Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Cercospora apiicola* Causing Leaf Spots and Stem Lesions on Celery in China

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Celery (*Apium graveolens* L.) is a vegetable crop cultivated widely in the Mediterranean, Europe, and parts of Asia. From March to May in 2014, leaf spots and stem lesions were observed on celery plants in Yanqing (116°03'E, 40°32'N), Beijing, and Chengdu (104°06'E, 30°67'N), Sichuan Province. Plants developed 0.3- to 1.8-cm-diameter subcircular leaf spots with brown centers surrounded by pale yellow halos. Spots on leaves were amphigenous. Necrotic areas on stems were subcircular to elongated, pale brown to brown. Plants in five greenhouses were surveyed with 30 to 60% disease incidence. Necrotic tissue from eight stems and 12 leaves was cut from the margins of lesions and divided into two parts. One part was treated with lactophenol and used for microscopic examination. The other part was surface sterilized with 4% sodium hypochlorite for 2 min, rinsed three times in sterile water, placed onto 2% malt extract agar, and incubated at 26°C for 7 days with natural daylight. Stromata on leaves and stems were not well developed. Four to ten conidiophores (15.3 to 56.5 × 2.8 to 5.5 µm), formed in fascicles, emerged through stomata or erupted through the cuticle. Conidia ($n = 50$) were 60 to 135 × 2.5 to 4.5 µm, solitary, septate, cylindrical to obclavate-cylindrical, hila thickened and darkened. Colonies were white to smoke-gray, and aerial mycelia were sparse to moderate. Morphological characteristics of the pathogen were similar to *Cercospora apiicola* (Groenewald et al. 2006, 2013). The gDNA of 20 isolates was extracted from mycelium using the Plant Genomic

DNA Kit (Tiangen, China). The internal transcribed spacers (*ITS*), actin (*ACT*), translation elongation factor 1- α (*TEF1*), and histone H3 (*HIS3*) regions were amplified with primer pairs ITS1/ITS4 (Groenewald et al. 2013), ACT-512F/ACT-783R (Carbone and Kohn 1999), EF1-728F/EF1-986R (Carbone and Kohn 1999), and CYLH3F/CYLH3R (Crous et al. 2006). Phylogenetic analysis of multiple genes (Bakhshi et al. 2018) was conducted with the neighbor-joining method using MEGA7. The sequences of our isolate (QC14030702) and five published sequences of *C. apiicola* were clustered into one clade with a 99% confidence level. The sequences of QC14030702 have been deposited in GenBank with accessions KU870468 for *ITS*, KU870469 for *ACT*, KU870470 for *TEF1*, and KU870471 for *HIS3*. Pathogenicity of the isolates was tested on plants (cv. Jia Yuan Xi Yang Qin). Because the pathogen sporulated poorly on various media, mycelial fragments were sprayed on leaves in a suspension of 1×10^6 /ml in a greenhouse (temperature $26 \pm 0.5^\circ\text{C}$, 98% relative humidity, photoperiod 12 h). Healthy plants were sprayed with sterilized water as controls. Three replicates of every isolate were conducted, and each replicate included five celery plants. After 7 days, leaf spots appeared on all inoculated plants, which were similar to those on celery in the field. All control plants remained asymptomatic. Reisolation of the fungus from infected tissues showed the same morphological and cultural characteristics of *C. apiicola* as the original isolates. *C. apiicola* has been reported in Greece, Korea, South Korea, and Venezuela on celery but has never been reported in China (Farr and Rossman 2020). *C. apiicola* potential threatens celery production, and this the first report of the disease in China.

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