

EVALUATION OF THE POTENTIALITY OF EIGHT ADVANCED POPULATIONS OF *BRASSICA RAPA* L. BASED ON YIELD AND YIELD CONTRIBUTING CHARACTERS

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ABSTRACT

In a study conducted at the experimental field of Sher-e-Bangla Agricultural University from November 2018 to February 2019, eight advanced populations of *Brassica rapa* L. were assessed to explore their variability, heritability, genetic advance, correlations and path coefficient considering twelve yield-contributing traits. Significant variation was observed among all populations for all traits. Minimum difference between phenotypic and genotypic variance was noted in most of the traits, while high genotypic and phenotypic coefficient of variation occurred in the number of secondary branches per plant, number of siliquae per plant, thousand seed weight, and seed yield per plant. Traits like days to first flowering, days to 50% flowering, and days to 80% maturity exhibited high heritability with low genetic advance. Conversely, the number of siliquae per plant demonstrated high heritability with high genetic advance, suggesting potentiality for trait selection. Correlation analysis identified significant positive associations between seed yield per plant and several traits. Path coefficient analysis highlighted direct positive effects on seed yield per plant from days to 80% maturity, root length, number of secondary branches per plant, and thousand seed weight. Chronologically, G6 performed the best showcasing most of the traits especially seed yield per plant and days to 80% maturity which can be considered as important breeding material for improvement of *B. rapa* L.

Keywords: Advanced population, Genetic advance, Heritability, Variability

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INTRODUCTION

The most economically important oleiferous genus within the family Brassicaceae is *Brassica*. The family belongs to 372 genera and 4060 accepted species bearing highly diversified morphology (<https://en.wikipedia.org/wiki/Brassicaceae>). *B. rapa* L. is commonly called turnip, turnip rape, field mustard, or turnip mustard and cultivated extensively for vegetables and edible oils in different parts of the world including Canada, China, Northern Europe and the Indian subcontinent (Islam et al., 2015). The genus *Brassica* has generally been aligned into three groups such as rapeseed, mustard and cole. Among the oil bearing plants *Brassica*, rape comprises of the diploid *B. rapa*, turnip rape (AA, 2n=20) and amphidiploids *B. napus* L., rape (AACC, 2n=38) (Yarnell, 1956).

Brassica plays a key role in industrial and culinary purposes while oil cakes are used as good organic fertilizer and good source of protein in animal feed. Rapeseed provides fat soluble vitamins (A, D, E and K) in the body. However, one of the two essential fatty acids is absent in many edible oils whereas mustard provides both the essential fatty acids named linoleic and linolenic acid to the human body (Khan et al., 2009). Rapeseed essential oil has strong antifungal properties due to the presence of allyl isothiocyanate in it. Besides, seeds of mustard and rapeseeds bear 42% oil and 25% protein and minerals which serves an eminent role to fulfill the need of the world population (Kaul and Das, 2006). *B. rapa* L. possesses first position in respect of area and production among the oilseed crops in our country (Naznin et al., 2015). In Bangladesh, 0.25 million hectares were covered by rapeseed with 0.92 metric tons (MT) per hectare yield during 2017-2018 (USDA, 2019). Bangladesh is passing through an enormous scarcity of edible oils because the cultivation area of mustard in Bangladesh is lower due to rice based cropping pattern and existing low yielding varieties, unavailability of locally developed hybrids and low management practices. In 2017-18, the utilization of total oils and fats was 3.0 million tons in Bangladesh therein 2.5 million tons were imported (FAO, 2019). A huge amount of foreign exchange is expended on imports of edible oils and oilseeds by Bangladesh to meet the rising demand of its population. Besides, farmers feel the necessity of short durational variety of mustard that can grow successfully in between the two rice crops. There is few improved short durational varieties available to replace the short durational but low yielding variety of *B. rapa* L. such as 'Tori-7' which can be compatible to the T. Aman-Mustard-Boro cropping pattern (Sharmin, 2016). In these circumstances, separate crossing programs have been thus inaugurated few years ago which ultimately led to the selection of eight promising advanced populations of *B. rapa* L. in subsequent generations. The present experiment was aimed at obtaining the early maturing and high yielding population to solve the current problems of the crop through comparing these eight advanced populations of *B. rapa* L.

MATERIALS AND METHODS

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka—during November 2018 to February 2019. The soil of the experimental plot was clay loam in texture and the land was medium high with medium fertility level. The seeds of eight advanced populations of *B. rapa* L. namely SAU1×BARI15, F7, yellow (G1), BARI9×BARI6, S5F15, Brown (G2), BARI6×BARI15, F6, yellow (G3), SAU2×BARI6, F6S4, yellow (G4), BARI6×BARI15, F9, 75 days, Yellow (G5), BARI9×BARI6, S5F15, yellow (G6), Yellow special, F9, 75 days (G7), TORI7×BARI15, F7, yellow (G8) used as experimental materials were brought from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 19 m × 13 m = 247 m². Each replication size was 19 m × 3 m and distance between replication to replication was 1m. The spacing between line to line was 30 cm and plant to plant was 10 cm. For studying various genetic parameters and inter-relationships, twelve characters of ten plants were taken into account such as days to first flowering, days to 50% flowering, days to 80% maturity, plant height, root length, number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliqua, number of seeds per siliqua, thousand seed weight, and seed yield per plant. The data obtained for different characters were analyzed statistically by using Statistix 10 software to find out the significance of the difference among the advanced populations of *B. rapa*. After evaluating the mean values of all the characters, analysis of variance was performed by the F-test. The significance of the differences among the treatments was estimated by least significant difference (LSD) test at 5% level of probability (Gomez and Gomez, 1984). Genotypic and phenotypic variance were estimated by the formula used by Johnson et al. (1955). Genotypic and phenotypic coefficient of variation were calculated by the help of the formula of Burton (1952). Heritability in broad sense was computed by using the formula given by Singh and Chaudhary (1985). Genetic advance in percentage of mean was computed by using the formula given by Comstock and Robinson (1952). Genotypic and phenotypic correlation obtained by the formula that was suggested by Al-Jibouri et al. (1958). Path coefficient analysis was done by following the outlined method of Dewey and Lu (1959).

RESULTS AND DISCUSSION

The knowledge on genetic variability, heritability, genetic advance and character association is a prerequisite for performing a successful breeding program to develop high yielding varieties.

Variability, heritability and genetic advance

The results of analysis of variance for all the characters under study are presented in Table 1. According to the table, there were significant variations among all advanced

populations of *B. rapa* L. for each character suggesting the presence of great genetic variability among the populations for effective selection.

Table 1. Analysis of variance of 12 important characters of 8 cross materials of *B. rapa* L.

Source of Variation	DF	DFP	DFPF	DM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
Replication	2	4.67	3.88	0.88	103.49	0.93	0.43	1.23	1527.5	0.06	12.4	0.18	1.69
Genotypes	7	28.85**	44.71**	96.67**	279.85**	2.64*	6.45**	33.30**	10901.90**	0.81**	34.32**	2.76**	33.91**
Error	14	1.9	5.64	9.26	58.96	0.93	0.4	1.17	883.4	0.12	3	0.11	0.76

** Significant at 1% level of significance * Significant at 5% level of significance

Here, DFF=Days to first flowering, DFPF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), RL=Root length (cm), PNB/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 siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P = Seed yield per plant

Among all the advanced populations, G2 was the earliest (25DAS) genotype followed by G6 (26.67DAS) in case of days to first flowering while G2 also took shortest (31 DAS) period followed by G1 (33DAS), G3 (33DAS), G4 (33DAS) and G6 (34.67) in case of days to 50% flowering. Shortest (79DAS) time for days to 80% maturity was observed in G7 followed by G5 (80DAS) and G6 (82.67DAS) among the advanced populations. G2 and G1 were the shortest (83.7cm) and tallest (108.96cm) population respectively. However, G3 had maximum (9.10) number of primary branches per plant while the maximum (9.20) number of secondary branches per plant was observed in G6. G1 showed maximum (218) number of siliquae per plant followed by G3 (212.60) and G6 (205.73) whereas largest (6.54) length of siliqua was exhibited in G4 followed by G2 (6.30) and G6 (6.03). Maximum (25.49) number of seeds per siliqua was observed in G5 followed by G8 (21.29) and G4 (19.82). Thousand seed weight was found highest (4.58) in G3 followed by G4 (3.87). Maximum (11.76g) seed yield per plant was found in G6 due to better performances in important yield contributing characters such as number of secondary branches per plant, number of siliquae per plant, length of siliqua.

Table 2. Mean performance of yield and yield contributing characters of eight advanced populations *Brassica rapa* L.

Advanced populations ↓	Character s →											
	DFF	DFFP	DM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
G1	29.33b	33.00b	92.00ab	108.96a	10.46c	8.47ab	5.37b	218.00a	5.11c	16.72de	3.68b	7.04b
G2	25.00c	31.00b	88.33bc	83.70b	11.27a-c	8.13a-c	8.63a	173.97ab	6.30a	19.05b-d	2.88c	7.83b
G3	29.33b	33.00b	94.00a	107.84a	11.61a-c	9.10a	5.13b	212.60a	5.47bc	14.25e	4.58a	6.84b
G4	29.67b	33.00b	91.00ab	105.26a	12.28ab	8.10a-c	3.17c	137.20b	6.54a	19.82bc	3.87b	7.84b
G5	31.67b	40.33a	80.00de	101.41a	11.09bc	4.40e	0.60d	59.67d	5.58bc	25.49a	1.77e	1.75d
G6	26.67c	34.67b	82.67de	85.85b	10.77bc	7.33cd	9.20a	205.73a	6.03ab	18.15cd	2.95c	11.76a
G7	35.00a	40.67a	79.00e	96.36ab	9.93c	6.40d	2.73c	124.90bc	5.22c	17.14c-e	2.05de	2.20d
G8	31.67b	39.33a	85.00cd	103.09a	12.78a	7.47b-d	0.33d	84.47cd	5.45bc	21.29b	2.45cd	3.75c
Min	25	31	79	83.70	9.93	4.40	0.33	59.67	5.11	14.25	1.77	1.75
Max	35	40.67	94	108.96	12.78	9.1	9.20	218	6.54	25.49	4.58	11.76
Grand mean	29.79	35.63	86.5	99.06	11.27	7.43	4.40	152.07	5.71	18.99	3.03	6.13
CV (%)	4.63	6.66	3.52	7.75	8.56	8.49	24.56	19.55	6.12	9.12	11.12	14.23
LSD	2.42	4.16	5.33	13.45	1.69	1.10	1.89	52.05	0.61	3.03	0.59	1.53
SE	1.13	1.94	3.03	6.27	0.81	0.52	0.88	24.27	0.29	1.41	0.28	0.73

Here, DFF= Days to first flowering, DFFP = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height (cm), RL=Root length, 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 siliqua (cm), NS/S = Number of seeds per siliqua, TSW = Thousand seed weight (g), SY/P =Seed yield per plant (g), LSD=Least Significant Difference, CV (%) = Percentage of Coefficient of variation, SE= Standard error

Table 3. Estimation of some genetic parameters of 8 advanced populations of *Brassica rapa* L.

Parameters	DFF	DFFP	DM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	SY/P
σ_g^2	8.98	13.02	29.14	73.63	0.57	2.02	10.71	3339.50	0.23	10.44	0.88	11.05
σ_p^2	10.89	18.66	38.39	132.59	1.50	2.42	11.88	4222.90	0.35	13.44	1.00	11.81
σ_e^2	1.90	5.64	9.26	58.96	0.93	0.40	1.17	883.40	0.12	3.00	0.11	0.76
GCV	10.06	10.13	6.24	8.66	6.71	19.14	74.46	38.00	8.37	17.02	31.03	54.26
PCV	11.08	12.13	7.16	11.62	10.87	20.94	78.41	42.73	10.37	19.31	32.96	56.10
h^2	82.50	69.79	75.89	55.53	38.04	83.54	90.18	79.08	65.17	77.68	88.61	93.56
GA	5.61	6.21	9.69	13.17	0.96	2.68	6.40	105.86	0.80	5.87	1.82	6.62
GA in (%) of mean	18.82	17.43	11.20	13.30	8.52	36.03	145.66	69.62	13.92	30.89	60.16	108.12

σ_g^2 = Genotypic variance, σ_p^2 = Phenotypic variance, σ_e^2 = Environmental variance, GCV= Genotypic coefficient of variation, PCV=Phenotypic Coefficient of variation, h^2 =Heritability, GA=Genetic advance

The phenotypic variance was higher than the genotypic variance for all the characters suggesting less environmental influence for the expression of the characters (Table 3). Difference between the genotypic and phenotypic variances was minimum in root length, number of primary branches per plant, length of siliqua, thousand seed weight and seed yield per plant indicating low environmental influence on them. High phenotypic coefficient of variation was noticed for all the studied characters over genotypic coefficient of variations. Moderate genotypic and phenotypic coefficient of variations were found in days to first flowering, days to 50% flowering and number of seeds per siliqua while number of secondary branches per plant, number of siliquae per plant, thousand seed weight and seed yield per plant showed high genotypic and phenotypic coefficient of variations.

For the selection of the best population, high heritability and high genetic advance are considered as a potential genetic tool. High heritability value shows the strategy for the selection of suitable character by the phenotypic performance of the respective genotype and genetic advance indicates the development for the choice of the best individual. High heritability with high genetic advance and high genetic advance in percentage of mean were found in case of number of siliquae per plant (79.08%, 105.86, 69.62%) indicated the prevalence of additive gene effect in the inheritance of the trait and during crop improvement there is a wider opportunity of the plant breeders for direct selection. High heritability along with low genetic advance was observed in days to first flowering (82.50%, 5.61), days to 50% flowering (69.79%, 6.21), days to 80% maturity (75.89%, 9.69), number of primary branches per plant (83.54%, 2.68), number of secondary branches per plant (90.18%, 6.40), number of seeds per siliqua (77.68%, 5.87), length of siliqua (65.17%, 0.80), thousand seed weight (88.61%, 1.82) and seed yield per plant (93.56%, 6.62) which indicated the prevalence of non-additive gene action and improvement through selection might not be so feasible for the characters.

Correlation coefficient

Seed yield is a complicated trait being influenced by various quantitative traits. Some of these traits are highly correlated with seed yield. The analysis of the interrelationship among those traits and their association with seed yield is very important for establishing selection criteria. Genotypic and phenotypic correlation coefficient among yield and yield contributing characters of 8 advanced populations of *B. rapa* L. is shown in table 6. The values of correlation coefficient range between -1.0 and 1.0. A calculated number higher than 1.0 or less than -1.0 indicates that there was an error in the measurement of correlation. A correlation of -1.0 exhibits a perfect negative correlation whereas a correlation of 1.0 exhibits a perfect positive correlation. A correlation of 0.0 exhibits no relationship between the movements of the two variables.

Days to first flowering showed highly significant and positive correlation with days to 50% flowering ($G=0.924^{**}$, $P=0.700^{**}$) at both genotypic and phenotypic level

suggesting that when days to first flowering increases, days to 50% flowering also increases. Correlation of days to 80% maturity with number of primary branches per plant ($G=0.963^{**}$, $P=0.703^{**}$), number of siliquae per plant ($G=0.644^{**}$, $P=0.588^{**}$), thousand seed weight ($G=0.998^{**}$, $P=0.809^{**}$) was highly significant and positive at both genotypic and phenotypic level enunciating a possible increase in number of primary branches per plant, number of siliquae per plant, thousand seed weight by increasing days to 80% maturity. Number of primary branches per plant and number of secondary branches per plant showed highly significant and positive correlation with number of siliquae per plant and seed yield per plant at both genotypic and phenotypic level indicating an increase in number of siliquae per plant and seed yield per plant by increasing number of primary branches per plant and number of secondary branches per plant. Number of siliquae per plant exhibited highly significant and positive association with thousand seed weight ($G=0.819^{**}$, $P=0.605^{**}$) and seed yield per plant ($G=0.784^{**}$, $P=0.741^{**}$) indicating that higher the thousand seed weight and seed yield per plant greater the number of siliquae per plant. Correlation of thousand seed weight with seed yield per plant ($G=0.609^{**}$, $P=0.535^{**}$) was highly significant and positive at both genotypic and phenotypic level suggesting that a possible increase in seed yield per plant by increasing thousand seed weight.

Path coefficient analysis

Path coefficient analysis is the most common statistical method utilized to determine the direct or indirect effects of yield contributing characters on seed yield per plant and measure the relative importance of each component on seed yield per plant. Partitioning of genotypic correlations into direct and indirect effects of important characters by path coefficient analysis of *B. rapa* L. is shown in table 5. According to the path coefficient analysis, direct positive effect on seed yield per plant was observed by days to 80% maturity (0.752), root length (0.471), number of secondary branches per plant (1.586) and thousand seed weight (1.283). On the other hand, negative direct effect on seed yield per plant was found by days to first flowering (-0.179), days to 50% flowering (-0.296), plant height (-0.452), number of primary branches per plant (-2.104), number of siliquae per plant (-1.535), length of siliqua (-0.625) and number of seeds per siliqua (-1.202). The residual effect (R) of path coefficient analysis was noted as 0.285 which indicated that the characters under study contributed 71.6% to the seed yield per plant. There are some other factors which contribute 28.5% to the seed yield per plant but are not utilized in the present study.

Table 4. Genotypic and phenotypic correlation coefficient among yield and yield contributing characters of 8 advanced populations of *Brassica rapa* L.

Characters		DFP	DFPF	DM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW
DFPF	r _g	0.924**										
	r _p	0.700**										
DM	r _g	-0.506*	-0.853**									
	r _p	-0.402 ^{NS}	-0.755**									
PH	r _g	0.613**	0.219 ^{NS}	0.475*								
	r _p	0.336 ^{NS}	-0.008 ^{NS}	0.402 ^{NS}								
RL	r _g	-0.058 ^{NS}	-0.052 ^{NS}	0.421*	0.190 ^{NS}							
	r _p	-0.234 ^{NS}	-0.184 ^{NS}	0.311 ^{NS}	0.348 ^{NS}							
NPB/P	r _g	-0.510*	-0.872**	0.963**	0.186 ^{NS}	0.276 ^{NS}						
	r _p	-0.438*	-0.670**	0.703**	0.115 ^{NS}	0.238 ^{NS}						
NSB/P	r _g	-0.856**	-0.769**	0.279 ^{NS}	-0.726**	-0.492*	0.523**					
	r _p	-0.759**	-0.703**	0.299 ^{NS}	-0.493*	-0.178 ^{NS}	0.451*					
NS/P	r _g	-0.613**	-0.831**	0.644**	-0.102 ^{NS}	-0.485*	0.839**	.821**				
	r _p	-0.549**	-0.702**	0.588**	-0.076 ^{NS}	-0.136 ^{NS}	0.653**	.810**				
LS	r _g	-0.639**	-0.541**	0.154 ^{NS}	-0.631**	0.303 ^{NS}	0.142 ^{NS}	.405*	0.011 ^{NS}			
	r _p	-0.569**	-0.454*	0.177 ^{NS}	-0.267 ^{NS}	0.503*	0.162 ^{NS}	.358 ^{NS}	0.062 ^{NS}			
NS/S	r _g	0.172 ^{NS}	0.621**	-0.625**	-0.148 ^{NS}	0.298 ^{NS}	-0.848**	-.555**	-0.898**	0.171 ^{NS}		
	r _p	0.163 ^{NS}	0.348 ^{NS}	-0.415*	-0.000 ^{NS}	0.275 ^{NS}	0.688**	-.478*	-0.750**	0.234 ^{NS}		
TSW	r _g	-0.435*	-0.846**	0.998**	0.424*	0.339 ^{NS}	0.907**	.413*	0.819**	0.202 ^{NS}	-0.758**	
	r _p	-0.385 ^{NS}	-0.679**	0.809**	0.374 ^{NS}	0.149 ^{NS}	0.796**	.319 ^{NS}	0.605**	0.138 ^{NS}	-0.595**	
SY/P	r _g	-0.847**	-0.831**	0.449*	-0.450*	-0.002 ^{NS}	0.652**	.856**	0.784**	0.573**	-0.477*	0.609**
	r _p	-0.773**	-0.715**	0.475*	-0.259 ^{NS}	0.091 ^{NS}	0.546**	.829**	0.741**	0.506*	-0.391 ^{NS}	0.535**

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

Table 5. Partitioning of genotypic correlations into direct and indirect effects of important characters by path coefficient analysis of *Brassica rapa* L.

Characters	DFP	DFPF	DM	PH	RL	NPB/P	NSB/P	NS/P	LS	NS/S	TSW	Genotypic correlation with yield
DFP	-0.179	-0.274	-0.381	-0.277	-0.027	1.073	-1.358	0.941	0.399	-0.206	-0.558	-0.847**
DFPF	-0.165	-0.296	-0.642	-0.099	-0.025	1.833	-1.219	1.275	0.338	-0.746	-1.085	-0.831**
DM	0.090	0.252	0.752	-0.215	0.198	-2.026	0.443	-0.989	-0.096	0.751	1.287	0.449*
PH	-0.110	-0.065	0.358	-0.452	0.089	-0.391	-1.152	0.157	0.394	0.178	0.544	-0.450*
RL	0.010	0.015	0.317	-0.086	0.471	-0.580	-0.780	0.744	-0.189	-0.358	0.435	-0.002 ^{NS}
NPB/P	0.091	0.258	0.725	-0.084	0.130	-2.104	0.830	-1.287	-0.089	1.018	1.164	0.652**
NSB/P	0.153	0.228	0.210	0.328	-0.232	-1.101	1.586	-1.260	-0.253	0.667	0.530	0.856**
NS/P	0.110	0.246	0.485	0.046	-0.228	-1.764	1.302	-1.535	-0.007	1.079	1.050	0.784**
LS	0.114	0.160	0.116	0.285	0.143	-0.299	0.643	-0.017	-0.625	-0.205	0.259	0.573**
NS/S	-0.031	-0.184	-0.470	0.067	0.140	1.783	-0.881	1.379	-0.107	-1.202	-0.972	-0.477*
TSW	0.078	0.250	0.751	-0.192	0.160	-1.908	0.655	-1.256	-0.126	0.911	1.283	0.609**

Bold figures indicate direct effects, Residual effect: 0.285

CONCLUSION

The results demonstrated significant variations among the populations, providing valuable insights for effective selection in breeding programs. The study not only identified promising populations with superior agronomic traits but also provided a comprehensive understanding of the interrelationships among key characteristics. This information is crucial for future breeding strategies aimed at developing high-yielding varieties of *B. rapa* L., addressing challenges in edible oil production and contributing to sustainable agriculture in the region. In these circumstances, G6 called BARI9× BARI6, S5F16, Yellow is regarded as the most promising population considering short days to 80% maturity, highest seed yield per plant, highest number of secondary branches per plant, high number of siliquae per plant and high length of siliqua which proves its potentiality to release as a variety or select as a prominent parental line for future hybridization strategy.

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