

International Journal of Plant & Soil Science

Volume 38, Issue 11, Page 89-94, 2026; Article no.IJPSS.168587
ISSN: 2320-7035

Evaluation of Powdery Mildew Resistance in Northwest Himalayan Bread Wheat Landraces and Doubled Haploid Lines

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: https://doi.org/10.9734/ijpss/2026/v38i116404

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://pr.sdiarticle5.com/review-history/168587

Original Research Article

Received: 13/08/2026
Accepted: 18/10/2026
Published: 02/11/2026

Abstract

Powdery mildew, caused by Blumeria graminis f. sp. tritici, is an important disease of bread wheat in the cool, humid hill environments of Himachal Pradesh. This study evaluated powdery mildew development in 50 bread wheat genotypes comprising 16 doubled haploid (DH) lines, 29 north-west Himalayan landraces and five checks. The trial was conducted at Palampur during the 2021–2022 Rabi season under natural epiphytotic conditions using a randomised block design with three replications. Disease reactions were recorded on a 0–9 scale at five Zadoks growth stages (Z20, Z30, Z41, Z51 and Z69). Disease progression was assessed using the area under the disease progress curve (AUDPC) and relative AUDPC (rAUDPC). No genotype remained entirely free from powdery mildew. The mean disease score increased from 1.24 at Z20 to 6.16 at Z69. AUDPC values ranged from 100.5 in DH-114 to 313.0 in T-79, with a mean of 200.5 (95% confidence interval: 185.4–215.6). Nine genotypes recorded AUDPC values below 150, including four DH lines, three landraces and two checks. Mean AUDPC was higher in landraces (215.8) than in DH lines (180.5), although the reported comparison among germplasm categories was not statistically significant (Kruskal–Wallis P = 0.082). These findings identify genotypes with relatively slow disease progression under the tested conditions and support their further evaluation as potential sources of resistance to powdery mildew.

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Cite as: *Prikshit, Chaudhary, H. K., Rana, V., Kumar, N., Kashyap, M., & Goswami, I. (2026). Evaluation of Powdery Mildew Resistance in Northwest Himalayan Bread Wheat Landraces and Doubled Haploid Lines. International Journal of Plant & Soil Science, 38(11), 89–94. https://doi.org/10.9734/ijpss/2026/v38i116404*

Keywords: Bread wheat; powdery mildew; Blumeria graminis f. sp. tritici; doubled haploid lines; Himalayan landraces; adult-plant resistance; disease progression; AUDPC; rAUDPC; germplasm screening.

1. Introduction

Wheat powdery mildew is caused by the fungus *Blumeria graminis f. sp. tritici*. Globally, this pathogen is considered one of the important fungal pathogens of wheat (Dean *et al.*, 2012), and contributes to losses associated with crop pathogens (Savary *et al.*, 2019). Favourable environmental conditions for this disease include cool and humid climates; thus, the Northern Hills Zone and some regions of the North-Western Plains Zone in India are particularly vulnerable (Rana *et al.*, 2006; Basandrai & Basandrai, 2017). Breeding resistant varieties is the most effective and affordable way to manage the disease; however, resistance controlled by a single gene quickly becomes ineffective following the development of corresponding virulence in the pathogen population. A recent population-genomic study of European wheat powdery mildew populations documented virulence variants able to evade Pm17-mediated recognition, illustrating the capacity of the pathogen to adapt (Jigisha *et al.*, 2025).

Screening large germplasm pools has demonstrated the limited availability of useful resistance. Field-based screening of elite bread wheat germplasm has also been used to identify potential sources of resistance to powdery mildew (Kushwaha *et al.*, 2024). Gupta *et al.* (2016) screened 370 varieties of Indian bread wheat, durum wheat, dicoccum wheat and triticale across four environments and found that only 23 varieties exhibited immunity, while 114 were highly susceptible. Phenotypic field evaluations of bread wheat have also differentiated lines for resistance to other foliar diseases, including yellow and stem rust (Solomon *et al.*, 2024).

The screening of a much larger pool of 19,460 genebank accessions at Wellington revealed the presence of resistance among bread wheat, durum, and emmer, although the proportion showing resistance varied considerably between these species (Vikas *et al.*, 2020). Research in Himachal Pradesh also highlighted stable sources of resistance and slow mildew development, even in lines with high susceptibility ratings (Basandrai & Basandrai, 2017; Sood *et al.*, 2020).

A meta-analysis of wheat powdery mildew resistance loci has identified genomic regions that may inform the further characterisation of resistance sources (Sharma *et al.*, 2024). A separate study identified a resistance allele from a wheat landrace that conferred resistance at both seedling and adult stages, providing an example of the potential value of landrace germplasm (Fu *et al.*, 2025).

North-west Himalayan landraces have been cultivated in their local environments for many years and are adapted to these conditions despite the presence of diseases, but they have not been properly evaluated for their response to powdery mildew. In contrast, doubled haploid (DH) lines were developed through crosses of wheat with maize and wheat with *Imperata cylindrica* at Palampur. They are homozygous and, therefore, require only one year to evaluate their response. A terminal score recorded near the end of the growing period indicates disease severity but does not provide information about the rate of disease progression. Two disease progress curves may have identical terminal values but differ substantially in the duration preceding disease development. Repeated scoring at successive crop stages and calculation of AUDPC account for this variation, making the approach preferable for differentiating genotypes in their response to powdery mildew. An evidence gap addressed by this study is the lack of stage-wise comparative information on powdery mildew development in the north-west Himalayan landraces and locally developed DH lines evaluated here.

Thus, 50 genotypes comprising landraces, DH lines and checks were scored at five growth stages, and AUDPC was calculated to rank them and select genotypes with slow disease development.

2. Materials and Methods

2.1 Plant Material and Field Layout

The experimental material consisted of 16 DH lines (DH-1 to DH-776) selected from the Molecular Cytogenetics and Tissue Culture Lab, 29 landraces (T-3 to T-101 and BK-1, BK-2) collected from the Mandi, Kinnaur, Kullu, and Chamba districts of Himachal Pradesh, and five checks (HPW-360, HPW-368, HPW-373, VL-892, and C-306).

These 45 genotypes and five checks were evaluated in a randomised block design with three replications during the 2021–2022 Rabi season, at the Experimental Farm of the Department of Genetics and Plant Breeding, CSK HPKV, Palampur. The crop was grown following the package of practices recommended by CSK HPKV to ensure healthy growth. To promote disease spread and minimise the likelihood of disease escape, infector rows consisting of a mixture of lines susceptible to powdery mildew were sown around the borders of the experimental plots and after every five test lines.

Disease scoring: To score powdery mildew, the 0–9 scale of Saari and Prescott (1975) was followed, which ranges from 0 (no symptoms) to 1–3 (flecks and small lesions, resistant); 4 (barely perceptible mycelium, moderately resistant); 5–6 (small to moderate lesions, moderately susceptible) and 7–9 (increasing mycelium and conidia up to a full compatible reaction, susceptible). Disease scoring was conducted at tillering (Z20), stem elongation (Z30), booting (Z41), ear emergence (Z51) and the end of anthesis (Z69), based on the Zadoks scale. The historical visual assessment and disease-management guidance for wheat rusts (Peterson *et al.*, 1948; Roelfs *et al.*, 1992) is distinct from the powdery mildew scale used in this investigation.

AUDPC: The area under the disease progress curve was computed using the trapezoidal rule (Shaner & Finney, 1977; Campbell & Madden, 1990).

$$AUDPC = \sum [(y_i + y_{i+1})/2] \times (t_{i+1} - t_i), \text{ where } i = 1 \text{ to } (n - 1)$$

where yi denotes the value of the powdery mildew severity rating at the i^{th} observation, ti denotes the Zadoks scale at the i^{th} observation, and n is the total number of observations. Relative AUDPC was expressed as a proportion of the maximum possible area under the curve ($9 \times 49 = 441$) that a rating of 9 could cover throughout the entire period.

Statistical treatment: The mean, standard deviation and 95% confidence interval (using the t-distribution) were calculated for each stage and AUDPC. The genotypes were classified into four classes based on AUDPC. The differences between DH, landrace and check genotypes were assessed using the Kruskal–Wallis test, while DH and landrace genotypes were tested using the Mann–Whitney test because the AUDPC values were not assumed to be normally distributed. The mean disease progress curves were calculated for all 50 genotypes.

3. Results and Discussion

Disease screening: Disease was observed from tillering to the end of anthesis, with scores increasing gradually. For the 50 genotypes evaluated, the mean scores were 1.24, 2.58, 3.74, 5.18 and 6.16 at Z20, Z30, Z41, Z51 and Z69, respectively (Supplementary Table 1). The table shows that the 95% confidence intervals for subsequent stages did not overlap, which means that the increase in the score from one stage to another was statistically significant and was unlikely to reflect random variation. The greatest increase in the mean score occurred between Z41 and Z51 and amounted to 1.44 points. The greatest divergence between the curves of the least and most affected genotypes also occurred between these stages.

None of the 50 genotypes was completely free from the disease. The minimum score at Z69 was 3, recorded for genotypes DH-114 and DH-1, while 19 genotypes recorded scores of 7 or higher. In this respect, the material differed from collections of exotic or improved lines, where some genotypes were resistant during the whole period.

Table 1. Mean powdery mildew score (0-9) at five Zadoks stages, with 95% confidence interval, for all genotypes and for the extreme groups

Group	Z20	Z30	Z41	Z51	Z69	AUDPC
All 50 genotypes	1.24 (0.95-1.53)	2.58 (2.28-2.88)	3.74 (3.42-4.06)	5.18 (4.80-5.56)	6.16 (5.75-6.57)	200.5
5 lowest AUDPC	0.2	1.2	2.4	3.0	4.0	116.8
5 highest AUDPC	2.2	4.4	5.4	7.4	8.6	294.9

The five genotypes with the lowest AUDPC values were DH-114, DH-1, HPW-373, DH-52 and T-10, whereas those with the five highest values were T-79, T-71, BK-2, T-32 and T-47 (Table 1). The low-AUDPC group had an initial mean disease score of 0.2, which increased to 4.0 by Z69, whereas the high-AUDPC group increased from 2.2 to 8.6. The low-AUDPC group showed an increase of 3.8 points, compared with 6.4 points in the high-AUDPC group. The mean AUDPC of the high-AUDPC group was approximately 2.5 times that of the low-AUDPC group (294.9 versus 116.8), the mean across all genotypes lay between these values, at 200.5.

AUDPC: AUDPC varied between 100.5 and 313.0 among the 50 genotypes, whereas rAUDPC varied between 22.8% and 71.0% (Supplementary Table 1). The mean AUDPC was 200.5 with a standard deviation of 53.1 (coefficient of variation 26.5%) and a 95% confidence interval of 185.4 to 215.6. This variation indicates differences among genotypes in accumulated disease severity. Genotypes were classified into four categories (Table 2). Nine genotypes had AUDPC values below 150, 17 between 150 and 200, 14 between 200 and 250, and 10 had values above 250.

Table 2. Classification of genotypes on the basis of AUDPC

AUDPC class	No.	rAUDPC (%)	Genotypes
Below 150	9	22.8-32.8	DH-114, DH-1, HPW-373, DH-52, T-10, DH-40, HPW-360, T-101, T-12
150-200	17	34.5-44.4	DH-86, T-96, T-93, HPW-368, DH-37, DH-7, T-64, T-78, T-31, DH-100, DH-59, T-20, DH-195, T-39, T-22, T-21, T-4
200-250	14	45.6-54.6	T-5, T-26, DH-51, T-50, T-60, VL-892, DH-3, DH-84, T-95, DH-206, T-41, DH-65, T-3, C-306
Above 250	10	57.8-71.0	T-19, BK-1, T-51, DH-776, T-94, T-47, T-32, BK-2, T-71, T-79

The highest AUDPC was almost three times the lowest AUDPC (313.0 compared to 100.5), suggesting that parental selection warrants consideration. Twenty-six genotypes had AUDPC values below the mean of 200.5, and 24 had values above it. The median was 194.0. The lowest AUDPC values were recorded for DH-114 (100.5), DH-1 (105.5) and HPW-373 (120.0), followed by DH-52 and T-10 (129.0) and DH-40 (134.0). Out of the nine genotypes with an AUDPC below 150, four were DH lines (DH-1, DH-40, DH-52 and DH-114), three were landraces (T-10, T-12 and T-101) and two were checks (HPW-360 and HPW-373). The distribution of genotypes across AUDPC classes varied by origin. Out of the ten genotypes with an AUDPC higher than 250, nine were landraces (T-19, T-32, T-47, T-51, T-71, T-79, T-94, BK-1 and BK-2), while one was a DH line namely DH-776 (269.0). Of the 16 DH lines, 10 had AUDPC values below the overall mean, compared with 13 of the 29 landraces. Among the checks, HPW-373, HPW-360 and HPW-368 had a low AUDPC (120.0, 139.5 and 162.0), while VL-892 (216.5) and C-306 (241.0) were above the mean (Fig. 1).

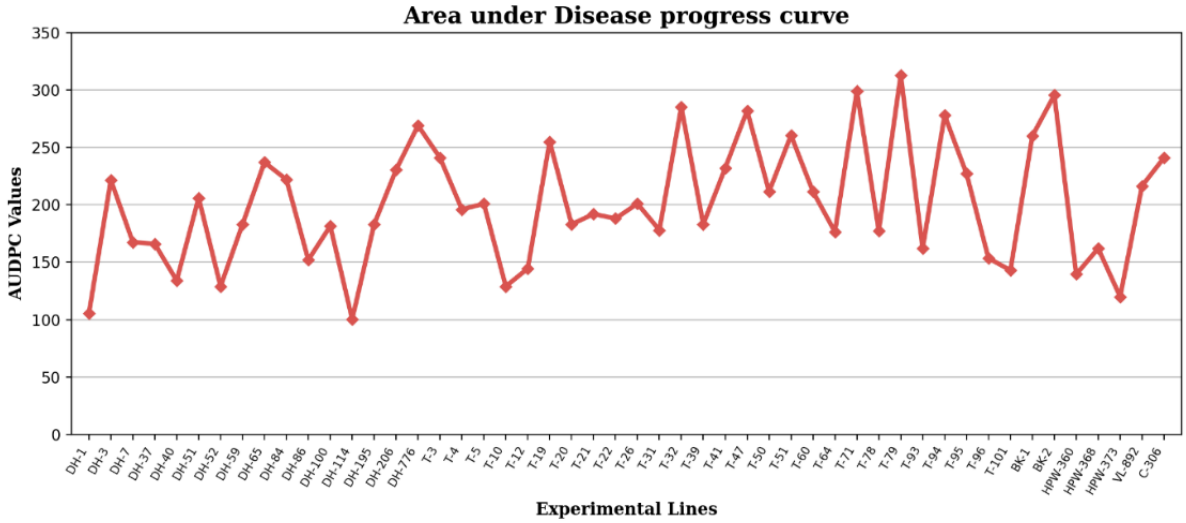


Fig. 1. Area under Disease progress curve of wheat lines for powdery mildew

The highest mean AUDPC was recorded for landraces (215.8; 95% CI 196.0-235.6), DH lines (180.5; 154.5-206.5) and checks (175.8; 112.1-239.5). The differences among the three categories were not statistically significant (Kruskal–Wallis P = 0.082) and the difference between the DH and landraces approached the conventional threshold (Mann–Whitney P = 0.052). These results therefore suggested only a trend towards slower mildew development in DH lines. It should also be considered that the landraces had not been selected for their disease reactions. Nevertheless, several landraces, including T-10, T-101 and T-12, showed relatively favourable performance and belonged to the lower AUDPC class, which makes this category worth further analysis. Considerable variation was observed among lines within each category (DH 100.5-269; landraces 129-313; checks 120-241), indicating that category averages alone are insufficient for evaluating individual lines.

DH-114 had the lowest AUDPC value (100.5), with a score of 3 at Z69 and scores of 1 or lower before Z30; it was followed by DH-1 (105.5), HPW-373 (120.0), DH-52 and T-10 (both 129.0), DH-40 (134.0) and HPW-360 (139.5). HPW-373 and HPW-360 are checks bred in Palampur; therefore, their performance supports the consistency of the scoring rather than representing a novel observation. T-101 (143.0) and T-12 (144.5), landraces of Kinnaur and Mandi, were the final two genotypes in this class. All of these lines reached the end of the growing season with scores of 3 to 5, corresponding to reactions ranging from resistant to moderately susceptible. Since a low AUDPC value accompanied by a moderate terminal score suggests slow mildew development, these lines may exhibit partial adult-plant resistance (Basandrai & Basandrai, 2017; Sood *et al.*, 2020).

4. Conclusion

Powdery mildew severity increased between tillering and the end of anthesis in all 50 evaluated wheat genotypes, and none remained free from disease throughout the observation period. Repeated disease scoring and calculation of AUDPC differentiated the genotypes according to their accumulated disease severity. AUDPC ranged from 100.5 in DH-114 to 313.0 in T-79, with an overall mean of 200.5. Nine genotypes had AUDPC values below 150: DH-114, DH-1, HPW-373, DH-52, T-10, DH-40, HPW-360, T-101 and T-12. These included four DH lines, three landraces and two checks. Although landraces had a higher mean AUDPC (215.8) than DH lines (180.5), the difference among the three germplasm categories was not statistically significant at the reported threshold (Kruskal–Wallis P = 0.082). The identification of landraces with relatively low AUDPC values indicates variation within this locally adapted germplasm. The identified low-AUDPC genotypes warrant further evaluation across seasons and locations before their resistance can be considered stable. They may provide material for subsequent investigation and breeding for powdery mildew resistance.

5. Limitations

This study was conducted at a single location, Palampur, during one Rabi season under natural epiphytotic conditions. Consequently, variation in disease pressure across locations and years was not evaluated, and the stability of genotype rankings remains uncertain. Resistance was assessed phenotypically through stage-specific scores and AUDPC, without identification of the underlying resistance genes or pathogen variants. The small check group also limits precision in comparisons among germplasm categories. Multi-season, multi-location screening and appropriate genetic and pathogen assessments would help establish whether the identified low-AUDPC genotypes consistently show reduced disease progression.

Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. Grammarly and ChatGPT were used solely to assist with grammatical refinement and reference

formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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Supplementary

Supplementary Table 1: Powdery mildew score (0-9) at five Zadoks stages, AUDPC and rAUDPC of 50 wheat genotypes

S. No.	Genotype	Z20	Z30	Z41	Z51	Z69	AUDPC	rAUDPC (%)
1.	DH-1	1	1	2	3	3	105.5	23.9
2.	DH-3	2	3	4	6	6	221.5	50.2
3.	DH-7	0	2	3	5	5	167.5	38.0
4.	DH-37	0	2	2	5	6	166	37.6
5.	DH-40	1	1	3	3	5	134	30.4
6.	DH-51	2	3	3	5	7	206	46.7
7.	DH-52	0	1	3	3	5	129	29.3
8.	DH-59	1	3	3	5	5	183	41.5
9.	DH-65	3	3	5	6	6	237	53.7
10.	DH-84	1	3	5	5	7	222	50.3
11.	DH-86	0	2	2	4	6	152	34.5
12.	DH-100	1	1	4	5	6	181.5	41.2
13.	DH-114	0	1	2	3	3	100.5	22.8
14.	DH-195	1	3	3	5	5	183	41.5
15.	DH-206	2	2	5	6	7	230.5	52.3
16.	DH-776	3	3	5	7	8	269	61.0
17.	T-3	2	4	4	6	7	241	54.6
18.	T-4	0	3	3	5	7	196	44.4
19.	T-5	1	2	4	5	7	201	45.6
20.	T-10	0	1	3	3	5	129	29.3
21.	T-12	1	2	3	3	5	144.5	32.8
22.	T-19	3	3	5	6	8	255	57.8
23.	T-20	2	3	3	4	6	183	41.5
24.	T-21	1	3	3	5	6	192	43.5
25.	T-22	2	2	4	5	5	188	42.6
26.	T-26	1	3	3	5	7	201	45.6
27.	T-31	0	3	3	5	5	178	40.4
28.	T-32	2	5	5	7	8	285	64.6
29.	T-39	1	3	3	5	5	183	41.5
30.	T-41	2	4	4	6	6	232	52.6
31.	T-47	1	3	5	8	9	282	63.9
32.	T-50	0	3	4	6	6	211.5	48.0
33.	T-51	2	3	6	6	8	260.5	59.1
34.	T-60	1	3	4	5	7	211.5	48.0
35.	T-64	0	2	3	5	6	176.5	40.0
36.	T-71	3	5	5	7	9	299	67.8
37.	T-78	2	2	3	5	5	177.5	40.2
38.	T-79	3	5	5	8	9	313	71.0
39.	T-93	1	1	3	5	5	162	36.7
40.	T-94	3	3	5	7	9	278	63.0
41.	T-95	1	3	5	6	6	227	51.5
42.	T-96	0	2	3	4	5	153.5	34.8
43.	T-101	0	1	3	4	5	143	32.4
44.	BK-1	3	3	5	7	7	260	59.0
45.	BK-2	2	4	7	7	8	295.5	67.0
46.	HPW-360	0	2	3	3	5	139.5	31.6
47.	HPW-368	1	1	3	5	5	162	36.7
48.	HPW-373	0	2	2	3	4	120	27.2
49.	VL-892	1	2	5	6	6	216.5	49.1
50.	C-306	2	4	4	6	7	241	54.6

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Peer-review history:
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