Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose Caused by *Colletotrichum fruticicola* on Tea in Taiwan

S. R. Lin,¹ S. Y. Yu,² T. D. Chang,² Y. J. Lin,² C. J. Wen,² and Y. H. Lin^{2,3,†}

¹ Section of Tea Agronomy, Tea Research and Extension Station, Executive Yuan, Taoyuan 324, Taiwan

² Department of Plant Medicine, National Pingtung University of Science and Technology, Pingtung 912, Taiwan

³ Plant Medicine Teaching Hospital, General Research Service Center, National Pingtung University of Science and Technology, Pingtung, Taiwan

S. R. Lin and S. Y. Yu contributed equally to this work.

Funding: Funding was provided by Ministry of Science and Technology, Taiwan, R.O.C. (MOST-105-2311-B-020-001 and MOST-108-2313-B-020-00). Plant Dis. 105:710, 2021; published online as <https://doi.org/10.1094/PDIS-06-20-1288-PDN>. Accepted for publication 2 September 2020.

Tea (*Camellia sinensis* [L.] O. Kuntze) is a popular beverage and cash crop that is widely cultivated in tropical and subtropical areas. In November 2017, diseased tea plants that exhibited brown blight disease were observed in Guanxi Township of Hsinchu County in Taiwan. In the plantation, 15% of tea trees (about 4,000 plants) had an average of 20% of the leaves with at least one lesion. The symptoms began as small, water-soaked lesions on young leaves and twigs and later became larger, dark brown, necrotic lesions 1 to 3 cm in diameter on leaves and 2 to 5 cm in length on twigs. Symptomatic leaf tissue (1 cm²) was surface sterilized with 1% NaClO (from commercial bleach, Clorox) for 1 min, washed with sterilized water three times, plated onto potato dextrose agar (PDA), and incubated under 12-h/12-h cycles of light and darkness at 25°C until sporulation to determine the causal agent. A fungus was consistently isolated from symptomatic leaf samples (80% isolation rate). The fungus initially produced white-to-gray fluffy aerial hyphae, which subsequently exhibited dark pigmentation. Acervuli and setae were absent. The conidia were hyaline, aseptate, smooth-walled, and cylindrical with obtuse to slightly rounded ends, with sizes of 9.54 to 15.78 × 3.23 to 5.26 (average 12.62 × 4.35, *n* = 30) µm. The majority had two rounded guttules. The appressoria were brown to dark brown, ovoid and slightly obtuse at the tip in shape, had lengths ranging from 3.59 to 10.31 µm (with an average of 7.18 µm, *n* = 30), and had diameters of 3.14 to 6.43 µm (with an average of

5.10 µm, *n* = 30). Morphological characteristics matched the descriptions of *Colletotrichum fruticicola* (Fuentes-Aragón et al. 2018; Liu et al. 2015). The internal transcribed spacer of nuclear ribosomal DNA (ITS), actin (ACT), chitin synthase (CHS-1), and Apn2-Mat1-2 intergenic spacer and partial mating-type Mat1-2 gene (ApMAT) sequences of the isolates were obtained to confirm this identification. The sequences showed close identity with those of *C. fruticicola* ex-type cultures ICMP18581 and CBS 130416 (Weir et al. 2012) of 99.65% for the ITS (JX010165), 99.29% for the ACT (JX009501), and 100.00% for the CHS-1 (JX009866), as well as close identity with the other ex-type culture LF506 (Liu et al. 2015) of 99.59% for the ApMAT (KJ954567), supporting the isolate's identification as *C. fruticicola*. The sequences were deposited in GenBank, with the following accession numbers: MN608177 (ITS), MN393175 (ACT), MT087546 (CHS-1), and MT087542 (ApMAT). Based on morphology and DNA sequence analysis, the associated fungus was identified as *C. fruticicola*. Pathogenicity tests were performed next according to the procedures described in Chen et al. (2017). Healthy leaves on tea plants (*Ca. sinensis* 'Chin-shin Oolong') were wounded by pinpricking in the middle of each counterpart and inoculated with conidial suspension (1 × 10⁷ conidia/ml, 10 µl). Both nonwounded and wounded healthy leaves were inoculated with the conidial suspension and sterile distilled water (a water control). The tea plants were covered with plastic bags to maintain high relative humidity for 2 days. One week after inoculation, anthracnose was observed on 40% of inoculated leaves, whereas all the control leaves remained healthy. The fungus was reisolated from the diseased plants and identified as *C. fruticicola* by resequencing of the four genes. To the best of our knowledge, this is the first report of anthracnose caused by *C. fruticicola* on tea in Taiwan, although the pathogen has been present in China and Indonesia (Farr and Rossman 2020; Shi et al. 2018; Wang et al. 2016).

References:

- Chen, Y., et al. 2017. Plant Dis. 101:1022.
- Farr, D. F., and Rossman, A. Y. 2020. Fungal Databases, Syst. Mycol. Microbiol. Lab., ARS, USDA. Retrieved March 23, 2020, from <https://nt.ars-grin.gov/fungal-databases/>.
- Fuentes-Aragón, D., et al. 2018. Mycobiology 46:92.
- Liu, F., et al. 2015. Persoonia 35:63.
- Shi, N. N., et al. 2018. Plant Dis. 102:241.
- Wang, C. Y., et al. 2016. Sci. Rep. 6:35287.
- Weir, B. S., et al. 2012. Stud. Mycol. 73:115.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: *Camellia sinensis*, appressorium, leaf brown blight

[†]Indicates the corresponding author.

E-mail: Y. H. Lin; pmhlin@mail.npust.edu.tw