the data for the number of seeds per siliqua showed highly significant difference (26.070**) among the genotypes of *Brassica* used in the present experiment. The mean square values regarding the character indicated the presence of variability among the genotypes (Table 2). Maximum number of seeds per siliqua was recorded in genotype G16 (22.89) which was followed by the genotypes G18 and G1 (21.70 and 21.61, respectively) and the minimum (12.05) was recorded in the genotypes, G12, which was statistically different from other genotypes.

The difference in magnitudes in between genotypic (7.49) and phenotypic (11.29) variances was relatively high for number of seeds per siliqua indicating large environmental influence on these characters (Table 4) and the moderate phenotypic and genotypic co-efficient of variations were 19.98% and 16.16%, respectively (Table 4) for this character of *Brassica* genotypes. The result indicated the existence of adequate variation among the population with possibility of high potential for selection low phenotypic co-efficient of variation regarding this in earlier noticed by Prakash *et al.* (2000) which also supported the results of the present experiment. Yogendra et al. (2002) also reported low phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) for this character.

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for 1000-seed weight indicating genotypic differences among the genotypes used under the present experiment (Table 2). From the mean value, it was found that the highest 1000-seed weight was recorded in the genotype G2 (3.79g) followed by G6 (3.50 g), while the lowest 1000 seed weight (2.21g) was in the G16 (Table 3).

The phenotypic variance (0.215) was considerably higher than the genotypic variance (0.103) and the phenotypic and genotypic co-efficient of variations were 16.02% and 11.10%, respectively, for 1000-seed weight of *Brassica* genotypes (Table 4). The result indicated the existence of inherent variability among the population with possibility of high potential for selection. Highest phenotypic and genotypic variances and genotypic and phenotypic co-efficient of variations for 1000-seed weight were also observed by Mishra and Yadav (1992), Uddin *et al.* (1995), Azad and Hamid (2000) and Venkatramana *et al.* (2001).

In the present experiment, the genotype mean square for seed yield per plant was found significant 5.876** (Table 2). The DMRT test indicated the existence of both significant and insignificant differences in different means. The seed yield per plant was recorded highest in the G1 (8.79), which was statistically similar with the genotypes G7 and G13, and the lowest mean value (4.22) was in G5 (Table 3). Shen *et al.* (2002) observed significant differences between F_1s and their parents for yield per plant. Katiyar *et al*. (2004) found significant variation

among parents and crosses indicated the presence of adequate genetic variance which reflected in differential performance of intervarietal cross combinations of *Brassica campestris.*

Seed yield per plant showed low values of genotypic (1.81) and phenotypic (2.26) variance with little differences indicating that they had some sort of interaction with environment and moderate GCV (20.81%) and PCV (23.26%) indicating that the genotypes are considerably variable for this character (Table 4). Bhardwaj and Singh (1969) reported GCV of seed yield per plant was 96.99% in *Brassica campestris*. Singh and Chaudhury (1987) also reported values 44.04% and 46.9% of GCV and PCV respectively for *Brassica juncea.*

Heritability and genetic advance

Findings of the heritability, genetic advance, and genetic advance in percentage of mean of individual character are discussed in this part of the thesis and the results related to this character are presented in Table 6.

Plant height showed very high heritability (78.16%) together with high genetic advance (23.70%) and genetic advance in percentage of mean (23.33) which indicated that most likely the heritability was due to additive gene effects and selection may be effective which was also earlier reported by Singh and Singh (1999).

Number of primary branches per plant showed high heritability (71.10%) coupled with low genetic advance (1.82%) and genetic advance in percentage of mean (32.18). These findings revealed that it was indicative of non-additive gene action. The high heritability was being exhibited due to favourable influence of environment rather than genotypes and selection for such traits may not be rewarding which was also earlier reported by Islam and Rasul (1998), Singh and Singh (1999).

High heritability (83.26%) coupled with low genetic advance (4.26%), and high genetic advance in percentage of mean (67.01) was calculated in respect of number of secondary branches per plant. These findings discovered the action of non-additive gene effect on the expression of this character as well as a scope pf improvement through selection may not be rewarding which was also earlier reported by Kumar *et al.* (1998). Days 50% flowering showed high heritability (78.70%) with genetic advance (7.89%) and genetic advance in percentage of mean (23.29) revealing that the character is governed by non-additive genes and heterosis breeding may be useful and also indicates that the character is least influenced by the environmental effects. The magnitude of heritability in broad sense (h^2b) of this character was high (62.81%) and low genetic advance (4.88%) and low genetic advance in percentage of mean (5.27). These findings revealed that it is indicative of non-additive gene action. The high heritability is being exhibited due to favorable influence of environment rather than genotypes and

Table 6. Heritability, genetic advance and genetic advance in percent of means for yield and yield contributing characters of 18 genotypes of *Brassica rapa*.

Genetic parameters → Characters ↓	Heritability h^2_b (%)	Genetic advance	GA in percent of means
		5%	**5%**
	78.16	23.70	23.33
No. of primary branches/plant	71.10	1.82	32.18
No. of secondary branches/plant	83.26	4.26	67.01
Days to 50% flowering	78.70	7.89	23.29
Days to maturity	62.81	4.88	5.27
Siliquae/plant	74.08	76.90	40.50
Siliqua length	65.57	0.68	17.53
No. of seeds/pod	65.47	4.53	26.94
1000-seed wt	47.99	0.46	15.84
Yield/plant	80.04	2.48	38.35

selection for such traits may not be rewarding. These results were reported by Alam *et al.* (1985) and Hossain (1988).

Number of siliquae per plant showed very high heritability (74.08%) coupled with very high genetic advance (76.90%) and very high genetic advance in percentage of mean (40.50). As this trait possessed high genetic advance, it was high potential for effective selection for further genetic improvement of this trait. Length of siliquae per plant showed very high heritability (65.57%) connected with very low genetic advance (0.68%) and genetic advance in percentage of mean (17.53) which exposed the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection. The magnitude of heritability in broad sense (h^2b) of this trait was high (65.47%) and low genetic advance (4.53%) and genetic advance in percentage of mean (26.94). These results indicate non-additive genes involvements in the expression of the character and this with limit scope of improvement by direct selection.

Very heritability (47.99%) associated with very low genetic advance (0.46%) and genetic advance in percentage of mean (15.84) was calculated in respect of 1000-seed weight of *Brassica* genotypes. These findings exposed the action of non-additive gene effect on the expression of this character as well as a scope of improvement through selection. High heritability (80.04%) coupled with low genetic advance (2.48%) and genetic advance in percentage of mean (38.35) was recorded in respect of yield per plant. These findings revealed that it is indicative of non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than genotypes and selection for such traits may not be rewarding. These results were reported by Alam *et al.* (1985) and Hossain (1988). Considering, inter genotypic variability, heritability, and genetic advance, % co-efficient of variation and other agronomic performance, G2, G14, G18, G1, G9, G12 , G16 and G17 may be considered to be better parents for future uses in hybridization programme.

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