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*Scientific Article*

# Resistance of melon genotypes to *Stagonosporopsis cucurbitacearum*

# Resistência de genótipos de melão a *Stagonosporopsis cucurbitacearum*

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**ABSTRACT** – Gummy stem blight, caused by the fungal pathogen *Stagonosporopsis cucurbitacearum* (syn. *Didymella bryoniae*), is a severe disease that results in significant yield losses in melon crops globally. The objective of this study was to evaluate and confirm resistance of melon genotypes to *S. cucurbitacearum*. Two experiments were conducted in a controlled environment using a randomized block design with four replications and eight plants per plot. Disease symptoms were assessed using a severity scale ranging from 0 (no visible symptoms) to 4 (stem necrosis with complete wilting and plant death) to determine disease reaction classes. Inoculation in both experiments utilized the toothpick method, in which a toothpick bearing a 5 mm diameter fungal colony disc was inserted directly into the plant stem (1 cm below the leaves). Twelve genotypes were evaluated in Experiment I and fourteen in Experiment II. In both experiments, genotypes exhibited genetic variability in their response to gummy stem blight symptoms, resulting in distinct disease reaction classes to *S. cucurbitacearum*. The genotypes PI482398, PI140471, PI157082, and PI420145 demonstrated stability in genetic resistance to *S. cucurbitacearum*, classified as highly resistant in both experiments, confirming prior findings. These genotypes are recommended for advancement in melon breeding programs as valuable sources of resistance.

**Keywords**: *Cucumis melo*. Gummy stem blight. Disease resistance. Genotype selection. *Didymella bryoniae*.

**RESUMO** – O crestamento gomoso, causado pelo patógeno fúngico *Stagonosporopsis cucurbitacearum* (sin. *Didymella bryoniae*), é uma doença severa que resulta em perdas significativas de produtividade em cultivos de melão em todo o mundo. O objetivo deste estudo foi avaliar e confirmar a resistência de genótipos de melão a *S. cucurbitacearum*. Dois experimentos foram conduzidos em ambiente controlado, utilizando um delineamento em blocos casualizados com quatro repetições e oito plantas por parcela. Os sintomas da doença foram avaliados por meio de uma escala de severidade variando de 0 (sem sintomas visíveis) a 4 (necrose do caule com murcha completa e morte da planta) para determinar as classes de reação à doença. A inoculação em ambos os experimentos foi realizada pelo método do palito, no qual um palito contendo um disco de colônia fúngica de 5 mm de diâmetro foi inserido diretamente no caule da planta (1 cm abaixo das folhas). Doze genótipos foram avaliados no Experimento I e quatorze no Experimento II. Em ambos os experimentos, os genótipos apresentaram variabilidade genética na resposta aos sintomas do crestamento gomoso, resultando em diferentes classes de reação à doença causada por *S. cucurbitacearum*. Os genótipos PI482398, PI140471, PI157082 e PI420145 demonstraram estabilidade na resistência genética a *S. cucurbitacearum*, sendo classificados como altamente resistentes em ambos os experimentos, confirmando resultados anteriores. Esses genótipos são recomendados para avanço em programas de melhoramento de melão como fontes valiosas de resistência.

**Palavras-chave**: *Cucumis melo*. Gomose do caule. Resistência a doenças. Seleção de genótipos. *Didymella bryoniae*.

**Conflict of interest:** The authors declare no conflict of interest related to the publication of this manuscript.



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## INTRODUCTION

*Stagonosporopsis cucurbitacearum* (Fr.) Aveskamp, Gruyter & Verkley (synonym *Didymella bryoniae* (Fuckel) Rehm) is a major fungal pathogen affecting cucurbit crops globally. This pathogen causes gummy stem blight, a disease that significantly reduces yield and impacts the economic returns of producers (Luo et al., 2022). In melon (*Cucumis melo* L.) crops, yield losses range from 15% to 30%, with severe cases reaching up to 80% (LIU et al., 2017). Symptoms initially manifest as brown to dark brown lesions on leaves, progressing rapidly to stem cankers with gummy exudate, and causing black rot in fruits, often leading to fruit abortion (RUANGWONG et al., 2021).

In the Northeast region of Brazil, gummy stem blight was first reported in 1973, causing yield losses of up to 50% in melon crops (MATTA; LUNA; BENEVIDES, 1974). This disease has also been associated with other cucurbit crops in the Northeast region (SILVA et al., 2016). Although multiple measures exist to mitigate the damage caused by gummy stem blight, chemical control through pesticide application remains the primary method, generating risks of environmental contamination, food safety concerns (HAN et al., 2023), and reduced efficacy due to selection pressure, which may lead to pathogen resistance (SANTOS et al., 2017).

Melon cultivation in Brazil has significant agricultural importance, with exports reaching approximately 222,400 Mg in 2022, valued at US$156.4 million (HORTIFRUTI BRASIL, 2023). However, due to the limited efficacy of plant protection products, research has focused on developing melon cultivars resistant to gummy stem blight, involving both the scientific community and private sector.

Genetic resistance to gummy stem blight in melon is conferred by five independent genes, four dominant (*Gsb-1*, *Gsb-2*, *Gsb-3*, *Gsb-4*) and one recessive (gsb-5) (HU et al., 2017). Identifying sources of resistance to *S. cucurbitacearum* depends on genetic variability within germplasm collections, making their characterization essential. Although resistance to gummy stem blight in melon has been documented, results have shown variations (ZHANG NING et al., 2017), potentially due to differences in pathogen aggressiveness (SANTOS et al., 2017), dormancy-braking capacity, and isolate variability. Therefore, confirming the resistance of genotypes is critical whenever feasible.

Characterizing the resistance of new melon genotypes and confirming resistance in previously identified resistant genotypes is crucial, as responses may vary due to differences among pathogen isolates and experimental conditions. The primary objective of this study was to identify potential variations in genes conferring resistance to gummy stem blight in melon. The findings aim to support plant breeders in transferring resistance genes to elite cultivars, thereby mitigating the damage caused by this pathogen. Thus, this study evaluated and confirmed the resistance of melon genotypes to *S. cucurbitacearum*.

## MATERIAL AND METHODS

### Experimental Area Characterization

Two experiments were conducted in a greenhouse and the Phytopathology Laboratory, in Jaboticabal, São Paulo, Brazil (21°14'05"S, 48°17'09"W, 614 m altitude). Experiment I was conducted from March 5 to May 7, 2018, and Experiment II from September 29 to November 8, 2018.

### Genetic Material

In Experiment I, the responses of 12 melon genotypes to gummy stem blight were evaluated (Table 1). In Experiment II, the same 12 genotypes, the JAB 11 line, and the 'Olimpic Express' hybrid were evaluated to confirm their resistance, to support subsequent steps of melon breeding programs, as pathogen isolates may vary in aggressiveness.

**Table 1**. Melon genotypes (*Cucumis melo* L.) inoculated with *Stagonosporopsis cucurbitacearum* for evaluation and confirmation of resistance to gummy stem blight.

| Genotype | Origin | Sexual expression | Nature | Classification |
|---|---|---|---|---|
| AC-09 | Brazil | Monoecious | Landrace | *C. melo* var. *momordica* |
| AC-29 | Brazil | Monoecious | Landrace | *C. melo* var. *momordica* |
| C-160 | Brazil | Monoecious | Landrace | Landrace |
| CNPH 111075 | Brazil | Monoecious | Landrace | Landrace |
| 'Ouro' | TOPSEED | Andromonoecious | Commercial | *C. melo* var. *inodorus* |
| Gaúcho' | TOPSEED | Andromonoecious | Commercial | *C. melo* var. *cantalupensis* |
| 'Caipira' | TOPSEED | Andromonoecious | Commercial | *C. melo* var. *cantalupensis* |
| PI482398 | Zimbabwe | Andromonoecious | Landrace | *C. melo* subsp. *melo* |
| PI157082 | China | Monoecious | Landrace | *C. melo* subsp. *melo* |
| PI140471 | NCRPIS USDA | Andromonoecious | Landrace | *C. melo* subsp. *melo* |
| PI420145 | Japão | Andromonoecious | Landrace | *C. melo* subsp. *melo* |
| JAB 11 | NEOM | Andromonoecious | Landrace | *C. melo* var. *reticulatus* |
| JAB 20 | NEOM | Andromonoecious | Landrace | *C. melo* var. *reticulatus* |
| 'Olimpic Express' | Sakata Seed Sudamerica | Andromonoecious | Commercial | *C. melo* var. *reticulatus* |

Landrace = non-commercial, indeterminate genotype; NCRPIS = North Central Regional Plant Introduction Station; NEOM = Center for Studies in Olericulture and Breeding.

### Experimental Procedure

Melon seedlings were grown in 128-cell expanded polystyrene trays filled with an autoclaved commercial substrate (Bioplant®), sterilized at 120 °C and 1 atm for one hour, and supplemented with 5 g $L^{-1}$ of 04-14-08 N-$P_2O_5$-$K_2O$ fertilizer formulation (TSUTSUMI; SILVA, 2004). Seeds were sown in staggered rows to avoid microclimate formation, which could promote disease development and compromise inoculation and evaluation processes. The plant rows at the borders were used as buffers, with the six central plants per plot evaluated. Seedlings were inoculated with *Stagonosporopsis cucurbitacearum* at the second fully expanded true leaf stage, 43 days after sowing, utilizing the toothpick method in both experiments.

Both experiments were conducted in a randomized block design with four replications and 24 plants per plot, evaluating 12 treatments in Experiment I and 14 in Experiment II. One replication was used as a control, with plants inoculated with a potato dextrose agar (PDA) disc

without the fungus to assess the impact of toothpick injury and PDA medium. The genotype JAB 20 was used as a susceptibility standard in Experiment I, while JAB 11 and JAB 20 were used in Experiment II.

Seedlings were maintained in a humid chamber during the first 72 hours post-inoculation. In Experiment I, temperatures in the humid chamber ranged from 17.1 to 47.6 ° C, with relative humidity ranging from 15.9% to 97%. Temperatures inside the greenhouse in Experiment I ranged from 11.4 to 37.5 °C, with relative humidity ranging from 16% to 96% (Figure 1). In Experiment II, temperatures in the humid chamber ranged from 22.0 to 48.7 °C, with relative humidity ranging from 11% to 90%. Temperatures inside the greenhouse in Experiment II ranged from 15.0 °C to 48.5 °C, with relative humidity ranging from 13% to 97% (Figure 2).

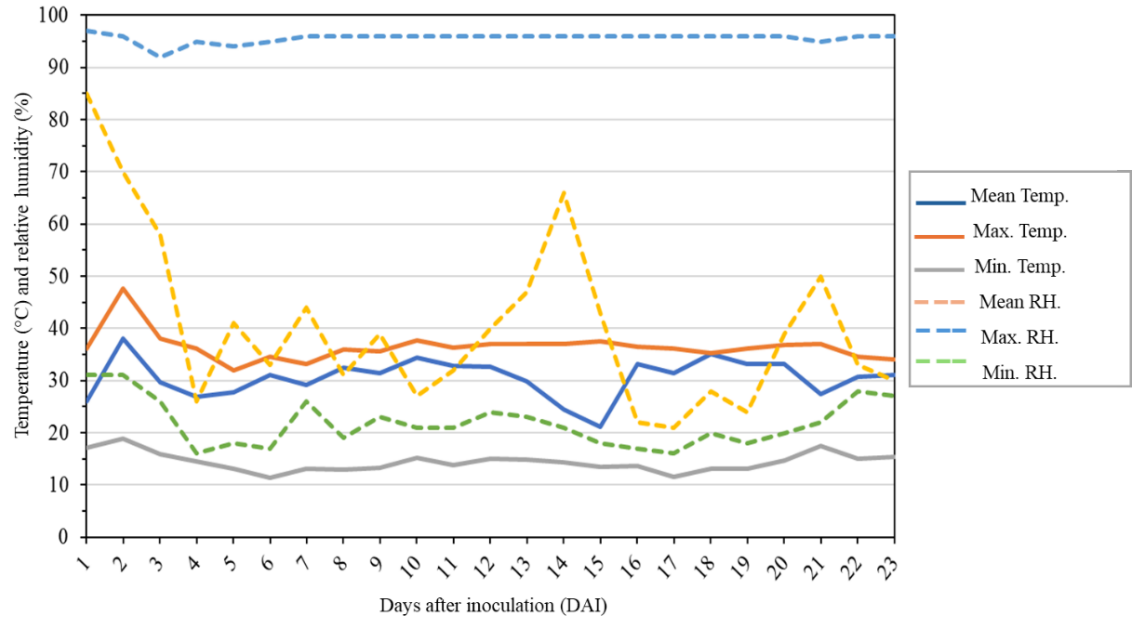


**Figure 1**. Mean, maximum, and minimum air temperatures and relative humidity (RH) inside the humid chamber up to three days after inoculation (DAI) and inside the greenhouse up to 21 DAI, in Experiment I.

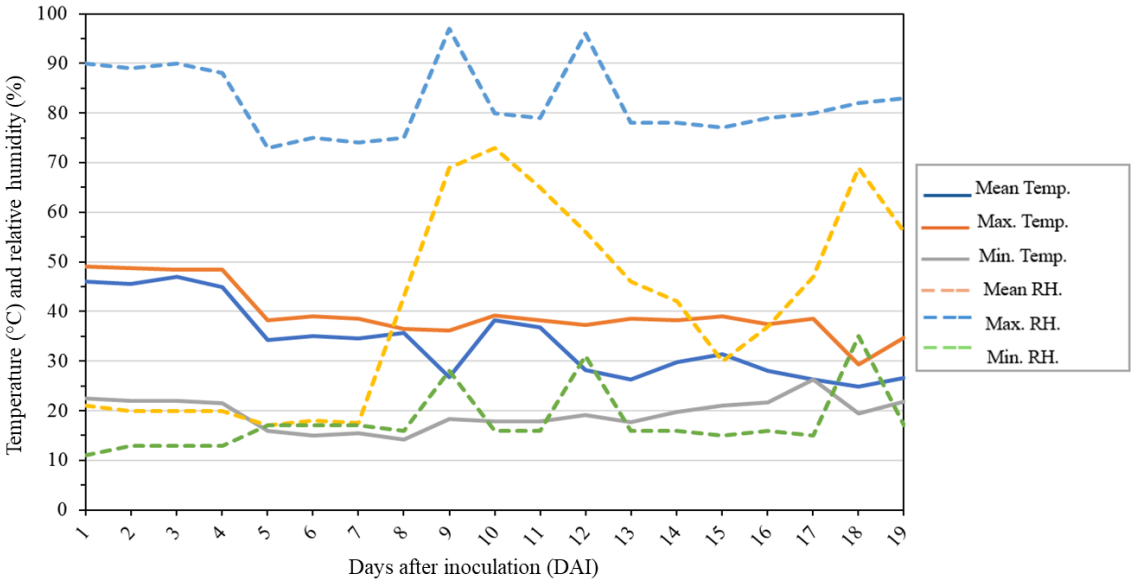


**Figure 2**. Mean maximum and minimum air temperatures and relative humidity inside the humid chamber up to three days after inoculation (DAI) and inside the greenhouse up to 14 DAI, in Experiment I.

**Fungal Isolation and Inoculation with *Stagonosporopsis cucurbitacearum***

The *S. cucurbitacearum* isolate used in Experiments I and II was obtained from infected melon plants from previous experiments conducted in the Olericulture and Aromatic Medicinal Plants Sector, Faculty of Agricultural and Veterinary Sciences, São Paulo State University (UNESP-FCAV). A direct isolation technique was employed to isolate the fungus, in which pycnidia and/or perithecia were removed from the stem surface and transferred to Petri dishes containing PDA medium.

The plates were incubated in a biochemical oxygen demand (BOD) chamber at 26 °C with a 12-hour photoperiod for three days to promote fungal growth. Subsequently, the mycelial growth was subcultured to obtain a pure fungal culture. After 12 days of subculturing, the *S. cucurbitacearum* isolate had colonized the entire plate, and 5 mm diameter discs of the culture medium with mycelium were used to inoculate the seedlings (Figure 3).

Inoculation in both experiments utilized the toothpick method, in which a toothpick bearing a 5 mm diameter fungal colony disc was inserted directly into the plant stem (1 cm below the leaves), as described by Verzignassi et al. (2004). Toothpicks were sterilized in boiling water for 30 minutes with three water changes to prevent contamination, followed by autoclaving in Petri dishes at 120 °C and 1 atm for 20 minutes (MEDEIROS et al., 2015).

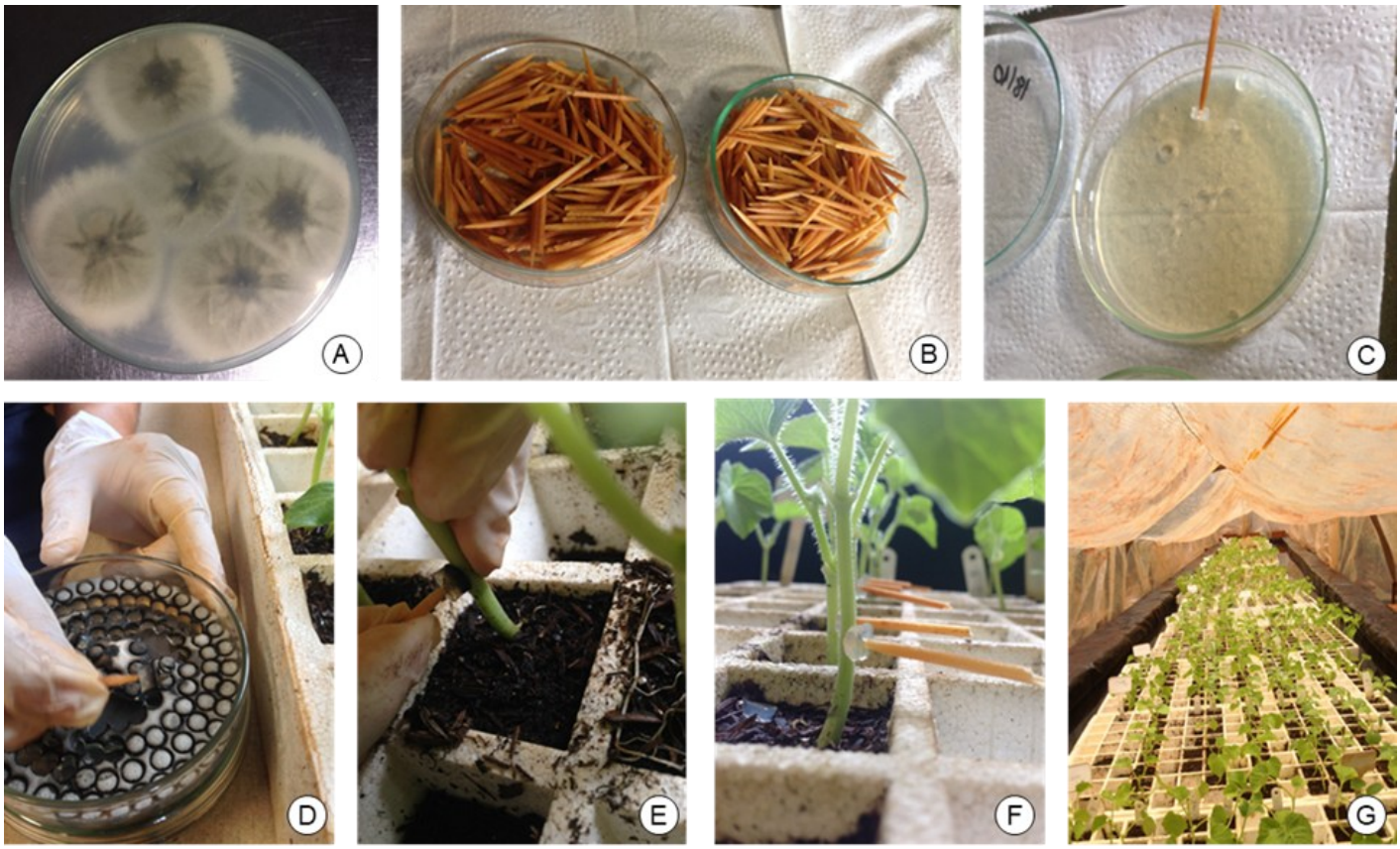


**Figure 3**. Fungal isolates of *Stagonosporopsis cucurbitacearum* (A), toothpicks used for inoculation (B); PDA discs for inoculation in the controls (C); PDA discs colonized with the fungus (D); inoculation of the fungus into the plant through toothpick insertion (E); control plants inoculated with PDA medium without the fungus (F); incubation of inoculated seedlings in the humid chamber (G).

**Resistance Evaluation**

Plants were incubated in a floating-type humid chamber (OLIVEIRA et al., 2009) for three days after inoculation (DAI) for the initial evaluation. Subsequently, the plants were transferred to the greenhouse, where they remained until the experiment concluded. In the greenhouse, seedlings were irrigated using an automated sprinkler system three times daily.

Evaluations were performed at 3, 7, 14, and 21 DAI in Experiment I, and at 3, 7, 14 DAI in Experiment II. A severity scale from 0 to 4 was used to assess disease symptoms in both experiments, as described by Dusi, Tasaki, and Vieira (1994), where 0 indicates no visible symptoms; 1 indicates a water-soaked lesion on the stem up to 1 cm in diameter; 2 indicates a water-soaked lesion on the stem greater than 1 cm in diameter; 3 indicates a partially necrotic lesion on the stem with partial plant wilting; and 4 indicates stem necrosis with complete wilting and plant death (Figure 4). Genotypes were subsequently classified into four disease reaction classes: highly resistant (0.1–1.0); moderately resistant (1.1–2.0); susceptible (2.1–3.0); and highly susceptible (3.1–4.0) (NORONHA et al., 2006). Evaluations were terminated when all plants in one of the plots containing the susceptibility standard reached the maximum severity score (4).

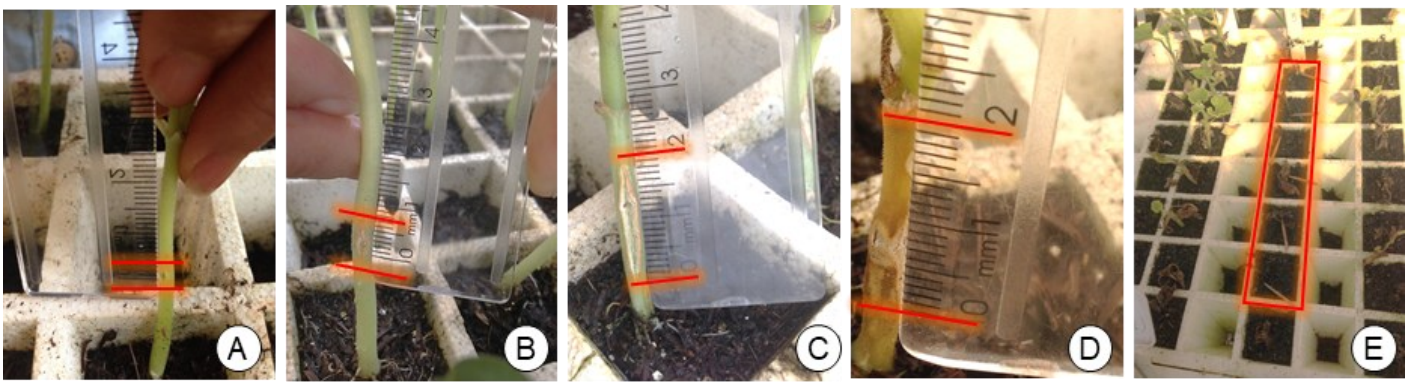


**Figure 4**. Disease severity scores for *Stagonosporopsis cucurbitacearum* in melon plants: Score 0 (no visible symptoms) (A); Score 1 (water-soaked lesion on the stem up to 1 cm in diameter) (B); Score 2 (water-soaked lesion on the stem greater than 1 cm in diameter) (C); Score 3 (partially necrotic lesion on the stem with partial wilting of the plant) (D); and Score 4 (stem necrosis with complete wilting and plant death) (E).

**Data Analysis**

Data were subjected to diagnostic analysis based on residuals. Since at least one of the assumptions of the analysis of variance was violated, data transformations were applied. Phenotyping data were transformed using $\sqrt{X+0.5}$ and subjected to analysis of variance. The experimental design utilized a split-plot arrangement, with genotypes as main treatments and evaluation days as secondary treatments. Following analysis of variance, genotypes were compared for significant effects and interactions within and between treatments. The least significant difference (LSD) multiple comparison test ($\alpha = 0.05$) was then applied. All statistical analyses were performed using the R Statistical Environment (R DEVELOPMENT CORE TEAM, 2020).

**RESULTS AND DISCUSSION**

Environmental conditions were favorable for the development of characteristic gummy stem blight symptoms in both experiments (Figures 1 and 2). The formation of pathogen reproductive structures, including pycnidia and/or perithecia, was observed on stem surfaces of susceptible and moderately resistant genotypes. Similar findings were reported by Santos et al. (2017) and Gomes (2018) when assessing melon genotype responses to gummy stem blight.

These symptoms manifested under temperatures ranging from 20 to 30 °C, with an optimum at 25 °C, and relative humidity of approximately 95%, representing ideal conditions for *Stagonosporopsis cucurbitacearum* development. However, disease occurrence has been documented even under relative humidity levels below 40% (LIMA et al., 2018).

The results confirmed genetic variability in genotype response to *S. cucurbitacearum* infection, as validated by the analysis of variance, which indicated significant effects for genotype (G), days after inoculation (DAI), and the G × DAI interaction (Table 2) ($p \leq 0.01$), in both experiments.

The assessment of potential damage caused by the *S. cucurbitacearum* isolate on the melon genotypes revealed varied levels of infection, with genotype JAB 20 exhibiting the highest scores (between 3.1 and 4.0 in the final evaluation) and being classified as susceptible. This result confirmed the pathogenicity of the *S. cucurbitacearum* isolate to melon seedlings and indicated that experimental and environmental conditions were favorable, as JAB 20 served as the susceptibility standard.

In general, symptoms in the JAB 20 genotype progressed rapidly, initially presenting as small water-soaked lesions that evolved into gummy stem exudation, followed by wilting. During the first evaluation, some seedlings in the JAB 20 plot exhibited scores greater than 1.0, with disease progression continuing until 21 DAI (Table 2). A broad range of disease severity was observed when analyzing the progression and disease reaction classes, resulting in three distinct groups, with seven genotypes classified as moderately resistant and four as highly resistant (Table 2).

Based on the mean scores across the four evaluations, genotype PI482398 showed no symptom development during the evaluation periods, unlike the other genotypes (Table 2). Its stability was evident from the second evaluation onward, with no variation in disease severity scores at 7 and 14 DAI (Table 2).

Genotypes PI482398, PI140471, PI157082, and PI420145 exhibited no progression of disease symptoms, with a mean score < 1.0, and were classified as highly resistant. The remaining genotypes were classified as moderately resistant, with scores > 1.0 and increasing disease severity across all evaluations. 'Caipira' had a score of 1, with a mean of 0.38 cm at 3 DAI, which remained below 1.0 at 7 DAI. However, in the final evaluation (21 DAI), its mean score reached 2.49 (Table 2).

**Table 2**. Resistance scores of melon genotypes to *Stagonosporopsis cucurbitacearum* at 2, 7, 14, and 21 days after inoculation (DAI) in Experiment I.

| Genotype | 3 DAI | 7 DAI | 14 DAI | 21 DAI | F-test | Mean | RC |
|---|---|---|---|---|---|---|---|
| JAB 20 | 1.45 (1.61) aC | 1.74 (2.52) aB | 1.82 (2.82) aAB | 1.91 (3.13) aA | 14.97** | (2.52) | S |
| 'OURO' | 1.31 (1.22) abC | 1.53 (1.83) abB | 1.70 (2.39) abA | 1.79 (2.72) abA | 17.46** | (2.04) | MR |
| AC-29 | 1.29 (1.16) abcC | 1.44 (1.58) bcB | 1.54 (1.86) bcAB | 1.66 (2.26) abcdA | 9.57** | (1.72) | MR |
| C-160 | 1.18 (0.89) bcdC | 1.45 (1.60) bcB | 1.54 (1.87) bcB | 1.70 (2.38) abcdA | 18.44** | (1.69) | MR |
| CNPH111075 | 1.15 (0.82) bcdC | 1.43 (1.54) bcB | 1.50 (1.74) bcdAB | 1.63 (2.15) bcdA | 15.71** | (1.56) | MR |
| 'GAÚCHO' | 1.10 (0.70) bcdC | 1.33 (1.28) bcdB | 1.47 (1.66) bcdAB | 1.53 (1.83) cdA | 14.19** | (1.37) | MR |
| 'CAIPIRA' | 0.94 (0.38) deD | 1.10 (0.71) defC | 1.44 (1.57) cdB | 1.73 (2.49) abcA | 48.04** | (1.20) | MR |
| AC-09 | 1.13 (0.77) bcdC | 1.22 (1.00) cdeBC | 1.35 (1.33) cdeAB | 1.47 (1.66) deA | 8.75** | (1.19) | MR |
| PI482398 | 1.13 (0.78) bcdA | 1.25 (1.06) cdeA | 1.25 (1.06) deA | 1.27 (1.11) efA | 1.56$^{ns}$ | (1.00) | HR |
| PI140471 | 1.04 (0.59) cdeB | 1.17 (0.87) defAB | 1.17 (0.87) eAB | 1.26 (1.10) efA | 3.24* | (0.86) | HR |
| PI157082 | 1.00 (0.51) deB | 1.07 (0.66) efAB | 1.15 (0.83) eA | 1.21 (1.00) fA | 3.26* | (0.74) | HR |
| PI420145 | 0.84 (0.21) eB | 0. 95 (0.40) fB | 1.15 (0.83) eA | 1.22 (1.00) efA | 12.08** | (0.61) | HR |
| F-test | 3.66** | 6.47** | 6.13** | 7.64** | | | |
| CV % (G) | 19.37 | | | | | | |
| CV % (DAI) | 6.53 | | | | | | |

CV = coefficient of variation; **. *, and ns = significant at 1%, 5%, and not significant at 5% by the F-test, respectively; Means followed by the same lowercase letter in the columns, or uppercase letter in the rows, are not significantly different by the LSD test at a 5% significance level.

Score means transformed using $\sqrt{X + 0.5}$ . RC = response classes based on original scores shown within parentheses: 0.0–1.0 = highly resistant (HR), 1.1–2.0 = moderately resistant (MR), 2.1–3.0 = susceptible (S), and 3.1–4.0 = highly susceptible (HS) (NORONHA et al., 2006).

Disease symptom progression varied across the three evaluations in Experiment II. Genotype CNPH111075 was the only one with a score of 0 (no visible symptoms) at 3 DAI; however, its mean score exceeded 3.0 by 14 DAI, resulting in a mean of 1.14, classified as moderately resistant. The susceptibility standard, JAB 20, consistently exhibited the highest mean scores across all evaluations, confirming its susceptibility (Table 3).

Disease progression was minimal in AC-29, PI482398, PI140471, PI420145, and PI157082, unlike the other genotypes, suggesting the presence of resistance mechanisms that limit disease advancement. Among these, PI157082 had the lowest mean severity scores across all evaluations, closely followed by PI420145 (Table 3).

The results revealed the formation of three disease reaction classes for *S. cucurbitacearum*, with the susceptibility standards JAB 20 and JAB 11 developing stem lesions that rapidly progressed to wilting and seedling death (score 4) by the final evaluation, confirming the isolate's virulence and the suitability of environmental conditions for fungal development. Additionally, the commercial hybrids 'Olimpic Express', 'Ouro', and 'Gaúcho' were grouped in the susceptible class, exhibiting similar symptom progression that continued until the final evaluation at 14 DAI (Table 3).

Genotypes PI482398, PI140471, PI420145, and PI157082 were classified as highly resistant, consistent with Experiment I results (Tables 1 and 2), highlighting the stability of their resistance to *S. cucurbitacearum* compared to the other genotypes.

In addition, AC-29, previously classified as moderately resistant in Experiment I (Table 2), was classified as highly resistant in Experiment II with a score < 1.0, though its resistance classification instability necessitates further experiments for reliable recommendations. Although AC-29 had the second-lowest mean severity score at 3 DAI, the disease may reach high levels in subsequent evaluations (Table 3), which may compromise the plant's full productive potential during its cycle. Differences in disease reaction classes between the two experiments were observed for 'Ouro' and 'Gaúcho', classified as moderately resistant in Experiment I but as susceptible in Experiment II (Tables 2 and 3). Control plants showed no gummy stem blight symptoms, indicating the absence of effects associated with mechanical injury from toothpick insertion or PDA medium.

Santos et al. (2017) classified genotypes JAB 11 and JAB 20 as susceptible and PI482398 and PI420145 as highly resistant. However, PI157082 and PI140471 were classified as moderately resistant, in contrast to the present study, where they were classified as highly resistant (Tables 2 and 3). Contrasting results were also observed for the genotypes C-160 and AC-29, which were classified as highly resistant by Santos et al. (2017).

Genotype AC-29 exhibited variation in resistance classification between the two experiments (Tables 2 and 3), likely due to differences in environmental conditions and in the isolate used, which, despite originating from the same location, was obtained from different plants at different times, potentially resulting in variation in isolate aggressiveness or pathogenicity. Another factor may be the genotype's genotypic instability, suggesting segregation of alleles for resistance genes. Although genotype AC-29 was classified as highly resistant in Experiment II, an increase in mean disease

score was observed, which could escalate to a higher disease severity class if further evaluations were conducted (Tables 2 and 3). These variations in gummy stem blight response across genotypes and environments may arise from differences in isolate virulence or pathogen-environment-genotype interactions (ZHANG NING et al., 2017; SEBLANI; MUNKVOLD, 2023).

**Table 3**. Resistance scores of melon genotypes to *Stagonosporopsis cucurbitacearum* at 2, 7, and 14 days after inoculation (DAI) in Experiment II.

| Genotype | 3 DAI | 7 DAI | 14 DAI | F-test | Mean | RC |
|---|---|---|---|---|---|---|
| JAB 20 | 1.54 (1.87) aB | 1.97 (3.39) aA | 2.12 (4.00) aA | 17.02** | 3.09 | S |
| 'Olimpic Express' | 1.47 (1.65) abB | 1.96 (3.33) aA | 2.12 (4.00) aA | 21.74** | 2.99 | S |
| JAB 11 | 1.44 (1.59) abC | 1.90 (3.10) aB | 2.12 (4.00) aA | 22.27** | 2.89 | S |
| 'OURO' | 1.22 (0.99) bcC | 1.82 (2.82) abB | 2.08 (3.83) aA | 36.52** | 2.55 | S |
| 'GAÚCHO' | 0.96 (0.42) cdeC | 1.60 (2.05) bcB | 2.08 (3.83) aA | 59.16** | 2.10 | S |
| 'CAIPIRA' | 1.10 (0.71) cdC | 1.63 (2.14) bcB | 1.95 (3.32) abA | 34.60** | 2.06 | MR |
| C-160 | 0.96 (0.42) cdeC | 1.45 (1.61) cB | 2.02 (3.59) abA | 52.91** | 1.87 | MR |
| AC-09 | 0.78 (0.11) eC | 1.15 (0.83) dB | 1.81 (2.78) bA | 51.03** | 1.24 | MR |
| CNPH111075 | 0.71 (0.00) eB | 0.87 (0.26) eB | 1.91 (3.15) abA | 79.98** | 1.14 | MR |
| AC-29 | 0.74 (0.11) eB | 1.15 (0.83) eB | 1.81 (2.78) cA | 19.00** | 0.52 | HR |
| PI482398 | 0.94 (0.38) deA | 0.94 (0.38) deA | 0.98 (0.46) dA | $0.09^{NS}$ | 0.41 | HR |
| PI140471 | 0.89 (0.30) deA | 0.93 (0.36) deA | 0.93 (0.36) dA | $0.07^{NS}$ | 0.34 | HR |
| PI420145 | 0.78 (0.11) eA | 0.84 (0.21) eA | 0.87 (0.26) dA | $0.41^{NS}$ | 0.19 | HR |
| PI157082 | 0.74 (0.05) eA | 0.82 (0.18) eA | 0.82 (0.18) dA | $0.40^{NS}$ | 0.14 | HR |
| F-test | 9.55** | 24.77** | 32.55** | | | |
| CV % (G) | 16.23 | | | | | |
| CV % (DAI) | 9.46 | | | | | |

CV = coefficient of variation; **. *, and ns = significant at 1%, 5%, and not significant at 5% by the F-test, respectively; Means followed by the same lowercase letter in the columns, or uppercase letter in the rows, are not significantly different by the LSD test at a 5% significance level.

Score means transformed using $\sqrt{X + 0.5}$ . RC = response classes based on original scores shown within parentheses: 0.0–1.0 = highly resistant (HR), 1.1–2.0 = moderately resistant (MR), 2.1–3.0 = susceptible (S), and 3.1–4.0 = highly susceptible (HS) (NORONHA et al., 2006).

Studies have suggested that differences in melon genotype resistance to *S. cucurbitacearum* may stem from variability in isolate aggressiveness. Santos et al. (2009) evaluated 86 melon genotypes with seven isolates and found all to be pathogenic, noting differences in aggressiveness; the BRSb isolate was the most aggressive, causing stem lesions with severity scores > 1.0, resulting in seedling damping-off.

Variations in severity scores can also be attributed to the onset and progression of the disease, which is influenced by plant-pathogen-environment interactions that vary with environmental conditions across experiments, leading to different results (CAMARGO, 2018). Thus, additional experiments replicating evaluations for unstable genotypes are essential before their inclusion in plant breeding programs.

Regarding disease progression, susceptible and moderately resistant genotypes in both experiments exhibited increasing disease levels across all evaluations, demonstrating a lack of resistance stability. In susceptible genotypes JAB 11 in Experiment I, and JAB 11, JAB 20, 'Olimpic Express', 'Ouro', and 'Gaúcho' in Experiment II symptoms progressed until the final evaluation, a pattern also observed in moderately resistant genotypes (Tables 2 and 3).

These findings indicate that moderately resistant genotypes with inconsistent disease severity responses should be further evaluated across generations for potential recommendation, as they lack sufficient resistance mechanisms to hinder pathogen development. Utilizing genotypes with only moderate resistance to *S. cucurbitacearum* may result in complete stand loss, either in early stages or during crop development, necessitating continuous disease monitoring throughout the entire cycle. Contrasting resistance classifications for melon genotypes to *S. cucurbitacearum* were reported by Santos et al. (2017) across multiple experiments.

Various management strategies, including genetic resistance, have been explored as potential methods for controlling *Stagonosporopsis cucurbitacearum* (HASSAN et al., 2018; ISLAM et al., 2020; ZHANG et al., 2025). Ongoing efforts to identify resistant genotypes aim to support breeders in melon breeding programs, facilitating subsequent steps such as determining genetic control of the trait and optimizing gene introgression strategies.

## CONCLUSION

The study confirmed the resistance of melon genotypes PI482398, PI157082, PI140471, and PI420145 to *Stagonosporopsis cucurbitacearum*, recommending their use in melon breeding programs to enhance resistance to this pathogen.

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