Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum truncatum* Causing Anthracnose on *Oxalis corniculata* in China

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Oxalis corniculata L., which belongs to the family Oxalidaceae R. Br., is a very common perennial herb. It is usually planted on bare land or in forests as a landscaping plant, and the whole plant can be used for its medicinal values of clearing heat, detoxification, and detumescence. In August 2019, typical symptoms of anthracnose on *O. corniculata* leaves were observed in the green belt on the campus of Shandong University of Technology (36.81°N, 117.99°E), Shandong Province, China. The disease incidence was above 40% from investigating more than 300 m² of planting area. Most *O. corniculata* are planted in the forest where the disease was found, mainly in an environment with high relative humidity and less ventilation. The infections on leaves appeared initially as tawny oval or irregular spots, and then the lesions enlarged gradually until the leaves died back or wholly withered, which greatly reduced the landscape effect of *O. corniculata*. Diseased leaves were collected by cutting into small pieces, sterilizing with 75% ethanol for 30 s and 2% sodium hypochlorite (NaClO) for 60 s, and rinsing with sterile deionized water three times. Each air-dried tissue segment was cultured on potato dextrose agar (PDA) and incubated at 25°C for 5 to 7 days in the dark (Zhu et al. 2013). Fifteen isolates were obtained from 20 symptomatic leaves

and the cultures were initially gray white, becoming grayish to dark green after 7 days, with copious gray aerial mycelium and black microsclerotia. Three isolates were verified by the amplification of DNA sequences of glyceraldehyde-3-phosphate dehydrogenase (GAPDH), actin (ACT), histone H3 (H3), and chitin synthase (CHS1) genes, using the primer pairs GDF1/GDR1, ACT-512F/ACT-783R, CYLH3F/CYLH3R, and CHS-79F/CHS-234R (Damm et al. 2019; Fu et al. 2019; Liu et al. 2013), respectively. The sequenced genes (GenBank accession nos. OK017473, OK159078, OK159076, and OK159077) shared 99.62 to 100.00% nucleotide identity with the corresponding genes of *Colletotrichum truncatum* strain UASB-Cc-10 (GenBank accession nos. KF322064.1, KF322055.1, KF322073.1, and KF319059.1, respectively), which was consistent with the morphological identification (Sawant et al. 2012). A pathogenicity test was performed with six healthy *O. corniculata* plants infected with mycelial plugs (about 3 mm in diameter) of three *C. truncatum* isolates from a 5-day-old culture, while negative controls on the same leaves were inoculated with sterile PDA plugs. All plants were placed in a greenhouse at 25 to 30°C with 90% relative humidity. The experiment was conducted three times. Five days later, all inoculated leaves had brown sunken spots, whereas no symptoms appeared on negative controls. The same pathogen, *C. truncatum*, was identified from the inoculated leaves on the basis of morphological and molecular characteristics as described above, confirming Koch's postulates. To our knowledge, this is the first report of anthracnose caused by *C. truncatum* on *O. corniculata* in China. The discovery of this new disease is beneficial to the application and protection of *O. corniculata*, a popular landscape and medicinal plant.

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