First Report of *Phytophthora helicoides* Causing Stalk Rot on Corn in China

X. Y. Xie, H. Z. Zhou, S. S. Fan, and X. J. Zhang[†]

Shandong Key Laboratory of Applied Microbiology, Ecology Institute, Qilu University of Technology (Shandong Academy of Sciences), Jinan 250103, China

Funding: The research was supported by the National Key Research and Development Project, China (foundation no. 2018YFD0200604) in 2018 and the Key Research and Development Project from the Department of Science & Technology of Shandong Province, China (foundation nos. 2019JZZY020610 and 2019GSF107043) in 2019. Plant Dis. 105:3766, 2021; published online as <https://doi.org/10.1094/PDIS-02-21-0429-PDN>. Accepted for publication 23 April 2021.

Corn (*Zea mays* L.) is one of the most important grain crops in the world, especially in China. Besides, corn stalks are often used in production of bio-fuels (Xue et al. 2017). Recently, the production and quality of corn have been severely influenced by corn stalk rot in China caused by *Fusarium* spp. (Yu et al. 2017). At the end of June 2019, a field survey of corn was carried out in Tai'an City, western Shandong Province, China. During the survey, the average daytime temperature ranged between 22 and 28°C with intermittent rainfall, and the relative humidity was 50 to 70%. In this survey, the symptomatic corn plants showed signs of necrosis and rotting on stalks and root collars. Five fields were surveyed, and symptomatic corn plants were observed in three fields. The incidence rate of disease was about 5%, and the disease was more of a problem in low-lying areas. A total of 28 symptomatic corn plants (seven to 12 per field), of hybrid Denghai-618, at the three- to four-leaf stage were collected and tested for the presence of pathogens. The diseased tissues were excised, surface sterilized with 75% ethanol for 30 s, rinsed three to five times with sterile distilled water, and plated on potato dextrose agar (PDA). All plates were incubated at 28°C for 48 h, and emerging colonies were subcultured onto PDA plates. Forty-two isolates were obtained, and 27 isolates were identified as *Fusarium* spp. The remaining 15 isolates had similar morphology, with colonies that were white and cottony in texture after incubation at 28°C for 3 days on PDA. The suitable temperature range for growth of hyphae was between 15 and 40°C, and sporangia were ellipsoidal, papillate, and 23 to 34 × 21 to 31 µm in diameter. Oogonia (smooth, 22 to 30 µm in diameter) were present in the cultures after 28 days at 28°C. The

isolates were identified using both morphological characteristics and DNA sequencing. Identity of the oomycete was confirmed using the BLAST algorithm available through GenBank with the DNA sequences of rDNA internal transcribed spacer region (ITS), cytochrome c oxidase I (*coxI*) gene, and cytochrome c oxidase II (*coxII*) gene, which were amplified using the primers ITS1/ITS4 (White et al. 1990), FM35/FM59, and FM66/FM58 (Martin 2000), respectively. The 15 isolates selected for sequence analysis had identical gene sequences, and hence, only sequences for isolate RMSD1 were submitted to GenBank (ITS, MW440691; *coxI*, MW450815; and *coxII*, MW450816). The ITS, *coxI*, and *coxII* sequences of the isolate RMSD1 showed 97% identity (751/774 bp), 99% identity (1,087/1,098 bp), and 99% identity (548/554 bp) with *Phytophthora helicoides* (HQ643382, FR774199, and AB108014, respectively). The pathogenicity of RMSD1 was tested on the corn hybrid Denghai-618. Three-leaf-stage corn plants ($n = 15$) were inoculated with mycelial agar disks (3 to 4 mm in diameter) colonized with RMSD1 placed on their root collars. Sterile PDA disks (3 to 4 mm in diameter) served as the negative control ($n = 9$). Inoculated plants were placed in the growth chamber at 28°C, 60% relative humidity, 16-h/8-h light regime cycle. Ten days postinoculation, the inoculated plants showed necrosis, with symptoms of stem rot similar to those observed in the field. The inoculation experiments were repeated twice with the same results, fulfilling Koch's postulates. The root collars and stems of the negative control remained asymptomatic, and *P. helicoides* was not isolated. Previously, *P. helicoides* has been reported as a pathogen of strawberry (Zhan et al. 2020) and kiwi fruits (Wang et al. 2015) from China, but not from corn. To our knowledge, it is the first report of *P. helicoides* causing corn stalk rot in China. In the future, *P. helicoides* can be considered as a potential candidate causing stem and collar rot of corn in China, but not the only one. There are other microbes that can produce similar symptoms on corn, and control methods for pathogenic oomycetes differ from those for fungi.

References:

- Martin, F. N. 2000. Mycologia 92:711.
- Wang, K. X., et al. 2015. Plant Dis. 99:725.
- White, T. J., et al. 1990. Page 315 in: PCR Protocols: A Guide to Methods and Applications. Academic Press, San Diego, CA.
- Xue, J. J., et al. 2017. Energy Convers. Manage. 142:143.
- Yu, C., et al. 2017. Physiol. Mol. Plant Pathol. 98:1.
- Zhan, Y. J., et al. 2020. Plant Dis. 104:2528.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: *Phytophthora helicoides*, corn stalk rot, corn, China

[†]Indicates the corresponding author.

X. J. Zhang; zhangxj@sdaas.org