Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Epicoccum sorghinum* Causing Leaf Sheath and Leaf Spot on Maize in China

T.-M. Chen, Y. J. Xie, Q. Sun, X.-C. Shi, S.-Y. Wang,[†] and P. Laborda[†]

School of Life Sciences, Nantong University, Nantong 226019, P.R. China

T.-M. Chen, Y. J. Xie, and Q. Sun contributed equally to this work.

Funding: National Natural Science Foundation of China (3201101306). Plant Dis. 105:3741, 2021; published online as <https://doi.org/10.1094/PDIS-04-21-0746-PDN>. Accepted for publication 28 May 2021.

In November 2020, leaf sheath on maize (*Zea mays*) was detected in southeastern Jiangsu (Nantong municipality; 120.54° E, 31.58° N) in China. Physiologically mature plants, at 13 weeks of cultivation (harvest stage), exhibited red-brown lesions in stem and leaves, and dried-up stems. The symptoms were observed on approximately 95% of the maize plants in a 0.8 ha maize field surrounded by old sorghum fields and the crop yield was decreased by 70 to 85% with respect to previous years, when no disease symptoms were detected. Small pieces of symptomatic tissue, approximately 0.3 cm² in size, were surface sterilized in 1.5% NaOCl for 1 min, and washed twice with sterile ddH₂O. The pathogen was isolated (one isolate was obtained) and cultured on potato dextrose agar (PDA) medium containing chloramphenicol (50 µg/ml) under darkness at 26°C for 3 days. Amplification of internal transcribed spacer (*ITS*), large subunit (*LSU*), actin (*ACT*), and β-tubulin (*TUB2*) genes was performed using *ITS1/ITS4*, *LR0R/LR7*, *ACT512F/ACT783R*, and *T1/Bt2b* primers, respectively (Ma et al. 2021). Sequences were submitted to GenBank under accession numbers MW800180 (*ITS*), MW800361 (*LSU*), MW845677 (*ACT*), and MW892439 (*TUB2*). Blast search revealed that the *ITS* sequence had 100% (492/492 bp) homology with *E. sorghinum* LY-D-1-1, MT604999, *LSU* had 98% (1,075/1,091 bp) homology with *E. sorghinum* GZDS2018BXT010, MK516207, *ACT* had 96% (214/222 bp) homology with *E. sorghinum* M3, MK044832, and *TUB2* had 99% (498/499 bp) homology with *E. sorghinum* BJ-F1, MF987525. A molecular phylogenetic tree was constructed using MEGA7 to confirm the identity of the pathogen. The evolutionary history was inferred by using the maximum

likelihood method based on the Tamura 3-parameter model, and the tree with the highest likelihood (−1774.9882) is shown in the supplementary material. *Bipolaris*, *Curvularia*, and *Fusarium* spp. found causing leaf spot on maize were included in the phylogenetic tree (Chang et al. 2016; Liu et al. 2021; Reyes Gaige et al. 2020). To confirm pathogenicity, a sterilized spatula was used to make wounds (3 mm diameter, 1 mm depth) on the stem and leaves of 2-week-old maize plants. A solution containing 1 × 10⁸ spores/ml (20 µl) was injected in the wound, while sterilized ddH₂O was used in the control experiment. Inoculated plants were maintained in a growth chamber at 28°C and 60% relative humidity for 7 days, observing fast-growing necrotic lesions in both stem and leaves. The pathogen was recovered from the infected plants and its identity was confirmed by morphological and sequence analyses. Microscope observations indicated the presence of chlamydospores, oval conidia (3 × 5 µm), and round pycnidia (60 to 100 µm diameter), and agree with those previously reported for the morphology of *E. sorghinum* (Bao et al. 2019). In the last 2 years, *E. sorghinum* was reported to cause leaf spot on a number of relevant agricultural crops in China, including taro, *Brassica parachinensis*, tea, rice, and wheat (Chen et al. 2021; Du et al. 2020; Li et al. 2020; Liu et al. 2020), confirming the expansion and host promiscuity of this pathogen. The pathogen was also reported to cause leaf spot on maize in Brazil in 2004 (Do Amaral et al. 2004); however, this is the first report of *E. sorghinum* causing leaf sheath and leaf spot on maize in China. Maize is an important agricultural crop in China with more than 168 million tons produced in 2019. The observed yield loss and disease incidence of the isolated strain suggest that *E. sorghinum* may be a threat to maize production in China.

References:

- Bao, X. T., et al. 2019. Plant Dis. 103:3282.
- Chang, J. Y., et al. 2016. Plant Dis. 100:1780.
- Chen, Q. H., et al. 2021. Plant Dis. 105:1212.
- Do Amaral, A. L., et al. 2004. Plant Pathol. 53:259.
- Du, Y., et al. 2020. Plant Dis. 104:3082.
- Li, Q., et al. 2020. Plant Dis. 104:3131.
- Liu, L. M., et al. 2020. Plant Dis. 104:2735.
- Liu, S., et al. 2021. Plant Dis. 105:2247.
- Ma, Y. M., et al. 2021. Plant Dis. 105:2251.
- Reyes Gaige, A., et al. 2020. Plant Dis. 104:2102.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: *Zea mays*, fungi, *Epicoccum sorghinum*, maize diseases

[†]Indicates the corresponding authors.

P. Laborda; pedro@ntu.edu.cn, and S.-Y. Wang; wangsuyan@ntu.edu.cn