Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Tar Spot of Maize (*Zea mays*) Caused by *Phyllachora maydis* in Pennsylvania

A. A. Collins,^{1,2,†} A. Y. Bandara,¹ S. R. May,¹ D. K. Weerasooriya,¹ and P. D. Esker¹

¹Department of Plant Pathology and Environmental Microbiology, Pennsylvania State University, University Park, PA 16802

²Southeast Agricultural Research and Extension Center, Pennsylvania State University, Manheim, PA 17545

Plant Dis. 105:2244, 2021; published online as <https://doi.org/10.1094/PDIS-11-20-2456-PDN>. Accepted for publication 17 March 2021.

In late September 2020, foliar symptoms consistent with tar spot caused by *Phyllachora maydis* Maubl. were observed in multiple noncommercial hybrids of corn (*Zea mays* L.) in a field in Lancaster County, Pennsylvania. Stromata were observed on leaf and sheath surfaces from the middle to upper canopy in affected areas, and incidence and severity differed by hybrid but ranged from 0 to 100% and from 1 to 40%, respectively. Signs were found on green tissue and tissue naturally desiccated upon maturity. Coinfection with gray leaf spot (*Cercospora zea-maydis*, Tehon & E. Y. Daniels) was ubiquitous, and no necrosis was directly attributable to tar spot. In October 2020, a second affected nonadjacent field was identified in Lancaster County, 20.6 km West of the initial site. Lesions were primarily restricted to a single noncommercial hybrid and the directly adjacent borders of surrounding plots. At this site, incidence ranged from 0 to 100% and severity ranged from 0 to 30%. The dark, raised, pseudostromatic structures (clypei) on the symptomatic leaves ranged in size from 0.5 to 1.2 × 0.7 to 4.1 mm ($n = 40$, average 0.8 × 1.4 mm). Microscopic examination of the clypei revealed single and multiple ascomata inside a clypeus. Ascomata contained cylindrical, unitunicate asci and abundant filiform paraphyses.

Asci contained hyaline, uniseriate, aseptate, ellipsoid to ovate ascospores ranging in size from 7.6 to 12.9 × 4.3 to 7.6 μm ($n = 40$, average 5.7 × 9.9 μm). Based on these characteristics, the fungus was identified as *Phyllachora maydis* Maubl., cause of tar spot on corn (Parbery 1967). For molecular confirmation, DNA was extracted from clypei. A segment of the internal transcribed spacer (ITS) region of the rDNA gene was amplified by PCR using ITS-1 and ITS-4 primers (Larena et al. 1999). Amplicons were subjected to Sanger sequencing, and resulting sequences were used as queries in BLASTN. With 100% coverage, queries showed 100% homology to three *P. maydis* GenBank accessions in NCBI: MG881846.1, MG881847.1, and MG881848.1 (McCoy et al. 2018). A representative sequence was deposited in GenBank (accession no. MW130254). Due to the obligate parasitic nature of the pathogen, completion of Koch's postulates was not attempted. While tar spot has been reported previously in the United States, this report represents the easternmost observation of its presence in the northern United States (Dalla Lana et al. 2019; Malvick et al. 2020; McCoy et al. 2018; Ruhl et al. 2016). The economic impact of tar spot in Pennsylvania is currently unknown, but recent reports indicate this disease may pose a threat to yield and quality in corn-producing regions of North America (Valle-Torres et al. 2020).

References:

- Dalla Lana, F., et al. 2019. Plant Dis. 103:1780.
- Larena, I., et al. 1999. J. Biotechnol. 75:187.
- Malvick, D.K., et al. 2020. Plant Dis. 104:1865.
- McCoy, A. G., et al. 2018. Plant Dis. 102:1851.
- Parbery, D. G. 1967. Aust. J. Bot. 15:271.
- Ruhl, G., et al. 2016. Plant Dis. 100:1496.
- Valle-Torres, J., et al. 2020. Plant Dis. 104:2541.

The author(s) declare no conflict of interest.

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Keywords: fungi, field crops, epidemiology, disease development and spread, *Phyllachora maydis*, tar spot

[†]Indicates the corresponding author.
A. A. Collins; collins@psu.edu