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Genetic Diversity Analysis of Restorer Lines of Rapeseed (*Brassica napus* L.)

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Abstract: Genetic diversity (GD) helps in the selection of valuable parents which is the key to improving heterosis breeding and thus GD within the collected or derived germplasm should be explored. The present study aims to quantify the GD of restorer lines of rapeseeds based on seed yield components. An experiment was conducted in a Randomized Complete Block Design with three replications. The first four principal components explained 35%, 24%, 16% and 10% of total variance, respectively. PC1 exhibited a positive relationship with branches/plant, pods/plant, thousand-seed weight, and seed yield/plant. The PC1 and PC2, projected branches/plant and pods/plant, showed a positive correlation with seed yield/plant. There were also positive correlations among plant height and days with first blooming and 100% flowering and maturity. Cluster study revealed that the restorer lines were clustered into 4 clusters where Tori was the only one (cluster 4) that did not coalesce with the rest of the R lines. Clusters 1-3 consist of 10, 13 and 11 R lines. Based on the above findings, diverse genotypes can be selected for the development of high-yielding variety through hybridization.

1 Introduction

The three *Brassica* species, *Brassica napus*, *Brassica campestris* and *Brassica juncea*, are recognized as important and the third global oil crop (Downey 1990). *Brassica napus* belongs to the family Brassicaceae and bears bright yellow flowers; it is an amphidiploid (2n=38), developed by a cross between *Bassica oleracea* (2n=18) *and Brassica rapa* (2n=20) (Kimber and McGregor 1995). The oil of *Brassica* species is known as mustard oil in Bangladesh and occupies the first position among all oilseed crops in terms of area and production (BBS 2022). There are a few varieties of *Brassica napus* released locally as BARI Sharisha 7, BARI Sharisha 8, BARI Sharisha 13, BARI Sharisha 18 and BU Sharisha 1; the first four varieties were released by Bangladesh Agricultural Research Institute (BARI) while the later variety was released by Bangabandhu Sheikh Mujibur Rahman Agricultural University. The yield of these varieties is not satisfactory compared to the world standard and ranges from 1.5-2.5 t/ha (Mandal et al 2002, Miah et al 2015). There is need of the

improvement of *Brassica napus* varieties with enhanced yields with early maturity, non-shattering characteristics, tolerant to stresses and acceptable oil quality.

The seeds of *Brassica napus* are considered a rich source of oil containing 40-45 % oil depending on the species and the climatic condition. The oil contains 20-25 % oleic acid, 5-7% saturated fatty acids and a high content of polyunsaturated fatty acids (10% linolenic acid and 17-21% linoleic acid). However, mustard oil as edible oil, faces a problem of containing a high level of erucic acid and glucosinolate (Mondal and Khajuria 2000, Mandal et al 2002). There are several ways to improve varieties of mustard with increased seed yield such as crossbreeding followed by selection, hybrid breeding, ideotype breeding and genomic approaches (Khush 2013). There is potential and great interest in the hybrid breeding of *Brassica napus* but the major obstacle is the shortage of diverse restorer lines giving hybrid vigor (Szała et al 2016). Knowledge of the genetic diversity of parental genotypes of any crop is essential for its improvement through successful breeding (Belaj et al 2002). Hence, breeders must have knowledge of genetic resources and the extent of genetic diversity of the crops (Kahani and Hittalmani 2015). The crosses between diverse genotypes yielded desirable recombinants in their progeny (Kahani and Hittalmani 2015). Typically, morphological, phenological and agronomic traits are used to estimate genetic diversity. Therefore, the main objective of this research is to assess the genetic diversity of the restorer lines of *Brassica spp*. through principal component and biplot analyses.

2 Materials and Methods

2.1 Climate and Site of the Experiment

The experiment was carried out in the Research Farm of Genetics and Plant Breeding Department of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur in the winter season (period from November to April). The soil of the experimental farm was acidic in nature with a pH of 5.5 and the soil texture was silt-loam. It was situated under a sub-tropical climatic zone having high rainfall during months from May to September, and scanty from October. During the experimental period, the average daily temperature was 26.92°C (max) and 17.33°C (min), rainfall was 8.52 mm per month and relative humidity was 85.63%.

2.2 Experimental Materials

Thirty-four selected R lines of *Brassica napus* and Tori (*Brassica rapa*) genotypes were used to study their genetic diversity and yield performance. The R lines were developed through the segregation of *Brassica napus* hybrids followed by selection based on different traits (flowering time, fertility status, plant height, pods/plant, pod length, seeds/pod, and seed yield/plant) (Islam et al 2020 a, b).

2.3 Soil Fertility and Crop Management

The fertility of the soil of the experimental field was ensured by applying urea, TSP, MoP, gypsum, Zinc sulfate and cow dung @ 270, 170, 100, 150, 5 kg/ha and 10 M ton/ha respectively. The whole quantity of cow dung, TSP, MoP, gypsum, zinc sulfate and half of the urea were applied during the final land preparation. The remaining urea was top-dressed 30 days after seedling emergence. Intercultural operations were done when necessary for the proper growth and development of the plants (Khaleque 1985 and Saha et al 2011). The first weeding and thinning was done after 10 days of emergence of seedlings and the second weeding was done 30 days after emergence and top dressing of urea. Irrigation was done when there was a shortage of water in the crop field. The foliar spray was applied with Malathion 57EC at an interval of 15 days to control aphid infestation as recommended by Khaleque (1985).

2.4 Experimental Design

The seeds of the restorer lines of rapeseed and Tori genotypes were planted with a row spacing of 30 cm and plant spacing of 15 cm within the row. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications.

2.5 Data Collection

Ten traits were selected to collect data i.e. days to first flowering (DFF), days to 100% flowering (DHF), days to maturity (DTM), primary branches/plant (NBP), plant height (PHT), pods/plant (NPP), pod length (PLT), seeds/pod (NSP), 100-seed weight (TSW) and seed yield/plant (SYP). Data on each trait was collected from five randomly selected competitive plants of each entry and replication.

2.6 Data Analysis

Data on different traits were analyzed by using the computer-based software ‘STAR’ (Statistical Tools for

Agricultural Research, http://bbi.irri.org). Analysis of variance was computed according to Panse (1957). Principal Components Analysis (PCA) was done by software R (Team RC 2021). The maximum amount of variance of the original image accounts for the first principal component and the remaining variances account for the subsequent components (Torbick and Becker 2009). Agglomerative hierarchical clustering was done following the method given by Anderberg (1973). PCA scores for 25 genotypes of F_2 generation were used as input for clustering. The data matrix was homogenized with column standardized function i.e., CA-Q Analysis. For linkage analysis, the resemblance coefficient was measured between pairs of genotypes, where 25 genotypes were taken in a data matrix and the data were converted into a distance matrix (similarity matrix). The distance matrix was transformed into a dendrogram using Ward's technique (Ward 1963).

3 Results and Discussion

3.1 Analysis of Variance

The analysis of variance (ANOVA) for 10 yield-related traits was carried out with 35 R lines of Brassica napus including Tori-7. ANOVA revealed highly significant variability among studied materials (**Table 1**) which confirms the presence of remarkable genetic variability among the lines. Box plot or box-whisker plot (**Fig 1A-1I and Fig 2**) present a graphical image of the concentration of the data. It also represents the extreme values far from most of the data. These values were used to compare how close or far one data was from the other data values.

3.2 Variability Analysis

Days to first flowering ranged from 28 to 67 days among the R lines of *Brassica napus* under study. It showed a normal distribution and the maximum values ranged from 32 to 49 (**Fig 1A**). There were five out layers which placed distant from the line of average values in the boxplot. The lowest value in the out layer was observed in Tori while the remaining layers were observed in BNR-037, BNR-038, BNR-042 and BNR-043. These five lines showed much variation from other lines and were late in the first flowering.

On the other hand, maximum values for days to 100% flowering ranged from 41 to 74 days. Boxplot showed four out layers which showed much more variability than the other lines and were distributed as positively skewed. Days to maturity varied from 73.66 to 117.66 days among the R lines. Rameeh (2015) reported a similar maturity range in oilseed mustard. Boxplot indicated that their maximum values ranged from 79 to 113 days. Three out layers were far distant from the others; these lines are Tori, BNR-042 and BNR-043 (**Fig 1C**). The boxplot revealed the greater spread of data (73.66 to 117.66 days) for days to maturity while the distribution for this set was positively skewed. The mean number of primary branches per plant ranged from 2.9 to 4.4 (**Fig 1D**). There were four out layers observed in this boxplot. Tori showed the maximum primary branches/plant which was more distant from the others; the distribution of this set was right-skewed. Plant height is a good indicator of the growth and development of a plant. Thirty-five R lines were studied and they ranged between 1.00 m to 1.80 m for plant height. The maximum value in the boxplot ranged from 1.0 to 1.8 cm for the character plant height. There was one out layer which was at 1.8 cm and the line was BNR 038 (**Fig 1E**). This line showed much variability with other lines and the distribution was right-skewed.

A significant amount of variation was observed for pods/plant among the R-lines. Rameeh (2012) reported similar results in rapeseed. Maximum values for the number of pods/plant varied between 100 and 230 (**Fig 1F**). There was a single-out layer for the number of pods/plant which was more than 600. 'Tori' represented the out layer and showed much more variability with other lines. This line represented the largest spread of values in the boxplot and a positively skewed distribution was observed.

The line BNR-018 produced the longest pod (8.50 cm) and the shortest in the line BNR-019 (5.19 cm). The maximum lines for pod length ranged from 6.3 to 8.5 cm. There was a single-out layer and it was the restorer line BNR-019 and its value was much less than that of the average value. This line showed much more variability than other lines. The distribution for this set was right-skewed. The line BNR-027 produced the highest number of seeds/pod (31.00) and the lowest in Tori (19.33). Box plot-8 represented the maximum number of seeds/pod which varied between 19.5 and 31. There were no out layers, which means that the lines showed less variability among themselves while the distribution of lines in the graph was left-skewed.

The thousand seed weight of the lines varied from 2.10 g to 3.93 g. The highest weight was observed in the line BNR-030 (3.86 g) followed by lines BNR-016 (3.63 g) and BNR-029 (3.53 g). Box plot-9 represented the majority of the lines for thousand seed weights ranging from 1.5 to 3.6 g. There were two out layers

which were represented by the lines BNR-030 and BNR-016. These lines did not show much more variability among each other and were distributed as negatively skewed. Seed yield per plant showed a significant amount of variability among the lines under study. Ali et al (2013), Chen et al (2014) and Islam et al (2020 a, b) also described significant variations

Table 1. Analysis of variance for 10 agronomic traits of 34 selected R lines of *Brassica napus* and Tori genotype

Source of variation	df	Mean sum of square									
		DFF	**DHF**	**DTM**	**NBP**	**PHT**	**NPP**	**PLT**	**NSP**	**TSW**	**SYP**
Replication	2	13.15	135.20	10.06	0.26	0.03	2349.84	0.23	3.98	0.00	6149621.67
Genotype	27	223.34**	513.26**	296.01**	1.33**	0.12**	20321.41**	1.18	20.74**	0.50	61412378.59**
Error	54	10.31	10.94	2.96	0.20	0.01	1080.42	0.05	2.95	0.00	2907884.13

*, ** represent significant at 5% and 1% level, respectively; df= degree of freedom. DFF- days to first flowering, DHF- days to 100% flowering, DTM-days to maturity, NBP-number of primary branches per plant, PHT- plant height, NPP- number of pods per plant, PLT- pod length, NSP- number of seeds per pod, TSW- thousand seeds weight, SYP-seed yield per plant.

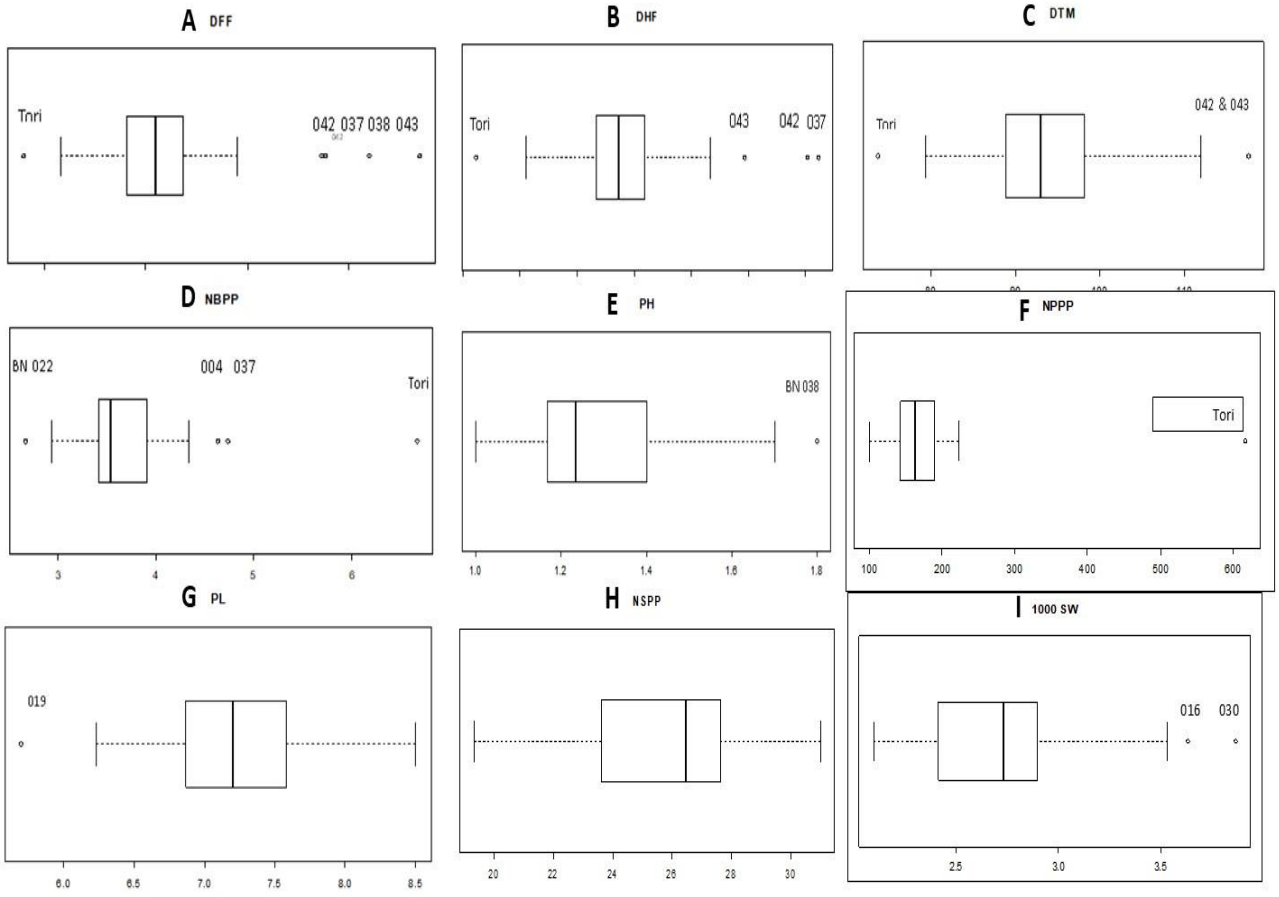

Fig 1. Boxplot - Upper and lower quartiles with median values for (A) days to first flowering, DFF; (B) days to 100% first flowering, DHF; (C) days to maturity, DTM; (D) number of primary branches per plant, NBPP; (E) plant height, PH; (F) number of pods per plant, NPPP; (G) pod length, PL; (H) number of seeds per pod, NSPP; and (I) thousand seeds weight, 1000-SW

in seed yield/plant in rapeseed mustard. Maximum seed yield/plant (32.45 g) was found in Tori-7 and the minimum in the line BNR-024 (6.36 g). **Fig 2** represented the variations among maximum lines which ranged from 7.0 to 17.0 g. There was a single-out layer which was represented by Tori-7 and yielded much more than the others; it showed extra variability with others. **Fig 2** represented the bigger spread of values and positively skewed distribution for seed yield/plant.

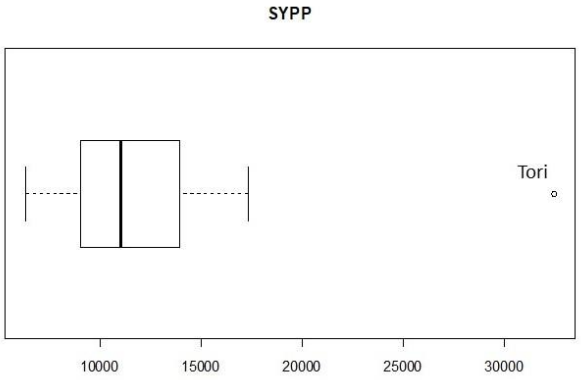

Fig 2. Boxplot presenting median value, quartiles, outliers for seed yield per plant, SYPP (g).

3.3 Principal Component Analysis

The principal component analysis (PCA) was employed to identify the key variance components and their roles (Héberger et al 2003). The PCA revealed ten principal components representing 100% of the total variance among the 35 selected R lines (**Table 2**). The first four components accounted for 86.05% of the variance, with PC1 contributing the most (35%). Paulauskas et al (2013) and Sandhu et al (2017) stated that four to five principal components contributed to maximum divergence in *Brassica napus* genotypes. The characters such as number of branches/plant (0.24), number of pods/plant (0.29), thousand seed weight (0.18), and seed yield/plant (0.29) contributed more positively to the PC1. On the other hand, first flowering time (-0.44), 100% flowering time (-0.46), maturity time (-0.45), height of the plant (-0.27), length of pod (-0.06) and seeds/pod (-0.17) showed negative relation with PC1. An eigenvalue less than one does not have any practical significance (Brejda et al 2000). The maximum Eigenvalue was considered the best attribute of the principal component (Ojha et al 2017). In addition, all the characters exhibited a positive correlation with PC2 except seeds/pod (-0.15). On the other hand, PC3 exhibited a positive association with days to first flowering time (0.06), days to 100% flowering time (0.05), maturity time (0.10), number of branches/plant (0.03), number of pods/plant (0.19); the rest of the characters showed a negative association. The component PC4 also exhibited a positive correlation with first flowering time (days), maturity time (days), number of branches/plant, height of the plant (m), number of pods/plant, thousand seed weight (g) and seed yield/plant (g).

Fig 3 shows that the maximum variation of the selected 10 characters lay between principal components 1 and principal component 4. Thus, these four principal components could be considered to explain variability. The rest principal components did not show a considerable amount of variation.

PC1 and PC2 were plotted to detect the association between the ten characters of *Brassica napus* R lines. The projection of PC1 and PC2 components revealed that branches/plant and pods/plant were positively associated with seed yield/plant. **Fig 4** shows that the genotype Tori presents in the second quartile. A number of primary branches/plant and pods/plant showed a positive relationship with the seed yield/plant and ultimately increased the yield in *Brassica napus*. Pod length and thousand seed weight had a very low impact on seed yield per plant. Again, days to first flowering time, days to 100% flowering time, and days to maturity time showed a positive relationship with each other. In the first quartile, the numbers 31, 32, 33 and 34 represent the *Brassica napus* R lines BNR-037, BNR-038, BNR-042 and BNR-043, respectively. Plant height also possessed a positive relationship with DFF, DHF and DTM. On the other hand, number of seeds per pod had no remarkable relationship with seed yield/plant (**Fig 4**). Thus, rapeseed lines placed in the desired quartile (upper or lower) and outliers for mean performances of specific characters can be selected for the improvement of *Brassica napus* variety.

3.4 Cluster Analysis

The primary gene pool of rapeseed only consists of the cultivated species *Brassica napus* which shows

maximum genetic diversity (Weise et al 2023). In general, the lines coming from the same sources and/or related by pedigree or derived from germplasm having common traits are clustered together. The cluster analysis separates the lines or accessions into different clusters (Ahmad et al 2014). The dendrogram was constructed using Euclidian distance among mean values

Table 2. Variation among *Brassica napus* R lines and Tori genotype accounted for ten principal components

Traits	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**
Days to first flowering (DFF)	-0.44	0.29	0.06	0.11	0.05	-0.17	0.02	-0.68	-0.44	0.00
Days to 100% flowering (DHF)	-0.46	0.26	0.05	-0.02	0.13	-0.26	-0.03	-0.01	0.78	0.02
Days to maturity (DTM)	-0.45	0.24	0.10	-0.15	0.15	-0.11	0.04	0.71	-0.41	0.03
Number of primary branches per plant (NBP)	**0.24**	**0.48**	0.03	0.07	0.11	0.14	-0.81	0.02	-0.02	-0.05
Plant height (PHT)	-0.27	0.21	**-0.40**	0.01	-0.77	0.32	-0.02	0.06	0.03	-0.01
Number of pods per plant (NPP)	**0.29**	**0.48**	0.19	0.04	-0.04	0.13	**0.35**	-0.01	0.03	0.69
Pod length (PLT)	-0.06	0.15	**-0.48**	-0.60	**0.44**	**0.37**	0.12	-0.08	-0.01	-0.01
Number of seeds per pod (NSP)	-0.17	-0.15	-0.32	**0.72**	**0.36**	**0.38**	0.10	0.01	0.06	0.16
Thousand seeds weight (TSW)	0.18	0.00	**-0.65**	0.05	0.00	-0.66	-0.09	0.05	-0.08	0.27
Seed yield per plant (SYP)	**0.29**	**0.46**	-0.12	**0.26**	0.06	0.08	0.42	0.05	0.03	-0.63
% of explained variance	0.35	0.25	0.16	0.10	0.05	0.03	0.03	0.01	0.00	0.00
Cumulative% of explained variance	0.35	0.59	0.75	0.86	0.91	0.94	0.97	0.99	0.99	1.0

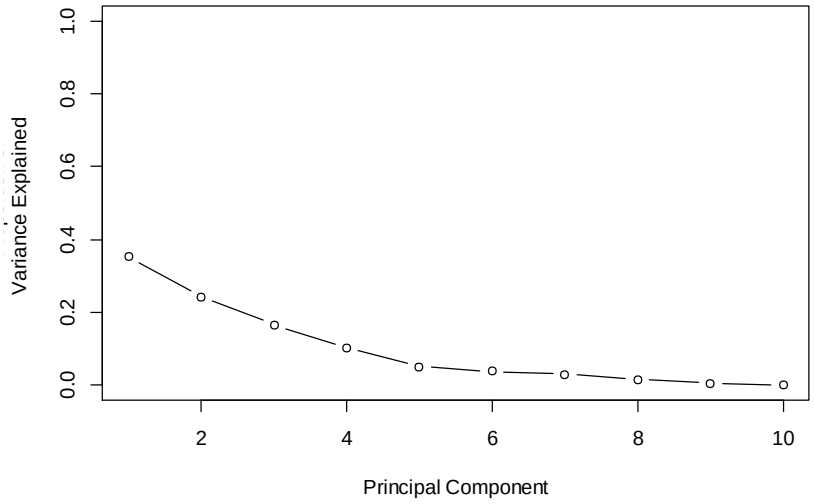

Fig 3. Scree plot showing eigenvalues in response to the number of components

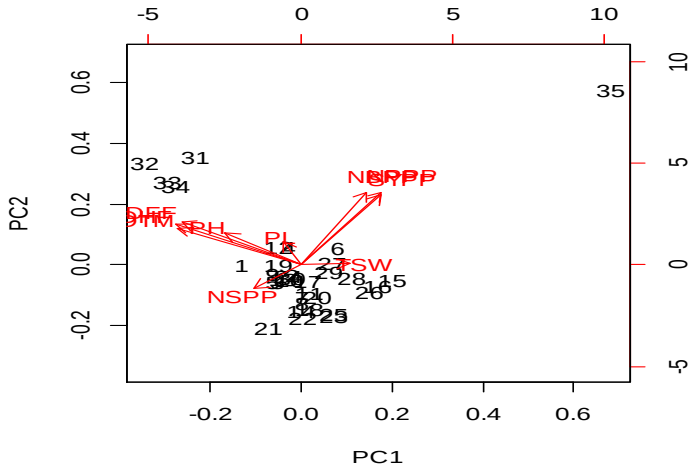

Fig 4. Principal component biplot for yield in Brassica genotypes

of morpho-agronomic traits and cluster analysis (**Fig 5**). All the *Brassica napus* R lines were divided into five main clusters (**Fig 5**). Sandhu et al (2017) used a similar method for determining the genetic diversity of some oil seed rape genotypes. In the dendrograms, genotypes are presented on the horizontal axis and the Euclidean distances are on the vertical axis. Based on cluster analysis, four major clusters existed within the material. The genotype Tori was the only one (cluster 4) that was not classified with the rest of the *Brassica napus* R lines. Ahmad et al (2014) reported a substantial amount of genetic diversity detected in restorer inbreds of *Brassica napus* L., but not within the same cluster.

Cluster 1 consists of 10 R lines (BNR-024, BNR-003, BNR-022, BNR-023, BNR-026, BNR-011, BNR-012, BNR-010, BNR-008 and BNR-009), cluster 2 consists of 13 lines (BNR-006, BNR-018, BNR-030, BNR-014, BNR-035, BNR-004, BNR-025, BNR-015, BNR-001, BNR-002, BNR-038, BNR-019 and BNR-020) and cluster 3 contains 11 lines (BNR-021, BNR-029, BNR-007, BNR-027, BNR-016, BNR-017, BNR-032, BNR-037, BNR-042, BNR-043 and BNR-13). All lines with late flowering and maturity are clustered in cluster 3. Paulauskas et al (2013) and Sandhu et al (2017) quantified genetic diversity in *Brassica napus* genotypes through principal components and cluster analysis. Restorer lines with genetic diversity can be utilized in the production of hybrids of *Brassica napus* (Ahmad et al 2014). The diverse genotypes are also a potentially valuable source for the improvement of rapeseed variety tolerant against biotic and abiotic stresses and heterosis. These lines can also be used to widen the genetic base of the germplasm (Wu et al 2014, Houmanat et al 2023).

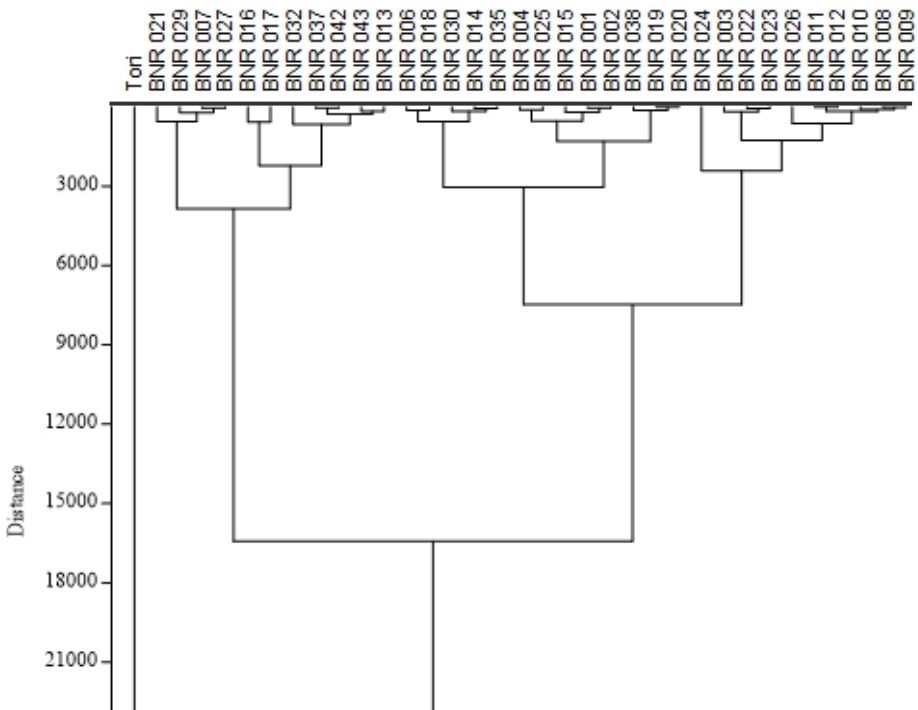

Fig 5. Dendrogram indicating the mutual relationships among 34 *Brassica napus* L. R lines and Tori-7 for seed yield-related traits

4 Conclusion

The variance estimated for seed yield and related traits of 35 *Brassica napus* R lines and Tori genotype showed highly significant genetic variations for most of the studied characters. Boxplot showed three out layers for days to maturity; the earliest one was Tori while the latest were BNR-042 and BNR-043. For thousand seed weight, there were two out layers, BNR-030 and BNR-016 which produce the heaviest or bold seeds among the lines. Biplot analysis exhibited positive correlations for plant height with days to first flowering, 100% flowering, and days to maturity. It was evident from principal component analysis that PC1 exhibited a positive relationship with branches/plant, pods/plant, thousand-seed weight, and seed yield/plant. Dendrogram grouped 35 genotypes into four major clusters where Tori remained in one (cluster 4) and the rest of the *Brassica napus* R lines were grouped into three clusters, 10 R lines in cluster 1, 13 R lines in cluster 2 and 11 R lines in cluster 3.

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References

Ahmad R, Farhatullah, Quiros CF, et al (2014) Genetic diversity analyses of *Brassica napus* accessions using SRAP molecular markers. *Plant Genetic Resources*. 12, 4-21. https://doi.org/10.1017/S147926211300021X

Ali I, Ahmed HM, Shah SA (2013) Evaluation and selection of rapeseed (*Brassica napus* L.) mutant lines for yield performance using augmented design. *Journal of Animal and Plant Sciences* 23, 1125-1130. https://www.scribd.com/document/372561072/28

Anderberg MR (1973) Cluster Analysis for Applications. London, Academic Press, 359 Pp. https://library.wur.nl/WebQuery/titel/354815

BBS (2022) Statistical Yearbook Bangladesh 2022. Byuro, Bangladesh. Parisaṃkhyāna (BBS), 42nd (ed) Statistical and Informatics Division, Ministry of Planning, Bangladesh, Dhaka. Pp 562. https://rb.gy/4oudc9

Belaj A, Satovic Z, Rallo L, et al (2002) Genetic diversity and relationships in olive (*Olea europaea* L.) germplasm collections as determined by randomly amplified polymorphic DNA. *Theoretical and Applied Genetics* 105, 638-644. https://doi.org/10.1007/s00122-002-0981-6

Brejda JJ, Moorman TB, Karlen DL, et al (2000) Identification of regional soil quality factors and indicators I. Central and Southern High Plains. *Soil Science Society of America Journal* 64, 2115-2124. https://doi.org/10.2136/sssaj2000.6462115x

Chen B, Xu K, Li J, et al (2014) Evaluation of yield and agronomic traits and their genetic variation in 488 global collections of *Brassica napus* L. *Genetic Resources and Crop Evolution* 61, 979-999. https://doi.org/10.1007/s10722-014-0091-8

Downey RK (1990) Brassica oilseed breeding-achievements and opportunities. *Plant Breeding Abstracts* 60, 1165-1170. http://surl.li/xmvmke

Héberger K, Csomós E, Simon-Sarkadi L (2003) Principal component and linear discriminant analyses of free amino acids and biogenic amines in Hungarian wines. *Journal of Agricultural and Food Chemistry* 51, 8055-8060. https://pubs.acs.org/doi/10.1021/jf034851c

Houmanat K, Nabloussi A, Rhazlaoui Y, et al (2023) Genetic relationship and diversity among some Moroccan and introduced rapeseed (*Brassica napus* L.) varieties as revealed by molecular markers. *Oilseeds and fats, Crops and Lipids* 30, 18. https://doi.org/10.1051/ocl/2023019

Islam AKMA, Chowdhury NK, Era FM, et al (2020a) Interrelationships among grain yield and related traits of candidate restorer lines of *Brassica napus* L. *Annals of Bangladesh Agriculture*, 24, 51-64. https://doi.org/10.3329/aba.v24i1.51935

Islam AKMA, Era FM, Chowdhury NK (2020b) Production of Restorer Lines from Segregating Progenies of *Brassica napus* L. Having Good Agronomic Value. *International Journal of Applied Sciences and Biotechnology* 8, 400-409. https://doi.org/10.3126/ijasbt.v8i4.31352

Kahani F, Hittalmani S (2015) Genetic analysis and traits association in F_2 inter varietal populations in rice under aerobic condition. *Journal of Rice Research* 3, 1000152. https://doi.org/10.4172/2375-4338.1000152

Khaleque MA (1985) A Guide Book on Production of Oil crops in Bangladesh. 1ST (ed) Ministry of Agriculture, Government of the People's Republic of Bangladesh, Pp 117.

Khush GS (2013) Strategies for increasing the yield potential of cereals: Case of rice as an example. *Plant Breeding* 132, 433-436. https://doi.org/10.1111/pbr.1991

Kimber DS, McGregor DI (1995) Brassica Oilseeds: Production and Utilization. Wallingford, CAB International, Pp 394. https://lib.ugent.be/catalog/rug01:000419818

Mandal S, Yadav S, Singh R, et al (2002) Correlation studies on oil content and fatty acid profile of some Cruciferous species. *Genetic Resources and Crop Evolution* 49, 551-556. https://doi.org/10.1023/A:1021210800414

Miah MA, Rasul MG, Mian MAK, et al (2015) Evaluation of rapeseed lines for seed yield stability. *International Journal of Agronomy and Agricultural Research* 7, 12-19. https://rb.gy/3gza9d

Mondal SK, Khajuria MR (2000) Genetic analysis for yield attributes in mustard. *Environment and Ecology* 18, 1-5. http://surl.li/jjfuud

Ojha GC, Sarawgi AK, Sharma B, et al (2017) Principal component analysis of morpho-physiological traits in rice germplasm accessions (*Oryza sativa* L.) under rainfed condition. *International Journal of Chemical Studies* 5, 1875-1878. https://rb.gy/69w8yn

Panse VG (1957) Genetics of quantitative characters in relation to plant breeding. International Symposium on Genetics and Plant Breeding in South Asia, sponsored by the Indian Society of Genetics and Plant Breeding and UNESCO South Asia Science Cooperation Office, New Delhi, January, *Indian Journal of Genetics* 17, 318-328. http://surl.li/jbzgec

Paulauskas A, Jodinskienė M, Griciuvienė L, et al (2013) Morphological traits and genetic diversity of differently overwintered oilseed rape (*Brassica napus* L.) cultivars. *Zemdirbyste-Agriculture* 100, 409-416. https://doi.org/10.13080/z-a.2013.100.052

Rameeh V (2012) Correlation and factor analyses of quantitative traits in rapeseed (*Brassica napus* L.). *International Journal of Agriculture Innovations and Research* 1, 12-18. https://rb.gy/vr2xmv

Rameeh V (2015) Genetic variability and interrelationships among quantitative traits in rapeseed (*Brassica napus* L.) advanced lines. *Journal of Agricultural Sciences – Sri Lanka* 10, 158–167. https://doi.org/10.4038/jas.v10i3.8069

Team RC (2021) R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. https://www.R-project.org

Saha SC, Yeasmin S, Islam AKMA, et al (2011) Performance of source nursery of pollen parent and CMS lines of *Brassica napus* L. *Journal of Agricultural Science* 3, 114-122.

Szała L, Sosnowska K, Popławska W, et al (2016) Development of new restorer lines for CMS ogura system with the use of resynthesized oilseed rape (*Brassica napus* L.). *Breeding science* 66, 516-521. https://doi.org/10.1270/jsbbs.15042

Sandhu R, Rai SK, Bharti R, et al (2017) Studies on genetic diversity among various genotypes of *Brassica napus* L. using morphological markers. *International Journal of Current Microbiology and Applied Sciences* 6, 469-480. https://doi.org/10.20546/ijcmas.2017.607.056

Torbick N, Becker B (2009) Evaluating principal components analysis for identifying *optimal* bands using wetland hyperspectral measurements from the Great Lakes, USA. *Remote Sensing* 1, 408-417. https://doi.org/10.3390/rs1030408

Ward Jr J H (1963) Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association* 58, 236–244. https://doi.org/10.1080/01621459.1963.10500845

Weise S, Hoekstra R, Kutschan KJ, et al (2023) Analysis of gaps in rapeseed (*Brassica napus* L.) collections in European genebanks. *Frontiers in Plant Science* 14, 1244467. https://doi.org/10.3389/fpls.2023.1244467

Wu J, Li F, Xu K, et al (2014) Assessing and broadening genetic diversity of a rapeseed germplasm collection. *Breeding Science* 64, 321-330. https://doi.org/10.1270/jsbbs.64.321