Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Chaetomium pseudocochliodes* Causing Petal Blight Disease of *Camellia reticulata* in Yunnan, China

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Camellia reticulata is a world-famous ornamental flower (Wang et al. 2021). In February 2021, infected flowers of *C. reticulata* ‘Shizitou’ were collected in Zixi Mountain, Chuxiong City, Yunnan Province, China (25°00′13″ N, 101°25′21″ E). Petal blight disease incidence ranged from 40 to 75% in the garden. The infected flowers showed symptoms of varying degrees of yellow-browning, dry or wet rot to wilting of the whole flower and even dropping. Three symptomatic flowers were randomly collected in the garden. Tissues from the infected flowers (5 × 5 mm) were surface disinfected with 75% ethyl alcohol for 30 s, rinsed in sterile water three times, air dried, and cultured in potato dextrose agar medium (PDA) at 25 ± 2°C in normal light for 5 to 7 days (Fang 1998). Similar fungal colonies were isolated from 50 to 75% of the infected flowers. Three isolates from different flowers showed similar colony morphology. After subculturing of hyphal tips on PDA for 5 to 7 days, the initially yellow colonies showed abundant white aerial mycelium with sporulation. The asci sporulation site is 24 (to 37) × 7 (to 14) μm,

and the stalk length is 17 to 42 μm, with eight biseriate acuminate ascospores. Mature ascospores are olive-brown or brown, lemon-like, double pointed, with slightly umbilical protrusions at both ends, flat on both sides, 9 (to 11.5) × 7 (to 9) × 5.5 (to 7) μm, with germ pores on the top (Wang et al. 2016). These morphological features are consistent with *Chaetomium pseudocochliodes*. Genomic DNA was extracted from the isolated strains. To identify this pathogen genetically, sequence analyses were conducted using the ITS1/ITS4 (Henson and French 1993), NL1/NL4 (Liu et al. 2011), and EF1-938F/EF1-2218R (Tan et al. 2016) primers for the internal transcribed spacer (ITS), large ribosomal subunit (LSU), and elongation factor 1-α (EF1-α) genes. The obtained sequences were deposited in GenBank with accession numbers MZ817067 (ITS), MZ817072 (LSU), and MZ820167 (EF1-α). Phylogenetic trees were constructed to determine the phylogenetic relationships based on the MEGA 6.0 maximum likelihood method. To confirm pathogenicity, tests were conducted with fungal plugs (5 mm) from a 7-day-old colony placed onto the surface of healthy petals. Sterile, water-absorbent cotton placed onto the healthy petal surface near the fungus plug and a plastic wrap cover over the Petri dish were used for moisturizing. Three replicates in each of three groups were included (three healthy petals per group, one for wounded inoculation, one for unwounded inoculation, and one for a sterile PDA plug). A sterile PDA plug was placed onto the surface of healthy petals as a control. After incubation at room temperature for 5 days (Ren 2019), three replicates in each of two groups of treated healthy petals with wounded inoculation showed obvious symptoms, and no symptoms appeared in the control. Unwounded inoculated petals showed symptoms after 7 to 10 days. The fungus was reisolated from the lesions of inoculated tissues. The reisolated fungal colonies showed identical morphology and high sequence similarity with ITS, LSU, and EF-1α of the initial isolate. No fungus was isolated from the controls. *C. pseudocochliodes* was first extracted from the roots of the *Panax notoginseng* in Wenshan, Yunnan (Wang et al. 2016). To our knowledge, this is the first report of petal blight caused by *C. pseudocochliodes* on *C. reticulata* in China.

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