Genetic Diversity, Correlations and Path Coefficient Analysis among the F5 Populations of Brassica Species

Sujon Kumar[1,2*], Barkat Ali[3], A. B. M. Khaldun[4], Shams Shaila Islam[5], M. Shalim Uddin[4,] M. A. Latif Akanda[4] and M. Shohidullah Miah[2]

[1]*Triticeae Research Institute, Sichuan Agricultural University, Chengdu 611130, Sichuan, China.*
[2]*College of Agricultural Sciences, International University of Business Agriculture and Technology, Dhaka 1230, Bangladesh.*
[3]*College of Horticulture, Sichuan Agricultural University, Chengdu 611130, Sichuan, China.*
[4]*Oilseed Research Centre, Bangladesh Agricultural Research Institute, Gazipur 1701, Bangladesh.*
[5]*Hajee Mohammad Danesh Science and Technology University, Dinajpur 5200, Bangladesh.*

Authors' contributions

This work was carried out in collaboration between all authors. Author SK designed the study and wrote the protocol and first draft. Authors BA and ABMK performed the statistical analysis and wrote the first draft of the manuscript. Authors SSI, MSU, MALA managed the analyses of the study and MSM revised the whole manuscript. All authors read and approved the final manuscript.

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ABSTRACT

The present study was carried out to estimate heritability, genetic variability, correlation and genetic advance among F_5 populations of ten genotypes *in Brassica* species. This study was executed following randomized complete block design (RCBD) with three replications during November 2017 to February 2018 at the experimental field of College of Agricultural Sciences, International University of Business Agriculture and Technology, Dhaka, Bangladesh. Aim of the research was to evaluate and select the best segregating genotypes for the yield and yield contributing traits towards variety development programs. Analysis of variance revealed that the genotypes were significantly different for all the characters studied. The relative phenotypic

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Corresponding author: Email: info.sujonkumar@gmail.com;

coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the traits studied. The high GCV value was observed for the days to 50% flowering (FF), plant height (PH), primary branches per plant (PBP), pod per plant (PP) and seed yield per plant (SYP) that indicated a high broad-sense heritability. A significant positive correlation with seed yield per plant was found in days to 50% flowering (0.578**), the plant height, (0.787**), pod length (PL) (0.406*), seeds per plant (SP) (0.369*), pod per plant (0.697**) and hundred seeds weight (HSW) (0.500**), but significantly negative correlation found in primary branches per plant (-0.046*). The results of path coefficient analysis revealed that days to 50% flowering (0.287), plant height (0.407), pod length (0.919), seeds per plant (0.033), pod per plant (0.035) and hundred seeds weight (0.795) had a positive direct impact on seed yield per plant and thus it was indicated that these traits could be exploited for the enhancement of yield performance of *Brassica* species. This study showed that based on the agronomic performance execution, genotypes G2, G5, G6 and G8 might be proposed for future hybridization programs in Bangladesh followed by variety development activities.

1. INTRODUCTION

Brassica ranked third most important sources of edible vegetable oils globally after palm and soybean [1]. The family Brassicaceae includes about 3,500 species and 350 genera. Rapeseed mustard were most important crops of this family. It is commonly grown in countries such as India, Canada, China, Pakistan, Poland, Bangladesh, Sweden and France [2]. Different types of Brassica varieties are developed through field breeding programs In Bangladesh aiming oil production. The genomic constitutions of the three diploid elemental species of Brassica are AA for *Brassica rapa* with diploid chromosome number 20, BB for *Brassica nigra* with chromosome number 16 and CC for *Brassica* oleracea having chromosome number 18. On the other hand, the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* L. (AACC) are the amphidiploids [3]. The oleiferous *Brassica* represented by rapeseed and mustard plays a pivotal role in vegetable oil production in Bangladesh. Undoubtedly, it is the most important edible oil crop, which covers the highest acreage of 66% of the total oil seed acreage of Bangladesh [4]. *Brassica rapa* or *Brassica napus* L occupied approximately 70% of the total cultivated mustard area in Bangladesh (Rashid et al., 2009). *Brassica* oil crops are the major group of species contributing edible oil supply chain in Bangladesh. Mustard and rapeseed seeds contain approximately 40%–45% oil and 25% protein [5].

In Bangladesh, 787025 ha of land was under rapeseed and mustard cultivation, which produced 361909 tons in 2018-19 [6]. The improvement of a crop is largely dependent on the nature and magnitude of available genetic variability, and the transfer of desired characters into new varieties. The success of breeding program can be enhanced when variability within the existing germplasm is high, which allows the plant breeder to more rapidly produce new varieties or improve existing ones [7,8,9,10].

Any plant breeding activity focused on maily creation of variability, selection of the best individual from the expanded resources and utilization of the best-selected individual to develop a new and superior variety. There is plenty of scope to increase yield per unit of area through plant hybridization programs. The knowledge on heritability and genetic advance [11], genetic variability [12], and character association for starting a fruitful breeding program targeting to develop high yielding varieties [13]. The genetic advance shows the progress for the choice of the best individuals [14], whereas high heritability value signifies the strategy for selection of suitable characters by the phenotypic performance of a corresponding genotype.

Analysis of correlation coefficient between the characters has remarkable importance in selecting crop breeding materials. Path coefficient analysis splits the correlation coefficient into direct and indirect effects [15] via pathways which allows an essential examination of components that greatly influenced a given correlation and can be useful in detailing an efficient selection technique [16]. By this way, the path coefficient analysis has proved to provide more particular data on the direct and indirect impact of each of the segment traits for seed yield [17]. Inter-varietal and inter-specific

hybridization are import for creating the genetic variation or accumulate gene of interest from wild species in mustard improvement program [18]. Genetic variability is an an important criterion for parent choice [19]. Consideration of more diverse parents in hybridization can build the possibility of achieving the highest level of heterosis [20] which provide the full range of variability in segregating generations. Thus the present investigation was conducted to evaluate variability, character association and the selection criteria for the best genotypes among the advanced generations of *Brassica* genotypes.

2. MATERIALS AND METHODS

This field experiment was conducted in the experimental field of College of Agricultural Sciences, International University of Business Agriculture and Technology, Dhaka, Bangladesh during November 2017 to February 2018. Geographically, the experimental field is situated at the altitude of 12.9m above mean sea level (23° 52' 25" N - 90° 23' 47" E). The experiment was carried out in the Agro ecological region of "Madhupur Tract" (AEZ No. 28, Bangladesh). The land was clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH range is 5.40–5.67 and organic carbon content is 0.82%. The experiment was conducted using ten F_5 lines materials. Seeds of F_5 of *Brassica* species were collected from the Oilseed Research Centre, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh, which were utilized as test materials (Table 1). Randomized complete block design (RCBD) was used with ten genotypes and three replications per treatment. The total area of the plot was 66m × 16m = 1056m^2 along with 66m × 3.5 m replication^{-1} plot and the distance between replication to replication was 1m. 30 cm spacing was used between plant-to-plant distances.

Different genotypes were matured at different times. Harvesting was done when 90% of the plant population of each plot reached to maturity. Data were recorded on five randomly chosen plants of each genotype for each replication on days to 50% flowering, plant height (cm), primary branches per plant, pod length (cm), seeds per pod, pods per plant, days to maturity, hundred seed weight (g), seed yield per plant (g).

Analysis of variance was calculated using MS Excel software and RStudio 4.0.3 software. The phenotypic and genotypic variance was evaluated by the method developed by HF and Comstock [21]. The genotypic (GCV) and phenotypic (PCV) coefficient of variation was computed followed by Burton (1952). Heritability and genetic advance were determined as described by many researchers such as Singh and Chaudhary (1985) and Allard [22]. The simple correlation coefficient was obtained by the method of Singh and Chaudhary (1985) and Clarke [23]. The path coefficient analysis was followed by the method carried out by Dewey and Lu [24].

3. RESULTS AND DISCUSSION

3.1 Variability, Heritability and Genetic Advance

Significant variations were observed for most of the characters among ten F_5 generations of *Brassica* species. The values of mean, range, CV%, phenotypic variances, genotypic variances, PCV and GCV for different yield related characters are shown in Table 2.

Table 1. Name and sources of studied Brassica genotypes

Genotype	Cross combination	Sources
G1	BARI Sarisha-7 × Tori-7	BARI, BD
G2	BARI Sarisha-8 × Tori-7	BARI, BD
G3	BARI Sarisha-13 × Rai-5	BARI, BD
G4	BINA Sarisha-4 × Rai-5	BARI, BD
G5	Rai-5 × BARI Sarisha-7	BARI, BD
G6	Tori-7 × BARI Sarisha-13	BARI, BD
G7	BINA Sarisha-4 × Tori-7	BARI, BD
G8	BARI Sarisha-8 × BINA Sarisha-4	BARI, BD
G9	BARI Sarisha-13 × BINA Sarisha-4	BARI, BD
G10	BINA Sarisha-4 × BINA Sarisha-4	BARI, BD

3.1.1 Days to 50% flowering (FF)

The lowest FF was observed in G6 (49.12 days) and the highest found in G3 (93 days) and the PCV (20.29) observed slightly higher than the GCV (20.19) However, FF exhibited low heritability (0.99%) with low genetic advance (2.26), and genetic advance mean is 41.41 which demonstrated that this attribute was controlled by non-additive gene (Table 2). Our results of high heritability and low genetic advance for this parameter was strongly supported by the results published by Akabari et al. [25], where they estimated high heritability (ns) 0.67 with low genetic advance 8.56 in Indian mustard [26] while they worked on 10 *Brassica napus* L. genotypes and found high heritability with high genetic advance 0.99 and 37.75 for FF. High heritability with low genetic advance for days FF are in accordance with that of Sadat et al. [27] published where they worked on F_2 and F_3 generations of rapeseed and found high heritability with low genetic advance 0.65 and 1.20. These results of high heritability are also in agreement with Oghan et al. (2009) where he obtained high heritability 0.73 for flowering time while worked on 21 progenies along with parents of *Brassica napus* L., while Muhammad et al. [28] reported low heritability for days to FF in F_2 populations of *Brassica* napus.

3.1.2 Plant height (PH)

From the results, highest PH was observed in G2 (156.37cm) whereas the minimum PH was observed in G4 (60.75cm). The PCV value (28.11) is slightly higher than GCV (20.36) value (Table 2). Plant height showed low heritability (0.94%) with the moderately low genetic advance (0.86) and the genetic advance in the percentage of mean is 27.38. The significant variation in our results strongly supported by the studies of Akabari et al. [25], Muhammad et al. [29] and Zare and Sharafzadeh (2011). In this study outcome, for low heritability was further supported by the results of Zebarjadi et al . [30] where they estimated low heritability 0.28 for plant height while working on rapeseed. Our results of high heritability for plant height was also supported by Aytaç and Kinaci [31] where they evaluated 10 winter rapeseed genotypes and high heritability and high genetic advance was further strengthen by the results of Akbar et al. [32] while they worked on eighteen lines of *Brassica juncea* L. and obtained high heritability with high genetic advance 0.84 and 11.05 for plant height. This figures revealed the possibility of the existence of the additive gene action in the

inheritance of this trait and indicating that this trait could be improved through the selection process [33].

3.1.3 Primary branches per plant (PBP)

Our findings observed that the highest PBP was in G5 (5.66) whereas the minimum was in G3 and G4 (2.12). PCV (22.49) value is comparatively higher than the corresponding GCV (17.29) value indicating the apparent variation not only due to genotypes but also due to the considerable influence of the environment (Table 2). Similar findings published by Varshney et al. [34] where significant differences occurred in PBP. Our finding of high heritability with low genetic advance was strongly consistent with the results of reports published by Iqbal et al. (2014) and Muhammad et al. [28] where high heritability 0.68 for branches plant^{-1} in *Brassica napus.* Low heritability coupled with low genetic advance was also found in the report by Ali et al. [35].

3.1.4 Pod length (PL)

The lowest PL (6.74cm) was found t in G3 and the highest (8.90cm) wasrecorded in G8. The PCV (9.19) found slightly higher than GCV (8.95). PL resulted low heritability (0.94%) with low genetic advance (0.26), and genetic advance in the percentage of the mean (17.97) demonstrated that this attribute might be controlled by non-additive gene. The result of high heritability and genetic advance for pod length was supported by the results of Singh et al. (2017), where they found high heritability (0.40) with high genetic advance (10.72) for a siliqua length while working on *Brassica rapa* and also similar reporting was found in previous work by Muhammad et al. [30]. Similarly, our results reflected by some previous reports from Nasim et al. [32], Zare and Sharafzadeh (2011) and Sadat et al. [27].

3.1.5 Seeds per pod (SP)

The highest SP was found in G8 (7.36), and the lowest was in G8 (4.12). The value of PCV and GCV were 12.76 and 7.77, respectively for the SP. SP displayed low heritability (0.37%) with low genetic advance (0.95), and genetic advance in the percentage of the mean (9.74). SP further showed a positive and significant correlation with seed yield per plant. Therefore, considering these traits as selection criteria will be advantageous in bringing improvement in *Brassica* species. These results are in conformity with the findings of [36,37].

Table 2. Estimation of range and genetic parameters in nine characters of 10 genotypes in *Brassica* species

Parameters	Range	Mean ± SE	MS	CV (%)	σ^2e	σ^2g	σ^2p	PCV	GCV	ECV (%)	Heritability	GA (5%)	GA (% mean)
FF	49.12-93.12	66.92±0.76	1.24***	4.89	1.74	182.77	184.52	20.29	20.19	1.97	0.99	2.26	41.41
PH	60.75-156.37	82.03±3.04	1.20***	8.30	27.86	503.98	531.85	28.11	27.36	6.43	0.94	0.86	27.38
PBP	2.12-5.66	3.50±0.29	0.19**	0.28	0.25	0.36	0.62	22.49	17.29	14.38	0.59	0.86	27.38
PL	6.74-8.90	7.42±0.08	0.02***	0.24	0.02	0.44	0.46	9.19	8.95	2.08	0.94	0.26	17.97
SP	4.12-7.36	5.47±0.31	1.28*	0.27	0.30	0.18	0.48	12.76	7.77	10.12	0.37	0.95	9.74
PP	20.00-55.50	28.99±3.03	16.48**	2.67	27.60	26.47	54.07	25.35	17.74	18.11	0.48	9.01	25.57
DM	79.58-107.13	95.85±3.04	1.54**	6.12	27.77	38.03	65.81	8.46	6.43	5.49	0.57	0.57	10.07
HSW	0.52-0.55	0.54±0.33	0.03***	0.80	0.33	4.67	5.00	13.80	13.33	3.57	0.93	0.99	26.54
SYP	13.69-53.99	30.27±1.11	12.19***	4.00	3.71	119.13	122.84	36.60	36.04	6.36	0.96	3.30	73.13

*Correlation is *p < 0.05, **p < 0.01, ***p < 0.001; ns: not significant level, respectively.*
Here, FF= Days to 50% flowering, PH= Plant height (cm), PBP= Primary branches per plant, PL= Pod length (cm), SP= Seeds per pod, PP= Pod per plant , DM= Days to maturity, HSW= Hundred seeds weight (g), SYP= Seed yield per plant (g), MS= Mean sum of square, CV(%)= Coefficient of variation, σ2p= Phenotypic variance, σ2g= Genotypic variance, σ2e=Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation, GA= Genetic advance
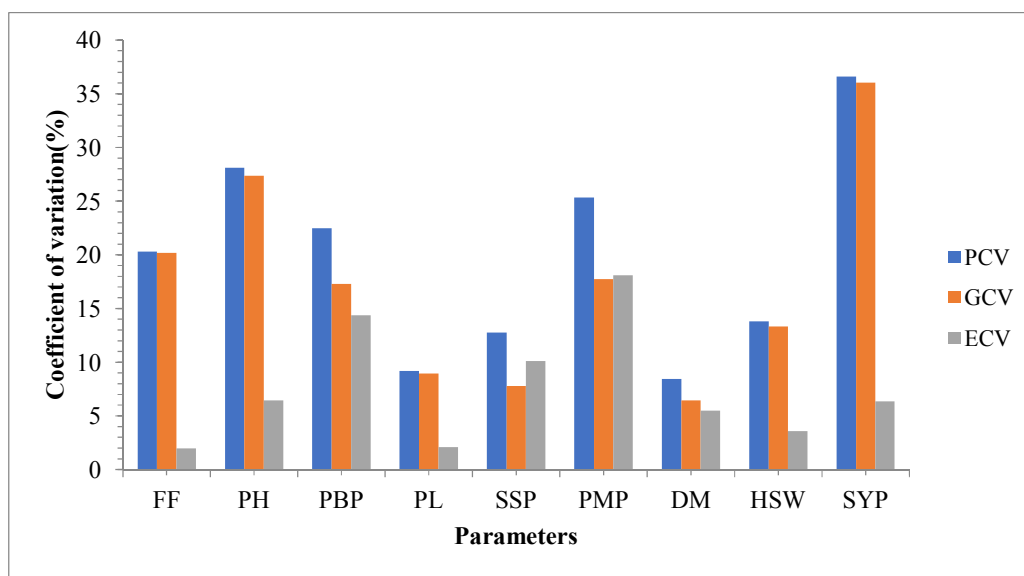

Fig. 1. Phenotypic, genotypic and environmental coefficient of variation in *Brassica* species.

3.1.6 Pods per plant (PP)

In this analysis, the PP was observed lowest (20.00) in G1 and highest (55.50) was observed in G2. The PCV (25.35) was slightly higher than the GCV (17.74). PP displayed low heritability (0.48%) with low genetic advance (9.01), and genetic advance in the percentage of the mean (25.57) demonstrated that this attribute was controlled by non-additive gene which indicating that medium variation exists among the different genotypes (Mahmud et al., 2008). Our findings showed similar pattern in Singh et al. (2016) where they reported high heritability 0.59 while

low genetic advance and further was consistent to the results of Nasim et al. [26] and Zhang and Zhou [38].

3.1.7 Days to maturity (DM)

Maturity duration took longest in G10 (107.13 days) where earliest maturity was observed in G2 (79.58 days). (Table 2). The PCV (8.46) observed higher than the GCV (6.43) (Table 2), which could imply that the environment had a significant role in the expression of this trait (Fig.1). DM demonstrates low heritability (0.57) with low genetic advance (0.57), 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 (10.07) (Table 2). The frequency of the F5 plants showing reduced maturity was comparatively higher than the crosses. Our results for this parameter produced similar findings of Majidi et al. [39] where they estimated high heritability 0.31 for days to ripening in *Brassica napus*. The results of high heritability with low genetic advance was strongly supported by Gupta et al. [40] where found the estimated high heritability 0.90 with low genetic advance 7.8 for days to maturity in interspecific hybridization of oilseed *Brassica*.

3.1.8 Hundred seed weight (HSW)

The highest HSW was observed in G2 (0.55 g) whereas the minimum was demontrated in G7 (0.52g). The PCV (13.80) and GCV (13.33) were close to each other (Table 2). This trait had low heritability (0.93%), low genetic advance (0.99) and genetic advance in the percentage of the mean (26.54), which revealed that this trait was controlled by non-additive genes. These results for high heritability and low genetic advance are showd similar results reported by Marjanovic et al. (2011). Moreover, our results of high heritability and low genetic advance for this parameter was strongly supported by Aytaç and Kinaci [31], and Akbar et al. [32].

3.1.9 Seed yield per plant (SYP)

The maximum SYP observed in G2 (53.99g), and the minimum was in G6 (13.69g). The values of PCV and GCV were 36.60 and 36.04. Similar pattern of variability was also observed by the reports of Yadava et al. (1993) and Khera et al. (1988). SYP showed the high heritability (0.96%) with the high genetic advance (3.30) and

moderately the high genetic advance in the percentage of the mean (73.13) (Table 2) and (Fig. 2) which indicated that this trait was similar with Sadat et al. [27] for high heritability while they worked on F_2 and F_3 generations of rapeseed and estimated high heritability 0.83 and 0.96 but the genetic advance was not in accordance with our results, they found high genetic advance 40.51 and 53.70 for SYP. Report of Aytaç and Kinaci, [31] also supports our results where they found high heritability (0.83) with low genetic advance (0.48) for SYP. Akbar et al. [32] also supports our findings of high heritability while they worked on eighteen lines of *Brassica juncea* L. and obtained high heritability (0.49) but he analyzed high genetic advance (33.59) which was not consistent to our findings.

3.2 Correlation Coefficient

Seed yield is a complex and cumulative product that may influences by several quantitative traits. Some of these traits contribute significantly to seed yield. The relationship analysis o among those traits and their association with seed yield is very much essential for selection pressure. The correlation co-efficient between pairs of the attribute for F_5 materials of *Brassica* genotypes is shown in Fig. 3.

FF showed a highly significant and positive correlation with PH and SYP, DM showed significantly positive and negative correlation with DM). It also exhibited interaction with PL, SP, PP and HSW. However, it had negative interaction with PBP. Insignificant association of these traits indicated that environmental factors largely influenced the associations between these traits.

PH showed highly significant and positive interaction with PP and SYP. It also shown positive interaction with SP, DM, and HSW. It had insignificant and negative interaction with PBP and PL. 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 Parveen [41]. The significant positive correlation between PH and SYP was also found by the report of Khan and Khan [42].

Primary branches per plant showed positive and highly significant interaction with PL and positively significant PP. These were suggesting if the PBP increases then the SYP also increases. It had insignificant and positive

correlation with SP, DM and HSW. However, insignificant and negative interaction was found in TSW. Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. 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 Varshney et al. [34].

The Pod length showed a significant and insignificantly positive correlation with SP, PP,

DM, HSW and SYP . Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. Rashid et al. (2015) also reported that PL had a positive and insignificant effect on SYP.

The Seeds per pod showed a highly significant and insignificantly positive correlation with PP, DM, HSW and SYP. Insignificant association of these traits indicated that environmental factors largely influence the association between these traits. Tyagi et al [33] also reported that SP had a positive and insignificant effect on SYP.
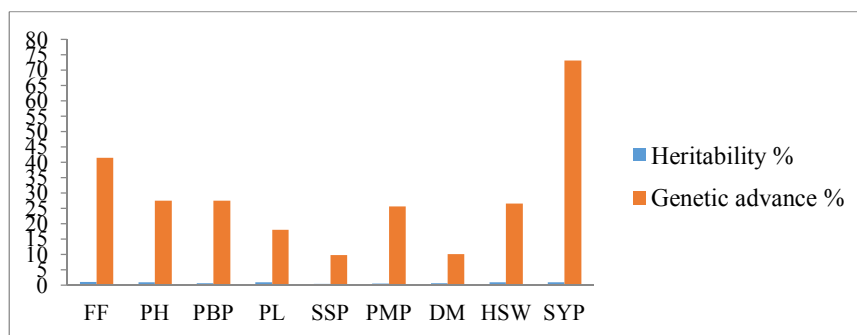

Fig. 2. Heritability and genetic advance over mean in *Brassica* species. X axis: Parameters; Y axis: Heritability and genetic advance (%)
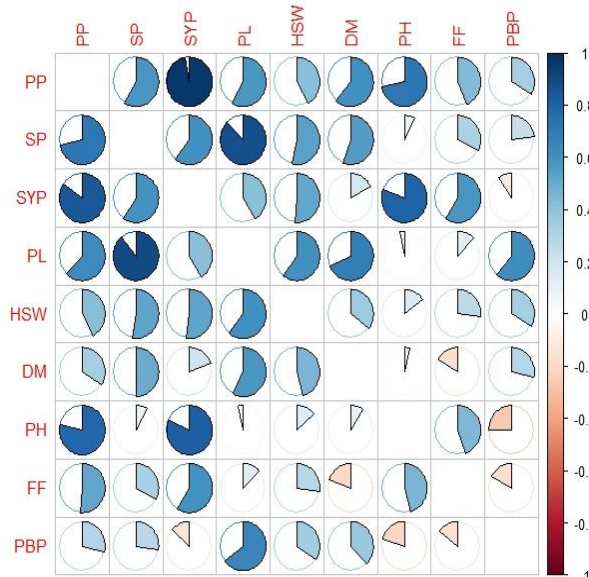

Fig. 3. Phenotypic and genotypic correlation matrices of among different pairs of yield and yield contributing characters for different genotype of Brassica species The correlogram with the phenotypic correlation in the lower diagonal and genotypic correlation in the upper diagonal
Here, FF= Days to 50% flowering, PH= Plant height (cm), PBP= Primary branches per plant, PL= Pod length (cm), SP= Seeds per pod, PP= Pod per plant, DM= Days to maturity, HFSW= Hundred seeds weight (g), SYP= Seed yield per plant (g).

Pods per plant showed a highly significant and insignificantly positive correlation with DM, HSW and SYP. Insignificant association of these traits indicated that environmental factors largely influenced the associations between these traits. Another research work [41] also revealed that PP had a highly significant and insignificantly positive interaction with SYP.

Days to maturity showed significant and insignificantly positive correlation with HSW and SYP. Insignificant association of these traits indicated that environmental factors largely influenced the associations between these traits.

3.3 Path Coefficient Analysis

Associated characters that determined by correlation coefficient may not provide an exact picture of the relative importance of the direct and indirect influence of each of yield contributing characters on seed yield. To get a clear picture of the inter-relationship between SYP and other yield attributes, direct and indirect effects using path analysis is very much important. 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 *Brassica* species is presented in (Table 3).

Path coefficient analysis revealed that FF had a positive direct effect (0.287) on SYP. Chauhan and Singh (1985) explained that FF had a positive direct effect on SYP. FF showed a positive indirect effect on PH, PBP, PL, SP, PP, DM, HSW .

Plant height had a positive direct effect on yield per plant. Also had a positive indirect effect via the FF, PBP, SP, PP and HSW (Table 3). Plant height showed negative indirect effect on PL and DM.

The PBP had a negative direct effect on SYP. This trait had a positive indirect effect via PL, SP, PP and HSW. On the other hand, the negative indirect effect was found on FF, PH and DM. Han [43] reported that SL had a negative direct effect on SYP.

Pod length had a direct positive effect on SYP. Some researchers like Mahla et al. [44] and Singh et al. [45] reported that the PL had the direct positive effect on seed yield per plant. This trait had indirect positive effect FF, on SP, PP and HSW. On the other hand, PL showed indirect negative effect via PH PBP and DM.

SP had a positive direct effect on SYP. It had a positive indirect effect via PH, PL, PP and HSW. Rashid [46] observed that the SP had a direct effect on SYP. On the other hand FF PBP and DM had negative indirect effect on the SP.

PP had a positive direct effect on seed yield per plant. This trait had a positive indirect effect on FF, PH, PL, SP and HSW. This trait had a negative indirect effect via PBP and DM.

DM had a negative direct effect on SYP. This trait had a positive indirect effect through PH, PL, SP, PP and HSW. In another research work reported [46] that it had a negative direct effect on SYP. On the contrary, in this study DM had negative indirect effect via FF (-0.056) and PBP (-0.188).

Table 3. Path coefficient analysis showing direct and indirect effects of different characters Seed yield per plant (SYP) of *Brassica* species

Parameters	Direct (Bold) and Indirect effect								Genotypic correlation with yield
	FF	**PH**	**PBP**	**PL**	**SP**	**PP**	**DM**	**HSW**	
FF	**0.287**	0.185	0.084	0.114	0.015	0.018	0.000	0.217	0.578**
PH	0.131	**0.407**	0.125	-0.035	0.002	0.027	-0.000	0.107	0.787**
PBP	-0.048	-0.102	**-0.501**	0.598	0.011	0.010	-0.001	0.271	-0.046*
PL	0.035	-0.015	-0.326	**0.919**	0.034	0.022	-0.002	0.480	0.406*
SP	-0.135	0.035	-0.177	0.928	**0.033**	0.028	-0.002	0.615	0.369*
PP	0.147	0.319	-0.146	0.575	0.027	**0.035**	-0.001	0.333	0.697**
DM	-0.056	0.037	-0.188	0.626	0.024	0.021	**-0.003**	0.364	0.140
HSW	0.078	0.055	-0.170	0.554	0.026	0.014	-0.001	**0.795**	0.500**

Residual effect: -0.0649
**, * Correlation is significant at the 0.01 and 0.05 level, respectively
Here, FF= Days to 50% flowering, PH= Plant height (cm), PBP= Primary branches per plant, PL= Pod length (cm), SP= Seeds per pod, PP= Pod per plant, DM= Days to maturity, HFSW= Hundred seeds weight (g), SYP= Seed yield per plant (g).

Path coefficient analysis revealed that HSW had positive direct effect on yield per plant followed by positive indirect effect via FF, PH, PL, SP and PP. Rashid et al. (2015) reported that HSW had a positive direct effect on SYP. On the other hand, this trait showed negative indirect effect on PBP (-0.170) and DM (-0.001).

The residual effect was -0.0649, indicated that about 67% of the variability was contributed by nine quantitative characters studied in the path analysis. This low residual effect might be due to the characters not included in the study, environmental factors, sampling error, etc.

4. CONCLUSION

Genetically diverse parents are desirable for selection genetic materials for future hybridization program that allow significant impact for development of a variety of interest. In this study our objectives are evaluate variability, character association and the selection criteria for the best genotypes among the advanced generations of *Brassica* genotypes. Therefore, considering the magnitude of agronomic performance of all the genotypes investigated, G2 (BARI Sarisha-8 × Tori-7) is hereby selected for higher seed yield per plant (SYP), and G5 (Rai-5 × BARI Sarisha-7) for higher primary branches per plant (PBP), G2 (BARI Sarisha-8 × Tori-7) for plant height (PH) or tallness, lowest days to 50% flowering (FF) and the lowest days to maturity (DM) G6 (Tori-7 × BARI Sarisha-13) and G2 (BARI Sarisha-8 × Tori-7); G8 (BARI Sarisha-8 × BINA Sarisha-4) and G8 (BARI Sarisha-8 × BINA Sarisha-4) for the highest pod length (PL) and highest seeds per plant (SP), G2 (BARI Sarisha-8 × Tori-7) for highest pod per plant (PP) and G2 (BARI Sarisha-8 × Tori-7) for highest hundred seeds weight (HSW). Keeping in mind all the objectives covering yield per plant, days to maturity, plant height and hundred seed weight G2 (BARI Sarisha-8 × Tori-7) and G6 (Tori-7 × BARI Sarisha-13) genotypes may be incorporated in the future *Brassica* variety development program.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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