Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Collar Canker and Dieback of *Camellia sinensis* Caused by *Fusarium solani* Species Complex in Henan, China

Wen Xu,¹ Fenghua Zhao,² Xiaoxu Deng,¹ Paul H. Goodwin,³ Mingcong Xia,¹ Jie Zhang,¹ Runhong Sun,¹ Juan Liang,¹ Chao Wu,¹ and Lirong Yang^{1,†}

¹ Institute of Plant Protection Research, Henan Academy of Agricultural Sciences, Henan Biopesticide Engineering Research Center, Henan International Joint Laboratory of Crop Protection, Zhengzhou, Henan, 450002, China

² Xinyang Academy of Agricultural Sciences, Xinyang, Henan, 464000, China

³ School of Environmental Sciences, University of Guelph, Guelph, Ontario, N1G 2W1, Canada

W. Xu and F. Zhao contributed equally to this work.

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Tea (*Camellia sinensis*) is a significant commercial crop in China. A collar canker and dieback disease of tea has recently been reported in Sri Lanka (Sinniah et al. 2017). In spring 2020, tea bushes with symptoms of fewer leaves, yellowing of leaves with cankers having cracks, and peeling of bark, premature falling in the early stage, and progressive dieback of branches followed by death of the whole tree that was partially covered with white-colored mold were observed in tea plantations over a 200-hm² area in Xinyang, Henan Province, China. To determine the causative agent, dead stems with white-colored mold were collected, cut into small pieces, surface-sterilized with 75% ethanol, rinsed twice with sterile distilled water, and then air-dried. The pieces were placed on potato dextrose agar (PDA) and incubated at 28°C for 7 days. A total of 19 fungal colonies were isolated and transferred to fresh PDA. Single-spore isolates were made for each, and they were all observed to produce white flocculent mycelium with the reverse side being pale yellow on PDA. The appearance of a representative strain, XYWLD-07, on PDA is shown in the supplementary materials. Macroconidia (14.26 to 42.13 × 3.53 to 6.79 μm) and microconidia (6.93 to 11.85 × 2.72 to 6.33 μm) were observed in the cultures. The genomic DNA from representative strain XYWLD-07 was extracted, and the internal transcribed spacer region (ITS) of ribosomal DNA, beta-tubulin, translation elongation factor 1-alpha (*TEF-1α*), RNA polymerase I beta subunit (*RPB1*), and RNA polymerase II beta subunit (*RPB2*) genes were amplified using the primer pairs

ITS1/ITS4 (5'-CTTGGTCATTTAGAGGAAGTAA-3'/5'-TCCTCCGCTTAT TGATATGC-3') (Gardes and Bruns 1993), Bt-F/Bt-R (5'-AACATGCGTGA GATTGTAAGT-3'/5'-TCTGGATGTTGTTGGGAATCC-3'), EF-1/EF-2 (5'-AT GGGTAAGGARGACAAGAC-3'/5'-GGARGTACCAGTSATCATGTT-3'), RPB-1F/IR (5'-TTTTCTCACAAAGGAGCAAAATCATG-3'/5'-GTTTAC CCAAGATATGGTTCGAAAGCC-3'), and RPB2-5F/11aR (5'-GGGGWG AYCAGAAGAAAGGC-3'/5'-GCRTGGATCTTTCRTCSACC-3') (O'Donnell et al. 2010), respectively. The PCR products were sequenced and deposited in GenBank (accession nos. MZ411431, MZ439920, OL982608, OM069738, and OM265212, respectively). BLASTn against NCBI nr and *Fusarium*-ID database revealed that the ITS sequence had 99.65% homology with BLAST sequences of *Fusarium solani* (GenBank accession nos. JN882257.1 and JN882255.1), the beta tubulin sequence had 96.92% similarity with BLAST sequences of *F. solani* (KU983876.1 and MN692929.1), *TEF-1α* gene sequence had 99.15 and 99.29% homology with BLAST sequences of *F. solani* (KM096405.1 and KM096409.1), *RPB1* gene sequence had 99.32 and 99.41% homology with BLAST sequences of *F. solani* (KU974331.1 and MT305119.1), and *RPB2* gene sequence had 98.15 and 98.20% homology with BLAST sequences of *F. solani* (MT305182.1 and MT305177.1). Furthermore, *TEF-1α*, *RPB1*, and *RPB2* gene sequences had more than a 98.52% match with *F. solani* sequences in *Fusarium*-ID databases. To test for pathogenicity, the inoculum was grown for 10 days at 25°C on 200 g of sterilized boiled wheat grain and sand (3:1, v/v) with a 20-ml spore suspension (10⁷ conidia/ml) of strain XYWLD-07. Two-year-old tea seedlings were planted in pots of autoclaved soil with 5% (m/m) strain XYWLD-07 inoculum, but controls were grown in autoclaved soil with only a sterile wheat/sand mix. The experiment was performed five times. After 30 days, collar canker symptoms appeared on inoculated tea branches, and the control was asymptomatic. The fungal pathogen was reisolated from the symptomatic tea tissues and again identified as *F. solani* based on the above analysis of the five gene sequences. *F. solani* has been previously identified as the causal agent of collar canker and dieback of *C. sinensis* in Sri Lanka (Sinniah et al. 2017) and India (Sarmah et al. 2017). To our knowledge, this is the first report of *F. solani* causing collar canker and dieback of *C. sinensis* in China. As this disease could result in death of tea bushes, effective management strategies should be investigated and applied.

References:

- Gardes, M., and Bruns, T. D. 1993. Mol. Ecol. 2:113.
O'Donnell, K., et al. 2010. J. Clin. Microbiol. 48:3708.
Sarmah, S. R., et al. 2017. J. Tea Sci. Res. 10:5376.
Sinniah, G. D., et al. 2017. Australas. Plant Dis. Notes 12:41.

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[†]Indicates the corresponding author.
L. Yang; luck_ylr@126.com