



Screening of okra (*Abelmoschus esculentus*) genotypes for resistance to powdery mildew caused by *Golovinomyces cichoracearum*

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Received: 15 August 2025; Accepted: 08 July 2026

ABSTRACT

Powdery mildew caused by *Golovinomyces cichoracearum* (DC.) V.P. Heluta, remains a major foliar disease, significantly reducing the yield of okra (*Abelmoschus esculentus* L.) under conducive environmental conditions. Identification of resistant okra genotypes offers an eco-friendly, sustainable and cost-effective approach for the management of powdery mildew. The present study was carried out at Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu with aim to evaluate okra genotypes for resistance against powdery mildew and identify resistance resources. The study evaluated 15 okra genotypes, including commercial varieties and hybrids, for resistance against powdery mildew under pot culture conditions during the *samba* seasons of 2022 and 2023. Disease severity was recorded at 50, 65 and 80 days after sowing (DAS) and quantified as percent disease index (PDI) using a 0–9 disease rating scale. Considerable and statistically significant variability was observed among the genotypes in disease severity and progression, allowing clear discrimination of resistance responses. Four genotypes, namely 'Arka Nikhita', 'Kasi Chaman', 'Pusa Makhmali' and 'Pusa A4' exhibited complete resistance, showing no visible symptoms or sporulation during both years of evaluation, confirming stable, resistant sources. In contrast, 'Sakthi' was categorised as highly susceptible, recording the highest mean PDI of 76.94%. This high susceptibility was associated with the highest conidial count (511.60/microscopic field) and the fastest apparent infection rate ($r = 0.1298$). Furthermore, seven genotypes including 'Raadhika Hybrid Okra' (72.79% PDI) and Farmers' variety (63.35% PDI), were classified as susceptible while three genotypes, namely 'Arka Abhay', 'COBH h1' and 'Traditional variety-Elephant Tusk Okra', showed moderate susceptibility. The simultaneous assessment of PDI, disease progression rates and conidial density proved reliable for discriminating genotypic resistance levels. This investigation successfully identified stable and resistant genotypes that can be utilised effectively in resistance breeding programmes and as components of integrated disease management (IDM) strategies for sustainable management.

Keywords: Disease severity, Percent disease index, Resistant genotypes, Sustainable management

Okra (*Abelmoschus esculentus* L.) is an important vegetable crop widely cultivated in tropical and subtropical regions. Among the diseases affecting okra, powdery mildew caused by *Golovinomyces cichoracearum* (DC.) V.P. Heluta is one of the most destructive foliar diseases, causing significant yield losses ranging from 17% to 86.6% under favourable environmental conditions (Sridhar and Sinha 1989, Lokesh *et al.* 2025). The disease initially appears as small white powdery patches on older leaves, which gradually spreads to younger foliage, forming a greyish-white coating that leads to necrosis, wilting and premature defoliation. Banvasi *et al.* (2020) reported a mean

disease incidence of 60.42% in okra under field conditions. Globally, powdery mildew and related fungal pathogens are responsible for considerable economic losses in agricultural production, with estimated annual losses of approximately US\$ 6.3 billion (Gan *et al.* 2025).

G. cichoracearum is an obligate biotrophic pathogen that derives nutrition from living epidermal tissues. Under favourable environmental conditions, the conidia germinate and penetrate host cells through appressoria and haustoria, resulting in rapid airborne secondary infection (Sundaramoorthy *et al.* 2025). Environmental factors, particularly temperature and relative humidity, play a critical role in the initiation and progression of powdery mildew disease (Diwakar *et al.* 2024). The optimum conditions for disease development range between 16.33–30.93°C, with relative humidity levels of 53.43–84.56% (Kavyashree *et al.* 2022). A regional survey conducted in Tamil Nadu reported disease severity as high as 90.13% in certain locations

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(Rajalakshmi *et al.* 2016). Similarly, Bachihal *et al.* (2013) demonstrated that yield losses in untreated plots (43.09 q/ha) were considerably higher than those recorded in treated plots (78.30 q/ha), indicating the economic importance of effective disease management.

Although fungicides are commonly used for the management of powdery mildew, repeated application increases production cost and may lead to environmental hazards and development of fungicide resistance. In this context, host plant resistance offers an economical, eco-friendly and sustainable approach for disease management. However, information on stable resistant sources against powdery mildew in okra under pot culture conditions remains limited. Therefore, the present investigation was undertaken to evaluate okra genotypes for resistance against powdery mildew and to identify resistant sources suitable for resistance breeding programmes and sustainable disease management in disease-prone regions.

MATERIALS AND METHODS

Experimental setup: The experiment was conducted during the *samba* seasons of 2022 and 2023 at Faculty of Agriculture, Annamalai University, Annamalai Nagar, (11°34'N, 79°72'E; at an elevation of 5.7 m asml), Tamil Nadu. The region receives an average annual rainfall of 1,200–1,400 mm, providing favourable climatic conditions for crop cultivation and disease development. The experiment was conducted under completely randomised design (CRD) with three replications under pot culture conditions. Regular irrigation was provided to maintain favourable humidity for disease development and no fungicidal treatments were applied during the experimental period. The plants were exposed to natural epiphytotic conditions for powdery mildew development and no artificial inoculation was carried out during the study. The experimental material comprised of 15 okra genotypes, including varieties and hybrids collected from different sources to ensure wide genetic variability (Table 1). In addition, hybrids and traditional landraces were collected from farming communities of Tamil Nadu to represent region-specific variability and field performance.

The Farmers' variety refers to a locally cultivated farmer-selected genotype collected from Krishnagiri district, whereas the traditional variety corresponds to the landrace locally known as 'Elephant Tusk Okra' collected from Salem district.

Screening of okra genotypes: Fifteen okra genotypes were screened for resistance against powdery mildew under pot culture conditions. Seeds were sown in earthen pots containing sterilised potting mixture and 3 plants/pot were maintained after thinning. Disease severity observations were recorded at 50, 65 and 80 days after sowing (DAS). For disease assessment, 25 leaves were randomly selected from each genotype and evaluated using a 0–9 disease rating scale. The percent disease index (PDI) was subsequently calculated based on disease severity scores. Detailed observations on symptom development, disease spread and sporulation were also recorded to differentiate the resistance response

Table 1 Source of collection of okra genotypes

Genotypes	Source of collection	Place
<i>Arka Anamika</i>	ICAR-IIHR	Bengaluru, Karnataka
<i>Arka Abhay</i>	ICAR-IIHR	Bengaluru, Karnataka
<i>Arka Nikhita</i>	ICAR-IIHR	Bengaluru, Karnataka
<i>Pusa Sawani</i>	ICAR-IARI	New Delhi
<i>Sakthi</i>	TNAU	Coimbatore, Tamil Nadu
<i>Parbhani Kranti</i>	VNMKV	Parbhani, Maharashtra
<i>Kasi Chaman</i>	ICAR-IIVR	Varanasi, Uttar Pradesh
<i>Akola Bahar</i>	PDKV	Akola, Maharashtra
<i>Pusa Makhmali</i>	ICAR-IARI	New Delhi
<i>Pusa A4</i>	ICAR-IARI	New Delhi
<i>Raadhika Hybrid</i>	Farmers seeds	Salem, Tamil Nadu
Farmers' local selection	Farmers seeds	Krishnagiri, Tamil Nadu
Traditional landrace (Elephant Tusk Okra)	Farmers seeds	Salem, Tamil Nadu
<i>Selvam Hybrid</i>	Farmers seeds	Cuddalore, Tamil Nadu
COBH h 1	TNAU	Coimbatore, Tamil Nadu

of the genotypes under uniform environmental conditions (Diwakar *et al.* 2020).

Disease assessment: The severity of powdery mildew disease was assessed for each entry using a 0–9 scale based on disease score chart for powdery mildew (McKinney 1923). The leaf area infected (%) was recorded and were graded as 0 for no signs or symptoms; 1 for 0–10% infection; 3 for 11–15% infection; 5 for 16–25% infection; 7 for 26–50% infection; and 9 for >50% infection. The observations were then converted into the percent disease index (PDI) using McKinney's formula:

$$\text{PDI} = \frac{\sum \text{Disease ratings}}{\text{Total number of leaves observed} \times \text{Maximum disease grade}} \times 100$$

The Disease Severity Grading Scale by Jamadar and Desai (1997) was used for categorising powdery mildew infection levels based on the percentage of leaf area affected (Table 2). Disease severity, apparent infection rate (*r*) and conidial density were assessed simultaneously to obtain a comprehensive understanding of genotypic resistance against powdery mildew. PDI indicates the extent of disease development, whereas the apparent infection rate reflects the speed of disease progression over time. In addition, conidial density provides information on pathogen sporulation and multiplication on host tissues. The combined assessment of these parameters improves the reliability of differentiating resistant and susceptible genotypes under uniform environmental conditions. The disease progression

Table 2 Disease severity grading scale for powdery mildew

Grade	(% leaf area infected)	Description
1	1–10% infection	Resistant
2	10–25% infection	Moderately resistant
3	25–50% infection	Moderately susceptible
4	50–75% infection	Susceptible
5	>75% infection	Highly susceptible

rate (r) at different intervals was determined using the formula provided by Van der Plank (1963):

$$r = \frac{2.3}{t_2 - t_1} \left(\log \frac{X_2}{1 - X_2} - \log \frac{X_1}{1 - X_1} \right)$$

Where r , apparent infection rate or disease spread; X_1 , Percent disease index at time t_1 ; X_2 , Percent disease index at time t_2 ; $t_2 - t_1$, Time interval (days) between two consecutive observations.

Microscopic observation of the pathogen: Microscopic examination of the pathogen was carried out using lactophenol blue staining. Infected leaf samples showing typical powdery mildew symptoms were gently scraped to collect conidia, which were stained with lactophenol blue and observed under a stereo binocular microscope and compound microscope at 10 $\times$ and 40 $\times$ magnifications. Morphological characteristics such as conidial shape, size and arrangement were compared with standard taxonomic descriptions to confirm the identity of *G. cichoracearum*, the causal organism of powdery mildew in okra (Barnett and Hunter 1998).

Statistical analysis: The experimental data was statistically analysed using WASP (Web Agri Stat Package) Version 2.0 developed by ICAR-Central Coastal Agricultural Research Institute, Goa. Analysis of variance (ANOVA) was performed to determine the significance of treatment differences at 5% probability level. Treatment means were compared using Duncan's Multiple Range Test (DMRT) as described by Gomez and Gomez (1984).

RESULTS AND DISCUSSION

Screening of different okra genotypes for powdery mildew resistance: Screening of 15 okra genotypes, including varieties and hybrids, for resistance against powdery mildew caused by *G. cichoracearum* under pot culture conditions during the *samba* seasons of 2022 and 2023 revealed significant variation in disease reaction among the genotypes (Table 3). The observed variability indicated the potential for identifying stable sources of resistance for sustainable management of powdery mildew in okra. Resistance responses of the genotypes were evaluated based on PDI, apparent infection rate (r) and conidial density.

Resistant genotypes exhibited lower conidial density and slower disease progression compared to susceptible genotypes, indicating restricted pathogen multiplication and sporulation. In contrast, susceptible entries showed

higher conidial production accompanied by increased disease severity and rapid epidemic development. Reduced sporulation is considered an important indicator of host resistance against powdery mildew pathogens, as it limits secondary spread of the disease under favourable environmental conditions. Similar relationships between reduced conidial density and enhanced resistance have been reported in powdery mildew patho-systems by Kulkarni *et al.* (2015).

Stable resistant sources: Four genotypes, namely 'Arka Nikhita', 'Kasi Chaman', 'Pusa Makhmali' and 'Pusa A4', exhibited complete resistance with a mean PDI of 0% (Table 3). These genotypes showed no visible symptoms or sporulation during both years of evaluation, indicating stable resistance against powdery mildew. The present findings are in agreement with Prabu *et al.* (2007), who reported resistant reactions in related *Abelmoschus* species against powdery mildew pathogens.

Highly susceptible genotype: In contrast, the genotype 'Sakthi' was categorised as highly susceptible (HS), recording the highest mean PDI of 76.94%. The genotype also exhibited the highest conidial density (511.60/microscopic field) and the fastest apparent infection rate ($r = 0.1298$) among all the tested genotypes. The high disease severity, rapid disease progression and increased sporulation observed in 'Sakthi' indicates its high susceptibility to powdery mildew.

Susceptible and moderately susceptible genotypes: Seven genotypes were classified as susceptible (S), exhibiting mean PDI values between 50% and 75%. This group included 'Raadhika Hybrid Okra' (72.79% PDI), 'Akola Bahar' (69.88% PDI), Farmers' variety (63.35% PDI), 'Selvam Hybrid Okra' (62.42% PDI), 'Pusa Sawani' (62.30% PDI), 'Arka Anamika' (53.90% PDI) and 'Parbhani Kranti' (52.96% PDI) (Table 3).

Three genotypes were categorised as moderately susceptible (MS), with PDI values ranging from 25% to 50%. These included 'COBH h 1' (49.19% PDI), 'Arka Abhay' (44.88% PDI) and Traditional variety ('Elephant Tusk Okra') (40.61% PDI). No genotype was categorised as moderately resistant (MR), indicating the absence of intermediate resistance among the evaluated genotypes (Table 3).

Disease severity, expressed as PDI, increased progressively from 50 to 80 DAS in susceptible and moderately susceptible genotypes. The simultaneous assessment of PDI, apparent infection rate (r) and conidial density was effective in differentiating resistant and susceptible genotypes. The apparent infection rate ranged from 0.0099 to 0.1298, with the highly susceptible genotype 'Sakthi' recording the maximum value, whereas the traditional variety ('Elephant Tusk Okra') exhibited the lowest r -value among the moderately susceptible genotypes. Higher disease severity and faster disease progression were associated with increased conidial density (Fig. 1). In contrast, relatively resistant genotypes exhibited lower conidial production and restricted sporulation, indicating reduced pathogen multiplication and disease spread.

Table 3 Screening of different okra genotypes for powdery mildew (2022 and 2023)

Genotypes	Powdery mildew intensity (PDI) 2022			Mean PDI 2022	Powdery mildew intensity (PDI) 2023			Mean PDI 2023	Mean PDI 2022 and 2023	Disease reaction	Mean 'r' values	Nos. of conidia/ microscopic field
	50 DAS	65 DAS	80 DAS		50 DAS	65 DAS	80 DAS					
<i>Arka Anamika</i>	48.23	55.00	63.65	55.63 ^f (48.23)	48.20	55.30	53.00	52.16 ^g (45.65)	53.90 ^f (47.06)	S	0.0484	326.55
<i>Arka Abhay</i>	41.83	45.00	47.06	44.63 ^{hi} (41.83)	42.20	46.10	47.05	45.12 ^{hi} (42.27)	44.88 ^c (42.27)	MS	0.0163	239.45
<i>Arka Nikhita</i>	-	-	-	-	-	-	-	-	-	R	-	-
<i>Pusa Sawani</i>	50.00	55.00	72.00	58.50 ^{ef} (49.89)	60.00	64.80	55.10	62.30 ^{ef} (52.40)	62.30 ^h (52.40)	S	0.0724	386.50
<i>Sakthi</i>	58.59	70.00	88.50	76.36 ^a (58.59)	72.00	78.10	77.70	76.94 ^{ab} (61.21)	76.94 ^k (61.21)	HS	0.1298	511.6
<i>Parbhani Kranti</i>	44.55	49.00	54.15	49.23 ^g (44.55)	50.20	54.10	54.60	52.96 ^f (46.23)	52.96 ^e (46.23)	S	0.0295	275.65
<i>Kasi Chaman</i>	-	-	-	-	-	-	-	-	-	R	-	-
<i>Akola Bahar</i>	53.21	64.00	75.15	64.12 ^{cd} (53.21)	66.30	71.20	72.10	69.88 ^{bc} (57.33)	69.88 ^{jk} (57.33)	S	0.0750	395.60
<i>Pusa Makhmali</i>	-	-	-	-	-	-	-	-	-	R	-	-
<i>Pusa A4</i>	-	-	-	-	-	-	-	-	-	R	-	-
<i>Raadhika Hybrid Okra</i>	54.87	67.00	78.68	66.85 ^{bc} (54.87)	69.40	73.90	74.80	72.79 ^b (52.47)	72.79 ^j (58.66)	S	0.0851	419.0
Farmers variety	56.00	69.00	84.00	69.68 ^{ab} (56.59)	61.00	66.70	67.00	63.35 ^{de} (52.93)	63.35 ⁱ (52.93)	S	0.1086	457.0
Traditional landrace ('Elephant Tusk Okra')	40.21	41.50	43.35	41.68 ⁱ (40.21)	37.10	42.00	42.70	40.61 ⁱ (39.60)	40.61 ^a (39.60)	MS	0.0099	218.30
<i>Selvam Hybrid Okra</i>	51.34	61.00	70.60	60.98 ^{de} (51.34)	58.90	65.40	62.90	62.42 ^{cd} (52.47)	62.42 ^h (52.47)	S	0.0631	368.0
COBH h1	45.00	48.00	50.63	47.88 ^{gh} (43.78)	45.00	50.10	50.50	49.19 ^{gh} (44.25)	49.19 ^d (44.25)	MS	0.0173	256.70

Values are means of three replications. Means followed by a common letter are not significantly different at 5% level. S, Susceptible; MS, Moderately susceptible; HS, Highly susceptible; R, Resistant; HR, Highly Resistant; -, Absence of disease symptoms; Mean 'r', mean of apparent infection rate values for 2022 and 2023; DAS, Days after sowing.

The resistance responses observed in the present investigation are consistent with previous reports of Diwakar *et al.* (2020) who reported reduced disease severity in resistant genotypes compared to susceptible local varieties under field conditions. Similarly, Ashwini *et al.* (2023) identified genotypes exhibiting lower disease severity against powdery mildew. The significant variability observed among the evaluated genotypes in the present study indicates the availability of useful resistance sources that may be effectively utilised in resistance breeding programmes for sustainable management of powdery mildew in okra.

The present investigation revealed considerable variability in the resistance response of okra genotypes against powdery mildew caused by *G. cichoracearum*

under pot culture conditions during the *samba* season of 2022 and 2023. Among the 15 evaluated genotypes, '*Arka Nikhita*', '*Kasi Chaman*', '*Pusa Makhmali*' and '*Pusa A4*' consistently exhibited complete resistance with the absence of visible symptoms and sporulation throughout the study period. In contrast, the genotype '*Sakthi*' recorded the highest disease severity, conidial density and apparent infection rate, indicating its high susceptibility to powdery mildew infection.

The assessment of PDI, apparent infection rate (r) and conidial density collectively proved to be effective in differentiating resistant and susceptible genotypes. Resistant genotypes exhibited reduced disease severity, slower disease progression and lower sporulation compared to susceptible

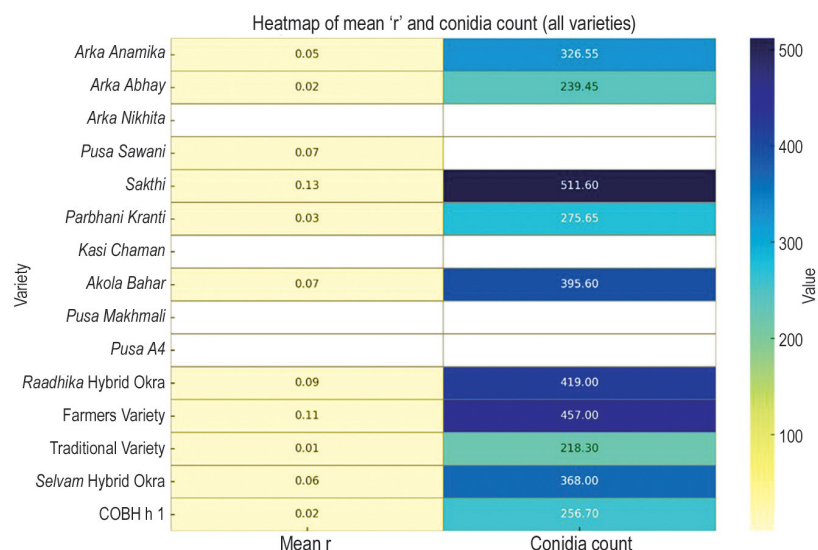


Fig. 1 Heatmap of mean 'r' and conidia count.

Mean 'r', Mean of apparent infection rate values for 2022 and 2023.

entries, indicating restricted pathogen multiplication and spread. The observed variability among the genotypes suggests the presence of useful genetic resistance sources that can be effectively exploited in future resistance breeding programmes.

The identified resistant genotypes can serve as valuable donor sources for the development of powdery mildew-resistant okra cultivars suitable for cultivation in disease-prone regions. Furthermore, incorporation of resistant varieties into integrated disease management (IDM) strategies can reduce dependence on chemical fungicides, minimise environmental hazards and promote sustainable crop protection practices. Therefore, the resistant genotypes identified in the present investigation may contribute significantly towards sustainable okra production and long-term management of powdery mildew disease.

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