Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Diaporthe eres* Causing Root Rot of *Coptis chinensis*

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The Chongqing coptis (*Coptis chinensis* Franchet) industry produces more than 60% of the Chinese coptis crop, and it has been exported to many countries and regions. Since 2008, root rot has become a serious and widespread disease on coptis plants in Shizhu county with an average incidence of 40% and yield losses up to 67%. Symptomatic coptis plants showed stunted growth, with the fibrous roots and main roots having brown or black, rotten, necrotic lesions. To our knowledge, *Fusarium solani*, *F. carminascens*, *F. oxysporum*, and *F. tricinctum* have been previously reported as pathogens of coptis root rot (Cheng et al. 2020; Luo et al. 2014; Wu et al. 2020), but non-*Fusarium* pathogens have not been reported yet. In order to identify new pathogens, 33 diseased roots were collected from Shizhu (30°18'N, 108°30'E) in October 2019. Small samples (0.5 cm in length) were cut from the border between diseased and healthy tissue and then put on PDA after surface sterilization. Cultures were incubated at 25°C in the dark until fungal colonies were observed. After subculturing for three times, three out of 21 isolates yielded a similar type of fungal colony. White, aerial, fluffy mycelium was formed and reached 8.3-cm diameter within 7 days, and dark pigmentation developed in the center. Colonies turned gray with age, and abundant dark brown pycnidia and black stromata were formed at maturity.

Alpha conidia were aseptate, hyaline, fusiform to ellipsoidal, often biguttulate, measuring 6.0 to 8.5 × 2.0 to 3.0 μm. Beta conidia were aseptate, hyaline, linear to hooked, measuring 18 to 30 × 1.0 to 1.5 μm. For further identification, a multigene phylogenetic analysis was carried out. The internal transcribed spacer (ITS), translation elongation factor 1α (*tef1-α*), histone H3 (*his3*), calmodulin (*cal*), and β-tubulin (*tub2*) gene regions were amplified with ITS1/ITS4, EF1-728F/EF1-986R, CYLH3F/H3-1b, CAL228F/CAL737R, and T1/Bt2b (Carbone and Kohn 1999; Crous et al. 2004; Glass and Donaldson 1995; White et al. 1990). GenBank accession numbers of isolate H13 were MT463391 for the ITS region, MT975573 for *tef1-α*, MT975574 for *his3*, MT975575 for *cal*, and MT975576 for *tub2*. BLAST results showed the ITS, *tef1-α*, *his3*, *cal*, and *tub2* sequences revealed 99.82% (553/554 base pairs), 100% (347/347 base pairs), 100% (474/474 base pairs), 99.39% (486/489 base pairs), and 99.14% (803/810 base pairs) homology, respectively, with those of *Diaporthe eres* (MN816416.1, KU557616.1, KC343564.1, KU557595.1, and KY569366.1). Thus, H13 was identified as *D. eres* based on its morphological and molecular characteristics. Pathogenicity of *D. eres* in coptis was investigated using the H13 isolate (one of the three isolates). The roots of 10 healthy 2-year-old coptis plants were individually inoculated with 5 ml of a 10⁶ conidia/ml suspension, and sterilized water was used to mock inoculate. Thirty days after inoculation, most of the inoculated coptis roots showed dark brown and rotten roots, similar to those observed in the field, whereas mock-inoculated roots appeared healthy. *D. eres* was recovered from symptomatic roots and identified based on morphology. To our knowledge, this is the first report of *D. eres* causing root rot of coptis not only in China but anywhere in the world.

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