Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Root Rot Caused by *Fusarium avenaceum* on *Coptis chinensis* in Chongqing, China

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Coptis chinensis Franchet is a perennial herb used as a traditional Chinese medicine. Annual production of *Coptis* is about 3,000 metric tons in Shizhu, Chongqing. In recent years, root rot has become a serious and widespread disease on *Coptis* in Shizhu with an average incidence of 40% and yield losses up to 67%. Infected plants were easy to pull from the soil, and most of the fibrous roots and main roots were brown or black compared with healthy roots that were yellow. Severely infected plants were wilted and necrotic. In October 2019, 33 diseased roots were collected from Shizhu (30°18'N, 108°30'E), and small samples (0.5 cm in length) were cut from the border between diseased and healthy tissue, successively sterilized with 75% ethanol and 2% sodium hypochlorite, rinsed three times with sterilized water, dried on sterilized filter paper, transferred onto potato dextrose agar (PDA), and incubated at 25°C for 7 days in the dark. Eighteen distinct fungal isolates (H1 to H18) were isolated, and Koch's postulates were conducted to verify the pathogenicity of individual isolates. The rhizosphere soil of healthy 2-year-old *Coptis* plants was inoculated by pouring 5 ml of conidial suspension (10⁶ conidia/ml) scraped from a culture of each isolate on PDA. Sterilized water was used to mock inoculate. For each isolate, six plants were inoculated. After 20 days, the roots of all plants inoculated with H15 or H18 were dark brown and rotten, whereas mock-inoculated plants were healthy. Isolates H15 and H18 were reisolated from

symptomatic plants. Isolate H15 formed abundant white mycelium on PDA and produced rose pigment in the agar. Conidia were long and slender, straight to slightly curved, with one to three septate. The apical cells were tapering and bent, and the foot cells were distinctly notched. Conidiogenous cells were monophialides and polyphialides. No chlamydospores were observed. Isolate H18 formed white sparse mycelium on PDA and produced no pigment in the agar. Conidia were relatively wide, straight and stout, with three to five septate. The apical cells were blunt and rounded, and the foot cells were barely notched. Conidiogenous cells were long monophialides. Chlamydospores were formed intercalary in the hyphae. For further identification, the internal transcribed spacer (ITS), β -tubulin, translation elongation factor 1 α (EF1 α), and RNA polymerase second largest subunit (RPB2) gene regions were amplified with ITS1/ITS4, Bt2a/Bt2b, EF1/EF2, and 5f2/7cr (Glass and Donaldson 1995; O'Donnell et al. 2010; White et al. 1990). GenBank accession numbers of H15 and H18 were MT463390 and MT463389 for the ITS region, MT465656 and MT465654 for β -tubulin, MT653321 and MT465651 for EF1 α , and MT653323 and MT653322 for RPB2. BLAST results showed the ITS, β -tubulin, EF1 α , and RPB2 sequences revealed 100% (533/533), 100% (265/265), 98% (622/632), and 99% (936/947) homology, respectively, with those of *Fusarium avenaceum* (MN186746.1, MH791368.1, KU238140.1, and MK185027.1) and 100% (537/537), 100% (227/227), 100% (688/688), and 99.03% (918/927) with *F. solani* in GenBank (MH857319.1, MN692929.1, KP674211.1, and MH300549.1), respectively. Thus, H15 and H18 were identified as *F. avenaceum* and *F. solani* based on morphological and molecular characteristics. To our knowledge, *F. solani* has been previously reported as a pathogen (Luo et al. 2014), and this is the first report of root rot on *Coptis* caused by *F. avenaceum* in the world. Identification of the pathogens is important for effective disease management and control.

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