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SCREENING OF RAPESEED (*BRASSICA NAPUS*) GENOTYPES AGAINST *ALTERNARIA* BLIGHT

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Abstract: *Alternaria* blight is a destructive fungal disease that infects rapeseed leaves and siliquae. The purpose of this study is to evaluate the disease severity of various mustard genotypes and to identify the superior rapeseed genotypes that are resistant to *Alternaria* blight. Twelve rapeseed genotypes were investigated. At 45, 55, and 65 days after sowing (DAS), genotype NAP16061 showed the lowest disease severity (12.43%, 15.06%, and 11.06%, respectively). NAP16001 had the fewest diseased pods (1.000, 1.133, and 1.700, respectively) at 45, 55, and 65 DAS, respectively. In terms of the quantities of healthy pods, NAP16001, NAP16068, and NAP16068 performed better. BARI SH13 had the lowest total numbers of leaves plant^{-1} and percent leaf area, while NAP16061 had the smallest average spot size on leaves. The greatest plant height was observed in NAP16066. Positive loadings for disease susceptibility parameters such as disease severity, percent disease severity, percent leaf area diseased, and diseased leaves plant^{-1} were observed in PC1. NAP16066, NAP16025, and NAP16001 showed a negative relationship with PC1, indicating resistance to *Alternaria* blight. Genotypes such as NAP16082 and NAP16068 were also negatively oriented along PC2, and exhibited moderate resistance, requiring further assessment. Cluster II includes the most sought-after genotypes with resistance to *Alternaria* blight disease, which clustered with NAP16001 and NAP16066.

Key words: *Brassica napus*, genotypes, mustard, PCA and hierarchical cluster, rapeseed.

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Introduction

Mustard crops, which belong to the genus *Brassica* under the family Brassicaceae, are among the common primary oilseed crops in Bangladesh. Rapeseed (*Brassica napus*), now commonly referred to as canola, is one of the most extensively cultivated oilseeds worldwide, especially in the Indian subcontinent (Goyal et al., 2020). In Bangladesh, mustard is a crucial oilseed crop, known locally as 'Sharisha', and along with grains, is vital in Bangladesh to the country agriculture for ensuring security and agricultural success (Laboni et al., 2024). It is intensively cultivated throughout the winter season (October–February), accounting for approximately 60% of total oilseed production and more than 80% of total oilseed production (Miah et al., 2015; BER, 2022). The crop is well-suited to nearly all of the country's agroclimatic zones. In addition to its utilization as an oil commodity, it is also employed as a condiment due to its medicinal properties (Thirumavalavan, 2025). The flavor of damaged perishable commodities, such as fruits, vegetables, dairy products, and meat, can be improved by adding *B. napus*, which contains pungent compounds, such as allyl isothiocyanate, which increase sensory acceptance (Liang et al., 2023; Torrijos et al., 2023). In comparison to other countries, rapeseed yields are particularly low in Bangladesh. *Brassica* spp. cultivation was conducted on approximately 814,288.54 acres of land, resulting in the production of 396,594.28 metric tons of mustard. However, the average mustard and rapeseed production in 2020–2021 was only 487.04 kg $acre^{-1}$ (BBS, 2021). In the fiscal year 2021–2022, mustard and rapeseed were the topmost planted oilseed crops in Bangladesh, covering 610,000 hectares and producing 822 thousand metric tons (Arafat, 2022).

Rapeseed, the third-largest source of edible oil after soybean and palm, contains approximately 38–46% on a dry weight basis of total oil and a high erucic acid content ranging between 40 and 47% (Mannekote et al., 2018; Chakroborty et al., 2025). Oil of *Brassica napus* is an important source of energy in human nutrition since it is free of cholesterol, which is commonly found in animal fats, and, notably, mustard oil contains crucial soluble vitamins A, D, E and K (Sharif et al., 2017), making it a popular choice for cooking and medical applications.

Several biotic and abiotic stressors can reduce the amount and quality of mustard crops, and among the biotic agents, *Alternaria brassicae* and *Alternaria brassicicola* are the main causal organisms of *Alternaria* leaf blight (Sharma et al., 2018). Of the two seed-borne fungal pathogens, only *A. brassicicola* has caused considerable yield losses of up to 70% (Gupta et al., 2020). In the initial stage, the *Alternaria* fungus develops dark brown lesions on leaves, stems, and siliquae that progressively limit photosynthetic activity, accelerate senescence, and subsequently hamper productivity (Nowakowska et al., 2019). The pathogen is significantly affected by weather, with the highest disease prevalence occurring during wet

seasons and in regions with considerable rainfall. *A. brassicae* can impact host species at all developmental stages, including the seed stage (Meena et al., 2010).

Disease-related mustard crop losses have an impact on the edible oil market prices of Bangladesh (Ahmed et al., 2018). Farmers in Bangladesh store their seeds using traditional practices, which lead to a major infestation of different fungi. *Alternaria* pathogens infect the varieties released in Bangladesh for farming (Hossain et al., 2018). However, the occurrence and severity of disease in the various released types in Bangladesh have received little attention. To provide superior genotypes for the successful rapeseed production, it is critically important to screen the resistant genotypes against the key diseases, such as *Alternaria* blight of rapeseed, and evaluate the effect of the disease on different rapeseed genotypes.

Material and Methods

Experimental setup

The experiment was conducted throughout the Rabi season from November 2021 to February 2022 on the farm of the Bangladesh Agricultural Research Institute, Rajbari, Dinajpur. The laboratory tests were conducted in the Post-graduation Laboratory, Department of Plant Pathology, Hajee Mohammad Danesh Science and Technology University, Dinajpur. The experimental site is situated in the subtropical zone, and the Dinajpur district of Bangladesh receives an average annual rainfall of 1542.10 mm. The area has a subtropical climate, with considerable rainfall from May to September and less precipitation from October to April (Yesmin et al., 2023; Bashir et al., 2025; Hasan et al., 2025; Rahman et al., 2024). Throughout the experiment, temperature, rainfall, and relative humidity data were collected from the meteorological station in Dinajpur, Bangladesh, and presented in Figure 1.

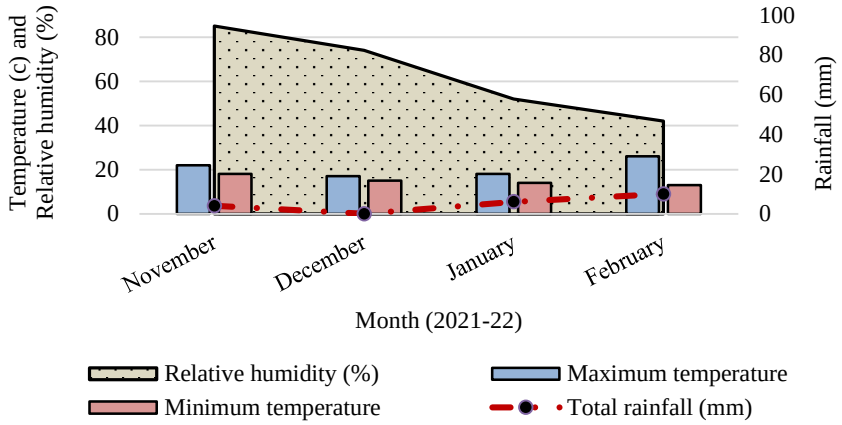

Figure 1. Monthly (November 2021 – February 2022) measurements of maximum and minimum temperatures, relative humidity, and rainfall in the Dinajpur District of Bangladesh (Data Source: Meteorological Station of Dinajpur, Bangladesh).

The soil in the experimental region was sandy loam (65% sand, 30% silt, and 5% clay). It had an acidic pH of 5.5 to 6.5 and limited water retention capacity. The initial soil study found 0.514% organic carbon and 0.04% total nitrogen. The soil contains 56 ppm of available phosphorus, 0.27 meq/100 g of exchangeable potassium, and 9.90 ppm of available sulphur (Sultana et al., 2025).

Field layout was completed following final land preparation. The experiment was designed in a randomized complete block design (RCBD) with three replicates. This study evaluated 12 mustard (*Brassica napus*) genotypes, including NAP0876, NAP16001, NAP16025, NAP16041, NAP16061, NAP16064, NAP16066, NAP16068, NAP16081, NAP16082, BARI SH8, and BARI SH13, collected from the Oilseed Research Centre (ORC) in Gazipur, Bangladesh, as planting materials. The entire field was divided into three blocks, each containing all the treatments once. The unit plot size was 3.6 m × 1.75 m, resulting in a total of 36 plots for the investigation. The distance between blocks was 1 m, and the spacing between individual plots was 0.5 m to facilitate intercultural operations and minimize border effects. The experimental field was prepared using appropriate tillage methods to provide a fine and well-aerated seedbed conducive to rapeseed cultivation. The land was initially plowed two to three times with a power tiller or country plow to achieve the desired soil tilth (Howlader et al., 2024). Each plowing was succeeded by laddering to fragment clods, equalize the soil, and enhance uniform moisture distribution. The final ground preparation resulted in a smooth, level area that was suitable for rapeseed seed germination and seedling establishment. Rapeseed seeds were seeded on 14 November 2019 and were harvested in March 2020.

Identification of *Alternaria* leaf blight

Alternaria leaf blight disease was characterized by the appearance of spots on plant parts such as leaves, stems, and siliquae. This kind of blight disease was distinguished by necrotic pinhead-like lesions surrounded by circular chlorotic regions or patches on leaves and siliquae (Tripathi et al., 2025). After observing the visual symptoms at 45, 55, and 65 DAS in the experimental field, the affected plant samples were covered with paper or poly bags and sent to the Laboratory of Plant Pathology, Hajee Mohammad Danesh Science and Technology University, for isolation, laboratory culture, and confirmation of *Alternaria brassicae* and *Alternaria brassicicola*.

Harvesting of crops and data collection

Five plants were randomly selected from each plot and tagged for data collection. When 80% of the plants showed signs of maturity, such as straw-colored leaves, stems, and siliquae, the crop was harvested for seed yield. At maturity, plants were collected by uprooting.

Data collection procedure

Plant height was measured in centimeters using a meter scale at both the vegetative and reproductive stages, and the average was recorded for each replication. Data were also collected as the average of five randomly selected plants from each plot. Plant height was measured from the ground surface to the top of the main shoot, with the mean height given in centimeters.

Five plants per plot were selected and tagged for the collection of data. The data on the number of total leaves were recorded at 45, 55 and 65 DAS by visual observation. The data on the number of total diseased leaves were recorded at 45, 55 and 65 days after sowing by visual observation from the five tagged plants per plot. The data on the number of healthy and diseased pods were also recorded by visual observation.

Average spot size on leaves was measured at 45, 55, and 65 DAT following sowing using a centimeter (cm) scale. The data on percent diseased leaf area were collected using visual scale observation of symptoms, and diseased leaf area data were recorded. The percentage of diseased leaves was estimated using the procedure below:

$$\%\ \text{Leaf area diseased} = \frac{\text{Infected leaf area diseased}}{\text{Total leaf area}} \times 100 \quad (1)$$

Disease severity was calculated by using the "0–5" scale (Conn et al., 1990). Disease severity was calculated using the following formula (Karim et al., 2024):

$$\%\ \text{Disease severity} = \frac{\text{Sum of all disease rating}}{\text{Total number of ratings} \times \text{Maximum disease rating}} \times 100 \quad (2)$$

Statistical analysis

The acquired data for the various parameters were compiled and tabulated. Statistical analysis was conducted using the Statistrix-10 application. The treatment means were compared using the least significant difference (LSD) test.

Results and Discussion

Plant height (cm)

The height of the plants exhibited significant variation among all 12 evaluated genotypes. At 45 DAS, the tallest plants measured 86.9 cm in NAP16066, followed by 82.76 cm in BARI SH8. At 55 DAS, the tallest plant height was noticed in NAP16066 (87.66 cm), followed by BARI SH8 (83.56 cm) (Figure 2). At 65 DAS, the tallest plant height recorded was 87.66 cm in NAP16066, followed by 83.60 cm in BARI SH8 and 78.53 cm in NAP16001 (Figure 2).

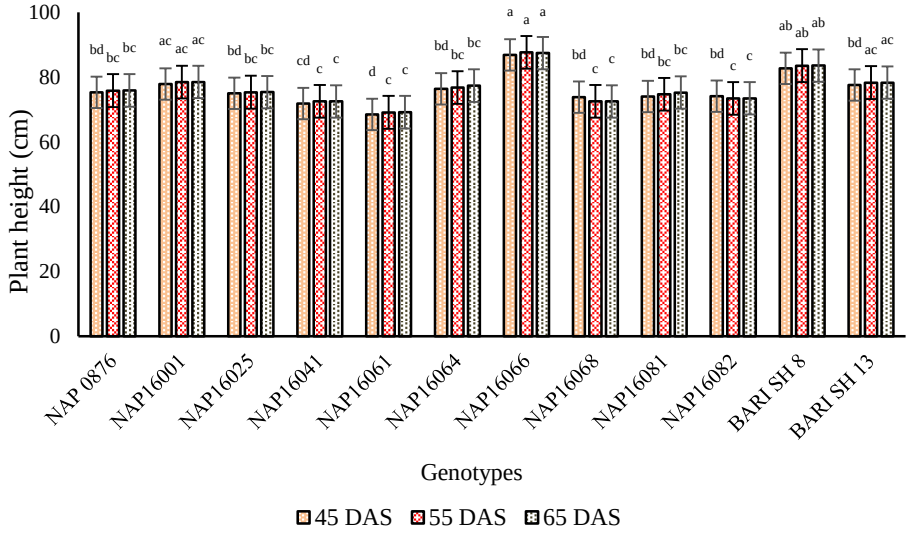

Figure 2. Plant height (cm) of 12 genotypes of *Brassica napus* recorded at different dates after sowing.

Number of total leaves plant^{-1}

The number of total leaves per plant varied considerably among the genotypes. At 45 DAS, the greatest number of leaves was recorded in BARI SH13 (12.67),

which was similar to NAP16064 (11.33). At 55 DAS, the highest number of leaves was again recorded in BARI SH13 (13.43) (Table 1). At 65 DAS, the highest number of leaves was recorded in NAP16061 (12.80), which was similar to BARI SH13 (11.03) and NAP16064 (10.93) (Table 1).

Table 1. Total number of leaves plant^{-1} and diseased leaves plant^{-1}of 12 genotypes of *Brassica napus* recorded at different dates after sowing.

Genotypes	Total number of leaves plant^{-1}			Diseased leaves plant^{-1}		
	45 DAS	55 DAS	65 DAS	45 DAS	55 DAS	65 DAS
NAP 0876	6.87 d	7.56 h	7.92 f	2.400 ef	2.920 ef	3.400 h
NAP16001	9.00 c	9.34 g	8.73 ef	3.120 d	3.920 d	4.510 f
NAP16025	9.457 c	9.81 fg	5.22 g	2.790 de	2.990 e	3.940 g
NAP16041	11.21 b	12.11 bd	10.87 bc	3.100 c	4.790 c	5.670 d
NAP16061	11.24 b	12.64 ac	12.80 a	2.780 de	3.390 d	3.950 g
NAP16064	11.33 b	12.47 ad	10.93 bc	4.020 c	4.400 cd	5.640 d
NAP16066	9.40 c	10.27 eg	9.25 de	3.950 c	4.830 c	5.630 d
NAP16068	11.05 b	10.653 ef	10.03 bd	5.580 a	6.810 a	7.930 a
NAP16081	10.77 b	11.36 ce	9.74 ce	4.800 b	5.840 b	5.100 e
NAP16082	10.47 b	11.28 de	9.29 de	4.870 b	5.840 b	6.860 b
BARI SH 8	11.20 b	13.21 ab	10.61 bc	4.390 bc	4.840 c	6.200 c
BARI SH 13	12.67 a	13.43 a	11.03 b	1.200 f	2.410 f	2.840 i
%CV	2.98	3.94	4.19	4.26	4.06	2.64
$LSD_{0.05}$	0.9102	1.2964	1.1954	0.4657	0.5279	0.3996

Means with the same letter within a column do not differ significantly at the 5% level of probability.

Number of diseased leaves plant^{-1}

The number of diseased leaves substantially varied among the genotypes. At 45 DAS, the lowest number of diseased leaves was recorded in BARI SH 13 (1.200), which was similar to NAP0876 (2.400) (Table 1). At 55 DAS, the minimum number of diseased leaves (2.410) was observed in BARI SH13. At 65 DAS, BARI SH13 again had the minimum number of diseased leaves (3.400), which was similar to NAP0876 (0.40) and NAP16025 (3.940) (Table 1).

Average spot size on leaf

The number of average spot sizes on the leaf differed substantially across genotypes at all data collection dates. At 45 DAS, the genotype with the smallest average spot size was NAP16061 (0.23 cm), followed by NAP16081 (0.62 cm) (Figure 3). At 55 DAS, the genotype with the smallest average spot size was observed in NAP160610 (0.23 cm), which was similar to BARI SH8 (0.56 cm). At

65 DAS, NAP16061 again had the smallest average spot size (0.23 cm), followed by NAP16064 (0.70 cm) (Figure 3).

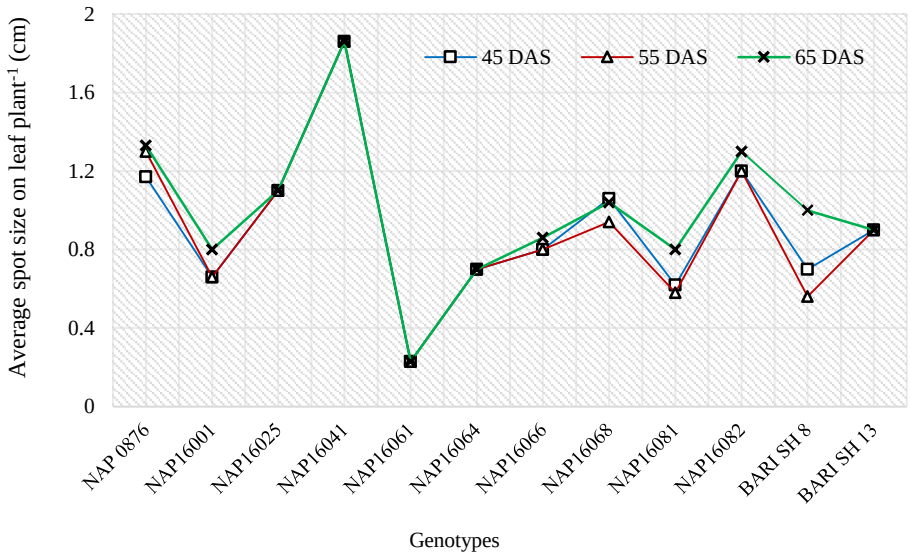

Figure 3. Average spot size on leaf plant^{-1} of 12 genotypes of *Brassica napus* recorded at different dates after sowing.

Percent leaf area diseased

Percent leaf area diseased varied significantly among the 12 genotypes of *Brassica napus*. At 45 DAS, NAP16061 had the lowest percentage of diseased leaf area (3.697%), which was comparable to BARI SH13 (3.700%), and NAP16064 (4.187%) (Table 2). At 55 DAS, the lowest percent disease leaf area was measured in NAP 16061 (5.477%), which was similar to BARI SH13 (6.321%), NAP16064 (6.610%) and NAP16041 (6.700%). At 65 DAS, NAP16061 again had the lowest percentage of diseased leaf area (3.167%) (Table 2).

Disease severity

The percent disease severity varied significantly among the 12 genotypes of *Brassica napus*. The minimal disease severity (12.56%) was observed at NAP 16061 (12.43%), followed by NAP16064 (12.56%) at 45 DAS (Table 2). At 55 DAS, NAP16061 showed minimum disease severity (15.06%), comparable to BARI SH13 (15.16%). At 65 DAS, NAP16061 performed better in the case of disease severity (11.06%), followed by BARI SH8 (24.00%) (Table 2).

Table 2. Percent leaf area diseased and disease severity (%) of 12 genotypes of *Brassica napus* recorded at different dates after sowing.

Genotypes	Percent leaf area diseased			Disease severity (%)		
	45 DAS	55 DAS	65 DAS	45 DAS	55 DAS	65 DAS
NAP 0876	9.143 d	9.53 e	13.96 e	20.50 f	21.86 f	27.09 i
NAP16001	9.743 c	11.40 c	16.11 cd	21.80 e	23.00 e	27.03 i
NAP16025	9.627 c	10.03 d	16.40 c	27.03 b	28.40 c	33.00 e
NAP16041	5.633 g	6.700 i	10.15 h	22.93 d	24.533 d	31.60 f
NAP16061	3.697 i	5.477 k	3.167 i	12.43 h	15.06 g	11.06 k
NAP16064	4.187 h	6.610 i	10.76 g	12.56 h	22.20 f	31.00 g
NAP16066	14.68 b	16.567 b	21.69 b	22.03 e	30.10 b	36.55 b
NAP16068	16.68 a	18.98 a	22.70 a	39.30 a	32.50 a	41.86 a
NAP16081	7.830 e	8.700 f	13.70 e	23.03 d	24.50 d	29.86 h
NAP16082	7.620 f	8.050 g	12.95 f	24.53 c	21.93 f	35.03 c
BARI SH 8	5.600 g	7.080 h	10.03 h	20.50 f	23.10 e	24.53 j
BARI SH 13	3.700 i	6.320 j	15.78 i	13.90 g	15.16 g	33.86 d
%CV	1.47	0.97	1.76	1	1.06	1.12
$LSD_{0.05}$	0.2031	0.1584	0.4152	0.3652	0.4267	0.5423

Means with the same letter within a column do not differ significantly at the 5% level of probability.

Number of healthy pods plant^{-1}

The number of healthy pods per plant differed substantially across all rapeseed genotypes. At 45 DAS, NAP16081 had the highest number of healthy pods (33.91), which was comparable to NAP16001 (27.53) and BARI SH8 (25.50) (Table 3). At 55 DAS, the genotype with the highest number of healthy pods was NAP16068 (53.00), followed by NAP16066 (43.00). At 65 DAS, the genotype with the highest number of healthy pods was NAP16066 (102.83), followed by NAP16064 (99.00), NAP16001 (88.27), and BARI SH13 (86.87) (Table 3).

Number of diseased pods plant^{-1}

The number of diseased pods per plant differed substantially across all rapeseed genotypes. At 45 DAS, NAP16001 had the fewest diseased pods (1.000), which was comparable to NAP16025 (1.400), NAP16064 (1.796), and NAP16066 (2.166) (Table 3). At 55 DAS, NAP16001 had the lowest number of diseased pods (1.133), which was comparable to NAP16025 (1.733), NAP16064 (2.133), and NAP16068 (2.500). At 65 DAS, NAP16001 had the fewest diseased pods (1.700), close to NAP16025 (2.000) (Table 3).

Table 3. Number of healthy and diseased pods per plant of 12 genotypes of *Brassica napus* recorded at different dates after sowing.

Genotypes	Number of healthy pods per plant			Number of diseased pods plant^{-1}		
	45 DAS	55 DAS	65 DAS	45 DAS	55 DAS	65 DAS
NAP 0876	18.6 h	19.33 k	51.53 a	3.4 b	3.7667 b	3.8533 de
NAP16001	27.533 b	38.66 d	88.27 h	1 g	1.1333 g	1.7 i
NAP16025	24.7 d	25.66 i	68.38 c	1.4 fg	1.7333 f	2 h
NAP16041	21.5 g	23.16 j	51.50 g	4.00 a	4.3743 a	5.2333 a
NAP16061	23.37 e	36.33 ef	69.99 h	2.6233 cd	3.2667 c	3.76 def
NAP16064	16.767 i	35.66 f	99.00 g	1.7967 ef	2.1333 e	2.8333 g
NAP16066	22.287 e	43.00 b	102.83 a	2.1667 de	2.89 d	3.62 ef
NAP16068	25.417 c	53.00 a	77.6 e	2.5 cd	3.3 c	3.863 de
NAP16081	33.907 a	41.33 c	73.47 f	2.8333 c	3 cd	3.4667 f
NAP16082	18.787 h	29.00 h	80.00 d	3.3667 b	3.7667 b	4 d
BARI SH 8	25.5 c	31.00 g	77.93 de	3.63 ab	3.9 b	4.45 c
BARI SH 13	22 fg	37.00 e	86.87 c	3.8033 ab	4.3067 a	4.79 b
CV	1.66	1.74	1.78	10.19	6.04	4.84
$LSD_{0.05}$	1.793	2.124	2.3374	0.4677	0.3201	0.2974

Means with the same letter within a column do not differ significantly at the 5% level of probability.

Principal component analysis (PCA)

Principal component analysis (PCA) indicated significant variance between genotypes in terms of disease-related and agronomic parameters (Figure 4). The first two principal components (PCs) explained 60.7% of the total variation, with PC1 accounting for 39.33% and PC2 for 21.37%. PC1 showed a positive loading of disease susceptibility traits such as disease severity (DS), percent disease severity (PDS), percent leaf area diseased (PLAD), and diseased leaves per plant (DP). Genotypes including BARI SH8, BARI SH13, NAP16081, and NAP16064 were positioned in the same manner, indicating higher disease susceptibility (Figure 4). Plant attributes, such as healthy pods per plant (HPP) and plant height (PH), were negatively linked with PC1, indicating a negative correlation with disease susceptibility. Genotypes involving NAP16066, NAP16025, and NAP16001 were concentrated in this region, showing disease resistance. The number of diseased pods (NDP) was similarly significantly associated with PC1, confirming this difference. PC2 (21.37% of the variance) exhibited additional differences between genotypes. Traits such as leaf per plant (LP) and DS were strongly correlated with PC2, but percent leaf area diseased (PLAD) and PDS had smaller impacts. NAP16082 and NAP16068 were found in the negative PC2 region, whereas NAP16061 was very susceptible (Figure 4).

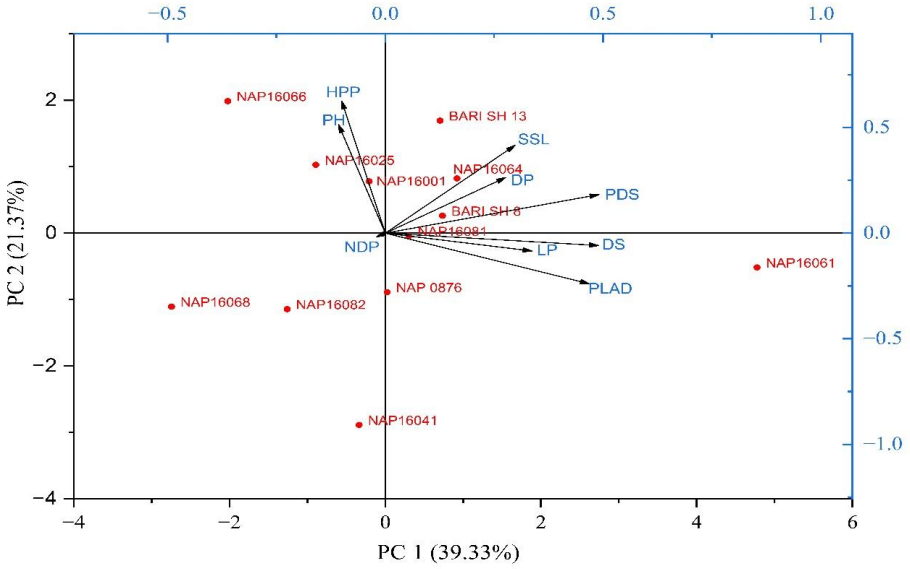

Figure 4. Expression of principal component analysis (PCA) across the genotypes.

Hierarchical cluster analysis (HCA)

The hierarchical clustering dendrogram illustrates the genetic relationships among the screened genotypes, providing insights into their diversity (Figure 5). The genotypes were divided into separate clusters based on genetic similarities. Cluster I contained NAP0876 and NAP16041, showing a strong genetic relationship. Cluster II was formed up of NAP16001 and NAP16066, with BARI SH13 as a subgroup. Cluster III possessed the genetically identical NAP16081 and NAP16082. Cluster IV included NAP16064 and NAP16025, which formed a moderately associated group. Finally, cluster V featured BARI SH8 and NAP16061, implying a genetic connection between these two genotypes. The clustering pattern demonstrated significant genetic heterogeneity among the tested genotypes (Figure 5).

The most significant and devastating disease of rapeseed is leaf blight, which is widely disseminated. Among the 12 genotypes studied, none were free of *Alternaria* infection; however, disease severity varied between genotypes. Talukdar and Das (2015) assessed rapeseed and mustard genotypes for resistance to *Alternaria* disease under field conditions in Assam, India, concluding that none of the genotypes exhibited strong resistance to *Alternaria* blight in rapeseed and mustard. The results showed that the highest plant height was observed in NAP16066, while the lowest disease severity was observed in NAP16061, BARI SH13, and BARI SH8. BARI SH13 genotypes performed better in terms of the total number of leaves, diseased

leaves, and percent leaf area diseased. The highest number of healthy pods was observed in NAP16001, NAP16066, and NAP16068, while the fewest diseased pods were noted in NAP16001. Significant diversity in disease resistance was identified among rapeseed genotypes through PCA, providing valuable insights for genotype selection (Ilieva et al., 2019). *Alternaria* blight resistance was observed in genotypes that were negatively associated with PC1, including NAP16066, NAP16025, and NAP16001. Similarly, NAP16082 and NAP16068, which were positioned negatively along PC2, showed modest resistance, requiring further investigation. Conversely, BARI SH8, NAP16064, and NAP16081 were significantly correlated with DS, PDS, and PLAD, suggesting that these genotypes were highly susceptible. Furthermore, NAP16041, situated at the extreme lower end of PC2, exhibited a novel disease tolerance mechanism, rendering it an appealing candidate for further investigation. NAP16066, NAP16025, and NAP16001 have been identified as potentially disease-resistant genotypes, underscoring their potential for use in screening programs. In contrast, genotypes particularly susceptible to *Alternaria* blight, such as NAP16061 and BARI SH8, showed poor disease resistance. In addition, the partitioned variance across these dimensions was accounted for by the significant contributions of multiple qualities to various principal components, as demonstrated by the research conducted by Neeru et al. (2015), Saleem et al. (2017) and Godara et al. (2022). These results underscore the effectiveness of PCA as a strategy for screening rapeseed genotypes for resistance to *Alternaria* blight.

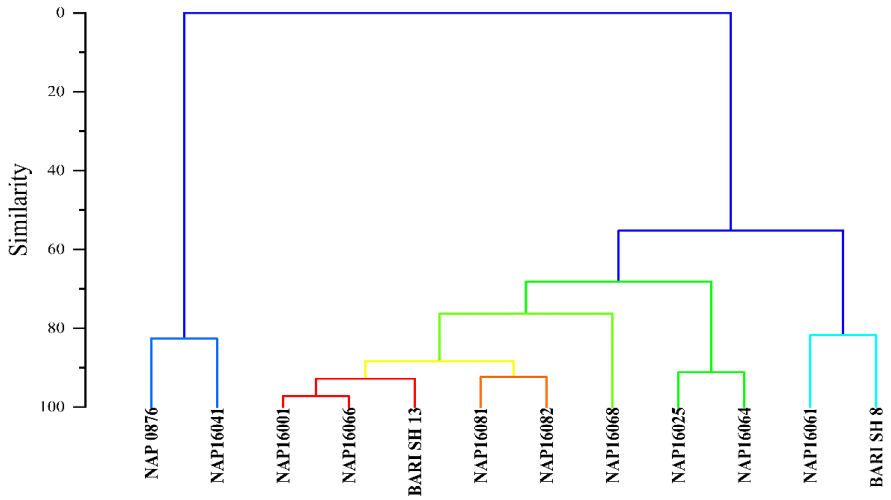

Figure 5. Hierarchical cluster analysis (HCA) dendrogram illustrating relationships among the genotypes.

The hierarchical clustering analysis effectively grouped the studied genotypes based on genetic similarity, providing valuable insights into their genetic relationships and diversity (Pathaichindachote et al., 2019). The observed clustering pattern demonstrated a high level of genetic variety, which is essential for mustard screening. The significant genetic association between NAP0876 and NAP16041 in cluster I revealed a high level of similarity, implying an individual disease tolerance mechanism. Similarly, in cluster II, the most desired genotypes, which were robust in resistance to *Alternaria* blight disease, clustered with NAP16001 and NAP16066. Cluster III (NAP16081 and NAP 16082) and cluster IV (NAP16068 and NAP16025) showed substantial resemblance, indicating that these genotypes were moderately to highly resistant to *Alternaria* blight. Finally, cluster V contained BARI SH8 and NAP16061, demonstrating a genetic association between the two genotypes that were most susceptible to *Alternaria* blight in this study. These findings are in alignment with Ghosh et al. (2019) and Blagojević et al. (2020).

Conclusion

The results showed that *Alternaria* blight resistance was suggested by genotypes that were negatively connected to PC1, such as NAP16066, NAP16025, and NAP16001. In a similar manner, NAP16082 and NAP16068, which were negatively oriented along PC2, demonstrated moderate resistance, requiring further investigation. NAP16066, NAP16025, and NAP16001 have been identified as possibly disease-resistant genotypes, highlighting their suitability for screening programs. Cluster I was significantly comparable, showing a particular disease tolerance mechanism, but cluster II contained the most desired genotypes with high resistance to *Alternaria* blight disease, clustering with NAP16001 and NAP16066.

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PROCENA GENOTIPOVA ULJANE REPICE (*BRASSICA NAPUS*) NA OTPORNOST PROTIV CRNE PEGAVOSTI

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R e z i m e

Crna pegavost (alternarioza) je razorna gljivična bolest koja inficira listove i ljuske uljane repice. Cilj ovog istraživanja bio je da se oceni intenzitet oboljevanja kod različitih genotipova kupusnjača i da se identifikuju superiorni genotipovi uljane repice otporni na crnu pegavost. Ispitano je dvanaest genotipova uljane repice. Naime, 45, 55 i 65 dana nakon setve (DNS), genotip NAP16061 je pokazao najmanji intenzitet oboljevanja (12,43%, 15,06% odnosno 11,06%). Genotip NAP16001 je imao najmanji broj zaraženih ljuski (1,000, 1,133 odnosno 1,700) 45, 55 odnosno 65 dana nakon setve. U pogledu broja zdravih ljuski, bolji su bili genotipovi NAP16001, NAP16068 i NAP16068. Genotip BARI SH 13 imao je najmanji ukupan broj listova po biljci i najmanji procenat lisne površine, dok je genotip NAP16061 imao najmanju prosečnu veličinu pega na listovima. Najveća visina biljaka je zabeležena kod genotipa NAP16066. Pozitivna opterećenja za parametre osetljivosti na bolest, kao što su intenzitet oboljevanja, procenat intenziteta oboljevanja, procenat zaražene lisne površine i broj zaraženih listova po biljci, primećene su kod prve glavne komponente (engl. *principal component 1 – PC1*). Genotipovi NAP16066, NAP16025 i NAP16001 pokazali su negativnu povezanost sa prvom glavnom komponentom, što ukazuje na otpornost na crnu pegavost.

Ključne reči: *Brassica napus*, genotipovi, gorušica, PCA i hijerarhijski klaster, uljana repica.

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