Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Root Rot of Tobacco Caused by *Fusarium brachygibbosum* in China

R. Qiu,^{1,†} J. Li,¹ W.-M. Zheng,² X.-H. Su,³ G.-Z. Xing,² S.-J. Li,^{1,†} Z.-Y. Zhang,³ C.-J. Li,¹ J. Wang,¹ Y.-G. Chen,¹ J.-K. Bai,¹ J. Zhao,¹ and W.-L. Ping¹

¹ Key Laboratory for Green Preservation & Control of Tobacco Diseases and Pests in Huanghuai Growing Area, Tobacco Research Institute, Henan Academy of Agricultural Sciences, Xuchang, 461000, China

² Henan Agriculture University, Zhengzhou, 450003, China

³ Sanmenxia Company of Henan Tobacco Company, Sanmenxia, 472000, China

Funding: Funding was provided by the Science and Technology Project of Henan Provincial Tobacco Company (2020410000270012), Independent Innovation Project of Hennan Academy of Agricultural Sciences (2020ZC18), and Research and Development Project of Henan Academy of Agricultural Sciences (2020CY010). Plant Dis. 105:4170, 2021; published online as <https://doi.org/10.1094/PDIS-01-21-0077-PDN>. Accepted for publication 14 May 2021.

Tobacco (*Nicotiana tabacum* L.) is an important cash crop in China, with an estimated production of 2.2 million tons every year (Berbec and Matyka 2020). In June 2020, a root rot disease was observed on tobacco (cv. Zhongyan 100) in four surveyed counties (Mianchi, Lushi, Duguan, and Lingbao) in Sanmenxia. Diseased plants exhibited leaf chlorosis and purplish to brown vascular discoloration of stem, taproot, and lateral roots. The disease incidence ranged from 15 to 40% in 11 surveyed fields, 36.7 ha in total. Twenty-five diseased tissues were surface sterilized in 75% ethanol and placed on potato dextrose agar (PDA) medium. Fifteen single-spore isolates were obtained from 25 diseased tissue samples. All cultures growing on PDA had white colonies with abundant aerial mycelia initially, turning into yellow to orange in the center and produced red pigmentation after 7 days of growth. The 7-day-old cultures grown on carnation leaf agar (CLA) produced macroconidia that were curved with 3 to 5 septa, had wide central cells, slightly pointy apex, and measured 17.0 to 45.9 μm long $\times$ 3.0 to 4.6 μm wide ($n = 50$). The microconidia formed on CLA were slightly curved, ovoid with zero to two septa, measuring 5.4 to 15.5 μm long $\times$ 2.0 to 3.2 μm wide ($n = 50$). Spherical chlamydospores (7.58 to 13.52 μm ; $n = 50$) were terminal or intercalary, single or in chains. Such characteristics were typical of *Fusarium*

brachygibbosum (Tirado-Ramírez et al. 2019). DNA from one representative single-spore isolate (MC1) was extracted, and the translation elongation factor 1- α (*EF1- α*), RNA polymerase I largest subunit (*RPB1*), and second largest subunit (*RPB2*) genes were amplified with primers *EF1/EF2*, *F5/G2R*, and *RPB2F/R*, respectively (O'Donnell et al. 1998, 2010), and sequenced. Sequences were submitted to GenBank under accession numbers MT947796 (*EF1- α*), MW679536 (*RPB1*), and MW430664 (*RPB2*). The consensus sequences showed 99.70%, 99.94%, and 100% identity to the sequences of *F. brachygibbosum* strain NRRL 34033 (accession nos. GQ505418.1, HM347172.1, and GQ505482.1, Wang et al. 2021). Morphological and molecular results confirmed this species as *F. brachygibbosum* (Al-Mahmooli et al. 2013; Rentería-Martínez et al. 2018). Pathogenicity tests were performed on tobacco seedlings grown on autoclaved tobacco specific substrate (Tobacco specific matrix, Ainong Biotechnology Co. Ltd, China). Healthy six-leaf stage tobacco seedlings ($n = 30$; Zhongyan 100) were inoculated by placing 7-day-old wheat seed (15 seeds per plant) infested with MC1 around the root. Thirty seedlings inoculated with sterile wheat seeds served as controls. All the plants were maintained in a growth chamber at $25 \pm 0.5^\circ\text{C}$ and 70% relative humidity. The assay was conducted three times. Typical symptoms of foliage chlorosis and root browning were observed 7 to 14 days after inoculation. The pathogen was reisolated from the necrotic tissue from all inoculated seedlings and was identified by sequencing partial *EF1- α* and *RPB2* genes. Control plants remained asymptomatic and no pathogen was recovered from the control plants. *F. brachygibbosum* is known as a pathogen of grains and cash crops in China (Shan et al. 2017; Xia et al. 2018). To our knowledge, this is the first report of *F. brachygibbosum* causing root rot on tobacco. We believe that our results will help to better understand rhizome fungal diseases affecting tobacco production in China.

References:

- Al-Mahmooli, I. H., et al. 2013. Plant Dis. 97:687.
- Berbec, A. K., and Matyka, M. 2020. Agriculture 10:551.
- O'Donnell, K., et al. 1998. Proc. Natl. Acad. Sci. USA 95:2044.
- O'Donnell, K., et al. 2010. J. Clin. Microbiol. 48:3708.
- Rentería-Martínez, M. E., et al. 2018. Mex. J. Phytopathol. 36:233.
- Shan, L. Y., et al. 2017. Plant Dis. 101:837.
- Tirado-Ramírez, M. A., et al. 2019. Plant Dis. 103:582.
- Wang, S., et al. 2021. Plant Dis. 105:1561.
- Xia, B., et al. 2018. Plant Dis. 102:2372.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: tobacco root rot, *Fusarium brachygibbosum*, China

[†]Indicates the corresponding authors.

R. Qiu; qiuui19840414@hotmail.com, and S.-J. Li; 13603749396@126.com