

Assessment of Rapeseed-Mustard Varieties for Resistance against White Rust (*Albugo candida*) Infection

ABSTRACT

The increasing prominence of rapeseed-mustard on the global stage as vital oilseed crop is attributed to its high yield, low moisture requirements, cost effective production, and adoptability to diverse farming condition indicating the potential for a forthcoming yellow revolution role in India's oilseed production, facing challenges from various factors affecting yield and seed quality. Notably, white rust stands out as a significant biotic stressor, causing substantial losses in both yield and seed quality, 17–34% yield particularly in oil content. To address this, utilizing resistant varieties is the most cost-effective and environmentally friendly approach for disease management. However, the available resistant sources are limited. In a recent study during the *Rabi* seasons of 2021-22 and 2022-23, thirty rapeseed mustard genotypes were assessed under white rust prevalent conditions. Out of 30 genotypes tested, none were found to be free of white rust disease infection and none were classified as resistant. However, 11 genotypes were registered as moderately resistance, while, 19 genotypes fell under the **were in the** susceptible category. Promisingly, some genotypes exhibited resistance to white rust, offering potential for developing superior cultivars to effectively manage the disease in regions where mustard cultivation is prevalent.

Aims: The study aimed to evaluate 30 rapeseed-mustard genotypes during the *Rabi* sessions of 2021-22 and 2022-23, focusing on their resistance to white rust. The primary objective was to identify genotypes with potential resistant traits, contributing to the development of superior cultivars for effective white rust management in regions where rapeseed-mustard cultivation is prominent.

Study design: Randomized Block Design.

Place and Duration of Study: Experimental field of the Department of Plant Pathology, College of Agriculture, BUAT, Banda session 2021-22 and 2022-23.

Result & Conclusion: None of the tested genotypes were found to be entirely free from white rust infection, and none of these achieved under resistance. However, the study identified 11 genotypes as moderately resistance and 19 genotypes fell into the susceptible category. Despite the challenges posed by white rust, some genotypes demonstrated resistance, offering promising potential for the development of advanced cultivars. This finding holds significant for regions where rapeseed-mustard cultivation faces the threat of white rust, providing the basis for future efforts enhancing crop resilience and productivity.

Keywords: Rapeseed-mustard, white rust, genotypes, resistance

1. INTRODUCTION

India stands as one of the world's leading producers of edible oils, with rapeseed-mustard being a significant annual oilseed crop, contributing around 25% to the nation's total oilseed production. Spanning 8.06 million hectares, it yields 11.75 million tonnes at a productivity rate of 1458 kg/ha (Anonymous, 2022). Ranking second in area after soybean, rapeseed-mustard is crucial due to its higher oil content (39-44%).(Singh *et al.*, 2022).

This agriculturally important crop has a rich cultivation history in India, China, and is gaining prominence in Australia. Predominantly grown during the Rabi season, its cultivation is concentrated in states such as Rajasthan, Madhya Pradesh, Uttar Pradesh, Haryana, West Bengal, Assam, Jharkhand, Gujarat, North Eastern States, and Bihar, collectively representing 96% of the crop's area and production. Despite the substantial oilseed cultivation, India remains a major importer of edible oil (Singh *et al.*, 2022). The mustard sector in India experiences fluctuations in area, production, and yield due to various biotic and abiotic stresses, as highlighted by Singh *et al.*, (2022).

Prominent biotic stresses leading to yield reduction in rapeseed-mustard include Alternaria blight (*Alternariabrassicae*), white rust (*Albugo candida*), Sclerotinia stem rot (*Sclerotiniasclerotiorum*), and downy mildew (*Hyaloperonospora parasitica*). Severe infections, particularly by Alternaria blight, white rust, and downy mildew, can result in economically significant yield losses ranging from 20% to 60% (Bisht *et al.*, 1994). To old reference due to lack of recent references on this, we cannot change this report.

When occurring together, white rust and downy mildew can cause a substantial impact, leading to a 37-47% reduction in pod formation and a 17-54.5% decrease in seed yield (Mukherjee *et al.*, 2001). Effective management strategies include the utilization of resistant varieties bioagent and botanical acknowledged for being cost-effective and environmentally friendly. Notably, germplasm screening has identified varying levels of host resistance against white rust, providing a promising avenue for mitigating these challenges (Ahmad *et al.*, 2014; Dharavath *et al.*, 2017).

The resistance to diseases, particularly through the presence of a single gene (R-gene) or multiple genes with modest effects, significantly influences crop production, quality assurance, environmental safety, and overall yield. Within Brassica species, considerable genotypic variability is observed concerning white rust resistance. Notably, *Brassica juncea*, a member of the Indian gene pool, displays high susceptibility to white rust, while the germplasm from East European origins exhibits varying degrees of resistance, ranging from highly resistant to moderately resistant (Chand *et al.*, 2022).

To ensure consistent and stable crop performance, the development of varieties with inherent resistance or tolerance to diseases, including white rust, emerges as an economically viable, environmentally safe, and sustainable strategy. The research focus is directed towards evaluating rapeseed-mustard genotypes for their resistance to white rust under field conditions, with a particular

emphasis on the cost-effectiveness and environmental advantages associated with the cultivation of resistant varieties.

2. MATERIALS AND METHODS:

This study involved the examination of 30 locally collected rapeseed-mustard cultivars. The cultivars were cultivated in a randomized block design with three replications during the *Rabi* seasons of 2021-22 and 2022-23 at the experimental field of the Department of Plant Pathology, College of Agriculture, BUAT, Banda (U.P.). Under conducive weather conditions, white rust progressed with temperatures ranging from 21.71 to 29.48°C and minimum temperature between 9.42 to 14.0°C. maximum relative humidity exceeded 90%, while minimum humidity varied from 36.14 to 56.42%, accompanied by a recorded rainfall of 12.30mm. The planting arrangement followed an augmented design with two rows for each genotype, each row extending 3 meters. The spacing was maintained at 30 cm between rows and 15 cm between individual plants. The incidence of white rust disease was systematically observed and recorded throughout the experimental period. 2022 and 2023

To analysed the percent disease index (PDI), observations on white rust occurrence were recorded every 10 days from 10 randomly selected plants of each row, both during the vegetative and true leaf stage (42nd days after sowing) under natural epiphytotic conditions.

Observations recorded on ten randomly selected plants from each row of each tagged genotype. The observation on disease severity of white rust disease was recorded at 10 days interval using 0-9 rating scale (Conn *et al*, 1990) (Table -1).

The intensity was calculated with formulae = $\frac{\text{Sum of all disease rating}}{\text{No. of leaves observed} \times \text{Max. disease rating}} \times 100$

The Area Under Disease Progress Curve (AUDPC) was calculated by the formula as under (Shaner and Finney 1977)

$$\text{AUDPC} = \sum_{i=1}^{n-1} \left[\frac{y_i + y_{i+1}}{2} \right] (t_{i+1} - t_i)$$

Where,

Y_i = White rust severity (%) at the 1st observation

$t_{(i+1)} - t_i$ = Time (days) between two disease scores

n = Total number of observations

Infection rate

Apparent infection rates per unit days helps estimated the progress of the disease in the filed on two different time points. Formula for weekly interval given by Vanderplank in 1963 was used to calculate the Logarithmic infection rates.

$$\text{Infection rate}(r) = \frac{2.3}{t_2 - t_1} \log_e \frac{x_2(1 - x_1)}{x_1(1 - x_2)}$$

Where

(r)= Apparent infection rate

t_1 = time during first observation

t_2 =time (days) during second observation

t_2-t_1 =time intervals between two observation

x_1 =per cent disease intensity value in decimal at corresponding t_1 time

x_2 =per cent disease intensity value in decimal at corresponding t_2 time

Log e= natural log

Table-1: Disease rating scale for evaluation of genotypes reaction:

Rating score	Leaf area covered (%)	Disease reaction
0	No symptoms	Immune(I)
1	< 5	Highly resistant(HR)
3	5-10	Resistant(R)
5	11-25	Moderately resistant (MR)
7	26-50	Susceptible (S)
9	>50	Highly susceptible (HS)

3. RESULTS AND DISCUSSION:

Data presented in table-2 & Fig-1 evident that combined mean of percent disease severity in different genotypes were ranged between 18.49 to 30.51% during crop session 2022 & 2023. Data are in accordance with that minimum percent disease severity was recorded in genotypes **Giriraj (18.49%)** differ statistically with **Tejashwani (20.40%)** followed by **RH746 (20.66%)**, **GSC7 (21.34%)**, **Krishna (21.35%)**, **PC6(21.53)** and **NRCHB101 (22.18%)**. The next group of genotypes that showed promising were **super express, RH406, DHM44, and PM29**, which obtained respective results of 22.30, 23.45, and 24.02% which, during crop sessions 2022 and 2023, shown non-significant differences in their effectiveness against the rapeseed-mustard white-rust.

For the genotypes **KMH8765, PHR126, PM30, RLC3, KMH721, Basanti, and RH749**, the reported percentages of disease severity (25.49, 25.65, 25.77, 25.83, 26.43, 26.47, and 27.44%) were statistically equivalent to each other. Subsequently, genotypes of **Radha, Dhakar, Peelasona, GSC6, and DRMR116540** were registered as promising; their respective genotypes were stated as 27.57, 27.68, 28.18, 28.59, and 28.66, however they were revealed to be comparable. A total of 56-92 (30.51%), **RCH (31.47%)**, **Ganga (30.28)**, **PGSH1707 (2.68%)**, **Nirmlabold (29.45)**, **Lahar (29.25)**, and **Kalasona (29.24)** had the highest percentage of disease severity. Similar to present findings **Li et al., (2007)** were screened out 44 genotypes of *Brassica juncea* against white rust and concluded that most of the genotypes of Indian gene pool showed moderate to susceptible reaction against white

rust disease. Previous researchers identified certain *Brassica* germplasms as resistant, but in the current study, the screened *Brassica* lines differed from those earlier findings. Some lines were identified as susceptible, while others fell into the moderately resistant category in the present research. The data presented in the table-2 indicates clear that the range of the pooled AUDPC of white rot in several cultivars of rapeseed mustard was 244.60 to 493.78. RCH1 recorded the highest pooled AUDPC (493.78), which was followed by 56-92 (482.05), Ganga (466.53), PGSH1707 (456.26), Nirmla bold (437.94), Lahar (426.33), Kalasona (412.03), DRMR116540 (407.56), GSC6 (406.95), Peelasona (394.92), Dhakar (384.98), Radha (381.75), RH 749 (370.75), KMH 721 (363.50), Basanti (362.94), RLC3 (352.53), PM 30 (346.58), PHR 126 (345.79), KMH 8765 (339.13), PM 29 (317.21), DHM 44 (311.44), RH 406 (297.58), Super express (298.42), NRCHB 101 (292.15), PC6 (279.40), Krishna (273.26), and GSC7 (273.22). Giriraj (244.60) genotypes had the lowest pooled AUDPC, followed by Tejashwani (256.50) and RH 746 (261.38).

The data in the table-2 revealed the apparent white rust disease infection rate in several rapeseed mustard cultivars during the 2022–2023 crop season. From the data, the genotypes Kala Sona (0.526) had the highest observed *r* value, followed by RCH-1 (0.515), GSC-6 (0.510), KMH-721 (0.497), 56-92 (0.493), PeelaSona (0.491), Lahar (0.490), RLC-3 (0.489), Dhakar, Radha, & NRCHB-101 (0.479), Ganga & PGSH-1707 (0.478), Basanti (0.473), PM-29 (0.472), PM-30 & PC-6 (0.470), PHR-126 (0.466), and Krishna (0.463). KMH-8765 (0.453), RH-749 & Nirmala Bold & DRMR-116540 (0.460), RH-406 (0.457), GSC-7 (0.484), and RH-746 (0.446). The genotypes Giriraj & Tejshwani had the lowest apparent infection rate (0.444), followed by DHM-44 & Super express (0.430).

The findings in the table-3 showed that all rapeseed mustard genotypes were infected with white rust disease, however the severity differed across genotypes. The data on per cent disease severity were classified into several categories (based on the diseaserating scale) to determine the reaction of genotypes to white rust disease. Out of 30 genotypes tested, none were found to be free of white rust disease infection and none were classified as resistant. However, 11 genotypes namely, Giriraj, RH-746, RH-406, NRCHB-101, PM-29, PC-6, GSC-7, Tejashwani, DHM-44, Krishna and Super express were registered under moderately resistance while, 19 genotypes namely, PM-30, GSC-6, RLC-3, RCH-1, PGSH-1707, PHR-126, RH-749, Nirmala Bold, Basanti, Kalasona, Peelasona, Radha, KMH-721, 56-92, Dhakar, KMH-8765, Ganga, Lahar and DRMR-116540 were registered moderately susceptible category.

In the current study, none of the assessed genotypes showed complete resistance to infection, aligning with Awasthi *et al.* (2012) findings that emphasized the susceptibility of key *B. juncea* varieties in India to white rust. The diverse responses of different genotypes to pathogens, varying in susceptibility, may stem from the complex interplay of resistance gene expression and the genetic background affecting genotype-pathogen interactions, as emphasized by Singh *et al.* (2021). The dynamics of how hosts and pathogens interact are significantly shaped by both macro and micro environmental factors, ultimately influencing the disease's severity, as discussed by Tamang *et al.* (2022).

Table-2: Pooled data of rapeseed mustard cultivars against white rust:

Pooled data of rapeseed-mustard cultivars against white rust 2022 and 23				
S. No.	Name of genotypes	Percent disease severity	Pooled AUDPC	Pooled r value
1	Giriraj	18.49 (25.45)	244.60	0.444
2	RH746	20.66 (27.01)	261.38	0.446
3	RH406	23.45 (28.94)	297.58	0.457
4	NRCHB101	22.18 (28.07)	292.15	0.479
5	PM29	24.02 (29.33)	317.21	0.472
6	PM30	25.77 (30.49)	346.58	0.470
7	PC6	21.53 (27.63)	279.40	0.470
8	GSC6	28.59 (32.30)	406.95	0.510
9	GSC7	21.34(27.49)	273.22	0.484
10	RLC3	25.83 (30.52)	352.53	0.489
11	RCH1	31.47 (34.10)	493.78	0.515
12	PGSH1707	29.68 (32.98)	456.26	0.478
13	PHR126	25.65 (30.39)	345.79	0.466
14	TEJASHWANI	20.40 (26.83)	256.50	0.444
15	DHM44	23.50 (28.98)	311.44	0.430
16	KRISHNA	21.35 (27.50)	273.26	0.463
17	RH749	27.44 (31.56)	370.75	0.463
18	NIRMLABOLD	29.45 (32.84)	437.94	0.460
19	BASANTI	26.47 (30.94)	362.94	0.473
20	KALASONA	29.24 (33.45)	412.03	0.526
21	GANGA	30.28 (33.18)	466.53	0.478
22	PEELASONA	28.18 (32.05)	394.92	0.491
23	RADHA	27.57 (31.66)	381.75	0.479
24	KMH721	26.43 (30.92)	363.50	0.497
25	56-92	30.51 (33.51)	482.05	0.493
26	DHAKAR	27.68 (31.73)	384.98	0.479
27	KMH8765	25.49 (30.31)	339.13	0.453
28	LAHAR	29.25 (32.72)	426.33	0.490
29	DRMR116540	28.66 (32.35)	407.56	0.460
30	SUPEREXPRESS	22.30 (28.16)	298.42	0.430
	C.D.		1.322	
	SE(m)		0.466	
	SE(d)		0.659	
	C.V.		2.649	

*Figure in parenthesis are angular transformed value

Table-3: Response of different genotypes against white rust of crucifers

Rating scale	Reaction	No. of genotypes	Name of genotypes
5	Moderately Resistant	11	Giriraj, RH-746, RH406, NRCHB-101, PM29, PC-6, GSC-7, Tejashwani, DHM- 44, Krishna, Super express.
7	Susceptible (S)	19	PM30, GSC-6, RLC-3, RCH-1, PGSH1707, PHR-126, RH-749, Nirmla Bold, Basanti, Kalasona, Peelasona, Radha, KMH-721, 56-92, Dhakar, KMH8765,

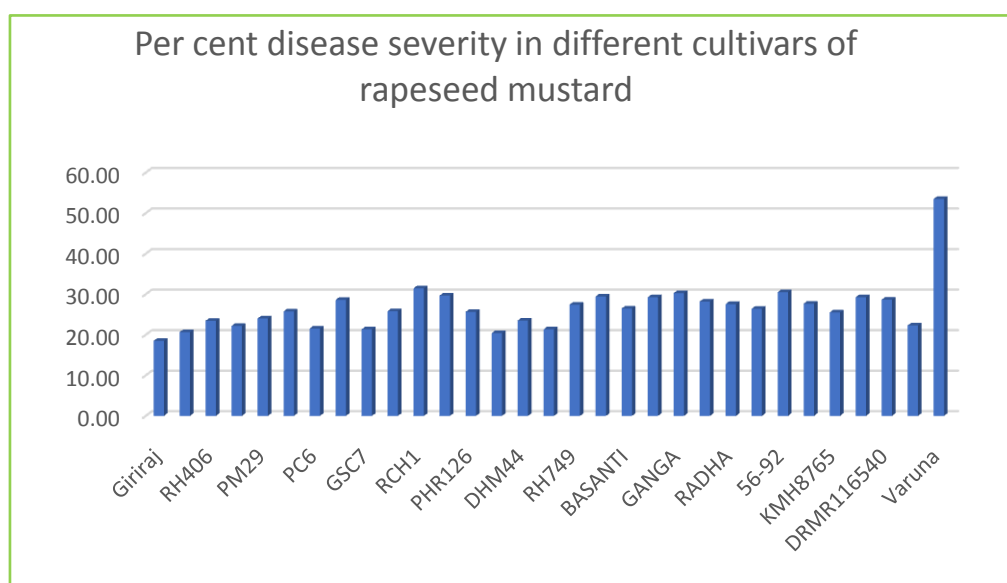


Fig-1:Per cent disease severity in different cultivars of rapeseed mustard

4. CONCLUSION:

Germplasm lines of rapeseed mustard have showed moderately resistant response in field screening trials against white rust disease while some of lines observed as a susceptible. These lines may be valuable in future breeding programs to develop resistant cultivars for commercial cultivation in farmer's fields. To address evolving diseases, identifying various resistance genes in crop species is crucial. India has recently made significant efforts to expand mustard cultivation in non-traditional locations for diversifying the cropping system. Thus, maintaining access to donor parents with high resistance against white rust disease is essential.

To achieve the goal, perform controlled lab tests on diverse genotypes for the disease. Confirm resistance in a controlled laboratory with artificial inoculation and molecular markers tied to resistant genes. Field testing is essential due to occasional disease escape. Hosts with more resistance genes prevent new pathogen races, as the pathogen requires virulent genes to overcome host resistance.

REFERENCES

1. Ahmad, HN, Perveen, R, Chohan S, Yasmeen G, Mehmood MA, & Hussain W. Screening of canola germplasm against *Albugo candida* and its epidemiological studies Pak. J. Phytopathol.. 2014; **26**(2): 169-173. <http://www.pakps.com>. Anonymous. Directorate of Economics and Statistics, Ministry of Agriculture and Farmers welfare. 2022; pp260.
2. Awasthi RP, Nashaat NI, Kolte SJ, Tewari AK, Meena PD, Bhatt R. Screening of putative resistant sources against Indian and exotic isolates of *Albugo candida* inciting white rust in rapeseed-mustard. J. Oilseed Brassica. 2012; **1**: 27–37.

3. Bisht IS, Agrawal RC, Singh R. White rust (*Albugo candida*) severity in mustard (*Brassica juncea*) varieties and its effects on seed yields. Plant Varieties & Seeds. 1994; 7(2): 85-89. ISSN : 0952-3863.
4. Chand S, Singh N, Prasad L, Nanjundan J, Meena VK, Chaudhary R. Inheritance and allelic relationship among Gene (s) for white rust resistance in Indian Mustard [*Brassica juncea* (L.) Czern&Coss]. Sustain. 2022; **14**(18):11620. <https://doi.org/10.3390/su141811620>.
5. Conn KL, Tewari JP, Awasthi RP. A disease assessment key for Alternaria black spot in rapeseed and mustard. Canadian Plant Dis. 1990; **70**:19-22.
6. Dharavath N, Mehera, B, Nath S, Patra SS, Rout S. Effect of different sowing dates and application of pesticides on growth and yield of mustard crop (*Brassica juncea*). Int. J. Pure App. Biosci. 2017; **5**(1): 178-187. DOI: <http://dx.doi.org/10.18782/2320-7051.2434>.
7. Li CX, Sivasithamparam K, Walton G, Salisbury P, Burton W, Banga Surinder, Banga SS, Shashi Chattopadhyay C, Kumar A, Singh R, Singh D, Agnohotri A, Liu SY, Li YC, Fu TD, Wang YF, Barbetti MJ. Expression and relationships of resistance to white rust (*Albugo candida*) at cotyledonary, seedling, and flowering stages in *Brassica juncea* germplasm from Australia, China, and India. Aust. J. Agric. Res. 2007; **58**(3): 259–264. <https://doi.org/10.1071/AR06237>. Mukherjee AK, Mohapatra T, Varshney A, Sharma R and Sharma RP. Molecular mapping of a locus controlling resistance to *A. candida* in Indian mustard. Plant Breed 2001; **120**: 483-487. <https://doi.org/10.1046/j.1439-0523.2001.00658.x>
- 8.
9. Shaner G, Finney RE. The effect of nitrogen fertilization on the expression of slow mildewing resistance in Knox wheat. Phytopathol. 1977; **67**:1051-1056.
10. Singh K, Akhtar J, Shekhawat N, Meena VS, Gupta A, Meena BR, Gupta V. Identification of new source of resistance against white rust. J. oilseed Brassica. 2022; **13**(2): 100-104.
11. Singh OW, Singh N, Kamil D, Singh VK, Devi TP, Prasad L. Morpho-Molecular Variability and Host Reactivity of *Albugo candida* Isolates Infecting Brassica juncea Genotypes in India. J. Plant Pathol. 2021; **103**:139–153.
12. Tamang S, Saha P, Bhattacharya S, Das A. Unveiling Genotype × Environment Interactions towards Identification of Stable Sources of Resistance in

Chickpea—Collar Rot Pathosystem Exploiting GGE Biplot Technique. Australas. Plant Pathol. 2022;**51**:47–58.

Plank, J. E. *Plant diseases: epidemics and control* (Vol. 111). New York: Academic press.1963.

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