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Elevated Air Temperature Suppresses Powdery Mildew Development in Cowpea

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ABSTRACT

Cowpea production can be severely affected by powdery mildew, a disease whose epidemiology is highly influenced by environmental conditions. In the context of climate change, understanding the effects of increasing temperatures on disease development is essential. In this study, 12 cowpea cultivars were evaluated under two daily temperature regimes: 20°C min–26°C average–33°C max (current condition) and 24.8°C min–30.8°C average–37.8°C max (warming scenario, +4.8°C). The experiment was conducted in growth chambers under a completely randomized design, with standardized inoculation. Evaluations were conducted on disease severity, area under the disease progress curve (AUDPC), number of lesions per leaf, number of conidia per counting field and conidial germination. Increased temperature prolonged the incubation period (i.e., from 7 to 9 days) and significantly reduced disease severity, AUDPC, lesion number, number of conidia per counting field and germination. Multivariate analysis indicated that temperature was the primary factor structuring disease response patterns, with limited differentiation among cultivars under the warming scenario. No cultivar showed resistance to the powdery mildew. The reduction in disease development is primarily attributed to the direct inhibitory effect of high temperature on pathogen development rather than to plant host resistance mechanisms. These results highlight the importance of temperature as a key driver of powdery mildew epidemiology under climate change conditions.

1 | Introduction

Cowpea (*Vigna unguiculata*) is a legume of great socioeconomic importance, especially for family farming in the north and northeast regions of Brazil (Freire Filho et al. 2020). Its wide adaptability to different soil and climate conditions, combined with its high nutritional value, makes cowpea an essential component in the diet of many families (Jayathilake et al. 2018).

However, in recent decades, rising global average temperatures and changes in precipitation patterns, including reduced water availability, have caused significant changes in agricultural systems, with direct effects on productivity (FAO 2021; IPCC 2023). Furthermore, climate change directly influences plant disease dynamics, as temperature impacts pathogen development, host susceptibility and epidemic progression.

In cowpea, these environmental changes represent an additional challenge, particularly in the management of climate-sensitive diseases such as powdery mildew. This disease, caused by the obligate biotrophic fungus, *Erysiphe vignae*, characterized by white powdery growth on leaves, stems and pods, reducing the photosynthetically active area and compromising plant

development and productivity (Braun and Cook 2012). Powdery mildew is most prevalent at temperatures between 14°C and 31°C and relative humidity between 55% and 95%. However, temperatures above this optimal range may suppress key stages of pathogen development, such as conidial germination and infection establishment.

In addition to its agronomic impacts, plant diseases, such as powdery mildew, pose a threat to food security and farmer income, especially in tropical regions where cowpea is cultivated under low-input systems (Omomowo and Babalola 2021). Given this scenario, it is essential to adopt adaptive strategies, including adjustments in cropping systems and improved epidemiological monitoring to mitigate disease outbreaks.

Although climate change is often associated with increased disease risk, powdery mildew pathogens exhibit well-defined thermal limits, and elevated temperatures can suppress disease development. Therefore, understanding pathogen-specific thermal responses is essential to correctly interpret disease dynamics under global warming scenarios.

Thus, this study aimed to evaluate the effect of increasing temperature on the epidemiology of powdery mildew in cowpea cultivars under controlled environmental conditions.

2 | Materials and Methods

2.1 | Experimental Conditions

The experiment was conducted in controlled-environment growth chambers, with set points for temperature, humidity and photoperiod. The plants were maintained in two temperature regimes (20°C–26°C–33°C and 24.8°C–30.8°C–37.8°C). The 20°C–26°C–33°C regime corresponds to the average values of the minimum, average and maximum temperatures of the sub-middle region of the São Francisco valley, which vary from 18°C to 22°C, 25°C to 27°C and 32°C to 34°C, respectively. The 24.8°C–30.8°C–37.8°C regime corresponds to the average temperature of the region, with an increase of 4.8°C, which corresponds to the simulation of the temperature increase, based on the scenarios brought by the IPCC (2021).

2.2 | Plant Material

The cowpea cultivars used in this study were developed by the Brazilian Agricultural Research Corporation (Embrapa), mainly by the Embrapa Meio-Norte (Teresina, PI) and Embrapa Semiárido (Petrolina, PE) breeding programmes. These cultivars are adapted to different agroecological conditions of Brazil, particularly the northeast semi-arid region and the Cerrado, with several cultivars specifically developed for the São Francisco Valley under irrigated and rain-fed conditions.

The main characteristics and origin of the cultivars used in this study are presented in Table S1.

2.3 | Experimental Design

The experimental design used was completely randomized in a 12×2 factorial scheme (i.e., cultivars × temperature regimes), with three replicates. Cowpea cultivars BRS Acauã, BRS Carijó, BRS Guariba, BRS Gurguéia, BRS Itaim, BRS Juruá, BRS Pajeú, BRS Potengi, BRS Pujante, BRS Rouxinol, BRS Tapaihum and BRS Tumucumaque were used. In the thermal regime 20°C–26°C–33°C the temperature variation throughout the day was applied as follows: 20°C from 8 PM to 6 AM, 26°C from 6 AM to 10 AM, 33°C from 10 AM to 3 PM, and 26°C from 3 PM to 8 PM. For the 24.8°C–30.8°C–37.8°C regime, the temperature variation was 24.8°C from 8 PM to 6 AM, 30.8°C from 6 AM to 10 AM, 37.8°C: from 10 AM to 3 PM, and 30.8°C: from 3 PM to 8 PM. Relative humidity was maintained at 50%–60%.

2.4 | Plant Growth Conditions

The experimental unit consisted of one pot containing a single plant. Three seeds of each cowpea cultivar were sown in 500 mL plastic pots filled with commercial substrate and maintained in growth chambers under different temperature regimes. After germination, seedlings were thinned to one plant per pot. Inoculation was performed at the V3 phenological stage (first fully expanded compound leaf). Non-inoculated control plants were maintained under the same environmental conditions to ensure that observed symptoms were exclusively associated with pathogen inoculation.

2.5 | Pathogen and Inoculation

To prepare the inoculum, cowpea leaves showing powdery mildew symptoms were collected, and conidia were obtained by gently scraping the lesions with a soft-bristled brush into distilled water containing 0.001% Tween 20. Although powdery mildew pathogens are typically dispersed as dry conidia, the use of aqueous suspension with Tween 20 has been reported as an effective method for uniform inoculation under controlled conditions (Ray and Chandran 2024). However, potential limitations regarding spore viability in water are acknowledged. The resulting suspension was sieved to remove impurities and subjected to counting in a Neubauer chamber to adjust the concentration to 10^5 conidia mL^{-1}. The application was carried out by spraying the suspension onto the adaxial and abaxial surfaces of the leaves until run-off. The initial inoculum of *E. vignae* was obtained from conidia of naturally infected cowpea leaves grown in a greenhouse.

2.6 | Pathogen Identification and Phylogenetic Analysis

To confirm the identity of the powdery mildew pathogen used in this study, molecular identification and phylogenetic analysis were performed as described below.

Genomic DNA was extracted from powdery mildew-infected leaves of *V. unguiculata*. The internal transcribed spacer

(ITS) region of rDNA was amplified using the universal primers ITS1 and ITS4 (White et al. 1990) and subjected to bidirectional Sanger sequencing using a SeqStudio Genetic Analyser (Thermo Fisher Scientific). The obtained sequence, available in File S1, was compared with reference sequences retrieved from GenBank, including representatives of *E. vignae* (MT628286, MW293895), *Erysiphe diffusa* (KM260706, KM260708–KM260712) and *Erysiphe polygoni* (LC163917, MK685172).

Sequence alignment was performed using MUSCLE (Edgar 2004), and poorly aligned regions were trimmed when necessary. Phylogenetic relationships were inferred using the neighbour-joining (NJ) method (Saitou and Nei 1987) based on the Jukes–Cantor (JC69) substitution model (Jukes and Cantor 1969). Node support was assessed by bootstrap analysis with 500 replicates (Felsenstein 1985). *Erysiphe glycines* (AB078807) was included as an outgroup to root the tree.

2.7 | Disease Assessment

Disease severity was assessed every 2 days using a diagrammatic scale adapted from Buffara et al. (2014), with intervals of 0%, 1%, 5%, 12%, 25%, 50%, 75% and 100% of affected leaf area. The incubation period was defined as the interval between inoculation and the observation of the first symptomatic leaf in each treatment. The area under the disease progress curve (AUDPC) was calculated from the severity data, according to the method described by Madden et al. (2007). Final disease severity was recorded at 18 days post-inoculation (dpi) for the 20°C–26°C–33°C regimen and at 20 dpi for the 24.8°C–30.8°C–37.8°C regimen.

In order to evaluate additional parameters, leaves were collected 15 days after the onset of infection. The number of lesions per leaf was quantified by directly counting all visible lesions. Leaf lesions were gently scraped to obtain a conidial suspension in Tween 20 solution (0.001%). Conidia were quantified using a Neubauer haemocytometer by counting conidia in quadrant A under an optical microscope. For each sample, counts were performed in replicate fields, and values were expressed as the mean number of conidia per counting field (no. conidia per field). Conidial germination (%) was evaluated by inoculating sporulated leaf fragments onto agar medium. After 24 h of incubation at room temperature, 100 conidia per replicate were randomly observed under an optical microscope (40×). Those with a germ tube equal to or greater than the length of the conidium itself were considered germinated (Pritchard and Bell 1967).

2.8 | Statistical Analysis

The grouping of cowpea cultivars and temperature regimes was performed using the unweighted pair group method with arithmetic mean (UPGMA) method, considering the quantitative variables: final severity, AUDPC, number of lesions per leaf, number of conidia per counting field and conidial germination (Cruz et al. 2012; Sneath and Sokal 1973). The data were previously standardized by *z*-score to zero mean and unit standard deviation, avoiding the influence of different scales, and the resulting Euclidean distance matrix was used for hierarchical clustering (Cruz et al. 2012; Hair et al. 2009).

The optimal number of clusters was defined by the silhouette method (factoextra), resulting in $k = 2$, and the silhouette index (cluster) evaluated the cohesion and separation between the groups. Multivariate divergence between cluster averages was assessed using the Mahalanobis distance, comparing D^2 values with the chi-square distribution to test significance.

In order to reduce dimensionality and identify the variables that contribute most to the observed variability, principal component analysis (PCA) was performed on the standardized data, aiding in the interpretation of the groupings.

All analyses were conducted in R (R Core Team 2024) with the packages factoextra (Kassambara and Mundt 2020), cluster (Maechler et al. 2025), MASS (Venables and Ripley 2002) and clusterSim (Walesiak and Dudek 2020).

3 | Results

3.1 | Incubation Period

The incubation period of powdery mildew in cowpea cultivars varied according to the different temperature regimes: 7 days in the 20°C–26°C–33°C regime and 9 days in the 24.8°C–30.8°C–37.8°C regime.

3.2 | Cluster Analysis

Cluster analysis separated the treatments into two distinct groups, with the daily temperature regime being the main factor in this division. Group 1 (GP1) included cultivars subjected to the 24.8°C–30.8°C–37.8°C regime, while Group 2 (GP2) comprised cultivars exposed to the 20°C–26°C–33°C regime (Figure 1).

The consistency of the clusters was assessed by the silhouette index, with $k = 2$. GP1 (24.8°C–30.8°C–37.8°C) had an average silhouette of 0.92, indicating excellent internal coherence, while GP2 (20°C–26°C–33°C) had a value of 0.61, reflecting moderate coherence. These results confirm the adequacy of the division into two groups and highlight the homogeneity of GP1.

3.3 | PCA

PCA resulted in the extraction of two components. The first principal component (PC1) explained 88.89% of the total variability and its most contributing variables (weight > 0.91) were the final severity, the area under the disease progress curve (AUDPC), the number of lesions per leaf, the number of conidia per counting field (no. conidia per field), the conidial germination, and the temperature regime, used as a supplementary variable. The second component (PC2) accounted for 9.50% of the variability, with no variable making a relevant contribution to explaining

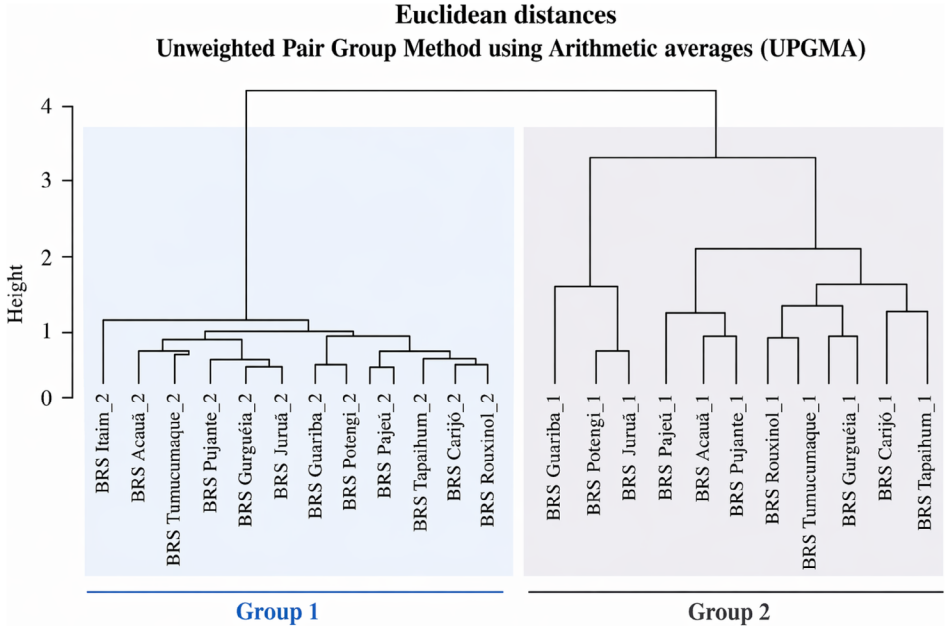

FIGURE 1 | Dendrogram showing hierarchical clustering (UPGMA) of cowpea cultivars based on epidemiological variables of powdery mildew under two temperature regimes (20°C minimum–26°C average–33°C maximum and 24.8°C minimum–30.8°C average–37.8°C maximum, respectively group 1 and 2). Clustering was based on Euclidean distances of standardized variables (final disease severity, AUDPC, number of lesions per leaf, number of conidia per counting field, and conidial germination).

TABLE 1 | Principal component analysis (PCA) of powdery mildew-infected cowpea cultivars grown in growth chambers under two daily temperature regimes (20°C minimum–26°C average–33°C maximum and 24.8°C minimum–30.8°C average–37.8°C maximum).

Variable	PC1	PC2
Final disease severity (%)	**−0.9713**	0.2202
AUDPC (%×days)	**−0.9541**	0.2292
No. of lesions per leaf	**−0.9171**	−0.3886
No. of conidia per counting field	**−0.9230**	−0.3758
Conidial germination (%)	**−0.9474**	0.2859
Temperature regime	**−0.9636**	0.2460
Cultivar	0.0497	0.1246
Eigenvalues	4.4444	0.4750
Total variance (%)	88.8883	9.5003
Cumulative variance (%)	88.8883	98.3886

Note: Values highlighted in bold indicate high factor loadings.
Abbreviation: AUDPC, area under the disease progress curve.

the results. Combined, the two components explained 98.39% of the total variance (Table 1).

Table 2 presents the contribution values of the five characteristics evaluated among the cowpea cultivars for the first two principal components (PC1 and PC2) of the PCA. PC1 showed a balanced distribution of contributions, with greater influence from the variables' final severity (21.23%), AUDPC (20.48%), and conidial germination (20.20%), indicating that this component is related to the general intensity of the disease in the cultivars. PC2 was

TABLE 2 | Principal component analysis (PCA) for contributions of five disease characteristics among cowpea cultivars infected with powdery mildew (caused by *Erysiphe vignae*) by the first two components.

Variable	PC1	PC2
Final disease severity (%)	**0.2123**	0.1021
AUDPC (%×days)	**0.2048**	0.1106
No. of lesions per leaf	0.1893	**0.3180**
No. of conidia per counting field	0.1917	**0.2974**
Conidial germination (%)	**0.2020**	0.1720

Note: Values highlighted in bold indicate high factor loadings.
Abbreviation: AUDPC, area under the disease progress curve.

most impacted by the number of lesions per leaf (31.80%) and number of conidia per counting field (29.74%), suggesting that this axis reflects the reproductive activity and infectious progress of the pathogen. This distinction between the components was fundamental for the separation of the groups observed in the hierarchical cluster analysis.

3.4 | Disease Variables

The mean values of the groups (Table 3) showed that all evaluated parameters were significantly lower in Group 1 compared to Group 2. The final severity of the disease was drastically reduced in Group 1 (3.13%) compared to Group 2 (73.61%). Similarly, the AUDPC showed an average of 17.42 in Group 1 and 268.39 in Group 2. Lower averages were also observed for the number of lesions per leaf (0.97 and 6.40), number of

conidia per counting field (0.96 and 6.40), and conidial germination (1.56% and 85.05%), respectively, for Group 1 and Group 2. These results demonstrated the suppressive effect of increased temperature on the development of the disease and the pathogen.

TABLE 3 | Average of groups of cowpea cultivars infected by powdery mildew (caused by *Erysiphe vignae*), grown in growth chambers under two daily temperature regimes (20°C minimum–26°C average–33°C maximum and 24.8°C minimum–30.8°C average–37.8°C maximum).

	Group 1 (24.8°C–30.8°C–37.8°C)		Group 2 (20°C–26°C–33°C)	
Variable	**Average**	**SD**	**Average**	**SD**
Final disease severity (%)	3.13	1.63	73.61	3.24
AUDPC (%×days)	17.42	9.98	268.39	49.16
No. of lesions per leaf	0.97	0.69	6.40	3.05
No. of conidia per counting field	0.96	0.59	6.40	2.99
Conidial germination (%)	1.56	1.64	85.05	10.28

Abbreviation: AUDPC, area under the disease progress curve.

The standard deviations were consistently higher in Group 2, subjected to the daily regime of 20°C–26°C–33°C, indicating greater variability in the response of the cultivars to infection by *E. vignae*. This pattern is particularly evident in AUDPC, whose SD in Group 2 (49.16) exceeded that of Group 1 (9.98), suggesting that, under lower mean daily temperatures, cultivars exhibit more distinct behaviours. In contrast, the increase in temperature promoted more uniform and controlled responses of the cultivars against the pathogen (Group 1).

3.5 | Multivariate Divergence (Mahalanobis D^2)

This greater heterogeneity observed in Group 2 was confirmed by multivariate divergence analysis, based on the generalized Mahalanobis distance (D^2), which showed wide variability among cowpea cultivars in their response to powdery mildew under the thermal regime of 20°C–26°C–33°C (Figure 2). The greatest dissimilarities were found between BRS Potengi and BRS Gurguéia ($D^2 = 35.90$), followed by BRS Tumucumaque and BRS Gurguéia ($D^2 = 33.11$). Other combinations with high divergence included BRS Gurguéia and BRS Carijó ($D^2 = 28.11$), BRS Gurguéia and BRS Acauã ($D^2 = 27.98$), and BRS Guariba and

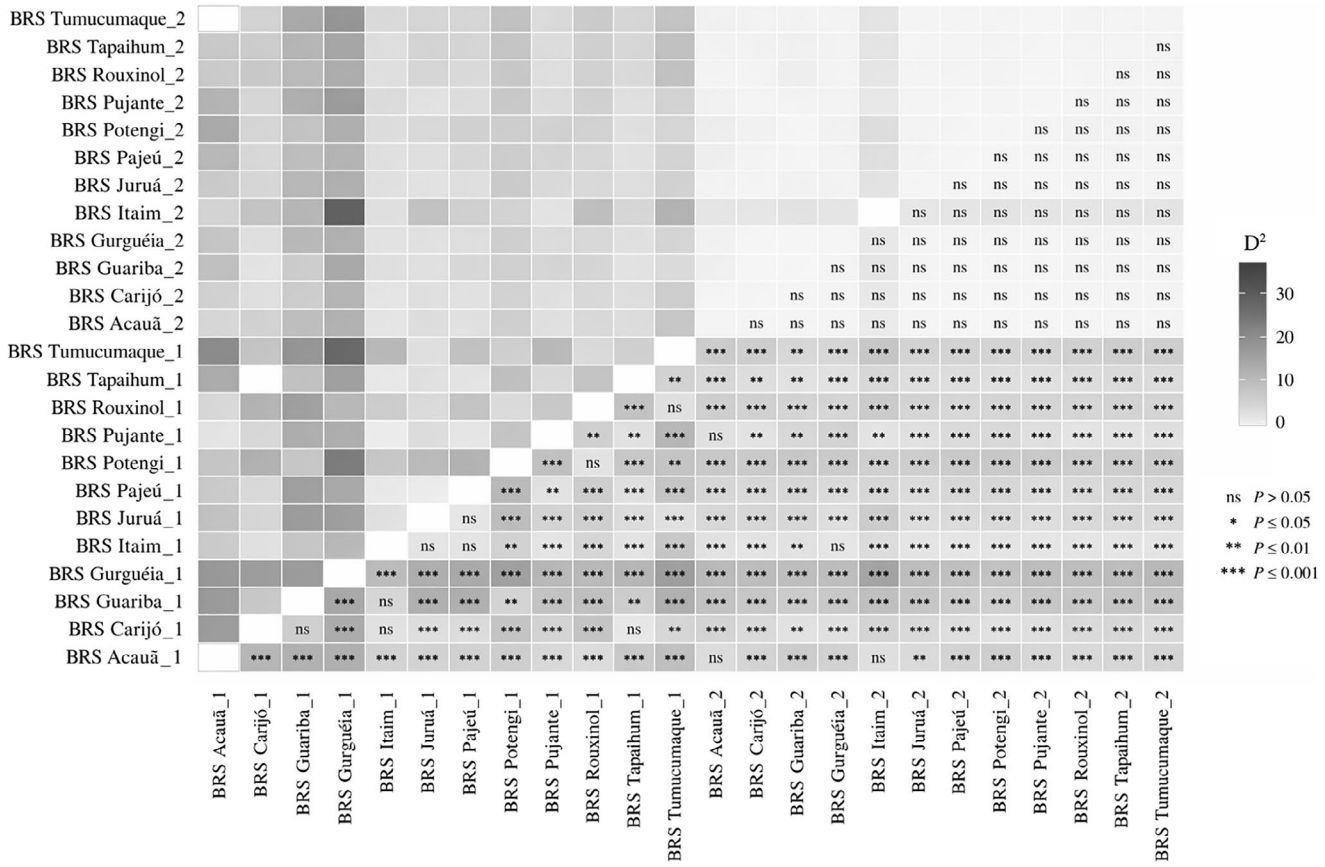

FIGURE 2 | Heatmap of Mahalanobis distances (D^2) among cowpea cultivars affected by powdery mildew under two temperature regimes (20°C minimum–26°C average–33°C maximum and 24.8°C minimum–30.8°C average–37.8°C maximum). Cultivars labelled '1' correspond to 20°C–26°C–33°C, and those labelled '2' to 24.8°C–30.8°C–37.8°C. Colour intensity indicates the magnitude of D^2 values. Significance of pairwise distances is indicated as ns (not significant), *$p \leq 0.05$, **$p \leq 0.01$, ***$p \leq 0.001$.

BRS Acauã ($D^2 = 26.83$), reinforcing the existence of variability among the cultivars evaluated.

Under the baseline temperature regime (20°C–26°C–33°C), some differences among cultivars were observed, with BRS Gurguéia showing the highest divergence (D^2 ranging from 17.33 to 35.90). This pattern was associated with higher AUDPC values (320.67) and lower conidial germination (63.89%) compared to other cultivars, such as BRS Tumucumaque, which presented lower AUDPC (202.33) and higher germination (100%).

BRS Guariba also showed divergence in relation to several cultivars (D^2 from 11.64 to 27.74), indicating variability in disease-related traits under this temperature condition.

However, under the elevated temperature regime (24.8°C–30.8°C–37.8°C), these differences were markedly reduced, with low and non-significant D^2 values observed among cultivars. This indicates that temperature had a stronger influence on disease development than genotype.

3.6 | Molecular Identification and Phylogenetic Analysis

The phylogenetic analysis based on ITS sequences revealed a clear clustering pattern among the evaluated *Erysiphe* species (Figure 3). The isolate (*E. vignae* present study) clustered within the *E. vignae* clade together with reference sequences MT628286 and MW293895. This clade was well separated from the *E. diffusa* cluster, which included sequences KM260706 and KM260708–KM260712, and from the *E. polygoni* cluster represented by LC163917 and MK685172.

The topology of the tree showed strong bootstrap support for the main clades, confirming the genetic distinction among these taxa. The isolate from *V. unguiculata* consistently clustered with *E. vignae*, indicating high sequence similarity and phylogenetic affinity with this species.

4 | Discussion

The results indicate that the powdery mildew incubation period in cowpea cultivars was significantly influenced by thermal regimes, being prolonged under 24.8°C–30.8°C–37.8°C. This delay in the appearance of symptoms confirms the inhibitory effect of high temperatures on critical stages of fungal development, such as conidial germination and appressoria formation (Milod et al. 2021; Pawełkowicz et al. 2025). Lengthening the latent period reduces the rate of epidemic progress (Araújo et al. 2021) and may promote the shift of sporulation to less susceptible stages of the crop, as observed by Asalf et al. (2016).

The homogeneity observed in Group 1 (cultivars under 4.8°C increase) can be attributed mainly to the direct effect of the elevated temperature on the pathogen. Thermo-biological evidence shows that temperatures above 30°C compromise the initial stages of infection, such as germination and penetration of conidia, reducing the efficiency of the powdery mildew inoculum (He et al. 2025; Milod et al. 2021). In this scenario, the disease is strongly suppressed, regardless of the genetic resistance of the cultivars, which in turn reduces selective pressure and results in more uniform responses among the genotypes evaluated.

Although relative humidity was maintained constant (50%–60%) across treatments, it is important to note that humidity is a key factor influencing powdery mildew development. By controlling this variable, the observed differences in disease development could be attributed primarily to the effects of temperature alone.

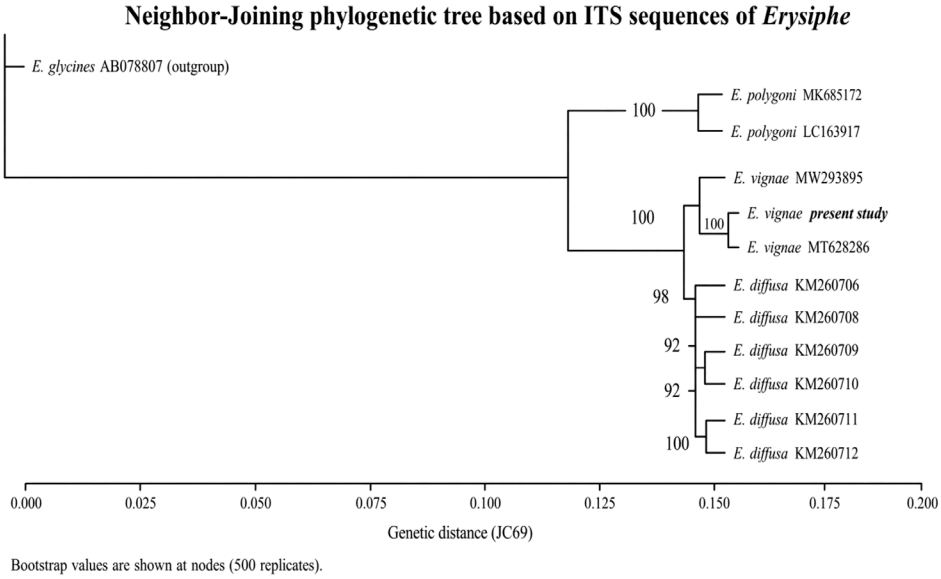

FIGURE 3 | Neighbour-joining phylogenetic tree based on rDNA ITS sequences of *Erysiphe*. The isolate (*E. vignae* present study) clustered within the *E. vignae* clade and was separated from the *E. diffusa* and *E. polygoni* clades. *E. glycines* AB078807 was used as the outgroup.

The influence of temperature was also evident in other epidemiological components. The reduction in the AUDPC under elevated temperatures may be explained by the simultaneous decrease in the infection rate, severity and duration of the epidemic. Recent studies show that increasing temperature reduces sporulation and accelerates the death of infectious structures, limiting the duration of lesions and, consequently, the temporal progression of the powdery mildew (Mieslerová et al. 2022). Thus, AUDPC becomes a sensitive indicator to capture the impact of heat stress on powdery mildew dynamics, because it integrates multiple stages of the epidemiological cycle.

Similarly, the number of lesions per leaf was reduced with a 4.8°C increase in air temperature, which is biologically related to the lower penetration efficiency of the fungus. Temperatures above the optimum reduce the plasticity of the germinal hypha and compromise the formation of appressoria, structures essential for the initial colonization of the host (He et al. 2025; Zhang et al. 2022). As a consequence, the establishment of new infections decreases, resulting in a lower density of lesions on the leaves.

The number of conidia per counting field was also directly affected by heat, because sporulation is a process highly dependent on enzymatic integrity and water availability in the colonized tissues. High temperatures compromise the viability of colonizing hyphae and reduce the sporulation rate, limiting the pathogen's ability to generate new infection cycles (Cao et al. 2021). This set of factors reduces the intensity of the epidemic and explains the low AUDPC values observed in the warmer regime.

Evidence from other pathosystems indicates that rising global average temperatures may compromise vital stages of the powdery mildew cycle. In cucurbits, temperatures above 35°C inhibit not only the germination of *Podosphaera xanthii* spores but also modulate the expression of virulence genes (Trecate et al. 2019). For cowpea, this effect would imply a delay in the establishment of the epidemic and a reduction in the rate of disease progression, especially in regions subject to heat waves.

The cluster analysis reinforced this trend, showing that the thermal regime was decisive in the formation of two distinct groups of cultivars, even overcoming the genetic differences between them. Although the present study did not directly assess the physiological mechanisms involved in the plant–pathogen interaction, the high coherence of Group 1 (silhouette = 0.92) under the 24.8°C–30.8°C–37.8°C regime suggests that the 4.8°C thermal increase acted as a leveller, suppressing phenotypic variability and directing responses toward common defence mechanisms. The reduction in disease development may be primarily associated with the direct inhibitory effect of high temperature on pathogen development rather than improved plant host resistance.

In contrast, the moderate coherence of Group 2 (silhouette = 0.61), observed under the 20°C–26°C–33°C regime, reflects the marked influence of cultivar genetic variability under pathogen-favourable conditions. In these situations, specific resistance mechanisms mediated by R genes or effector-triggered susceptibility (ETS) interactions tend to manifest themselves differently, resulting in greater heterogeneity among genotypes (Schwarczinger et al. 2021; Zhang et al. 2021).

PCA confirmed the dominance of the thermal regime in the data variability, with PC1 explaining 88.89% of the total variance. The strong correlation (> 0.91) between epidemiological variables (disease severity, AUDPC, number of lesions per leaf, number of conidia per counting field, and germination) and the thermal regime highlights the central role of temperature as a modulator of disease development. This finding converges with recent studies that highlight temperature as one of the main elements in modelling epidemics under climate change scenarios (Angelotti et al. 2024; Lahlali et al. 2024; Tang et al. 2017). The significant contribution of AUDPC in PC1 (20.48%) reinforces its usefulness as a summary parameter of the temporal progression of the disease, validating its use as an indicator sensitive to thermal variations and plant–pathogen interaction (Shikha et al. 2024).

The results of this study indicate that although none of the evaluated cowpea cultivars exhibited resistance to powdery mildew, increasing temperatures had a pronounced effect on the pathogen. This suggests that global warming scenarios may reduce inoculum pressure and disease severity, directly impacting management practices. These findings may lead to scrutiny around the use of fungicides in tropical and semi-arid environments, reducing production costs and environmental impacts, and supporting breeding programmes in the selection of more stable genotypes under heat stress.

The phylogenetic placement of the isolate obtained from *V. unguiculata* within the *E. vignae* clade is consistent with recent taxonomic revisions of powdery mildew fungi infecting Fabaceae. Historically, powdery mildew pathogens in legumes were frequently identified as *E. polygoni sensu lato*; however, molecular studies have demonstrated that this taxon represents a complex of cryptic species rather than a single species with a broad host range (Braun and Cook 2012; Takamatsu et al. 2015).

In this context, *E. vignae* has been described as a distinct powdery mildew species infecting *Vigna* spp., based on molecular phylogenetic analyses and host association (Kelly et al. 2021). In contrast, *E. diffusa* is commonly associated with *Glycine max* and is phylogenetically distinct from powdery mildew species infecting *Vigna* (Takamatsu et al. 2015). The clear separation observed between *E. vignae* and *E. diffusa* in the present study reinforces this host-associated differentiation.

Previous studies have shown that powdery mildew isolates infecting legumes were historically assigned to the *E. polygoni* complex due to morphological similarity, underscoring the importance of molecular approaches for accurate species delimitation (Braun and Cook 2012; Cunnington et al. 2003). More recent phylogenetic studies have reinforced the existence of cryptic diversity and host specialization within *Erysiphales* (Vaghefi et al. 2022). In this context, *E. vignae* has been described as a distinct species associated with *Vigna* hosts based on molecular phylogenetic evidence (Kelly et al. 2021). These findings are consistent with the topology obtained in the present study, in which the isolate clustered within the *E. vignae* clade with strong bootstrap support.

Although the ITS region is widely used for fungal identification, it may present limited resolution among closely related species within *Erysiphales*, and additional loci are sometimes required for precise delimitation (Schoch et al. 2012). Nevertheless, the congruence between phylogenetic clustering and host association observed in this study provides strong evidence supporting the identification of the present isolate as *E. vignae*.

Therefore, considering both molecular data and host association, the pathogen detected on *V. unguiculata* is best interpreted as *E. vignae*, although the more conservative designation *E. cf. vignae* may be adopted in the absence of multilocal data.

Temperature plays a key role in the development of powdery mildew in cowpea. Elevated temperature regimes prolonged the incubation period and reduced disease severity, AUDPC, number of conidia per counting field, and germination, while also promoting more homogeneous responses among cultivars. These findings indicate that increasing temperature can suppress disease development primarily through direct effects on the *E. vignae* pathogen, highlighting the importance of environmental factors in shaping disease dynamics under climate change scenarios.

Author Contributions

Camila Barbosa dos Santos: investigation, validation, methodology. **Emília Hamada:** project administration, funding acquisition, resources, writing – review and editing. **Francislene Angelotti:** conceptualization, project administration, supervision, writing – review and editing, investigation, methodology. **Jadson Lima da Silva:** investigation, methodology, validation. **Layana Alves do Nascimento:** investigation, methodology, validation, formal analysis, writing – original draft, data curation, funding acquisition. **Márcia Vitória de Macedo:** data curation, formal analysis, writing – original draft. **Natoniel Franklin de Melo:** investigation, supervision, methodology. **Samuel Cavalcante do Amaral:** methodology, formal analysis, investigation. **Weslley Oliveira da Silva:** investigation, methodology. **Tailane Amorim Luz:** investigation, validation, methodology.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The datasets generated and analysed during the current study are available from the corresponding author upon reasonable request. The ITS sequence obtained in this study is available in the Supporting Information (File S1).

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **File S1:** ITS sequence of *Erysiphe vignae* isolate obtained in this study. **Table S1:** Origin, agronomic characteristics, and adaptation of cowpea cultivars used in the study, developed by Embrapa breeding programmes.