Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Corynespora cassiicola* Causing Leaf Spot on *Jasminum sambac* in China

Wei Gao,[†] Yong Wang, Hai-Yan Ben, Li-Juan Yang, and Jin-Pin Yu

Institute of Plant Protection, Tianjin Academy of Agricultural Sciences, Tianjin, 300381, China

Funding: Funding was provided by the National Key Research and Development Program of China (2017YFD02016). Plant Dis. 105:501, 2021; published online as <https://doi.org/10.1094/PDIS-06-20-1222-PDN>. Accepted for publication 2 September 2020.

Jasminum sambac (Linnaeus) Aiton belonging to Oleaceae family, has been cultivated in China for over 1,500 years. It is an important tea crop in South China and a popular ornamental plant in North China. In June 2015, *Corynespora* leaf spot on *J. sambac* was first observed in Caozhuang flower plant base in Tianjin (117°20' E, 39°13' N). In a series of investigations, the disease incidence of *Corynespora* leaf spot on *J. sambac* in Tianjin could range up to 20%. It was also found in flower planting greenhouses in Beijing and Hebei region. The initial symptoms appeared as small circular spots with gray white in the center and dark brown in the edge. The lesions expanded rapidly to 5 to 10 mm in diameter, surrounded by an obvious yellow halo. The infected leaves were covered with the circular spots and fell off at last. Fifty-six typical leaf samples were collected from 20 greenhouses, directly observed with a microscope (Nikon 80i), and isolated with a tissue separation method. Conidiophores were either solitary or in clusters, straight or curved and unbranched, with three to 10 septate, pale to dark brown in color. Those measured 80.6 to 234.8 µm long and 4.5 to 8.0 µm wide and were formed with zero to eight successive cylindrical proliferations ($n = 50$). Conidia borne from conidiophore, were single or in chains, obclavate to cylindrical, smooth. The average size of 50 conidia was 43.6 to 130.7 µm long × 6.4 to 13.5 µm wide, with four to eight pseudosepta ($n = 50$). The infected leaves were cut into small pieces, sterilized with 75% ethanol, rinsed in sterilized distilled water, and then plated on potato dextrose agar. The isolated plates were incubated at 25°C for 5 days. Thirty-five pure isolates were obtained from diseased leaves. The colonies were pale brown on the front and dark brown on the

underneath, with thick aerial mycelia. Morphological characteristics of the pathogen from the infected leaves and purified strains matched the description of *Corynespora cassiicola* (Ellis and Holliday 1971). To confirm the pathogenicity, conidial suspensions (10^6 conidia/ml) of 35 isolated strains were sprayed on the healthy plants at the seedling stage of *J. sambac*, respectively, five plants per strains. Ten healthy plants were sprayed only with sterilized water as a control. Conidial suspensions were prepared by washing conidia from the pure *C. cassiicola* cultures. Conidial suspensions were adjusted to a concentration of 1×10^6 conidia/ml with the hemocytometer. All of these inoculated plants were incubated in an artificial climate room at 90% relative humidity, $25 \pm 2^\circ\text{C}$. After 7 days, small circular spots, similar to the field samples, were observed on all inoculated plants, whereas the control plants displayed no symptoms. The same pathogens were reisolated from the inoculated leaves, which fulfilled Koch's postulates. For molecular identification, rDNA-ITS and two housekeeping genes (TUB2 and EF-1 α) were amplified and sequenced (Zhu et al. 2020). The sequences of three high-pathogenicity isolates showed 99% homology to *C. cassiicola* (MK571399) with 464 bp for rDNA-ITS, 100% homology to *C. cassiicola* (MN512639) with 469 bp for TUB2 gene, and 98.61% homology to *C. cassiicola* (MH263735) with 287 bp for EF-1 α gene. All nine obtained sequences were submitted to GenBank (MT334575 to 77 for rDNA-ITS, MT886387 to 89 for TUB2, and MT886390 to 92 for EF-1 α). The molecular identification and morphological characteristics showed that the isolated strains from *J. sambac* were identified as *C. cassiicola*. *C. cassiicola* has an extensive host range, covering 397 host plants (Farr and Rossman 2020). Recently, *C. cassiicola* has been reported on *Jasminum mesnyi* in China (Zhang et al. 2018). To our knowledge, this is the first report of leaf spot caused by *C. cassiicola* on *J. sambac* in China and also worldwide.

References:

- Ellis, M. B., and Holliday, P. 1971. CMI Descriptions of Pathogenic Fungi and Bacteria, No. 303. Commonwealth Mycological Institute, Kew, U.K.
- Farr, D. F., and Rossman, A. Y. 2020. Fungal Databases, Syst. Mycol. Microbiol. Lab., ARS, USDA. Retrieved August 13, 2020, from <https://nt.ars-grin.gov/fungal-databases/>.
- Zhang, Y. L., et al. 2018. Plant Dis. 102:2643.
- Zhu, J. Z., et al. 2020. Can. J. Plant Pathol. 42:125.

The author(s) declare no conflict of interest.

Keywords: *Corynespora cassiicola*, *Jasminum sambac*, fungi

[†]Indicates the corresponding author.

E-mail: W. Gao; gaowei5277@163.com