VARIABILITY AND HERITABILITY STUDY IN SOME SELECTED GENOTYPE OF RAPESEED (*Brassica rapa* L.)

N. J. Shelly[1*], M. S. R. Bhuiyan[2], F. Mahmud[2], J. Rahman[2] and M. A. Alam[3]

[1]Department of Biochemistry, Faculty of Agriculture, Sher-e-Bangla Agricultural University (SAU), Dhaka; [2]Department of Genetics and Plant Breeding, Faculty of Agriculture, Sher-e-Bangla Agricultural University (SAU), Dhaka; [3]Plant Breeding Division, Spices Research Centre, Bangladesh Agriculture Research Institute (BARI), Bogura. Bangladesh

Abstract

A field experiment was conducted in the research field of Sher-e-Bangla Agricultural University (SAU), Dhaka, Bangladesh to study variability and heritability in *Brassica rapa* L. for developing short durable, high yielding varieties. The experiment had laid out in a randomized complete block design with three replications and consisted of seven genotypes viz., G_1 (BARI Sarisha-14), G_2 (Brown Special), G_3 (Yellow Special), G_4 (Tori-7), G_5 (BARI Sarisha-17), G_6 (BARI Sarisha-15) and G_7 (BARI Sarisha-6). The result revealed that G_7 had the highest yield plant^{-1} (6.91 g) and longest duration (108 days) while G_4 had the lowest yield plant^{-1} (4.12 g) and G_2 had the shortest duration (79 days). High genotypic and phenotypic coefficient of variation for number of secondary branches plant^{-1} (95.4 % and 99.4 %), number of siliqua plant^{-1} (29.6 % and 30.3%), plant height (25.2 % and 25.4 %) and number of seeds siliqua^{-1} (26.76% and 27.2%) had estimated. High heritability with high genetic advance and gain had observed for days to 80% maturity (99.9%, 21% and 23.4 %), plant height (98.55%, 53.99% and 51.6 %) and number of siliqua plant^{-1} (95.4 %, 101.3 % and 59.4 %). While high heritability with low genetic advance and high genetic gain were observed for number of primary branches plant^{-1} (92.1%, 0.70% and 188.4%), number of secondary branches plant^{-1} (92.02%, 7.47 % and 188.43 %), length of siliqua (98.3%, 1.104% and 29.96), 1000 seed weight (84.6 %, 1.23% and 32.01%) and yield plant^{-1} (97.4 %, 2.01% and 38.47%). Days to 80% maturity, plant height and number of siliqua plant^{-1} showed high heritability with high genetic advance and genetic gain indicated additive gene action and selection could be useful for these traits. While high heritability with low genetic advance had observed for number of primary and secondary branches plant^{-1}, length of siliqua, 1000 seed weight and yield plant^{-1} indicated non additive gene action and selection might be ineffective for these traits.

Keywords: Additive gene, Genetic advance, Genetic gain, Heritability, Variance

Introduction

Mustard and rapeseed have become the major oilseed crops occupying the third position among the oilseed crops in the world and the world area harvested under mustard

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and rapeseed is 38,509,853 MT, and production is 75,711,806 MT (FAOSTAT, 2020). The climate and soil conditions of Bangladesh is also preferable for mustard and rapeseed production (Chowdhury *et al.,* 2014). In Bangladesh total cultivated area under rapeseed and mustard cultivation is 0.589 million hectares which produces 1.34 ton ha^{-1} in 2020-21 and *B. rapa* occupies the 1st position in respect of area and production (AIS, 2022). Although short durable, low yielding and pest susceptible variety (Tori-7) of *B. rapa* is popular in Bangladesh but there is still lack of improved short durable and high yielding varieties. As a result, Bangladesh is suffering from an acute shortage of edible oil and therefore, it is very important to develop new varieties with such desirable traits. Varietal improvement requires a laborious and long term breeding activities, which depends on the extent and nature of genetic variability, heritability, and genetic advance present in the genotypes (Islam *et al.,* 2020 and Snehi *et al.,* 2020). The more the variability in the breeding population the more effective selection will be achieved (Rauf and Rahim, 2018). Genetic variability and heritability had estimated by different morphological parameters that involve polygenic inheritance of gene action (Ali *et al*., 2013, Azam *et al.,* 2013 and Iqbal *et al*., 2014). Polygenic inheritance of gene action has higher environmental influences so heritability estimation is very much important to ensure an effective selection process as it shows the influence of genes and environment on different morphological traits (Sultana *et al.,* 2021). Heritability and phenotypic variance along with the selection intensity can give the most accurate estimate of genetic advance for effective selection (Parvin *et al*., 2020). High heritability along with high genetic advance for a particular trait indicated most effective selection condition (Bibi *et al*., 2016; Rauf and Rahim, 2018 and Mazurkievicz *et al*., 2019). For developing a high yielding variety, it is very important to estimate the individual role of different morphological traits on higher yield (Ejaz-Ul-Hasan *et al.*, 2014). Therefore, the present study had conducted to estimate the variability, heritability and genetic advance for yield and yield related attributes in *B. rapa* (main oil yielding species in Bangladesh) for developing short durable and high yielding genotypes. This would provide a guide for effective selection in the breeding population in formulating the most appropriate breeding technique for improvement of various traits.

Materials and Methods

Study area

The experiment had conducted in the research field of SAU, Dhaka, Bangladesh from October/20 to March/21.

Plant materials

The plant materials of the present study consisted of seven genotypes of *B. rapa* collected from Bangladesh Agricultural Research Institute (BARI) and Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh, which included G$_1$ (BARI Sarisha-14), G$_2$ (Brown Special), G$_3$ (Yellow Special), G$_4$ (Tori-7), G$_5$(BARI Sarisha-17), G$_6$ (BARI Sarisha-15) and G$_7$ (BARI Sarisha-6).

Materials and Methods

The experiment had laid out in a randomized complete block design (RCBD) with three replications. The genotypes had randomly distributed to each replication having row spacing of 30 cm and plant distance of 10 cm. Three rows of each accession had sown in each replication. Ten plants had selected at random from each replication and data on ten quantitative parameters namely; days to 50% flowering, days to 80% maturity, plant height, number of primary branches plant[-1], number of secondary branches plant[-1], number of siliqua plant[-1], siliqua length, number of seeds siliqua[-1], 1000 seed weight and seed yield plant[-1] had noted.

Statistical analysis

Means separated using Least Significant Difference test. The analysis of variance for different characters had carried out using mean data in order to assess the genetic variability among populations as given by Cochran and Cox (1957). The broad sense heritability (h_{bs}^2) was estimated for all characters as the ratio of genotypic variance to the total of phenotypic variance as suggested by Lush (1949) and Hanson *et al*. (1956) and had categorized according to Robinson *et al*. (1966). Genetic advance had measured and categorized using the formula given by Johnson *et al*. (1955). Genotypic and phenotypic co-efficient of variation had been calculated by the formula of Burton (1952) and had categorized as suggested by Sivasubramanian and Madhamenon (1973).

Results and Discussion

Analysis of variance

Analysis of variance was performed for ten quantitative characters including yield and yield-attributing traits for selected *B. rapa* genotypes (Table 1) and observed that mean sum of squares due to genotypes were significant for all the studied traits at 1% level of significance, thus exhibiting the presence of considerable genetic variability except primary branches plant[-1]. Singh *et al.,* (2013), Tripathi *et al.,* (2013) and Shekhawat *et al*., (2014) also reported considerable genetic variability for all these traits in their experiments, as mean sum of squares due to genotypes were significant. Abideen *et al.,* (2013) also studied non-significant differences in primary branches plant[-1] among the genotypes. This might be due to environmental effects.

Mean performance

Significant variation in days to 50% flowering and 80% maturity had observed which ranged from 34.33 to 58.86 days and 79.33 to 108.00 days respectively (Table 2). Days to 50% flowering was maximum in G_7 (58.86 days) and the minimum in G_4 (34.33 days) while days to 80% maturity was maximum in G_7 (108.00 days) and the minimum in G_2 (79.33 days). The result matched with the findings of Karmokar (2018) and Ullah

(2018) who reported days to 50% flowering for different lines and varieties of *B. rapa* ranged from 33.00 to 57.33 days and 27.33 to 55.66 days respectively while days to 80% maturity ranged from 78.00 to 89.67 and 78.33 to 87.33 days respectively. Minimum days of 50% flowering indicated short durable population. Plant height ranged from 67.86 to 149.23 cm. The highest plant height was recorded in G_7 (149.23 cm) and lowest in G_4 (67.86 cm) (Table 2). The result differed from the findings of Karmokar (2018) and Ullah (2018) who reported that, the plant height for different lines and varieties of *B. rapa* ranged from 80.77 to 111.47 cm and 94.56 to 107.73 cm respectively. This might be due to environmental effects. The number of primary and secondary branches plant^{-1} ranged from 6.53 to 9.13 and 0.13 to 9.80 respectively (Table 2). The maximum primary branches plant^{-1} had recorded in G_6 (9.13) and the minimum was in G_5 (6.53) while the secondary branches plant^{-1} had found to be the maximum in G_4 (9.80) and the minimum was in G_6 (0.13). The more branches plant^{-1} indicating more siliqua that ultimately increased yield plant^{-1}.The result had supported by Karmokar (2018) who reported that number of primary and ranged from 59.48 to 124.29, 96.54 to 124.44 and 78.00 to 180.33 respectively. Number of seeds siliqua^{-1} ranged from 11.85 to 30.97 (Table 2). It was maximum in G_5 (30.97) followed by G_6 (24.11) which was statistically similar with G_1 (23.99) while the minimum number was in G_4 (11.85). Ali *et al.,* (2002) observed that the hybrid of *B. rapa* produced an excellent number of seeds siliqua^{-1} (25.06) while Karmokar (2018) and Ullah (2018) found that the seeds siliqua^{-1} for different lines and varieties of *B. rapa* ranged from 11.98 to 16.22 and 12.83 to 20.87 respectively. The result of the present study exceeded the range of this finding. Which might be due to the differences in size and shape of siliqua in different genotypes. The siliqua length ranged from 3.04 to 4.57 cm. The highest siliqua length had measured in G_2 (4.57 cm) followed by G_7 (4.14 cm) while the lowest in G_4 (3.04 cm) preceded by G_1 (3.18 cm) and G_5 (3.36 cm) (Table 2). secondary branches plant^{-1} for different lines and varieties of *B. rapa* ranged from 5.13 to 10.33 and 0.50 to 10.93 respectively but higher than the findings of Ullah (2018) who estimated that the range was between 5.67 to 4.12 and 1.45 to 2.27 respectively. This might be due to environmental effects. Number of siliqua plant^{-1} ranged from 90.64 to 246.53 (Table 2). It was maximum in G_4 (246.53) followed by G_2 (219.66) while the minimum number was in G_1 (90.64). The findings exceeded the range reported by Naznin *et al.,* (2015), Karmokar (2018) and Ullah (2018) who reported that the number of siliqua plant^{-1} for different lines and varieties of *B. rapa*.

Table 1. Analysis of variance for seed yield and seed yield attributing traits in *Brassica rapa* genotype

Source of variation	Df	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of siliqua plant^{-1}	Siliqua length (cm)	No. of seed siliqua^{-1}	1000 Seed Weight (g)	Seed yield plant^{-1} (g)
Genotypes	6	235.11**	311.89**	2101.65**	2.24	44.13**	7726.9**	0.88**	101.46**	1.35**	2.96**
Replications	2	26.09	20.67	1.15	0.66	0.69	404.7	0.02	1.18	0.02	0.58
Error	12	0.09	0.08	10.24	1.02	1.24	124.2	0.01	0.91	0.08	0.03
CV (%)		0.66	0.32	3.05	13.69	28.06	6.54	1.97	4.41	7.20	3.09
LSD		0.52	0.51	5.70	1.80	1.98	19.83	0.13	1.70	0.50	0.29

Df = Degree of freedom, CV = Co-efficient of variation, LSD = Least Significant Difference, ** = Significant at 1%

Table 2. Mean performance for yield and yield contributing traits for seven genotypes of *Brassica rapa* L.

Sl. No.	Genotypes	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	Number of primary branches plant[-1]	Number of secondary branches plant[-1]
1.	G_1	39.11 e	84.33 e	85.36 d	7.06 b	3.13 c
2.	G_2	34.33 g	79.33 g	109.73 b	7.26 b	7.66 b
3.	G_3	42.00 d	87.00 d	114.10 b	7.40 ab	0.46 d
4.	G_4	36.00 f	81.33 f	67.86 e	6.66 b	9.80 a
5.	G_5	53.33 b	98.33 b	97.33 c	6.53 b	3.73 c
6.	G_6	45.33 c	90.66 c	114.86 b	9.13 a	0.13 d
7.	G_7	58.86 a	108.00 a	149.23 a	7.66 ab	0.83 d
	Min.	34.33	79.33	67.86	6.53	0.13
	Max.	58.86	108.00	149.23	9.13	9.80
	Mean	44.13	89.85	104.78	7.39	3.96
	CV%	0.66	0.32	3.05	13.68	28.06
	LSD	0.51	0.50	5.69	1.79	1.97

G_1 (BARI Sarisha-14), G_2 (Brown Special), G_3 (Yellow Special), G_4 (Tori-7), G_5 (BARI Sarisha-17), G_6 (BARI Sarisha-15) and G_7 (BARI Sarisha-6). (Note: BARI: Bangladesh Agriculture Research Institute)

Sl. No.	Genotypes	Number of siliqua plant[-1]	Siliqua length (cm)	Number of seeds siliqua[-1]	1000 seed weight (g)	Seed yield plant[-1] (g)
1.	G_1	90.64 e	3.18 e	23.99 b	3.33 ef	4.93 c
2.	G_2	219.66 b	4.57 a	19.06 d	3.52 de	5.22 c
3.	G_3	145.99 d	3.74 c	20.61 cd	4.55 ab	5.11 c
4.	G_4	246.53 a	3.04 f	11.85 e	2.86 f	4.12 d
5.	G_5	106.56 e	3.36 d	30.97 a	3.90 cd	6.09 b
6.	G_6	161.63 cd	3.73 c	24.11 b	4.10 bc	5.20 c
7.	G_7	172.73 c	4.14 b	20.80 c	4.75 a	6.91 a
	Min.	90.64	3.04	11.85	2.86	4.12
	Max.	246.53	4.57	30.97	4.75	6.91
	Mean	170.54	3.68	21.63	3.86	5.22
	CV%	6.53	1.96	4.40	7.20	3.08
	LSD	19.82	0.13	1.69	0.49	0.28

G_1 (BARI Sarisha-14), G_2 (Brown Special), G_3 (Yellow Special), G_4 (Tori-7), G_5 (BARI Sarisha-17), G_6 (BARI Sarisha-15) and G_7 (BARI Sarisha-6). (Note: BARI: Bangladesh Agriculture Research Institute)

Similar result had been observed by Karmokar (2018) and Ullah (2018) who reported that siliqua length for different lines and varieties of *B. rapa* ranged from 4.67 to

5.96 cm and 5.07 to 6.38 cm respectively. 1000 seed weight ranged from 2.86 to 4.75. The highest 1000 seed weight had recorded in G_7 (4.75 g) and the lowest in G_4 (2.86 g) while significant variation for seed yield plant[-1] was observed among the genotypes and it ranged from 4.12 to 6.91 g (Table 2). The highest yield was recorded in G_7 (6.91 g) followed by G_5 (6.09 g) and the lowest yield was recorded in G_4 (4.12 g) preceded by G_1 (4.93 g). The higher 1000 seed weight indicated that the seeds are bigger and contained higher amount of oil. These result matched with the findings of Karmokar (2018) and Ullah (2018) who reported that 1000 seed weight for different lines and varieties of *B. rapa* ranged from 3.33 to 4.53 g and 2.50 to 3.63 g respectively and for seed yield plant[-1] it ranged from 3.53 to 7.31 g and 5.65 to 7.48 g respectively.

Variability

For days to 50% flowering and days to 80% maturity phenotypic variance (78.42 and 104.02 respectively) were higher than the genotypic variance (78.34 and 103.94 respectively). High values of phenotypic coefficient of variation (PCV) (20.12 %) and genotypic coefficient of variation (GCV) (20.11 %) had observed for days to 50 % flowering while 80 % maturity exhibited moderate GCV and PCV of 11.34 and 11.35 % respectively (Table 3). The difference between genotypic and phenotypic variances and PVC and GVC were relatively low for these traits. Hussain *et al.,* (2014) and Rout *et al.,*(2019) also found similar result that indicated the less influence of environment on the expression of the characters. The high value for PVC and GVC had estimated here but Sikarwar *et al.*, 2017; found low PCV and GCV that may be due to environmental factors. For plant height, Genotypic and phenotypic variance were 697.14 and 707.37 respectively with large environmental influence (10.23). The PCV and GCV also had the higher values, 25.38 and 25.19 % respectively (Table 3). Iqbal *et al.,* (2015), Naznin *et al.,* (2015) and Aktar *et al*., (2019) also found the similar results. High PCV and GCV values for this traits had supported by Gupta *et al.,* (2019), indicated the existence of inherent variability among the studied genotypes for this trait. The genotypic and phenotypic variance were recorded as 0.40 and 1.43 respectively along with low GCV (8.64 %) and moderate PCV (16.18 %) for of primary branches plant[-1] while for secondary branches plant[-1], the genotypic and phenotypic variance were recorded as 14.30 and 15.53 respectively along with very high GCV (95.35 %) and PCV (99.39 %) (Table 3). Relatively low differences between genotypic and phenotypic variance for number of primary branches plant[-1] indicated less environmental influences, this result matched with Hussain *et al.,* 2014; and Naznin *et al.,* 2015; Iqbal *et al.,* 2015; and Rout *et al.,* 2019; also estimated low GCV and moderate PCV but Sikarwar *et al.*, 2017; and Gupta *et al.,* 2019; reported high GCV and PCV for this trait. For number of siliqua plant[-1], phenotypic variance (2658.44) was higher than genotypic variance (2534.23) (Table 3).

Table 3. Genetic variance estimation for ten yield and yield contributing traits of *Brassica rapa L. genotype*

Traits	Phenotypic Variance $(\sigma^2 p)$	Genotypic Variance $(\sigma^2 g)$	Environ-mental Variance $(\sigma^2 e)$	Phenotypic coefficient of variation (PCV) (%)	Genotypic coefficient of variation (GCV) (%)
Days to 50% flowering	78.42	78.34	0.08	20.12	20.11
Days to 80% maturity	104.02	103.94	0.08	11.35	11.34
Plant height (cm)	707.37	697.14	10.23	25.38	25.19
Number of primary branches plant[-1]	1.43	0.40	1.03	16.18	8.64
Number of secondary branches plant[-1]	15.53	14.30	1.23	99.39	95.35
Number of Siliqua plant[-1]	2658.44	2534.23	124.21	30.23	29.52
Length of siliqua (cm)	0.297	0.292	0.005	14.80	14.67
Number of seeds siliqua[-1]	34.42	33.52	0.9	27.12	26.76
1000 seeds weight (g)	0.50	0.42	0.08	18.36	16.89
Seed yield plant[-1] (g)	1.004	0.978	0.026	19.17	18.92

High genotypic variance indicates the better transmissibility of the character from parent to their offspring. Higher value of PCV (30.23%) and GCV (29.52%) had also estimated for this trait indicated the existence of inherent variability among the studied genotypes but differences between phenotypic and genotypic variance was relatively higher (124.21) indicated influence of environment (Table 3). The result matched with Aktar *et al*., (2019), Gupta *et al.,* (2019) and Rout *et al.,* (2019). The genotypic variance (34.42), phenotypic variance (33.52), environmental variance (0.90), high GCV (26.76) and high PCV (27.12) had estimated for number of seeds siliqua[-1] (Table 3). Very low environmental influences and high GCV, PCV indicated presence of additive gene effects and hence the selection might be effective for this trait. Sikarwar *et al.,* (2017), Aktar *et al*., (2019) and Rout *et al.,* (2019) also estimated similar result for this trait. The genotypic and phenotypic variance for siliqua length was 0.297 and 0.292 respectively with environmental variance 0.005 (Table 3). Very low difference between genotypic and phenotypic variance indicated very low environmental influences and the preponderance of additive gene effects, hence, the selection, based on these traits might be effective. Naznin *et al.,* (2015) and Rout *et al.,* (2019) also found least difference between phenotypic and genotypic variances for this trait. Moderate GCV (14.67%) and PCV (14.80 %) values were estimated for this trait (Table 3). Salam *et al.,* (2017) also reported moderate GCV and PCV values for this trait. Very low genotypic, phenotypic and environmental variance (0.42, 0.50 and 0.08 respectively), moderate GCV and PVC (16.89 % and 18.36 % respectively) had observed for 1000 seed weight (Table 3). Yield

plant[-1] also exhibited low genotypic, phenotypic and environmental variance (1.00, 0.98 and 0.02 respectively) with moderate estimates of PCV (19.17%), low GCV (18.92%) (Table 3). Low environmental influences focused on additive gene effects. Aktar *et al.* (2019) and Rout *et al.,* 2019; also reported less environmental influences for these traits.

Heritability and genetic advance

Days to 50% flowering and 80% maturity showed high heritability (99.89 % and 99.92 % respectively) with high genetic advance (20.22 % and 20.99 % respectively) and high genetic gain (41.40 % and 23.36 % respectively) (Fig. 1). High heritability and high genetic advance and gain indicating that this trait was under additive gene control and selection for genetic improvement for these traits would be effective. Sikarwar *et al.,* (2017), Salam *et al.,* (2017), Singh *et al.,* (2018), Aktar *et al.,* (2019) and Gupta *et al.,* (2019) also observed similar result. High heritability (98.55%) coupled with high genetic advance (53.99 %) and genetic gain (51.53 %) had estimated for this trait (Fig. 1). High heritability coupled with high genetic advance and high genetic gain implied that this trait had governed by additive gene action and selection might be effective for further genetic improvement of this trait. Similar result had observed by Bibi *et al.,* (2016), Salam *et al.,* (2017), Singh *et al.,* (2018) and Gupta *et al.,* (2019) for plant height. Low heritability 28.49 % with low genetic advance (0.70%) and low genetic gain 9.50% had estimated for number of primary branches plant[-1] that indicated non-additive gene effects and selection might be ineffective for this trait. The result agreed with Mekonnen *et al.,* (2014) but did not matched with Naznin *et al.,* (2015), Sikarwar *et al.,* (2017) and Rout *et al.,* (2019) who studied high heritability with high genetic advance for number of primary branches plant[-1]. While for number of secondary branches plant[-1], high heritability 92.02 % with low genetic advance (7.47%) and very high genetic gain 188.43% were estimated (Fig.1).
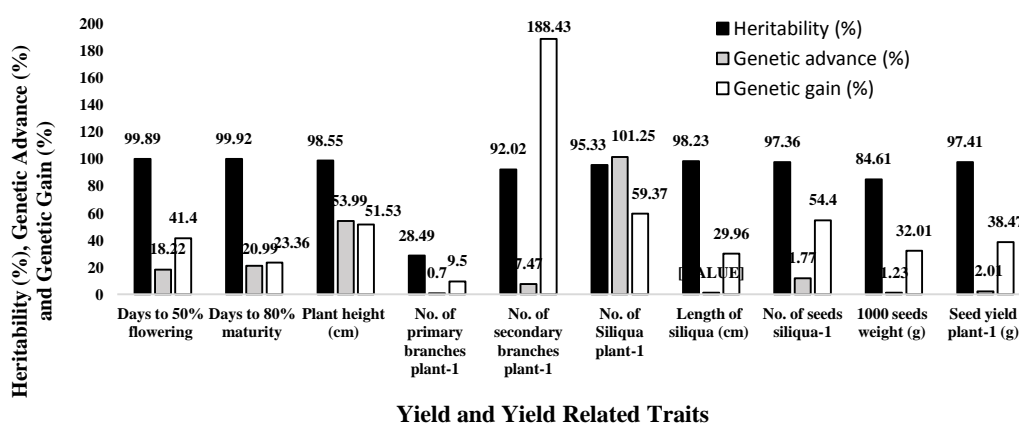

Fig. 1. Heritability, genetic advance and genetic gain for yield and yield related traits of *B. rapa* genotype

Which reflected non-additive gene action, as high estimates of heritability and low genetic advance had found. The result agreed with Khan *et al.*(2013) but did not matched with Sikarwar *et al.* (2017), Singh *et al.* (2018), Gupta *et al.*(2019) and Rout *et al.*(2019) who studied high heritability with high genetic advance for number of secondary branches plant[-1].Therefore, selection might be ineffective for this trait. High heritability (95.33%) with very high genetic advance (101.25%) and high genetic gain (59.37%) had estimated for number of siliqua plant[-1] (Fig. 1). Which indicated selection for this trait could be useful for future breeding program due to prevalence of additive gene action. The result of the present study supported by Sikarwar *et al.*, 2017; Rauf and Rahim (2018), Aktar *et al*., 2019; Gupta *et al.,* 2019; and Rout *et al.*, 2019). High heritability (97.36%), moderate genetic advance (11.77%) and high genetic gain (54.40%) had recorded for number of seeds siliqua[-1] indicated presence of additive gene effects and hence the selection might be effective for seeds siliqua[-1]. Sikarwar *et al.*, 2017; Aktar *et al*., 2019; Gupta *et al.,* 2019; and Rout *et al.,*2019; also estimated similar result for this trait. While high heritability (98.23%) with low genetic advance (1.10%) and high genetic gain (29.96%) had observed for siliqua length (Fig. 1).High heritability estimates with high genetic gain speculate the presence of additive gene effects but very low genetic advance with high heritability indicated that high heritability occurs due to environmental effects, so, selection for genetic improvement of this trait would be ineffective. Khan *et al.,* 2013; also found similar results for siliqua length but Bibi *et al.,* (2016), Salam *et al.,* 2017; Sikarwar *et al.,* 2017; and Singh *et al.,* 2017; reported high heritability estimates with high genetic gain for this trait. High heritability (84.61%), low genetic advance (1.23%) and high genetic gain (32.01%) had observed for 1000 seed weight while seed yield plant[-1] also exhibited high heritability (97.40%), low genetic advance (2.01) and high genetic gain (38.47%) (Fig.1). High heritability with high genetic gain focused on additive gene effects but very low genetic advance with high heritability indicated that high heritability occurs due to environmental effects, so, selection for genetic improvement of these traits would be ineffective for future breeding program. The result of the present study matched with Khan *et al.,* 2013; while Yared and Misteru (2016), Salam *et al.,* 2017; Singh *et al.,* 2018; Aktar *et al*., 2019; and Rout *et al.,* 2019; reported high heritability with high genetic advance for these traits.

Conclusion

Significant variations were observed among the genotypes for all the studied traits. All the characters except plant height, number of siliqua plant[-1] showed least difference between genotypic and phenotypic variances, which indicated low environmental influence on those characters. Hence, selection will be beneficial for those traits. The high genotypic and phenotypic coefficient of variation were observed for number of secondary branches plant[-1], number of siliqua plant[-1], plant height and number of seeds siliqua[-1] indicated these characters could be improved by phenotypic selection. High heritability coupled with high genetic advance and genetic gain had observed for days to 80% maturity, plant height and number of siliqua plant[-1] indicated selection for these traits could be useful for future breeding program due to prevalence of additive gene action. While high heritability coupled with low genetic advance and high genetic gain were observed for number of primary branches plant[-1], number of secondary

branches plant[-1], length of siliqua, 1000 seed weight and seed yield plant[-1] indicated that, high heritability occurs due to environmental effects, so, selection for genetic improvement of these traits would be ineffective. However, high heritability coupled with moderate genetic advance and high genetic gain were estimated for days to 50% flowering and number of seeds siliqua[-1] indicated medium possibility of selection.

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Conflicts of Interest

The authors declare no conflicts of interest regarding publication of this paper.

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