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<u>Int. J. Expt. Agric. 5(2): 24-29 (March 2015)</u> GENETIC DIVERSITY OF MORPHOLOGICAL TRAITS OF BRASSICA NAPUS PARENTS AND F₇ FAMILY LINES

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GENETIC DIVERSITY OF MORPHOLOGICAL TRAITS OF BRASSICA NAPUS PARENTS AND F7 FAMILY LINES

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ABSTRACT

Awal MA, Uddin MK, Uddin SKN, Jahan SE, Rahman L (2015) Genetic diversity of morphological traits of *Brassica napus* parents and F₇ family lines. *Int. J. Expt. Agric.* 5(2), 24-29.

The research was conducted to test the performance of twelve selected F_7 family lines evolved from the cross products of two *Brassica napus* varieties in comparing with their parents affiliated to some yield contributing characters. The characters, days to 50% germination, number of primary branches per plant, days to 50% flowering, average pollen fertility (%), plant height at maturity, number of siliqua per plant, beak length, number of seeds per siliqua, seed yield per plant were studied. There were significant variations among the varieties for all the characters except pollen fertility. But highly significant variations were found among the family lines and their parents in respect to morphological characters. The insignificant variation among genotypes tested for some traits denoted that, although the cross products are from two different parents, but have possibly been reached good balance due to high selection pressure in previous generations for types having better combinations. The family line 459 belonging to ED (BINA sarisha-5 × BINA sarisha-4) and family line 111 belonging to DE (BINA sarisha-4 × BINA sarisha-5) were found to be better in performance and have unveiled near close trails with parents in respect to the aforementioned traits. In general, genotypic correlation coefficients were higher than their corresponding phenotypic ones. Grain yield per plant had significant positive correlation with days to 50% flowering, average plant height at maturity, average number of siliqua per plant. Path coefficient analysis suggested that number of seeds per siliqua contributed maximum to seed yield through positive direct effect followed by average plant height.

Key words: Brassica napus, F7 lines, genetic diversity, morphological traits

INTRODUCTION

Mustard belongs to the genus Brassica under the family Cruciferae. Brassica has three species that produce edible oil, namely Brassica napus, B. campestris and B. juncea. These three species produce a total of 40.19 million tons of seed annually from an area of 26.8 million hectares in the world (FAO 2001). Vegetable oils and fats (lipids) constitute an important ingredient of human diet. Oils of plant origin are nutritionally superior to that of animal origin (Singh 2000). Due to insufficient production, a huge amount of foreign exchange involving over 160 Million US dollar is being spent every year for importing edible oils in Bangladesh (Raquibullah et al. 2006). At present, about 233.60 thousand hectares of land are under rapeseed and mustard cultivation in Bangladesh with a production of 228 thousand metric tons of mustard seed (BBS 2008). This quantity can meet only a fraction of the cooking oil, needed in the country. The grain yield and oil content of the mustard and rapeseed groups ranged between 600 to 3000 kg/ha and 30% to 45% respectively, depending upon the species, the variety and the climatic conditions under which they are grown (Kakroo and Kumar, 1991; Varshney et al. 1986). To utilize the variability, it is necessary to assess the genetic variations in respect of genotypic and phenotypic co-efficient of variation and other relevant parameters which have been reported by many authors. (Kumar et al. 1996; Nanda et al. 1995; Biswas 1989; Lebowitz 1989; Yadava et al. 1985; Thurling 1983). If a plant breeding programme is to be advanced more rapidly and efficiently, knowledge of inter-relationships between yield and yield contributing characters is necessary. Thus, determination of correlation between characters has a considerable importance in selection practices since it helps in the construction of selection indices and also permits for the prediction of correlated response. Therefore, considering the above facts, the present study was undertaken aiming at finding out the genetic variation in morphological traits of the progeny lines and their parents, the correlation co-efficient, the path co-efficient pattern of different characters and the better genotype based on performance of individual character as well as characters together.

MATERIALS AND METHODS

Experimental site and duration

The study has been conducted as the partial fulfillment of MS degree at the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh during July, 2008 to December, 2009 and the Experimental Farm of the same department that located at $24^{0}75'$ N latitude and $90^{0}50'$ E longitude at an elevation of 18m above the mean sea level has been used for the experiment.

Soil and climate

The experimental area was characterized by non-calcareous dark grey floodplain soil belonging to the Sonatola Soil Series under the Old Brahmaputra Floodplain (Agro-Ecological Zone 9) (FAO 1998). Soil of the experimental field was slightly acidic with a pH value of 6.17, low in organic matter and fertility level. The land type was medium high with silty loam texture and the climate of the place was characterized by wet summer and dry winter.

Materials used

For the present study, two *Brassica napus* parents and 12 F_7 lines were included in the experiment. The source and characteristics of the parental varieties and the progeny lines are listed in tables 1 and 2.

Table 1. Characteristics of the parents used in the study programme

Name of variety	Species	Ecotypes	Flower color	Plant height	Maturity	Source	
BINA Sarisha-4 (D)	B. napus	Rapeseed	Yellow	Medium	100-105	GPB	
BINA Sarisha-5 (E)	B. napus	Rapeseed	Yellow	Medium	100-105	GPB	
GPB = Department of Genetics and Plant Breeding, BAU, Mymensingh, Bangladesh							

Table 2. List of progeny lines used in this study

Serial No.	Name of progeny lines	Cross	Species
01.	Line 456 ED	BINASarish-5×BINASarish-4	B. napus
02.	Line 301 DE	BINASarish-4×BINASarish-5	B. napus
03.	Line 262 DE	BINASarish-4×BINASarish-5	B. napus
04.	Line 154 DE	BINASarish-4×BINASarish-5	B. napus
05.	Line 532 ED	BINASarish-5×BINASarish-4	B. napus
06.	Line 104 DE	BINASarish-4×BINASarish-5	B. napus
07.	Line 459 ED	BINASarish-5×BINASarish-4	B. napus
08.	Line 111 DE	BINASarish-4×BINASarish-5	B. napus
09.	Line 551 ED	BINASarish-5×BINASarish-4	B. napus
10.	Line 486 DE	BINASarish-4×BINASarish-5	B. napus
11.	Line 540 ED	BINASarish-5×BINASarish-4	B. napus
12.	Line 460 ED	BINASarish-5 \times BINASarish-4	B. napus

Note: 6 cross products between BINA-4 (D) and BINA-5 (E) and 6 reciprocal cross products

Experimental design and layout

Field layout was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The unit plot size was 3m x 1.5m with 30cm distances between line and 50cm distances between plots. Number of rows in each plot was 5. The distance between rows was 50cm and between plants 5cm for proper development and growth of plants.

Sowing of seeds

Selected parental materials and seeds of 12 family lines of Brassica *napus* were sown in lines in the experimental plots. The Seeds were placed at about 1.5cm deep in the soil.

Intercultural operations

Intercultural operations such as weeding, thinning, irrigation and top dressing were done in all the plots. The first weeding was done after 10 days of sowing. At that time, thinning was done for maintenance of a distance of 5-6cm from plant to plant in each row. Second weeding was done after irrigation at 25 days of sowing. Malathion 57EC @ 2ml/L and Rovral-5 WP were sprayed at regular interval to protect crops from aphids and *Alternaria* blight respectively.

Tagging and harvesting of sample plants

At 50% flowering stage, ten plants were selected at random from the 3 middle rows of each plot. The samples were then tagged properly for collecting the data of various morphological characters. Harvesting was done depending upon the maturity of the fruit.

Data of tagged plant were collected for nine quantitative characters according to followings procedure.

- i. *Days required for 50% germination*: The Data were recorded when approximately fifty percent of the seedling were seen above the ground.
- ii. *Days required for 50% flowering*: The Data were taken when approximately fifty percent of the plants of a plot have open flowers.
- iii. **Pollen fertility** (%): The young flowers at anthesis were collected from the plant. Everyday freshly opened flowers were collected from the field between 10-10.30a.m. A drop of 0.5% acetocarmine was taken on a clean slide. Pollen grains were colleted from the bursted anthers into the acetocarmine. A clean cover glass was placed on the materials. The slide was then placed under a compound microscope under low power. Pollen grains which took stain, uniform, either round or oval in shape were considered as viable pollens and those greenish in color, smaller in size and deformed were considered as sterile pollen. The number of viable and sterile pollens was counted from three independent observations and percentages of fertile pollens were calculated.
- iv. *Plant height at maturity (cm)*: The plant height was measured in centimeters from the soil level to the tip of the tallest raceme.

- v. *Number of primary branches per plant:* The branches that developed from the main stem were considered as primary branches. The total number of primary branches per plant was counted and recorded.
- vi. *Number of siliqua per plant*: The number of fertile siliqua per plant was counted and averaged to find out the number of siliqua per plant.
- vii. **Beak length (cm):** From the base of the beak upto tip of the siliqua was considered as beak length and was measured in cm. Data on beak length was taken from 10 siliqua from each of the selected plants.
- viii. *Number of seeds per siliqua*: Ten siliqua from each of the selected plants were taken. Number of seeds per individual siliqua was counted and the average number of seeds per siliqua was determined from total number of seeds obtained divided by the total number of siliqua or individual siliqua.
- ix. Seed yield per per plant (g): Seed yield per plant was obtained from randomly selected plants and average of 10 plants per replication was designated as seed yield per plant.

For Statistical analysis, the analysis of variance for each character under study was performed by F test (Cochran and Cox, 1957); Duncan's New Multiple Range Test (DMRT) was performed according to Steel and Torrie (1960); Genotypic and phenotypic correlation coefficients were estimated using the formula suggested by Singh and Chaudhary (1985); Path coefficient analysis was done according to the procedure stated by Dewey and Lu (1959). After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula used by Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

Analysis of variance

The present study was undertaken with a view to determining the performance among 14 Brassica genotypes belonging to two *B. napus* and their 12 family lines like the study performed by Baradaran *et al.* (2007). The analysis of variance for the characters *viz.*, days required for 50% germination, days to 50% flowering, pollen fertility (%), plant height at maturity (cm), number of primary branches, number of siliqua per plant, beak length (cm), number of seeds per siliqua and seed yield per plant (g) of 14 genotypes varieties have been presented in Table 3. The results of analysis of variance showed that significant variation exists among the genotypes for all the characters except pollen fertility but in a similar study Khan *et al.* (2005) found a wide range of genetic variation existed among all the characters except 1000 grain weight. In another study, Ali *et al.* (2003) found Genotypic and phenotypic coefficients of variability were in seed yield per plant and pods per plant, respectively. The mean performances of the genotypes were presented in Table 4.

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Characters	Replication (df=2)	Genotype (df=13)	Error (df=26)
Days to 50% germination	0.18	0.61*	0.28
Days to 50% flowering	2.64	23.58**	2.21
Average plant height	37.38	85.37*	34.99
Average pollen fertility	1.07	3.60^{NS}	1.53
Average percent siliqua set	145.65	65.42**	19.09
Average seeds/siliqua	21.82	11.36**	4.58
Average beak length	0.01	0.17**	0.21
No. of primary branches/plant	0.01	0.16*	0.07
Seed yield/plant	71.88	55.36**	12.91

Table 3. Analysis of variance (mean square values) for various important characters of 14 genotypes

df = degrees of freedom, ** = significant at 1% level, * = significant at 5% level, NS = Non-significant

Table 4. Mean performance of parents and family lines (ED/DE) in respect of considered character

	Days to	Days to	Plant	Pollen	Siliana/	Seeds/	Book	No. of primary	Seed
Genotypes	50%	50%	6 height fertility	fertility	/ nlent	siliqua	longth	branches/	yield/
	germination	flowering	(cm)	(%)	plan	siliqua	lengui	plant	plant
456 ED	4.117	40.000	65.367	90.350	76.007	25.267	1.310	2.347	22.333
301 DE	4.583	42.000	72.467	92.597	85.267	24.600	1.110	2.447	23.333
262 DE	4.440	39.000	78.367	92.493	79.860	27.933	1.107	2.700	27.333
154 DE	4.463	42.333	83.700	91.177	76.110	22.000	1.113	2.200	24.000
BINA-4	4.300	38.000	74.700	94.513	75.783	25.200	1.187	2.667	20.333
532 ED	3.533	40.667	71.100	94.207	67.237	21.433	1.587	2.533	21.000
104 ED	2.897	48.000	77.900	91.663	78.627	24.267	1.080	2.200	22.000
459 ED	4.177	45.667	73.767	91.487	79.680	27.600	1.047	2.170	34.333
111 DE	4.133	44.000	79.453	92.627	84.793	24.400	1.147	2.200	27.667
551 ED	4.517	43.000	74.033	92.647	78.520	22.600	1.790	2.700	23.333
486 DE	3.933	42.333	70.133	92.310	82.070	27.133	1.170	2.200	24.000
BINA-5	3.817	38.000	68.100	92.590	75.297	25.533	1.003	2.363	21.000
540 ED	3.883	41.000	65.513	91.583	73.057	25.067	1.093	2.790	17.667
460 ED	3.900	42.000	70.420	92.367	76.740	24.000	1.569	2.167	18.000

DE = BINA Sharisha- 4 × BINA Sharisha- 5, ED = BINA Sharisha- 5 × BINA Sharisha- 4

The insignificant variation among the genotypes tested for the considered traits indicated that the seedling vigour through seed viability and pollen fertility have had almost no variation in the selected lines as well as parents where coefficient of variation (CV%) ranged from 1.34% to 15.41% for all characters studied (not shown) mean that there exists considerable variation in some genotypes while others have shown almost no variation which is similar to many previous study (Badsra and Chaudhary, 2001; Das *et al.* 1998; Kardam and Singh, 2005). That has possibly become so, as the genotypes used were mostly genetically balanced which was due to continuous selection of the lines for high fruit setting in its previous generations. While studying the *Brassica juncea* with ten agro-morphological characters Sudan *et al.* (2004) found that analysis of variance showed significant difference among them for all the characters indicating the existence of genetic variation and provided scope for selection of superior genotypes (data not shown) which is identical to current study. It was found that among 14 genotypes, Binasarisha-5, family lines 104ED, 532ED, 540ED and 460ED took shorter days to initiate 50% germination while family line 301DE took longer days (4.583). Similarly, family line 104ED took maximum days (48.00) to initiate 50% flowering while Binasarisha-4, Binasarisha-5 took the shorter days. Plant height at maturity was found to be the highest in line 154DE (83.700) and the lowest in 456 ED (65.367). Among all the genotypes, family line 301DE had the highest number of siliqua per plant (85.267).

Association of characters

The results of genotypic (g) and phenotypic (p) correlation coefficients among seed yield and yield contributing characters in all possible combinations were presented in Table 5. Most of the genotypic correlation coefficients were found to be larger than their corresponding phenotypic correlation coefficients indicating inherent relationships of deliberate characters which is similar to experiments conducted by other researcher (Massimo *et al.* 2006; Kashyap and Mishra, 2004).

Characters		No. of primary branches per plant	Avg. days to 50% flowering	Avg. pollen fertility (%)	Avg. plant height at maturity	Avg. no. of siliqua set per plant	Avg. no. of seed per siliqua	Avg. beak length	Avg. plant height	Seed yield per plant
Avg. days to 50% germination	G P	-0.352 -0.241	0.864** 0.729**	-0.449 -0.332	0.081 0.045	0.332 -0.321	0.156 0.024	0.253 0.242	-0.320 -0.205	-0.419 -0.353
No. of primary branches per plant	G P		0.024 0.023	-0.153 -0.201	0.858** 0.815**	0.984** 0.980**	0.726** 0.725**	-0.633* -0.583*	-0.529 -0.350	0.801** 0.796**
Avg. days to 50% flowering	G P			- 0.823** -0.686*	0.391 0.381	0.000 -0.001	0.155 0.157	0.183 0.137	- 0.720** -0.567	0.011 0.015
Avg. pollen fertility (%)	G P				-0.523 -0.489	-0.245 -0.221	-0.145 -0.093	-0.192 -0.194	0.953** 0.578*	0.286 -0.236
Avg. plant height at maturity	G P					- 0.765** - 0.752**	-0.631* -0.632*	-0.640* -0.618*	-0.325 -0.348	0.489 0.480
Avg. no. of siliqua per plant	G P						-0.694* -0.680*	-0.481 -0.454	-0.497 -0.350	0.883** 0.880**
Avg. no. of seed per siliqua	G P							0.755** 0.736**	-0.085 0.097	-0.380 -0.311
Avg. beak length	G P								-0.080 0.056	-0.102 -0.108
Avg. plant height	G P								0.000	-0.405 -0.330

Table 5. Correlation coefficients among different quantitative characters of 14 genotypes in matrix form

G = Genotype, P = Phenotype, ** = Significant at 1% level, * = Significant at 5% level

Genotypic and phenotypic correlation coefficients showed that the genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients for most of the characters studied where number of primary branches per plant and average no. of siliqua per plant showed highly significant positive genotypic correlation with seed yield per plant. Singh *et al.* (2004) found similar result in an identical experiment but high heritability coupled with high genetic advance as percentage of mean was observed for days to flowering, followed by 1000-seed weight, days to maturity and plant height. In the current study significant positive phenotypic relationships were found in same characters with seed yield per plant.

Path coefficient analysis

Path analysis at genotypic level was done to see the direct and indirect effects of yield contributing characters on seed yield (Table 6). The analysis revealed that average number of seeds per siliqua (3.801) had the highest positive direct effect on seed yield followed by average plant height (2.730) which is similar to the study conducted by Kashyap and Mishra (2004) but Sudan *et al.* (2004) found the different result as path analysis indicated that number of primary branches was the most important character with the highest direct effect on seed yield.

Characters	Days to 50% germination	Days to 50% flowering	Average plant height	Average pollen fertility	Average percent siliqua set	Average seeds/ siliqua	Average beak length	No. of primary branches/ plant	Seed yield/ plant
Days to 50% germination	<u>1.535</u>	-0.4980	-0.3058	0.0011	-0.7441	0.0494	0.1699	0.1221	0.330
Days to 50% flowering	-0.6019	<u>1.270</u>	1.1493	-0.0334	-0.6335	-0.3877	-0.0840	-0.2462	0.433
Average plant height	-0.1719	0.5348	<u>2.730</u>	0.0000	-0.3804	-1.8359	-0.4029	-0.0876	0.386
Average pollen fertility	0.01995	-0.5196	0.0000	<u>0.082</u>	0.4676	-1.0378	0.6224	0.1915	-0.174
Average percent siliqua set	0.6817	0.4802	0.6197	-0.0282	<u>-1.676</u>	1.3684	-0.8229	-0.1543	0.474
Average seeds/siliqua	0.01996	-0.1296	-1.3186	-0.0223	-0.6034	<u>3.801</u>	-1.268	-1.240	0.467
Average beak length	0.1366	-0.05590	-0.5760	0.0267	0.7223	-0.0253	<u>1.909</u>	0.0488	-0.312
No. of primary branches/plant	0.4836	-0.8067	-0.6170	0.0404	0.6670	-0.1216	0.2406	0.388	0.274

Table 6. Genotypic path-coefficient analysis for yield components towards yield

Residual effect: -1.5874, Underline and bold figure indicated the direct effects

Path analysis showed that all the considered characters but average percent siliqua set per plant were positive where average number of seeds per silliqua showed highest positive direct effect (3.801) on yield while highest negative direct effect was observed in number of average percent of silliqua set per plant (-1.676).

CONCLUSION

Seed yield is an end product of interactions of several yield components. Correlation and path coefficients analysis can furnish a basis in determining the relative contribution of each character to seed yield. Hence, from the prevailing probation, it can be concluded that number of seeds/siliqua and number of primary branches/ plant had strong positive association along with high direct effect on seed yield. Therefore, selection of this character would be more effective for yield improvement.

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