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 F_3 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 23^0 74' N latitude and 90^0 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 m × 14 m = 784 m^2 along with 56 m × 3.5 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 F_3 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^2g	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^2p= Phenotypic variance, σ^2g= Genotypic variance, σ^2e=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

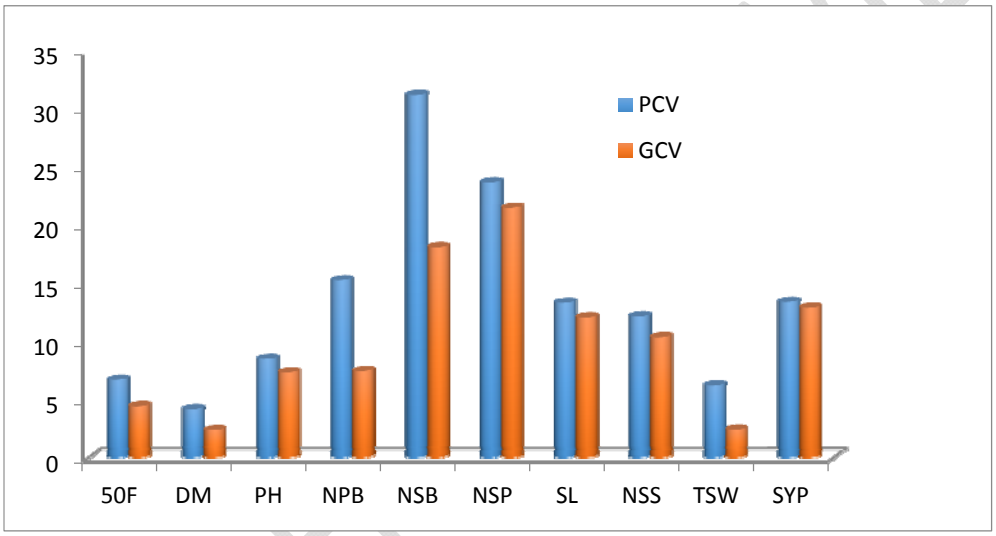
Here, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.

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)

123 Maturity delayed the maximum in G32 (91.50 days), and the earliest maturity was
124 observed in G19 (79.50 days) (Table 2a). The PCV (4.16) was higher than the GCV (2.34)
125 (Table 2b), which proposed that the environment has a significant role in the expression of
126 this trait. Days to maturity demonstrates low heritability (31.70) with low genetic advance
127 (2.36), and the genetic advance in the percentage of the mean indicated that this trait was
128 controlled by the non-additive gene and medium probability of choosing genotypes that
129 would mature earlier (2.71) (Table 2b). The frequency of the segregating plants showing
130 reduced maturity was comparatively higher than the other crosses.



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

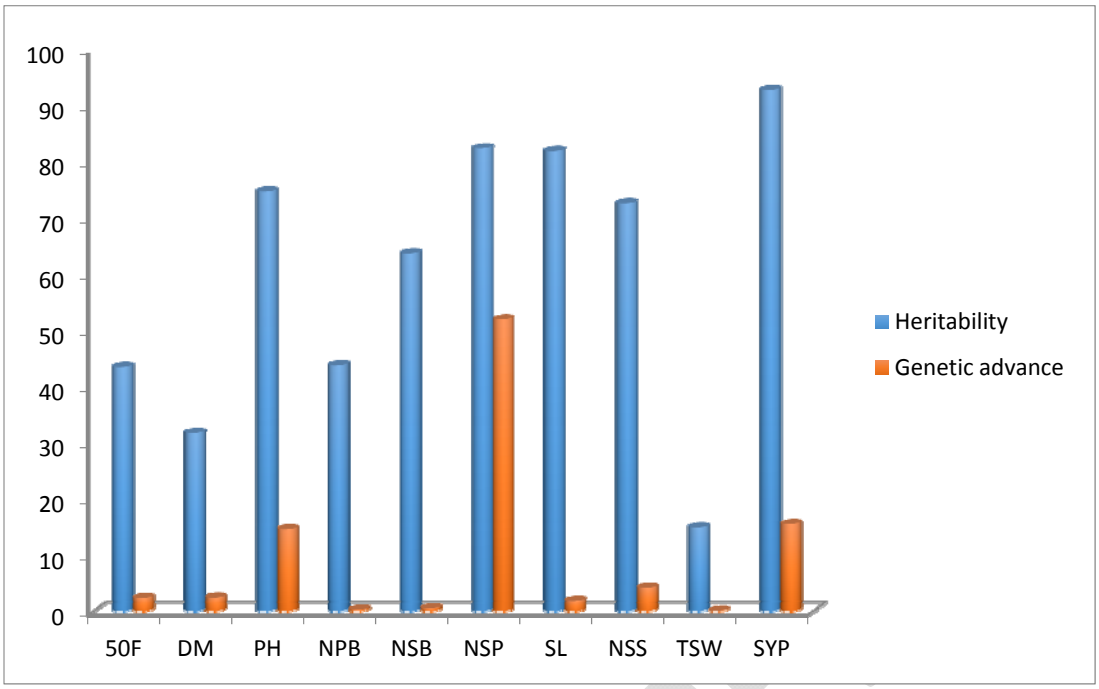

Figure 2. Heritability and genetic advance over mean in *Brassica napus* L.

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

149 considerable influence of the environment (Table 2b). [28] also found significant differences
150 in the NPB. The NPB displayed low heritability (43.73%) with the low genetic advance
151 (0.23) and the genetic advance in the percentage of the mean (7.46), which uncovered that the
152 non-additive gene controlled this trait. As a whole, the low heritability and the consequent
153 low genetic advance indicated the lower plausibility of choosing genotypes for this attribute
154 [29]. However, some of the individual plants showed quite a reasonable lower primary
155 branches which were selected for further study in the next generation. Low heritability
156 coupled with low genetic advance was also found by [30].

157 **Number of secondary branches per plant (NSB)**

158 The highest NSB was observed in G55 (3.38) whereas the minimum number was in
159 G18 (0.88) (Table 2a). The PCV value (31.23) is higher than the corresponding GCV value
160 (18.12) (Table 2b). It indicated the presence of considerable variability among the genotypes
161 for this trait. [31] found the highest GCV for the NSB while working on 24 genotypes of *B.*
162 *napus* L. [28] found significant differences for the NSB. Moderately high heritability (63.66)
163 along with the low genetic advance (0.46) and the genetic advance in the percentage of the
164 mean (16.62) (Table 2b) revealed that the non-additive gene controlled this trait [16, 32]. As
165 a whole, the moderately high heritability and the consequent low genetic advance indicated
166 the lower possibility of selecting genotypes. Moderately high heritability coupled with low
167 genetic advance was also found by [33].

168 **Number of siliqua per plant (NSP)**

169 The NSP was observed the highest in G14 (223.80) and the lowest in G24 (85.35)
170 (Table 2a). PCV (23.68) had a similar trend as GCV (21.49) (Table 2b). The difference
171 between the PCV (23.68) and GCV (21.49) indicated the existence of adequate variation
172 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 siliqua 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). Siliqua 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 siliqua (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)

196 Thousand seed weight was found the maximum in G15 (3.87g) whereas the minimum
197 was found in G50 (3.14g) (Table 2a). The PCV (6.19) and GCV (2.39) were close to each
198 other (Table 2b). This trait had low heritability (14.89%), low genetic advance (0.07) and
199 genetic advance in the percentage of the mean (1.90) revealed that this trait was controlled by
200 non-additive gene. High heritability for this trait was also observed by [38].

201 **Seed yield per plant (SYP, g)**

202 Seed yield per plant was found the maximum in G8 (76.72 g), and the minimum was
203 in G24 (45.62 g) (Table 2a). The values of PCV and GCV were 13.40 and 12.91. Similar
204 variability was also found by [39, 40]. Seed yield per plant showed the high heritability
205 (92.76%) with the high genetic advance (15.48) and moderately the high genetic advance in
206 the percentage of the mean (25.61) (Table 2b) indicated that this trait was controlled by the
207 additive gene and selection for this character would be effective [32]. High heritability
208 coupled with the high genetic advance for this trait was also observed by [33]. High
209 heritability and genetic advance for SYP were reported by [37] while working with 22
210 genotypes of *B. napus* L.

211 The knowledge of variability is prerequisite for simultaneous selection and significant
212 improvement of rapeseed genotypes. The NSB and number of silique per plant demonstrates
213 the presence of broader variability suggesting that these traits could be the excellent
214 candidate for developing new high yielding rapeseed varieties [41]. GCV is a good indicator
215 that imparts information on the existence of genetic variability present in various quantitative
216 traits, but it is lack of providing the clear picture about the heritable variation contributed to
217 GCV [42]. In the current investigation, we found a cross-link between GCV and PCV for PH,
218 NSP, SL, NSS, and SYP indicating that environment influenced less for the expression of
219 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	-0.299**	-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%.

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].

283 The NSP showed a significant and positive correlation with SYP (G= 0.549, P=
284 0.531) (Table 3) whereas the insignificant and positive interaction was found in NSS (G=
285 0.039, P= 0.013), TSW (G= 0.200, P= 0.071) (Table 3). Insignificant association of these
286 traits indicated that environmental factors largely influence the association between these
287 traits. [49] reported that NSS had a positive and insignificant effect on SYP.

288 Siliqua length showed a highly significant and positive correlation with SYP (G=
289 0.037, P= 0.048) and NSS (G= 0.489, P= 0.341) (Table 3) indicated that the traits were
290 governed by same gene and simultaneous improvement would be effective. [50] reported that
291 if SL increased then SYP will increase. Insignificant and negative correlation found with
292 TSW (G= -0.018, P= -0.009). Number of seeds per silique showed positive interaction with
293 TSW (G= 0.849, P= 0.230) and SYP (G= 0.074, P= 0.047) (Table 3).

294 Thousand seed weight showed insignificant and positive interaction with SYP (G=
295 0.663, P= 0.304) (Table 3). Insignificant association of these traits indicated that
296 environmental factors largely influence the association between these traits. [51] found
297 positive associations which support the results.

298 **Path Coefficient analysis**

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

305 other characters were causal (independent) variables. Estimation of the direct and indirect
306 effect of path coefficient analysis for *B. napus* L. is presented in Table 4.

307 Path coefficient analysis revealed that 50F had a positive direct effect (0.390) on SYP.
308 [52] explained that 50F had a positive direct effect on SYP. 50F showed a positive indirect
309 effect on DM (0.036), PH (0.125), NSP (0.027) and negative effect on NPB (-0.072), NSB (-
310 0.069), SL (-0.006), NSS (-0.195) and TSW (-0.388) (Table 4).

311 Days to maturity had a positive direct effect (0.575) on SYP. This trait had a positive
312 indirect effect through NPB (0.172), NSB (0.163), NSP (0.036), SL (0.052), NSS (0.010) and
313 TSW (0.169) (Table 4). [53] revealed that DM had a positive direct effect on yield. On the
314 other hand, DM had negative indirect effect via 50F (-0.208) and PH (-0.306).

315

316 **Table 4.** Path coefficient analysis showing direct and indirect effects of different characters on yield
317 of mustard
318

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**

319 Residual effect: **0.3123**
320 **, * Correlation is significant at the 0.01 and 0.05 level, respectively
321
322
323 Plant height had a positive direct effect (0.582) on yield per plant. Also had a positive
324 indirect effect via the NSP (0.037) and SL (0.005) (Table 4). Plant height showed negative
325 indirect effect on 50F (-0.186), DM (-0.192), NPB (-0.037), NSS (-0.113), NSS (-0.016) and
326 TSW (-0.173).

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

332 The number of secondary branches had a positive direct effect (0.182) on SYP. It had
333 a positive indirect effect via DM (0.052), PH (0.035), NPB (0.390), NSP (0.048), NSS

334 (0.166) and TSW (0.054) (Table 4). [53] observed that the NSB had a direct effect on SYP.
335 On the other hand 50F (-0.032) and SL (-0.047) had negative indirect effect on the NSB.

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

339 Siliqua length had a direct negative effect (-0.124) on SYP. [56] reported that SL had
340 a negative direct effect on SYP. This trait had indirect positive effect 50F (0.020), on NPB
341 (0.270), NSB (0.069) and NSP (0.015). On the other hand, SL showed indirect negative effect
342 via DM (-0.011) PH (-0.022), NSS (-0.061) and TSW (-0.005).

343 The NSS had a direct negative effect (-0.425) on SYP. This trait had an indirect
344 positive effect on 50F (0.179), NPB (0.394) and NSP (0.004) (Table 4). On the other hand,
345 this trait showed indirect negative effect via DM (-0.008), PH (-0.022), NSB (-0.071), SL (-
346 0.208) and TSW (-0.245).

347 Path coefficient analysis revealed that TSW had positive direct effect on yield per
348 plant (0.289) followed by positive indirect effect via 50F (0.523), PH (0.347), NPB (0.112)
349 and NSS (0.361) (Table 4). [33] reported that TSW had a positive direct effect on SYP. On
350 the other hand, this trait showed negative indirect effect on DM (-0.337), NSB (-0.034), NSP
351 (-0.019) and SL (-0.002).

352 **Selection of parents for future hybridization**

353 Selection of genetically diverse parents is the prime task for any plant breeding
354 activities. Therefore, considering the magnitude agronomic performance the genotypes G8
355 (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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