Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Leaf Spot Caused by *Colletotrichum siamense* on *Philodendron bipinnatifidum* in Guangxi, China

Ping Ning,¹ Mengmeng Lu,² Li'an Ma,² and Tiejun Deng^{3,†}

¹Guangxi Agricultural Vocational College, Nanning, Guangxi, China

²College of Life Sciences, Yangtze University, Jingzhou, Hubei, 434025, China

³Institute of Plant Protection, Guangxi Academy of Agricultural Sciences and Guangxi Key Laboratory of Biology for Crop Diseases and Insect Pests, Nanning, Guangxi, 530007, China

M. Lu and P. Ning contributed equally to this work.

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Philodendron bipinnatifidum belongs to the Araceae family, and its graceful plant architecture and function of purifying air and water has important ornamental value (Yu et al. 2019). *P. bipinnatifidum* is often cultivated in parks and along roadsides. In August 2019 and June 2020, leaf spot disease was observed on over 80% of *P. bipinnatifidum* plants in Qingxiushan Park (22°47'23.35" N, 108°23'4.26" E), Nanning, Guangxi, China. The disease was also frequently observed on *P. bipinnatifidum* in some other places in Nanning. Symptoms began as small, round, brown spots. As the disease developed, the center of the lesions became sunken, with a dark-brown border. Under severe conditions, some spots were joined into larger irregular spots, and even whole leaves died. For fungal isolation, small pieces (5 by 5 mm) were cut from the margin between lesions and healthy tissues of symptomatic leaves, disinfected with 75% ethanol for 10 s and 1% sodium hypochlorite solution for 1 min, and washed by sterile water for three times. More than 100 morphologically similar colonies with white mycelia and a dark-green pigment were obtained after 5 days of incubation on potato dextrose agar (PDA) at 25°C. Isolates GBZ6-1, GBZ9-1, and GBZ9-2 were selected for intensive study, and their mycelial growth rates averaged 14.5, 14.6, and 13.2 mm/day, respectively. Isolates could produce orange conidia on PDA for 7 days. Conidia were elliptical, aseptate, and colorless, with sizes

of 15.4 ± 0.14 by 5.8 ± 0.1 , 15.6 ± 0.14 by 5.3 ± 0.1 , and 15.0 ± 0.16 by 6.3 ± 0.1 μm for GBZ6-1, GBZ9-1, and GBZ9-2, respectively. Appressoria were mostly brown, ovoid, conidial appressoria and averaged 7.62 to 9.31 by 5.84 to 7.42 μm , and mycelial appressoria were 8.06 to 9.22 by 6.28 to 6.92 μm . Genomic DNA was extracted by the DNAsecure Plant Kit (Tiangen Biotech Co., Ltd., Beijing, China) and the rDNA *internal transcribed spacer region* (ITS), *actin* (ACT), *calmodulin* (CAL), *chitin synthase* (CHS-1), and *glyceraldehyde-3-phosphate dehydrogenase* (GAPDH) genes (Weir et al. 2012) were sequenced. Phylogenetic analysis was performed using RAXML (version 2.0) based on sequences of multiple loci (ITS, ACT, CAL, CHS-1, and GAPDH). The results showed that three isolates were identified as *Colletotrichum siamense* (accessions MW116805 to MW116816, for ACT, CAL, CHS-1, and GAPDH of GBZ6-1, GBZ9-1, and GBZ9-2; MW073391 to MW073393 for ITS of GBZ6-1, GBZ9-1, and GBZ9-2). According to the cultural and conidial morphology, as well as phylogenetic analysis, these isolates were identified as *C. siamense*. Pathogenicity tests were conducted on 1-year-old plants. Young, healthy leaves of three plants were artificially wounded by gently scratching with a sterile needle and 10 μl of conidial suspension (10^6 spores/ml) was applied per wound site for each isolate. Wounded leaves were inoculated with 10 μl of water as controls. All plants were sprayed with water and covered with plastic bags to maintain high humidity. Symptomatic lesions were observed on the inoculated leaves after 15 days at 28°C, whereas no symptoms were observed on the control leaves. To fulfill Koch's postulates, fungi were reisolated from symptomatic leaves and were morphologically identical to the inoculated isolates (Xue et al. 2020). To our knowledge, this is the first report of leaf spot caused by *C. siamense* on *P. bipinnatifidum* worldwide. This research may accelerate the development of future epidemiological studies and management strategies for anthracnose caused by *C. siamense* on *P. bipinnatifidum*.

References:

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[†]Indicates the corresponding author.
T. Deng; dtiejun@163.com