Journal of Biology, Agriculture and Healthcare
ISSN 2224-3208 (Paper) ISSN 2225-093X (Online)
Vol.13, No.2, 2023

Heritability, Genetic Advance, Correlation and Path Coefficient Analysis in Advanced Generation of Brassica napus L.

E. Parvin[1] F. Mahmud[2] M. M. Haque[3*]
1. Scientific Officer, Bangladesh Institute of Research and Training on Applied Nutrition (BIRTAN), Dhaka, Bangladesh
2. Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh
3. Senior Scientific Officer, Bangladesh Institute of Research and Training on Applied Nutrition (BIRTAN), Dhaka, Bangladesh
* Corresponding author: Senior Scientific Officer, Bangladesh Institute of Research and Training on Applied Nutrition (BIRTAN), Dhaka, Bangladesh, Mobile: +8801723778056, Email: maksudulhq@gmail.com

Abstract

Broad sense heritability and selection response were measured among forty rapeseed (*Brassica. napus* L. genotypes for seed yield and yield related traits. The experiment was designed in Randomized Complete Block with three replications. High heritability with moderate genetic advance was observed for days to 1st flowering, days to 50% flowering, days to 80% flowering and Days to maturity indicating medium possibility of selecting genotypes. The significant positive correlation with seed yield per plant were found in Days to 1st flowering (G = 0.383, P = 0250), Days to 80% flowering (G = 0.738, P = 0.091), Days to maturity (G= 0.102, P= 0.033), Number of primary branches per plant (G = 0.816, P = 0.597), Number of secondary branch (G = 606, P = 433) and Siliqua per plant (G = 0.885, P = 0.626). In addition, there were non-significant positive correlation with seed yield per plant was also found in Plant height (G = 0.082, P = 0.139), Number of seeds per siliqua (G = -0.314, P 0.069) and Thousand seed weight (G=0.237, P=0.162). The path coefficient studies indicated that plant height, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

Keywords: Heritability, Genetic Advance, Correlation Coefficient, Path Coefficient Analysis, *Brassica rapa* L.
DOI: 10.7176/JBAH/13-2-03
Publication date: January 31st 2023

Introduction

Rapeseed (*Brassica napus* L.) is relatively young species that resulted from spontaneous hybridizations between the diploid *Brassica rapa* L. Rapeseed is the second most important oilseed crop in the world after soybean for oil while, in terms of area and production, rapeseed and mustard graded as the world's third most important edible oil crop. Canada, China, Northern Europe and the Indian sub-continent are the leading counties in the production of rapeseed. Rapeseed is considered as the most valuable source of vegetable oil in Europe. The seeds of present varieties normally contain 40-45% oil, 25% protein and 20% polysaccharides. These are used in the production of biodiesel (green diesel), industrial lubricants and hydraulic oils, detergents, soaps and recyclable plastics [1]. Rapeseed oil is primarily used in food and the oil cake contains high biological proteins as well as appropriate amounts of calcium and phosphorus. Oil and fat are a good source of energy and also comprises fat-soluble vitamins like A, D, E, and K. After oil extraction the remaining meal, having 38-44% high quality protein, is used as an animal feed and fertilizer for several crops [5].

Heritability is a measure of the expression of a character. The estimates of heritability alone give no indication of the associating genetic progress that would result from selecting the best plants. Heritability along with phenotypic variance and the selection intensity, however, promise the estimation of genetic advance or response to selection, which is more useful in the selection of promising lines [3-5]. the study of heritability and genetic advance is very useful in order to estimate the scope for improvement by selection. Heritability levels show the reliability with which the genotype will be recognized by its phenotype expression [6]. Since selection response has an additional superiority over heritability, it can act as a directorial factor for plant breeders in selection programs. In order to estimate the selection effects, heritability along with selection response is much more useful than the heritability alone for the genetic improvement of a character. Broad sense heritability and expected response to selection along with its percentage was determined in this particular experiment among *Brassica napus* genotypes for seed yield and its related traits. Heritability is a key of transmissibility of traits and as such partition the total variance into genetic and environmental components [7-8].

Determination of correlation coefficient between the characters has considerable importance in selecting breeding materials. Path coefficient technique splits the correlation coefficient into direct and indirect effects [9] via alternative aspects or pathways and in this way allows an essential examination of components that influence a given correlation and can be useful in detailing an efficient selection strategy [10]. Therefore, the path coefficient analysis has been found to provide more particular data on the direct and indirect impact of each of the segment characters upon seed yield [11]. Inter-varietal and inter-specific hybridization are essential for creating the variation or transfer gene of interest from wild species in rapeseed improvement programme [12]. Genetic variability is one of the criteria for parent choice [13]. Consideration of more diverse parents (inside the farthest point) in hybridization could build the possibility of acquiring the most extreme heterosis [14] and give the full range of variability in segregating generations.

Heritability can also help in determining the choice of breeding system. It plays a main role in bringing improvement in the crop plants. Genetic gain is the amount of increase in performance that is achieved through artificial genetic improvement. The objectives of the present study were to estimate the genetic coefficient of variation, broad sense heritability, and the relationship among yield associated traits for improving seed yield in spring type rapeseed advanced lines.

MATERIALS AND METHODS

Twenty two progressive genotypes of *B. napus* were grown in randomized complete block design with three replications. The advanced lines of *Brassica napus* L. for the trial were collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU) and three released varieties collected from Bangladesh Agricultural Research Institute (BARI) as presented in Table 1.

Table 1. List of the 40 *Brassica napus L.* genotypes used in the experiment with their sources

Genotype No.	Name/Acc No.	Source	Genotype No.	Name/Acc No.	Source
G1.	Nap-0717-2	BARI	G21.	Nap-10014	BARI
G2.	Nap-0733-1	BARI	G22.	Nap-10012	BARI
G3.	Nap-0762	BARI	G23.	Nap-0130	BARI
G4.	Nap-08-4	BARI	G24.	Nap-2012	BARI
G5.	Nap-0837	BARI	G25.	Nap-2013	BARI
G6.	Nap-0865	BARI	G26.	Nap-2022	BARI
G7.	Nap-0869	BARI	G27.	Nap-9906	BARI
G8.	Nap-0876	BARI	G28.	Nap-9908	BARI
G9.	Nap-0885	BARI	G29.	Nap-248	BARI
G10.	Nap-205	BARI	G30.	Nap-2001	BARI
G11.	BARI-8	BARI	G31.	Nap-9901	BARI
G12.	BARI-13	BARI	G32.	Nap-9904	BARI
G13.	Nap-10007	BARI	G33.	Nap-9905	BARI
G14.	Nap-10009	BARI	G34.	Nap-2057	BARI
G15.	Nap-10015	BARI	G35.	Nap-2037	BARI
G16.	Nap-10017	BARI	G36.	Nap-206	BARI
G17.	Nap-10019	BARI	G37.	Nap-2066	BARI
G18.	Nap-10020	BARI	G38.	Nap-179	BARI
G19.	Nap-1005	BARI	G39.	Nap-94006	BARI
G20.	Nap-1007	BARI	G40.	Nap-108	BARI

Estimation of heritability:

Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary [15].

$$h^2{}_b(\%) = \frac{\delta^2{}_g}{\delta^2{}_p} \times 100$$

Where, $h^2{}_b$ = Heritability in broad sense, $\delta^2{}_g$ = Genotypic variance and $\delta^2{}_p$ = Genotypic variance

Estimation of genetic advance:

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard [16].

$$GA = \frac{\delta^2{}_g}{\delta^2{}_p} \,.\, K \,.\, \delta_p$$

Where, GA = Genetic advance, $\delta^2{}_g$ = Genotypic variance, $\delta^2{}_p$ = Phenotypic variance, δ_p = Phenotypic standard deviation and K = Selection differential which is equal to 2.06 at 5% selection intensity.

Estimation of genetic advance in percentage of mean:
Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson [17].

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{\bar{\text{x}}} \times 100$$

Estimation of simple correlation co-efficient:
Simple correlation co-efficient (r) was estimated with the following formula [15].

$$r = \frac{\sum xy - \frac{\sum x \cdot \sum y}{N}}{\sqrt{[\{\sum x^2 - \frac{(\sum x)^2}{N}\}\{\sum y^2 - \frac{(\sum y)^2}{N}\}]}}$$

Where, $\sum$ = Summation, x and y are the two variables correlated and N = Number of observation

Path co-efficient analysis:
Path co-efficient analysis was done according to the procedure employed by Dewey and Lu [18] also quoted in Singh and Chaudhary [15] and Dabholkar [19], using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variable.
In order to estimate direct & indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$
$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$
$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (Unknown). P's in the above equations may be conveniently solved by arranging them in matrix from.

Total correlation, say between x1 and y is thus partitioned as follows:
P_{yx1} = The direct effect of x1 on y, $P_{yx2}r_{x1x2}$ = The indirect effect of x1 via x2 on y and $P_{yx3}r_{x1x3}$ = The indirect effect of x1 via x3 on y.
After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below [15]:

$$P^2_{RY} = 1 - \sum P_{iy} \,.\, riy$$

Where, P^2_{RY} = (R^2); and hence residual effect, $R = (P^2_{RY})^{1/2}$, P_{iy} = Direct effect of the character on yield and Riy = Correlation of the character with yield.

RESULT AND DISCUSSION

Heritability and genetic advance

High heritability with moderate genetic advance was observed for days to 1st flowering, days to 50% flowering, days to 80% flowering and Days to maturity indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for Number of primary branches per plant, Thousand-seed weight (gm), Length of siliqua (cm), Seed yield per plant (gm) and Number of secondary branches per plant indicating that non-additive gene effects were involved for the expression of these characters and selection for such traits might not be rewarding. This results support the reports of Malik *[20]*. In some of the crosses the frequency of the segregating plants showing reduced maturity was comparatively higher than the other crosses. Low heritability coupled with low genetic advance for this trait was also observed by Sharma [21].

Plant height shows high heritability 99.287% with moderately high genetic advance of 28.994 and genetic advance in percentage of mean of 17.244%, revealed the possibility of predominance of additive gene action in the inheritance of this trait and indicating that this trait could be improved through selection process (Table 2). High variability in plant height for *B. juncea*, *B. rapa* and *B. napus* was also observed by Varshney *[22]*. Chandola [24] observed high genetic advance for plant height while working with 30 varieties of *Brassica rapa.* Heritability and genetic advance in percentage of mean are shown in Figure 1.

As a whole, the low heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes for this trait. However, some of the individual plants showed quite a reasonable lower primary branches which were selected for further study in the next generation. Low heritability coupled with low genetic advance was also found by Singh *[24]*. Yadava *[25]* found high heritability and genetic advance for number of primary branches per plant. Moderately high heritability coupled with low genetic advance was also found by Singh *[24]*. Sheikh *[26]* found high heritability coupled with high genetic advance for number of secondary branches per plant while working with 24 genotypes of toria. Number of siliqua per plant exhibited very high heritability 99.986% with high genetic advance 43.295 and genetic advance in percentage of mean 25.749%. Mahmud *[27]* reported that the number of siliqua per plant were highly heritable coupled with high genetic advance. Siliqua length showed high heritability (59.934%) with low genetic advance (0.678) and low genetic advance in percentage of mean 0.404% indicated that this trait was controlled by non-additive gene (Table 2).

Thousand seed weight exhibited high heritability 79.197% with low genetic advance 0.586 and genetic advance in percentage of mean 0.349%. Johnson *[28]* reported that heritability estimates along with genetic group were more useful in prediction selection of the best individual. High heritability for this trait was also observed by Yadava *[25]*. Singh [24] reported the high heritability and genetic advance for thousand seed weight. Seed yield per plant showed high heritability 49.197% with high genetic advance (1.385) and moderately high genetic advance in percentage of mean 0.823% indicated this trait was controlled by additive gene and selection for this character would be effective. High heritability and genetic advance for seed yield per plant was reported by Singh [29] while working with 22 genotypes of *Brassica napus*.

Correlation coefficient of characters

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. Breeders always look for genetic variation among traits to select desirable type. Correlation co-efficient between pairs of trait for 40 materials of *B. napus* are shown in Table 3 & 4.

Correlation coefficients among the characters were studied to determine the association between yield and yield components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values.

In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. The significant positive correlation with seed yield per plant were found in Days to 1st flowering (G = 0.383, P = 0250), Days to 80% flowering (G = 0.738, P = 0.091), Days to maturity (G= 0.102, P= 0.033), Number of primary branches per plant (G = 0.816, P = 0.597), Number of secondary branch (G = 606, P = 433) and Siliqua per plant (G = 0.885, P = 0.626). In addition, there were non-significant positive correlation with seed yield per plant was also found in Plant height (G = 0.082, P = 0.139), Number of seeds per siliqua (G = -0.314, P 0.069) and Thousand seed weight (G=0.237, P=0.162). Insignificant association of these traits indicated that the associations between these traits were largely influenced by environmental factors. Parveen [30] also revealed that insignificant and positive interaction with yield per plant. Shalini *[31]* also observed that plant height was highly associated with seed yield. Similar result was reported by Srivastava *[32]*. Significant positive correlation between plant height and seed yield was found by Verma and Sachan [33]. Chaudhary *[34]* found positive correlation of plant height with number of seed per siliqua, number of siliqua per plant. Basalma [35] reported opposite result for this trait. Malik *[36]* reported similar result for number of primary branches and seed yield both at genotypic and phenotypic level. Tyagi *[37]* reported that number of seed per siliqua had positive and insignificant effect on seed yield per plant. Indicated that if siliqua length increased then yield per plant decreased. Nasim *[38]* reported that seed yield per plant was significantly and negatively with siliqua length. Ahmed [39] also found similar results for this trait. Tuncturk and Ciftci [40] reported positive correlation between seed yield with 1000-seed weight which did not support the present findings.

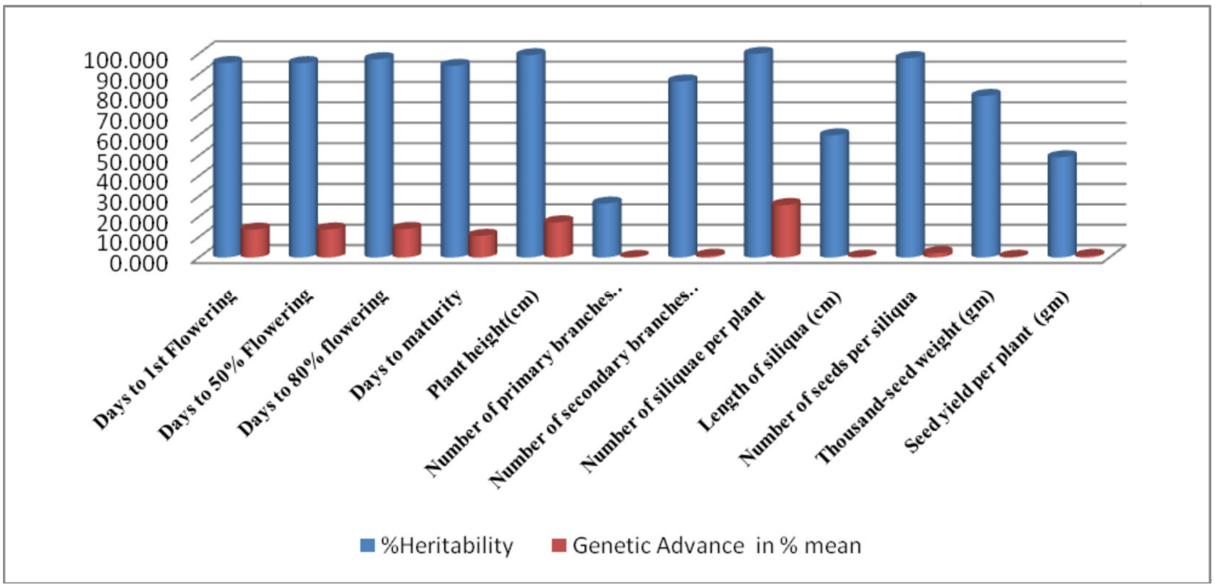

Figure 1. Heritability and genetic advance over mean in *Brassica napus L*

Path Co-efficient analysis

Association of character 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 hector. 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 at phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable and days to 1st flowering, days to 50% flowering, days to 80% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, length of siliqua (cm), number of seeds per siliqua and thousand-seed weight (gm) were causal (independent) variables. Estimation of direct and indirect effect of path co-efficient analysis for *Brassica napus* is presented in Table 4.

Table 2.Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus* L.

Characters	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae per plant	Length of siliqua (cm)	Number of seeds per siliqua	Thousand -seed weight (gm)	Seed yield per plant (gm)
Days to 1st flowering	0.383**	-0.712**	-0.322**	0.116	0.092	0.123	0.117	-0.125	0.293**	-0.055	-0.214**
Days to 50% flowering		-0.092	-0.215**	-0.207*	-0.011	0.083	-0.107	0.237**	-0.018	-0.321**	0.281**
Days to 80% flowering			0.738**	-0.339	-0.525**	-0.643**	-0.259	-0.325**	0.482**	-0.612**	-0.595**
Days to maturity				0.302**	0.912**	0.976**	-0.593**	0.497**	0.102	-0.723	0.13
Plant height(cm)					0.082	0.176	0.940**	0.618**	-0.415*	0.09	-0.590**
Number of primary branches per plant						0.597*	-0.364	0.151	-0.165	0.813**	0.443*
Number of secondary branches per plant							0.606*	-0.114	0.223	-0.473*	0.064
Number of siliquae per plant								0.885**	0.950**	-0.277	0.564**
Length of siliqua (cm)									-0.260	0.293	0.195
Number of seeds per siliqua										-0.314	0.312
Thousand-seed weight (gm)											0.237
Seed yield per plant (gm)											0.342

** = Significant at 1%. , * = Significant at 5%.

Table 3. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of *Brassica napus L.*

Characters	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae per plant	Length of siliqua (cm)	Number of seeds per siliqua	Thousand -seed weight (gm)	Seed yield per plant (gm)
Days to1st flowering	0.250**	0.043	-0.127	-0.009	0.076	0.087	0.082	-0.043	0.106	-0.011	-0.069
Days to 50% flowering		-0.041	0.014	-0.06	-0.122	0.012	-0.09	-1.906**	0.043	-0.034	0.164
Days to 80% flowering			0.091	-0.07	-0.358	-0.426*	0.047	-0.292	-0.402*	0.053	0.212*
Days to maturity				0.104	-0.1	-0.015	0.097	0.087	0.033	-0.165	0.279
Plant height(cm)					0.139	0.037	0.267	0.138	-0.266	0.073	-0.252
Number of primary branches per plant						0.472*	-0.009	0.490*	-0.064	0.441*	0.533**
Number of secondary branches per plant							0.433*	0.431*	0.145	0.036	0.397
Number of siliquae per plant								0.626**	0.287	0.137	0.648*
Length of siliqua (cm)									-0.185	0.315	0.126
Number of seeds per siliqua										0.069	0.258
Thousand-seed weight (gm)											0.162
Seed yield per plant (gm)											0.405

** = Significant at 1%; * = Significant at 5%

Path co-efficient analysis revealed that Days to 1st Flowering, Days to 50% Flowering, Days to 80% flowering, Days to maturity, Plant height (cm), Number of secondary branches per plant, Number of siliquae per plant, Length of siliqua (cm), Thousand-seed weight (gm) and Seed yield per plant (gm) had the positive direct effect on yield per plant. Whereas, Number of primary branches per plant and Number of seeds per siliqua had the negative direct effect on yield per plant. It is mainly due to high positive direct effect and positive indirect effects of others characters and selection would be effective for this trait. The path coefficient studies indicated that plant height, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program. Chauhan and Singh [41] revealed that days to 50% flowering had positive direct effect on yield per plant. Rashid [42] revealed that days to maturity had positive direct effect on yield. Han [43] and Singh [44] also reported direct positive result for plant height. Singh *[45]* reported that number of primary branches per plant had direct positive effect on seed yield. Yadava *[46]* found the number of secondary branch had the highest positive direct effect on seed yield. Rashid [42] observed that number of secondary branches per plant had the highest direct effect on seed yield per plant. Shalini *[31]* found the number of siliqua per plant had the highest direct effect on seed yield. Sheikh *[26]* revealed that siliqua per plant had highly positive direct effect on seed yield. Singh *[47]* reported that siliqua length had negative direct effect on yield per plant. Rashid [42] reported that number of seeds per siliqua had direct positive effect on yield per plant. Parveen [30] also found similar results for this trait. Siddikee [48] reported that thousand seed weight had the highest positive direct effect on seed yield per plant. Kudla [49] reported that thousand seed weight had positive direct effect on seed yield.

CONCLUSIONS

From this High heritability with moderate genetic advance was observed for days to 1st flowering, days to 50% flowering, days to 80% flowering and Days to maturity indicating medium possibility of selecting genotypes. On main raceme indicating that phenotypic selection for these traits would be effective so we can easily manipulate these changes. Some plants showed high heritability for short duration and yield contributing characters were selected from some of the cross combinations of the intervarital crosses of *Brassica napus L* for further selection. The plant height, number of primary branches per plant, number of secondary branches per plant and number of siliqua per plant were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program.

Table 4. Path coefficient analysis showing Direct (Diagonal) and indirect effects of different characters on yield of *Brassica napus* L.

Characters	Days to 1st flowering	Days to 50% flowering	Days to 80% flowering	Days to maturity	Plant height(cm)	Number of primary branches per plant	Number of secondary branches per plant	Number of siliquae per plant	Length of siliqua (cm)	Number of seeds per siliqua	Thousand-seed weight (gm)	Genotypic correlation with yield
Days to 1st flowering	0.2717	0.4193	0.9135	0.2494	-0.1367	-0.1400	0.0727	0.0187	0.0011	-0.0142	-0.0110	0.1825
Days to 50% flowering	0.2686	0.4225	0.9175	0.2511	-0.1352	-0.1403	0.0733	0.0187	0.0015	-0.0140	-0.0108	0.1823
Days to 80% flowering	0.2682	0.4208	0.9210	0.2517	-0.1344	-0.1388	0.0718	0.0186	0.0019	-0.0139	-0.0100	0.1849
Days to maturity	0.0470	0.2049	0.4669	0.2842	-0.1244	-0.1396	0.0705	0.0140	0.0048	0.0150	-0.0231	0.3435**
Plant height(cm)	0.3524	0.3893	0.3978	0.7560	-0.2113	-0.1318	0.0688	0.0302	-0.0178	-0.0164	0.0282	0.3065**
Number of primary branches per plant	-0.1583	-0.2440	-0.9318	0.6439	0.1000	-0.2784	0.1019	0.0078	-0.0074	0.0140	-0.0342	0.2901*
Number of secondary branches per plant	0.7099	0.9878	0.2224	0.4382	0.0703	0.1373	0.2067	0.0282	-0.0240	-0.0187	0.0401	0.3581**
Number of siliquae per plant	0.6764	0.7041	0.6101	0.1945	0.0691	-0.0235	0.0633	0.0922	-0.0044	0.0010	0.1723	0.4966**
Length of siliqua (cm)	-0.1255	-0.1722	-0.4713	-0.0840	-0.0507	-0.0280	0.0671	0.0055	-0.0740	-0.0063	0.0286	0.0255
Number of seeds per siliqua	0.6927	0.7055	0.5819	0.2787	-0.0500	-0.0563	0.0556	-0.0013	-0.0067	-0.0693	0.0254	0.0075
Thousand-seed weight (gm)	0.2058	0.2054	0.4030	-0.0668	0.0134	0.0215	-0.0186	0.0358	0.0048	-0.0040	0.4440	0.4219

Residual Effect (R) = 0.2729

**, * Correlation is significant at the 0.01 and 0.05 level, respectively.

Reference

1. Friedt W., Snowdon R., Ordon F., Ahlemeyer J., *Progress in Botany*. 168 (2007) 152.
2. Marjanovic J.A., Genetic divergence and variability of rapeseed (*Brassica napus* L.). PhD thesis, Faculty of Agriculture, University of Novi Sad, Serbia. (2005).
3. Johnson H.W., Robinson H. F., and Comstock R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47: 314-318.
4. Igbal S., Mahmood T., Tahira A. L. I., Anwar M., and Sarwar M. (2003). Path coefficient analysis in different genotypes of soybean (*Glycine max* L.). *Pakistan Journal of Biological Science*, 6: 1085-1087.
5. Roham M. M., Igbal A. S. M., Arifin M. S., Akhtar Z., and Husanuzzaman M. (2003). Genetic variability, correlation and path analysis in mungbean, *Asian Journal of Plant Science*, 2: 1209-1211.
6. Chandrababu R. J., and Sharma R. K. (1999). Heritability estimates in almond (*Prunus dulcis* Miller). *Horticultural Science,* 79: 237-243.
7. Falconer, D.S., and T.F.C. Mackay.(1996): Introduction to Quantitative Genetics (4th Ed.) Longman, Essex, UK.
8. Marwede, V., A. Schierholt, C. Mollers and H.C. Becker, (2004). Genotype x environment interactions and heritability of tocopherol contents in Canola. Crop Sci., 44:728-731.
9. Sarwar G, Rashid MH, Parveen S, Hossain MS. Correlation and path coefficient analysis for agro-morphological important traits in aman rice genotypes (*Oryza sativa* L.). Adv. Biores. 2015;6(4): 40-47.
10. Sabaghnia N, Dehghani H, Alizadeh B, Mohghaddam M. Interrelationships between seed yield and 20 related traits of 49 canola genotypes in non-stressed and water stressed environments. Spanish J. Agri. Res. 2010;8:356-370.
11. Behl RK, Chowdhury BD, Shing RP, Shing DP. Morphophysiological determinates of oil yield in *Brassica juncea* under dryland conditions. Indian J. Genet. Pl. Breed. 1992;52(3):280-284.

12. Parveen S, Rashid MH, Bhuiyan MSR. Assessment of breeding potential of rapeseed germplasm using D2 analysis. J. Expt. Biosci. 2015;6(1): 59-64.
13. Bhatt GM. Comparison of various methods of selecting parent for hybridization in common bread wheat (*Triticum aestivum*). Aus. J. Agric. Res. 1973;24:457-464.
14. Taiana T, Rashid MH, Parveen S, Hossain MS, Haque MA. Selection strategies to choose better parents in tomato using genetic parameters. 2015;4(1):33-39.
15. Singh, R.K. and Chaudhary, B.D. (1985).Biometrical methods in quantitative genetic analysis.Kalyani Publishers, New Delhi, India.p. 56.
16. Allard, R.W. (1960). Principles of Plant Breeding. John Willey and Sons. Inc. New York.
17. Comstock, K. and Robinson, P.R. (1952). Estimation of genetic advance. *Indian J. Hill.* 6(2): 171-174.
18. Dewey, D.R. and Lu, K.H. (1995). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 5l :515-518.
19. Dabholkar, A.R. (1992). Elements of Biometrical Genetics. Concept publishing, New Dhelhi, India.
20. Malek, M.A., Das. M.L. and Rahman, A. (2000). Genetic variability, character association and path analysis in rapeseed. *Bangladesh J. Agric. Sci*. 27(1): 25-59.
21. Sharma, S.K., Rao, D., Singh, D.P., Harbir, S. and Singh, H. (1994). Correlation analysis of yield, biomass and its partitioning components in Indian mustard (*Brassica juncea* L. Czern. Coss.). *Hariana Agril. Univ. J. Res.* 27(2-4): 149-152.
22. Varshney, S.K., Rai, B. and Singh, B. (1986). Component analysis of harvest index in *Brassica* oilseeds. *Indian J. Agric. Res*. 20(3): 129-134.
23. Chandola, R.F., Dixit, P.K., Sharina, K.N., Saxena, D.K. (1977). Variability in *B. juncea* under three environments. *Indian J. Agric. Sci*. 47(9): 680-683.
24. Singh, R.P., Malik, B.P. and Singh, D.P. 1997. Variation for morpho-physiological characters in genotypes of Indian mustard. *Indian J. Agric. Sci*., 57: 227-230.
25. Yadava, C.K. (1983). Studies on genetics of yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss). Thesis Abst. 9(2): 186-187.
26. Sheikh, F.A., Rathen, A.G. and Wani, S.A. (1999). Path analysis in toria (*Brassica campestris* L.) var. toria. *Adv. P1. Sci.* 12(2): 385-388.
27. Mahmud, F., Rasul, M.G and Rahim, M.A. (2008). Genetic diversity analysis in some advanced lines of *Brasssica napus*., *Sci. Asia*, 34:432-434.
28. Johnson, H.W., Robinson, H.F. and Comstock. R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.* 47: 314-318.
29. Singh, M. Singh, H.L. and Dixit, R.K. 2004. Studies on genetic variability, heritability, genetic advance and correlation in Indian mustard *(Brassica juncea (L.)* Czem and Coss.). Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. *Plant-Archives*. 4(2): 291294
30. Parveen, S. (2007). Variability study in F_2 progenies of the inter-varietal crosses of *Brassica rapa*. MS thesis, Department of Genetics and Plant Breeding, Shere-e-Bangla Agricultural University, Dhaka.
31. Shalini, T.S., Sheriff, R.A., Kulkarmi, R.S. and Venkataramana, P. (2000). Correlation and path analysis in Indian mustard germplasm. Research on. crops Dept. of Genetics and Plant Breeding. University of Agricultural Science, India. 1(2): 226-229.
32. Srivastava P.P. Salara. B.S. and Gowda, M.V.C. (1983). Variability and correlation studies in groundnut (*Arachis hypogaea*). *Crop improv.* 25(1): 122-123.
33. Verma, S. K. and J. N. Sachan. 2000. Genetic divergence in Indian mustard. *Crop Research Hisar.* 19(2): 271-276.
34. Chaudhury, P.K., P. and Kumar, A. (1990). Association and Interdependence of morphophysiological characters under moisture stress in *Brassica. Beitrage Zar Tropichen Landuitshaft*. 18(1): 43-47.
35. Basalma, D. (2008). The correlation and path analysis of yield and yield components of different winter rapeseed (*Brassica napus* ssp. *oleifera* L.) cultivars. *Res. J. Agric. Biol. Sci.* 4(2):120-125.
36. Malik. V., Singh, H. and Singh, D. (1995). Gene action of seed yield and other desirable characters in rapeseed. Analysis Biol (Ludhiana). 11(1/2): 94-97.
37. Tyagi, M.K. Chauhan, J.S., Kumar, P.R. and Singh K.H. (2001). Estimaiton of heterosis in Indian mustard [*Brassica juncea. (*L) Czren and Coss]. *Annl. Agril. Bio. Res*. 6 (2): 193-200.
38. Nasim, M., Rahman, L., Quddus, M.A. and Shah-E-Alam, M. (1994). Correlation and path analysis in *Brassica campestris* L. *Bangladesh J. Agril. Sci*. 21(10): 15-23.
39. Ahmed, M.R. (1993). Study of agronomic value of resynthesized rapeseed lines and early generations of crosses "rsyn-lines x improved varieties. *Iranian J. Agril. Sci.* 24(3/4):1-13.
40. Tuncturk, M. and Ciftci, V. (2007). Relationships between yield and some yield components in rapeseed (*Brassica napus* ssp. *Oleifera* L.) cultivars by using correlation and path analysis. *Pakistani. J. Bot.*

39(1):81-84.

41. Chauhan, J. and Singh, P. 1985. Association of some morphophysiological determinants with seed yield in Toria (Brassica campestris L. var. Toria).Thesis Abstract , XI-1: 4243.
42. Rashid, M. H. (2007). Characterization and diversity analysis of the oleiferous *Brassica* species. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.
43. Han, J.X. (1990). Genetic analysis of oil content in rape *Brassica napus. Oil Crops of Chaina.* 2: 1-6.
44. Singh, B. 2004. Character association and path analysis under dryland condition in India mustard (*B. juncea*). *Cruciferae* Newslet., 25: 99-100.
45. Singh, M. Singh, H.L. and Dixit, R.K. 2004. Studies on genetic variability, heritability, genetic advance and correlation in Indian mustard *(Brassica juncea (L.)* Czem and Coss.). Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. *Plant-Archives*. 4(2): 291294
46. Yadava, C.K. (1983). Studies on genetics of yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss). Thesis Abst. 9(2): 186-187.
47. Singh, R.K. and Chaudhary, B.D. (1985). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India. p. 56.
48. Siddikee, M. A. (2006). Heterosis inter genotypic variability, correlation and path analysis of quantitative characters of oleiferous *Brassica campestris* L. MS Thesis, Dept. of Genetics and Plant Breeding, SAU, Dhaka.
49. Kudla, M. (1993). Comparative analysis of winter swede rape genotypes. *Biuletyn instytutu Hodowli Roslin*. 90: 99-107.