Diseases Caused by Fungi and Fungus-Like Organisms

Root Rot of *Angelica sinensis* Caused by *Clonostachys rosea* and *Fusarium acuminatum* in China

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Angelica sinensis, a perennial plant in the Apiaceae, is a source of one of the most important traditional medicines in China. This medicinal herb has been mainly cultivated in Gansu, Sichuan, Yunnan, Shanxi, Hubei, and Qinghai provinces. In June 2020, angelica plants in a field in the village of Sada, Minhe County, Haidong City, in Qinghai Province (36°19'9.47"N, 102°51'30.83"E, elevation: 2,437 m), displayed symptoms of yellowing, stunting, root rot, and wilting. Severe brown discoloration of vascular tissue in the stems of infected plants was observed. Root rot seriously affected the quality and yield of *A. sinensis*. The incidence of root rot in the fields reached 15% in 2020 and 18% in 2021. Fungi were isolated from diseased roots using a single spore method. The identity of isolates was confirmed by sequencing the nuclear ribosomal internal transcribed spacer (ITS) using the primers ITS1/ITS4 (White et al. 1990) and the translation elongation factor 1- α (*TEF1- α*) gene using the primers EF-1/EF-2 (O'Donnell et al. 1998). BLAST analysis of the ITS and *TEF1- α* sequences of isolates DG-1, DG-1-1, DG-1-2, DG-2, DG-2-1, DG-5, and DG-5-1 in the NCBI database showed 99 to 100% nucleotide identity to those of *Clonostachys rosea* (NCBI accession nos. MZ424803 to MZ424809 [ITS] and MZ451383 to MZ451389 [*TEF1- α*]). BLAST analysis of the ITS and *TEF1- α* sequences of isolates DG-3, DG-3-1, and DG-4 in the NCBI database produced matches of 99.1% or better to *Fusarium acuminatum* (NCBI accession nos. MZ424810 to MZ424812 [ITS] and MZ441148 to MZ441150 [*TEF1- α*]).

Conidia of *C. rosea* were hyaline, round or oval, and aseptate with an average length and width of 6.5 to 8.5 $\times$ 2.5 to 3.5 μ m. Chlamydospores were round or oval with an average length and width of 9.9 to 16.2 $\times$ 8.1 to 13.6 μ m. Conidiophores of *C. rosea* were hyaline, septate, and *Verticillium*-like, and conidiogenous cells were slender and cylindrical. Macroconidia of *F. acuminatum* were hyaline, falciform, zero to five septate, and had an average length and width of 22.5 to 39.5 $\times$ 2.5 to 4.5 μ m. Microconidia were rare. Chlamydospores were oval with an average length and width of 9.5 to 14.3 $\times$ 8.1 to 11.8 μ m. Conidiophores of *F. acuminatum* were hyaline, septate, and branched. A pathogenicity test was performed by inoculating a conidial suspension of 1 $\times$ 10⁷/ml in 0.025% Tween 20 onto the roots of *A. sinensis*. Inoculated roots were incubated in a humid, dark chamber at 26°C for 24 h and then with 12 h light/12 h dark for 6 days. The pathogenicity assay was repeated three times for each isolate. Root rot was observed 7 days after inoculation, and mycelia were observed on the surface of the lesions. Two isolates were recovered from the lesions and named DG-2-D and DG-3-1-D. The colonial morphology of these two isolates and the original isolates DG-2 and DG-3-1 was identical after 6 days of inoculation on potato dextrose agar. The two isolates recovered were identified as *C. rosea* and *F. acuminatum*, respectively, by amplifying and sequencing a portion of the *TEF1- α* gene. To our knowledge, this is the first report of *C. rosea* causing root rot of *A. sinensis* in China. *F. acuminatum* was reported to cause root rot of *A. sinensis* in Gansu province, China, in 2021 (Niu et al. 2021). *C. rosea* has been previously reported to cause root rot of soybean in the United States (Bienapfl et al. 2012). The disease must be considered in existing management practices, and our findings provide a foundation for management of this disease.

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