Diseases Caused by Fungi and Fungus-Like Organisms

Brown Culm Rot of *Dendrocalamus latiflorus* Caused by *Diaporthe guangxiensis* in Sichuan Province, China

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Dendrocalamus latiflorus Munro, the most widely cultivated bamboo species in southern China, has high ornamental value and is used in gardens, and culms are also used for buildings and as fibers and edibles (Gao et al. 2011). In June 2020, brown culm rot of bamboo was observed in Yibin city, Sichuan Province, in an area of approximately 1,000 ha. Disease incidence was approximately 60%, of which 30% of the plants had died. At the end of June, the lesions expanded but did not surround the base of the culm. From the end of June to the beginning of September, the lesions expanded upward and formed a streak, of which the color gradually deepened to purple-brown and black-brown. At the same time, the disease spots at the base of the culm also expanded horizontally. After the spots surrounded the base of the culm, the diseased bamboo died. Ten culms showing typical symptoms were collected and cut into 5 × 5-mm pieces at the junction of infected and healthy tissues. The tissues were sterilized for 1 to 2 min in 3% sodium hypochlorite, decontaminated in 75% alcohol for 3 to 5 min, placed on modified potato glucose agar with streptomycin sulfate (50 µg/ml), and incubated at 26°C. Two isolates were obtained by the single-spore method (Sivan et al. 1992). The isolates both produced white round colonies similar to *Diaporthe guangxiensis* and two types of conidia: one was α type (5.5 to 8.2 × 1.0 to 2.8 µm, *n* = 30), colorless, single-celled, undivided, and oval, containing two oil droplets; and the other was β type (21.1 to 30.2 × 0.8 to 1.4 µm, *n* =

30), colorless, single celled, and hook shaped. Genomic DNA was extracted from the two isolates by using a fungal genomic DNA extraction kit (Solarbio, Beijing). The products were amplified by polymerase chain reaction with primers for the internal transcribed spacer 1 (ITS) region (White et al. 1990), calmodulin (CAL) gene (Carbone and Kohn 1999), translation elongation factor 1-alpha (TEF) gene (Glass and Donaldson 1995), and beta-tubulin (TUB) gene (Soares et al. 2018). The amplified products were sequenced and blasted in GenBank (accession nos. MW380383, MW431318, MW431317, and MW431316 for ITS, CAL, TEF, and TUB, respectively). The ITS, CAL, TEF, and TUB sequences showed 100, 99.33, 100, and 99.80% identity to *D. guangxiensis* JZB320094 (accession nos. MK335772.1, MK736727.1, MK523566.1, and MK500168.1 in GenBank), respectively. To evaluate the pathogenicity of the isolates, five plants were each inoculated with two isolates. The cortex of potted bamboo was injured locally with a sterilized needle, and the bamboo culms were inoculated with 100 µl of conidial suspension (10⁵ CFU/ml). The surface of the inoculation wound was covered with gauze soaked with sterilized water. Five plants inoculated with sterile water were used as controls. The treated plants were maintained in a greenhouse at a temperature of 22 to 29°C and relative humidity of 70 to 80%. One month later, all inoculated plants showed similar symptoms as those observed in the field. *D. guangxiensis* was reisolated from all inoculated plants. The pathogenicity test was repeated three times with similar results. This is the first report of *D. guangxiensis* causing brown culm rot of *D. latiflorus* in China. These results will facilitate an enhanced understanding of factors affecting bamboo and the design of effective management strategies of the pathogenic species on bamboo and thus to develop corresponding control measures.

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