



Etiology of brown rot in strawberry (*Fragaria x ananassa*) in the State of Mexico

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ABSTRACT

Background/Objective. In a strawberry crop established in a greenhouse in Montecillo, Texcoco, State of Mexico, in 2022, brownish brown leaf spots and rotting of fruits with asymmetric sunken lesions were observed, which extended and acquired a brown color. The objective of the present work was to identify the causal agent of brown rot in fruits and strawberry plants.

Materials and Methods. Symptomatic fruits and leaves were collected, from which fungal isolates were obtained to perform pathogenicity tests on plants and fruits, in plants by two inoculation methods: spraying via foliar and via root; in fruits by immersion. Concentrations of 2×10^6 conidia mL⁻¹ were used. The ITS region of the rDNA was amplified and sequenced by PCR with the universal primers ITS1-ITS4.

Results. *Pilidium concavum* was morphologically and molecularly identified as the causal agent of brown spot and brown rot on strawberry. It was found to be pathogenic in strawberry fruits cv. Aromas and in plants less than two months old. It showed variation in virulence, in affected plants it varied from 40 to 50%, in fruits it reached 100%.

Conclusion. The result determines that *Pilidium concavum* is a pathogen that produces brown leaf spot and brown rot in strawberry fruits. It allows new lines of research related to the impact of the disease on strawberry production, yield and quality in Mexico. This research is the first report of *Pilidium concavum* as a strawberry pathogen in the State of Mexico.

Keywords: *Pilidium concavum*, strawberry, pathogenicity, virulence.

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INTRODUCTION

Strawberry (*Fragaria x ananassa*) is one of the most important fruits worldwide from an economic, commercial, and nutritional perspective (Giampieri *et al.*, 2012; Ikegaya, 2023). However, several pathogens affect its life cycle, including fungi, bacteria, viruses, and nematodes (Petrasch *et al.*, 2019). Fungi have the greatest impact on reducing yield and nutritional, commercial, and economic quality. They can infect all parts of the plant, causing severe damage and even plant death (Garrido *et al.*, 2011; Azam *et al.*, 2019). Among the most damaging fungal and oomycete pathogens affecting strawberries are *Botrytis cinerea*, *Colletotrichum* sp., *Sphaerotheca macularis*, *Phytophthora* sp., *Verticillium* sp., and *Diplocarpon earlianum* (Reddy, 2016). Additionally, new emerging pathogens have gained increasing economic and scientific significance over time.

Emerging pathogens pose a significant threat to strawberry productivity, as their incidence and severity can increase rapidly, resulting in substantial losses (Milgroom, 2017; Ristaino *et al.*, 2021). According to Pedraza Herrera *et al.* (2022), emerging diseases are caused by pathogens that have undergone changes in their incidence, geographic distribution, or host range, as well as alterations in their pathogenesis, evolution, or have been newly discovered or recognized. Among the new diseases caused by emerging pathogens are leaf spot and root and crown rot caused by *Neopestalotiopsis* sp. (Rebollar-Alviter *et al.*, 2020; Baggio *et al.*, 2021), fruit rot caused by *Neofusicoccum* sp. (Zhan *et al.*, 2021), leaf spot and anthracnose caused by *Pestalotiopsis* sp. (Morales-Mora *et al.*, 2019), and brown leaf spot and fruit rot caused by *Pilidium concavum* (Fernández-Ortuño *et al.*, 2014).

The presence of brown necrotic spot and rot on strawberry has been reported to date in only nine countries: India, Venezuela, Poland, Brazil, Belgium, China, the USA, Iran, and South Korea (Fernández-Ortuño *et al.*, 2014; Park *et al.*, 2017). The severity of the damage caused by this disease varies considerably, ranging from 3% to 50% infection in greenhouse plants, and up to 70% in stored fruit (Lopes *et al.*, 2010; Debode *et al.*, 2011). The pathogen responsible for this disease is *Pilidium concavum*, which has a broad host range in both wild and cultivated plants. Affected wild plants include *Fallopia japonica*, *Hieracium caespitosum*, *Aesculus hippocastanum*, *Greyia radlkoferi*, while cultivated hosts include *Olea europaea*, *Fragaria x ananassa*, *Paeonia suffruticosa*, *Bergenia crassifolia*, *Rosa rugosa*, *Eucalyptus* spp., *Prunus domestica*, *Vaccinium corymbosum*, *Vitis vinifera*, and *Ilex paraguariensis* (Aguin *et al.*, 2016; Karimi *et al.*, 2016; Lopez *et al.*, 2020). The spread of emerging pathogens to new geographical areas presents additional challenges for governments, farmers, and scientists, as they must be prepared to confront an expanding range of diseases that threaten food security and economic stability. Due to the incidence of brown toasted rot on strawberry fruit and leaves in Montecillo, Texcoco, Mexico, this study was designed to identify the causal agent of brown toasted rot in strawberry fruit plants through pathogenicity tests, morphological characteristics, and molecular assays.

A random sampling was conducted, and ten strawberry plants showing symptoms of leaf spot, flower peduncle necrosis, and fruit rot were collected. This was carried out in October and November of 2022 in the greenhouse at the Colegio de Postgraduados, Montecillo Campus, Texcoco, Mexico, located at coordinates 19°27'37"N 98°54'12"W. The samples were labeled, packaged in paper bags, and transported in a cooler for processing in the Phytosanitary-Phytopathology Laboratory at the Colegio de

Postgraduados, Montecillo Campus, State of Mexico. The samples were cut into 1 cm square tissue pieces, disinfected with 1% sodium hypochlorite for three minutes, and five tissue pieces from each sample were placed on potato-dextrose-agar (PDA; Bioxón®, Becton Dickinson de México) and in a humid chamber. Isolations were obtained from fruit and leaves. The re-isolation of the microorganism associated with symptomatic leaflets and fruit from the humid chamber was done on agar-water (AA; BD Bioxón®, Becton Dickinson de México) following the procedure described by the National Service of Health, Safety, and Agro-food Quality (SENASICA, 2018). The cultures were incubated under natural white light at a laboratory temperature of 25 ± 2 °C for 72 hours until mycelial growth was observed. To purify the isolation, a hyphal tip was transferred to PDA. Monosporic isolations were obtained through serial dilutions, which were plated on AA at 1.6% and incubated for 18 hours; then, a germinated conidium was transferred to PDA medium, and the cultures were incubated at 25 ± 2 °C. The isolates were stored at 15°C in test tubes with slanted PDA, supplemented with sterile mineral oil (Montesinos et al., 2015). Morphological identification was carried out using taxonomic keys reported by Barnett and Hunter (2006) and species-specific keys by Palm (1991) and Rossman et al. (2004). Semi-permanent preparations with 50% glycerol on glass slides were made to observe them under a BX51 compound microscope (Olympus, Japan). Mycelial coloration and conidial morphology and morphometry were determined by examining 100 conidia per isolate at 14 days after plating.

For the pathogenicity tests, inoculations were performed on mature strawberry fruits that were uniform in size and color, as well as on strawberry seedlings of the *Aromas* variety. Pathogenicity was assessed on both wounded and non-wounded fruits, which were previously disinfected. Wounds were made using a sterile needle to a depth of 1 cm in each fruit. Five fruits were used per treatment. Inoculation was carried out by immersing the fruits for 3 minutes in a conidial suspension of 2×10^6 conidia mL^{-1} , adjusted using a hemocytometer. Control fruits were immersed in sterile distilled water for 3 minutes. The fruits were placed in a plastic dome with sterile wet towels as humid chambers and incubated at 25 ± 2 °C under natural white light. Incidence was evaluated as the percentage of fruits affected by the pathogen, and severity was evaluated as the percentage of tissue affected.

For the plant tests, seedlings aged 1-2 months, 3-4 months, and older than 4 months were used. They were inoculated by spraying with spore suspensions of 2×10^6 conidia mL^{-1} , both foliar and root inoculations. Ten plants were assigned per treatment. Control plants were sprayed with sterile distilled water. The plants were incubated in a growth chamber with a 12-hour light and 12-hour dark photoperiod, at 80% relative humidity, for seven days. Incidence and severity were evaluated every 24 hours up to 20 days after inoculation. Incidence was assessed as the percentage of leaflets affected by the pathogen, and severity was measured using a visual scale with seven severity classes (Figure 1). Asymptomatic plant leaflets were disinfected and incubated in a humid chamber for five days, after which incidence was evaluated. The pathogenicity tests were performed in triplicate. Incidence and severity data were adjusted to a normal distribution, and the Tukey test was applied for mean comparison ($P \leq 0.05$).

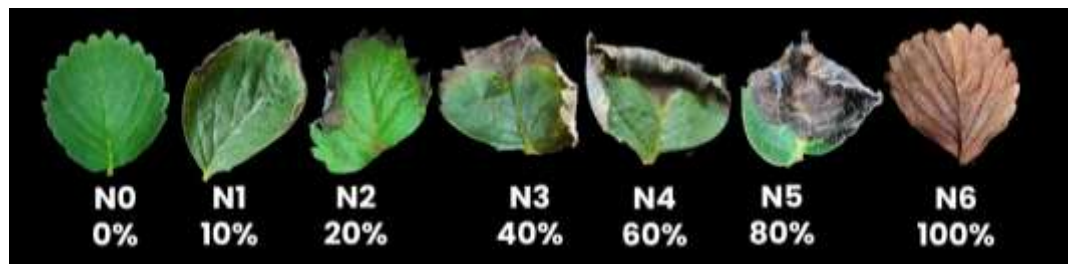


Figure 1. Visual scale for evaluating the severity of brown toasted leaf spot on strawberry. Designed by the authors.

For molecular identification, mycelium and conidia were collected to extract genomic DNA, following the method of Ahrens and Seemüller (1992). The ribosomal gene (rDNA) regions of the internal transcribed spacers ITS1 and ITS2 were then amplified by PCR using the universal primers ITS5 and ITS4 (Martin and Rygielwicz, 2005), using the Sanger method at Macrogen (Korea). The obtained sequences were purified and aligned with sequences deposited in the Gene Bank of the National Center for Biotechnology Information (NCBI) based on BLAST searches and literature. Sequences with 100% similarity were aligned in MEGA11 software, version 11.0.13 (Tamura *et al.*, 2021), using the Clustal algorithm, and compared with sequences in GenBank at NCBI, supported by the BLAST tool. The most similar sequences were extracted for phylogenetic analysis, constructing a neighbor-joining tree using the Bootstrap method and the Tajima-Nei model. *Chaetomella raphigera* (accession number MH860747) was used as the outgroup, and the sequences of the isolates were deposited in the NCBI Gene Bank. Symptoms observed on the fruits of strawberry cv. *Aromas* include asymmetric, sunken, wet lesions that are pink in color, without a chlorotic halo on the epicarp. The lesions expand, turning brown with masses of white conidia that turn pink-red and eventually brown on the lesion surface (Figure 2A-B). On the leaves, lesions begin at the margin or apex as brown, asymmetric spots, progressing toward the leaf base, characteristic of "toasted" leaves (Figure 2D-E).

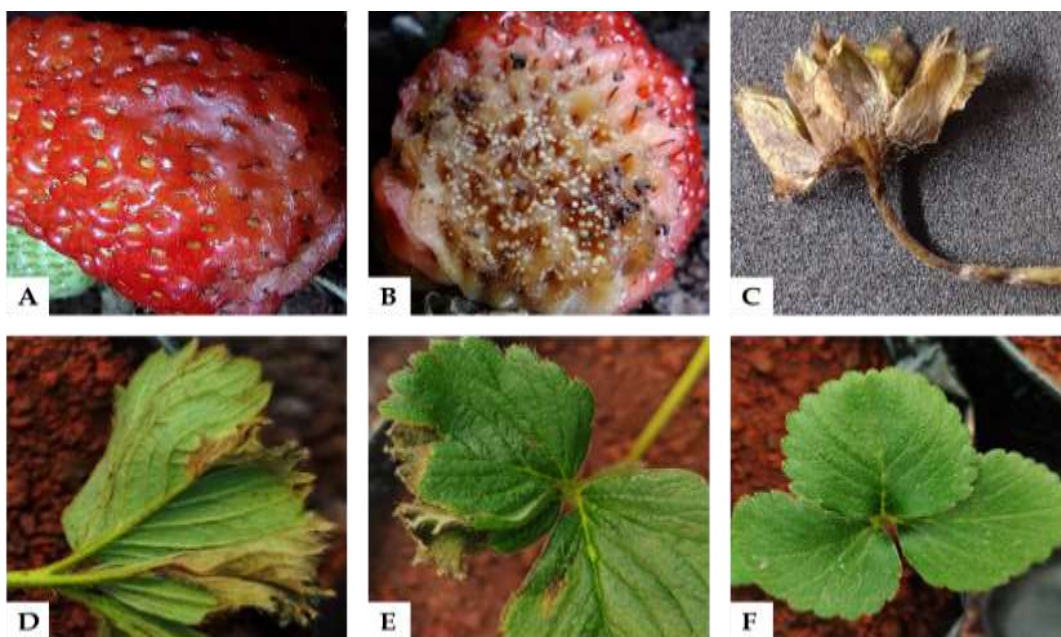


Figure 2. A) Fruit with sunken, wet lesions. B) Fruit with brown rot and fungal structures. C) Brown constriction on the flower peduncle. D-E) Leaves with toasted brown edges. F) Healthy leaves.

The isolate on PDA medium formed colonies with circular shapes, ranging from regular to irregular, and the presence of white mycelium was minimal to absent (mass-like form) with regular edges. The base color of the colony grew from cinnamon to brown. After 12 days of incubation on PDA medium, the colony edges developed a light to dark brown pigmentation. After 14 days of incubation, sporodochia were observed, forming in concentric circles with a gelatinous appearance, a black base, and disc-shaped to hemispherical structures, ranging from light brown to dark brown, suborbicular, measuring 354 to 658 μm in length and 370 to 688 μm in width. The conidiophores were hyaline, unicellular, cylindrical, and filiform, measuring 17.64 to 48.04 μm in length and 0.83 to 2.49 μm in width. Conidia were hyaline, aseptate, fusiform, canoe-shaped to allantoid, measuring 5.84 to 10.95 μm in length and 1.29 to 3.63 μm in width. (Figure 3). No sexual stage was observed. These characteristics correspond to those described by Palm (1991) and Rossman (2004) for *Pilidium*, reported as a facultative parasite with symptoms similar to those described by Debode *et al.* (2011) and Fernández-Ortuño *et al.* (2014).

The sequence alignment in the GenBank database (NCBI) showed 100% similarity with *Pilidium concavum* and *P. lythri*. In the phylogenetic tree (Figure 4), the isolate grouped with the reference isolates of *P. concavum* and *P. lythri*. Additionally, it was confirmed that *P. concavum* is more closely related to *P. pseudoconcavum*, with a support value of 94%. The isolates were registered in the GenBank database with accession numbers OR568456 and OR568457. The presence of *P. concavum* as a pathogen of leaves and fruits has been reported in several countries, including India (Phatak and Payak, 1965), Venezuela (Cedeño *et al.*, 2001), Poland (Gołębniak and Jarosz, 2003), Brazil (Lopes *et al.*, 2010), Belgium (Debode *et al.*, 2011), China (Geng *et al.*, 2012), the USA (Fernández-Ortuño *et al.*, 2014), Iran (Ayoubi *et al.*, 2016), and Korea (Park *et al.*, 2017). However, no reports of damage caused by this pathogen had been made in Mexico.

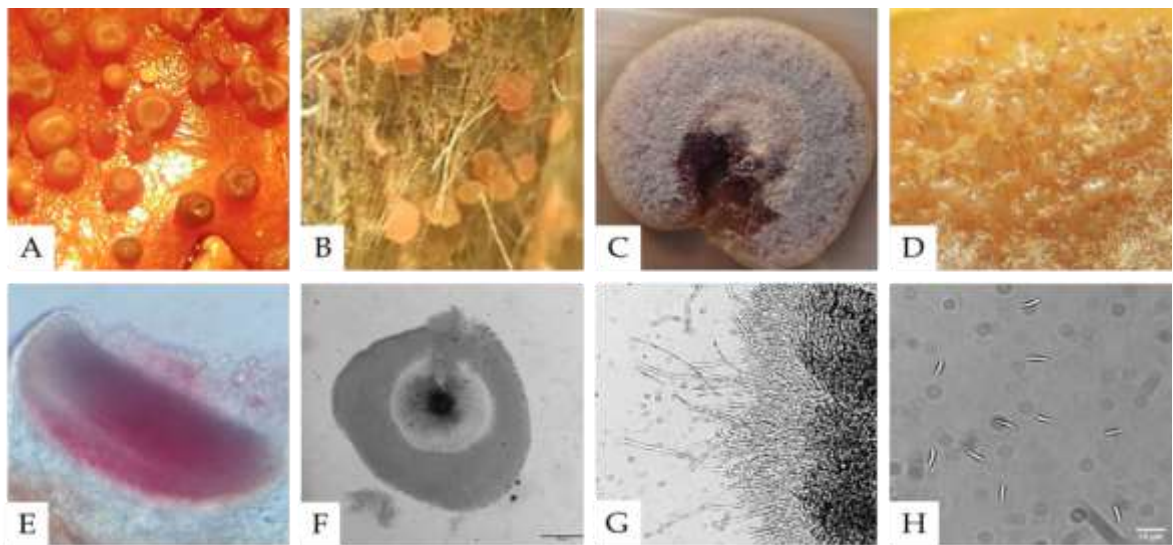


Figure 3. A) Sporodochia on strawberry fruit. B) Sporodochia on the underside of the leaf. C-D) Gelatinous colony with conidial mass on PDA medium. E-F) Longitudinal and transverse sections of the sporodochium. G) Hyaline, cylindrical, filiform conidiophores. H) Hyaline, aseptate, allantoid conidia.

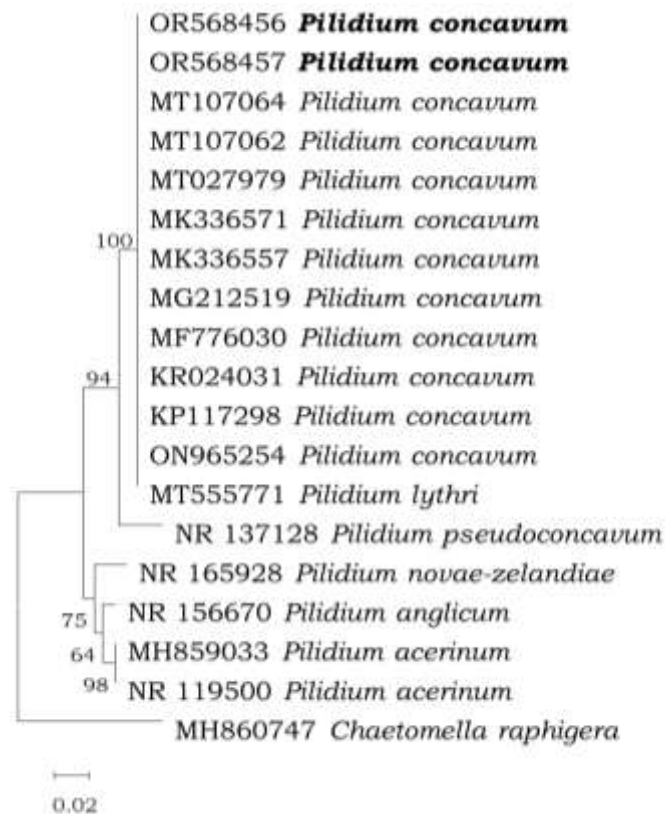


Figure 4. Phylogenetic tree based on Neighbor Joining of the ITS rDNA sequence, showing a phylogenetic affinity of the Mexico isolate (in bold) with *Pilidium concavum* above 95% of the node. Bar scaling 0.02 represents nucleotide substitutions per site.

The taxonomy of this fungus is not well defined and has undergone reclassifications based on recent morphological characteristics and phylogenetic analyses. The genus *Pilidium* of the family *Chaetomellaceae*, class *Leotiomyces*, was first described as *P. acerinum* (Alb. and Schwein) (Rossman *et al.*, 2004). Currently, the recognized species in the genus are *P. acerinum*, *P. lythri* (also known as *P. concavum*), *P. pseudoconcavum*, *P. eucalyptorum*, and *P. septatum* (Rossman *et al.*, 2004; Kirk *et al.*, 2011; Crous *et al.*, 2013; 2015). According to Palm (1991) and Rossman *et al.* (2004), *P. concavum* was shown to be related to the anamorph *Hainesia lythri*, *Dacryomyces lythri* (teleomorph *Discohainesia oenotherae*), *Peziza oenotherae*, *Pezizella oenotherae*, and *Sclerotiopsis testudinacea* as morphotypes of the same species, and thus are considered synonyms. However, *Pilidium* is the oldest generic name used and includes several phytopathogenic species. Recently, Rossman (2014) transferred *P. concavum* as a synonym of *P. lythri*, so referring to either name is now considered valid for the same species (Johnston *et al.*, 2014).

In the pathogenicity tests, three days after inoculation, sunken lesions were observed on wounded fruits, ranging in color from opaque pink to brown, with initial white conidial masses that turned pink and eventually brown (Figure 5A). The incidence and severity were both 100%. On non-wounded fruits, symptoms with fungal structures appeared on the fifth day after inoculation, with incidence and severity also at 100% (Figure 5D). The structures and spores on the symptomatic fruits were morphologically identical to the colonies originally used for inoculum production. The control fruits showed no symptoms of the disease. These tests confirmed that the causal agent of brown rot in strawberry fruit is *P. concavum*, as reported in similar studies by Debode *et al.* (2011) and Karimi *et al.* (2016) on strawberry fruit.

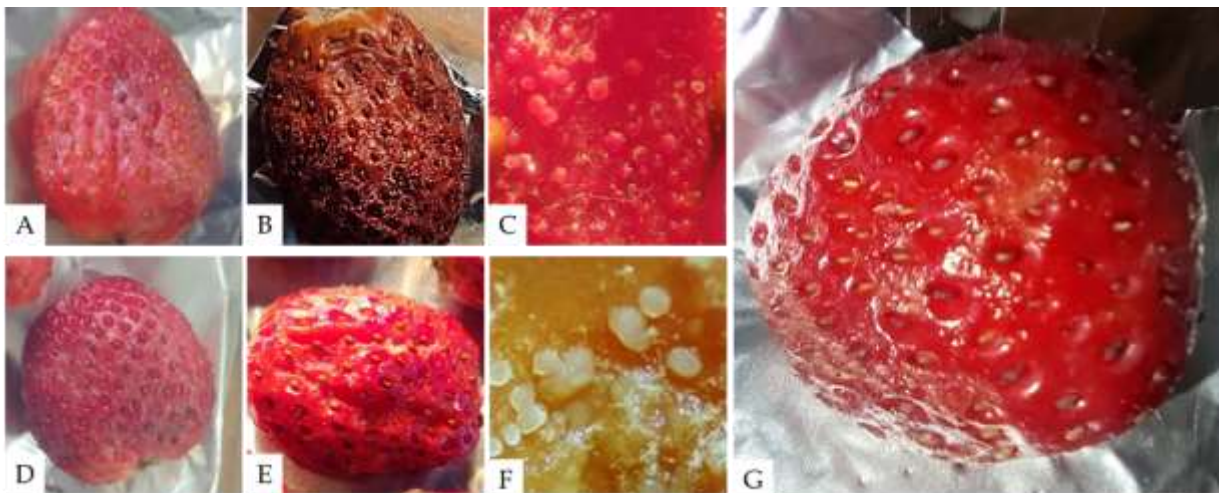


Figure 5. Pathogenicity tests on strawberry fruit inoculated with a concentration of 2×10^6 conidia mL^{-1} of *Pilidium concavum*. A) Fruit with a wound inoculated with the fungus. B) Wounded fruit showing symptoms 72 hours post-inoculation (hpi). C) Sporodochia of the fungus on the wounded fruit. D) Unwounded fruit inoculated with the fungus. E) Unwounded fruit showing symptoms 96 hours post-inoculation. F) Sporodochia of the fungus on the unwounded fruit. G) Control inoculated with sterile distilled water, showing no symptoms at 96 hours post-inoculation.

The inoculated seedlings, approximately 1 to 2 months old, showed mild symptoms on new shoots and leaves (Figure 6) 20 days after inoculation. Inoculation on leaves showed 50% incidence with 20% severity. Most symptoms were observed on new shoots (new leaves) and senescent mature leaves. In contrast, in the plants inoculated via the roots, the incidence was 40%, and symptoms appeared on senescent leaves and new leaves with 10% severity. Asymptomatic leaflets, after 5 days in a humid chamber, showed orange to brown sporodochia on the leaves (Figure 7). Fungal structures were observed in 90% of the leaf-inoculated treatment and 80% of the root-inoculated treatment. No structures were observed on stems or roots, only on leaves. The microorganism was reisolated, and its identity was confirmed through morphological identification. It is inferred that the fungus is a potential pathogen for nursery seedlings. This aligns with reports by Debode *et al.* (2011) and Fernández-Ortuño *et al.* (2014), who reported infections in nurseries and transplant batches. The infection was systemic. Plants inoculated through the roots showed structures on the leaves when exposed to a humid chamber, results similar to those obtained by Lopez *et al.* (2020), who inoculated *Ilex paraguariensis* plants via roots and observed damage on the leaves. In this study, plants at the fruiting stage showed fruit rot symptoms 6 months after inoculation, suggesting that the inoculum remained latent in the plants and caused damage when conditions became favorable. According to Hipol *et al.* (2014), *P. concavum* is part of the endophytic fungi group, as it belongs to the Leotiomycetes class of the Pezizomycotina subphylum, which includes common endomycorrhizal endophytic fungi. Therefore, it may have the ability to be endophytic in strawberry plants. Inoculation of 3-month-old and older-than-4-month-old strawberry plants did not induce brown rot symptoms on the leaves. However, when these plants developed and fruited 6 months after inoculation, the fruits and flower buds showed symptoms with fungal structures of *P. concavum*.



Figure 6. Strawberry plants (*Fragaria x ananassa*) cv. Aromas less than three months old, 15 days post-inoculation (dpi) with a suspension of 2×10^6 conidia per mL of *Pilidium concavum*. A) Inoculated via foliar; B) Inoculated via root routes; C) Control inoculated with sterile distilled water.



Figure 7. **A)** Asymptomatic strawberry leaves after 28 days post-inoculation (dpi), placed in a humid chamber. **B)** Formation of sporodochia on the leaves after 5 days in the humid chamber.

P. concavum is a fungus with a wide host range. Its importance lies in its ability to affect economically valuable crops, especially olive fruit (Arzanlou *et al.*, 2013), *Ilex paraguariensis* (López *et al.*, 2020), grape clusters (Aguin *et al.*, 2016), and strawberry (Debode *et al.*, 2011). Thus, the evolution of this pathogen, its geographical distribution, host range, and its interaction with plants have increasing relevance in the context of global climate change. This phenomenon affects plant communities in all aspects, from growth and reproduction to resistance and susceptibility (Zhao *et al.*, 2017; Tito *et al.*, 2018). Additionally, climate change alters the population and behavior of microorganisms, modifying their interactions with hosts (Cohen and Leach, 2020). This may lead to the adoption of new invasion strategies through changes in the virulence system, which could, in turn, compromise plant resistance (Cheng *et al.*, 2019). As a result, plant-microorganism interactions may shift from a mutualistic to a pathogenic association, or vice versa (González *et al.*, 2021). This study reports *Pilidium concavum* as the species responsible for brown toasted rot in strawberry fruits and leaves in Montecillo, Texcoco, State of Mexico. Morphological characteristics, pathogenicity tests, molecular characterization, and a literature review showed no genetic diversity between the isolates from leaflets and fruits, although further studies are needed, along with monitoring regions where strawberries are cultivated. Symptoms were more frequently associated with fruits, which contributed to the difficulties in replicating symptoms in leaves. Additional research is needed to clarify the origin of the new pathogen, its disease cycle, and to develop integrated management strategies for the disease in nurseries and postharvest.

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