Diseases Caused by Fungi and Fungus-Like Organisms

Leaf Blight on *Photinia × fraseri* Caused by *Pestalotiopsis trachicarpicola* in China

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Plant Dis. 106:1520, 2022; published online as <https://doi.org/10.1094/PDIS-06-21-1351-PDN>. Accepted for publication 15 October 2021.

Photinia × fraseri is a well-known green plant mainly distributed in the Yangtze River and Yellow River Basin, in the east and southwest of China (Guan et al. 2013). In October 2020, typical leaf blight symptoms on roughly 10% of leaves on a *Photinia × fraseri* shrub were observed on the campus of Sichuan Agricultural University (30°42'19" N, 103°51'29" E). Initially, chlorotic lesions with brown margins occurred on the leaf margin, then large patches formed causing leaf necrosis, and finally lesions dried and formed acervuli 2 to 4 months later. Five single conidium isolates were collected (Chomnunti et al. 2014) and cultured on potato dextrose agar (PDA) at 25°C. All isolates shared similar morphological characteristics; they were white and thin, and the reverse was yellowish. Mycelium was hyaline, sparsely septate, and 1 to 4 µm in diameter. Conidiogenesis occurred after 7 days. Conidiogenous cells were discrete, lageniform, smooth, thin-walled, and colorless. Conidia were fusiform, straight to slightly curved, 4-septate, 21 to 30 × 5 to 7 µm ($\bar{x}$ = 27 × 6.0 µm, n = 30); basal cells were obconic with truncate base, hyaline, thin- and smooth-walled, 4 to 7 µm long ($\bar{x}$ = 5.5 µm, n = 30); three median cells were doliiform with thick walls, concolorous, olivaceous, constricted at the septa, and septa and periclinal walls were darker than the rest of the cell, 14 to 20 µm long ($\bar{x}$ = 17 µm, n = 30); apical cells were hyaline, conic to cylindrical, 3.0 to 6.5 µm long ($\bar{x}$ = 4.5 µm, n = 30), with 2 to

4 (mostly 3) tubular apical appendages arising from the upper portion, rarely branched, 7.5 to 18 µm long ($\bar{x}$ = 12 µm, n = 50); basal appendages were single, unbranched, 3 to 10 µm long ($\bar{x}$ = 6.5 µm, n = 30). DNA was extracted from the representative strain (SICAUCC 21-0012), and the internal transcribed spacer (ITS) region, large subunit of the nrDNA, translation elongation factor 1- α (*tef1- α*), and partial sequences of β -tubulin (*tub2*) were amplified by polymerase chain reaction and sequenced with primers ITS5/ITS4, LR0R/LR5, 728F/1567R, and Bt2a/Bt2b, respectively (Ariyawansa and Hyde 2018; Zhang et al. 2012). The sequences were deposited in GenBank (accession nos. MZ453106, MZ453108, MZ467300, and MZ467301, respectively). The nucleotide BLAST showed 99% (ITS, 0 gaps), 100% (*tub2*, 0 gaps), and 100% (*tef1- α* , 0 gaps) identities with the ex-type *Pestalotiopsis trachicarpicola* Yan M. Zhang & K. D. Hyde (IFRDCC 2440). The fungus was identified as *P. trachicarpicola* in combination with phylogeny and morphology (Maharachchikumbura et al. 2012; Zhang et al. 2012). To conduct Koch's postulates, five healthy 6-year-old *P. × fraseri* were inoculated with 10 µl spore suspension (10⁶ conidia/ml) onto the wounded sites (five leaves per plant, ~1 to 2 years old) via sterile pin, and five healthy plants were treated with sterile dH₂O as controls (Yang et al. 2021). The plants were placed in a greenhouse at 25°C with relative humidity >80%. After 2 months, leaf blight symptoms gradually emerged on inoculated leaves, and the controls were symptomless. Fungal isolates from symptomatic plants showed similar morphological characteristics as SICAUCC 21-0012, and the pathogen was not isolated from asymptomatic plants. To our knowledge, this is the first report of leaf blight caused by *P. trachicarpicola* on *Photinia × fraseri* in China. Disease management should be adopted properly to restore and improve its ornamental value.

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The author(s) declare no conflict of interest.

Keywords: China, leaf blight, *Pestalotiopsis trachicarpicola*, *Photinia × fraseri*

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