



## Research Article

### Genetic variability and character association of Bangladeshi popular varieties of mustard (*Brassica rapa* L.)

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#### ARTICLE INFO

##### Article History

Received: 12 August 2020

Revised: 12 October 2020

Accepted: 21 October 2020

**Keywords:** Variability, Heritability, Genetic advance, Correlation, Path Coefficient, *Brassica rapa*

#### ABSTRACT

A study was conducted to estimate genetic variability, correlation and direct and indirect effects of yield attributes on seed yield of fourteen Bangladeshi varieties of *Brassica rapa*. High heritability coupled with high genetic advance was recorded in a number of secondary branches plant<sup>-1</sup>, a number of siliqua plant<sup>-1</sup> and a number of seeds siliqua<sup>-1</sup> indicating the effects of additive genes in controlling the traits. Significant and positive association with seed yield plant<sup>-1</sup> were observed in the number of primary branches plant<sup>-1</sup>, a number of seeds siliqua<sup>-1</sup>, while a negative association was found in days to maturity. The path analysis revealed that the days to first flowering, number of secondary branches plant<sup>-1</sup> and 1000 seed weight were the main contributors to seed yield. The results suggest that days to first flowering, number of primary and secondary branches plant<sup>-1</sup> and 1000 seed weight may be considered for selection to improve the seed yield in *B. rapa*.

#### Introduction

*Brassica rapa* is the most popular and major oilseed crop in Bangladesh. The oil crop covers about 70% of the total oilseed crops acreage in Bangladesh, contributing the lion's share to the total edible oil production in Bangladesh. Being a short duration crop compared to other *Brassica* spp (*Brassic napus* and *Brassicajuncea*), *B. rapa* fits well into the cropping patterns, e.g, T. Aman Rice-Mustard-Boro Rice or T. Aman Rice-Mustard-Maize (Karim et al., 2014). The crop occupies the first position among the oilseed crops in Bangladesh with a cultivated area of 7,87,025 acres, which

produces 3,61,909 metric tonnes of oilseed during 2015-2016 (BBS, 2016).

Bangladesh is self-sufficient in the production of cereal crops; however, the scenario of oilseed production of the country is very discontented. According to MPOC (2019), the consumption of edible oil and fat is about 3 million tonnes. Due to insufficient domestic production, almost 90% of these annual requirements of oils and fats are met through import. USDA (2019) reports that Bangladesh spent Tk. 14,448 crore in the fiscal year 2017-18 for importing both soybean and palm oil to meet the domestic requirement.

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Therefore, to fulfill the edible oil's requirements, the country needs to increase the acreage of oilseed crops with high yielding modern varieties using modern agronomic practices. However, there is limited scope to increase acreage due to pressure of other rabi season crops and also limited scope to increase the yield ha<sup>-1</sup>, because farmers usually cultivate the existing low yielding mustard varieties with low inputs and management. Short duration variety like Tori-7 of *Brassica rapa* is still popular in Bangladesh because it can fit well into the T. Aman rice – Mustard - Boro rice cropping pattern. Unfortunately, to date, there is no improved short duration variety of *B. rapa* available to replace Tori-7. However, farmers are being advised to cultivate the improved Tori and BARI Shorisha 14 and BARI Shorisha 15 varieties to replace the Tori-7 local cultivar. The above scenario indicates there should be an attempt to develop short duration and high yielding mustard varieties with more oil percentage in seeds to fulfill the requirement of edible oils of the country through increasing productivity.

For a successful breeding program, analysis of genetic variability and the correlation among the yield and its contributing traits would be of great importance (Mary and Gopalan, 2006). Development of high-yielding variety requires knowledge of the existing genetic variability (genetic and environmental) with respect to yield and its components along with quality traits. Nevertheless, estimates of heritability in conjunction with genetic advances, the change in mean value among successive generations should also be considered (Sikarwar et al.,

2017). Seed yield is a complex character that is determined by several components reflecting positive-negative and direct-indirect effects (Marjanovic-Jeromela et al., 2008). So, determination of correlation coefficients and path analysis are important biometrical procedures to evaluate breeding materials for the improvement of yield (Pal et al., 2019). The objectives of the present investigation were to study the variability and nature of gene actions governing the yield and components as well as the nature and degree of association among the traits, direct and indirect relation with the yield contributing characters.

#### **Materials and Methods**

The plant materials of the present study consisted of fourteen varieties of *Brassica rapa* commonly found in Bangladesh (Table 1), which were collected from Plant Genetic Resources Centre (PGRC) of Bangladesh Agricultural Research Institute (BARI), Bangladesh Institute Nuclear Agriculture (BINA) and local farmers from Manikgonj, district of Bangladesh. The field experiment was conducted at the research field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The experiment was laid out in a randomized complete block design (RCBD) manner with three replicates. The total experimental area was 200 m<sup>2</sup>. The varieties were randomly distributed to each replication. Seeds of the fourteen varieties were sown using the solid line sowing method on 17 November 2016, maintaining the spacing of 30 cm × 8cm in a separate block for each variety. Variety to variety distance in each replication was maintained at 50 cm. All the recommended agronomic

**Table 1. Mustard (*B. rapa*) varieties used in the experiment.**

Symbol	Varieties	Source
G1	Tori-7	BARI
G2	BARI sarisha-3	BARI
G3	Sonali sarisha	BARI
G4	BARI sarisha-6	BARI
G5	BARI sarisha-9	BARI
G6	BARI sarisha-12	BARI
G7	BARI sarisha-14	BARI
G8	BARI sarisha-15	BARI
G9	BARI sarisha-17	BARI
G10	Improved Tori	BARI
G11	Sonali Tori	BARI
G12	Torsha	BARI
G13	Maghi	Local (Manikgonj)
G14	BINA sarisha-10	BINA

package of practices was followed (weeding, thinning staking, irrigation, drainage, etc.) as recommended for commercial mustard production following BARI's, 2018. Malathion-57 EC @ 2mL/liter with Rovral 50WP under Iprodione group @ 2g/liter of water was applied for controlling the Aphid and Alternaria leaf spot infections.

The crop was harvested at different dates according to maturity when 80% of the plants showed signs of maturity. Ten plants of each variety were selected randomly to record data on eleven characters *viz.* plant height (cm), number of primary branches plant<sup>-1</sup>, number of secondary branches plant<sup>-1</sup>, days to 1<sup>st</sup> flowering, days to 50% flowering, days to maturity, number of siliqua plant<sup>-1</sup>, siliquae

length (cm), number of seeds siliqua<sup>-1</sup>, 1000-seed weight (g) and seed yield plant<sup>-1</sup> (g).

The analysis of variance for different characters was carried out using mean data to assess the genetic variability among varieties following the method of Cochran and Cox (1957). The level of significance was tested at 5% and 1% using the F test. Estimation of genotypic and phenotypic variance, heritability, genetic advance, and genetic advance in percent of mean was made according to Johnson et al. (1955). The genotypic and phenotypic correlation coefficient and path co-efficient were measured according to Dewey and Lu (1959). The heat maps were created using the online heat mapper tool ([www.heatmapper.ca](http://www.heatmapper.ca)).

## Results and Discussion

The mean values over three replications with maximum and minimum values of eleven phenotypic characters of fourteen mustard varieties (*B. rapa*) are presented in Table 2. Analysis of variance of the eleven characters of fourteen mustard varieties revealed highly significant variations among the varieties for all the traits (Table 2). Days to first flowering and 50% flowering varied significantly, ranging from 22 to 38 and 26 to 43 days after sowing (DAS), respectively. The number of days to maturity varied from 79 to 92 days. Significant variations were also observed in plant height, number of primary and secondary branches plant<sup>-1</sup>, which ranged from 76.03 to 107.13 cm; 3.98 to 6.57 and 1.0 to 9.2, respectively. Interestingly, a considerable variation was observed in the siliqua plant<sup>-1</sup>, which varied from 50.17 to 181.87. Notable variation was also observed in seed yield plant<sup>-1</sup>,

which were recorded to range from 3.9 to 9.09 g. The results also indicated that the varieties were genetically quite different from each other and could be used as valuable germplasms for creating variations and novel recombination for further improvement of *B. rapa*.

The genotypic variations are due to genetic factors and their interactions with the surrounding environmental factors, while the phenotypic variance is the cumulative effect of genotypic and environmental variances (Shompa et al., 2020). In our study, we estimated the coefficient of variations in the phenotypic (PCV), genotypic (GCV) and environmental (ECV) aspects of eleven characters of all the varieties (Table 2, Figure 1A). In the present study, higher (>20%), moderate (10-20%), and low (< 10%) PCV and GCV were observed in different traits. The high PCV and GCV were found in the number of secondary branches plant<sup>-1</sup> (NSB), number of siliqua plant<sup>-1</sup> (NSP), number of seeds siliqua<sup>-1</sup> (NSS) and seed yield plant<sup>-1</sup> (SYP) (Figure 1A), while days to first flowering (DFF), days to 50% flowering (D50% F), plant height (PH), number of primary branches plant<sup>-1</sup> (NPB) and 1000-seed weight (TSW) showed moderate PCV and GCV. On the other hand, days to maturity (DM) and siliqua length (LS) showed low (<10%) PCV and GCV. These findings of the present investigation are in agreement with those of Aktar et al. (2019), Meena et al. (2017) and Gupta et al. (2019).

Again, that the PCV was higher or slightly higher than the GCV of all the characters (Fig. 1A), suggests that considerable environmental

influences exist on the expression of genes controlling these traits. The slightly higher PCV values indicate that the characters are largely controlled by genetic factors and less influenced by environmental factors. This emphasizes the need for direct selection for the effective improvement of all traits studied. On the other hand, a higher difference between PCV and GCV indicates that the characters are highly influenced by the environment (Gupta et al., 2019; Sikarwar et al., 2017). In which case, direct selection may not be effective for crop improvement.

Estimation of heritability ( $h^2$ ) coupled with genetic advance (GA), is considered as an important index in the selection of traits in a breeding program (Gupta et al., 2019). High heritability, coupled with high GA, is considered as right selection criteria. In the present experiment, high heritability, coupled with high GA in the percentage of the mean was observed in the number of secondary branches plant<sup>-1</sup> (65.03, 95.92), number of siliqua plant<sup>-1</sup> (57.92, 46.79), number of seeds siliqua<sup>-1</sup> (87.69, 67.93), while high heritability and moderate GA in the percentage of the mean were observed in 1000-seed weight (93.12, 5.7) and seed yield plant<sup>-1</sup> (62.02, 31.55) (Figure 1B). The high heritability coupled with high GA in the number of secondary branches plant<sup>-1</sup>, number of siliqua plant<sup>-1</sup>, number of seeds siliqua<sup>-1</sup> are probably due to the effect of additive gene action for the expression of these traits, indicating that direct selection based upon these characters would be effective for genetic improvement of the traits (Manjunath et al., 2017). On the contrary, high heritability and moderate GA

**Table 2. Estimation of mean performance in terms of eleven parameters of *Brassica rapa* varieties.**

Parameters	Range		Mean	CV(%)	SD	MSS	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$
	Max.	Min.							
Days to First flowering	22.00	38.00	28.98	4.80	1.39	83.40**	29.32	27.15	1.97
Days to 50% flowering	26.67	43.00	33.24	5.89	1.96	91.20**	32.96	29.12	3.83
Days to maturity	79.00	92.00	85.00	2.68	2.27	40.00**	16.78	11.61	5.17
Plant height (cm)	76.03	107.13	91.41	5.65	5.16	325.03**	126.12	99.46	26.66
Primary branches plant <sup>-1</sup>	3.98	6.57	5.20	17.99	0.94	1.71 <sup>ns</sup>	1.16	0.28	0.87
Secondary branches plant <sup>-1</sup>	1.00	9.20	5.37	42.35	2.27	33.99**	14.78	9.61	5.17
Siliqua plant <sup>-1</sup>	50.17	181.87	130.32	25.44	33.15	5636.22**	2611.26	1512.48	1098.77
Length of siliqua (cm)	4.86	6.01	5.22	5.89	0.31	0.40**	0.20	0.10	0.09
Seeds siliqua <sup>-1</sup>	12.33	34.60	19.45	13.19	2.57	147.26**	53.48	46.89	6.58
1000 seed weight (g)	2.20	3.83	2.99	3.51	0.11	0.45**	0.16	0.15	0.01
Seed yield plant <sup>-1</sup> (g)	3.90	9.09	6.62	15.22	1.01	5.99**	2.68	1.66	1.02

\*\*and 'ns' indicate significant at 1% level and non-significant, respectively.

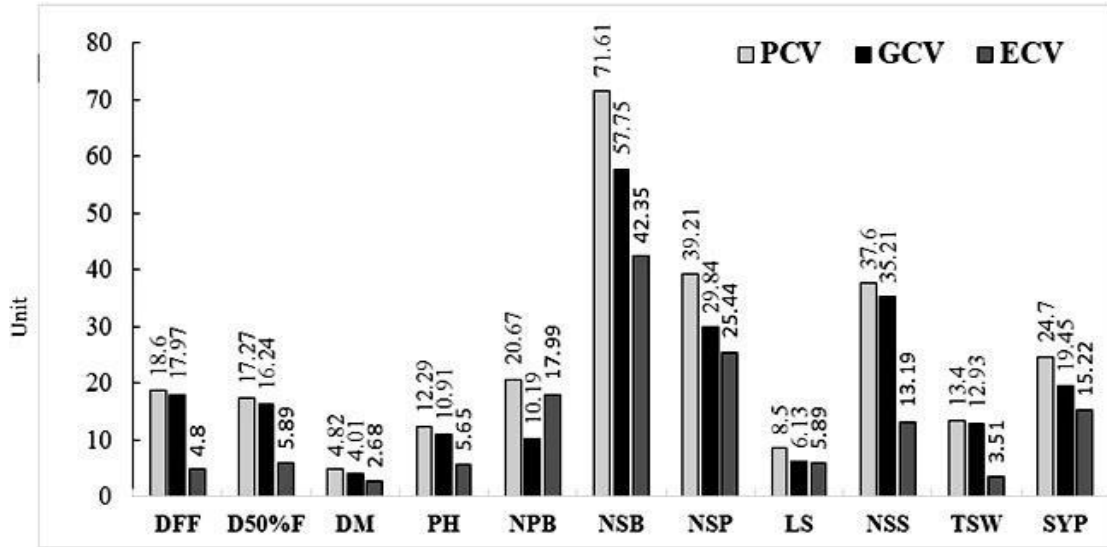
MSS,  $\sigma^2_p$ ,  $\sigma^2_g$ , the and  $\sigma^2_e$  indicate the mean sum of the square, phenotypic, genotypic, and environmental, variance respectively.

in 1000-seed weight and seed yield plant<sup>-1</sup> could be due to the effects of both additive and interactions of additive x additive, additive x dominance, or additive x recessive gene interaction effects. This genetic phenomenon states that the traits are controlled by interactions of genes, and non-additive effects govern these traits proving that direct selection for such characters would be less effective for the improvement of 1000-seed weight and seed yield plant<sup>-1</sup>.

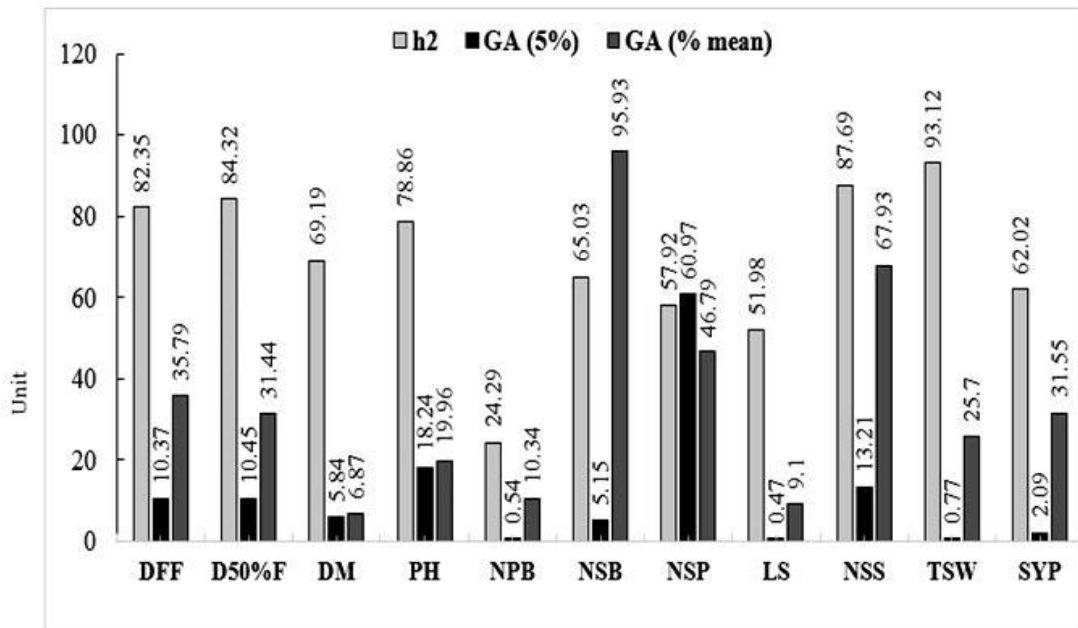
Pal et al. (2019) and Sikarwar et al. (2017) reported that days to first and 50% flowering had high percentage of the mean.

In two other studies, Naznin et al. (2015) and Bind et al. (2014) found high heritability coupled with the high genetic advance in days to maturity, number of the secondary branches plant<sup>-1</sup> and number of seeds siliqua<sup>-1</sup> in mustard. Mekonnen et al. (2014) reported that pods plant<sup>-1</sup> had high heritability with moderately genetic advances, while Aktar et al. (2019) found high heritability with a low genetic advance in percent of the mean for days to maturity, and selection for such trait might not be rewarding.

A



B



**Fig. 1. Estimation of genetic variability in eleven parameters of fourteen *Brassica rapa* varieties:**  
**A)** phenotypic (PCV), genotypic (GCV) and environmental (ECV) co-efficient of variation;  
**B)** heritability (h<sup>2</sup>), genetic advance (GA), and genetic advance in percent of the mean (GA%).

Information on character associations helps identify the correlated characters with yield and determine the extent and nature of the relationship among the yield attributes. Hence, to identify the most correlated traits with seed yield in the mustard varieties, we estimated genotypic and phenotypic correlation coefficients among 11 characters presented in Table 3 and Figure 2. In most instances, there was a close agreement between genetic correlations and phenotypic correlations. The genotypic correlations were higher than phenotypic correlations for the studied traits. Seed yield plant<sup>-1</sup> had a positive correlation with days to first flowering, days to 50% flowering, plant height, number of primary branches plant<sup>-1</sup>, number of secondary branches plant<sup>-1</sup>, number of seeds siliqua<sup>-1</sup>, and 1000-seed weight. However, a significant and positive correlation coefficient was observed only with the number of primary branches plant<sup>-1</sup> (0.34, 0.531), a number of seeds siliqua<sup>-1</sup> (0.468, 0.419) at both genotypic and phenotypic levels. Similar reports on a positive correlation of seed yield plant<sup>-1</sup> were found with days to 50% flowering, plant height, number of primary branches plant<sup>-1</sup>, number of secondary branches plant<sup>-1</sup>, number of seeds siliqua<sup>-1</sup> and 1000-seed weight (Begum et al., 2018; Uddin et al., 2013; Malek et al., 2000).

Interestingly, days to maturity, number of siliqua plant<sup>-1</sup>, and length of siliqua were negatively correlated with seed yield plant<sup>-1</sup>, but among the traits, only days to maturity (-0.601) were significantly and negatively associated with seed yield plant<sup>-1</sup> (Table 3). In contrast to our results, Pal et al. (2019) and Begum et al. (2018) reported a positive association of seed yield plant<sup>-1</sup> with days to

maturity in mustard. In general, the early maturity trait reduces the yield potential in the mustard crop.

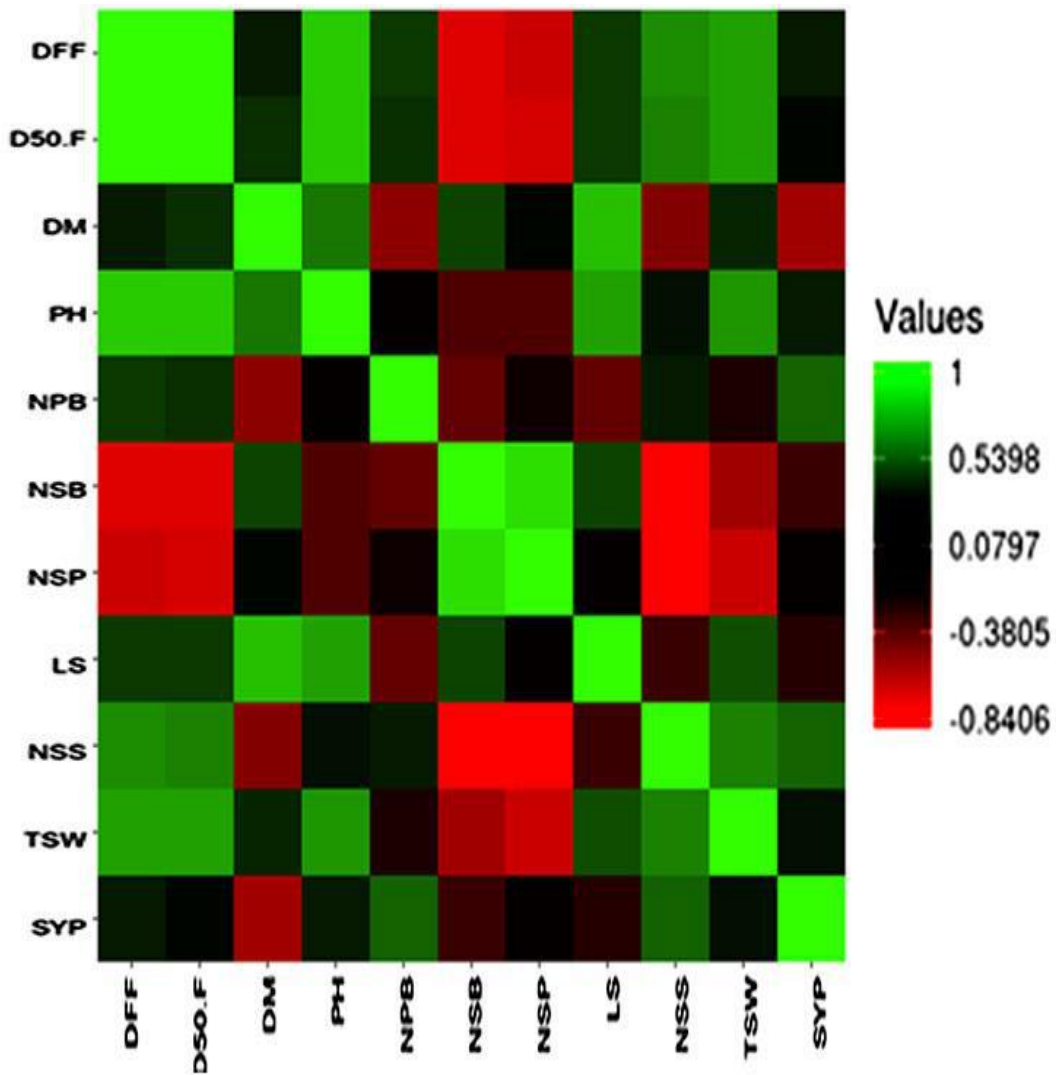
Our results of the character association study elucidate that the number of primary branches plant<sup>-1</sup> and number of seeds siliqua<sup>-1</sup> might be the most important yield attributes in *Brassica rapa* as these traits had a strong and positive association with seed yield, necessitating improvement of seed yield through a selection of these traits. On the other hand, a significant negative association between days of maturity and seed yield plant<sup>-1</sup> inferred that early maturity would decrease the seed yield performance in the mustard crop, while an increase of days to maturity would increase the seed yield performance. Therefore, based on the correlation study, it could be suggested that selection should be made based upon the characters that are positively and significantly associated with yield. If a positive correlation exists, simultaneous improvement is possible through single selections, in contrast, when a negative correlation exists, it would be challenging to exercise simultaneous selection of the characters (Newell and Eberhart, 1961).

Simple correlation does not consider the complex, direct, and indirect relationships between the various traits related to the dependent variables. So, to get a clear picture of the interrelationship between seed yield and other yield contributing characters, direct and indirect effects, we calculated the path analysis (Table 4). The results of the present investigation on path coefficient analysis revealed that days to first flowering (6.314), number of secondary branches plant<sup>-1</sup> (1.916), and 1000 seed weight (0.18) had

**Table 3. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for fourteen varieties of *Brassica rapa*.**

Traits		DEF	D50%F	DM	PH	NPB	NSB	NSP	LS	NSS	TSW
<b>D50% F</b>	G	0.999 <sup>**</sup>									
	P	0.927 <sup>**</sup>									
<b>DM</b>	G	0.159	0.250								
	P	0.196	0.240								
<b>pH</b>	G	0.847 <sup>**</sup>	0.839 <sup>**</sup>	0.524 <sup>**</sup>							
	P	0.724 <sup>**</sup>	0.722 <sup>**</sup>	0.445 <sup>**</sup>							
<b>NPB</b>	G	0.333 <sup>*</sup>	0.290	-0.742 <sup>**</sup>	-0.060						
	P	0.233	0.203	-0.175	0.205						
<b>NSB</b>	G	-0.787 <sup>**</sup>	-0.840 <sup>**</sup>	0.366 <sup>*</sup>	-0.238	-0.576 <sup>**</sup>					
	P	-0.586 <sup>**</sup>	-0.498 <sup>**</sup>	0.289	-0.097	-0.052					
<b>NSP</b>	G	-0.752 <sup>**</sup>	-0.793 <sup>**</sup>	0.077	-0.317 <sup>*</sup>	-0.335 <sup>*</sup>	0.953 <sup>**</sup>				
	P	-0.510 <sup>**</sup>	-0.488 <sup>**</sup>	0.120	-0.070	0.278	0.805 <sup>**</sup>				
<b>LS</b>	G	0.319 <sup>*</sup>	0.314 <sup>*</sup>	1.017 <sup>**</sup>	0.813 <sup>**</sup>	-0.404 <sup>**</sup>	0.393 <sup>*</sup>	0.065			
	P	0.206	0.258	0.492 <sup>**</sup>	0.429 <sup>**</sup>	-0.199	0.219	0.020			
<b>NSS</b>	G	0.584 <sup>**</sup>	0.545 <sup>**</sup>	-0.435 <sup>**</sup>	0.156	0.209	-0.948 <sup>**</sup>	-0.970 <sup>**</sup>	-0.170		
	P	0.548 <sup>**</sup>	0.522 <sup>**</sup>	-0.342 <sup>*</sup>	0.137	0.178	-0.666 <sup>**</sup>	-0.667 <sup>**</sup>	-0.082		
<b>TSW</b>	G	0.665 <sup>**</sup>	0.684 <sup>**</sup>	0.187	0.633 <sup>**</sup>	-0.031	-0.521 <sup>**</sup>	-0.703 <sup>**</sup>	0.418 <sup>**</sup>	0.584 <sup>**</sup>	
	P	0.625 <sup>**</sup>	0.627 <sup>**</sup>	0.198	0.549 <sup>**</sup>	0.019	-0.433 <sup>**</sup>	-0.525 <sup>**</sup>	0.259	0.502 <sup>**</sup>	
<b>SYP</b>	G	0.165	0.074	-0.601 <sup>**</sup>	0.154	0.340 <sup>*</sup>	0.240	-0.109	-0.068	0.468 <sup>**</sup>	0.155
	P	0.165	0.148	-0.325 <sup>*</sup>	0.199	0.531 <sup>**</sup>	0.033	0.256	-0.022	0.419 <sup>**</sup>	0.152





**Fig. 2. Correlation matrix showing correlation between different traits of mustard.**

The green and red colors in the legend indicate highest and lowest values, respectively. DFF= days to first flowering, D50%F= days to 50% flowering, DM= days to maturity, PH= plant height (cm), NPB= no. of primary branches per plant, NSB= no. of secondary branches per plan, NSP= no. of siliqua per plant, LS= length of siliqua (cm), NSS= no. of seeds per siliqua, TSW=1000 seed weight (g), SYP= seed yield per plant (g).

**Table 4. Partitioning of genotypic correlations into direct (bold) and indirect effects on eleven parameters for fourteen varieties of *Brassica rapa* by path analysis.**

Trait	DFE	D50%F	DM	PH	NPB	NSB	NSP	LS	NSS	TSW	r <sub>g</sub> with yield
<b>DFE</b>	<b>6314</b>	-4.506	-0.065	-0.623	-0.066	-1.509	0.696	-0.158	-0.026	0.11	0.165
<b>D50%F</b>	6311	<b>-4.512</b>	-0.103	-0.618	-0.057	-1.611	0.734	-0.155	-0.024	0.11	0.074
<b>DM</b>	1.004	-1.128	<b>-0.416</b>	-0.386	0.146	0.702	-0.071	-0.503	0.019	0.03	-0.601**
<b>PH</b>	5.350	-3.785	-0.215	<b>-0.735</b>	0.012	-0.456	0.293	-0.402	-0.007	0.10	0.154
<b>NPB</b>	2.104	-1.308	0.305	0.044	<b>-0.198</b>	-1.105	0.310	0.200	-0.009	-0.01	0.340*
<b>NSB</b>	-4.971	3.789	-0.150	0.175	0.113	<b>1.916</b>	-0.882	-0.195	0.042	-0.08	0.240
<b>NSP</b>	-4.750	3.577	-0.032	0.233	0.066	1.828	<b>-0.926</b>	-0.032	0.043	-0.11	-0.109
<b>LS</b>	2.015	-1.416	-0.418	-0.598	0.080	0.754	-0.060	<b>-0.494</b>	0.007	0.07	-0.068
<b>NSS</b>	3.689	-2.458	0.179	-0.115	-0.041	-1.818	0.897	0.084	<b>-0.047</b>	0.09	0.468**
<b>TSW</b>	4.20	-3.09	-0.08	-0.47	0.01	-1.00	0.65	-0.21	-0.03	<b>0.18</b>	0.155

\*\* and \* indicates significant at 1% and 5%, respectively. Residual effect: **0.302**.

DFE= days to First flowering, D50%F= days to 50% flowering, DM= days to maturity, PH= plant height (cm), NPB= no. of primary branches per plant, NSB= no. of secondary branches per plan, NSP= no. of siliqua per plant, LS= length of siliqua (cm), NSS= no. of seeds per siliqua, TSW=1000 seed weight (g), SYP= seed yield per plant (g).

a highly-positive and direct effect on seed yield plant<sup>-1</sup>. On the other hand, direct and negative effects on seed yield plant<sup>-1</sup> were contributed through days to 50% flowering (- 4.512), days to

maturity (- 0.416), plant height (- 0.735), number of primary branches plant<sup>-1</sup> (- 0.198), number of siliqua plant<sup>-1</sup> (- 0.926), siliqua length (- 0.494) and number of seeds siliqua<sup>-1</sup> (- 0.047) (Table 4).

The direct relationship between first flowering and seed yield plant<sup>-1</sup> indicates that an early flowering variety usually has higher seed yield than a late flowering variety, so selection based on this character would increase the yield in *B. rapa*. Again, the number of secondary branches and seed yield plant<sup>-1</sup> had a positive direct relationship (Table 4), but the correlation between the traits was negative and non-significant (Table 3), suggesting that seed yield plant<sup>-1</sup> could be improved through direct selection of secondary branches plant<sup>-1</sup>, reducing the undesired indirect effects. Pal et al. (2019) observed that the number of secondary branches plant<sup>-1</sup> and siliquae plant<sup>-1</sup> had the highest direct effect on seed yield plant<sup>-1</sup>. Again, the trait, 1000-seed weight, was found to have a positive direct effect (0.18) on yield plant<sup>-1</sup> (Table 4). The value of the direct effect of the trait was very close to the correlation coefficient (0.155) (Table 3). This result suggests that selection could be made based upon this trait for yield improvement in *B. rapa*. Naznin et al. (2015) and Belete (2011) also found that thousand seed weight had a positive direct effect on seed yield plant<sup>-1</sup>.

The magnitude of 'residual effect' (0.302) (Table 4) indicates that traits included in the path analysis explained about 70% of the variation in seed yield. However, the remaining variation in seed yield (30%) can be attained by incorporating other yield-related contributing traits in the path analysis as far as studies involving the association of traits are concerned. Rauf and Rahim (2018) reported a residual value of 0.211 in *B. napus*.

## Conclusion

Based on the present study, the traits *viz.* number of primary branches plant<sup>-1</sup>, number of secondary branches plant<sup>-1</sup>, number of siliqua plant<sup>-1</sup>, number of seeds siliqua<sup>-1</sup> and 1000-seed weight might be selected for selection indices as these traits were seen to be less affected by environmental factors and had high heritability coupled with genetic advances. Moreover, the present findings suggest that days to first flowering, number of secondary branches plant<sup>-1</sup> and 1000 seed weight could be selected as important characters for seed yield improvement in *Brassica rapa* as these traits were found to be directly and strongly associated with seed yield trait.

## Acknowledgment

The authors duly acknowledge the Ministry of Science and Technology, GoB for providing the research grant, and Sher-e-Bangla Agricultural University for providing the research field to conduct the study.

## Conflicts of Interest

The authors have no competing interests

## References

- Aktar T, Nuruzzaman M, Rana MS, Huda MM, Hossain MM and Hassan L. Genetic parameters and diversity studies of yield and yield contributing characters in brassica genotypes. *J. Bangladesh Agril. Univ.* 2019; 17(3): 295-300.
- Bangladesh Agricultural Research Institute (BARI). Annual Report 2017-2018, Bangladesh Agricultural Research Institute. Gazipur, Bangladesh, 2018.

- Bangladesh Bureau of Statistics (BBS). Annual Agricultural Statistics 2015-16, Bangladesh Bureau of Statistics. Statistic Division, Ministry of Planning, Dhaka, Bangladesh, 2016.
- Begum MM, Uddin ME, Sezanur S, Hossain MS, Rahman RF, Rezanur MR and Faruquee HM. Genetic variation, character association and genetic divergence analysis among mustard (*Brassica spp.* L.) in Bangladesh. *Biotechnol. Res.* 2018;4(1):40-47.
- Belete YS. Genetic variability, correlation and path analysis studies in Ethiopian mustard (*Brassica carinata* A. Brun) genotypes. *Intl. J. Plant Breed. Genet.* 2011; 5(4): 328-338.
- Bind D, Singh D and Dwivedi VK. Genetic variability and character association in Indian mustard [*Brassica juncea* (L) Czerns & Coss.]. *Agric. Sci. Digest.* 2014; 34(3): 183-188.
- Cochran WG and Cox GM. Experimental design. New York. John Wiley & Sons, 1957; 546- 568.
- Dewey DR and Lu HK. A correlation and path coefficient analysis of components of creasted wheat grass and seed production. *Agron. J.* 1959; 51: 515- 518.
- Gupta MC, Roy HS and Bhadauria SS. Genetic variability analysis in F2/F3 population derived through inter-specific hybridization in oilseed Brassica. *Elect. J. Plant Breed.* 2019; 10(3): 1275-1282.
- Johnson HW, Robinson HF and Comstock RE. Estimation of genetic and environmental variability in soybean. *Agron. J.* 1955; 47: 314-318.
- Karim MM, Siddika A, Tonu NN, Hossain DM, Meah MB, Kawanabe T, Fujimoto R and Okazaki K. Production of high yield short duration *Brassica napus* by interspecific hybridization between *B. oleracea* and *B. rapa*. *Breed. Sci.* 2014; 63(5): 495-502.
- Malek, MA, Das, ML and Rahman A. Genetic variability, character association and path analysis in rapeseed. *Bangladesh J. Agril. Sci.* 2000; 27(1): 25-59.
- Marjanovic-Jeromela A, Marinkovic R, Mijic A, Zdunic Z, Ivanovska S and Jankulovska M. Correlation and path analysis of quantitative traits in winter rapeseed (*Brassica napus* L.). *Agric. Conspec. Sci.* 2008; 73(1): 13-18.
- Mary SS and Gopalan A. Dissection of genetic attributes yield traits of fodder cowpea in F3 and F4. *J. Appl. Sci. Res.* 2006; 2: 805-808.
- Manjunath H, Phogat DS, Kumari P and Singh D. Genetic analysis of seed yield and yield attributes in Indian mustard (*Brassica juncea* (L.) Czern and Coss.). *Electronic J. Plant Breed.* 2017; 8(1):182-186.
- Meena HS, Kumar A, Singh VV, Meena PD, Ram B and Kulshrestha S. Genetic variability and inter-relation of seed yield with contributing traits in Indian mustard (*Brassica juncea*). *J. Oilseed Brassica*, 2017; 8(2): 131-137.
- Mekonnen TW, Wakjira A and Genet T. Correlation and path coefficient analysis among yield component traits of Ethiopian mustard (*Brassica carinata* a. Brun) at Adet, Northwestern, Ethiopia. *J. Plant Sci.* 2014; 2(2): 89-96.
- MPOC, Malaysian Palm Oil Council. Oils and Fats Market Scenario of Bangladesh. Wisma Sawit, Jalan Perbandaran, Kelana Jaya, Selangor Darul Ehsan, Malaysia, 2019.

- Naznin S, Kawochar MA, Sultana S and Bhuiyan MSR. Genetic variability, character association and path analysis in *Brassica rapa* l. genotypes. *Bangladesh J. Agril. Res.* 2015; 40(2): 305-323.
- Newell LC and Eberhart SA. Clone and progeny evaluation in the improvement switchgrass, *Panicum Virgatum* L. *Crop Sci.* 1961; 51(10): 613-616.
- Pal S, Dubey N, Avinash H, Khan SJ and Reddy JP. Estimation of genetic variability, correlation and path analysis for yield and yield contributing characters in Indian mustard (*Brassica juncea* L.). *J. Pharmacog. Phytochem.* 2019; sup. 1: 102-105.
- Rauf MA and Rahim MA. Genetic variability studies among yield and its contributing traits in mustard (*Brassica napus* L.). *Adv. Zool. Bot.* 2018; 6(4): 101-108.
- Shompa BN, Fatima K, Jony M, Sarker S, Ullah MJ, Chowdhury AK and Rahman J. Selection of dwarf stature yield potential lines from F<sub>3</sub> populations of white maize (*Zea mays* L.). *J. Genet. Resour.* 2020; 6(2): 95-105.
- Sikarwar RS, Navneet Satankar N, Munesh Kumar Kushwah MK and Singh AK. Genetic variability, heritability and Genetic Advance Studies in Yellow Sarson (*Brassica rapa* var. Yellow Sarson). *Intl. J. Agric. Innova. Res.* 2017; 5(5): 2319-1473.
- Uddin, MS, Bhuiyan, MSR, Mahmud F and Kabir K. Study on correlation and path coefficient in F<sub>2</sub> progenies of rapeseed. *Acad. J. Plant Sci.* 2013; 6(1): 13-18.
- USDA, United States Department of Agriculture. Grain and Feed Annual. USDA Foreign Agricultural Service, Bangladesh, 2019.