



International Journal of Horticulture and Food Science

E-ISSN: 2663-1067

P-ISSN: 2663-1075

NAAS Rating (2026): 4.74

www.hortijournal.com

IJHFS 2026; 8(7): 49-56

Received: 27-04-2026

Accepted: 29-05-2026

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Evaluation of cucumber (*Cucumis sativus* L.) germplasm for resistance to downy mildew (*Pseudoperonospora cubensis*) based on percent disease index and area under disease progress curve

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DOI: <https://www.doi.org/10.33545/26631067.2026.v8.i7a.798>

Abstract

Downy mildew, caused by *Pseudoperonospora cubensis* (Berk. & Curt.) Rostov, is one of the most destructive foliar diseases of cucumber (*Cucumis sativus* L.), resulting in severe yield losses and deterioration of fruit quality under humid and moderate temperature conditions. The rapid evolution of pathogen populations and the emergence of new virulent races have reduced the effectiveness of fungicide-based disease management, making host plant resistance the most economical and environmentally sustainable strategy for disease control. The present investigation was conducted to evaluate fifty cucumber genotypes for resistance to downy mildew under natural epiphytotic conditions using Percent Disease Index (PDI) and Area Under Disease Progress Curve (AUDPC) as quantitative measures of disease severity. Disease observations were recorded at regular intervals following disease initiation, and genotypes were classified into different resistance categories based on their disease response. Significant variation was observed among the evaluated germplasm for both PDI and AUDPC, indicating the existence of substantial genetic variability for downy mildew resistance. Genotypes exhibiting consistently low PDI and AUDPC values were identified as potential sources of resistance, whereas highly susceptible genotypes recorded rapid disease progression and higher AUDPC values. A strong positive correlation between PDI and AUDPC suggested that both parameters effectively described disease development, while AUDPC provided a more comprehensive assessment of temporal disease progression. The identified resistant genotypes constitute valuable genetic resources for cucumber improvement programmes and may serve as donor parents for breeding durable downy mildew-resistant cultivars. The findings also demonstrate the usefulness of integrating PDI and AUDPC for accurate phenotypic characterization of disease resistance in cucumber germplasm.

Keywords: *Cucumis sativus*, downy mildew, *Pseudoperonospora cubensis*, disease resistance, germplasm evaluation, PDI, AUDPC, screening, breeding

1. Introduction

Cucumber (*Cucumis sativus* L.) is one of the most economically important vegetable crops belonging to the family Cucurbitaceae and is cultivated extensively throughout tropical, subtropical, and temperate regions of the world. It is valued for its tender fruits, refreshing taste, nutritional quality, and versatility in fresh consumption, processing, and pickling. Cucumber fruits are rich in water, dietary fibre, vitamins C and K, potassium, magnesium, and several bioactive compounds with antioxidant properties. The crop plays a significant role in improving nutritional security while providing substantial income to vegetable growers due to its short duration, high productivity, and year-round market demand. Globally, cucumber occupies several million hectares, with major production concentrated in Asia, particularly China and India, where it contributes significantly to vegetable production and rural livelihoods.

Despite its economic importance, cucumber productivity is constrained by numerous biotic stresses, among which downy mildew is regarded as one of the most devastating foliar diseases.

The disease is caused by the obligate oomycete *Pseudoperonospora cubensis* (Berk. & Curt.) Rostov, a pathogen capable of infecting several economically important cucurbit crops including cucumber, muskmelon, watermelon, pumpkin, bottle gourd, bitter melon, and squash. Since its first description during the nineteenth century, downy mildew has become one of the most widespread diseases of cucurbits, causing severe epidemics in regions characterized by moderate temperatures, prolonged leaf wetness, and high relative humidity. The pathogen has a worldwide distribution and remains a major challenge to sustainable cucumber production in both open-field and protected cultivation systems.

Downy mildew primarily attacks the foliage, resulting in angular chlorotic lesions delimited by leaf veins on the upper leaf surface. Under favorable environmental conditions, grey to purplish sporulation develops on the abaxial leaf surface, representing the sporangiophores and sporangia of the pathogen. As infection progresses, lesions coalesce rapidly, leading to extensive chlorosis, necrosis, premature defoliation, reduced photosynthetic area, and impaired assimilate translocation. Severe infections may result in complete collapse of the foliage, drastically reducing fruit size, marketable yield, and fruit quality. Yield losses ranging from 30% to nearly complete crop failure have been reported during severe epidemics, particularly when susceptible cultivars are grown under conducive environmental conditions.

The epidemiology of downy mildew is strongly influenced by environmental factors. Disease development is favoured by temperatures between 15 and 25°C, relative humidity above 90%, prolonged dew periods, and frequent rainfall or overhead irrigation, which facilitate sporulation, dispersal, and infection. Owing to the polycyclic nature of the disease, repeated infection cycles occur throughout the cropping season, resulting in rapid disease escalation. Climate variability, changing rainfall patterns, and increased humidity in many cucumber-growing regions have further intensified disease incidence and increased the frequency of epidemics.

Management of downy mildew largely depends on repeated fungicide applications. However, intensive reliance on fungicides has raised serious concerns regarding the development of fungicide-resistant pathogen populations, environmental contamination, increased production costs, and pesticide residues on fresh produce. Moreover, the emergence of new physiological races and highly virulent populations of *P. cubensis* has frequently overcome previously deployed resistance genes, leading to the breakdown of resistance in commercial cultivars. These challenges highlight the urgent need to identify novel and durable sources of resistance that can be incorporated into cucumber breeding programmes.

Host plant resistance represents one of the most effective, economical, and environmentally sustainable approaches for managing downy mildew. The identification of resistant germplasm provides valuable donor parents for breeding programmes and reduces dependence on chemical disease control. Germplasm evaluation under natural or artificial disease pressure remains the cornerstone for discovering new resistance sources. Reliable phenotyping is therefore essential to distinguish resistant, moderately resistant, and susceptible genotypes and to facilitate the genetic

improvement of cucumber.

Among the quantitative methods used for disease assessment, the Percent Disease Index (PDI) is one of the most widely adopted parameters for estimating disease severity at specific observation dates. PDI provides a snapshot of disease intensity and enables comparison among genotypes based on symptom expression. However, because disease development is dynamic and progresses continuously throughout the crop growth period, single-time assessments may not accurately reflect the overall disease burden experienced by the plant.

To overcome this limitation, the Area Under the Disease Progress Curve (AUDPC) has become a standard epidemiological parameter for evaluating temporal disease development. AUDPC integrates disease severity over multiple observation dates, providing a cumulative measure of disease intensity throughout the epidemic. Compared with single disease observations, AUDPC offers a more robust estimate of disease progression, host resistance, and epidemic development. Consequently, the combined use of PDI and AUDPC has been widely recommended for comprehensive evaluation of disease resistance in breeding and pathology research.

Although several studies have reported sources of resistance to downy mildew in cucumber, the continuous evolution of *P. cubensis* populations necessitates periodic re-evaluation of available germplasm. Furthermore, many cucumber collections remain inadequately characterized under Indian agro-climatic conditions, where disease pressure varies considerably across environments. Comprehensive evaluation of diverse germplasm under natural epiphytotic conditions can facilitate the identification of stable resistance sources and broaden the genetic base available for resistance breeding (FAOSTAT (2024); Zitter *et al.* (1996)^[13]; Lebeda *et al.* (2011))^[7].

The present investigation was therefore undertaken to evaluate a diverse panel of fifty cucumber genotypes for resistance to downy mildew using PDI and AUDPC as complementary disease assessment parameters. The specific objectives of the study were to (i) quantify the variability in disease response among cucumber genotypes, (ii) identify promising resistant germplasm based on disease severity and disease progression, (iii) compare the effectiveness of PDI and AUDPC for phenotypic evaluation, and (iv) identify potential donor genotypes for utilization in future cucumber improvement programmes aimed at developing durable resistance to downy mildew. The outcomes of this study are expected to contribute valuable information for disease resistance breeding and support the development of sustainable disease management strategies in cucumber.

2. Materials and Methods

2.1 Experimental Site

The experiment was conducted during the kharif 2023 and kharif 2024 seasons at the Experimental Farm of the Division of Vegetable Science, ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India. The experimental farm is situated at 28°38' N latitude and 77°10' E longitude at an elevation of approximately 228.6 m above mean sea level. The region experiences a subtropical climate characterized by hot summers, a monsoon season with high relative humidity, and cool winters. The kharif season receives substantial rainfall, creating favourable environmental conditions for the natural development of

downy mildew.

2.2 Experimental Material

A total of 50 cucumber (*Cucumis sativus* L.) genotypes, designated CCUH-2501 to CCUH-2550, were used in the present investigation. The germplasm represented a diverse collection maintained at the Division of Vegetable Science, ICAR-IARI, New Delhi. The genotypes were selected to represent broad genetic diversity and were evaluated for their reaction to downy mildew under natural epiphytotic conditions.

2.3 Experimental Design and Crop Raising

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications during each season.

Each genotype was represented by one plot in each replication, consisting of 10 healthy plants. Standard agronomic practices recommended for cucumber cultivation in the region were followed throughout the crop growth period. Appropriate doses of farmyard manure and fertilizers were applied before sowing and during crop growth according to the recommended package of practices. Irrigation, intercultural operations, and weed management

were carried out uniformly for all experimental plots. No fungicides effective against downy mildew were applied during the experimental period to allow natural disease development.

2.4 Disease Development

The experiment was conducted under natural epiphytotic conditions, where downy mildew developed naturally during the cropping season. Disease development was favoured by the prevailing environmental conditions of moderate temperature, prolonged leaf wetness, and high relative humidity during the kharif season.

Observations on disease severity were initiated immediately after the appearance of the first visible symptoms of downy mildew and continued at regular intervals until disease development reached maximum severity.

2.5 Disease Assessment

Disease severity was recorded on 10 randomly selected plants from each plot in every replication.

On each selected plant, disease severity was assessed on all fully expanded leaves using the standard 0-9 disease rating scale, where:

Disease Rating	Disease Severity
0	No visible symptoms
1	Up to 5% leaf area infected
3	6-10% leaf area infected
5	11-25% leaf area infected
7	26-50% leaf area infected
9	More than 50% leaf area infected with severe chlorosis, necrosis and defoliation

Disease observations were recorded at seven-day intervals from disease initiation until crop maturity. The average disease score for each genotype was calculated from observations recorded on ten plants in each replication.

2.6 Estimation of Percent Disease Index (PDI)

- The Percent Disease Index (PDI) was calculated according to the method described by Wheeler (1969)^[12].
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$$PDI = \frac{\sum \text{Disease Ratings}}{\text{Number of leaves observed} \times \text{Maximum disease rating}} \times 100$$

where:

- Σ Disease Ratings = Sum of disease scores of all observed leaves
- Maximum disease rating = 9

- Number of leaves observed = Total leaves assessed on ten plants.

The mean PDI for each genotype was calculated by averaging the observations recorded from all three replications.

Based on the final PDI values, the genotypes were categorized into different disease reaction classes.

PDI (%)	Disease Reaction
0-10	Resistant (R)
10.1-25	Moderately Resistant (MR)
25.1-50	Moderately Susceptible (MS)
50.1-75	Susceptible (S)
>75	Highly Susceptible (HS)

2.7 Estimation of Area Under Disease Progress Curve (AUDPC)

Disease progression over time was quantified by calculating the Area Under Disease Progress Curve (AUDPC) using disease severity observations recorded at successive observation dates according to the method of Shaner and Finney (1977)^[11]:

AUDPC was calculated by the formula given below:

$$AUDPC = \sum_{i=1}^{n-1} \frac{y_i + y_{i+1}}{2} \times (t_{i+1} - t_i)$$

Where y_i is an assessment of a disease (percentage) at the i^{th} observation, t_i is time (in days,) at the i^{th} observation, and n is the total number of observations

The AUDPC values were computed separately for each genotype in each replication and averaged across replications and seasons. Lower AUDPC values indicated slower disease development and greater resistance, whereas higher values reflected rapid disease progression and susceptibility (Wheeler (1969); Shaner & Finney (1977)^[11]; Jenkins & Wehner (1983))^[5].

2.8 Statistical Analysis

Data on foliar disease score, PDI, and AUDPC recorded during the two seasons were subjected to statistical analysis using analysis of variance (ANOVA) appropriate for a Randomized Complete Block Design (RCBD).

The statistical model included:

- Genotype (G)

- Season (S)
- Genotype $\times$ Season interaction (G $\times$ S)

The significance of treatment effects was tested at the 5% probability level ($P \leq 0.05$).

Mean comparisons among genotypes were performed using the Least Significant Difference (LSD) (or Critical Difference, CD) test at the 5% level of significance.

Descriptive statistics, including mean, standard deviation, coefficient of variation (CV), minimum, and maximum values, were computed for all disease parameters.

2.9 Experimental Summary

Particular	Description
Crop	Cucumber (<i>Cucumis sativus</i> L.)
Number of genotypes	50 (CCUH-2501 to CCUH-2550)
Seasons	Kharif 2023 and Kharif 2024
Experimental design	Randomized Complete Block Design (RCBD)
Replications	3
Plants per plot	10
Disease assessment	Natural epiphytotic conditions
Disease observations	fortnightly after symptom appearance
Parameters recorded	Foliar disease score, PDI, AUDPC
Statistical analyses	ANOVA

3. Results

3.1 Variability in Downy Mildew Severity among Cucumber Genotypes

Considerable variation was observed among the fifty cucumber genotypes for downy mildew severity at different crop growth stages, indicating the presence of substantial genetic variability for disease resistance. Disease severity progressively increased from 30 DAS to 75 DAS in all genotypes, although the rate of disease development differed markedly among genotypes.

At 30 DAS, the Percent Disease Index (PDI) ranged from approximately 11.1 to 42.2% among the evaluated genotypes. The lowest disease severity was recorded in genotype CCUH-2535 (11.11%), followed by CCUH-2511, CCUH-2514, CCUH-2532, and CCUH-2537, indicating comparatively higher levels of resistance during the initial stages of disease development. In contrast, genotypes CCUH-2544, CCUH-2541, CCUH-2545, CCUH-2547, CCUH-2501, and CCUH-2513 exhibited relatively higher disease severity at the early growth stage, suggesting greater susceptibility to downy mildew.

Disease severity increased substantially by 45 DAS, with PDI values ranging from approximately 34.4 to 71.1%. Several genotypes that exhibited low disease severity during the early growth stage continued to maintain comparatively lower PDI values, whereas susceptible genotypes showed rapid disease progression.

By 60 DAS, disease development accelerated in most genotypes, with PDI values varying between approximately 47.8 and 98.9%. The majority of susceptible genotypes recorded disease severity exceeding 70%, while a few genotypes maintained comparatively lower disease intensity.

At the final observation (75 DAS), PDI values ranged from approximately 65.6 to 100%, indicating severe disease

pressure under natural epiphytotic conditions. Several genotypes, including CCUH-2513, CCUH-2516, CCUH-2517, CCUH-2518, CCUH-2527, and CCUH-2549, reached nearly complete disease severity (100%), whereas genotype CCUH-2535 consistently recorded the lowest final disease severity (66.67%), followed by CCUH-2534, CCUH-2543, CCUH-2532, and CCUH-2538.

These observations clearly demonstrated differential disease progression among the evaluated germplasm and confirmed the existence of useful variation for downy mildew resistance.

3.2 Disease Progression among Genotypes

Disease progression followed a characteristic increasing trend throughout the crop growth period. Across all genotypes, PDI increased steadily from 30 DAS to 75 DAS, indicating continuous pathogen multiplication and favourable environmental conditions for disease development.

However, the rate of disease progression varied considerably among genotypes. Resistant and moderately resistant genotypes exhibited slower disease development, whereas susceptible genotypes showed rapid increases in disease severity between successive observations. The slower disease progression observed in resistant genotypes suggests the presence of effective host defence mechanisms capable of restricting pathogen colonization.

3.3 Area Under Disease Progress Curve (AUDPC)

Significant variation was observed among cucumber genotypes for AUDPC, reflecting differences in cumulative disease development throughout the cropping period. AUDPC values ranged from approximately 1850 to 3400. The lowest AUDPC value was recorded in CCUH-2535 (1850), indicating slow disease progression and superior

resistance. Other genotypes exhibiting relatively low AUDPC values included CCUH-2534, CCUH-2538, CCUH-2532, CCUH-2519, and CCUH-2511. In contrast, the highest AUDPC values were observed in CCUH-2516 (3400), followed by CCUH-2513, CCUH-2517, CCUH-2545, CCUH-2527, and CCUH-2544, indicating rapid disease development and high susceptibility.

The wide range in AUDPC values further confirmed substantial genetic variability for resistance to downy mildew among the evaluated cucumber germplasm.

3.4 Identification of Resistant and Susceptible Genotypes

Based on disease severity and AUDPC, the evaluated cucumber germplasm could be broadly grouped into resistant and susceptible categories.

Genotypes such as:

- CCUH-2535
- CCUH-2534
- CCUH-2538
- CCUH-2532
- CCUH-2519

- CCUH-2511

Consistently exhibited comparatively lower PDI values throughout the crop growth period and recorded the lowest AUDPC values. These genotypes may therefore be considered promising sources of resistance to downy mildew.

Conversely,

- CCUH-2516
- CCUH-2517
- CCUH-2513
- CCUH-2545
- CCUH-2527
- CCUH-2544

Recorded high disease severity at successive observations and accumulated the highest AUDPC values, indicating high susceptibility to the disease.

Table 1: The Percent Disease Index (PDI) and AUPDC of downy mildew in 50 genotypes in Kharif 2024 and 2025

Genotypes	Kharif season 2024					Kharif season 2025				
	PDI 30 DAS	PDI 45 DAS	PDI 60 DAS	PDI 75 DAS	AUDPC	PDI 30 DAS	PDI 45 DAS	PDI 60 DAS	PDI 75 DAS	AUDPC
CCUH-2501	34.99	64.07	72.21	89.59	2978.45	35.55	65.55	73.95	92.30	3051.38
CCUH-2502	29.04	43.97	65.87	87.68	2523.04	30.57	45.75	68.80	88.50	2611.24
CCUH-2503	28.83	65.42	73.37	93.41	2998.68	31.40	66.00	73.95	95.85	3053.63
CCUH-2504	32.74	51.21	86.58	95.48	3028.52	35.50	53.90	86.80	96.45	3100.13
CCUH-2505	26.96	41.97	64.92	88.99	2472.94	30.55	44.10	68.30	89.10	2583.38
CCUH-2506	26.58	59.20	71.15	92.30	2846.88	28.90	60.40	73.70	90.90	2910.00
CCUH-2507	29.04	51.71	69.59	86.58	2686.67	27.85	51.80	71.95	87.15	2718.75
CCUH-2508	25.47	53.16	74.37	93.16	2802.67	27.15	51.05	74.45	89.30	2755.88
CCUH-2509	18.94	41.15	69.49	93.36	2501.92	21.85	43.35	72.35	93.55	2601.00
CCUH-2510	27.94	42.40	66.79	95.37	2562.71	27.40	41.95	69.60	90.30	2556.00
CCUH-2511	13.82	42.71	61.96	89.59	2345.58	17.25	45.20	64.35	89.55	2444.25
CCUH-2512	24.97	52.73	73.67	94.72	2793.73	27.00	50.70	71.55	90.30	2713.50
CCUH-2513	34.58	61.71	92.57	99.60	3320.58	34.00	60.75	93.95	99.20	3319.50
CCUH-2514	14.27	53.42	67.48	92.70	2615.83	17.60	52.75	68.95	92.30	2649.75
CCUH-2515	15.03	49.59	76.38	94.37	2710.04	17.95	51.40	75.20	93.15	2732.25
CCUH-2516	19.00	66.64	97.29	99.85	3350.38	21.40	63.80	99.45	100.00	3359.25
CCUH-2517	15.88	70.66	93.47	100.00	3331.00	17.20	70.35	92.40	100.00	3320.25
CCUH-2518	20.60	42.71	82.26	100.00	2778.92	23.20	43.95	84.35	99.50	2844.75
CCUH-2519	21.10	40.36	58.19	90.59	2315.88	23.80	44.15	61.60	89.35	2434.88
CCUH-2520	21.71	52.82	79.25	95.08	2856.92	21.90	52.25	82.80	99.35	2935.13
CCUH-2521	27.58	57.14	76.98	94.32	2926.17	29.30	56.10	82.30	97.90	3030.00
CCUH-2522	21.76	59.54	75.63	92.10	2881.63	29.05	59.50	77.95	91.30	2964.38
CCUH-2523	26.28	52.27	69.54	91.80	2712.79	25.15	54.30	72.90	92.20	2788.13
CCUH-2524	20.60	59.30	66.18	91.61	2723.71	23.10	59.50	67.90	88.50	2748.00
CCUH-2525	23.47	60.09	73.07	94.47	2881.96	26.10	62.60	75.05	91.10	2943.75
CCUH-2526	22.76	49.54	74.92	83.16	2661.38	25.00	51.55	77.65	87.90	2784.75
CCUH-2527	23.86	63.37	91.10	100.00	3246.04	25.35	65.25	94.25	100.00	3332.63
CCUH-2528	23.21	49.45	75.02	94.32	2748.54	25.08	51.35	76.50	93.95	2810.48
CCUH-2529	22.76	43.02	65.57	82.60	2419.04	24.15	49.65	67.50	86.35	2586.00
CCUH-2530	23.36	51.76	58.94	82.15	2451.75	25.70	53.95	61.70	85.30	2567.25
CCUH-2531	28.19	50.90	70.29	85.37	2669.67	31.25	52.30	71.90	85.37	2737.67
CCUH-2532	14.27	36.08	60.59	81.71	2169.88	17.05	36.55	62.70	85.25	2256.00
CCUH-2533	17.14	48.09	70.29	84.31	2536.71	19.40	47.75	73.85	86.75	2620.13
CCUH-2534	20.60	45.04	56.98	67.53	2191.21	22.35	46.60	60.45	76.95	2350.50
CCUH-2535	11.71	37.08	48.94	67.53	1884.63	13.85	36.55	52.00	75.00	1994.63
CCUH-2536	17.99	61.66	83.37	99.44	3056.25	19.85	62.30	86.15	100.00	3125.63
CCUH-2537	15.27	51.21	82.86	98.14	2861.58	16.85	51.55	83.95	100.00	2908.88
CCUH-2538	18.04	33.52	61.15	83.51	2181.71	20.55	35.75	63.50	87.50	2299.13
CCUH-2539	27.58	59.20	67.29	93.41	2804.88	29.60	61.25	67.10	95.00	2859.75

CCUH-2540	32.87	55.43	73.93	89.49	2858.13	31.70	55.30	73.45	91.40	2854.50
CCUH-2541	38.14	49.45	69.99	91.15	2761.33	38.55	51.55	72.95	93.54	2858.18
CCUH-2542	29.19	59.15	72.52	94.92	2905.96	31.85	56.85	73.10	92.55	2882.25
CCUH-2543	20.70	46.98	80.46	77.48	2647.96	22.65	48.65	79.05	84.80	2721.38
CCUH-2544	42.86	57.24	83.21	91.20	3112.29	42.55	54.50	85.15	97.00	3141.38
CCUH-2545	38.19	69.35	86.69	86.93	3278.96	40.65	67.00	88.34	100.00	3384.96
CCUH-2546	25.12	47.48	88.94	91.46	2920.71	27.50	49.50	91.00	100.00	3063.75
CCUH-2547	38.69	51.15	86.23	84.11	2981.71	39.35	51.75	88.10	95.35	3108.00
CCUH-2548	27.08	56.74	77.13	94.92	2923.13	27.15	56.80	80.10	96.52	2981.04
CCUH-2549	24.92	59.45	74.97	100.00	2953.25	28.15	58.90	76.15	97.30	2966.63
CCUH-2550	40.56	57.03	78.79	97.54	2956.54	28.05	57.90	82.35	98.04	3049.42
CD(0.05)	6.66	2.97	3.01	2.63		4.30	5.15	4.34	6.18	
CD(0.01)	8.88	3.96	4.01	3.50		5.74	6.86	5.78	8.25	
CV (%)	13.29	2.82	2.02	1.44		8.08	4.81	2.85	3.33	
SE(m)	2.34	1.05	1.06	0.92		1.51	1.81	1.53	2.18	
SE(d)	3.31	1.48	1.50	1.31		2.14	2.56	2.16	3.08	

3.5 Relationship between PDI and AUDPC

Genotypes exhibiting higher disease severity at 75 DAS consistently recorded higher AUDPC values, indicating a strong positive association between final disease severity and cumulative disease development.

Genotype	PDI 2024	PDI 2025	Disease reaction
CCUH-2535	67.53	75.00	Least susceptible
CCUH-2534	67.53	76.95	Moderately resistant
CCUH-2532	81.71	85.25	Slow disease progression
CCUH-2517	100.00	100	Highly susceptible
CCUH-2518	100.00	99.5	Highly susceptible
CCUH-2527	100.00	100	Highly susceptible

This trend demonstrates that genotypes with lower disease intensity also experienced slower disease progression, resulting in reduced AUDPC values. Thus, AUDPC effectively complemented PDI by integrating disease development over time and provided a more comprehensive assessment of host resistance.

3.6 Overall Disease Response

Natural epiphytotic conditions during the experimental season were highly conducive for downy mildew development, as evidenced by the progressive increase in disease severity across all genotypes. Nevertheless, considerable differences among genotypes in both PDI and AUDPC indicated the presence of exploitable genetic variability for resistance. The identification of genotypes with consistently lower disease severity and reduced AUDPC highlights their potential utility as donor parents in cucumber breeding programmes aimed at developing durable downy mildew-resistant cultivars.

4. Discussion

Downy mildew, caused by *Pseudoperonospora cubensis*, is one of the most destructive foliar diseases affecting cucumber worldwide. The disease develops rapidly under conditions of high relative humidity, moderate temperatures, and prolonged leaf wetness, resulting in severe defoliation, reduced photosynthetic activity, and substantial yield losses. The present study demonstrated considerable variation in disease severity among the evaluated cucumber genotypes, indicating the presence of exploitable genetic diversity for resistance to downy mildew. Such variability is essential for identifying resistant donor parents and developing cultivars with durable resistance through breeding programmes.

The progressive increase in Percent Disease Index (PDI) from 30 to 75 DAS across all genotypes reflected the polycyclic nature of downy mildew and the favourable environmental conditions prevailing during the kharif season. Similar disease progression has been reported in cucumber under natural epiphytotic conditions, where repeated infection cycles and continuous sporulation accelerate epidemic development. However, the magnitude of disease progression differed significantly among genotypes, suggesting differences in host-pathogen interactions and the expression of resistance mechanisms.

Several genotypes, including CCUH-2535, CCUH-2534, CCUH-2532, CCUH-2538, CCUH-2519, and CCUH-2511, consistently exhibited lower disease severity throughout the crop growth period and accumulated comparatively lower AUDPC values. The slower increase in disease severity in these genotypes suggests the presence of partial or quantitative resistance that restricts pathogen colonization and slows epidemic development. Unlike race-specific resistance, quantitative resistance generally reduces the rate of disease development rather than completely preventing infection and is considered more durable because it is controlled by multiple genes and is less likely to be overcome by evolving pathogen populations.

In contrast, genotypes such as CCUH-2516, CCUH-2517, CCUH-2513, CCUH-2527, CCUH-2544, and CCUH-2545 exhibited rapid disease progression, reaching very high PDI values by the final observation and recording the highest AUDPC values. These genotypes appear to possess limited resistance against *P. cubensis*, allowing rapid pathogen multiplication and disease spread under favourable environmental conditions. Such highly susceptible genotypes may serve as susceptible checks in future screening experiments and can also be valuable in genetic studies aimed at understanding the inheritance of downy mildew resistance.

The present investigation demonstrated that disease severity increased continuously with crop age, indicating that resistance should not be assessed solely on the basis of early disease observations. Genotypes showing low disease severity during the initial stages occasionally developed severe symptoms at later growth stages, emphasizing the importance of repeated disease assessments throughout the epidemic. Therefore, multiple observations at regular intervals provide a more reliable estimation of host response than a single disease score.

Among the disease assessment parameters evaluated, both

Percent Disease Index (PDI) and Area Under the Disease Progress Curve (AUDPC) effectively differentiated resistant and susceptible genotypes. However, AUDPC provided a more comprehensive estimate of disease development because it integrated disease severity over time rather than representing disease intensity at a single observation. Genotypes with lower AUDPC values maintained reduced disease severity throughout the cropping period, whereas susceptible genotypes accumulated significantly higher AUDPC values due to rapid disease progression. The strong positive association observed between final PDI and AUDPC indicates that both parameters are closely related; however, AUDPC better reflects the temporal dynamics of disease development and is therefore considered a superior parameter for quantitative assessment of resistance.

The wide variation observed for both PDI and AUDPC indicates substantial genetic variability within the evaluated cucumber germplasm. Such variability is highly desirable in breeding programmes because it provides opportunities for selecting superior parents possessing stable resistance. The identification of moderately resistant genotypes with slower disease progression is particularly important because quantitative resistance generally provides longer-lasting protection than single major resistance genes, which are often overcome by new pathogen races.

The observed differences among genotypes may be attributed to several structural and biochemical defence mechanisms operating within the host plant. Resistant genotypes may possess thicker cuticles, enhanced stomatal defence, rapid hypersensitive responses, increased lignification, accumulation of phenolic compounds, and elevated activities of defence-related enzymes such as peroxidase, polyphenol oxidase, phenylalanine ammonia-lyase, and β -1,3-glucanase. Activation of salicylic acid-mediated signalling pathways and other induced defence responses may further contribute to restricting pathogen establishment and sporulation. Future investigations involving molecular characterization and transcriptomic analyses of the identified resistant genotypes would facilitate the identification of candidate genes associated with downy mildew resistance and accelerate marker-assisted breeding Cohen (1981)^[2]; Savory *et al.* (2011)^[10]; Ojiambo *et al.* (2015)^[9]; Keinath (2015)^[6].

Host plant resistance remains the most sustainable approach for managing downy mildew because it minimizes dependence on repeated fungicide applications, reduces production costs, and decreases environmental contamination. The emergence of fungicide-resistant populations of *P. cubensis* and increasing concerns regarding pesticide residues further emphasize the importance of developing resistant cultivars. Consequently, the resistant and moderately resistant genotypes identified in the present study constitute valuable genetic resources for future breeding programmes aimed at developing high-yielding cucumber cultivars with durable resistance to downy mildew.

Although the present study successfully identified promising resistant sources, the stability of resistance should be confirmed through multi-location and multi-season evaluations under diverse environmental conditions. Since disease development is strongly influenced by climatic factors and pathogen variability, validation across environments will help identify genotypes possessing broad-spectrum and stable resistance. Integration of phenotypic

screening with molecular marker analysis, quantitative trait locus (QTL) mapping, genome-wide association studies (GWAS), and genomic selection could further accelerate the development of resistant cultivars (Call *et al.* (2012)^[1]; Naegle *et al.* (2014)^[8]; Li *et al.* (2018)).

Overall, the findings demonstrate that combining PDI with AUDPC provides a robust and comprehensive approach for evaluating downy mildew resistance in cucumber. The identified resistant germplasm offers valuable opportunities for both conventional and molecular breeding aimed at enhancing disease resistance while reducing dependence on chemical disease management.

5. Conclusion

The present investigation revealed substantial genetic variability among the fifty cucumber genotypes evaluated for resistance to downy mildew under natural epiphytotic conditions. Disease severity increased progressively from 30 to 75 DAS, reflecting favourable environmental conditions for disease development and the polycyclic nature of *Pseudoperonospora cubensis*. Nevertheless, marked differences in disease progression among genotypes demonstrated the existence of valuable resistance sources within the evaluated germplasm.

Both Percent Disease Index (PDI) and Area Under the Disease Progress Curve (AUDPC) effectively differentiated resistant and susceptible genotypes, with AUDPC providing a more comprehensive assessment by integrating disease severity over time. Genotypes CCUH-2535, CCUH-2534, CCUH-2532, CCUH-2538, CCUH-2519, and CCUH-2511 consistently exhibited lower disease severity and reduced AUDPC values, indicating slower disease progression and greater levels of resistance. In contrast, CCUH-2516, CCUH-2517, CCUH-2513, CCUH-2527, CCUH-2544, and CCUH-2545 were highly susceptible and experienced rapid disease development throughout the assessment period.

The study confirms that integrating sequential disease observations with AUDPC analysis provides a reliable framework for identifying durable sources of resistance in cucumber. The resistant genotypes identified here represent valuable donor lines for breeding programmes aimed at developing high-yielding cultivars with improved resistance to downy mildew. Future work should focus on validating these resistant sources across multiple environments, elucidating the genetic basis of resistance through QTL mapping and genome-wide association studies, and developing molecular markers to facilitate marker-assisted selection. Such integrated approaches will contribute to sustainable cucumber production by reducing dependence on fungicides and enhancing resilience to one of the crop's most economically important diseases.

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