Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Maize Stalk Rot Caused by *Epicoccum laticollum* on Maize (*Zea mays*) in China

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Maize (*Zea mays* L.) is the most important crop in Heilongjiang province. In July 2021, maize stalk rot was observed on approximately 10% of maize in a 2.4 ha field of Xiangfang District, Harbin City (N45°44'23", E126°43'19"). Infected plants showed softening of the stalks at the lower internodes, and the pith tissue was disintegrated and brown to reddish. Fifteen symptomatic plants were collected from the field. The discolored stalk pith tissues were cut into small pieces (4 × 2 mm), superficially disinfected with 1% NaClO for 3 min and 70% ethanol for 10 s, and washed three times with sterile distilled water. The disinfected tissues were placed on potato dextrose agar (PDA) amended with streptomycin sulfate (50 mg/liter) and incubated at 25°C for 1 week. Twenty-one cultures were obtained using hyphal tip technology and cultured on PDA for 7 days at 25°C for morphological and molecular analyses. The mycelia of the cultures were initially white but became grayish with time, and reddish-brown diffusible pigments were produced. A dark green discoloration was produced on malt extract agar (MEA) using the NaOH spot test. Pycnidia were brown, predominantly spheroidal, and 80.1 to 130.2 × 110.5 to

220.6 μm. Conidia were ellipsoidal, aseptate, and 4.3 to 6.8 × 2.1 to 3.2 μm. The isolates were initially identified as *Epicoccum laticollum* based on morphological features (Chen et al. 2017). To confirm the identity of *E. laticollum*, primers TUB2Fd/TUB4Rd, LR0R/LR5, ITS1/ITS4, and RPB2-5F2/fRPB2-7cR (Valenzuela-Lopez et al. 2018) were used to amplify beta tubulin (*tub2*), nuclear large subunit rDNA (LSU), internal transcribed spacer (ITS), and *RPB2* genes, respectively, for the representative isolate JF3. These sequences were deposited in GenBank (accession nos. OK490498, OK445527, OK483136, and OK490497) and had 100% (276/276 bp), 100% (842/842 bp), 100% (501/501 bp), and 100% (589/589 bp) nucleotide identity, respectively, with *E. laticollum* isolate GZDS2018BXT010 (GenBank accession nos. MK516208, MK516207, MK516206, and MK852278). To fulfill Koch's postulates, pathogenicity tests for all isolates were performed by individually inoculating surface-disinfected stalks of five healthy maize plants (10-leaf stage) between the second and third stem nodes with 20 μl conidial suspension at a concentration of 10⁶ conidia/ml as described by Zhang et al. (2016). Five other healthy surface-disinfected maize plants inoculated with sterile distilled water served as a control. All plants were kept at 25 ± 0.5°C in a greenhouse with a photoperiod of 12 h and approximately 90% relative humidity. After 10 days, all inoculated plants showed symptoms that were similar to those of the infected maize plants observed in the field, whereas the control plants were asymptomatic. The *Epicoccum* isolates were reisolated from symptomatic plants, and species identification was performed using the morphological and molecular methods described above. To our knowledge, this is the first report of *E. laticollum* causing maize stalk rot in China. This report will assist with monitoring the distribution of the disease and developing management recommendations.

References:

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The author(s) declare no conflict of interest.

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