



Variability, Correlation and Path Analysis in F₂ Progenies of Inter-Varietal Crosses of *Brassica Rapa*

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Abstract: Eight F₂ populations generated through inter-variety crosses, along with three check varieties of *Brassica rapa* were evaluated to study the variation in different characters, correlation between pairs of different characters and the direct and indirect effect of different characters on seed yield per plant to select the plants with higher yield potential. From the values of mean, range and (CV%) of seed yield and yield contributing characters it was confirmed that there were considerable variation present among all the genotypes used in the experiment. The values of phenotypic variances were higher than the corresponding genotypic variances. Number of branches per plant, length of siliqua, seeds per siliqua, 1000 seed weight and yield per plant showed least difference between phenotypic and genotypic variances. The values of GCV and PCV indicated that there was least variation present among most of the characters studied. The number of branches per plant, days to 50% flowering, days to maturity and length of siliqua had showed high heritability with low genetic advance and genetic advance in percentage of mean. Yield per plant had significant and highest positive correlation with plant height, days to 50% maturity, length of siliqua and seeds per siliqua. The path co-efficient analysis revealed that siliqua per plant had the highest positive direct effect followed by seeds per siliqua, length of siliqua and plant height. Sixteen most promising plants with higher yield were selected for cultivation.

Key words: *Brassica rapa*, Correlation, Genetic variability, F₂ segregating population, Path analysis

Introduction

Brassica rapa, commonly known as field mustard or turnip mustard is a widely cultivated as an oil seed crop. In Bangladesh more than 150 thousand metric ton of local rape and mustard was produced from a total 431 thousand acre of cultivable land 743 thousand metric ton of hybrid rape and mustard produced from a total of 146 thousand acre of cultivable land in the year 2009-2010 (BBS, 2010). The genus *Brassica* has generally been divided in to three groups namely –rape seed, mustard and cole. The rape seed groups includes the diploid *Brassica rapa*, turnip rape (AA, 2n=20) and amphidiploid *Brassica napus* L, rape (AACC, 2n=38) while the mustard groups include species like *Brassica juncea* Czern and Coss; *Brassica nigra* Koch and *Brassica carinata* Braun (Yin, 1989). All these species have many cultivated varieties suited to different agro-climatic conditions. In the oleiferous *Brassica* group, a considerable variation of genetic nature exists among different species and varieties within each species in respect of different morphological characters (Malik *et al.* 1995; Kakroo and Kumar, 1991).

In Bangladesh there is limited scope to increase acreage due to pressure of other crops. There is limited scope to increase yield because farmers usually cultivate the existing low yielding varieties with low input and management and almost all cultivars are brown seeded and smaller in size (2-2.5

g/1000 seeds). Short duration variety like Tori-7 of *B. rapa* is still popular in Bangladesh because it can fit well into the T. Aman – Mustard – Boro cropping pattern. There is no improved short duration variety of *B. juncea* is available to replace short duration Tori -7. So we need to develop higher yielding short duration *Rapa* variety. A study of correlation between different qualitative characters provides idea of association that could be effectively utilized in selection for a better plant type. Thus the present research work was undertaken to study the variability in F₂ segregating generations to select the desired plant types and to find out the relationship among the different traits and their contribution to the yield.

Materials and Methods

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, during November, 2009 to March, 2010. A total number of eleven different populations obtained from eleven different cross consideration materials were used in this experiment where eight were F₂ segregating generations and three were checks varieties. All the Materials were collected from Department of Genetics and Pant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. The materials used in that experiment are SS 75 × SAU 1, SS 75 × BARI 15, BARI 15 × BARI 6, BARI 6 × TORI 7, BARI 15 × SS 75, R TORI 7 × SAU 1, BARI 11 × TORI 7, BARI 10 × BARI 15, BARI sharisha 11, BARI sharisha 15 and SAU sarisha 1.

The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area under the experiment was $56\text{ m} \times 14\text{ m} = 784\text{ m}^2$. Each plot size was $56\text{ m} \times 3.5\text{ m}$, and the distance between plots to plot was 1 m. The spacing between lines was 30 cm. The data were recorded on forty selected plants for each cross and ten selected plants for each parent on the plant height (PH), number of branches per plant (NBP), days to 50% flowering (50%DF), days to 50% maturity (50%DM), number of siliqua per plant (NSP), siliqua length (SL), number of seeds per siliqua (NSS), 1000 seed weight (SW) and yield per plot (YP). The data were statistically analyzed for different components. Phenotypic and genotypic variance was estimated according to Johnson *et al.* (1955). Heritability and genetic advance were measured as suggested by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Simple correlation coefficient was obtained using the formula suggested by Clarke (1973); Singh and Chaudhary (1985) and path co-efficient analysis was done following the method outlined by Dewey and Lu (1959).

Results and Discussion

The estimates of genotypic variance, phenotypic variance, environmental variance, genotypic (GCV) and phenotypic coefficients of variation (PCV), heritability (h^2b), genetic advance (GA) and genetic advance as percentage of mean for the characters are given in Table 1. In the study, significant variations

were observed for most of the characters among 8 F_2 materials of *Brassica rapa*. The least difference between phenotypic and genotypic variances were observed for NBP, SL, NSS, SW and YP indicating that these characters were less responsive to environmental factors for their phenotypic expression. The highest difference between genotypic and phenotypic variance was observed for NSP followed by PH indicating large environmental influences on these characters. 50%DF and 50%DM had moderate differences for genotypic and phenotypic variance indicating environment had less influence on these characters. A narrow difference between PCV and GCV supported the speculation that environment had little effect on characters under the present study. The highest and lowest GCV were found in YP and 50%DM respectively. PH and NSP had high heritability with high genetic advance, Genetic advance in percentage of mean revealed possibility of predominance of additive gene action in the inheritance of these traits. These traits could be improved through selection process. The high heritability with low genetic advance and genetic advance in percentage of mean were estimated for NBP, 50%DF, 50%DM and SL. The results indicated the lower possibility of selecting genotypes. Similar results have also been reported by Varshney *et al.* (1986), Malik *et al.* (1995), Yadava *et al.* (1982), Sharma (1984) and Kakroo and Kumar (1991). Johnson *et al.* (1955) reported that heritability estimates along with genetic gain were more useful in predicting selection of the best individual.

Table 1. Estimation of some genetic parameters in respect of F_2 genotypes

Parameters	σ^2_g	σ^2_p	σ^2_e	h^2b	GA	GA in % mean	GCV	PCV
PH	119.31	29.87	149.17	79.98	20.12	18.75	10.18	11.38
NBP	0.46	0.93	1.39	33.18	0.81	8.84	7.45	12.93
50%DF	12.59	3.19	15.77	79.81	6.53	15.24	8.28	9.27
50%DM	2.48	3.88	6.36	39.01	2.03	2.08	1.62	2.59
NSP	3706	606	4312	85.9	116	51.2	26.8	28.9
SL	0.17	0.23	0.40	42.11	0.55	0.79	8.07	12.44
NSS	11.08	0.96	12.04	92.03	6.58	40.89	20.69	21.57
SW	0.39	0.06	0.44	87.53	1.20	42.19	21.89	23.40
YP	6.69	0.77	7.46	89.67	5.04	60.95	31.25	33.00

Correlation co-efficient

Seed yield is a complex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. Correlation co-efficient between pairs of trait for F_2 materials of *B. rapa* (Table 2) revealed that the genotypic correlation coefficients in most of the cases were higher than their phenotypic

correlation coefficients indicating the effects of environment suppressed the phenotypic relationship between these characters. In few cases, phenotypic correlation coefficient were same or higher than their genotypic correlation coefficients suggesting that both environmental and genotypic correlations in these cases acted in the same direction and finally maximize their expression at phenotypic level. Seed yield had positive and highly significant association with 50%DF, SL and NSS both at genotypic and

phenotypic levels. Das *et al.* (1998) reported that seed yield per plant was positively correlated with length of siliqua. Dhillon *et al.* (1997) and Tyagi *et al.* (1996) reported that no. of seeds per siliqua had positive and significant effects on seed yield per

plant. PH had significant and negative association with seed yield at both genotypic and phenotypic level. Similar associations were also reported by Chowdhury *et al.* (1993) and Yadava *et al.* (1978).

Table 2. Genotypic and phenotypic correlations co-efficient among different

Parameters		NBP	50%DF	50%DM	NSP	SL	NSS	SW	YP
PH	r _g	0.591**	0.522*	0.125	-0.812**	-0.292	-0.458*	-0.341	-0.678**
	r _p	0.287	0.334	-0.017	-0.539*	-0.252	-0.122	-0.065	-0.409*
NBP	r _g		0.933**	0.990**	-0.315	0.320	0.590**	0.263	0.572**
	r _p		0.389	0.401*	-0.021	0.144	0.17	0.022	0.337
50%DF	r _g			0.773**	-0.485*	-0.399*	0.107	0.115	-0.289
	r _p			0.651**	0.07	-0.039	0.257	-0.014	0.162
50%DM	r _g				0.249	0.384	0.649**	0.495*	0.856**
	r _p				0.298	0.369	0.474*	0.330	0.671**
NSP	r _g					0.013	-0.073	-0.012	0.529*
	r _p					0.177	0.14	-0.049	0.528*
SL	r _g						0.999**	0.695**	0.703**
	r _p						0.741**	0.636**	0.605**
NSS	r _g							0.783**	0.619**
	r _p							0.724**	0.651**
SW	r _g								0.310
	r _p								0.428*

Path co-efficient analysis

Association of characters determined by correlation co-efficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on seed yield per plant. In order to find out a clear picture of the inter-relationship between seed yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica rapa* is presented in Table 3. NSP had

maximum positive direct effect on seed yield followed by NSS and SL. The direct effect revealed that the characters viz., NSP, NSS and SL having high positive correlation with YP, also had direct positive influence with YP. The results also had close agreement with the findings of Yadava *et al.* (1996), Chaudhury *et al.* (1987) and Uddin *et al.* (1995). The residual effect of the present study was 0.434 indicating 57% of the variability of seed yield per plot was contributed by the characters studied in the path analysis.

Table 3. Path coefficients analysis of genotypic correlation showing direct (bold) and indirect effect of yield contributing characters on yield of *B. rapa* in F₂

Characters	PH	NBP	50%DF	50%DM	NSP	SL	NSS	SW	r _g with yield
PH	0.388	-0.078	0.151	0.001	-0.802	-0.153	-0.374	0.189	0.678
NBP	0.229	-0.132	0.271	0.010	-0.311	0.168	0.482	-0.146	0.572
50%DF	0.202	-0.123	0.290	0.008	-0.479	-0.210	0.087	-0.064	-0.289
50%DM	0.049	-0.131	0.224	0.010	0.245	0.202	0.530	-0.274	0.856
NSP	-0.315	0.042	-0.141	0.002	0.987	0.007	-0.060	0.007	0.529
SL	-0.113	-0.042	-0.116	0.004	0.013	0.526	0.817	-0.385	0.703
NSS	-0.178	-0.078	0.031	0.006	-0.072	0.526	0.817	-0.434	0.619
SW	-0.132	-0.035	0.033	0.005	-0.012	0.366	0.640	-0.554	0.310

Residual (R) = 0.434

Conclusion

Considering heritability, genetic advance, genetic advance in % of mean, correlation, path coefficient analysis for the characters under study and comparing the crosses with three check varieties sixteen most promising plants with good yield and yield

contributing characters were selected from the crosses BARI 15 × SS 75, TORI 7 × SAU 1 and BARI 11 × TORI 7.

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