



Genetic Variability, Correlation and Path Coefficient Analysis in Advanced Generation of *Brassica napus* L.

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Authors' contributions

This work was carried out in collaboration between all authors. Author MNE designed the study and wrote the protocol and first draft. Authors MEH and MHU performed the statistical analysis and wrote the first draft of the manuscript. Authors FM and SP managed the analyses of the study. Authors MA, MMH and MSM managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

The present study was conducted involving 62 F₃ genotypes of *Brassica napus* L. at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh to ponder the genetic variability, phenotypic, genotypic and environmental coefficient of variation, heritability and genetic advance, correlation, path coefficient and genetic diversity analysis in a randomized complete block design (RCBD) with sixty-two genotypes (treatments) with three replications during November 2014 to February 2015. The investigations aimed to select the best segregating genotypes for the yield improvement of *Brussica napus* (rapeseed). Analysis of variance indicated

that the genotypes were found significantly different for all the characters considered. The relative phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits investigated. The high GCV value was observed for the number of silique per plant (NSP), plant height (PH), silique length (SL), number of seed per silique (NSS) and seed yield per plant (SYP) indicated high broad sense heritability. The significant positive correlation with seed yield per plant (SYP) was found in plant height (PH) (0.368**), the number of primary branches per plant (NPB) (0.332**), number of secondary branches per plant (NSB) (0.382**), number of silique per plant (NSP) (0.549**), and silique length (SL) (0.037**). The results of path coefficient analysis uncovered that plant height (PH) (0.582), days to 50% flowering (50F) (0.390), days to maturity (DM) (0.575), number of primary branches per plant (NPB) (0.678), number of secondary branches per plant (NSB) (0.182), and thousand seed weight (TSW) (0.289) had a positive direct impact on seed yield per plant (SYP) and thus it was concluded that these traits could be exploited for the enhancement of yield potential of rapeseed. This study showed that based on the agronomic performance execution, genotypes G8, G14, G19, G21, G47, and G55 might be proposed for future hybridization program in Bangladesh and this could help rapeseed breeders to upgrade their breeding activities.

Keywords: *Brassica napus*; correlation path analysis; genetic advance; heritability.

1. INTRODUCTION

Brassica oil is one of the world's most important edible vegetable oils. In Bangladesh, different types of *Brassica* species are developed through breeding programs. The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *B. rapa*, BB for *B. nigra* and CC for *B. oleracea* having the diploid chromosome number of 20, 16, and 18 respectively. On the other hand, the species *B. juncea* (AABB), *B. carinata* (BBCC) and *B. napus* L.(AACC) are the amphidiploids [1]. Approximately, 70% of the total cultivated mustard in Bangladesh is occupied of either *B. rapa* or *B. napus* L [2]. *Brassica* oil crops are the most critical group of species that supply essential edible oil in Bangladesh [3]. Mustard and rapeseed seeds contain 40%–45% oil and 25% protein [3].

The per capita consumption of consumable oil in Bangladesh is 8 g/day when contrasted with a need of 40 g/day [4]. The shortage of edible oil has turned into a constant problem for the country [5]. The average per hectare yield of oilseed crops in Bangladesh was 740 kg, and average world production was 2400 kg [6]. The productivity of oilseed crops in Bangladesh is comparatively lower than that which obtains in most of the oilseed growing countries of the world. The logical reason behind such poor yield in Bangladesh might be attributed to the lack of improved varieties and poor management practices [7]. Besides, the cultivated area of mustard is comparatively lower than other crops such as due to the consequence of rice-

dependent cropping pattern, and as such, it is strenuous to change [8].

A plant breeding program may be divided into three main steps viz. developing germplasm with various genetic resources, selection of the best individual from the expanded resources and utilization of the best selected individual to develop a suitable and superior variety. There is plenty of scope to increase yield per unit of area through breeding unrivaled varieties. The knowledge on genetic variability [9], heritability and genetic advance [10] and character association is a prerequisite for starting a fruitful breeding program expected to develop high yielding varieties [8]. High heritability value indicates the strategy for selection of suitable character by the phenotypic performance of the respective genotype and genetic advance shows the progress for the choice of the best individual [11].

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 [12] 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 [13]. 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 [14]. Inter-varietal and inter-specific hybridization are essential for creating the variation or transfer gene of interest

from wild species in rapeseed improvement programme [15]. Genetic variability is one of the criteria for parent choice [16]. Consideration of more diverse parents (inside the farthest point) in hybridization could build the possibility of acquiring the most extreme heterosis [17] and give the full range of variability in segregating generations. This present investigation was undertaken to evaluate the variability, character association and the selection criteria for the best genotypes among the advanced generations of *B. napus*.

2. MATERIALS AND METHODS

The present research was carried out at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during November 2014 to February 2015. The area of the trial site is 23° 74' N latitude and 90° 35' E longitudes with 8.2 meters above from the ocean level. The experiment was carried out in the Agro-ecological region of "Madhupur Tract" (AEZ No. 28). The land was clay loam in texture and olive gray with common fine to medium distinct dark

yellowish brown mottles. The pH range is 5.47–5.63 and organic carbon content is 0.82%.

The healthy seeds of sixty-two F₃ of *B. napus* L. were collected from the Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were utilized as test materials (Table 1). Randomized complete block design (RCBD) was used with sixty-two genotypes (treatments) and three replications per treatment. The total area of the plot was 56m × 14m = 784m² along with 56m × 3.5m replication⁻¹ plot and the distance between replication to replication was 1m. 30cm spacing was used between the line to line.

The data were recorded on ten randomly selected plants for each cross and each parent on days to 50% flowering (50F), days to 80% maturity (DM), plant height (PH) (cm), number of primary branches per plant (NPB), number of secondary branches per plant (NSB), number of siliqua per plant (NSP), siliqua length (SL) (cm), number of seeds per siliqua (NSS), thousand seed weight (TSW) (g) and seed yield per plant (SYP) (g).

Table 1. List of sixty two genotypes of advanced generation *B. napus* used for the experiment

Genotypes	F ₃ Populations	Genotypes	F ₃ Populations
G1	BS-7 × Nap-206	G32	Nap-2012 × Nap-2013
G2	BS-7 × Nap-2012	G33	Nap-2012 × Nap-2022
G3	BS-7 × Nap-2013	G34	Nap-2037 × Bs-13
G4	BS-7 × Nap-2057	G35	Nap-2037 × Nap-206
G5	BS-13 × Nap-179	G36	Nap-2037 × Nap-248
G6	BS-13 × Nap-206	G37	Nap-2037 × Nap-2001
G7	BS-13 × Nap-2001	G38	Nap-2037 × Nap-2012
G8	BS-13 × Nap-2013	G39	Nap-2037 × Nap-2013
G9	BS-13 × Nap-2022	G40	Nap-2037 × Nap-2022
G10	BS-13 × Nap-2057	G41	Nap-2037 × Nap-2057
G11	Nap-179 × Nap-206	G42	Nap-2057 × Nap-248
G12	Nap-179 × Nap-2001	G43	Nap-2057 × Nap-2012
G13	Nap-179 × Nap-2012	G44	Nap-2057 × Nap-2022
G14	Nap-179 × Nap-2013	G45	Nap-9908 × Bs-13
G15	Nap-179 × Nap-2022	G46	Nap-9908 × Nap-206
G16	Nap-179 × Nap-2057	G47	Nap-9908 × Nap-248
G17	Nap-206 × Nap-2012	G48	Nap-9908 × Nap-2001
G18	Nap-206 × Nap-2013	G49	Nap-9908 × Nap-2012
G19	Nap-206 × Nap-2022	G50	Nap-9908 × Nap-2013
G20	Nap-206 × Nap-2057	G51	Nap-9908 × Nap-2022
G21	Nap-248 × Nap-159	G52	Nap-9908 × Nap-2037
G22	Nap-248 × Nap-206	G53	Nap-9908 × Nap-94006
G23	Nap-248 × Nap-2012	G54	Nap-94006 × Bs-13
G24	Nap-248 × Nap-2013	G55	Nap-94006 × Bs-7
G25	Nap-248 × Nap-2022	G56	Nap-94006 × Nap-179
G26	Nap-248 × Nap-2057	G57	Nap-94006 × Nap-206
G27	Nap-2001 × Nap-179	G58	Nap-94006 × Nap-2001
G28	Nap-2001 × Nap-206	G59	Nap-94006 × Nap-2012
G29	Nap-2001 × Nap-248	G60	Nap-94006 × Nap-2013
G30	Nap-2001 × Nap-2013	G61	Nap-94006 × Nap-2022
G31	Nap-2001 × Nap-2022	G62	Nap-94006 × Nap-2057

Analysis of variance was calculated using MS Excel software using MSTAT-C software. The phenotypic and genotypic variance was evaluated by Johnson et al. [18]. The genotypic (GCV) and phenotypic (PCV) coefficient of variation was computed by Burton [19]. Heritability and genetic advance were determined as described by many researchers [20,21]. The simple correlation coefficient was obtained by the method of [20,22] and path coefficient analysis was carried out by Dewey and Lu [23].

3. RESULTS AND DISCUSSION

3.1 Variability, Heritability and Genetic Advance

Significant variations were observed for most of the characters among sixty two F₃ materials of *B. napus* L. The values of mean, range CV%, phenotypic variances, genotypic variances, PCV

and GCV for different yield related characters are shown in Tables 2a and 2b.

3.1.1 Days to 50% flowering (50F)

The days to 50% flowering were observed the lowest (32.50 days) in G19 and highest (44 days) was observed in G48 (Table 2a). The PCV (6.68) was slightly higher than the GCV (4.40) (Table 2b). Days to 50% flowering (50F) exhibited low heritability (43.46%) with low genetic advance (2.28), and genetic advance in the percentage of the mean (5.98) demonstrated that this attribute was controlled by non-additive gene (Table 2b).

3.1.2 Days to maturity (DM)

Maturity delayed the maximum in G32 (91.50 days), and the earliest maturity was observed in G19 (79.50 days) (Table 2a). The PCV (4.16) was higher than the GCV (2.34) (Table 2b), which could imply that the environment had a

Table 2a. Estimation of range and genetic parameters in ten characters of 62 genotypes in *B. napus* L.

Parameters	Range	Mean	MS	CV (%)	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$
50F	32.50-44.00	38.12	9.30**	5.02	6.49	2.82	3.67
DM	79.50-91.50	86.98	17.22**	3.44	13.08	4.14	8.93
PH	90.73-136.00	111.81	156.52**	4.26	89.59	66.92	22.67
NPB	2.30-3.94	3.09	0.27**	13.32	0.22	0.05	0.17
NSB	0.88-3.38	2.14	0.59**	15.44	0.45	0.15	0.30
NSP	85.35-223.80	129.17	1706.54**	9.94	935.67	770.88	164.79
SL	6.86-14.26	7.97	2.05**	5.67	1.13	0.92	0.20
NSS	16.73-29.20	22.66	13.09**	6.36	7.59	5.51	2.08
TSW	3.14-3.87	3.46	0.05**	5.71	0.05	0.01	0.04
SYP	45.62-76.72	60.45	126.52**	3.61	65.64	60.89	4.75

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

Here, 50F= Days to 50% flowering, DM= Days to maturity, PH=Plant height, NPB= Number of primary branches per plant, NSB= Number secondary branches per plant, NSP= Number of siliqua per plant, NSS= Number of seed per siliqua, SL= Siliqua length(cm), TSW=Thousand seed weight(g), SYP=Seed yield per plant, MS= Mean sum of square, CV(%)= Coefficient of variation, $\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance, $\sigma^2 e$ =Environmental variance.

Table 2b. Estimation of range and genetic parameters in ten characters of 62 genotypes in *B. napus* L.

Parameters	PCV	GCV	ECV	Heritability (%)	Genetic advance (5%)	Genetic advance (% mean)
50F	6.68	4.40	5.02	43.46	2.28	5.98
DM	4.16	2.34	3.44	31.70	2.36	2.71
PH	8.47	7.32	4.26	74.70	14.57	13.03
NPB	15.26	7.43	13.32	43.73	0.23	7.46
NSB	31.23	18.12	25.44	63.66	0.46	16.62
NSP	23.68	21.49	9.94	82.39	51.91	40.19
SL	13.32	12.06	5.67	81.90	1.79	22.49
NSS	12.15	10.35	6.36	72.60	4.12	18.18
TSW	6.19	2.39	5.71	14.89	0.07	1.90
SYP	13.40	12.91	3.61	92.76	15.48	25.61

Here, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

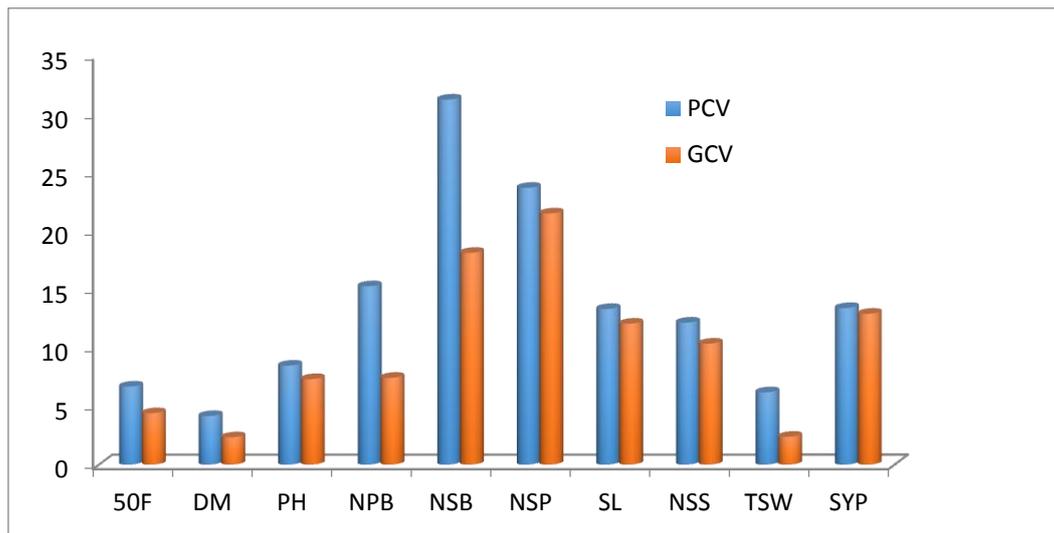


Fig. 1. Genotypic and phenotypic coefficient of variation in *Brassica napus* L. X axis: Parameters; Y axis: Coefficient of variation (%)

significant role in the expression of this trait (Fig. 1). Days to maturity demonstrates low heritability (31.70) with low genetic advance (2.36), and the genetic advance in the percentage of the mean indicated that this trait was controlled by the non-additive gene and medium probability of choosing genotypes that would mature earlier (2.71) (Table 2b). The frequency of the segregating plants showing reduced maturity was comparatively higher than the other crosses.

3.1.3 Plant height (PH, c)

In this investigation, the highest PH was observed in G19 (136c) whereas the minimum PH was observed in G13 (90.73c) (Table 2a). The PCV (8.47) value is slightly higher than GCV (7.32) value (Table 2b). The most noteworthy variation in PH among parents and their hybrid was observed by many researchers [24,25]. Plant height showed high heritability (74.70%) with the moderately high genetic advance (14.57) and the genetic advance in the percentage of mean (13.03) (Table 2b), uncovered the likelihood of the prevalence of the additive gene action in the inheritance of this trait and indicating that this trait could be improved through the selection process [26]. High variability in PH for *B. juncea*, *B. rapa*, and *B. napus* L. was likewise seen by Afrin et al. [27].

3.1.4 Number of primary branches per plant (NPB)

The highest NPB was observed in G47 (3.94) whereas the minimum was in G26 (2.30) (Table

2a). PCV (15.26) value is comparatively higher than the corresponding GCV (7.43) value indicating the apparent variation not only due to genotypes but also due to the considerable influence of the environment (Table 2b). Varshney et al. [28] also found significant differences in the NPB. The NPB displayed low heritability (43.73%) with the low genetic advance (0.23) and the genetic advance in the percentage of the mean (7.46), which uncovered that the non-additive gene controlled this trait. As a whole, the low heritability and the consequent low genetic advance indicated the lower plausibility of choosing genotypes for this attribute [29]. 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 Ali et al. [30].

3.1.5 Number of secondary branches per plant (NSB)

The highest NSB was observed in G55 (3.38) whereas the minimum number was in G18 (0.88) (Table 2a). The PCV value (31.23) is higher than the corresponding GCV value (18.12) (Table 2b). It indicated the presence of considerable variability among the genotypes for this trait. Singh et al. [31] found the highest GCV for the NSB while working on 24 genotypes of *B. napus* L. Varshney et al. [28] found significant differences for the NSB. Moderately high heritability (63.66) along with the low genetic advance (0.46) and the genetic advance in the

percentage of the mean (16.62) (Table 2b) revealed that the non-additive gene controlled this trait [16,32]. As a whole, the moderately high heritability and the consequent low genetic advance indicated the lower possibility of selecting genotypes. Moderately high heritability coupled with low genetic advance was also found by Rashid et al. [33].

3.1.6 Number of siliqua per plant (NSP)

The NSP was observed the highest in G14 (223.80) and the lowest in G24 (85.35) (Table 2a). PCV (23.68) had a similar trend as GCV (21.49) (Table 2b). The difference between the PCV (23.68) and GCV (21.49) indicated the existence of adequate variation among the genotype. The high heritability (82.39) with the high genetic advance (51.91) and the genetic advance in the percentage of the mean (40.19) was observed for this trait revealed the possibility of the predominance of additive gene action in the inheritance of this trait. This trait possessed high variation; it is the high potential for active selection for further genetic improvement of this character [32]. Singh et al. [34] also observed high heritability coupled with the high genetic advance for this trait. Singh et al. [34] reported that the NSP were highly heritable coupled with high genetic advance.

3.1.7 Length of silique (SL)

Length of silique was observed the highest in G21 (14.26c), and the minimum length of the pod was observed in G55 (6.86c) (Table 2a).

Relatively medium PCV (13.32) and GCV (12.06) was found for this trait (Table 2b). Silique length showed the high heritability (81.90) with the low genetic advance (1.79), and the low genetic advance in the percentage of the mean (22.49) indicated that this trait was controlled by non-additive gene (Table 2b).

3.1.8 Number of seeds per silique (NSS)

The NSS was observed highest in G21 (29.20), and the lowest was in G55 (16.73) (Table 2a). The value of PCV and GCV were 12.15 and 10.35 respectively for the number of seeds per silique (Table 2b) which indicating that medium variation exists among the different genotypes [35]. Similar variability was also recorded by Kwon et al. [36]. Number of seeds per silique showed high heritability (72.60%) coupled with the high genetic advance (4.12) and the high genetic advance in the percentage of the mean (18.18) (Table 2b) indicated that this trait was controlled by additive gene and choice for this character would be helpful [15,17,32]. High heritability coupled with the high genetic advance for this trait was likewise seen by Kumar and Singh [37].

3.1.9 Thousand seed weight (TSW, g)

Thousand seed weight was found the maximum in G15 (3.87g) whereas the minimum was found in G50 (3.14g) (Table 2a). The PCV (6.19) and GCV (2.39) were close to each other (Table 2b). This trait had low heritability (14.89%), low genetic advance (0.07) and genetic advance in

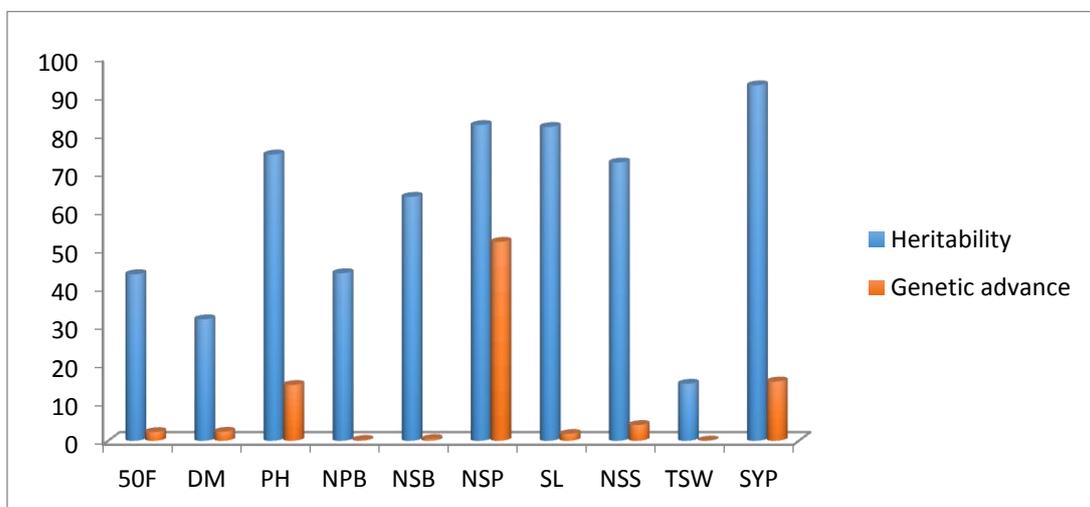


Fig. 2. Heritability and genetic advance over mean in *Brassica napus* L. X axis: Parameters; Y axis: Heritability and genetic advance (%)

the percentage of the mean (1.90) revealed that this trait was controlled by non-additive gene. High heritability for this trait was also observed by Singh [38].

3.1.10 Seed yield per plant (SYP, g)

Seed yield per plant was found the maximum in G8 (76.72g), and the minimum was in G24 (45.62g) (Table 2a). The values of PCV and GCV were 13.40 and 12.91. Similar variability was also found by [39,40]. Seed yield per plant showed the high heritability (92.76%) with the high genetic advance (15.48) and moderately the high genetic advance in the percentage of the mean (25.61) (Table 2b) indicated that this trait was controlled by the additive gene and selection for this character would be effective [32]. High heritability coupled with the high genetic advance for this trait was also observed by Rashid et al. [33]. High heritability and genetic advance for SYP were reported by Kumar and Singh [37] while working with 22 genotypes of *B. napus* L.

The knowledge of variability is prerequisite for simultaneous selection and significant improvement of rapeseed genotypes. The NSB and number of silique per plant demonstrates the presence of broader variability suggesting that these traits could be the excellent candidate for developing new high yielding rapeseed varieties [41]. GCV is a good indicator that imparts information on the existence of genetic variability present in various quantitative traits, but it is lack of providing the clear picture about the heritable variation contributed to GCV [42]. In the current investigation, we found a cross-link between GCV and PCV for PH, NSP, SL, NSS, and SYP indicating that environment influenced less for the expression of these traits. The highest GCV and PCV value observed for traits- NPB, NSB, and NSP suggesting that selection for these traits would be rewarding to isolate more promising lines. Moderate GCV and PCV value were found for SL, NSS, and SYP indicating that vigorous selection method is utilized for the improvement of these parameters. The descriptors such as 50F, DM, PH, and TSW displayed low GCV and PCV value recommended breeder to find out the high variability source for these traits for the future improvement.

GCV along with the heritable components estimation would render the outcome for proper selection for utilizing them in the future breeding program [43]. Genetic and environmental factors

are the contributors to the observed variation in a population. Genetic factors are the only heritable portion from generation after generation. We cannot solely confirm the expected genetic gain in the next generation unless we consider heritability in conjunction with the genetic advance [44] because it provides reliability for the selection of the trait of interest from the variable entries [44]. Characters have high heritability and high genetic advance as a percentage of mean is considered as a powerful genetic tool in the selection round of the best genotype. These characters are governed by the additive gene action and have a less chance to influence by the environment [45]. We found high heritability coupled with high genetic advance as a percentage of the mean for the trait NSB and NSP. Thus these traits have a less tendency to guide by the environment. Three types of heritability was found in corn- low (0-20%), medium (20-60%) and high (above 60%) [46].

3.2 Correlation Coefficient

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. The correlation co-efficient between pairs of the attribute for F_3 materials of *B. napus* L. is shown in (Table 3).

Days to 50% flowering showed a highly significant and positive correlation with DM ($G=0.533$, $P=0.182$) indicated that if 50F increased then DM also increased. It also exhibited interaction with NSP ($G=0.458$, $P=0.316$), SL ($G=0.051$, $P=-0.056$) and SYP ($G=0.201$, $P=0.132$). However, it had negative interaction with NSP ($G=-0.282$, $P=-0.206$) (Table 3). Insignificant association of these traits indicated that environmental factors largely influenced the associations between these traits.

Days to maturity showed significant and positive correlation with NSS ($G=0.018$, $P=0.074$), SL ($G=0.091$, $P=0.037$) and NSP ($G=0.063$, $P=0.132$) (Table 3). It had negative correlation with SYP ($G=-0.065$, $P=-0.04$), TSW ($G=-0.586$, $P=-0.109$) (Table 3). Insignificant association of these traits indicated that environmental factors largely influenced the associations between these traits. Another research work [47] also revealed that DM had an insignificant and positive interaction with SYP.

Plant height showed highly significant and positive interaction with NPB (G= 0.055, P = 0.078), NSB (G= 0.194, P= 0.187), NSP (G= 0.396, P= 0.375), SL (G= 0.038, P= 0.039), NSS (G= 0.038, P= 0.041) and SYP (G= 0.368, P= 0.317) (Table 3). Highly significant positive associations between PH and other characters indicate that the same gene governed the traits and simultaneous improvement would be effective. It had insignificant and negative interaction with TSW (G= -0.597, P= -0.234) (Table 3). Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. These findings are showed resemblance to the reports of [47]. The significant positive correlation between PH and SYP was found by Khan and Khan [48].

Number of primary branches per plant showed positive and significant interaction with NSB (G= 0.575, P= 0.626), NSP (G= 0.397, P= 0.276) and SYP (G= 0.332, P= 0.167)(Table 3). These were suggesting if the NPB increases then SYP also increases. It had insignificant and positive correlation with SL (G= 0.398, P= 0.160) and NSS (G= 0.581, P= 0.163). However, insignificant and negative interaction was found in TSW (G=-0.165, P= -0.164) (Table 3). Insignificant association of these traits indicated

that environmental factors largely influence the association between these traits. Number of secondary branch showed highly significant and positive interaction with NSP (G= 0.507, P= 0.414) and SYP (G= 0.382, P= 0.236) indicated that the same gene governed the traits, and simultaneous improvement would be effective, and branching was an important contributor to yield, independent of its association with plant canopy size. It had insignificant correlation with SL (G= 0.381, P= 0.180) and NSS (G= -0.284, P= 0.188).However, it had a significant and negative interaction with a TSW (G = -0.188, P= -0.190) (Table 3). Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. These findings are showing similar to the reports of [28].

The NSP showed a significant and positive correlation with SYP (G= 0.549, P= 0.531) (Table 3) whereas the insignificant and positive interaction was found in NSS (G= 0.039, P= 0.013), TSW (G= 0.200, P= 0.071) (Table 3). Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. Tyagi et al. [49] reported that NSP had a positive and insignificant effect on SYP.

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

Parameters		DM	PH	NPB	NSB	NSP	SL	NSS	TSW	SYP
50F	G	0.533**	0.320**	-0.184	-0.176	-0.282	0.051	0.458	-0.341**	0.201
	P	0.182*	0.169**	-0.083	-0.02	-0.206	-0.056	0.316	-0.314**	0.132
DM	G		0.330	-0.299**	-0.284	0.063**	0.091**	0.018**	-0.586	-0.065
	P		0.074	0.032	-0.016	0.132**	0.037**	0.074**	-0.109	-0.04
PH	G			0.055**	0.194*	0.396**	0.038**	0.038**	-0.597	0.368**
	P			0.078**	0.187*	0.375**	0.039**	0.041**	-0.234	0.317**
NPB	G				0.576**	0.397**	0.398	0.581	-0.165	0.332**
	P				0.626**	0.276**	0.160	0.163	-0.164	0.167*
NSB	G					0.507**	0.381	-0.284	-0.188*	0.382**
	P					0.414**	0.180	0.188	-0.190*	0.236**
NSP	G						-0.159	0.039	0.200	0.549**
	P						0.136**	0.013	0.071	0.531**
SL	G							0.489**	-0.018	0.037**
	P							0.341**	-0.009	0.048**
NSS	G								0.849	0.074
	P								0.230*	0.047
TSW	G									0.663
	P									0.304

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

Here, 50F= Days to 50% flowering, DM= Days to maturity, PH=Plant height, NPB= Number of primary branches per plant, NSB= Number secondary branches per plant, NSP= Number of siliqua per plant, SL= Siliqua length (cm), NSS= Number of seed per siliqua, TSW=Thousand seed weight (g), SYP=Seed yield per plant (g)

Siliqua length showed a highly significant and positive correlation with SYP (G=0.037, P=0.048) and NSS (G= 0.489, P= 0.341) (Table 3) indicated that the traits were governed by same gene and simultaneous improvement would be effective. Nasim et al. [50] reported that if SL increased then SYP will increase. Insignificant and negative correlation found with TSW (G=-0.018, P=-0.009). Number of seeds per silique showed positive interaction with TSW (G= 0.849, P= 0.230) and SYP (G= 0.074, P= 0.047) (Table 3).

Thousand seed weight showed insignificant and positive interaction with SYP (G=0.663, P=0.304) (Table 3). Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. Saini and Kumar [51] found positive associations which support the results.

3.3 Path Coefficient Analysis

Association of character determined by correlation coefficient may not provide an exact picture of the relative importance of the direct and indirect influence of each of yield components on seed yield per hectare. To find out a clear view of the inter-relationship between SYP and other yield attributes, direct and indirect effects were worked out using path analysis at the phenotypic level which also measured the relative importance of each component. Seed yield per plant was considered as a resultant (dependent) variable, and all other characters were causal (independent) variables. Estimation of the direct and indirect effect of path

coefficient analysis for *B. napus* L. is presented in Table 4.

Path coefficient analysis revealed that 50F had a positive direct effect (0.390) on SYP. Chauhan and Singh [52] explained that 50F had a positive direct effect on SYP. 50F showed a positive indirect effect on DM (0.036), PH (0.125), NSP (0.027) and negative effect on NPB (-0.072), NSB (-0.069), SL (-0.006), NSS (-0.195) and TSW (-0.388) (Table 4).

Days to maturity had a positive direct effect (0.575) on SYP. This trait had a positive indirect effect through NPB (0.172), NSB (0.163), NSP (0.036), SL (0.052), NSS (0.010) and TSW (0.169) (Table 4). In another research work [53], it was revealed that had a positive direct effect on yield. On the contrary, in this study DM had negative indirect effect via 50F (-0.208) and PH (-0.306).

Plant height had a positive direct effect (0.582) on yield per plant. Also had a positive indirect effect via the NSP (0.037) and SL (0.005) (Table 4). Plant height showed negative indirect effect on 50F (-0.186), DM (-0.192), NPB (-0.037), NSS (-0.113), NSS (-0.016) and TSW (-0.173).

The NPB had a positive direct effect on SYP (0.678) (Table 4). This trait had a positive indirect effect via DM (0.203), PH (0.032), NSB (0.105) and NSP (0.037). On the other hand, the negative indirect effect was found on 50F (-0.125), SL (-0.049), NSS (-0.247) and TSW (-0.048). Many researchers [54,55] reported that the NPB had the direct positive effect on seed yield.

Table 4. Path coefficient analysis showing direct and indirect effects of different characters on seed yield per plant (SYP) of mustard

Parameters	Direct (Bold) and Indirect effect									Genotypic correlation with yield
	50F	DM	PH	NPB	NSB	NSP	SL	NSS	TSW	
50F	0.390	0.036	0.125	-0.072	-0.069	0.027	-0.006	-0.195	-0.388	-0.201*
DM	-0.208	0.575	-0.306	0.172	0.163	0.036	0.052	0.010	0.169	0.065
PH	-0.186	-0.192	0.582	-0.037	-0.113	0.037	0.005	-0.016	-0.173	0.368**
NPB	-0.125	0.203	0.032	0.678	0.105	0.037	-0.049	-0.247	-0.048	0.332**
NSB	-0.032	0.052	0.035	0.390	0.182	0.048	-0.047	0.166	0.054	0.382**
NSP	0.110	0.006	0.230	0.269	0.092	-0.094	-0.020	-0.017	-0.058	0.549**
SL	0.020	-0.011	-0.022	0.270	0.069	0.015	-0.124	-0.061	-0.005	0.037
NSS	0.179	-0.008	-0.022	0.394	-0.071	0.004	-0.208	-0.425	-0.245	-0.074
TSW	0.523	-0.337	0.347	0.112	-0.034	-0.019	-0.002	0.361	0.289	0.663**

Residual effect: 0.3123

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

Here, 50F= Days to 50% flowering, DM= Days to maturity, PH=Plant height, NPB= Number of primary branches per plant, NSB= Number secondary branches per plant, NSP= Number of siliqua per plant, SL= Siliqua length (cm), NSS= Number of seed per siliqua, TSW=Thousand seed weight (g), SYP=Seed yield per plant (g).

The number of secondary branches per plant (NSB) had a positive direct effect (0.182) on SYP. It had a positive indirect effect via DM (0.052), PH (0.035), NPB (0.390), NSP (0.048), NSS(0.166) and TSW (0.054) (Table 4). Rashid [53] observed that the NSB had a direct effect on SYP. On the other hand 50F (-0.032) and SL (-0.047) had negative indirect effect on the NSB.

The NSP had a negative direct effect (-0.094) on seed yield. This trait had a positive indirect effect on 50F (0.110), DM (0.006), PH (0.230), NPB (0.296) and NSB (0.092) (Table 4). This trait had a negative indirect effect via SL (-0.020), NSS (-0.017) and TSW (-0.058).

Siliqua length had a direct negative effect (-0.124) on SYP. Han [56] reported that SL had a negative direct effect on SYP. This trait had indirect positive effect 50F (0.020), on NPB (0.270), NSB (0.069) and NSP (0.015). On the other hand, SL showed indirect negative effect via DM (-0.011) PH (-0.022), NSS (-0.061) and TSW (-0.005).

The NSS had a direct negative effect (-0.425) on SYP. This trait had an indirect positive effect on 50F (0.179), NPB (0.394) and NSP (0.004) (Table 4). On the other hand, this trait showed indirect negative effect via DM (-0.008), PH (-0.022), NSB (-0.071), SL (-0.208) and TSW (-0.245).

Path coefficient analysis revealed that TSW had positive direct effect on yield per plant (0.289) followed by positive indirect effect via 50F (0.523), PH (0.347), NPB (0.112) and NSS (0.361) (Table 4). Rashid et al. [33] reported that TSW had a positive direct effect on SYP. On the other hand, this trait showed negative indirect effect on DM (-0.337), NSB (-0.034), NSP(-0.019) and SL(-0.002).

The residual effect was 0.3123, indicated that about 69% of the variability was contributed by nine quantitative characters studied in the path analysis. This low residual effect might be due to the characters not included in the study, environmental factors, sampling error, etc.

4. CONCLUSION

Selection of genetically diverse parents for future hybridization is the prime task for any plant breeding activity. Therefore, considering the magnitude of agronomic performance of all the genotypes investigated, G8 (Nap BS-13 X Nap-

2013) is hereby selected for higher seed yield per plant (SYP), and G47 (Nap-9908 X Nap-248) for higher number of primary branches per plant (NPB), G19 (Nap-206 X Nap-2022) for plant height (PH) or tallness, lowest days to 50% flowering (50F) and the lowest days to maturity (DM); G21(Nap-248 X Nap-159) for the highest siliqua length (SL) and highest number of seeds per siliqua (NSS), G14(Nap-179 X Nap-2013) for highest number of siliqua per plant (NSP) and G55 (Nap-94006 X BS-7) for highest number of secondary branches per plant (NSB).

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Nath UK, Naz S, Rahman MM. Genetic divergence of *Brassica campestris*, *Brassicajuncea* parents and their hybrids. Pakistan J. Biol. Sci. 2003;6(10):936-938.
2. Rashid MH, Bhuiyan MSR, Akbar MA, Parveen S. Diversity analysis of the germplasm oleiferous *Brassica* species. J. Sher-e-Bangla Agric. Univ. 2009;3(1):30-34.
3. BBS. Statistical Yearbook of Bangladesh. Bangladesh Bureau of Statistics. Statistics Division, Ministry of Planning. Govt. of the People's Republic of Bangladesh, Dhaka; 2011.
4. Kaul AK, Das ML. Oil seeds in Bangladesh Canada Agric. Sector team. Ministry of Agric. Govt. of the Peoples Republic of Bangladesh; 1978.
5. Parveen S, Bhuiyan MSR, Hossain MS, Rashid MH. Variability study in F_2 progenies of the inter-varietal Crosses of *Brassica rapa*. J. Sher-e-Bangla Agric. Univ. 2008;2(2):34-40.
6. FAO. FAOSTAT Database of Agriculture (Crops); 2011. Available:<http://www.fao.org>
7. Rashid MH, Parveen S, Bhuiya MSR. Genetic variability, correlation and path coefficient analysis in nineteen *Brassica rapa* germplasm. J. Sher-e-Bangla Agric. Univ. 2010;4(1):84-89.
8. Parveen S, Rashid MH, Bhuiyan MSR. Genetic variation and selection criteria for seed yield related traits in rape seed (*Brassica napus* L.). Bangladesh J. Pl. Breed. Genet. 2013;26(2):15-22.
9. Rahman MM, Chowdhury MAZ, Hossain MG, Amin MN, Muktadir MA, Rashid MH.

- Gene action for seed yield and yield contributing characters in turnip rape (*Brassica rapa* L.). J. Expt. Biosci. 2011;2(2):67-76.
10. Sarwar G, Hossain MS, Rashid MH, Parveen S. Assessment of genetic variability for agro-morphological important traits in aman rice (*Oryza sativa* L.). Int. J. Appl. Sci. Biotechnol. 2015;3(1):73-79.
 11. Sarwar G, Rashid MH, Parveen S, Hossain MS. Evaluation of genetic diversity in agromorphological traits of forty two aman rice genotypes (*Oryza sativa* L.) using D² analysis. American J. Experimental Agri. 2015;8(5):280-288.
 12. 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.
 13. 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.
 14. 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.
 15. Parveen S, Rashid MH, Bhuiyan MSR. Assessment of breeding potential of rapeseed germplasm using D² analysis. J. Expt. Biosci. 2015;6(1): 59-64.
 16. 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.
 17. 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.
 18. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agron. J. 1955;47: 314-318.
 19. Burton GW. Quantitative inheritance in grass pea. Proc. 6th Grassl. Cong. 1952;1: 277-283.
 20. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India; 1985.
 21. Allard RW. Principles of plant breeding. John Willey and Sons. Inc. New York; 1960.
 22. Clarke GM. Statistics and experimental design. Edward Arnold. London; 1973.
 23. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J. 1995;51:515-518.
 24. Malik V, Singh H, Singh D. Gene action of seed yield and other desirable characters in rapeseed. Analysis Biol (Ludhiana). 1995;11(1/2):94-97.
 25. Rao TS. Genetics of yield components in brown sarson. Geneticalberica. 1977;29(3/4):219-227.
 26. Tyagi MK, Chauhan JS, Kumar PR, Singh KH. Estimation of heterosis in Indian mustard [*Brassica juncea* (L.) Czern and Coss.]. Annals Agric. Bio. Res. 2001;69(2): 193-200.
 27. Afrin T, Bhuiyan MSR, Rashid MH, Parveen S. Variability and comparative analysis among advanced generations of *Brassica rapa* L. Plant Knowledge J. 2016;5(1):18-26.
 28. Varshney SK, Rai B, Singh B. Component analysis of harvest index in *Brassica* oilseeds. Indian J. Agric. Rev. 1986;20(3): 129-134.
 29. Chowdhury BD, Thakural SK, Singh DP, Singh P. Genetics of yield and its components in Indian mustard. Narendra Deva J. Agril. Res. 1987;3(1):37-43.
 30. Ali MA, Md. Bhuiyan MSR, Rashid MH, Parveen S, Robbani MG, Sonom M. Breeding for an ideal plant type in *Brassica rapa* L. Plant Knowledge J. 2016;5(1): 36-43.
 31. Singh RP, Malik BPS, Singh DP. Variation for morphological characters in genotypes of Indian mustard. Indian J. Agric. Sci. 1987;57(4):225-230.
 32. Lekh R, Hari S, Singh VP, Raj L, Singh H. Variability studies in rapeseed and mustard. Ann. Agril. Res. 1998;19(1):87-88.
 33. Rashid MH, Parveen S, Bhuiyan MSR. Morphological attributes species identification of oleiferous *Brassica* species and better parents selection criteria for *Brassica juncea*. Int. J. Current Res. 2015;7(9):19847-19854.
 34. Singh RS, Singh P, Dixit RK. Combining ability analysis of yield and developmental traits in Indian canola (*Brassica campestris* L. var. yellow sarson). Farm Sci. 1987; 12(2):170-174.
 35. Mahmud F, Rasul MG, Rahim MA. Genetic diversity analysis in some advanced lines

- of *Brassica napus*. Sci. Asia. 2008;34:432-434.
36. Kwon BS, Lee JI, Chae YA. Genetic studies on some agronomic characters in rapeseed. Korean J. Pl. Breed. 1989;21(1):22-27.
 37. Kumar V, Singh D. Genetics of yield and its components in Indian mustard (*Brassica juncea* L. Czern and Coss). Crop Res. 1994;7(2):243-246.
 38. Singh H. Genetic variability, heritability and drought indices analysis in *Brassica* species. J. oilseeds Res. 1986;3(2):170-177.
 39. Yadava YP, Singh H, Singh D. Gene action for seed yield and its attributes under research. Indian J. Genet. Pl. Breed. 1993;6(1):168-172.
 40. Khera MK, Singh P. Sensitivity and performance of some *Brassica napus* genotypes in stress and non-stress environments. Crop Improve. 1988;15(2): 209-211.
 41. Ejaz-ul-hasan, Mustafa HSB, Bibi T, Mahmood T. Genetic variability, correlation and pathanalysis in advanced lines of rapeseed (*Brassica napus* L.) for yield components. Cercetări Agronomice în Moldova. 2014;157(1):71-79.
 42. Awas G, Mekbib F, Ayana A. Variability, heritability and genetic advance for some yield and yield related traits and oil content in ethiopian coriander (*Coriandrum sativum* L.) Genotypes. Int. J. Plant Breed. Genet. 2015;9:116-125.
 43. Burton GW, DeVane EH. Estimations of heritability in tall festca (*Festuca arundinacea*) from replicated clonal materials. Agron. J. 1953;45:478-481.
 44. Ahsan MZ, Majidano MS, Bhutto H, Soomro AW, Panhwar FH, Channa AR, Sial KB. Genetic variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum* L. accessions. J. Agric. Sci. 2015;7(2):147-151.
 45. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 3rd Edn. ICAR. New Delhi; 1995.
 46. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agron. J. 1949;41:353-359.
 47. Parveen S. Variability study in F₂ progenies of the inter-varietal crosses of *Brassica rapa*. MS thesis, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka; 2007.
 48. Khan RSA and Khan FA. Evaluation of genetic potential of some *Brassica germplasm* collections. Int. J. Agri. Biol. 2003;5(4):30-31.
 49. Tyagi PK, Singh K, Rao V, Kumar A. Correlation and path coefficient analysis in Indian mustard (*Brassica juncea* L.). Crop Res. Hisar. 1996;11(3):319-322.
 50. Nasim M, Rahman L, Quddus MA, Shah-E-Alam M. Correlation and path analysis in *Brassica campestris* L. Bangladesh J. Agril. Sci. 1994;21(10):15-23.
 51. Saini HC, Kumar RP. Model plant architecture through association and path co-efficient analysis in Indian Colza. Indian J. Agric. Res. 1995;29(3):109-115.
 52. Chauhan J, Singh P. Association of some morpho-physiological determinants with seed yield in toria (*Brassica campestris* L var. toria). Thesis Abst. 1995;XI(1):42-43.
 53. Rashid MH. Characterization and diversity analysis of the oleiferous *Brassica* species. MS thesis, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka; 2007.
 54. Mahla HR, Jambhulkar SJ, Yadav DK, Sharma R. Genetic variability, correlation and path analysis in Indian Mustard. [*Brassica juncea* (L.) Czern and Coss.]. Indian J. Genet. Pl. Breed. 2003;63(2):171-172.
 55. Singh RP, Khera MK, Gupta VP. Variability and correlation studies for oil and seed yield in gobhisarson. Crop Improv. 1991;18(2):99-102.
 56. Han JX. Genetic analysis of oil content in rape *Brassica napus*. Oil Crops of China. 1990;2:1-6.

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