Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Leaf Brown Blight Caused by *Neopestalotiopsis formicarum* on Jabuticaba in Taiwan

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Jabuticaba (*Plinia cauliflora* (Mart.) Kausel) originated from Brazil (Lorenzi 2000). The production of jabuticaba is growing globally because of its value in the food and pharmaceutical industries (Benvenuti et al. 2021). In August 2019, jabuticaba plants with symptoms of leaf blight were observed in a field in the Meinong District of Kaohsiung City, Taiwan. Disease incidence was 40%. Symptoms first presented as small, water-soaked lesions on young leaves, and then dark brown lesions of 1 to 3 cm in diameter on mature leaves. Six symptomatic leaves were collected from six jabuticaba plants to verify the causal agent. Tissues (5 × 5 mm²) were cut from the margin of symptomatic leaves. Samples were sterilized in 1% sodium hypochlorite for 60 s, rinsed with sterile distilled water three times, and placed in 1% water agar in the dark for 5 days at room temperature. Resultant fungal colonies were purified by subculturing fungal hyphal tips on potato dextrose agar in a growth chamber (28°C, 12 h photoperiod) until fungal conidia appeared. The fungi initially produced white, cottony, aerial mycelium, after which concentric black conidiomata appeared on the plates after 7 days of incubation. The five-celled conidia were fusiform to ellipsoid, straight to slightly curved, with sizes of 24.00 to 44.00 × 6.00 to 13.00 μm (avg. size, 32.00 × 9.37 μm; *n* = 120). The apical and basal cells were hyaline, and three median cells were pale brown and versicolorous. Conidia had two to three apical appendages and a conical basal cell with a truncate base. Based on

these characteristics, which were common among isolates from diseased samples, the causal pathogen was identified as *Neopestalotiopsis* sp. (Solarte et al. 2018). Internal transcribed spacer (ITS), translation elongation factor 1α (TEF), β-tubulin, and large ribosomal subunit (LSU) DNA sequences were obtained from these isolates and deposited in GenBank (MN723897, ITS; MN813055, TEF; MN813054, β-tubulin; and MN860104, LSU). Sequences demonstrated high sequence identity with those of *Neopestalotiopsis formicarum* ex-type cultures CBS 362.72 (Maharachchikumbura et al. 2014): 99.44% for ITS (KM199358), 99.38% for TEF (KM199517), 98.86% for β-tubulin (KM199455), and 100.00% for LSU (KM116248). The phylogenetic relationship of *Neopestalotiopsis* species supported the identification of our isolates as *N. formicarum*. Three independent three-isolate inoculation experiments were performed to fulfill Koch's postulates. Surface-sterilized leaves on live plants were punctured with a needle and inoculated with 5 μl of conidial suspension (1 × 10⁵ conidia/ml). Inoculated plants were kept in a growth chamber (25°C, 70% relative humidity) for 7 days. Control plants were inoculated with sterile distilled water and kept under the same conditions. Inoculated leaves developed brown lesions around wounds after 7 days. The pathogen was reisolated from diseased plants, following the steps used for the original procedure, with identical characteristics as the initial isolates. This is the first report of leaf brown blight caused by *N. formicarum* on jabuticaba in Taiwan. *N. formicarum* was recently considered as a new threat to jabuticaba (Gualberto et al. 2021). In addition, it has a broad host range on many tropical crops, such as guarana and banana (Gualberto et al. 2021). *Neopestalotiopsis* spp. have been reported to cause economically important fruit diseases (Gualberto et al. 2021). Therefore, *N. formicarum* may become a potential risk to tropical fruit production.

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