Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum gloeosporioides* Causing Anthracnose on *Canna edulis* in China

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Canna edulis Ker has been an important economic plant in southern China. The tuberous stems are the most valued plant part and in the past were routinely used as animal feed. In June 2019, leaf spot disease was detected on *C. edulis* plants in Chengmai, Hainan Province. Symptoms of the disease were characterized by oval-shaped, initially pale to yellow lesions that become necrotic (brown) with yellow borders. As the lesions expanded, the disease could encompass the entire leaves, which were seen as concentric rings typical of anthracnose disease. A survey of *C. edulis* plants revealed that the disease caused serious damage during the summer in Hainan Province, with 50 to 60% incidence in plants. To isolate the pathogen, 10 pieces of diseased leaf samples were plated, and seven pieces yielded fungal colonies after 5 to 6 days of incubation at 25°C. The colonies were single-spored to obtain pure cultures. Pure cultures on potato dextrose agar (PDA) appear white to gray, with white margins and aerial hyphae, and the reverse of the colonies was gray to brown. Conidia were single-celled, hyaline, cylindrical to slightly curved with a rounded apex and truncated base, and measured 13.3 to 18.1 (length) × 3.7 to 5.5 (width) μm ($n = 50$). The morphological characteristics and measurements of this fungal pathogen matched the previous descriptions of *Colletotrichum gloeosporioides*

(Prihastuti et al. 2009). Isolate JO-3 was identified by molecular analysis; sequences of the internal transcribed spacer (ITS), actin (ACT), and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) regions were obtained. These loci were amplified from isolates using the primer pairs ITS1/ITS4 (Mills et al. 1992), ACT-512F/ACT-783R (Weir et al. 2012), and GDF/GDR (Templeton et al. 1992), respectively. A BLAST search of GenBank showed that the ITS (MN913584), ACT (MN919196), and GAPDH (MN919195) sequences of the isolate were 99, 100, and 100% homologous with *C. gloeosporioides* (GenBank accession nos. MH930419, JX009931, and KX885158). Maximum likelihood trees based on concatenated sequences of the three genes were constructed using MEGA7.0. The results showed the strains isolated from *C. edulis* were closely related to *C. gloeosporioides*, as supported by high bootstrap values. Pathogenicity testing was performed with isolate JO-3 by depositing 10-μl droplets of a suspension (1×10^6 conidia/ml) on the surfaces of five artificially wounded leaves (a small hole made with a pushpin) of 10 healthy 1-year-old *C. edulis* plants. An equal number of control leaves were inoculated with sterile water to serve as a negative control. The test was conducted three times. Plants were kept at 25°C with 80% humidity and observed for symptoms every day. One week after inoculation, all the inoculated plants showed symptoms of yellow sunken spots similar to those observed in the field. No symptoms were observed on the controls. The fungus reisolated from the infected tissues showed the same cultural and morphological characteristics of the strain inoculated, fulfilling Koch's postulates. *C. gloeosporioides* was previously reported as the causal agent of anthracnose on *Hymenocallis littoralis* (Zhao et al. 2019), *Abelmoschus esculentus* (L.) Moench (Shi et al. 2019), and *Sorbaria sorbifolia* (Li et al. 2019) in China. To our knowledge, this is the first report of anthracnose on *C. edulis* caused by *C. gloeosporioides* in China. This disease can seriously affect the yield and quality of *C. edulis* in China. Given its wide host range, *C. gloeosporioides* has great potential to become an economically important plant pathogen.

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