Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Tar Spot on Corn Caused by *Phyllachora maydis* in Georgia, United States

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Plant Dis. 106:2262, 2022; published online as <https://doi.org/10.1094/PDIS-11-21-2456-PDN>. Accepted for publication 22 January 2022.

Tar spot is a major foliage disease of corn (*Zea mays*) caused by the fungus *Phyllachora maydis*. This disease can reduce the quality of silage, stover, husks, and grain (Valle-Torres et al. 2020). It was identified in the United States for the first time in 2015 in northern Illinois and Indiana (Ruhl et al. 2016). As of 2020, it has also been confirmed in Iowa, Michigan, Wisconsin, Ohio, Florida, Missouri, Minnesota, and Pennsylvania (Collins et al. 2021; Telenko et al. 2020). In early August 2021, tar spot symptoms and signs were observed in late-planted, hybrid corn in southwestern Georgia in both Tift and Calhoun Counties. Where it occurred, incidence was nearly 100%, and severity ranged from approximately 1 to 20% leaf coverage. As of November 2021, tar spot has been confirmed in 13 counties throughout southern Georgia.

The symptoms on leaves were chlorotic lesions, and the signs were black, raised, and circular to irregular-shaped structures (stromata or clypei) ranging from 0.2 to 8 mm on the surface of the leaves. The stromata were present on both green and necrotic leaf tissue. Southern corn rust (*Puccinia polysora*) was often, but not always, observed on leaves with tar spot. Microscopic observations of stromata included single and clustered ascomata (60 × magnification) that contained cylindrical, unitunicate asci with ellipsoid, hyaline, and aseptate ascospores and abundant filiform paraphyses (400 × magnification). For molecular confirmation, stromata were surface sterilized with 95% ethanol and separated from the leaf tissue, and DNA was then extracted using the Qiagen DNeasy Plant Mini-Kit (Qiagen, Inc., Valencia, CA). PCR was conducted with the universal ITS1 and ITS4 primers to amplify the internal transcribed spacer (ITS) region of the rDNA. The amplicons were Sanger sequenced (Genewiz, Inc., South Plainfield, NJ), and a consensus sequence of a representative lesion was deposited in GenBank (accession number OK649959). Using the BLASTn algorithm, our sequence shared 100 and 99.2% coverage and 97.2 and 98.4% similarity to *P. maydis* GenBank accessions MG881848 and MK184990, respectively. *P. maydis* is an obligate parasite that cannot be cultured, so Koch's postulates were not performed. Inoculum of *P. maydis* may have been transported to Georgia from Florida by wind or other weather events, but this has not been confirmed.

References:

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The author(s) declare no conflict of interest.

Keywords: corn, fungi, obligate biotroph, tar spot

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