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Genetic Variability and Trait Association for Important Agro-Morphological Traits in Advanced Populations of *Brassica Rapa* L.

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Abstract

The study was conducted at Sher-e-Bangla Agricultural University using eight advanced *Brassica rapa* L. populations to assess character variation, heritability, genetic advance, and correlations with seed yield per plant. ANOVA revealed significant variations among all populations for all the characters studied. High GCV and PCV were observed for the traits, including number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, and seed yield per plant. High heritability with high genetic advance was observed for plant height and number of siliquae per plant. Seed yield per plant showed a strong positive correlation with branches, root length, siliquae traits, and seed weight at both genotypic and phenotypic levels. Direct positive effects on per-plant seed yield were found in days to first flowering, plant height, number of siliquae per plant, and length of siliquae through path coefficient analysis. The highest per plant seed yield was observed in P3 (11.7g) followed by P4, P1, P6, and P5, with per-plant seed yields of 9.2g, 8.027g, 6.667g and 5.967g, respectively. Based on their higher per-plant yield potential and favorable combination of yield-contributing characters, five advanced populations- P3, P4, P1, P6, and P5- were selected from the eight.

Keywords: Co-efficient of variation, Genetic advance, Heritability, Path coefficient, Residual effect

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Introduction

B. rapa commonly known as field mustard or turnip mustard taxonomically belongs to the family Brassicaceae. The crop is mainly cultivated for vegetable oil production (Yellow sarson) and for vegetable purposes (Chinese cabbage). It has been traditionally cultivated from central Asia to Europe and northern America (Gomez Campo, 1999). It is the world's second most important source of edible vegetable oil (69.2 million tons) after soybean (337.9 million tons) (FAO, 2020). Vegetable oils are a high value agricultural commodity used in cooking foods and bakery products and as a renewable source of biofuels in addition to many industrial uses. They are considered a high energy food and contain a number of fat-soluble vitamins (A, D, E and K). Poor intake of fat and oil lowers the availability of' fat soluble vitamins that causes dietary imbalance and food wastage. In a balanced diet, 20-25% of calories come from fats and oils and the average body requirement of fats and oil is about 37g/day (Rahman, 1981). The seeds of *B. rapa* contain 42% oil and 25% protein (Khaleque, 1985).

Global oilseeds production in 2019/20 stood around 572.5 million tons (FAO, 2020) where rapeseed contributed 69.2 million tons (FAO, 2020). *B. rapa* is the main oil yielding species of *Brassica* genus in Bangladesh (FAO, 2017). It occupies the first position in respect of acreage and production among the oil crops cultivated in Bangladesh (Naznin *et al*., 2015). About 7,63,855 acres of land was sown to rapeseed and mustard during 2019-20 and the total oilseeds production was about 3,58,249 tons national average yield of 469 kg/acre in the country (BBS, 2021). The production is way lower as compared to the developed countries. The total utilization of oilseeds in Bangladesh was 3.0 million tons out of which 2.5 million tons was imported (FAO, 2020). In Bangladesh over 80% of total edible oil consumed in the country is imported from outside.

Due to factors including land scarcity, pressure from other crops, longer growing times, lower yields, etc., there is little possibility of mustard expansion in Bangladesh (Rashid *et al*., 2010). The Boro-Fallow-T. Aman cropping pattern is the most common crop rotation system in Bangladesh. According to Nasim *et al*. (2017), cropping patterns that involve only rice cultivation occupy approximately 51% of the net cropped area, highlighting a substantial reliance on rice-centric agriculture. As rice is their main cereal crop, farmers in Bangladesh are not willing to switch over to other cropping systems. Bangladeshi farmers can, however, grow a short-duration mustard type during this fallow season without interfering with their two main rice crops. Most farmers like to grow Tori-7 since it is a traditional Maghi Sarisha. According to Ali *et al*. (2016), Tori-7 has a shorter maturity period (81 days) and yields 10.89 g/plant. The Boro-Mustard-T. Aman cropping pattern can work effectively with Tori-7, despite its lower than ideal yield.

A selection method has been employed over several generations to develop eight advanced populations of *B. rapa* by crossing different mustard types, aiming to address the problems of low yield and longer maturity duration in the rice-based farming systems of Bangladesh. The crosses are made to engender suitable traits, such as early maturation, better plant architecture, and increased seed yield. This study aims to assess these advanced populations to identify the best mustard genotype suited for short cultivation periods, which may be efficiently integrated into rice-based cropping systems and enhance mustard production.

Materials and Methods

The experiment was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. The seeds of eight advanced populations of *B. rapa* were obtained from the Department of Genetics and Plant Breeding (GEPB), Sher-e-Bangla Agricultural University (SAU). Those seed materials contained populations from $F_6 - F_{10}$ generations.

Table 1. The names of experimental materials along with their sources are listed here.

Advanced populations	Abbreviated forms	Generations	Source
SAU Sarisha 2 × BARI Sarisha 15	P1	F_7	GEPB, SAU
SAU Sarisha 1 × BARI Sarisha 15	P2	F_6	GEPB, SAU
BARI Sarisha 6 × BARI Sarisha 15	P3	F_9	GEPB, SAU
SAU Sarisha 1 × BARI Sarisha 15	P4	F_7	GEPB, SAU
BARI Sarisha 15×SS75 (Sonali Sarisha)	P5	F_{10}	GEPB, SAU
SAU Sarisha 1 × BARI Sarisha 15	P6	F_7	GEPB, SAU
Tori-7 × BARI Sarisha 15	P7	F_6	GEPB, SAU
BARI Sarisha 6 × BARI Sarisha 15	P8	F_6	GEPB, SAU

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications following 30cm × 10cm planting geometry. The total area of the experiment was $19m \times 13m = 247m^2$. Each replication size was $19m \times 3m = 57m^2$ and the distance between replications was 1m. For studying different genetic parameters and their inter-relationship, data were recorded on twelve different traits such as days to first flowering, days to 50% flowering, days to 80% maturity, plant height (cm), root length (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliquae (cm), number of seeds per siliquae, thousand seed weight (g) and seed yield per plant (g). The data obtained were analyzed statistically for different components to find out the significance of the difference among the advanced populations of *B. rapa* for the studied traits. After evaluating the mean values of all the characters, analysis of variance was done using the F-test. The significance of the differences among the treatments was estimated by the least significant difference (lsd) test at 5% level of probability (Gomez and Gomez, 1984). Genotypic and phenotypic variance and coefficient of variation were estimated by the formulae used by Johnson *et al.* (1955) and Burton (1952) respectively. Heritability in broad sense was computed by technique given by Singh and Chaudhary (1985). Genetic advance was measured using the formula of Allard (1960) while genetic advance in percentage of mean was computed according to the formula given by Comstock and Robinson (1952). Genotypic and phenotypic correlation were found out using the formula suggested by Al-Jibouri *et al*. (1958) while path coefficient analysis was done employing the method proposed by Dewey and Lu (1959).

Results and Discussion

Among all the studied advanced populations (Table 3), P3 proved to be the earliest population taking 25.67 days to first flowering (DFF) followed by P6 (26.67 DFF), P1 (27.67 DFF), P4 (29.67 DFF), P2 (31.67 DFF) P5 (31.67 DFF), P8 (31.67 DFF) and P7 (35.33 DFF). As regards days to 50% flowering (DFPF), P3 took least number of days (30.67 DAS) while P7 recorded highest number of DFPF. P3 matured earliest of all the studied genotypes taking just 76.67 days followed by P4 (78.67 DTM), P6 (78.67 DTM), P1 (80 DTM), P8 (82.33 DTM), P5 (85.67 DTM), P2 (88.67 DTM) and P7 (89.33 DTM). P8 turned out to be the tallest population (125.04 cm) while P5 recorded the shortest height (93.57 cm). P3 had the maximum number of primary branches per plant (9.07) and maximum number of secondary branches per plant (6.83) while P8 showed minimum level of expression for these two traits with values of 5.0 and 2.57 respectively. P3 showed maximum number of siliquae per plant (217.97) followed by P4 (187.5), P1 (182.87), P6 (125.56), P2 (110.07), P5 (103.61), P8 (100.13) and P7 (87.91) whereas longest siliquae were exhibited in P1 (6.44 cm) followed by P3 (6.07 cm), P6 (6.07 cm), P4 (6.04 cm), P5 (6.0 cm), P2 (5.7 cm), P8 (5.03 cm) and P7 (4.67 cm). The maximum number of seeds per siliqua was observed in P6 (24.43) followed by P4 (23.31) P3 (23.3), P1 (22.14), P2 (18.84), P5 (18.35), P8 (18.07) and P7 (16.1). Thousand seed weight (g) was found highest in P3 (3.53 g) followed by P4 (3.37 g), P1 (3.1 g), P5 (3.07 g), P8 (2.9 g), P7 (2.83 g), P2 (2.43 g) and P6 (2.67 g). Seed yield per plant (g) remained highest in P3 among all the studied populations due to better expression in important yield contributing characters such as number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, thousand seed weight (g), etc. The co-efficient of variation varied within the range of 1.89%—23.88%.

The analysis of variance for some morphological, yield and yield contributing characters are presented in Table 2 indicating that significant variations existed among all the populations for all the studied characters. The significant differences among the studied populations indicate the presence of actual genetic variability in the material used and provide a good opportunity for yield improvement. We studied heritability, genetic advance, genetic advance in percentage of mean, genotypic co-efficient of variation and phenotypic co-efficient of variation to determine the existence of genetic variability for all the analyzed traits (Figure. 1 & 2). As expected, phenotypic co-efficient of variation was greater than genotypic co-efficient of variation for all the studied characters. Phenotypic co-efficient of variation and genotypic co-efficient of variation were the highest for number of secondary branches per plant (PCV=44.153%, GCV=37.135%) followed by number of siliquae per plant (PCV=36.193%, GCV=34.749%) and seed yield (PCV=33.747%, GCV=31.341%). Low variability was recorded for days to 80% maturity (PCV=6.047%, GCV=5.773%) followed by plant height (PCV=9.947%, GCV=9.712%). Heritability is the proportion of genetic variance in phenotypic variance, expressed as a percentage. In the present study, heritability was high (above 50%) for most of the studied characters. The highest estimate of heritability was observed for plant height (95.325%) followed by number of siliquae per plant (92.176%) and days to 80% maturity (90.351%). High heritability indicated that the characters were less influenced by the variation in the environment conditions. Since high heritability does not always lead to high genetic advance, heritability with genetic advance considered together should be used in predicting the ultimate effect of selecting superior varieties (Ali *et al.,* 2002). Genetic advance was the highest for the number of siliquae per plant (95.838) followed by plant height (21.389) and days to maturity (9.326). Genetic advance in percentage of mean was the highest for number of siliquae per plant (68.725%) followed by number of secondary branches per plant (64.34%) and seed yield (59.96%). Panse (1957) stated that high heritability coupled with high genetic advance indicates the additive gene effects while high heritability coupled with low genetic advance indicates the non-additive gene effects for control of a particular character. The present study indicated that the number of siliquae per plant showed high heritability with high genetic advance and genetic advance in percentage of mean, which indicated that this character can be considered for selection based phenotypic improvement in *B. rapa.*

For measuring the mutual relationship of different morphological and yield and yield contributing characters of eight advanced populations of *B. rapa,* correlation co-efficient analysis was done. The estimates of genotypic correlation co-efficient and phenotypic correlation co-efficient are presented in Table 4 and 5. According to Cruz *et al.* (2012), beyond significance, it should also be considered the magnitude and direction to interpret correlations correctly. As regards direction, the correlations can be positive (indicating a trend of increasing one variable leads to an increase in the other one; while negative correlation suggests a possibility of inverse relationship between traits (Nogueira *et al.,* 2012). The values of correlation co-efficient range between -1.0 to +1.0. A correlation of -1.0 exhibits a perfect negative correlation whereas a correlation of 1.0 exhibits a perfect positive correlation. A correlation of 0 exhibits no linear relationship between the movements of the two variables. For most traits, genotypic correlation co-efficient were greater than phenotypic correlation coefficients. This indicated that genetic factors contributed more than the environmental factors to the correlations (Almeida *et al.,* 2010, Parveen *et al*., 2013).

The occurrence of genotypic correlation between two traits can eventually happen due to pleiotropism or gene binding imbalance. Pleiotropism is one of the major causes of high correlations since one gene can influence the expression of more than one character. Accordingly, this fact improves the simultaneous selection of two or more traits by the selection of only one of them (Falconer and Mackay, 1996).

The strong positive correlation of days to 1st flowering and days to 50% flowering with days to 80% maturity indicates that the higher the days to flowering the more the maturity days. The strong positive correlation of number of primary branches per plant and number of secondary branches per plant with number of siliquae per plant indicates that the more the branches of plant the more the number of siliquae per plant. The strong positive correlation between length of siliquae and number of seeds per siliquae indicates that longer siliquae contain more seeds which ultimately increases yield. The strong positive correlation between thousand seed weight and seed yield indicates that if thousand seed weight increases seed yield increases.

Although correlation co-efficients are useful for quantifying the magnitude and direction of correlations between traits, they may result in misconceptions to selection strategies as a high magnitude of a correlation between two traits can occur due to the indirect effect of a third trait or a group of traits (Cruz *et al*., 2012). Consequently, path analysis is a method that helps breeding programs in performing indirect selection by confirming the obtained results from correlation analysis between traits and avoiding misconceptions throughout the selection.

According to the path co-efficient analysis (Table 6), direct positive effect on seed yield per plant was observed by days to first flowering, plant height, number of siliquae per plant and length of siliquae. These traits showed the highest level of influence on seed yield. Number of siliquae per plant showed positive indirect effect on seed yield per plant via plant height (cm) (0.54407), root length (1.14935), number of primary branches per plant (2.05348), number of secondary branches per plant (2.11512), length of siliquae (1.46116), number of seeds per silique (1.64963) and thousand seed weight (1.82525). Therefore, the number of siliquae per plant can be considered as a valuable option for selection in *B. rapa* breeding in the case of an indirect selection for high seed yield. The residual effect (R) of path co-efficient analysis was 0.12035 which reported that the traits under study contributed 88% to the seed yield per plant. It was said that there were some other factors that contributed 12% to the seed yield per plant that were not included in the present study but could had a significant effect on seed yield per plant.

Table 2. Analysis of variance for 12 important characters of eight advanced populations of *Brassica rapa* L.

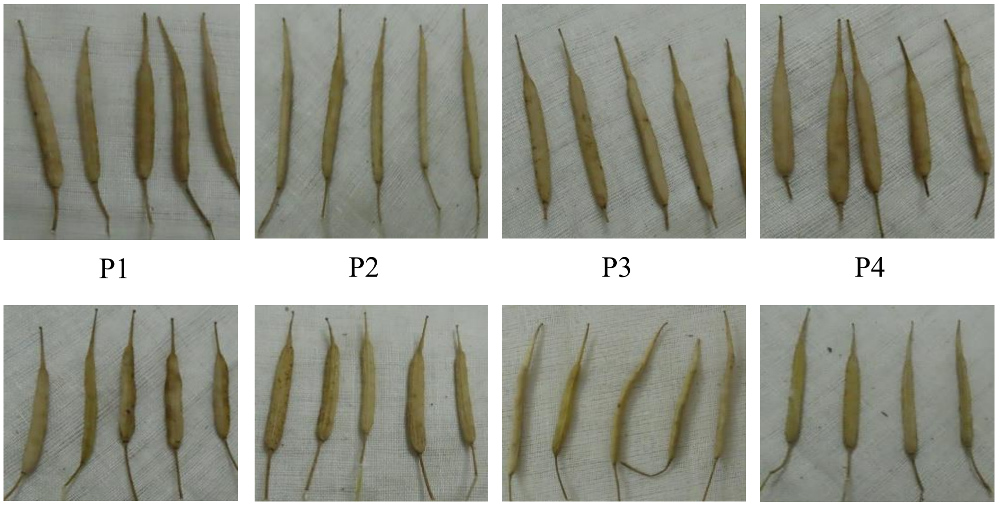
Source of Variation	Degrees of freedom	Mean sum of square											
		DFF	DFPF	DTM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
Replication	2	0.1250	10.0417	2.38	22.18	2.11	1.3362	0.2788	125.15	0.0162	1.21	0.0488	0.7306
Populations	7	30.95**	48.33**	70.48**	344.83**	6.36**	7.84**	9.17**	7243.7**	1.08**	28.48**	0.5566*	16.09**
Error	14	3.078	5.47	2.42	5.55	0.9399	1.88	1.11	199.32	0.0766	1.83	0.1930	0.8117

** Significant at 1% level of significance * Significant at 5% level of significance, DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), NPB/P = Number of primary branch per plant, NSB/P = Number of secondary branch per plant, NS/P = Number of siliquae per plant, LS = Length of siliqua (cm), NS/S = Number of seed per siliqua, TSW = Thousand seed weight (g), SY/P = Seed yield per plant.

Table 3. Mean performance and CV% of eight advanced populations of *B. rapa*

AP	DFF	DFPF	DTM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
P1	27.67cd	32.00 cd	80.00 cd	103.28 e	10.45 cd	8.97 a	5.53 ab	182.87 b	6.44 a	22.14 a	3.100 ab	8.027 bc
P2	31.67 b	40.33 a	88.67 a	114.31 c	11.77 bc	5.73 b	3.70 bc	110.07 cd	5.70 b	18.84 b	2.433 bc	5.773 de
P3	25.67 d	30.67 d	76.67 e	120.86 b	13.73 a	9.07 a	6.83 a	217.97 a	6.07 ab	23.30 a	3.533 a	11.7 a
P4	29.67 bc	35.67 bc	78.67 de	109.77 d	12.85 ab	7.30 ab	6.80 a	187.50 b	6.04ab	23.31 a	3.367 a	9.2 b
P5	31.67 b	40.33 a	85.67 b	93.57 g	9.83 d	6.20 b	3.17 c	103.61 cd	6.00 ab	18.35 bc	3.067 ab	5.967 de
P6	26.67 cd	34.67 cd	78.67 de	110.53 cd	10.68 cd	7.40 ab	4.00 bc	125.56 c	6.07 ab	24.43 a	2.267 c	6.667 cd
P7	35.33 a	40.60 a	89.33 a	98.67 f	10.37 cd	5.03 b	2.70 c	87.91 d	4.67 c	16.10 c	2.833 a-c	4.8 e
P8	31.67 b	39.33 ab	82.33 c	125.04 a	12.97 ab	5.00 b	2.567 c	100.13 d	5.03c	18.07 bc	2.900 abc	5.467 de
Mean	30.00	36.71	82.50	109.50	11.58	6.84	4.41	139.45	5.75	20.57	2.938	7.2
SE	1.43	1.91	1.2709	1.92	0.79	1.12	0.86	11.53	0.23	1.10	0.359	0.7356
lsd	3.07	4.096	2.7257	4.12	2.40	1.84	1.70	24.72	0.48	2.37	0.770	1.5778
CV%	5.85	6.37	1.89	2.15	8.37	20.07	23.88	10.12	4.81	6.58	14.96	12.51

Here, AP= Advanced populations, DFF=Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length (cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliquae, TSW = Thousand seed weight (g), SY/P = Seed yield per plant (g), lsd=least significant difference, SE=Standard Error, CV%=Percentage of co-efficient of variation.



P1 P2 P3 P4

P5 P6 P7 P8

Plate 1. A pictorial view showing siliquae of different advanced populations

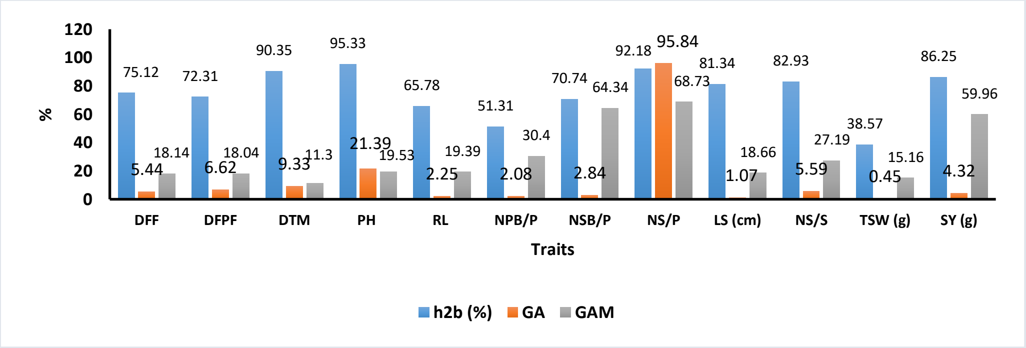


Fig. 1. Heritability, Genetic advance and Genetic advance in percent of mean for some yield contributing characters of 8 advanced populations of *B. rapa*

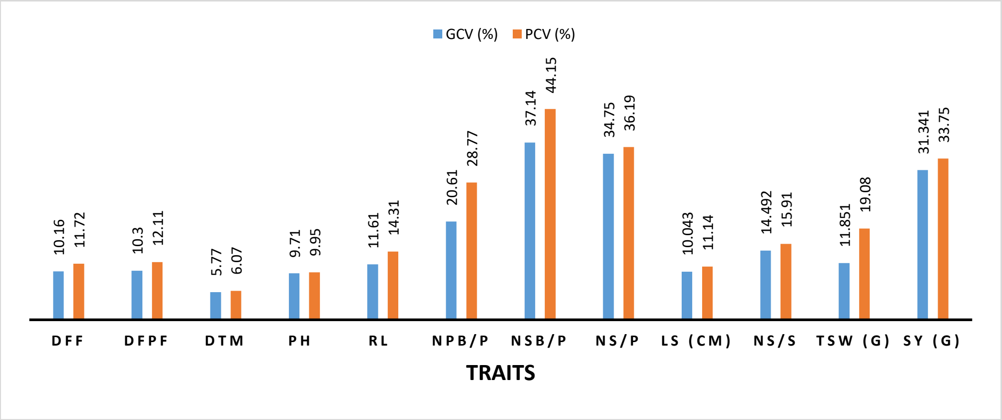


Fig. 2. Genotypic and phenotypic co-efficient of variation of 12 characters of advanced populations of *Brassica rapa* L.

Table 4. Genotypic correlation co-efficient among yield and yield contributing characters of 8 advanced populations of *B. rapa*

Traits	DFF	DFPF	DTM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
DFF	1											
DFPF	0.996**	1										
DTM	0.976**	0.934**	1									
PH	-0.397^{NS}	-0.282^{NS}	-0.428*	1								
RL	-0.424*	-0.352^{NS}	-0.483*	0.913**	1							
NPB/P	-0.997**	-0.993**	-0.886**	0.057^{NS}	0.209^{NS}	1						
NSB/P	-0.802**	-0.971**	-0.827**	0.223^{NS}	0.644**	0.930**	1					
NS/P	-0.848**	-0.957**	-0.823**	0.263^{NS}	0.556**	0.994**	0.994**	1				
LS	-0.895**	-0.775**	-0.641**	-0.087^{NS}	-0.020^{NS}	0.960**	0.739**	0.707**	1			
NS/S	-0.995**	-0.912**	-0.947**	0.283^{NS}	0.386^{NS}	0.925**	0.833**	0.799**	0.856**	1		
TSW	-0.312^{NS}	-0.662**	-0.544**	0.100^{NS}	0.664**	0.859**	0.891**	0.884**	0.307^{NS}	0.251^{NS}	1	
SY/P	-0.860**	-0.928**	-0.820**	0.340^{NS}	0.664**	0.981**	0.997**	0.984**	0.632**	0.780**	0.830**	1

Here, *= Significant at 5% level of probability, **= Significant at 1% level of probability

DFF=Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length(cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliquae, TSW = Thousand seed weight (g), SY/P = Seed yield per plant (g).

Table 5. Phenotypic correlation co-efficient among yield and yield contributing characters of 8 advanced populations of *B. rapa*

Traits	DFF	DFPF	DTM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
DFF	1											
DFPF	0.722^{**}	1										
DTM	0.748^{**}	0.785^{**}	1									
PH	-0.319^{NS}	-0.276^{NS}	-0.409^{*}	1								
RL	-0.204^{NS}	-0.330^{NS}	-0.498^{*}	0.795^{**}	1							
NPB/P	-0.593^{**}	-0.796^{**}	-0.668^{**}	0.093^{NS}	0.156^{NS}	1						
NSB/P	-0.582^{**}	-0.604^{**}	-0.619^{**}	0.180^{NS}	0.307^{NS}	0.749^{**}	1					
NS/P	-0.665^{**}	-0.814^{**}	-0.765^{**}	0.284^{NS}	0.461^{*}	0.802^{**}	0.899^{**}	1				
LS	-0.650^{**}	-0.551^{**}	-0.598^{**}	-0.087^{NS}	-0.025^{NS}	0.684^{**}	0.600^{**}	0.645^{**}	1			
NS/S	-0.808^{**}	-0.744^{**}	-0.790^{**}	0.249^{NS}	0.189^{NS}	0.714^{**}	0.712^{**}	0.729^{**}	0.666^{**}	1		
TSW	-0.123^{NS}	-0.215^{NS}	-0.328^{NS}	-0.034^{NS}	0.256^{NS}	0.101^{NS}	0.393^{NS}	0.473^{*}	0.148^{NS}	0.093^{NS}	1	
SY/P	-0.643^{**}	-0.747^{**}	-0.761^{**}	0.320^{NS}	0.510^{*}	0.693^{**}	0.806^{**}	0.938^{**}	0.598^{**}	0.688^{**}	0.586^{**}	1

Here, *= Significant at 5% level of probability, **= Significant at 1% level of probability

DFF=Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length(cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliquae, TSW = Thousand seed weight (g), SY/P = Seed yield per plant (g).

Table 6. Partitioning of genotypic correlation with seed yield per plant into direct and indirect component of 8 genotypes of *B. rapa*

Direct Effects	DFF	DFPF	DTM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
DFF	1.01102	-0.14772	-0.48724	-0.35888	0.36804	0.78087	0.04842	-1.75231	-0.53851	0.20106	0.01495	-0.860^{**}
DFPF	1.04442	-0.143	-0.46633	-0.25499	0.30553	0.75481	0.05862	-1.97733	-0.46618	0.18436	0.03175	-0.928^{**}
DTM	0.98675	-0.13358	-0.49923	-0.38624	0.41882	0.61149	0.04993	-1.70041	-0.38549	0.1915	0.02612	-0.820^{**}
PH	-0.40164	0.04036	0.21344	0.90338	-0.79265	-0.03937	-0.01346	0.54407	-0.05235	-0.05715	-0.00482	0.340^{NS}
RL	-0.42876	0.05034	0.24092	0.82509	-0.86786	-0.14416	-0.03886	1.14935	-0.01231	-0.07812	-0.03185	0.664^{**}
NPB/P	-1.14362	0.15636	0.44221	0.05152	-0.18123	-0.69034	-0.05615	2.05348	0.57738	-0.18691	-0.04124	0.981^{**}
NSB/P	-0.8108	0.13884	0.41286	0.20146	-0.55857	-0.64199	-0.06038	2.11512	0.44463	-0.16831	-0.04273	0.997^{**}
NS/P	-0.85769	0.13689	0.41097	0.23795	-0.48291	-0.6863	-0.06183	2.06556	0.42551	-0.16145	-0.0424	0.984^{**}
LS	-0.90512	0.11083	0.31993	-0.07863	0.01776	-0.66263	-0.04463	1.46116	0.60152	-0.17312	-0.01473	0.632^{**}
NS/S	-1.00549	0.13041	0.4729	0.25537	-0.33536	-0.63826	-0.05027	1.64963	0.51512	-0.20216	-0.01203	0.780^{**}
TSW	-0.31503	0.09461	0.27179	0.09073	-0.57598	-0.5933	-0.05377	1.82525	0.1846	-0.05069	-0.04798	0.830^{**}

Residual effect 0.12035

Here, DFF=Days to first flowering, DFPF = Days to 50% flowering, DTM = Days to 80% maturity, PH = Plant height (cm), RL=Root length(cm), NPB/P = Number of primary branches per plant, NSB/P = Number of secondary branches per plant, NS/P = Number of siliquae per plant, LS = Length of siliquae (cm), NS/S = Number of seeds per siliquae, TSW = Thousand seed weight (g), SY/P = Seed yield per plant (g).

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