

Original Research Article

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

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 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 RCBD with three replications during November 2014 to February 2015. The investigations aimed to select the best segregating genotypes for the yield improvement of rapeseed. Analysis of variance indicated that the genotypes were found significantly different for all the characters considered. The relatively phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits inspected. The high GCV value was observed for the NSP. PH, NSP, SL, NSS, and SYP indicated high broad sense heritability. The significant positive correlation with SYP was found in PH (0.368**), the NPB (0.332**), NSB (0.382**), NSP (0.549**), and SL (0.037**). The results of path coefficient analysis uncovered that PH (0.582), 50F (0.390), DM (0.575), NPB (0.678), NSB (0.182), and TSW (0.289) had a positive direct impact on SYP and thus it was concluded that these traits could be exploited for the enhancement of yield potential of rapeseed. Based on the agronomic execution genotypes G8, G14, G19, G21, G47, and G55 might be proposed for future hybridization program on Bangladesh and helps rapeseed breeders to amend their breeding activities.

Key words: *Brassica juncea*, *Brassica rapa*, Genetic advance; Genetic advance percentage of mean; Heritability.

INTRODUCTION

Brassica oil is the world's most important edible vegetable oils. In Bangladesh, different types of *Brassica* species are developed through the breeding program. 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) is 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 our country is 8 g/day when contrasted with a need of 40 g/day [4]. The shortage of edible oil has turned into a constant issue 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 the oilseed growing countries of the world. The logical reason behind such poor yield in Bangladesh might be credited because of the lack of improved varieties and poor management practices [7]. Besides, the cultivated area of mustard is comparatively lower than other crops as a 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 germplasms with various genetic resources, selection of the best individual from the expanded resources and utilized the best selected individual to develop a suitable and

superior variety. There is plenty of scopes 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 expecting 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 showed 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 should 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*.

MATERIALS AND METHODS

The present research was led at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during November 2014 to February 2015. The area of the trial site is 23⁰ 74' N latitude and 90⁰ 35' E longitudes with 8.2 meters above from the ocean level. The soil

of the experimental site in 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 F_3 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 three replications. The total area of the plot was $56 \text{ m} \times 14 \text{ m} = 784 \text{ m}^2$ along with $56 \text{ m} \times 3.5 \text{ m}$ replication⁻¹ plot and the distance between replication to replication was 1 m. 30 cm spacing was used between the line to line.

The data were recorded on ten randomly selected plants for each cross and each parent on 50F, days to 80% maturity, PH (cm), NPB, NSB, NSP, SL (cm), NSS, 1000 seed weight (g) and 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 [18]. The genotypic (GCV) and phenotypic (PCV) coefficient of variation was computed by [19]. Heritability and genetic advance were determined as described by [20, 21]. The simple correlation coefficient was obtained by the method of [20, 22] and path coefficient analysis was carried out by [23].

RESULTS AND DISCUSSION

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 were shown in Table 2a and 2b.

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

Parameters	Range	Mean	MS	CV (%)	σ^2_p	σ^2_g	σ^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, σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, σ^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.

Days to 50% flowering (50F)

The days to 50% flowering were observed the lowest (32.50 days) in G19 and most noteworthy (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 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).

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 proposed that the environment has a significant role in the expression of this trait. 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.

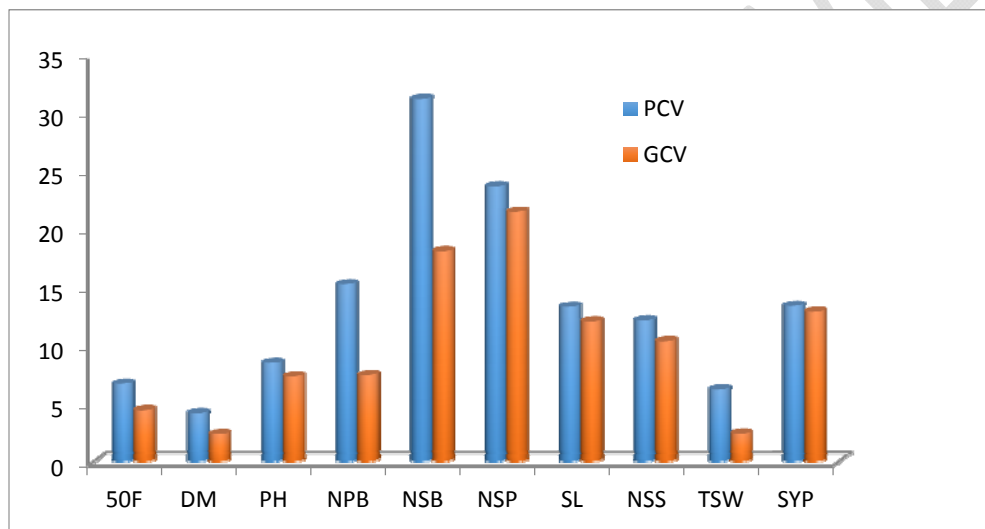


Figure 1. Genotypic and phenotypic coefficient of variation in *Brassica napus* L.

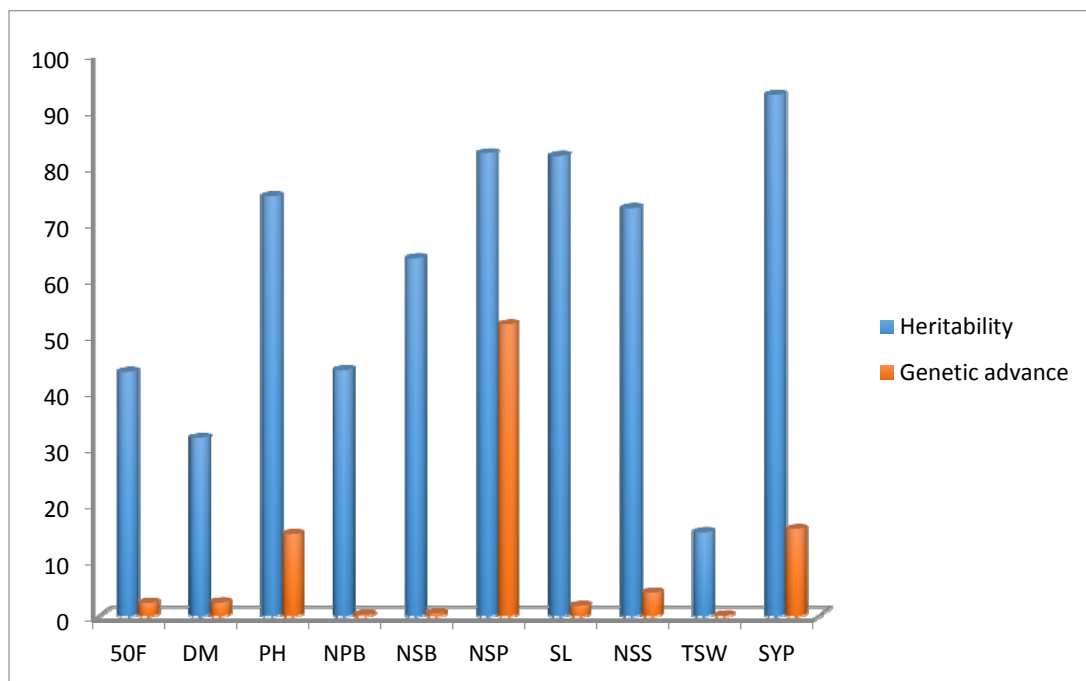


Figure 2. Heritability and genetic advance over mean in *Brassica napus* L.

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 [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 [27].

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). [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 [30].

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. [31] found the highest GCV for the NSB while working on 24 genotypes of *B. napus* L. [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 [33].

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]. [34] also observed high heritability coupled with the high genetic advance for this trait. [34] reported that the NSP were highly heritable coupled with high genetic advance.

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).

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 [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 [37].

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 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 [38].

Seed yield per plant (SYP, g)

Seed yield per plant was found the maximum in G8 (76.72 g), and the minimum was in G24 (45.62 g) (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 [33]. High heritability and genetic advance for SYP were reported by [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].

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.

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	-	-0.284	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%.

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. [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 [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. [49] reported that NSS had a positive and insignificant effect on SYP.

Silique 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. [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. [51] found positive associations which support the results.

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 hectore. 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. [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). [53] revealed that DM had a positive direct effect on yield. On the other hand, DM had negative indirect effect via 50F (-0.208) and PH (-0.306).

Table 4. Path coefficient analysis showing direct and indirect effects of different characters on yield of mustard

Parameter s	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	-	-	0.027	-	-	-	-0.201*
DM	-	0.575	-	0.172	0.163	0.036	0.052	0.010	0.169	0.065
PH	-	-	0.582	-	-	0.037	0.005	-	-	0.368**
NPB	-	0.203	0.032	0.678	0.105	0.037	-	-	-	0.332**
NSB	-	0.052	0.035	0.390	0.182	0.048	-	-	-	0.382**
NSP	0.110	0.006	0.230	0.269	0.092	-	-	-	-	0.549**
SL	0.020	-	-	0.270	0.069	0.015	-	-	-	0.037
NSS	0.179	-	-	0.394	-	0.004	-	-	-	-0.074
TSW	0.523	-	0.347	0.112	-	-	-	-	-	0.663**

Residual effect: **0.3123**

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

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). [54 and 55] reported that the NPB had the direct positive effect on seed yield.

The number of secondary branches 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). [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. [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). [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).

Selection of parents for future hybridization

Selection of genetically diverse parents is the prime task for any plant breeding activities. Therefore, considering the magnitude agronomic performance the genotypes G8 (Nap BS-13 X Nap-2013) for higher SYP, and G47 (Nap-9908 X Nap-248) higher NPB, G19

(Nap-206 X Nap-2022) for tallness, lowest 50F and the lowest DM, G21(Nap-248 X Nap-159) for the highest SL and highest NSS, G14(Nap-179 X Nap-2013) highest NSP and G55 (Nap-94006 X BS-7) for highest NSB.

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