Original Research Article

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

ABSTRACT

The present study was conductedinvolving 62 F_3 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 siliqua 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 siliqua 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

25 thousand seed weight (TSW) (0.289) had a positive direct impact on seed yield per plant

26 (SYP) and thus it was concluded that these traits could be exploited for the enhancement of

27 yield potential of rapeseed. This study showed that based on the agronomic performance

28 execution, genotypes G8, G14, G19, G21, G47, and G55 might be proposed for future

29 hybridization program in Bangladesh and this could help rapeseed breeders to upgrade their

30 breeding activities.

31 **Key words:** *Brassica napus;* Correlation path analysis; Genetic advance; Heritability.

32 **INTRODUCTION**

33 *Brassica* oil is one of the world's most important edible vegetable oils. In Bangladesh,

34 different types of *Brassica* species are developed through breeding programs. The genomic

35 constitutions of the three diploid elemental species of *Brassica* are AA for *B. rapa*, BB for *B.*

36 *nigra* and CC for *B. oleracea* having the diploid chromosome number of 20, 16, and 18

37 respectively. On the other hand, the species *B. juncea* (AABB), *B.carinata* (BBCC) and *B.*

38 napusL.(AACC) are the amphidiploids[1]. Approximately, 70% of the total cultivated

39 mustard in Bangladesh is occupied of either *B.rapa* or *B.napus* L [2].*Brassica* oil crops are

40 the most critical group of species that supply essential edible oil in Bangladesh [3]. Mustard

41 and rapeseed seeds contain 40%–45% oil and 25% protein [3].

42   The per capita consumption of consumable oil in Bangladesh is 8 g/day when

43 contrasted with a need of 40 g/day [4]. The shortage of edible oil has turned into a constant

44 problem for the country [5]. The average per hectare yield of oilseed crops in Bangladesh was

45 740 kg, and average world production was 2400 kg [6]. The productivity of oilseed crops in

46 Bangladesh is comparatively lower than that which obtains in most of the oilseed growing

47 countries of the world. The logical reason behind such poor yield in Bangladesh might be

48 attributed to the lack of improved varieties and poor management practices [7]. Besides, the

49 cultivated area of mustard is comparatively lower than other crops such as due to the

50 consequence of rice-dependent cropping pattern, and as such, it is strenuous to change [8].

51 A plant breeding program may be divided into three main steps viz. developing

52 germplasm with various genetic resources, selection of the best individual from the expanded

53 resources and utilization of the best selected individual to develop a suitable and superior

54 variety. There is plenty of scope to increase yield per unit of area through breeding unrivaled

55 varieties. The knowledge on genetic variability [9], heritability and genetic advance [10] and

56 character association is a prerequisite for starting a fruitful breeding program expected to

57 develop high yielding varieties [8]. High heritability value indicates the strategy for selection

58 of suitable character by the phenotypic performance of the respective genotype and genetic

59 advance shows the progress for the choice of the best individual [11]

60 Determination of correlation coefficient between the characters has considerable

61 importance in selecting breeding materials. Path coefficient technique splits the correlation

62 coefficient into direct and indirect effects [12] via alternative aspects or pathways and in this

63 way allows an essential examination of components that influence a given correlation and can

64 be useful in detailing an efficient selection strategy [13]. Therefore, the path coefficient

65 analysis has been found to provide more particular data on the direct and indirect impact of

66 each of the segment characters upon seed yield [14]. Inter-varietal and inter-specific

67 hybridization are essential for creating the variation or transfer gene of interest from wild

68 species in rapeseed improvement programme [15]. Genetic variability is one of the criteria

69 for parent choice [16]. Consideration of more diverse parents (inside the farthest point) in

70 hybridization could build the possibility of acquiring the most extreme heterosis [17] and

71 give the full range of variability in segregating generations. This present investigation was

72   undertaken to evaluate the variability, character association and the selection criteria for the

73   best genotypes among the advanced generations of *B. napus*.

74   **MATERIALS AND METHODS**

75   The present research was carried out at the experimental farm of Sher-e-Bangla

76   Agricultural University, Dhaka during November 2014 to February 2015. The area of the trial

77   site is $23^0 74^{'}$ N latitude and $90^0 35'$ E longitudes with 8.2 meters above from the ocean level.

78   The experiment was carried out in the Agro-ecological region of "Madhupur Tract" (AEZ

79   No. 28). The land was clay loam in texture and olive gray with common fine to medium

80   distinct dark yellowish brown mottles. The pH range is 5.47–5.63 and organic carbon content

81   is 0.82%.

82   The healthy seeds of sixty-two F_3 of *B. napus* L. were collected from the Dept. of

83   Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, which were utilized as

84   test materials (Table 1). Randomized complete block design (RCBD) was used with sixty-

85   two genotypes (treatments) and three replications per treatment. The total area of the plot was

86    $56m \times 14m = 784m^2$ along with $56m \times 3.5m$ replication^{-1} plot and the distance between

87   replication to replication was 1m. 30cm spacing was used between the line to line.

88   The data were recorded on ten randomly selected plants for each cross and each

89   parent on days to 50% flowering (50F), days to 80% maturity (DM), plant height (PH) (cm),

90   number of primary branches per plant (NPB), number of secondary branches per plant

91   (NSB), number of siliqua per plant (NSP), siliqua length (SL) (cm), number of seeds per

92   siliqua(NSS), thousand seed weight (TSW) (g) and seed yield per plant (SYP) (g).

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

94

Genotypes	F₃ Populations	Genotypes	F₃ 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

A. Variability, Heritability and Genetic advance

102   Significant variations were observed for most of the characters among sixty two F_3

103 materials of *B.napus* L.Thevalues of mean, range CV%, phenotypic variances, genotypic

104 variances, PCV and GCV for different yield related characters are shown in Table 2a and 2b.

105 **Table 2a.** Estimation of range and genetic parameters in ten characters of 62 genotypes in *B.napus* L.
106

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

107
108 **, * Correlation is significant at the 0.01 and 0.05 level, respectively.
109 Here, 50F= Days to 50% flowering, DM= Days to maturity, PH=Plant height, NPB= Number of
110 primary branches per plant, NSB= Number secondary branches per plant, NSP= Number of siliqua
111 per plant, NSS= Number of seed per siliqua, SL= Siliqua length(cm), TSW=Thousand seed weight(g),
112 SYP=Seed yield per plant, MS= Mean sum of square, CV(%)= Coefficient of variation, $\sigma^2 p$=
113 Phenotypic variance, $\sigma^2 g$= Genotypic variance,$\sigma^2 e$=Environmental variance.

114
115
116 **Table 2b.** Estimation of range and genetic parameters in ten characters of 62 genotypes in *B.napus* L.
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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

118

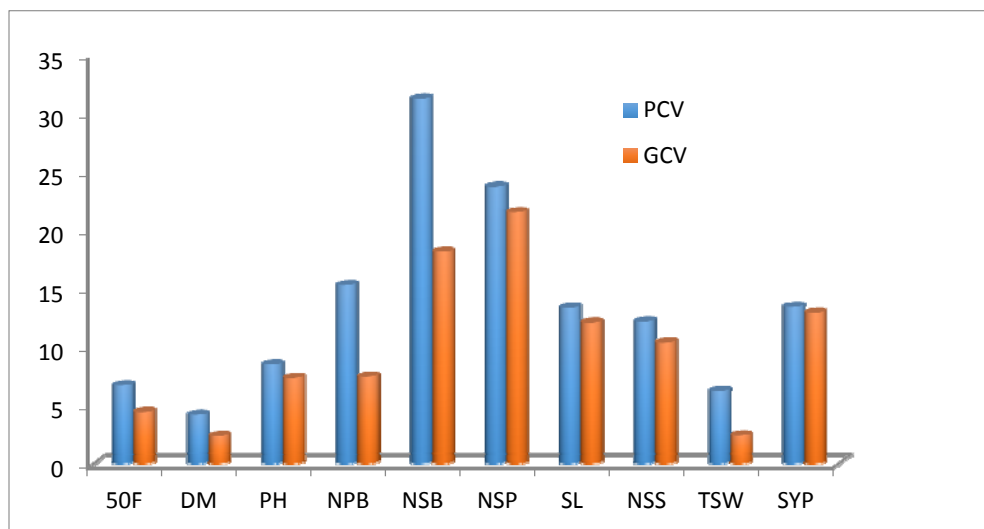119 Here, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV =
120 Environmental coefficient of variation.
121

Days to 50% flowering (50F)

123   The days to 50% floweringwere observed the lowest (32.50 days) in G19 and highest

124 (44 days) was observed in G48 (Table 2a). The PCV (6.68) was slightly higher than the GCV

125 (4.40) (Table 2b). Days to 50% flowering (50F) exhibited low heritability (43.46%) with low

126 genetic advance (2.28), and genetic advance in the percentage of the mean (5.98)

127 demonstrated that this attribute was controlled by non-additive gene (Table 2b).

Days to maturity (DM)

129   Maturity delayed the maximum in G32 (91.50 days), and the earliest maturity was

130 observed in G19 (79.50 days) (Table 2a). The PCV (4.16) was higher than the GCV (2.34)

131 (Table 2b), which could implythat the environment had a significant role in the expression of

132 this trait(Figure 1). Days to maturity demonstrateslow heritability (31.70) with low genetic

133 advance (2.36), and the genetic advance in the percentage of the mean indicated that this trait

134 was controlled by the non-additive geneand medium probability of choosing genotypes that

135 would mature earlier (2.71) (Table 2b). The frequency of the segregating plants showing

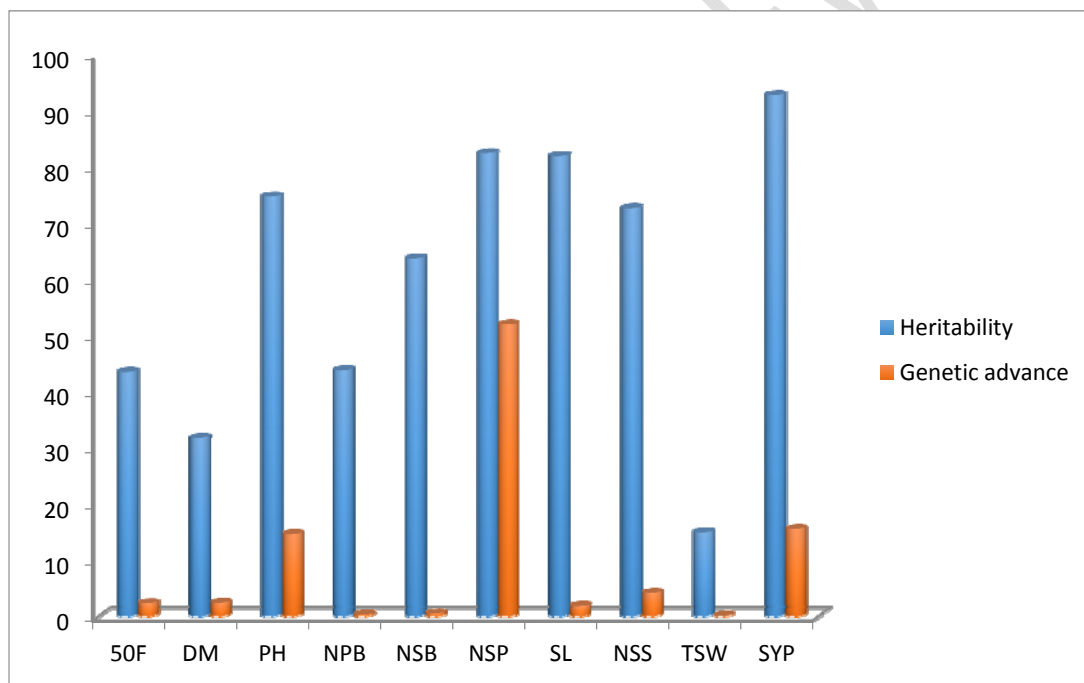136 reduced maturity was comparatively higher than the other crosses.

137

Figure 1. Genotypic and phenotypic coefficient of variation in *Brassica napus*L.<mark>X axis: Parameters; Y axis: Coefficientof variation (%)</mark>

140

142 **Figure 2.** Heritability and genetic advance over mean in *Brassica napus*L.<mark>X axis: Parameters; Y axis: Heritability and genetic advance (%)</mark>

144 **Plant height (PH, c)**

145   In this investigation, the highest PH was observed in G19 (136c) whereas the

146 minimum PH was observed in G13 (90.73c) (Table 2a). The PCV (8.47) value is slightly

147 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) valueindicating 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 inthe NPB.The NPBdisplayed low heritability (43.73%) with the low genetic advance (0.23) and the genetic advance in the percentage of the mean (7.46), which uncoveredthat 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]foundthe highest GCV for theNSB 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 themean (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 activeselection 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)

195   The NSS was observed highest in G21 (29.20), and the lowestwas in G55 (16.73)

196   (Table 2a). The value of PCV and GCV were 12.15 and 10.35 respectively for the number of

197   seeds per silique (Table 2b)which indicating that medium variation exists among the different

198   genotypes [35]. Similar variability was also recorded by [36].Number of seeds per silique

199   showed high heritability (72.60%) coupled with the high genetic advance (4.12) and the high

200   genetic advance in the percentage of the mean (18.18) (Table 2b)indicated that this trait was

201   controlled by additive gene and choice for this character would be helpful [15, 17, 32]. High

202   heritability coupled with the high genetic advance for this trait was likewise seen by [37].

203   **Thousand seed weight (TSW, g)**

204   Thousand seed weight was found the maximum in G15 (3.87g) whereas the minimum

205   was found in G50 (3.14g) (Table 2a). The PCV (6.19) and GCV (2.39) were close to each

206   other (Table 2b). This trait had low heritability (14.89%),low genetic advance (0.07) and

207   genetic advance in the percentage of the mean (1.90)revealed that this trait was controlled by

208   non-additive gene. High heritability for this trait was also observed by [38].

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

210   Seed yield per plant was found the maximum in G8 (76.72g),and the minimum was in

211   G24 (45.62g) (Table 2a). The values of PCV and GCV were 13.40 and 12.91.Similar

212   variability was also found by [39, 40]. Seed yield per plant showed the high heritability

213   (92.76%) with the high genetic advance (15.48) and moderately the high genetic advance in

214   the percentage of the mean (25.61)(Table 2b)indicated that this trait was controlled by the

215   additive gene and selection for this character would be effective[32]. High heritability

216   coupled with the high genetic advance for this trait was also observed by [33]. High

217   heritability and genetic advance for SYPwere reported by [37] while working with 22

218   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

244 heritability coupled with high genetic advance as a percentage of the mean for the trait NSB

245 and NSP. Thus these traits have a less tendency to guide by the environment. Three types of

246 heritability was found in corn- low (0-20%), medium (20-60%) and high (above 60%) [46].

247 **B. Correlation coefficient**

248   Seed yield is a complex product being influenced by several quantitative traits. Some

249 of these traits are highly associated with seed yield. The analysis of the relationship among

250 those traits and their association with seed yield is very much essential to establish selection

251 criteria. The correlation co-efficient between pairs of the attributefor F_3 materials of *B. napus*

252 L. isshown in (Table 3).

253   Days to 50% flowering showed a highly significant and positive correlation with DM

254 (G= 0.533, P= 0.182) indicated that if 50F increased then DM also increased. It also exhibited

255 interaction with NSP (G= 0.458, P= 0.316), SL (G= 0.051, P= -0.056) and SYP (G= 0.201, P

256 = 0.132). However, it had negative interaction with NSP (G= -0.282, P=-0.206) (Table 3).

257 Insignificant association of these traits indicated that environmental factors largely influenced

258 the associations between these traits.

259 **Table 3.** Genotypic and phenotypic correlation coefficients among different pairs of yield and yield

260 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**

		SL	NSS	TSW	SYP
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%.

<mark>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)</mark>

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. <mark>Another research work [47] also revealed</mark> 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 traitsand 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

284 insignificant and positive correlation withSL (G= 0.398, P= 0.160)andNSS (G= 0.581, P=

285 0.163). However, insignificant and negative interaction was found inTSW (G=-0.165, P= -

286 0.164) (Table 3). Insignificant association of these traits indicated that environmental factors

287 largely influence the association between these traits.Number of secondary branch showed

288 highly significant and positive interaction with NSP (G= 0.507, P= 0.414) and SYP (G=

289 0.382, P= 0.236) indicated that the same gene governed the traits,and simultaneous

290 improvement would be effective, and branching was an important contributor to yield,

291 independent of its association with plant canopy size. It had insignificant correlation with SL

292 (G= 0.381, P= 0.180) and NSS (G= -0.284, P= 0.188).However, it had asignificant and

293 negative interaction witha TSW (G = -0.188, P= -0.190) (Table 3). Insignificant association

294 of these traits indicated that environmental factors largely influence the association between

295 these traits. These findings are showing similar to the reports of [28].

296   The NSPshowed a significant and positive correlation with SYP (G= 0.549, P= 0.531)

297 (Table 3)whereas the insignificant and positive interaction was found in NSS (G= 0.039, P=

298 0.013), TSW (G= 0.200, P= 0.071) (Table 3). Insignificant association of these traits

299 indicated that environmental factors largely influence the association between these

300 traits.[49]reported that NSP had a positive and insignificant effect on SYP.

301   Siliqua length showed a highly significant and positive correlation with SYP

302 (G=0.037, P=0.048) and NSS (G= 0.489, P= 0.341) (Table 3) indicated that the traits were

303 governed by same gene and simultaneous improvement would be effective. [50]reported that

304 if SL increased then SYPwill increase. Insignificant and negative correlation found with

305 TSW (G=-0.018, P=-0.009). Number of seeds per silique showed positive interaction with

306 TSW (G= 0.849, P= 0.230) and SYP (G= 0.074, P= 0.047) (Table 3).

307   Thousand seed weight showed insignificant and positive interaction with SYP

308 (G=0.663, P=0.304) (Table 3). Insignificant association of these traits indicated that

309 environmental factors largely influence the association between these traits.[51] found

310 positive associations which support the results.

311 <mark>**C. Path Coefficient analysis**</mark>

312   Association of character determined by correlation coefficient may not provide an

313 exact picture of the relative importance of the direct and indirect influence of each of yield

314 components on seed yield per <mark>hectare</mark>. To find out a clear viewof the inter-relationship

315 between SYP and other yield attributes, direct and indirect effects were worked out using

316 path analysis at the phenotypic level which also measured the relative importance of each

317 component. Seed yield per plant was considered as a resultant (dependent) variable, and all

318 other characters were causal (independent) variables. Estimation of the direct and indirect

319 effect of path coefficient analysis for *B.napus* L. is presented in Table 4.

320   Path coefficient analysis revealed that 50F had a positive direct effect (0.390) on SYP.

321 [52]explainedthat 50F had a positive direct effect on SYP.50F showed a positive indirect

322 effect on DM (0.036), PH (0.125), NSP (0.027) and negative effect on NPB (-0.072), NSB (-

323 0.069), SL (-0.006), NSS (-0.195) and TSW (-0.388) (Table 4).

324   Days to maturity had a positive direct effect (0.575) on SYP. This trait had a positive

325 indirect effect through NPB (0.172), NSB (0.163),NSP (0.036), SL (0.052), NSS (0.010) and

326 TSW (0.169) (Table 4). <mark>In another research work [53], it was revealed that</mark>had a positive

327 direct effect on yield. On the contrary, in this study DM had negativeindirect effect via 50F (-

328 0.208) and PH (-0.306).

329

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

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

<mark>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)</mark>

Plant height had apositive 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 apositive 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 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). [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 anegative 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) andNSP (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 viaDM (-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 via50F (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 onDM (-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

372 effect might be due to the characters not included in the study, environmental factors,

373 sampling error, etc.

374 **CONCLUSION**

375 Selection of genetically diverse parents for future hybridization is the prime task for any plant

376 breeding activity. Therefore, considering the magnitude of agronomic performance of all the

377 genotypes investigated, G8 (Nap BS-13 X Nap-2013) is hereby selected for higher seed yield

378 per plant (SYP), and G47 (Nap-9908 X Nap-248) for higher number of primary branches per

379 plant (NPB), G19 (Nap-206 X Nap-2022) for plant height (PH) or tallness, lowest days to

380 50% flowering (50F) and the lowest days to maturity (DM); G21(Nap-248 X Nap-159) for

381 the highest siliqua length (SL) and highest number of seeds per siliqua (NSS), G14(Nap-179

382 X Nap-2013) for highest number of siliqua per plant (NSP) and G55 (Nap-94006 X BS-7) for

383 highest number of secondary branches per plant (NSB).

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