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ORIGINAL RESEARCH ARTICLE

Yield potency assessment and characters association of promising lines of mustard (*Brassica rapa* L.) in southern region of Bangladesh

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ABSTRACT

Mustard (*Brassica spp.*) is a major oilseed crop and the world's third-largest source of vegetable oil. During the rabi season of 2022–2023, the experiment was carried out at the Regional Agricultural Research Station, Bangladesh Agricultural Research Institute (BARI), Barishal, to evaluate the performance of 12 genotypes of *Brassica rapa* L., including the check variety BARI Sarisha-14. The experiment was conducted under a randomized complete block design (RCBD) design with three replications. Analysis of variance demonstrated highly significant ($p \leq 0.01$) differences for the traits viz., plant height, no. of primary branches, no. of secondary branches, and no. of seeds per siliqua, whereas no. of siliqua per plant, 1000 seed weight, and yield kg per hectare had a significant difference at $p \leq 0.05$. Among the examined accessions, the unweighted pair group method with arithmetic mean (UPGMA) cluster analysis identified four different clusters. Cluster II (28.91%) with only one accession had the highest average yield, followed by Cluster I (26.25%) and Cluster IV (22.68%) with the best agronomic features. Furthermore, we observed 1.6% and 11.93% greater (+) mean yield compared to the grand mean yield (1502.33 kg ha^{-1}) for cluster I and cluster II, respectively. Correlation analysis examines the positive and highly significant association among the yield and its related traits. Principal component analysis (PCA) revealed a total proportion of variation of 54.86% for PC1 and 16.89% for PC2. The genotypes BC-100614(8)–7 gave a 7.20% higher yield than the check variety. Considering the statistical results, maturity period, yield, and yield contributing characters of *Brassica rapa* L. genotypes BC-100614(8)-7 (1681 kg ha^{-1}), BC-100614(8)-1 (1594 kg ha^{-1}) and BC-100614(7)-3 (1565 kg ha^{-1}) were noted as promising lines among the evaluated genotypes and suggested for future breeding programs.

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Keywords: *Brassica rapa* L.; yield potency; phenotypic association; PCA analysis; promising breeding lines; trait selection

1. Introduction

Rapeseed-mustard belongs to the family of Cruciferae under the genus *Brassica and is the* most important oilseed crop, a source of vegetable oil, as well as a widely expanding oilseed crop in Bangladesh[1]. There are about ten distinct oil crops in Bangladesh that produce fats and oils of varying quality and quantity. Among them, rapes (*Brassica campestris* L. and *Brassica napus* L.) and mustard (*Brassica juncea* L.) are key sources of vegetable fats. In Bangladesh, the most widely cultivated species are *Brassica rapa* and *Brassica juncea.* Both the plant species that are grown in Bangladesh, *Brassica juncea* and *Brassica campestris*, are together referred to as "mustard"[1,2].

In Bangladesh, the usage of edible oil is rising daily. Bangladesh's agricultural sector includes mustard production and cultivation as essential components. Since ancient times, Bangladesh has cultivated mustard, as a significant edible oilseed crop[3]. Mustard seeds provide 40–45% oil, 20–25% protein, and 12–18% carbohydrates[4]. Mustard is high in fat-soluble vitamins such as A, D, E, and K, as well as energy (approximately 9 kcalg^{-1})[5]. Its oil not only serves as an excellent fat alternative in our daily diet but also stimulates the nation's economy[6].

The area devoted to growing mustard has grown dramatically in recent years. Examining the current domestic mustard output in Bangladesh and projecting the future is crucial for fulfilling the rising demand. Bangladesh produced 11.64 lakh tones of mustard oil seed in the current fiscal year of 2022-2023 against a target of 11.12 tones due to a rise in acreage as well as a high yield[7]. Despite the production rate increasing in terms of our demand, oil production is still not remarkable. As a result, a considerable volume of oil and oil seeds are imported into our country each year. Increasing mustard production might be one strategy to reduce the country's edible oil demand-supply mismatch[8].

Bangladesh Agricultural Research Institute (BARI) has created a variety of high-yielding mustard varieties with yield potentials of up to 2.5–2.8 t ha^{-1} in recent years, as well as launched some promising lines in terms of global climate change[9]. Although these new types have a lot of potential, there are several difficulties that make it tough to produce the optimum results. If these problems could be solved, we could become self-sufficient in the production of edible oil. To fit into the pre-existing cropping pattern, the majority of farmers in our nation grow the traditional variety, Tori-7. When compared to other recently established contemporary varieties, the yield of the native Tori-7 is incredibly low. Consequently, the yield potential of newly developed, promising lines is very high. In light of the foregoing, the present experiment was undertaken under regional conditions to find out early lines of *Brassica rapa* L. with better agronomic traits for yield and wider adaptability.

2. Materials and methods

The experiment was carried out at Rahmatpur, Barishal, during Rabi 2022–2023, with 12 genotypes of *Brassica rapa* L. with yellow seed coat color and one control, BARI Sarisha-14. The experiment was designed with three replications in a randomized complete block design. The plot measured 3 m × 0.9 m. Continuous seed planting in rows 30 cm apart was carried out at Rahmatpur on November 18, 2022. After a few days of germination, the seedlings were trimmed to 5 cm apart. Fertilizers were administered at a rate of 120:80:60:40:4:1 kg ha^{-1} of N:P:K:S:Zn and Boron derived from Urea, TSP, MOP, Gypsum, Zinc Sulphate, and Boric acid[9]. During the last stage of land preparation, half of the urea and all other fertilizers were applied.

The remaining urea was sprayed at the bloom initiation stage. To ensure a satisfactory yield, all intercultural operations were completed on schedule. Days to 50% flowering, days to maturity, plant height (cm), number of primary and secondary branches per plant, number of siliqua per plant, number of seeds per siliqua, 1000 seed weight (g), and seed yield per plot were all recorded. The yield of the plot was converted to kilograms per hectare (kg ha^{-1}). All the data was statistically examined. The meteorological data during the cropping season is listed in **Table 1**.

Table 1. Meteorological data during the cropping season.

Parameter	November	December	January	February
Average high temperature °C	30.72	26.48	26.24	29.82
Average low temperature °C	24.23	17.5	16.18	18.85
Average precipitation (mm)	1.75	8.28	69.27	1.37
Average relative humidity (%)	51.03	48.97	78.22	58.75

3. Statistical analysis

For all of the morphological features presented, an analysis of variance was performed with Statistical Analysis System (SAS) version 9.4. The significant differences were separated using List Significant Difference (LSD) at 5%. According to Khalikqi et al.[10], Pearson's correlation was utilized to determine the associations between yield and yield component qualities using "proc corr" in the SAS software. The Euclidian Distance Method, as well as Dices' and Jaccard's similarity of coefficient data, were used to investigate genetic diversity. In addition, the genetic inter-relationship (showing dendrogram) among *Brassica rapa* L. genotypes was estimated using the Unweighted Pair Group Method using Arithmetic Average (UPGMA) and the algorithm and sequential, agglomerative, hierarchic, and non-overlapping (SAHN) methods. For this study, NTSYSpc version 2.1 (Numerical Taxonomy Multivariate Study System), Exeter Software, Setauket, NY, USA, software 4.0, was used. Principal component analysis (PCA) was performed using comparable software to generate the two-dimensional (2D) plots described by Khan et al.[11].

4. Results and discussion

4.1. Mean square (MS) of analysis of variance (ANOVA)

Table 2 shows the results of an analysis of variance (ANOVA) for nine characteristics from 12 genotypes and one control. Among the genotypes, highly significant ($p \leq 0.01$) mean square accounted for plant height (PH), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), and number of seeds per siliqua (NSPS), whereas the number of siliqua per plant (NSPP), 1000 seed weight (TSW), and yield (kg ha^{-1}) had significant differences ($p \leq 0.05$). This incidence revealed the presence of highly significant genetic variability among the genotypes in terms of statistically significant traits. However, among the replications, only the trait plant height (PH) and number of seeds per siliqua (NSPS) showed significant differences ($p \leq 0.05$). Fayyaz and Amin[12] also found that there was significant genetic and environmental variability among the genotypes due to variance in the analysis of variance.

Table 2. Mean square of ANOVA for yield and yield components of *Brassica rapa* L.

Source	DF	D50%F	DM	PH	NPBPP	NSBPP	NSPP	NSPS	TSW	Yield
Rep	2	3.86	6.78	59.69*	0.14	0.09	78.78	24.69*	0.06	817.33
Gen	11	2.47	3.47	78.08**	0.71**	0.69**	150.27*	38.02**	0.23*	37009.75*
Error	22	4.22	2.57	9.30	0.06	0.10	50.32	7.36	0.09	10534.45
R-square	-	0.27	0.48	0.83	0.85	0.78	0.62	0.74	0.57	0.64

Note: *denotes significance level at $p \leq 0.05$; ** denotes significance level at $p \leq 0.01$; Rep = replication; Gen = genotype; DF = degree of freedom; LSD = least significant difference; D50%F = days to fifty percent flowering; DM = days to maturity; PH = Plant height (cm); NPBPP = no. of primary branch per plant; NSBPP = no. of secondary branch per plant; NSPP = no. of siliqua per plant; NSPS = no. of seeds per siliqua; TSW = 1000 seed weight (g) and seed yield (kg ha^{-1}).

4.2. Mean performance of genotypes

The statistical results revealed that the evaluated *Brassica rapa* L. genotypes significantly differed in terms of plant height (cm), the number of siliqua per plant, no. of seeds per siliqua, thousand seed weight, and seed yield (**Table 3**). The highest plant height (89 cm) was recorded in BC-110714(7)-8, which was statistically similar to the genotypes BC-100614(4)-10 (86.66 cm) and BC-100614(4)-11 (86.33 cm). The lowest plant height (73.66 cm) was recorded in BC-100614(4)-5. The highest number of siliqua per plant (92) was counted in genotype BC-100614(8)-7, followed by the genotypes BC-100614(8)-1(85) and BARI Sharisa-14(85), whereas the lowest was recorded as 70 for the genotype BC-100614(7)-8. The highest seed per siliqua (34) was observed for the genotype BC-100614(8)-7, followed by BC-100614(8)-1(31). The genotypes BC-100614(4)-19 and BC-100614(7)-8 had the lowest number of seeds per siliqua. The 1000 seed weights were almost similar for all the genotypes. The highest seed yield (1681.67 kg ha^{-1}) was produced in BC-100614(8)-7, followed by BC-100614(8)-1 (1594.67 kg ha^{-1}) (**Figure 1**, **Table 3**), which produces 7.2% and 2% higher yield than the check variety BARI Sharisa-14 (**Table 3**). Days to 50% flowering range from 30 to 32 days, while the maturity period ranges from 84 to 87 days. Bazzaz et al.[13] reported a similar statement when conducting research on heat stress in late-sown mustard (*Brassica spp.*) varieties. Among the tested genotypes, the accession BC-100614(4)-10 is considered early mature as well as a short-duration line with a yield of 1553.67 kg ha^{-1}. Sharif et al.[14] reported 1730 kg ha^{-1} yield, and Helal et al.[15] reported 800 to 1460 kg ha^{-1} when evaluated in 3 and 12 lines, respectively.

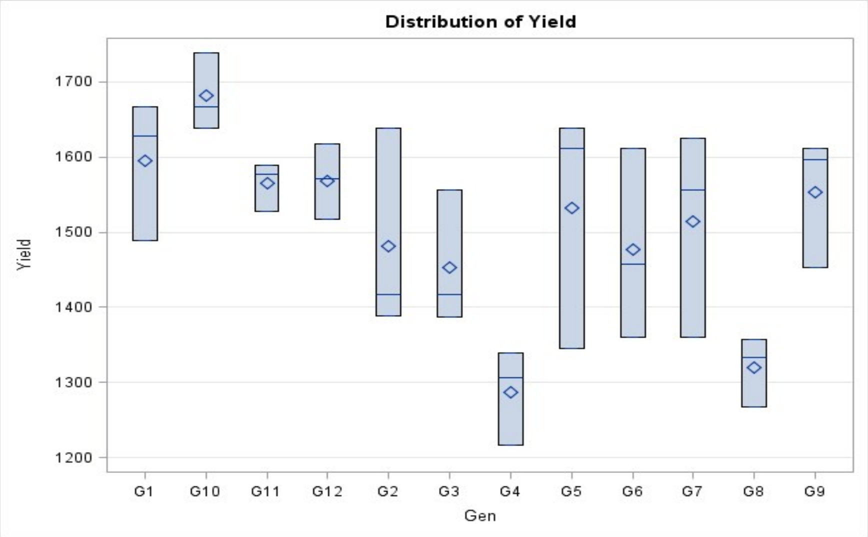

Figure 1. The distribution of yield (kg per hectare) of 1.2 genotypes of *Brassica rapa* L.

Table 3. Mean performance and relative position of *Brassica rapa* L. genotypes.

Genotype	D50%F	DM	PH	NPBPP	NSBPP	NSPP	NSPS	TSW	Yield	Relative position (%)
BC-100614 (8)-1	30.33a	84.33bc	82.33b–d	5.33b	6.38ab	85.33ab	31ab	2.96ab	1594.67ab	101.66
BC-100614 (4)-2	31.66a	84.66a–c	77.33d–f	4.46d–f	5.36de	71c	26c–e	2.53bc	1481.67bc	94.45
BC-100614 (4)-4	30.33a	84.33bc	74.33ef	4.3ef	5.09e	75.66bc	25.66c–e	2.7b	1453.33b–d	92.65
BC-100614 (4)-5	30.66a	86a–c	73.66f	4.5d–f	5.52c–e	70.66c	30a–c	2.56bc	1287.67d	82.09
BC-100614 (4)-11	32.33a	84.33bc	86.33ab	4.73cd	5.58c–e	72.33c	26c–e	2.8ab	1531.67ab	97.64
BC-100614 (4)-19	30.66a	85.33a–c	81cd	4.26f	5.31de	74.33bc	22.33e	2.13c	1476.67bc	94.14
BC-100614 (7)-8	30.33a	85.33a–c	89a	4.36d–f	5.51c–e	70c	22.33e	2.46bc	1514ab	96.51
BC-100614 (8)-2	32a	87ab	85a–c	4.34d–f	5.60c–d	73.66bc	24.33de	2.63bc	1319.33cd	84.11
BC-100614 (4)-10	32.66a	84c	86.66ab	4.7c–e	5.82cd	76.66bc	26.33c–e	2.63bc	1553.67ab	99.04
BC-100614 (8)-7	30.33a	84.66a–c	77.33d–f	5.8a	6.81a	92.33a	34.33a	3.23a	1681.67a	107.20
BC-100614 (7)-3	30a	85.33a–c	85.33a–c	5.23b	6.03bc	80.33a–c	29.33bc	2.7b	1565ab	99.77
BARI Sharisa-14	31.33a	87.33a	79.33de	4.97bc	5.66cd	85.33ab	27.66b–d	2.96ab	1568.67ab	100.00
Mean	31.06±0.32	85.22±0.29	81.47±0.97	4.75±0.09	5.73±0.09	77.31±1.52	27.11±0.71	2.69±0.06	1502.33±22.55	-
StD	1.91	1.76	5.81	0.52	0.53	9.13	4.24	0.37	135.28	-
CV (%)	6.16	2.06	7.14	11.00	9.32	11.81	15.64	13.71	9.00	-
Maximum	37.00	90.00	92.00	5.90	6.95	95.00	38.00	3.40	1739.00	-
Minimum	28.00	81.00	68.00	3.90	4.90	61.00	20.00	2.00	1217.00	-
LSD = 0.05	3.48	2.71	5.16	0.43	0.53	12.01	4.59	0.52	173.80	-

Note: Means with the same letter are not significantly different. *and **denote significance level at $p < 0.05$ & $p < 0.01$ respectively; LSD = least significant difference; StD = standard deviation; CV = coefficient of variation; D50%F = days to fifty percent flowering; DM = days to maturity; PH = Plant height (cm); NPBPP = no. of primary branch per plant; NSBPP = no. of secondary branch per plant; NSPP = no. of siliqua per plant; NSPS = no. of seeds per siliqua; TSW = 1000 seed weight (g) and seed yield (kg ha^{-1}).

4.3. Clustering pattern and Principal component analysis

As indicated by a dendrogram, the UPGMA (average linkage) cluster analysis identified distinct clusters showing linkages among tested accessions (**Figure 2**). With a dissimilarity coefficient of 0.022, the accessions were grouped into four primary clusters based on their evaluated quantitative features. To pick the optimal cluster number and readability, the dendrogram was cut off at 0.022 using Mojena[16] stopping criterion. Cluster I absorbed the most accessions (9) with an average yield of 1526.59 kg ha^{-1}, accounting for 26.25% of the cluster mean yield. Cluster II (28.91%) had the highest average yield (1681.67 kg ha^{-1}) with just one accession (**Table 3**), followed by Cluster I (1526.59 kg ha^{-1}; 26.25%) and Cluster IV (1319.33 kg ha^{-1}; 22.68%) with the best agronomic features. Cluster III genotypes (1287.67 kg ha^{-1}; 22.14%), on the other hand, indicated limited yielding potential. Furthermore, clusters I and II had 1.6% and 11.93% higher (+) mean yields compared to the grand mean yield (1502.33 kg ha^{-1}) respectively, whereas cluster III (14.28%) and cluster IV (12.18%) had lower (−) yields. In terms of yield, genotypes in clusters I and II (BC-100614(8)–7) provide greater yields than genotypes in clusters III and IV (**Table 4**) and were recognized as potential accessions for future crop development. Khan et al.[11] discovered a similar tendency in their studies on Bambara groundnut.

Table 4. Relative proportion of grand mean yield for four clusters based on the UPMGA clustering pattern.

Cluster	No. of Genotypes	Average yield (kg ha^{-1})	RPGY (%)
I	9 [BC-100614(8)-1, BC-100614(4)-2, BC-100614(4)-4, BC-100614(4)-11, BC-100614(4)-19, BC-100614(7)-8, BC-100614(7)-3, BARI Sharisa-14, BC-100614(4)-10]	1526.59 (26.25%)	1.6 (+)
II	1 [BC-100614(8)-7]	1681.67 (28.91%)	11.93 (+)
III	1 [BC-100614(4)-5]	1287.67 (22.14%)	14.28 (−)
IV	1 [BC-100614(8)-2]	1319.33 (22.68%)	12.18 (−)

Note: Grand average yield = 1502.33 kg/ha; relative proportion of grand average yield = RPGY (%); "(+)" = yield higher; "(−)" = yield lower.

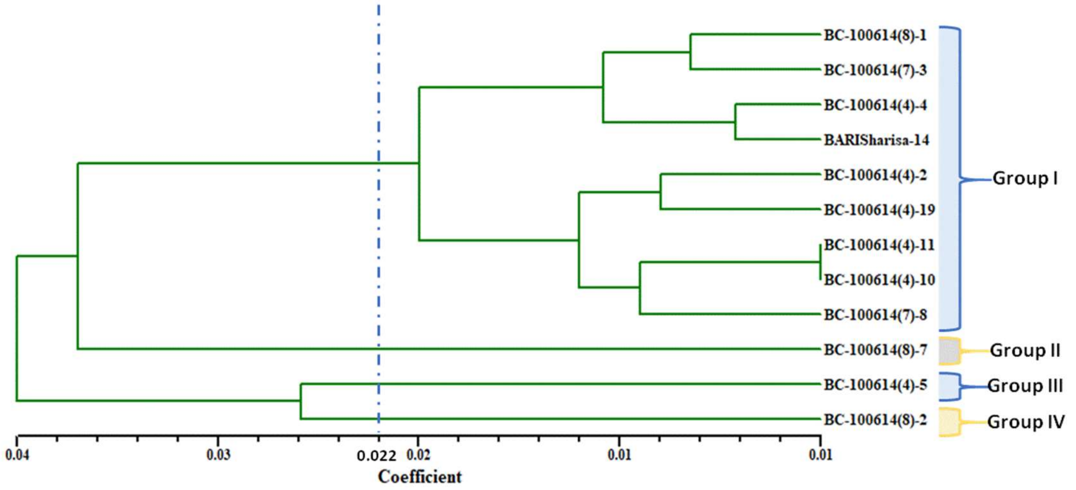

Figure 2. Cluster analysis revealed a dendrogram for 12 *Brassica rapa* L. genotypes based on the UPGMA method of SAHN clustering.

4.4. Principal component analysis

According to our findings, the first principal component (PC1) accounted for greater variation (54.86%) than the second main component (PC2) (16.89%), whereas the third principal component (PC3) accounts for 83.17% of all variances (**Table 5**). The majority of the overall variance is explained by the first axis (PC1) of any principal component analysis (PCA)[17]. The variables such as no. of primary branch per plant, no. of secondary branch per plant, no. of siliqua per plant, no. of seeds per siliqua, 1000 seed weight (g), and seed yield (kg ha^{-1}) occupied high values in PC1. These traits were positioned in the positive (+ve) quartile and very close to each other (**Figure 3**) in the component pattern plot, indicating that there is a significant contribution of these traits to yield. In combination with principal component analysis, cluster analysis investigated the relationships between genotypes in terms of seed yield and associated agronomic parameters[11]. The two-dimensional (2D) graphical explanation (**Figure 3**) showed that while a small number of accessions were distributed at large distances, the majority were spread at modest distances, as shown by the eigenvector in **Table 5**. The farthest genotypes from the centroid were BC-100614(8)-7, BC-100614(4)-5, and BC-100614(8)-2, whereas other accessions were near the centroid. Khan et al.[17] classified the 44 Bambara groundnut accessions based on quantitative features using PCA analysis.

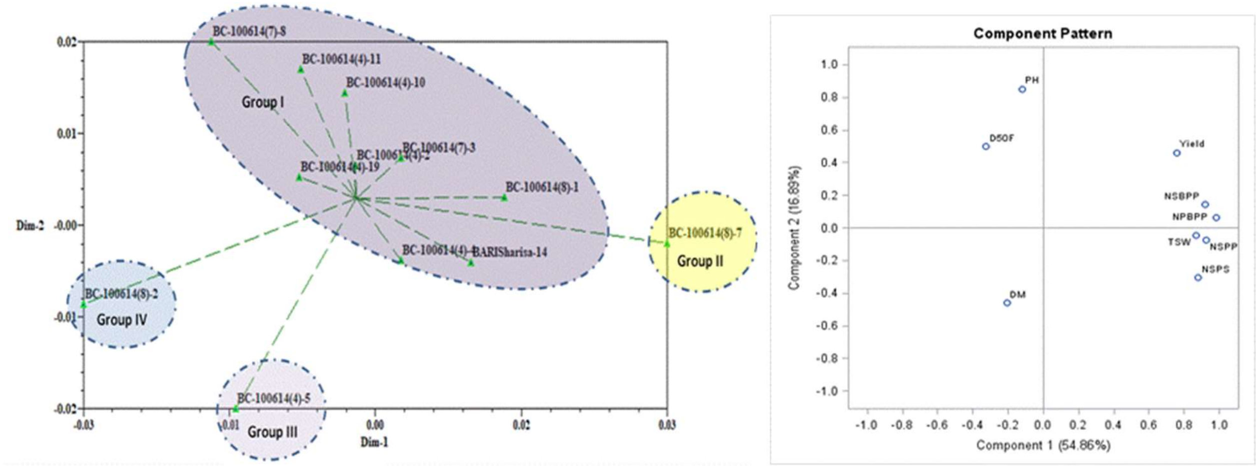

Figure 3. Two-dimensional (2D) graph showing the relationship among 12*Brassica rapa* L. genotypes using PCA revealed by NTSYSpc and component pattern plot for 9 morphological traits revealed by PCA using SAS.

Table 5. Principal component analysis for nine quantitative traits of *Brassica rapa* L. genotypes.

Parameters	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**
Eigenvalue	4.937	1.520	1.027	0.819	0.402
Proportion of variance (%)	54.86	16.89	11.41	9.1	4.46
Cumulative variance (%)	54.86	71.75	83.17	92.26	96.72
	Eigenvectors				
D50%F	−0.147	0.404	0.444	0.718	0.118
DM	−0.093	−0.372	0.781	−0.358	0.149
PH	−0.054	0.690	0.262	−0.409	−0.317
NPBPP	0.442	0.050	0.067	−0.048	−0.122
NSBPP	0.414	0.118	0.112	−0.089	−0.435
NSPP	0.417	−0.063	0.128	−0.104	0.395
NSPS	0.397	−0.245	−0.008	0.252	−0.398
TSW	0.391	−0.035	0.234	0.277	0.116
Yield	0.341	0.375	−0.192	−0.167	0.576

Note: PC = principal component; D50%F = days to fifty percent flowering; DM = days to maturity; PH = Plant height (cm); NPBPP = no. of primary branch per plant; NSBPP = no. of secondary branch per plant; NSPP = no. of siliqua per plant; NSPS = no. of seeds per siliqua; TSW = 1000 seed weight (g) and seed yield (kg ha^{-1}).

4.5. Characters association analysis

The phenotypic correlation among the nine quantitative traits of twelve *Brassica rapa* L. genotypes is given in **Table 6**. The trait yield revealed a positively moderate ($0.25 \leq r \leq 0.75$) and highly significant association with the number of primary branches per plant ($r = 0.50$; $p \leq 0.01$), the number of secondary branches per plant ($r = 0.42$; $p \leq 0.05$), the number of siliqua per plant ($r = 0.48$; $p \leq 0.05$), and the thousand seed weight ($r = 0.33$; $p \leq 0.05$). A positively strong ($0.75 \leq r \leq 1.00$) and highly significant association was noted for the number of primary branches with secondary branches per plant ($r = 0.83$; $p \leq 0.01$). A positive and highly significant association was noted for the number of primary and secondary branches per plant with the number of siliqua per plant, the number of seeds per siliqua, and 1000 seed weight. Number of seeds per siliqua had a positive and highly significant interrelation with 1000 seed weight ($r = 0.56$; $p \leq 0.01$). A weak ($0 \leq r \leq 0.25$) and non-significant association was found with yield and the number of seeds per siliqua ($r = 0.22$; $p \geq 0.05$), whereas the traits days to 50% flowering and days to maturity had a negative correlation with yield, indicating that early maturity reduces the yield potentiality of genotypes. The presence of positive and highly significant correlation coefficients between the yield and yield-related traits reported in this study was a sign that the morphological traits measured correctly predicted the yield and were suitable for genotype selection in subsequent breeding programs to improve heterosis or vigor. According to Khan et al.[18] the positive association also suggests that these features should be better explored in order to create genotypes that are desired.

Table 6. Pearson's correlation coefficients (r) among nine quantitative traits of *Brassica rapa* L. genotypes.

Traits	**D50%F**	**DM**	**PH**	**NPBPP**	**NSBPP**	**NSPP**	**NSPS**	**TSW**	**Yield**
D50%F	1.00	0.21	0.21	−0.05	−0.07	−0.13	0.04	0.19	−0.02
DM	-	1.00	0.06	−0.12	−0.12	−0.06	−0.19	0.05	−0.05
PH	-	-	1.00	−0.05	0.10	−0.20	−0.22	−0.07	0.14
NPBPP	-	-	-	1.00	0.83**	0.53**	0.65**	0.69**	0.50**
NSBPP	-	-	-	-	1.00	0.55**	0.55**	0.44**	0.42*
NSPP	-	-	-	-	-	1.00	0.41*	0.25	0.48*
NSPS	-	-	-	-	-	-	1.00	0.56**	0.22
TSW	-	-	-	-	-	-	-	1.00	0.33*
Yield	-	-	-	-	-	-	-	-	1.00

Note: "**" correlation is significant at the 0.01 level; "*" correlation is significant at the 0.05 level; D50%F = days to fifty percent flowering; DM = days to maturity; PH = Plant height (cm); NPBPP = no. of primary branch per plant; NSBPP = no. of secondary branch per plant; NSPP = no. of siliqua per plant; NSPS = no. of seeds per siliqua; TSW = 1000 seed weight (g) and seed yield (kg ha^{-1}).

5. Conclusion

The genotypes BC-100614(8)-7, BC-100614(8)-1, BC-100614(7)-3, BC-100614(4)-10, and BC-100614(4)-11 were chosen for further varietal evaluation under a regional yield trial in the following year after being found to be promising in terms of all statistical parameters and trait performance, particularly maturity period, yield, and yield contributing characters. The traits number of primary branches, number of secondary branches, number of siliqua per plant, and thousand seed weight showed a statistically meaningful association with yield, indicating that these traits are beneficial for the selection of genotypes for future breeding schemes.

Author contributions

Conceptualization, MHK and BCK; methodology, MHK; software, MHK; validation, MHK, BCK and MSU; formal analysis, MHK; investigation, MHK; resources, MHK; data curation, MHK; writing—original draft preparation, MHK; writing—review and editing, MRI (M. Rafiqul Islam), MA, MAUZ, MRI (M. Rashedul Islam), AKD, RU and MGR; visualization, MHK; supervision, MHK, BCK and MSU; project administration, MHK and BCK; funding acquisition, MHK, BCK. All authors have read and agreed to the published version of the manuscript.

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Conflict of interest

The authors declare no conflict of interest.

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