Diseases Caused by Oomycetes

First Report of *Phytophthora nicotianae* Causing Stem Canker of *Catalpa bungei* (Chinese Catalpa) in China

Lin Chang,¹ Kang Liu,¹ Liang-gui Wang,² Xiu-lian Yang,² and Hui Sun^{1,†}

¹ Collaborative Innovation Center of Sustainable Forestry in Southern China, College of Forestry, Nanjing Forestry University, Nanjing 210037, China

² College of Landscape Architecture, Nanjing Forestry University, Nanjing 210037, China

Funding: The study was supported by Jiangsu Agricultural Science and Technology Innovation Fund project (CX(19)2038) and the research funding for Priority Academic Program Development (PAPD) of Jiangsu Higher Education Institutions. Plant Dis. 106:1309, 2022; published online as <https://doi.org/10.1094/PDIS-08-21-1778-PDN>. Accepted for publication 2 October 2021.

Chinese catalpa (*Catalpa bungei* C.A. Mey) is native to China and has been widely cultivated as an important tree species for timber and ornamental purposes (Tao et al. 2019). The properties and high durability of the wood can resist the damage caused by microorganisms and insects (Jia et al. 2010; Xiao et al. 2019). In September 2020, stem cankers were observed in 5-year-old and 3-year-old *C. bungei* trees in a pilot experiment field covering 16 ha in Shuyang City (Jiangsu Province, China) and in a nursery in Binhai City (Jiangsu Province, China), respectively. The disease incidence in both locations was about 1 to 3%. Typical disease symptoms included small to large, dark-brown and irregular, sunken cankers around and along the stem less than 2 m from the stem base. The phloem and xylem of the symptomatic stem were dark brown, and the xylem had more necrosis than the phloem. The cross section of the diseased stem was partially necrotic. Symptomatic stems were collected in both locations for pathogen isolation. In total, seven different purified isolates from the diseased samples were obtained using potato dextrose agar (PDA) following standard isolation protocol (Huang et al. 2019). In order to determine the pathogenicity, 3-year-old Chinese catalpa seedlings were artificially inoculated with each of the seven isolates in April 2021. After removing the bark of the stem by a sterilized punch (diameter = 6 mm), an agar plug (diameter = 6 mm) precolonized by the isolate was inoculated to the stem and the inoculation point was sealed with Parafilm. The agar plug without precolonization was used as control. Six tree seedlings were inoculated for each isolate. Ten days after inoculation, only the treatment with isolate QS.1 showed obvious discoloration around the inoculation point in all

inoculated seedlings (100% infection rate). One month after inoculation, a canker around the inoculation point was formed (3.4 ± 1.0 cm) and spread to the xylem, similar to the symptoms observed in the field. Isolate QS.1 was reisolated successfully from the inoculated stem based on morphological characteristics, confirming Koch's postulates and QS.1 as the causal pathogen. Isolate QS.1 formed white colonies with abundant aerial mycelia on V8 juice agar and produced a large amount of persistent and papillary ovoid sporangia with a size of ~ 22 to $45 \mu\text{m}$ (average $31 \mu\text{m}$) by ~ 18 to $39 \mu\text{m}$ (average $23 \mu\text{m}$) in 10% aqueous solution of V8. The spore was spherical with a thick wall and diameter of $24 \pm 3.9 \mu\text{m}$. The morphology of QS.1 is similar to that of *Phytophthora nicotianae* (Erwin and Ribeiro 1996). The genomic DNA of representative isolate QS.1 was extracted from mycelium by a modified CTAB method (Murray and Thompson 1980). The rDNA internal transcribed spacer (*ITS*) region, β -*tubulin*, and *EF1- α* genes were amplified and sequenced with primers ITS1/ITS4 (White et al. 1990), BTub_F1/TUBUR1 (Kroon et al. 2004), and EF1A_for/EF1A_rev (Blair et al. 2008), respectively. The BLAST results of these sequences (867 bp with accession no. MZ646302, 1,119 bp with accession no. MZ672116, and 876 bp with accession no. MZ675589, respectively) showed 99, 100, and 100% identity with sequences of *P. nicotianae* (accession nos. KJ494902, KY205750, and MH359041, respectively). Based on the morphological characteristics and DNA analysis, isolate QS.1 was identified as *P. nicotianae*. To the best of our knowledge, this is the first report of *P. nicotianae* causing stem canker on Chinese catalpa. This disease may pose potential threat on catalpa due to the increase in catalpa planting for economic and ecological purposes in China.

References:

- Blair, J. E., et al. 2008. Fungal Genet. Biol. 45:266.
- Erwin, D. C., and Ribeiro, O. K. 1996. Phytophthora Diseases Worldwide. American Phytopathological Society, St. Paul, MN.
- Huang, W. L., et al. 2019. Chin. Agric. Sci. Bull. 35:135.
- Jia, J. W., et al. 2010. For. Res. 23:382.
- Kroon, L. P., et al. 2004. Fungal Genet. Biol. 41:766.
- Murray, G. M., and Thompson, W. F. 1980. Nucleic Acids Res. 8:4321.
- Tao, L. I., et al. 2019. J. Fujian Forestry Sci. Technol. 46:134.
- White, T. J., et al. 1990. Page 315 in: PCR Protocols: A Guide to Methods and Applications. Academic Press, San Diego, CA.
- Xiao, Y., et al. 2019. Sci. Silvae 55:58.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: *Catalpa bungei*, *Phytophthora nicotianae*, stem canker, tree disease

[†]Indicates the corresponding author.
H. Sun; hui.sun@njfu.edu.cn