Genetic variability and characters association in rape seed (*Brassica napus* L)

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ABSTRACT

Genetic variability, correlation and path coefficient analysis were done for yield and its component characters in twenty two diverse genotypes of rape seed. The highest genotypic coefficient of variation (GCV) was recorded for seed yield per plant (31.33%) followed by siliqua per plant (20.07%). Heritability estimates in broad sense were higher for the characters days to maturity (83.92%), days to flowering (72.49%) and thousand seed weight (68.13%). Days to maturity, days to flowering, thousand seed weight and length of siliqua had high heritability along with low genetic advance suggests non-additive gene action was observed controlling these characters. Correlation coefficient of days to flowering (0.406*), primary branches per plant (0.514**), length of siliqua (0.548**), siliqua per plant (0.864**), seeds per siliqua (0.335*) was positive and significantly associated with seed yield per plant at genotypic level. Primary branches per plant (1.588), days to maturity (0.185), length of siliqua (0.740), siliqua per plant (0.569) and thousand seed weight (0.590) showed positive direct effect on seed yield. Selection based on these traits would give better response for the improvement of seed yield in rapes. The results of this study are expected as the basic information on genetic variation and relationship of component traits which can be used in rape seed breeding.

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Introduction

Rapeseed (*Brassica napus* L., 2n=38) is an important oil seed crop belonging to the family Cruciferae. Rapeseed is the second most important oil crop in the world after soybean (Hasan *et al.*, 2006). Besides that, rapeseed is also very important as a key crop for the raw material supply in the biodiesel (green diesel) industry (Marjanovic-Jeromela, 2005). Rapeseed and mustard grown in Bangladesh comprise of three species viz. *B. campestris* L., *B. juncea* L. and newly introduced *B. napus* and it occupies the first position in respect to area and production among the oil crops grown in Bangladesh (Anonymous, 2007). In general, the *B. napus* varieties have high seed and oil productivity with bold seeds. High yield potential of *B. napus* is mainly due to elongate flower raceme with moderate number of large siliqua accommodating more number of bold seeds and also due to higher number of plants that can be accommodated per unit area. The yield of rapeseed and mustard is generally low in Bangladesh as compared with the world average. The main problems for this low yield are the use of low yielding local indigenous cultivars, unavailability of locally developed hybrids and low management practices. The present seed yield per hectare of mustard in Bangladesh is far below the level attained in the developed countries of the world. With good management and use of hybrid varieties, the present yield level could be increased.

Genetic variability is a prerequisite for a successful breeding program of any crop species and a critical survey of genetic variability is essential before initiating an improvement program aiming to develop high yielding varieties. Selection which is the retention of desired genotypes and elimination of undesirable ones is a major and important process in breeding for improvement of one or more plant attributes (Chopra, 2000). The utilization of any criterion for selection is linked with high genetic coefficient of variation and estimates of heritability as

the magnitudes of heritability and other genetic parameters for a character would vary from location to location (Ramachandran *et al.*, 1982). It is also necessary to know the correlation of among the component characters and with yield. Path analysis partitions the components of correlation coefficient into its direct and indirect effects and visualizes the relationship in more meaningful way. Therefore, the present study was undertaken to study the variability and relationship between yield and its components in rape seed.

Materials And Methods

Twenty two genotypes of rape seed were grown in a randomized complete block design with three replications at the experimental field, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur, Bangladesh. The experimental materials were collected from Plant Genetic Resources Center, Bangladesh Agricultural Research Institute, Gazipur 1706. The seeds were sown in the rows 50cm apart and seeds in 5cm apart in the rows. Intercultural operations were done as and when necessary. Yield contributing data have been recorded from the mean of ten harvested plants selected randomly from each genotype in each replication. Data were recorded on ten characters namely days to flowering (DF), number of primary branches per plant (PB), plant height (PH), length of inflorescence (LI), days to maturity (DM), length of siliqua (LS), siliqua per plant (SP), seeds per siliqua (SS), 1000-seed weight (TSW) and seed yield per plant (SYP). Genotypic and phenotypic coefficients of variation were calculated by the formula suggested by Burton (1952) and Al-Jibouri *et al.* (1958). The broad sense heritability and genetic advance in percentage of mean were calculated following Lush (1949), Hanson (1961) and Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were calculated according to Miller *et al.*, (1958). Genotypic correlation coefficient were

further partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959).

Results and Discussion

Genetic Variability, Heritability and Genetic Advance:The estimates of genotypic variance ($\sigma^2 g$), phenotypic variance ($\sigma^2 p$), genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability ($h^2 b$), genetic advance (GA) and genetic advance in percent of mean (GA%) for seed yield and yield contributing characters are presented in Table 1. The estimates of GCV and PCV indicated that there were considerable variations for all the characters. Primary branches per plant, length of siliqua and thousand seed weight showed minimum variation. The GCV and PCV were the highest for number of siliqua per plant and seed yield per plant (20.27% & 32.41% and 31.33% & 43.44%, respectively) indicating higher degree of genetic variability in these traits. Heritability in broad sense ranged from 28.68 (PB) to 83.92% (DM), whereas the expected genetic advance varied from 0.29% (PB) to 49.46% (SP). Almost all the characters except days to maturity (83.92%), days to flowering (72.49%), thousand seed weight (68.13%) and length of siliqua (62.65%) showed low heritability. Days to maturity, days to flowering, thousand seed weight and length of siliqua had high broad sense heritability along with low genetic advance suggests non-additive gene action was present controlling these characters. The high heritability is exhibited due to influence of favorable environments rather than genotypes and selection for such trait may not be rewarding. High heritability for days to 50% flowering was also reported by (Tyagi *et al.*, 2000); days to 50% maturity by (Siddique and Gupta, 1991); pod length by (Roquib and Patnaik, 1997). Low heritability and high genetic advance for siliqua per plant indicates that the character is governed by additive gene effects. The low heritability is due to high environmental effects. Selection may be effective in such case. Both heritability and genetic advance were low for primary branches per plant, which suggest that the character is highly influenced by environmental effects and selection for this character will not be effective.

DF= days to flowering, PB= number of primary branches per plant, PH= plant height, LI= length of inflorescence, DM= days to maturity, LS= length of siliqua, SP= siliqua per plant, SS= seeds per siliqua, TSW= thousand seed weight, SYP= seed yield per plant The characters with high values of genetic coefficient of variation and heritability accompanied by high genetic advance in percentage of mean indicating that might be transmitted to their hybrid progenies. Earlier Burton (1952), Chaudhary and Sharma (2003), Sharma *et al.* (2003) and Gupta *et al.* (2006) also suggested that high GCV along with high heritability and genetic advance provided better view scope for selecting high yielding genotypes. This result suggests that improvement of these would be effective through phenotypic selection. High heritability is considered to be helpful in making selection of superior genotypes on the basis of phenotypic performance. The high value of heritability and genetic advance show that variation is attributable to a high degree of additive effect and the character can be improved by selection (Panse, 1957).

Correlation Coefficients:

Correlation coefficients both at genotypic and phenotypic level between seed yield and its component characters are presented in Table 2. The correlation studies revealed that in

general estimates of genotypic correlation coefficient were higher than corresponding phenotypic correlation coefficient, which indicated a strong inherent association among different traits under study and the apparent association may be largely due to genetic reason. The lower phenotypic values might be due to environmental interactions (Table 2). Similar observations were noticed in peas earlier (Chaudhary and Sharma, 2003; Kumar and Sharma, 2006).

DF= days to flowering, PB= number of primary branches per plant, PH= plant height, LI= length of inflorescence, DM= days to maturity, LS= length of siliqua, SP= siliqua per plant, SS= seeds per siliqua, TSW= thousand seed weight, SYP= seed yield per plant The difference between genotypic and phenotypic correlation was in general low, indicating the environmental effects did not have much influence on these characters. In some cases, phenotypic correlation coefficients were same or higher than their genotypic correlation coefficients suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level.

Correlation coefficient among seed yield per plant and other yield contributing characters revealed that seed yield was positively and significantly associated with days to flowering, primary branches per plant, day to flowering, length of siliqua, siliqua per plant, seeds per siliqua at genotypic level. It indicated that these characters have the major contribution towards the seed yield of rape. A very weak association was observed between days to maturity, length of inflorescence and 1000-seed weight with seed yield per plant in this study suggested that environment played role in determining these traits. Jiban *et al.* (1998) also evaluated the major contribution to genetic variability for number of siliqua per plant and number of seeds per siliqua in Toria. So selection would be effective for improving seed yield per plant in rape by selecting the characters days to flowering, primary branches per plant, day to flowering, length of siliqua, siliqua per plant, seeds per siliqua (Table 2). The highly significant and positive correlation was due to the substantial influence of the traits and these traits were genetically linked up with the seed yield. It is therefore indicated by importance may be given to select plants with longer siliqua, higher number of siliqua per plant and seeds per siliqua.

Path Analysis: Path coefficient analysis (Table 3) revealed that primary branches per plant, days to maturity, length of siliqua, siliqua per plant and thousand seed weight had positive direct effect on seed yield per plant. Positive and higher values of direct effect of primary branches per plant, length of siliqua and siliqua per plant on seed yield per plant were the reflection of significant positive correlation of these traits with seed yield. Though days to maturity showed positive direct effect on seed yield but its indirect effects through days to flowering, plant height, length of inflorescence and length of siliqua were negative which consequently reduce the correlation of this character with seed yield per plant. Similar results also observed for thousand seed weight. This result suggests that while using these characters as a criterion for selection, other causal characters must be considered simultaneously which confirm earlier findings of Chaudhary and Sharma (2003).

Residual effect= 0.009, Bold values are direct effect DF= days to flowering, PB= number of primary branches per plant, PH= plant height, LI= length of inflorescence, DM= days to maturity, LS= length of siliqua, SP= siliqua per plant, SS= seeds per siliqua, TSW= thousand seed weight, SYP= seed yield per

plant In spite of significant correlation with seed yield per plant, days to flowering showed negative direct effect but indirect effects via primary branches per plant, days to maturity, number of siliqua per plant and thousand seed weight had positive and high value. High positive indirect effect on seed yield via primary branches per plant, days to maturity, number of siliqua per plant and thousand seed weight might be due to significant positive correlation of days to flowering with those characters (Table 2). The genotypic residual effect (0.009) indicated that the character studied contributed 99% of the yield. It is suggested that maximum emphasis should be given on the above characters in selecting *Brassica napus* genotype with higher seed yield. If the value of residual effect is moderate or high, it indicates that besides the character studied, there are some other attributes which contribute for yield.

Acknowledgements

Table 1. Estimation of genetic components of variation for seed yield and its component characters in rape seed

Character	σ^2_g	σ^2_e	σ^2_p	GCV%	PCV%	h^2_b (%)	GA	GA (%)
DF	2.96	1.12	4.08	4.59	5.39	72.49	3.02	8.04
PB	0.07	0.18	0.25	8.10	15.13	28.68	0.29	8.94
PH	38.45	76.91	115.36	6.64	11.51	33.33	7.37	7.90
LI	26.81	26.89	53.69	8.58	12.15	49.93	7.54	12.49
DM	8.76	1.68	10.44	2.86	3.12	83.92	5.59	5.39
LS	0.11	0.07	0.18	5.67	7.16	62.65	0.55	9.24
SP	1504.05	2419.44	3923.49	20.07	32.41	38.33	49.46	25.60
SS	3.41	2.76	6.17	8.70	11.72	55.21	2.82	13.32
TSW	0.15	0.07	0.22	10.21	12.36	68.13	0.66	17.35
SYP	9.20	8.50	17.70	31.33	43.44	51.99	4.51	46.53

Table 2. Genotypic (r_g) and phenotypic (r_p) correlations among yield and its component characters in rape seed

Character		PB	PH	LI	DM	LS	SP	SS	TSW	SYP
DF	r_g	0.72**	0.12	0.13	0.68**	-0.07	0.32	0.37**	0.14	0.41*
	r_p	0.27	0.29	0.08	0.54**	-0.06	0.22	0.32	0.02	0.32*
PB	r_g		0.29	0.05	0.43*	0.02	0.24	0.56**	0.03	0.51**
	r_p		0.14	0.18	0.27	0.19	0.38*	0.24	-0.15	0.42*
PH	r_g			0.63**	0.18	-0.16	0.28	-0.33	0.32	0.12
	r_p			0.56**	0.18	-0.17	0.49**	-0.01	-0.06	0.39*
LI	r_g				0.13	-0.34	0.17	-0.46**	0.39**	-0.01
	r_p				0.17	-0.25	0.33	-0.25	0.10	0.13
DM	r_g					-0.24	0.06	-0.01	-0.29	0.09
	r_p					-0.17	0.11	0.06	-0.22	0.15
LS	r_g						0.36	0.60**	0.31	0.55**
	r_p						0.04	0.59**	0.12	0.29
SP	r_g							0.05	0.20	0.86**
	r_p							0.01	-0.03	0.83**
SS	r_g								0.17	0.34*
	r_p								-0.03	0.35*
TSW	r_g									0.30
	r_p									0.08

Table 3. Path analysis showing direct (diagonal) and indirect (off-diagonal) effects of yield components on seed yield in rape seed

Character	DF	PB	PH	LI	DM	LS	SP	SS	TSW	SYP
DF	-0.45	1.14	-0.10	-0.02	0.13	-0.05	0.18	-0.49	0.08	0.41*
PB	-0.33	1.59	-0.24	-0.01	0.08	0.01	0.14	-0.75	0.02	0.51*
PH	-0.06	0.45	-0.85	-0.12	0.03	-0.12	0.16	0.43	0.19	0.12
LI	-0.06	0.07	-0.54	-0.19	0.02	-0.25	0.10	0.61	0.23	-0.01
DM	-0.31	0.68	-0.15	-0.06	0.19	-0.18	0.04	0.01	-0.17	0.09
LS	0.03	0.03	0.14	0.07	-0.04	0.74	0.20	-0.80	0.18	0.55**
SP	-0.14	0.38	-0.24	-0.03	0.01	0.27	0.57	-0.07	0.12	0.87**
SS	-0.17	0.89	0.28	0.09	-0.01	0.44	0.03	-1.33	0.10	0.34**
TSW	-0.06	0.05	-0.27	-0.07	-0.05	0.23	0.12	-0.23	0.59	0.30

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