

## Variability and comparative analysis among advanced generations of *Brassica rapa* L.

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### Abstract

Variability and comparison analysis among the fifteen F<sub>4</sub> population considering different morphological attributes of *Brassica rapa* obtained through inter-varietal crosses were evaluated in randomized complete block design with three replications in the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during October 2012-March 2013 to find out the best genotype as well as trait for improving the yield in future. Highly significant variation was observed among the genotypes for almost all of the characters studied. The cross combination SAU sarisha 1 x SAU sarisha 3 performed the best for highest yield per plant along with most of the traits. So it can be used for developing superior genotypes. The number of secondary branches per plant exhibits the highest value for heritability while the primary branches per plant shows lowest value. Yield per plant, thousand seed weight, siliquae length, days to 50% flowering, days to 50% maturity and plant height showed moderate heritability. Hence selection based on this character will be judicious and effective for future *B. rapa* breeding program.

**Keywords:** genetic advance; heritability; morphological; variability; genotypes.

**Abbreviations:** CV (%)\_coefficient of variation; D50%F\_days to 50% flowering; df\_degrees of freedom; D 50% M\_days to 50% maturity; ER\_error; GA\_genetic advance; GA%\_genetic advance percentage of mean; MS\_mean sum of square; PBP\_number of primary branches per plant; PH\_plant height; SBP\_number of secondary branches per plant; SE\_standard error; SPP\_number of siliquae per plant; SPS\_number of seeds per siliquae; SL\_siliquae length; TSW\_1000 seed weight; YPP\_yield per plant.

### Introduction

*Brassicaceae* is a medium-sized and economically important family of flowering plants (Angiosperms), informally known as the mustards, mustard flowers, the crucifers or the cabbage family (Wikipedia). The family contains over 330 genera and about 3,700 species, according to the Royal Botanic Gardens, Kew. The genus *Brassica* has generally been divided into three groups' namely-rapeseed, mustard and cole. The rapeseed group includes the diploid *B. rapa*, turnip rape (AA, 2n=20) and amphidiploids *B. napus* L, rape (AACC, 2n=38) (Yarnell et al., 1956). *Brassica* have the great economic and commercial value and play a major role in our daily diet. *Brassica* vegetables are full of indole-3-carbinol, a compound which enhances DNA repair in cells and tissues and appears to block the growth regarding cancer tissues. *B. rapa* L. is a plant consisting of various widely cultivated subspecies. The oilseeds are sometimes also called *canola*. In Bangladesh, rapeseed and canola are the major source of edible oil. Edible oil plays a key role as a source of high energy component of food in human nutrition. Many edible oils lack one of the two essential fatty acids; on the other hand mustard provides both the essential fatty acids to the human body-linoleic acid and linolenic acid (Khan et al., 2009). Significantly, it contains the lowest amount of saturated fatty acids among the vegetable oils, higher amounts of which causes attendant heart problems (Khan et al., 2009). Mustard seeds contain 40-45% oil and 20-25% protein and minerals (Mondal and Wahhab, 2001). Mustard (*Brassica* spp.) is one of the most important oilseed crops throughout the world after oil-palm and soybeans (FAO, 2010). It occupies first position of the list in respect of area and production among the oilseed crops

grown in this country (BBS, 2010). Bangladesh is now self-sufficient in rice (USAID, 2006) and for this the dominant cropping pattern Transplanted aman (wet season rice)-fallow-boro (dry season rice) plays an important role which covers about 1.8 million hectare (about 22% of the total land) of land (Elahi et al., 1999). The late harvest of medium duration T. aman rice and increased cultivation of boro rice under this cropping pattern causes the decline of mustard area. In the year of 2006-07, it covered 5,20,045 acres land and the production was 1,88,880 metric ton, where in the year of 2010-11 it covered 6,23,294 acres land and the production was 2,46,494 metric tons (Yearbook 2011 of Agricultural Statistics of Bangladesh). A very brief comparison between of mustard in 2006-07 to 2010-2011 indicates an increase of land 19.85%, when the production is increased by more than 30.5% (Yearbook 2011 of Agricultural Statistics of Bangladesh). The demand of edible oil is increasing day by day with the increasing population. The present per capita oil consumption is only 10 g per day as compared to the total need of 22 g per day. To fulfill the shortage of edible oil Bangladesh has to import a large quantity of edible oil every year. Development of improved varieties of oil seeds with short durational, better quality, higher yields are the most important issues with high priority (Current & Future challenges as reported by MoA for SYFP 2011 to 2015). The Bangladesh Rice Research Institute has recommended the T. Aman-Mustard-Boro cropping pattern for the irrigated ecosystem (BARC, 2001; Khan et al. 2004) with the inclusion of 65-70 days mustard variety, Tori-7 in the transition period between T. Aman and Boro to address

the issue. But the farmers harvest poor yield from Tori-7 that can be increased manifold by introducing high yielding varieties (Alam and Rahman. 2006; Bask et al., 2007). There is no HYV to replace this short durational low yielding local variety. One major technique of plant breeding is the deliberate interbreeding (crossing) of closely or distantly related individuals to produce new crop varieties or lines with desirable properties. Plants are crossbred to introduce traits or genes from one variety or line into a new genetic background. Generally we use crossed materials for yield improvement (hybrids often out yield traditional open pollinated selections by 50-100% due to its improved vigor, improved genetic disease resistance, improved fruit setting under stress, and higher female or male flower ratios), extended or reduced growing season (hybrids often mature up to 15 days earlier than local open pollinated varieties). For many crops, the hybrid's relative advantage over the open pollinated is most pronounced under stress conditions and quality improvement (hybrids have helped stabilize product quality at a higher and more uniform level– this implies improved consumption quality). For example, a short durational *B. rapa* may be crossed with a high-yielding but moderate or long durational *B. rapa*, the goal of the cross being to introduce short durational *B. rapa* without losing the high-yield characteristics. Progeny from the cross (F<sub>1</sub>) would then be crossed with the high-yielding parent to ensure that the progeny were most like the high-yielding parent, (backcrossing). The progeny from that cross (F<sub>2</sub>, F<sub>3</sub>, F<sub>4</sub> etc.) would then be tested for yield (selection) and short durational, high-yielding plants would be further developed. Achievement of any crop improvement depends upon the presence of genetic variability, heritability, correlation as well as genetic gain in selection (Khan et al., 2006). Heritability is a key of transmissibility of traits and as such partition the total variance into genetic and environmental components (Marwede et al., 2004). Additive genes are considered to control traits with high heritability and genetic advance and the phenotypic selection thus would be effective (Aytaç and Kinaci, 2009). Developing high yielding varieties need critical evaluation of existing genetic variability, heritability and genetic advance (Mahmood et al., 2003; Akbar et al., 2003). In order to make the selection more effective, both heritability and genetic advance will be considered instead of heritability alone (Johnson et al., 2003). Therefore, the aim of the present study is to estimate genetic variability, heritability, genetic advance of F<sub>4</sub> materials generated by crossing among six varieties of *B. rapa*. The selected progenies are expected to be short durational, high yielding and yellow seeded. By comparing among them, we could able to select the best ones to mitigate the demand of edible oil.

## Results and Discussion

### ANOVA, variability, heritability and genetic advance

The genotypes for almost all characters showed significant difference in this study, indicating the presence of enough variability among the genotypes for effective selection to pick up the best genotypes.

### Days to 50% flowering

From ANOVA, it was found that there were highly significant variations (23.09) at 1% level of probability among the genotypes for days to 50% flowering.

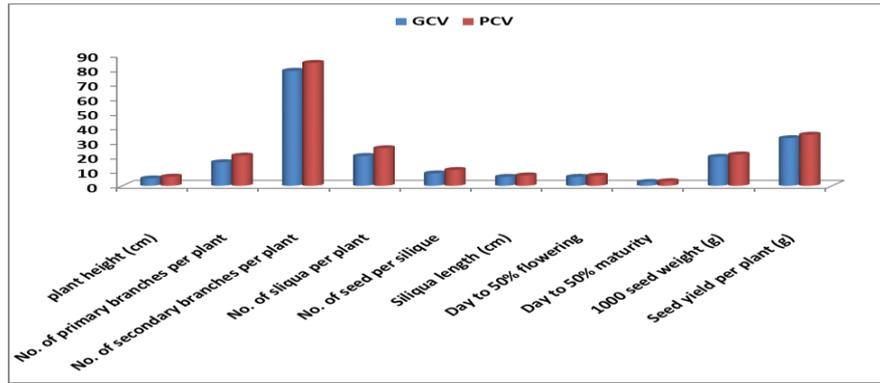
**Table 1.** Materials used in experiment.

Sl. No.	Designation
1	BARI sarisha 6 X BARI sarisha 15
2	BARI sarisha 6 X SAU sarisha 1
3	BARI sarisha 6 X Tori 7
4	BARI sarisha 6 X SAU sarisha 2
5	BARI sarisha 6 X SAU sarisha 3
6	BARI sarisha 15 X SAU sarisha 1
7	BARI sarisha 15 X Tori 7
8	BARI sarisha 15 X SAU sarisha 2
9	BARI sarisha 15 X SAU sarisha 3
10	SAU sarisha 1 X Tori 7
11	SAU sarisha 1 X SAU sarisha 2
12	SAU sarisha 1 X SAU sarisha 3
13	Tori 7 X SAU sarisha 2
14	Tori 7 X SAU sarisha 3
15	SAU sarisha 2 X SAU sarisha 3

Minimum days to 50% flowering was observed in Tori 7 x SAU sarisha 3 (37.67 days) and maximum was in BARI sarisha 6 x BARI sarisha 15 (48.00 days) (Table 3), where the mean was 43.16 days (Table 4). Genotypic and phenotypic variance of days to 50% flowering was found 7.05 and 8.99 respectively indicating moderate environmental influence on their phenotypic expression for the trait of the genotypes; the GCV and PCV were 6.15 and 6.95 respectively indicating low variability due to influence of genotypes and environment both for the character (Table 5). Jahan et al. (2014) mentioned the high genotypic and phenotypic coefficient of variation for days to 50% flowering. It exhibited high heritability (78.41%), moderate genetic advance (4.84) and genetic advance in percentage of mean (11.22%) (Table 5), refers that the character is governed by additive genes and selection for this character may will be effective. Afrin et al. (2011) reported high heritability for this trait with low genetic advance and also low genetic advance in percentage of mean. But Jahan et al. (2014) observed high heritability with low genetic advance and genetic advance in percentage of mean and concluded that the character is governed by non-additive genes.

### Days to 50% maturity

For days to 50% maturity highly significant variations were observed among the genotypes (16.37) at 1% level of probability. Minimum days to 50% maturity was found in SAU sarisha 2 x SAU sarisha 3 (78.33 days), maximum was found in BARI sarisha 6 x BARI sarisha 15 (86.67 days) (Table 3), where the mean was 82.78 days. Genotypic and phenotypic variance of days to 50% maturity was found 4.81 and 6.74 respectively indicating moderate environmental influence on their phenotypic expression for the trait of the genotypes; the GCV and PCV were 2.65 and 3.14 respectively indicating the variability for the character is influenced by genotypes and environment both (Table 5). Jahan et al. (2014) reported high genotypic and phenotypic coefficient of variation for days to 50% maturity. It exhibited moderate heritability (71.35%), low genetic advance (3.82) and low genetic advance in percentage of mean (4.61%) (Table 5), refers that the character is mostly governed by non-additive genes and selection of genotypes for minimum days to maturity may will not be effective. Jahan et al. (2014) observed high heritability with low genetic advance and genetic advance in percentage of mean and concluded that the character is governed by non-additive genes.



**Fig 1.** Genotypic and phenotypic coefficient of variability in 15 genotypes of *Brassica rapa*.

### Plant height

Plant height showed highly significant variations (98.01) at 1% level of probability of the studied genotypes. Highest plant height was found in SAU sarisha 1 x SAU sarisha 3 (116.20 cm), lowest one was SAU sarisha 1 x Tori 7 (96.41 cm) (Table 3) and the mean was 104.28 cm (Table 4). From Table 5, higher phenotypic variance (42.58) was observed than the genotypic variance (27.71) in this study, the PCV (6.26) closer to GCV (5.05) gave information that the genotypes and environment both are responsible for variation of plant height. Highest phenotypic and genotypic variances and genotypic and phenotypic coefficient of variations for plant height were also observed by Venkatramana et al. (2001) in their studies. It exhibited moderate heritability (65.08%), moderate genetic advance (8.75) and moderate genetic advance in percentage of mean (8.39%) (Table 5), refers that the character is mostly controlled by non-additive genes and the tallest plant selection may will not be effective. Afrin et al. (2011) reported high heritability with high genetic advance in percentage of mean for this trait.

### Number of primary branches per plant

Primary branches per plant showed significant variations among the genotypes (1.56) at the level of 1% probability. Uddin et al. (2013) reported significant differences for number of primary branches per plant. Maximum number of primary branches were observed in SAU sarisha 2 x SAU sarisha 3 (5.31), minimum was in Tori 7 x SAU sarisha 3 (2.86) (Table 3) and the mean was 4.05 (Table 4). Phenotypic and genotypic variance were 0.70 and 0.43 respectively, indicated that there was lower environmental effect on the phenotypic traits. The PCV and GCV was 20.74 and 16.19 respectively which stated that the existence of inherent variability among the population. It exhibited low heritability (60.92%), low genetic advance (1.05) and moderate genetic advance in percent mean (25.99%) (Table 5). These results revealed the predominance of non-additive gene action in the inheritance of this trait which limits the scope of improvement by direct selection. Afrin et al. (2011) found low heritability with high genetic advance in percentage of mean.

### Number of secondary branches per plant

The data of analysis of variance in referred that the number of secondary branches per plant showed statistically significant differences (2.72) among the genotypes. Table 3 presented that the SAU sarisha 2 x SAU sarisha 3 (3.40) and

SAU sarisha 1 x SAU sarisha 3 (3.31) were significantly different from all other genotypes. The lowest no. of secondary branches were in BARI sarisha 6 x SAU sarisha 2 (0.23) and the mean value was 1.18 (Table 4). According to table 5 the phenotypic and genotypic variances were 0.99 and 0.87, which indicated low environmental influence to the genotypes for expression of this character. The higher difference between PCV (84.51) and GCV (79.07) indicating highly variable genotypes for this character. Lekh et al. (1998) reported the highest genotypic coefficient of variation for the number of secondary branches per plant. High heritability (87.56) along with moderate genetic advance (1.80) and high genetic advance in percentage of mean (152.13) suggesting the predominance of additive gene action in the inheritance of this trait. It provides a wider scope to the breeders for direct selection during crop improvement. Afrin et al. (2011) found high heritability along with high genetic advance in percentage of mean for this trait.

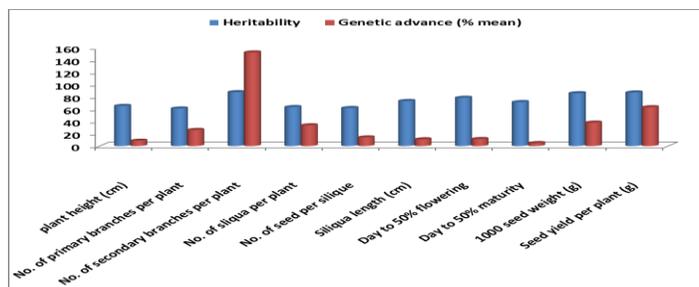
### Number of siliqua per plant

From ANOVA table, no. of siliqua per plant showed highly significant differences (1310.74) among the genotypes at the level of 1% probability. Among the lines, SAU sarisha 1 x SAU sarisha 3 showed highest number of siliqua per plant (138.40) with highest number of seeds per siliqua (19.31), siliqua length (5.52 cm) giving highest yield per plant (4.56 g) (Table 3). BARI sarisha 6 x SAU sarisha 2 giving the lowest no. of siliqua per plant (69.07) (Table 3) and the mean performance (93.22) was figured from Table 4. Number of siliqua per plant of BARI sarisha 6 x Tori 7 (124.60), BARI sarisha 15 x Tori 7 (115.30), BARI sarisha 15 x SAU sarisha 1 (107.50), BARI sarisha 6 x SAU sarisha 1 (100.10) showed better performance than others. The genotypic (365.83) and phenotypic variances (579.08) showed significant differences, which indicating the large environmental influence over genotypes. The PCV (25.81) was much higher than GCV (20.52) also referring environmental influence to express this trait and the existing of adequate variation among the genotypes. Highest phenotypic and genotypic variances and genotypic and phenotypic coefficient of variations for number of siliqua per plant were also observed by Azad and Hamid (2000) and Venkatramana et al. (2001). The medium heritability (63.18%) along with high genetic advance (31.32) and medium genetic advance in percentage mean (33.59%) indicating non-additive gene action. Selection based on this character may not be effective for future breeding program. High heritability and high genetic advance was reported by Afrin et al. (2011) and Akbar et al. (2007) also found higher

**Table 2.** Mean Sum of Squares from the ANOVA of 15 F<sub>4</sub> populations of *Brassica rapa* in respect of ten characters.

Source of variation	d. f.	Mean Square									
		PH	PBP	SBP	SPP	SPS	SL	D50%F	D50%M	TSW	YPP
Replication	2	40.42	0.18	0.40	161.40	1.21	0.03	1.12	2.29	0.04	0.01
Treatment	14	98.01**	1.56**	2.72**	1310.74**	7.75**	0.33**	23.09**	16.37**	1.01**	1.99**
Error	28	14.87	0.28	0.12	213.24	1.33	0.04	1.94	1.93	0.06	0.09

\*\* = Significant at 1%. PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliquae per plant, SPS = Number of seeds per siliquae, SL = Siliquae length (cm), D50%F = Days to 50% flowering, D50%M = Days to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g).



**Fig 2.** Heritability and genetic advance (% mean) in 15 genotypes of *Brassica rapa*

**Table 3.** Mean performance of ten characters of mustard.

Genotypes↓	Characters→									
	PH	PBP	SBP	SPP	SPS	SL	D50%F	D50%M	TSW	YPP
BARI 6xBARI 15	99.84d-f	3.50ef	1.13b-d	99.40b-f	15.24e-g	4.56f	48.00a	86.67a	2.26e	1.94e-g
BARI 6xSAU 1	104.1c-e	4.16b-e	1.48b	100.1b-e	14.63fg	4.74ef	46.00a-c	84.33ab	3.18b	2.57c-e
BARI 6 xTori 7	108.1bc	4.55a-c	0.663c-f	124.6ab	17.54a-d	5.09b-d	43.67c-f	84.33ab	2.78cd	3.45b
BARI 6xSAU 2	102.3c-f	3.66c-f	0.23f	69.07g	17.41a-d	5.25a-d	46.33ab	84.67ab	3.30b	2.39d-f
BARI 6xSAU 3	99.61d-f	3.30ef	0.62d-f	88.38c-g	16.82b-e	4.96c-d	42.00d-f	81.33c-e	2.63c-e	1.26i
BARI 15xSAU 1	108.2bc	4.50a-d	0.86b-f	107.5b-d	17.73a-d	4.50f	46.00a-c	84.67ab	2.49de	2.49c-f
BARI 15xTori 7	104.9cd	4.58a-c	1.31bc	115.3a-c	16.63c-f	5.36ab	44.00b-e	83.67bc	1.62f	2.20d-g
BARI 15xSAU 2	105.3cd	4.98ab	0.45ef	82.77d-g	18.18a-c	4.64ef	44.33b-d	80.67d-f	2.70cd	3.04bc
BARI 15xSAU 3	105.1cd	3.50ef	0.90b-f	75.30e-g	18.64a-c	4.93de	43.33d-f	84.67ab	2.95bc	2.20d-g
SAU 1xTori 7	96.41f	3.56d-f	0.95b-e	80.63d-g	18.09a-c	5.14b-d	41.33fg	82.67b-d	2.58c-e	1.68g-i
SAU 1xSAU 2	107.0b-d	3.48ef	0.80c-f	76.00e-g	18.28a-c	5.42ab	42.33d-f	84.00b	4.09a	2.23d-g
SAU 1xSAU 3	116.2a	4.90ab	3.31a	138.4a	19.31a	5.52a	41.67e-g	81.33c-e	3.34b	4.56a
Tori 7xSAU 2	97.40ef	3.80c-f	1.22b-d	94.47c-g	13.97g	5.31a-c	39.33gh	81.00de	2.60c-e	1.52hi
Tori 7xSAU 3	112.6ab	2.86f	0.32ef	71.10fg	18.96ab	5.23a-d	37.67h	79.33ef	2.48de	2.13e-g
SAU 2xSAU 3	97.10ef	5.31a	3.40a	75.20e-g	15.81d-g	5.36ab	41.33e-g	78.33f	3.347b	2.767cd

PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliquae per plant, SPS = Number of seeds per siliquae, SL = Siliquae length (cm), D50%F = Days to 50% flowering, D50%M = Days to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g).

**Table 4.** Estimation of genetic parameters in ten characters of 15 genotypes in mustard.

Parameters	Range	Mean	MS	CV (%)	SE
PH	96.41-116.20	104.28	98.00**	3.70	3.148
PBP	2.87-5.32	4.05	1.56**	12.96	0.428
SBP	0.23-3.40	1.18	2.72**	29.81	0.287
SPP	69.07-138.45	93.22	1310.74**	15.67	11.923
SPS	13.97-19.31	17.15	7.75**	6.73	0.942
SL	4.50-5.52	5.07	0.32**	3.71	0.153
D50%F	37.67-48.00	43.16	23.08**	3.23	1.138
D50%M	78.33-86.67	82.78	16.36**	1.68	1.135
TSW	1.62-4.10	2.83	1.00**	8.10	0.187
YPP	1.26-4.56	2.43	1.99**	12.66	0.251

\*\* = Significant at 1%. PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliquae per plant, SPS = Number of seeds per siliquae, SL = Siliquae length (cm), D50%F = Days to 50% flowering, D50%M = Days to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g), MS = Mean sum of square, SE = Standard error and CV (%) = Coefficient of variation.

**Table 5.** Estimation of genetic parameters in twelve characters of 19 genotypes in mustard.

Traits	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$	PCV	GCV	ECV	$h^2_b$	GA (5%)	GA%
PH	42.58	27.71	14.87	6.26	5.05	3.70	65.08	8.75	8.39
PBP	0.70	0.43	0.28	20.74	16.19	12.96	60.92	1.05	25.99
SBP	0.99	0.87	0.12	84.51	79.07	29.81	87.56	1.80	152.13
SPP	579.08	365.83	213.24	25.81	20.52	15.67	63.18	31.32	33.59
SPS	3.47	2.14	1.33	10.87	8.53	6.73	61.65	2.37	13.80
SL	0.13	0.10	0.04	7.15	6.12	3.71	73.12	0.55	10.77
D50%F	8.99	7.05	1.94	6.95	6.15	3.23	78.41	4.84	11.22
D50%M	6.74	4.81	1.93	3.14	2.65	1.68	71.35	3.82	4.61
TSW	0.37	0.32	0.05	21.53	19.94	8.11	85.81	1.08	37.99
YPP	0.73	0.63	0.09	35.12	32.76	12.66	87.00	1.53	62.96

PH = Plant height (cm), PBP = Number of primary branches per plant, SBP = Number of secondary branches per plant, SPP = Number of siliquae per plant, SPS = Number of seeds per siliquae, SL = Siliquae length (cm), D50%F = Days to 50% flowering, D50%M = Days to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g),  $\sigma^2_p$  = Phenotypic variance,  $\sigma^2_g$  = Genotypic variance,  $\sigma^2_e$  = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation and ECV = Environmental coefficient of variation.

**Table 6.** Performance of some selected yellow seeded plants from F<sub>4</sub> materials of different cross combinations of *Brassica rapa*.

Cross Combinations	Plant No.	SPP	D50%F	TSW	YPP
	6	217	86	3.00	3.00
BARI sarisha 6 x BARI sarisha 15	17	228	88	3.00	5.60
	29	93	86	2.30	3.33
	9	138	83	4.00	5.80
BARI sarisha 6 x SAU sarisha 1	19	75	85	2.10	4.30
	26	166	85	4.00	5.20
BARI sarisha 6 x Tori 7	13	183	85	3.00	6.20
BARI sarisha 6 x SAU sarisha 2	5	52	83	6.00	3.40
BARI sarisha 6 x SAU sarisha 3	27	215	84	5.00	4.50
	8	131	85	2.00	4.10
BARI sarisha 15 x SAU sarisha 1	23	255	85	2.50	3.90
BARI sarisha 15 x Tori 7	4	75	82	2.00	3.90
	1	218	79	3.95	4.90
	12	92	82	3.00	4.10
BARI sarisha 15 x SAU sarisha 2	23	186	81	3.00	5.90
	13	91	85	3.00	5.90
	30	76	85	3.00	5.60
	1	126	84	3.40	3.71
SAU sarisha 1 x Tori 7	13	107	82	2.80	3.03
	23	51	82	2.50	4.50
	10	79	86	2.10	3.90
SAU sarisha 1 x SAU sarisha 2	11	225	84	4.00	4.10
	21	75	82	4.00	4.70
SAU sarisha 1 x SAU sarisha 3	3	208	82	4.00	14.90
	2	113	80	4.00	5.90
Tori 7 x SAU sarisha 3	20	147	78	3.00	5.53
	21	70	80	2.20	3.46

SPP = Number of siliquae per plant, D50%F = Days to 50% flowering, D50%M = Days to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g).

**Table 7.** Performance of some selected brown seeded plants from F<sub>4</sub> materials of different cross combinations of *Brassica rapa*.

Cross Combinations	Plant No.	SPP	D50%F	TSW	YPP
BARI sarisha 6 x BARI sarisha 15	18	97	88	3.50	3.75
	23	189	86	3.00	3.80
	1	145	83	4.00	4.20
BARI sarisha 6 x SAU sarisha 1	16	57	85	4.00	6.10
	24	174	85	3.00	3.60
BARI sarisha 6 x Tori 7	7	456	84	2.00	10.60
BARI sarisha 6 x SAU sarisha 2	6	101	83	3.00	3.40
	30	216	86	3.00	4.30
BARI sarisha 15 x SAU sarisha 1	12	465	84	3.00	5.70
BARI sarisha 15 x Tori 7	12	263	85	1.50	4.82
BARI sarisha 15 x SAU sarisha 2	18	215	82	3.00	7.40
BARI sarisha 15 x SAU sarisha 3	11	223	85	2.50	5.80
SAU sarisha 1 x Tori 7	14	118	82	3.30	4.42
SAU sarisha 1 x SAU sarisha 2	23	115	82	4.00	3.30
SAU sarisha 1 x SAU sarisha 3	2	355	86	5.00	11.20
	14	118	84	3.20	3.60
Tori 7 x SAU sarisha 2	22	107	82	2.50	3.10
Tori 7 x SAU sarisha 3	6	145	80	2.28	3.08
SAU sarisha 2 x SAU sarisha 3	2	128	78	3.00	5.92

SPP = Number of siliquae per plant, D50%F = Days to 50% flowering, D50%M = Days to 50% maturity, TSW = 1000 seed weight (g), YPP = Yield per plant (g).

GCV, broad base heritability and genetic advance for this trait.

#### Number of seeds per siliquae

Number of seeds per siliquae showed highly significant variations (7.75) among the genotypes from ANOVA at 1% level of probability. Among the lines, SAU sarisha 1 x SAU sarisha 3 showed highest number of seeds per siliquae (19.31) along with highest siliquae length (5.52 cm) giving highest yield per plant (4.56 g) (Table 3). Tori 7 x SAU sarisha 2 giving the lowest no. of seeds per siliquae (13.97) (Table 3) and the mean performance (17.15) was figured from Table 4. The genotypic (2.14) and phenotypic variances (3.47) showed lower differences, which indicating the lower environmental influence over genotypes. The PCV (10.87) was higher than GCV (8.53) referring moderate variation among the genotypes with some environmental influence for the expression of this character. Yogendra et al. (2002) reported low phenotypic coefficient of variation and genotypic coefficient of variation for this character. The low heritability (61.65%) along with moderate genetic advance (2.37) and low genetic advance in percentage mean (13.80%) indicating non-additive gene action. Selection based on this character will not be rewarding for future breeding programme. Afrin et al. (2011) reported moderate heritability (43.72%) with very high genetic advance in percentage of mean.

#### Siliquae length

In the present study analysis of variance of the data for siliquae length showed significant differences among the genotypes. The mean square values (0.33) regarding the siliquae length indicated the presence of variability among the genotypes. The longest siliquae was found in SAU sarisha 1 x SAU sarisha 3 (5.52 cm) giving highest yield per plant (4.56 g) (Table 3). BARI sarisha 6 x BARI sarisha 15 (4.56 cm) and BARI sarisha 15 x SAU sarisha 1 (4.50 cm) giving the shortest siliquae (Table 3) and the mean performance (5.07) was figured from Table 4. The genotypic (0.10) and phenotypic variances (0.13) showed lowest differences, which indicating the lowest environmental influence on genotypes. The PCV (7.15) was higher than

GCV (6.12) referring moderate variation among the genotypes with some environmental influence for the expression of this character. Jahan et al. (2014) also reported similar result. The moderate heritability (73.12%) along with low genetic advance (0.55) and low genetic advance in percentage mean (10.77%) indicating non-additive gene action. Selection based on this character will not be rewarding for future breeding program. Afrin et al. (2011) reported moderate heritability with moderate genetic advance in percentage of mean.

#### Thousand seed weight

According to the ANOVA significant variations in thousand seed weight (1.01) were presented among the studied genotypes at 1% level of probability. From table 3, highest seed weight (4.09 g) was found in SAU sarisha 1 x SAU sarisha 2 gave moderate yield (2.23 g) as it had moderate number of siliquae per plant (80.63) but higher no. of seeds per siliqua (18.28). SAU sarisha 2 x SAU sarisha 3 (3.35 g), SAU sarisha 1 x SAU sarisha 3 (3.34 g), BARI sarisha 6 x SAU sarisha 2 (3.30 g) and BARI sarisha 6 x SAU sarisha 1 (3.18 g) were giving the higher seed weight among the genotypes. According to the table 4, the mean value was 2.83 g, which is much lower than above mentioned genotypes. There were very little differences between the phenotypic variance (0.37) and genotypic variance (0.32) indicating very low environmental effect on them. Moderate difference between PCV (21.53) and GCV (19.94) showed moderate variation in genotypes (Table 5). Highest phenotypic and genotypic variances and genotypic and phenotypic coefficient of variations for 1000-seed weight were also observed by Azad and Hamid (2000) and Venkatramana et al. (2001). Heritability for this trait was higher (85.81%) with moderate genetic advance (1.08) and moderate genetic advance in percentage mean (37.99%) indicating this trait is governed by non-additive gene which includes dominance and epistasis. The high heritability along with considerable genetic advance in percentage of mean was reported by Afrin et al. (2011). Singh et al. (2002) reported the high heritability and genetic advance 1000 in seed weight.

### **Yield per plant**

Yield per plant showed highly significant variations (1.99) among the genotypes from ANOVA at 1% level of probability. Among the lines, SAU sarisha 1 X SAU sarisha 3 showed highest yield per plant (4.56 g) (Table 3). BARI sarisha 6 V SAU sarisha 3 giving the lowest yield per plant (1.26 g) (Table 3) and the mean performance (2.43 g) was figured from Table 4. The genotypic (0.63) and phenotypic variances (0.73) showed lower differences, which indicating the lower environmental influence over genotypes. The PCV (35.12) was higher than GCV (32.76) referring moderate variation among the genotypes with some environmental influence for the expression of this character. The high heritability (87.00%) along with moderate genetic advance (1.53) and high genetic advance in percentage mean (62.96%) indicating additive gene action. Selection based on this character will be rewarding for future breeding programme. Aytac and Kinaci (2009) mentioned the high heritability and genetic advance for seed yield.

### **Selection of plant material**

Variability was found for most of the studied character in almost all the F<sub>4</sub> materials of different cross combinations. Selection was carried out among the studied populations as per objectives. Thirty one most promising plants with yellow seed were selected from different cross combinations (Table 6). There were large variations for number of siliquae per plant ranging from 51-255 siliquae. The genotypes showed variations regarding maturity duration (78-86 days). The most short durational cross combination was Tori 7 x SAU sarisha 3 (78 days) bearing 5.53g seed per plant which was high in comparison with others. The exceptionally highest yield per plant (14.90 g) was obtained from cross combination SAU sarisha 1 x SAU sarisha 3 and also it had higher number of siliquae per pant (208) and it takes 82 days to mature. 1000 seed weight was as much as 6 g from BARI sarisha 6 x SAU sarisha 2 cross combination.

On the other hand twenty five most promising plants from different cross combinations with brown seed were selected (Table 7). There were also variations for number of siliquae per plant (57- 465). Maturity duration ranged from 79 to 86 days. The exceptionally highest seed yield per plant (11.20 g) was obtained from the SAU sarisha 1 x SAU sarisha 3 cross combination and also it had higher number of siliquae per pant (355) and it takes 86 days to mature. In this combination 1000 seed weight (5 g) was also higher comparing to others. So from the table 6 and table 7 we can conclude that cross combination SAU sarisha 1 x SAU sarisha 3 is the best promising line.

## **Materials and Methods**

### **Experimental site**

The present research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during October 2012-March 2013. The location of the site is 23° 74' N latitude and 90° 35' E longitude with an elevation of 8.2 meter above sea level.

### **Soil and climate**

The experimental site was suited in the subtropical climate zone, wet summer and dry winter is the climatic feature of this region. The soil of the experimental site belongs to Agro-

ecological region of "Madhupur Tract" (AEZ No. 28). The soil of the plots was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The land was medium high with medium fertility level. The p<sup>H</sup> was 5.47 to 5.63 and organic carbon content is 0.45%. During the Rabi season the rainfall generally is scant and temperature is moderate with short day length.

### **Plant materials**

The experiment was conducted using fifteen F<sub>4</sub> generation materials of *B. rapa* (included in table 1). There were 100 plants in each cross combination and the total population was 1500. The F<sub>4</sub> progenies were selected from F<sub>3</sub> progenies of the previous year based on their variation and performance in different traits. The F<sub>1</sub>'s were obtained through half diallel crossing among five parents. All the F<sub>4</sub> materials were collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh.

### **Field Experiment**

The experimental plot was prepared by several ploughing and cross ploughing followed by laddering and harrowing with tractor and power tiller to bring about good tilth. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly.

A Randomized Complete Block Design was used in the experiment with three replications. The field was divided into three blocks; the blocks were subdivided into 15 plots. Genotypes were randomly assigned into 15 plots in each block. The plot size was 125 m<sup>2</sup> (5m×25m). Block to block and plot to plot distance were 1.5 m and .3 m respectively. The seed sowing was carried out on 30 October, 2012 in the seedbed. The seeds were placed at about 1.5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. Seed germination started after 3 days of sowing. Intra and inter row distance were maintained @ 0.1 m and 0.3 m respectively. Urea, Triple Super Phosphate, Muriate of Potash, Gypsum, Zinc oxide, Boron @ 250, 175, 85, 250, 3, 1 kg/ha and Cowdung 10 ton/ha were used in the experiment. Half of Urea and rest of the fertilizers were applied in final land preparation and the remaining of the Urea was applied in the plot after 25 days of seed sowing.

### **Intercultural operations**

Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots. One post sowing irrigation was given with cane after sowing of seeds to bring proper moisture condition of the soil to ensure uniform germination of the seeds. A good drainage system was maintained for immediate release of excess rain or irrigation water from the experimental plot during the growing period. The first weeding was done after 15 days of sowing. At the same time, thinning was done for maintaining a distance of 10 cm from plant to plant in rows of 30 cm apart. Second weeding was done after 35 days of sowing. The crop was protected from the attack of aphids by spraying Malathion-57 EC (Organophosphate) @ 2 ml/liter of water. The insecticide was applied for the first time approximately before one week of flower initiation and it was applied for another two times at an interval of 15 days. To protect the crop from the *Alternaria* spot, Rovral-50 WP (Dicarboximide) was sprayed at the rate of 25g in 10 ml

water at 50% flowering stage for the first time and it was again applied for two times at an interval of 15 days.

### **Crop harvesting**

Harvesting was started from 15 February, 2013 depending upon the maturity of the plants. When 80% of the plants showed symptoms of maturity i.e. straw color of siliquae, leaves, stem and desirable seed color in the matured siliquae, the crop was assessed to attain maturity. Ten plants were selected at random from F<sub>4</sub> progenies in each replication.

### **Recording data**

Data were recorded on various plant traits i.e. plant height (cm), number of primary branches per plant, number of secondary branches per plant, siliquae length (cm), number of siliquae per plant, number of seeds per siliquae, 1000 seeds weight (g), seed yield per plant (g), seed coat color, days to 50% flowering and days of maturity.

### **Statistical analysis**

All the collected data of the study were analyzed for different characters. Analysis of variance (ANOVA), mean, range were calculated by using MSTATC software program and then the analysis of variance for different characters was measured followed by the Duncan's new multiple range test (DMRT) (Steel and Torrie, 1980), to test the significant differences between means. Phenotypic and genotypic variance was estimated by the formula used by Johnson et al. (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic coefficient of variation was calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller et al. (1958), Johnson et al. (1955) and Hanson et al. (1956).

### **Conclusion**

Highly significant variation was observed among the genotypes for almost all the characters studied revealed the presence of considerable variability among the studied genotypes. The cross combination SAU sarisha 2 x SAU sarisha 3 showed earliest maturity of 78 days with moderate yield per plant (2.77 g). Highest yield per plant (4.56 g) was observed in SAU sarisha 1 x SAU sarisha 3 cross combination with tallest plant (116.2 cm), higher number of primary branches per plant (4.90), maximum number of secondary branches per plant (3.31), maximum number of siliquae per plant (138.4), maximum number of seeds per siliqua (19.31) and longest siliqua (5.52cm). So we can conclude that, SAU sarisha 1 x SAU sarisha 3 cross combination can be used for future breeding program.

Number of siliquae per plant showed highest range of variation (69.07-138.45) which refers a wide range of variation for this character. Highest mean value was observed in plant height (104.28). The phenotypic variance and phenotypic coefficient of variation were higher than corresponding genotypic variance and genotypic coefficient of variation for all the studied character. It suggests that, environmental influence is present in some extent for the expression of the genotypes. On the other hand number of primary branches per plant, number of secondary branches per plant, seeds per siliquae, siliquae length, thousand seed weight and yield per plant showed least difference between

phenotypic and genotypic variance indicating less environmental influence for the expression of these characters. The number of secondary branches per plant (87.56%) exhibits the highest value for heritability while the primary branches per plant (60.92) shows lowest value. Yield per plant, thousand seed weight, siliquae length, days to 50% flowering, days to 50% maturity and plant height showed moderate heritability.

From the above results we can conclude that, number of primary branches per plant, plant height, number of siliquae per plant, number of secondary branches per plant, number of seeds per siliquae and thousand seed weight are the most influencing yield contributing character for the studied genotypes. Therefore these can be used for future breeding programme for improvement of *Brassica rapa*.

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