Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Root Rot of *Schisandra chinensis* Caused by *Fusarium acuminatum* in Northeast China

B.-Y. Shen, W.-S. Sun,[†] K. Liu, and J.-T. Zhang

Liaoning Research Institute of Cash Crops, Liaoyang 111000, China

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Wuweizi (*Schisandra chinensis* [Turcz.] Baill.) is used for traditional medicine in northeastern China. In August 2019, root rot of *S. chinensis* with an incidence of 30 to 50% was observed in a commercial field in Liaozhong City (41°29'57" N, 122°52'33" E) in the Liaoning province of China. The diseased plants were less vigorous, stunted, and had leaves that turned yellow to brown. Eventually, the whole plant wilted and died. The diseased roots were poorly developed with brown lesions and would eventually rot. To determine the causal agent, symptomatic roots were collected, and small pieces of root with typical lesions were surface sterilized in 2% NaOCl for 3 min, rinsed three times in distilled water, and plated onto PDA medium. After incubation at 26°C for 5 days, whitish-pink or carmine to rose-red colonies on PDA were transferred to carnation leaf agar (CLA). Single spores were isolated with an inoculation needle using a stereomicroscope. Five single conidia isolates obtained from the colonies were incubated at 26°C for 7 days, and abundant macroconidia were formed in sporodochia. Macroconidia were falcate, slender, with a distinct curve to the latter half of the apical cell, mostly three to five septate, and measured 31.3 to 47.8 × 4.8 to 7.5 μm (*n* = 50). Microconidia were oval and irregularly oval, zero to one septate, and measured 5.0 to 17.5 × 2.5 to 17.5 μm (*n* = 50). Chlamydospores formed in chains within or on top of the mycelium. Morphological characteristics of the isolates agreed with *Fusarium acuminatum* (Leslie and Summerell 2006). To confirm the identity, the partial sequence of the translation elongation factor 1 alpha (*TEF1-α*) gene of five isolates was amplified using the primers EF-1 (ATGGGTAAGGARGACAAG) and EF-2 (GGAGTACCAGTSATCATGTT) (O'Donnell et al. 2015) and sequenced. The rDNA internal transcribed spacer (*ITS*) region for the five isolates was also amplified using the

primers ITS1 (TCCGTAGGTGAACCTGCGG) and ITS4 (TCCTCCGCTATTGATATGC) (White et al. 1990) and sequenced. Identical sequences were obtained, and one representative sequence of isolate WW31-5 was submitted to GenBank. BLASTn analysis of the *TEF1-α* sequence (MW423624) and *ITS* sequence (MZ145386) revealed 100% (708/685 bp, 563/563 bp) sequence identity to *F. acuminatum* MH595498 and MW560481, respectively. Pathogenicity tests were conducted in a greenhouse. Inocula of *F. acuminatum* were prepared from the culture of WW31-5 incubated in 2% mung bean juice on a shaker (140 rpm) at 26°C for 5 days. Ten roots of 2-year-old plants of *S. chinensis* were immersed in the conidial suspension (2×10^5 conidia/ml) for 6 h, and another 10 roots were immersed in sterilized distilled water in a plastic bucket for 6 h. All these plants were planted into pots with sterilized field soil (two plants per pot). Five pots were planted with inoculated plants and another five pots planted with uninoculated plants served as controls. All 10 pots were maintained in a greenhouse at 22 to 26°C for 21 days and irrigated with sterilized water. The leaves of the inoculated plants became yellow, gradually dried up, and finally all the aboveground parts died. The roots of the inoculated plants were rotted. Noninoculated control plants had no symptoms. *F. acuminatum* was reisolated from the roots of inoculated plants and had morphology identical to the original isolate. The experiment was repeated twice with similar results. *F. acuminatum* has been reported as a pathogen causing root rot of ginseng (Wang et al. 2016) but had not yet been reported on wuweizi in China. To our knowledge, this is the first report of root rot of *S. chinensis* caused by *F. acuminatum*. We also observed the disease in Benxi City of Liaoning Province in 2020, and it has become an important disease in the production of *S. chinensis*. An effective control method should be adopted to reduce losses.

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[†]Indicates the corresponding author.
W.-S. Sun; sunwensong12@126.com