Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium proliferatum* Associated with Basal Rot Disease of *Bambusa pervariabilis* × *Dendrocalamopsis grandis* in China

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Bambusa pervariabilis × *Dendrocalamopsis grandis* is a cultivated bamboo used in ecological construction in the Yangtze River basin. It has easy reproduction, wide adaptability, and strong resistance and has high economic, ecological, and social benefits (Peng et al. 2020). A 68-hm² area of bamboo with basal rot disease was discovered in Renshou County, Sichuan Province, China (29°41'N, 104°11'E), in June 2020. Incidence was 34.8%, and 5% of plants died. The pathogen first invaded the first section of the base of the stalk, appearing as black to yellowish-brown strips or lumps of disease spots, and rapidly developed horizontally and vertically, causing the whole plant to wither in severe cases. Diseased tissues were collected from the base of a 4-year-old stalk with a sterile blade. One hundred 5 × 5 × 2 mm pieces of diseased tissue were sterilized with 3% NaClO for 30 s and 75% ethanol for 90 s, rinsed three times with sterile distilled water (SDW), dried on sterile filter paper, plated onto PDA amended with streptomycin sulfate (Solarbio, 50 µg/ml), and incubated at 25°C for 7 days with light. Five isolates were obtained, of which four had similar morphology. Using monospore isolation (Leslie and Summerell 2006) and culturing on PDA, the fungus produced round colonies ~8.4 mm in diameter and a white to purple surface after 7 days at 25°C. For identification by typical spores, the fungus was cultured on carnation leaf agar at 25°C for 7 days. Microconidia of isolates BD2002, BD2004, BD2008, and BD2010 were elliptical, ovoid, without septa, and 4.56 to 15.53 × 1.36 to 6.98 µm (*n* = 100). Macroconidia were rod-shaped or slightly curved, tapering apically with three to five septa, and 18.86 to 52.99 × 1.56 to 6.42 µm (*n* = 100). Based on morphology, the isolates were identified as *Fusarium* sp. (Leslie and Summerell 2006). For molecular identification, DNA

of the four isolates was extracted with a fungal genomic DNA extraction kit. PCR was performed with primers ITS1/ITS4 for the ITS rDNA region (White et al. 1990), Bt2a/Bt2b for β -tubulin (*TUB*) (Glass and Donaldson 1995), EF1F/EF2R for translation elongation factor 1 α (*TEF*) (Carbone and Kohn 1999), 5f2/7cr for RNA polymerase II genes (*RPB2*) (O'Donnell et al. 2010), H3-1a/H3-1b for histone H3 (*HIS*) (Jacobs et al. 2010), and NMS1/NMS2 for mitochondrial small subunit (*mtSSU*) rDNA (Stenglein et al. 2010). A BLASTn search in GenBank showed all isolates had the highest similarity with *Fusarium proliferatum* (Matsushima) Nirenberg. The BD2010 ITS had 99.61% similarity to *F. proliferatum* Z23-28 (FJ648201.1); *HIS* had 99.57% similarity to *F. proliferatum* M06A_4G_4 (KX681532.1); and the *TUB*, *TEF*, *RPB2*, and *mtSSU* sequences showed 99.67, 99.10, 99.06, and 99.57% similarity, respectively, to *F. proliferatum* ITEM2287 (LT841243.1, LT841245.1, LT841252.1, and LT841247.1). BD2010 sequences were deposited in GenBank (ITS, OK325614; *TUB*, OK377026; *TEF*, OK377027; *RPB2*, OK377028; *HIS*, OK377029; and *mtSSU*, OK338638). To test pathogenicity, 30 healthy 4-year-old plants were grown in individual pots. Five plants per isolate were punctured at the base with a sterile syringe and inoculated with 100 µl of 1 × 10⁶ conidia/ml suspension. Five controls were inoculated with 100 µl of SDW. The inoculation site was wrapped with wet gauze to maintain moisture. Plants were watered every 7 days and kept in a greenhouse at 25 to 28°C, 70 to 80% RH, and a 12-h light/dark cycle. After a month, 20 plants inoculated with a conidial suspension of BD2002, BD2004, BD2008, or BD2010 showed the same symptoms as seen in the field, but plants inoculated with the other fungus and controls were asymptomatic. The test was conducted three times, and the results were consistent. Fungi were reisolated from diseased parts and identified as *F. proliferatum* by morphological and molecular comparison. This is the first report of basal rot disease caused by *F. proliferatum* on *B. pervariabilis* × *D. grandis* in China. This research will help develop control strategies for basal rot disease in this species.

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The author(s) declare no conflict of interest.

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