Diseases Caused by Bacteria and Phytoplasmas

First Report of Bacterial Leaf Streak of Corn Caused by *Xanthomonas vasicola* pv. *vasculorum* in Wisconsin

C. L. Groves,¹ S. Lueloff,¹ B. Hudelson,¹ B. Kasiborski,^{2,3} M. J. Stulberg,² R. Bates,⁴ J. Chaky,⁴ B. Mueller,¹ and D. L. Smith^{1,†}

¹ Department of Plant Pathology, University of Wisconsin–Madison, Madison, WI 53706

² Science and Technology, Plant Protection and Quarantine, APHIS, USDA, Beltsville, MD 20705

³ Department of Plant Pathology, North Carolina State University, Raleigh, NC 27695

⁴ Corteva Agriscience, Johnston, IA 50131

The findings and conclusions in this publication are those of the authors and should not be construed to represent any official USDA or U.S. Government determination or policy.

Funding: This work was supported, in part, by the U.S. Department of Agriculture, Animal and Plant Health Inspection Service and the National Plant Diagnostic Network. Plant Dis. 104:3055, 2020; published online as <https://doi.org/10.1094/PDIS-04-20-0700-PDN>. Accepted for publication 22 May 2020.

In July 2018, corn (*Zea mays* L.) plants displaying symptoms of bacterial leaf streak were collected from a field in Pierce County, Wisconsin. The field was not irrigated, and the severity of bacterial leaf streak within the field was low. Symptoms of bacterial leaf streak consisted of long, linear, mostly necrotic lesions confined to the interveinal spaces of the leaf. Some lesions had yellow-colored margins. A symptomatic leaf sample was submitted to the University of Wisconsin–Madison Plant Disease Diagnostics Clinic (PDDC) for identification. The PDDC identified *Xanthomonas vasicola* pv. *vasculorum* (Xvv) directly from the sample tissue using polymerase chain reaction (PCR) diagnostic assays Xvv3, which amplifies a putative membrane protein, and Xvv5, which targets a putative exported protein (Lang et al. 2017a, 2017b). Resulting PCR products of the expected sizes (207 bp for Xvv3 and 200 bp for Xvv5) were identified, purified, and sequenced. A BLASTn search revealed that the

Xvv3 and the Xvv5 sequences shared 100% sequence identity with strains of Xvv (accession nos. CP025272 and CP028127). The Wisconsin Xvv sequences were submitted to GenBank (accession nos. MT005285 and MT005286). Bacterial identity was confirmed by the USDA APHIS Beltsville Lab using the qPCR 4909 assay (Stulberg et al. 2020) and partial gene sequencing of *dnaK* (Ah-You et al. 2009). A pure culture of the pathogen was obtained by surface disinfecting symptomatic leaf pieces in 70% ethanol, blotting dry, and placing a small, freshly excised leaf piece into a tube containing 200 µl of sterile water. Veins were oriented vertically with the lower end of the leaf piece submerged in the water. After 20 min, a loop of the water was streaked onto nutrient agar and incubated at 30°C. After 2 days, round, yellow colonies were selected and tested using the qPCR 4909 assay to confirm Xvv. A pure isolate from this process, designated Xvv2018-988, was used to test pathogenicity by inoculating four Burpee's Golden Bantam sweet corn plants. At approximately the V7 growth stage, a solution of 1.0×10^8 CFU/ml suspended in sterile water was sprayed onto the leaves. Inoculated plants were covered with plastic bags and placed in the shade for 24 h to maintain humidity. The bags were removed after 24 h and the plants maintained in direct light. Two control plants were mock inoculated by spraying with sterile water. By 6 days postinoculation, three of the four inoculated plants developed symptoms consistent with bacterial leaf streak, whereas neither of the water-inoculated control plants developed symptoms. The pathogen was reisolated from symptomatic tissues as described above and tested using the Xvv-specific qPCR 4909 assay. All reisolated bacterial colonies were identified as Xvv. This is the first report of bacterial leaf streak of corn caused by Xvv in Wisconsin. This pathogen has caused significant epidemics in other U.S. corn-producing states. Thus, this disease should be monitored in Wisconsin to identify other potentially yield-limiting outbreaks.

References:

- Ah-You, N., et al. 2009. Int. J. Syst. Evol. Microbiol. 59:306.
Lang, J. M., et al. 2017a. Detection of *Xanthomonas vasicola* pv. *vasculorum* from corn leaves. Protocol for isolation of Xvv, Option 2, lab communication. USDA-APHIS-PPQ, Beltsville, MD.
Lang, J. M., et al. 2017b. Phytopathology 107:1312.
Stulberg, M. J., et al. 2020. Phytopathology 110:1174.

The author(s) declare no conflict of interest.

Keywords: field crops, cereals and grains, pathogen detection

[†]Indicates the corresponding author.

E-mail: damon.smith@wisc.edu (D.L.S.)