Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Root Rot Caused by *Macrophomina phaseolina* on *Atractylodes lancea* in China

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The dried root of cang-zhu (*Atractylodes lancea* Thunb. DC), which belongs to the Asteraceae (Compositae), is a perennial herb that has been widely used as a traditional medicine for treating digestive disorders, rheumatic diseases, influenza, and night blindness in China, Japan, and Thailand, and it has been listed in Chinese pharmacopoeia for centuries (such as “Shen-nong-ben-cai-jing”) (Na-Bangchang et al. 2017). From May to October 2017 and 2018, root rot disease was observed on approximately 5 to 15% of plants in commercial nurseries of *A. lancea* in Chengkou, Fuling, Shizhu, and Wuxi counties in Chongqing city, and Ganluo and Yanyuan counties in Sichuan province. The disease resulted in approximately 5% yield loss of the crop. Initially, the lower mature leaves on the infected *A. lancea* plants became yellow and wilted. Stems and roots of symptomatic plants were rotted, and some plants eventually wilted and died. Black, irregular lesions were observed in the pith cavity of split stems and roots of the infected plants. The disease was more severe with extended rainy days or high air humidity conditions. In 2017 to 2018, root and stem samples were collected from six symptomatic plants in Chengkou and Wuxi counties. Small slices of infected tissues (about 3 × 3 mm) were surface sterilized with 1% sodium hypochlorite for 3 min, rinsed using sterile distilled water, and grown on potato dextrose agar (PDA) at 28°C in an incubator with 12 h light/day. Colonies on PDA plates were initially circular with hyaline mycelia, and they turned to gray or dark gray 5 days after incubation. In the meantime, dark, smooth, and oblong microsclerotia (averaging 117.7 × 173.6 μm) were observed microscopically among the

aerial mycelia. According to these morphological characteristics, the isolate was assumed to be *Macrophomina phaseolina* (Smith and Wyllie 1999). Three isolates were selected for molecular identification, and genomic DNA was extracted using a TianGen DNA secure plant kit (Tiangen, Beijing, China). PCR amplification of the internal transcribed spacer with primers ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3') resulted in an amplicon of 583 bp from each isolate that was sequenced. All sequences were identical, and BLASTN of one obtained sequence (GenBank accession no. MK418648) revealed 100% identify (583/583 bp) with several *M. phaseolina* strains (GenBank accession nos. MK408587, MN298740.1, and KR012878.1). A pathogenicity test was performed by inoculating the roots of 2-year-old *A. lancea* plants with *M. phaseolina* under greenhouse conditions (20 to 25°C). The roots of the *A. lancea* plants were washed with water and surface disinfested in 70% alcohol and planted in sterilized soil. A 5-mm-diameter mycelial agar plug was placed on the exposed root base of each healthy *A. lancea* plant (10 plants for each treatment) (Keeling 1982). This experiment was conducted with three replicates. After 5 days, all inoculated plants, except for the noninoculated control plants, showed similar necrotic symptoms to those observed in the field on the roots. *M. phaseolina* was reisolated from diseased tissues of the inoculated plants but not from the noninoculated control plants, thereby fulfilling Koch's postulates. This pathogen has been reported on other hosts that are economically important including blueberry (Santos et al. 2019), sacha inchi (Wang et al. 2020), and strawberry (Qamar et al. 2019). To our knowledge, this is the first report of *M. phaseolina* causing root rot in *A. lancea*. The global demand for *A. lancea* is growing at an annual rate of more than 10%. Because China produces more than 70% of the world's *A. lancea*, root rot caused by *M. phaseolina* is an economic threat to the global production of *A. lancea*. Consequently, the epidemiology and management of this disease need to be investigated.

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