Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose on *Cinnamomum camphora* (Camphor Tree) Caused by *Colletotrichum fioriniae* and *Colletotrichum siamense* in China

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The camphor tree (*Cinnamomum camphora*) is native to east Asia, and it produces pharmaceutical metabolites such as camphor and linalool (Chen et al. 2020). In September 2020, severe anthracnose symptoms were observed on *C. camphora* leaves in Nanchang, and estimated incidences ranged from 30 to 80%, which could inhibit leaf growth and reduce their biomass. The lesions appeared on the leaves of annual branchlets, with irregular dead areas appearing on leaf tips or margins, sometimes moving onto the shoots and small twigs. For pathogen isolation, 15 leaves with typical symptom were randomly collected in Jiangxi Agricultural University (N28°45'38", E115°50'0.006") and the fungi were isolated from the symptomatic-asymptomatic junction and cultured on potato dextrose agar (PDA) at 25°C in darkness. A total of 40 isolates were obtained from tissue samples, of which 32 were identified as belonging to *Colletotrichum* spp. following published works (Damm et al. 2012a, b; Weir et al. 2012). Based on the morphologies of conidia, all 32 isolates were classified into two categories. For more precise identification, the representative isolates YK1 and YK18 were selected to analyze using morphological characters after 7 days of incubation and multiple genes, including ITS (White et al. 1990), ACT,

GAPDH, TUB (Damm et al. 2009), and RPB2 (Réblová et al. 2011). Sequences were deposited in GenBank with accession numbers MZ229311 to MZ229326. Conidia of isolate YK1 were aseptate, primarily fusiform, and measured 14.07 to 21.21 × 4.99 to 6.79 μm (*n* = 51) and acervuli were 60.24 to 113.56 × 44.24 to 102.63 μm (*n* = 6). Conidia of YK18 were one-celled, cylindric with obtuse ends, and measured 13.28 to 16.51 × 4.10 to 5.82 μm (*n* = 52) and acervuli were 73.85 to 131.70 × 63.93 to 105.66 μm (*n* = 6). Acervuli of YK1 and YK18 were produced on alfalfa stems 40 days after inoculation and were dark brown to black in color. All the YK1 and YK18 genes showed >99% similarity to multiple *C. fioriniae* and *C. siamense* accessions, respectively. The phylogram reconstructed from the combined dataset using W-IQ-TREE (Trifinopoulos et al. 2016) showed that YK1 and YK18 clustered with *C. fioriniae* and *C. siamense*, respectively. Pathogenicity of both species was tested in the field by inoculating 10 surface-sterilized mature leaves with a puncture wound and 10 nonwounded young leaves with 20 μl of a conidial suspension (10⁵ conidia ml⁻¹). Leaves treated with sterilized water under the same conditions served as controls. After 4 to 7 days, the inoculated leaves developed typical dark brown to black lesions, similar to symptoms observed in the field, and controls remained symptomless. To fulfill Koch's postulates, *C. fioriniae* and *C. siamense* were consistently reisolated, and confirmed morphologically and molecularly. *C. siamense* has been found to cause anthracnose on *C. camphora* in China (Xu 2017). To our knowledge, this is the first report of anthracnose on *C. camphora* with *C. fioriniae* in China. In addition, this is an indication of the complexity of pathogens causing anthracnose on camphor tree, which can pose a serious threat to the production of *C. camphora* in China.

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