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RESEARCH ARTICLE

Screening of field resistance to downy mildew (*Pseudoperonospora cubensis*) disease in an indigenous and exotic collection of cucumber

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Abstract

An experiment was conducted to identify sources of resistance to downy mildew in cucumber. A total of 148 genotypes, along with susceptible checks, were evaluated under natural epiphytotic field conditions using percent disease index (PDI) and area under the disease progress curve (AUDPC) as criteria. Disease severity was recorded on a 0 to 9 scale at fortnightly intervals on 10 randomly selected plants per genotype, for a total of four assessments until crop termination. Genotypes were classified into four reaction groups based on average PDI: highly resistant (0–20%), moderately resistant (21–40%), moderately susceptible (41–60%) and highly susceptible (>60%). Substantial variability in disease response was observed. Only two genotypes, PI-197086 and PI-197088, were highly resistant, with the lowest PDI (≤ 20%) and AUDPC values (788.54–885.24), indicating slow disease development. Four genotypes (Gol Kheera-1, Gol Kheera-2, IC-345573 and IC-613461) were moderately resistant (AUDPC 1048.93–1269.25), while five (IC-332344, IIHR-82, IC-398675, Pusa Uday and PI-330628) were moderately susceptible. The remaining majority, including several commercial cultivars and advanced lines, were highly susceptible (PDI >60%). The predominance of susceptible entries highlights the vulnerability of current cucumber germplasm and the narrow genetic pool for disease resistance. PI-197086 and PI-197088 represent promising primary donors, with moderately resistant genotypes providing additional diversity for durable resistance breeding.

Keywords: AUDPC, PDI, Cucumber, Screening, Downy mildew and resistance.

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Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important salad crops in the family Cucurbitaceae. It has a chromosome number of 2n = 14 and a genome size of 367 Mb organized into seven linkage groups (Yang et al., 2022). In India, cucumber occupies an area of 1.31 lakh hectares with the production of 17.59 lakh MT with a productivity of 13.42 MT/ha (www.indiastat.com). In India, cucumber is cultivated for immature fruits for fresh consumption and for processing, primarily as pickles (Dey et al., 2023). However, numerous biotic and abiotic stresses significantly reduce yield. Among biotic constraints, foliar diseases such as powdery mildew and downy mildew are particularly damaging. Rainfall, dew, and irrigation create a favourable microclimate for disease development (Thomas, 1996), and temperatures between 5 and 30°C with sufficient moisture promote disease progress. Downy mildew is widespread in both the Northern and Southern Hemispheres and occurs on all continents (Call, 2012; Lebeda & Cohen, 2011).

The host range of the downy mildew pathogen, *Pseudoperonospora cubensis* (Berk. & Curt.) Rostov., includes around 60 vegetable species across about 20 genera in the Cucurbitaceae (Lebeda, 1992; Lebeda & Cohen, 2011). In its

native habitats, nine cucurbit species are affected, with the genus *Cucumis* serving as the principal host (Cohen, 1981; Lebeda & Urban, 2007). Six *Ps. cubensis* pathotypes have been identified worldwide based on differential host ranges within the Cucurbitaceae (Cohen et al., 2003). In India, the disease can cause 70 to 100% yield losses (El-Nagdy & Abdel-Hafez, 1990; Kumar et al., 2026) and leads to substantial declines in both yield and fruit quality (Colucci & Holmes, 2010). Management relies primarily on repeated fungicide applications, which impose strong selection pressure and can lead to resistance in pathogen populations (Holmes et al., 2006). Moreover, routine fungicide use can harm non-target organisms and disrupt ecosystems (Kibria et al., 2010; Komarek et al., 2010). In most cases, cucumber downy mildew primarily affects the foliage. Early symptoms appear on the undersides of leaves as small, water-soaked lesions. These lesions are typically angular, delimited by leaf veins, and show varying degrees of chlorosis. Sporulation occurs on the abaxial (lower) leaf surface. Over time, chlorotic lesions become necrotic; severely affected leaves can become entirely necrotic and die. Highly susceptible cultigens develop extensive chlorosis and necrosis, whereas more resistant cultigens exhibit a hypersensitive response (HR) characterized by limited sporulation and small necrotic or chlorotic flecks (Call et al., 2012).

Historically, many downy mildew-resistant U.S. breeding lines and elite cultivars derive their resistance from the Indian accession PI 197087. Dhillon et al. (1999) identified nine resistant cultivars of Asian and European origin. In a four-year screening of 1,300 cucumber cultigens in Poland, Call (2012) identified six with high levels of resistance: PI 330628, PI 197088, PI 197086, PI 197085, Ames 2353, and Ames 2354. Nonetheless, several previously resistant sources have since become susceptible to downy mildew. Consequently, discovering and deploying novel resistance sources is critical to provide growers with durable, environmentally sound, and cost-effective management options. In light of these considerations, the current breeding program aims to evaluate 148 indigenous cucumber germplasm accessions for downy mildew resistance in order to identify novel resistant genotypes.

Material and Methods

A total of 148 cucumber genotypes (Table 1) from the national gene bank were screened for downy mildew under natural epiphytotic conditions at the research farm of ICAR–Indian Institute of Vegetable Research (ICAR-IIVR), Varanasi, during the late *Kharif* season of 2024–25. Each genotype, along with susceptible and resistant checks, was planted on raised beds (6 × 1.5 m) at 60 cm plant-to-plant and 1.2 m row-to-row spacing. Ten plants per genotype were maintained per plot. Standard agronomic practices were followed, and no fungicide was applied throughout the crop cycle. Two lines, PI 197086 and PI 197088, were used as resistant checks, and Pusa Uday (IARI, New Delhi) and Kalyanpur Green (CSAU&T, Kanpur) served as susceptible checks. One row of infector was planted at every ten rows to ensure that the disease propagated uniformly.

Natural epiphytotic field screening technique

Natural field screening was conducted at the Vegetable Research Farm, ICAR–Indian Institute of Vegetable Research (ICAR-IIVR), Varanasi, Uttar Pradesh, during 2024–2025. Cucumber genotypes/varieties were sown in the late *Kharif* season (September) following recommended practices (Chattopadhyay et al., 2007). Standard cultural and plant-protection practices were adopted as needed; however, no fungicide was applied throughout the crop cycle. All genotypes were evaluated under open-field, natural epiphytotic conditions. Downy mildew severity was recorded at 30, 45, 60, and 75 days after sowing (DAS) using the 0-9 rating scale (Jenkins and Wehner, 1983), and scores were converted to percent disease index (PDI) for analysis.

Disease assessment

The scoring of downy mildew disease incidence was started a month after planting and at fortnightly intervals (30, 45, 60, and 75 DAS) for four times until the plant growth cycle ended. A scoring of 0-9 scale was followed. The disease reaction of the genotype was classified into four groups based on their PDI data, i.e., 0- 20% (resistant), 21 to 40% (moderately resistant), 41 to 60% (susceptible), and >60% (highly susceptible) (Reddy, 2002). Disease score data of all the plants in each genotype has been converted to PDI using the following formula: Per cent disease index (PDI) was calculated with the help of the following formula.

$$PDI = \frac{Sum\ of\ numerical\ value}{Number\ of\ leaves\ graded \times Maximum\ rating} \times 100$$

Based on PDI, the disease reaction of the genotype will be classified into four groups according to the following scale (Reddy, 2002). Disease reaction was categorized based on percent disease index (PDI) values, wherein genotypes exhibiting 0 to 20% PDI were classified as resistant (R), those with 21 to 40% PDI as moderately resistant (MR), genotypes showing 41 to 60% PDI as susceptible (S), and those recording more than 60% PDI were considered highly susceptible (HS).

Area under the disease progress curve

Area under the disease progress curve (AUDPC) is another criterion that represents the speed of progression of the pathogen in plant tissue and is used to differentiate between resistant and susceptible genotypes. Disease incidence data recorded at a weekly interval were used to calculate the area under the disease progress curve (AUDPC) as a measure of quantitative disease resistance involving repeated disease assessments. The AUDPC was computed based on the disease scores using the following formula (Jeger and Rollinson 2001).

Table 1: List of cucumber genotypes used for screening of resistance against the downy mildew disease under the natural epiphytotic condition

S. No.	*Genotype*	*S. No.*	*Genotype*	*S. No.*	*Genotype*	*S. No.*	*Genotype*	*S. No.*	*Genotype*
1.	Mirpur	31.	DC-48	61.	IC-396662	91.	IC-347816	121.	EC-1184695
2.	Yogesh C-2	32.	DC-61	62.	EC-398512	92.	IIHR-27	122.	EC-1184697
3.	DC-401	33.	DC-92-1	63.	IIHR-82	93.	IIHR-375	123.	EC-1184698
4.	740-B-1	34.	DC-44	64.	IC-398675	94.	IC-394652	124.	EC-1184699
5.	Yogesh C-3	35.	DG-60	65.	IC-429942	95.	EC-1184714	125.	EC-1184700
6.	Super Salad	36.	DC-1-1	66.	IC-613475	96.	EC-1184653	126.	EC-1184701
7.	Punjab Navin	37.	WBC-39-1	67.	IC-345573	97.	EC-1184654	127.	EC-1184702
8.	Summer Green	38.	DC-40	68.	IIHR-336	98.	EC-1184655	128.	EC-1184703
9.	Calarib Mizo-7	39.	DC-106	69.	IC-432030	99.	EC-1184657	129.	EC-1184704
10.	Cucumber Beejo	40.	DC-605	70.	IC-345570	100.	EC-1184658	130.	EC-1184705
11.	Pahari Barsati	41.	WBC-29-1	71.	IC-423365	101.	EC-1184659	131.	EC-1184706
12.	Yogesh C-1	42.	WBC-39-2	72.	IC-341153	102.	EC-1184661	132.	EC-1184707
13.	EC-443605	43.	DC-55	73.	IC-326133	103.	EC-1184662	133.	EC-1184708
14.	DC-92-2	44.	DC-773	74.	IC-350202	104.	EC-1184664	134.	EC-1184709
15.	WBC-30	45.	DG-1-1	75.	IC-312851	105.	EC-1184667	135.	EC-1184710
16.	WBC-1-1	46.	DC-43	76.	IC-345635	106.	EC-1184668	136.	EC-1184711
17.	PCUC-8	47.	CCUH-8	77.	IC-526685	107.	EC-1184669	137.	EC-1184713
18.	WBC-22	48.	EOM-400	78.	IIHR-271	108.	EC-1184670	138.	Pusa Uday
19.	WBC-23-1	49.	HS-5	79.	IC-398521	109.	EC-1184671	139.	Pusa Long Green
20.	Kalayanpur Green	50.	Swarna Sheetal	80.	IC-354128	110.	EC-1184678	140.	Pahari Harit
21.	WBC-13	51.	EC-1041419	81.	IC-432027	111.	EC-1184681	141.	PI197086
22.	WBC-5	52.	EC-1041452	82.	IC-613484	112.	EC-1184682	142.	PI197087
23.	WBC-29-2	53.	DG-1-1	83.	IC-341130	113.	EC-1184683	143.	PI-197088
24.	WBC-35-2	54.	IC-613476	84.	IC-612082	114.	EC-1184687	144.	PI 330628
25.	WBC-21	55.	IC-432028	85.	IC-354358	115.	EC-1184688	145.	Punjab Naveen
26.	WBC-26	56.	IC-398523	86.	IC-613473	116.	EC-1184689	146.	Gol Kheera-1
27.	WBC-1	57.	IC-312852	87.	IC-339713	117.	EC-1184691	147.	Gol Kheera-2
28.	WBC-10	58.	IC-400685	88.	IC-345753	118.	EC-1184692	148.	IC-613461
29.	WBC-36-2	59.	IC-332344	89.	IC-352969	119.	EC-1184693		
30.	KPS-301	60.	IC-347785	90.	IC-976759	120.	EC-1130883		

$$\mathrm{Ak} = \sum_{i=1}^{Ni-1} \left(\frac{y_i + y_{i+1}}{2} \right) \left(t_{i+1} - t_i \right)$$

where y_i is the proportion of disease on the i th observation, t_i is the time (days) of observation expressed as days after sowing (DAS), and N is the total number of disease severity readings (PDI) taken throughout the experimental period.

Results

In the late Kharif season of 2024, a natural epiphytic screening of 148 cucumber genotypes against downy mildew was carried out at the experimental fields of ICAR–IIVR, Varanasi, using the susceptible checks Pusa Uday and Kalayanpur Green. The percent disease index (PDI) and the related area under the disease progress curve (AUDPC) showed significant variance across the assessed cucumber genotypes.

Among the 148 genotypes evaluated, only two genotypes, PI-197086 and PI-197088, were highly resistant, with PDI ranging from 0 to 20% and AUDPC values between 788.54 and 885.24 (Table 2; Figure 1). Four genotypes, Gol Kheera-1, Gol Kheera-2, IC-345573 and IC-613461, showed moderate resistance with PDI of 21 to 40% and AUDPC

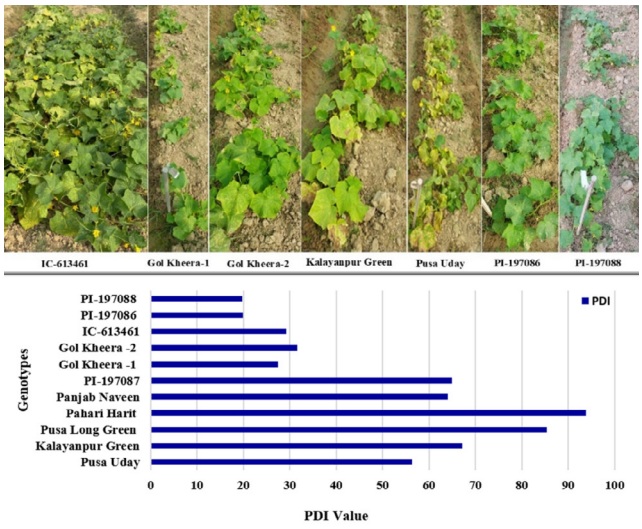

Figure 1: Disease reaction of cucumber genotypes and resistant and susceptible checks against downy mildew under natural epiphytotic conditions, showing representative disease symptoms and percent disease index (PDI).

ranging from 1048.93 to 1269.25 (Figure 1). Five genotypes (IC-332344, IIHR-82, IC-398675, Pusa Uday and PI-330628) were moderately susceptible, exhibiting PDI values of 41 to 60% and AUDPC between 2328.41 and 3084.66.

The majority of the genotypes evaluated fell into the highly susceptible category, with PDI exceeding 60%. This group showed a wide AUDPC range (from 2629.15 upwards) and included both local cultivars and advanced breeding lines, such as Mirpur, Yogesh C-2, Macher Sasa/DC-401, 740-B-1, Yogesh C-3, Super Salad, Punjab Navin, Summer Green, Calarib Mizo-7, Cucumber Beejo, Pahari Barsati, Yogesh C-1, EC-443605, DC-92-2, WBC-30, WBC-1-1, PCUC-8, WBC-22, WBC-23-1, Kalayanpur Green, WBC-13, WBC-5, WBC-29-2, WBC-35-2, WBC-21, WBC-26, WBC-1, WBC-10, WBC-36-2, KPS-301, DC-48, DC-61, DC-92-1, DC-44, DG-60, DC-1-1, WBC-39-1, DC-40, DC-106, DC-605, WBC-29-1, WBC-39-2, DC-55, DC-773, DG-1-1, DC-43, CCUH-8, EOM-400, HS-5, Swarna Sheetal, EC-1041419, EC-1041452, IC-613476, IC-432028, IC-398523, IC-312852, IC-400685, IC-347785, IC-396662, EC-398512, IC-429942, IC-613475, IIHR-336, IC-432030, IC-345570, IC-423365, IC-341153, IC-326133, IC-350202, IC-312851, IC-345635, IC-526685, IIHR-271, IC-398521, IC-354128, IC-432027, IC-613484, IC-341130, IC-612082, IC-354358, IC-613473, IC-339713, IC-345753, IC-352969, IC-976759, IC-347816, IIHR-27, IIHR-375, IC-394652, and a large set of exotic introductions (EC-1184714, EC-1184653, EC-1184654, EC-1184655, EC-1184657, EC-1184658, EC-1184659, EC-1184661, EC-1184662, EC-1184664, EC-1184667, EC-1184668, EC-1184669, EC-1184670, EC-1184671, EC-1184678, EC-1184681, EC-1184682, EC-1184683, EC-1184687, EC-1184688, EC-1184689, EC-1184691, EC-1184692, EC-1184693, EC-1130883, EC-1184695, EC-1184697, EC-1184698, EC-1184699, EC-1184700, EC-1184701, EC-1184702, EC-1184703, EC-1184704, EC-1184705, EC-1184706, EC-1184707, EC-1184708, EC-1184709, EC-1184710, EC-1184711, EC-1184713), along with Pusa Long Green, Pahari Harit, PI-197087 and Punjab Naveen (Table 3).

Area under disease progress curve

The AUDPC indicates the progress of the disease in a given crop growth period (Table 2). The resistant genotypes PI-197086 and PI-197088 showed less AUDPC values of 822.72 and 788.54, respectively, compared with other genotypes screened for resistance. The highest AUDPC value was recorded in genotype Pahari Harit 4257.33 with an average PDI of 93.75, followed by Pusa Long Green 3747.33 with an average PDI of 87.33, and the susceptible check was Pusa Uday 3084.66 with an average PDI of 56.34, and Kalayanpur Green 2873.21 with an average PDI of 67.11.

Discussion

The present study evaluates a total of 148 genotypes of cucumber against the Downy mildew disease caused by

Table 2: Scale to score of downy mildew disease incidence

Scale	*Percentage of disease*	*Description of scores*
0	0	No disease
1	0–3	Few small leaf lesions
2	3–6	Few lesions on few leaves with no stem lesions
3	6–12	Few lesions on few leaves or with superficial stem lesions
4	12–25	Few well-formed leaf lesions or superficial stem lesions
5	25 –50	Few well-formed leaf lesions or enlarging stem lesions
6	50 –75	Many large leaf lesions or deep stem lesions with abundant sporulation, or plant more than 50% defoliated
7	75– 87	Many large coalescing leaf or stem lesions, over 75% of plant area affected or defoliated
8	87– 99	Plants largely defoliated, leaves or stems with abundant sporulation lesions
9	100	Plants dead

Table 3: Grouping of cucumber genotypes according to plant disease index and AUDPC

PDI Range	*AUDPC Range*	*Genotypes*
0–20 %	788.54–885.24	PI-197086, PI-197088
21–40 %	1048.93–1269.25	Gol Kheera-1, Gol Kheera-2, IC-345573, IC-613461
41–60%	2328.41–3084.66	IC-332344, IIHR-82, IC-398675, Pusa Uday, PI-330628
>60%	2629.15–4257.33	Mirpur, Yogesh C-2, Macher Sasa/DC-401, 740-B-1, Yogesh C-3, Super Salad, Punjab Navin, Summer Green, Calarib Mizo-7, Cucumber Beejo, Pahari Barsati, Yogesh C-1, EC-443605, DC-92-2, WBC-30, WBC-1-1, PCUC-8, WBC-22, WBC-23-1, Kalayanpur Green, WBC-13, WBC-5, WBC-29-2, WBC-35-2, WBC-21, WBC-26, WBC-1, WBC-10, WBC-36-2, KPS-301, DC-48, DC-61, DC-92-1, DC-44, DG-60, DC-1-1, WBC-39-1, DC-40, DC-106, DC-605, WBC-29-1, WBC-39-2, DC-55, DC-773, DG-1-1, DC-43, CCUH-8, EOM-400, HS-5, Swarna Sheetal, EC-1041419, EC-1041452, DG-1-1, IC-613476, IC-432028, IC-398523, IC-312852, IC-400685, IC-347785, IC-396662, EC-398512, IC-429942, IC-613475, IIHR-336, IC-432030, IC-345570, IC-423365, IC-341153, IC-326133, IC-350202, IC-312851, IC-345635, IC-526685, IIHR-271, IC-398521, IC-354128, IC-432027, IC-613484, IC-341130, IC-612082, IC-354358, IC-613473, IC-339713, IC-345753, IC-352969, IC-976759, IC-347816, IIHR-27, IIHR-375, IC-394652, EC-1184714, EC-1184653, EC-1184654, EC-1184655, EC-1184657, EC-1184658, EC-1184659, EC-1184661, EC-1184662, EC-1184664, EC-1184667, EC-1184668, EC-1184669, EC-1184670, EC-1184671, EC-1184678, EC-1184681, EC-1184682, EC-1184683, EC-1184687, EC-1184688, EC-1184689, EC-1184691, EC-1184692, EC-1184693, EC-1130883, EC-1184695, EC-1184697, EC-1184698, EC-1184699, EC-1184700, EC-1184701, EC-1184702, EC-1184703, EC-1184704, EC-1184705, EC-1184706, EC-1184707, EC-1184708, EC-1184709, EC-1184710, EC-1184711, EC-1184713, Pusa Long Green, Pahari Harit, PI-197087, Punjab Naveen

the fungus *Ps. Cubensis*. The clear stratification of genotypes into distinct PDI and AUDPC classes indicates substantial variability for resistance to the target disease within the evaluated cucumber germplasm (Figure 1). Only two highly resistant genotypes, PI197086 and PI197088, fell in the lowest PDI (0–20%) and AUDPC (788.54–885.24) class; their consistently low disease severity and slow disease progress suggest stable and potentially durable resistance that can be exploited as primary donor parents in resistance breeding programmes. The small number of resistant and moderately resistant genotypes, contrasted with the large proportion classified as highly susceptible (PDI > 60%), reflects the vulnerability of the existing cucumber gene pool and the narrow genetic base for resistance in cultivated and widely grown types. Many popular or regionally adapted cultivars and breeding lines, such as Mirpur, Punjab Navin/Punjab Naveen, Pusa Long Green, Summer Green and several WBC and DC lines, showed high PDI and elevated AUDPC values, indicating rapid disease development and poor field tolerance, which is consistent with earlier observations in cucurbits that high yielding or widely cultivated varieties often lack adequate resistance and require introgression from resistant or exotic sources. The moderate resistance observed in Gol Kheera1, Gol Kheera2, IC345573 and IC613461 (PDI 21–40% with comparatively lower AUDPC) is also noteworthy;. However, these do not reach the resistance level of PI197086 and PI197088, they may harbour different or complementary resistance loci and can serve as secondary donors. The identification of resistant and moderately resistant cucumber genotypes in the present study is consistent with earlier reports. Bommesh et al. (2017) and Pitchaimuthu et al. (2012) also documented resistant genotypes against downy mildew, while Bhutia et al. (2005), after screening 114 genotypes, reported ten resistant, 18 moderately resistant, 37 moderately susceptible and 49 susceptible entries; other researchers, including Criswell et al. (2008), Reshmi (2006) and Wan et al. (2010), have likewise identified resistant sources. According to Petrov et al. (2000), resistant plants show small, chlorotic, watersoaked lesions, whereas susceptible cultigens exhibit pronounced yellowing, chlorosis and heavy sporulation; the reaction patterns observed in the present study closely correspond to these descriptions. Our findings also agree with reports from Poland and North Carolina, where only 20 out of 1,300 cucumber cultigens screened from 2005 to 2009 showed high resistance and none were immune (Call 2012), reaffirming the scarcity of strong resistance to downy mildew in cucumber germplasm and highlighting a few promising lines, particularly PI197986 and PI197088, for resistance breeding. The disease progress curves showed large variation in average PDI among genotypes under field conditions, and, in line with Lebeda (1999), field resistance was associated with delayed onset of infection and a slower rate of disease progression under high disease pressure. AUDPC quantified the resistance reaction over time and was similar among most genotypes, except for four notable entries with clearly lower values, indicating that effective resistance sources are rare. Because the pathogen is obligate and strongly influenced by the environment, pathogen progression is generally slower in resistant genotypes, which delay and limit colonisation and symptom expansion (Mhada et al. 2015); low temperatures can delay symptom development and leaf colonisation, whereas higher temperatures can hasten lesion formation and chlorosis, sometimes inhibiting pathogen growth (Cohen 1977). Neykov and Dobrev (1987) described genotypes with small necrotic lesions covering less than 25% of leaf area as resistant, and the present findings are in line with those

of Bjoern & Kampmann (2000). Cohen et al. (2000). Low AUDPC at weekly intervals, combined with lower sporangial counts and reduced symptomatic leaf area, reflects "slow mildewing" moderate resistance, which has often proved more durable than complete resistance, as reported in watermelon (Tetteh et al. 2010).

Combining such moderate resistance sources with highly resistant genotypes through hybridization and selection could enhance the durability and breadth of resistance, particularly if underlying mechanisms differ (e.g., partial resistance, slowed disease development or tolerance). The large cluster of genotypes in the moderately susceptible (41–60% PDI) and highly susceptible (>60% PDI) groups, including both indigenous IC lines and exotic EC accessions, suggests that resistance is neither widespread nor randomly distributed in available germplasm (Figure 1); moreover, the wide AUDPC range among susceptible entries indicates substantial variability in disease progress rate even in highly affected genotypes. Some lines with high final PDI but intermediate AUDPC may still be useful as parents for desirable agronomic or horticultural traits, provided resistance is introgressed from identified resistant sources. From a practical perspective, these results underscore the urgent need to incorporate resistance into commercially important cultivars, as relying solely on chemical control is unsustainable due to economic, environmental and resistance management concerns. The strong resistance expressed by PI197086 and PI197088 under field conditions implies that these accessions may carry major resistance genes or favourable combinations of minor genes; their systematic use in crossing programmes, coupled with phenotypic or marker assisted selection, could speed development of resistant hybrids and open-pollinated varieties suited to diverse agroclimatic zones. At the same time, the high proportion of susceptible entries among both IC and EC accessions underscores the importance of continued germplasm exploration and prebreeding, including the screening of wild relatives and underutilised cucurbit species to broaden the resistance base.

Overall, the findings demonstrate that although most of the evaluated cucumber germplasm is highly susceptible to downy mildew, a few accessions, particularly PI197086 and PI197088, offer promising and urgently needed resistance sources; their strategic deployment, together with moderate resistance sources like Gol Kheera1, Gol Kheera2, IC345573 and IC613461, will be essential for developing durable, disease resistant cucumber cultivars and for enhancing the resilience and sustainability of cucumber production.

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सारांश

खीरे में डाउनी मिल्ड्यू के प्रति प्रतिरोध के स्रोतों की पहचान के उद्देश्य से यह प्रयोग किया गया। इसमें कुल 148 जीनोटाइप्स तथा संवेदनशील और प्रतिरोधी मानक किस्मों का मूल्यांकन प्राकृतिक रूप से रोग-प्रसार वाली (एपिफाइटोटिक) परिस्थितियों में किया गया। आकलन के लिए 'प्रतिशत रोग सूचकांक' (प्र.रो.सू) और 'रोग प्रगति वक्र का क्षेत्रफल' (AUDPC) को आधार बनाया गया। प्रत्येक जीनोटाइप से यादृच्छिक रूप से चुने गए 10 पौधों पर 0–9 के पैमाने पर रोग की तीव्रता का मूल्यांकन पखवाड़े के अंतराल पर, फसल की समाप्ति तक कुल चार बार किया गया। औसत प्र.रो.सू के आधार पर जीनोटाइप्स को चार वर्गों में विभाजित किया गया: अत्यधिक प्रतिरोधी (0–20%), मध्यम प्रतिरोधी (21–40%), मध्यम संवेदनशील (41–60%) तथा अत्यधिक संवेदनशील (>60%)। जीनोटाइप्स में रोग प्रतिक्रिया के स्तर पर उल्लेखनीय भिन्नता देखी गई। केवल दो जीनोटाइप्स, पीआई-197086 और पीआई-197088, अत्यधिक प्रतिरोधी पाए गए; इनमें प्र.रो.सू (≤20%) और AUDPC (788.54–885.24) मान सबसे कम थे, जो रोग के धीमे प्रसार का संकेत देते हैं। चार जीनोटाइप्स, गोल खीरा -1, गोल खीरा-2, आईसी-345573 और आईसी -613461 मध्यम प्रतिरोधी (AUDPC 1048.93–1269.25) पाए गए, जबकि पाँच जीनोटाइप्स, आईसी -332344, आईआईएचआर -82, आईसी -398675, पूसा उदय और पीआई-330628 मध्यम संवेदनशील रहे। शेष अधिकांश जीनोटाइप्स, जिनमें कई व्यावसायिक किस्में और उन्नत पंक्तियाँ शामिल थीं, अत्यधिक संवेदनशील (प्र.रो.सू >60%) पाए गए। संवेदनशील जीनोटाइप्स की अधिकता यह दर्शाती है कि उपलब्ध खीरा जर्मप्लाज्म में रोग के प्रति प्रतिरोध का स्तर सीमित है और आनुवंशिक विविधता अपेक्षाकृत कम है। पीआई-197086 और पीआई-197088 प्रभावी प्रारंभिक दाता के रूप में उपयोगी हैं, जबकि मध्यम प्रतिरोधी जीनोटाइप्स दीर्घकालिक और टिकाऊ प्रतिरोध विकसित करने हेतु अतिरिक्त आनुवंशिक विविधता प्रदान करते हैं।