Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium miscanthi* Causing Ear Rot on Maize in China

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Maize (*Zea mays* L.), an important food and feed crop worldwide, can be infected by *Fusarium* pathogens that can contaminate grain with mycotoxins. From August to October in 2018 and 2019, a field survey for maize ear rot was conducted in 76 counties of Guizhou province. The incidence ranged from 3 to 15% at individual fields in different areas. A total of 175 diseased maize ears with similar symptoms, including kernels covered with white, pink, or salmon-colored mold or exhibiting a white streaking (“starburst”) symptom, were collected from fields. Symptomatic kernels were surface sterilized by soaking for 30 s in 70% alcohol and for another 2 min in 2% sodium hypochlorite solution, followed by five rinses with sterile water. Each kernel was cut in half and placed on potato dextrose agar (PDA). After incubation at 28°C in the dark for 5 days, colonies displaying morphological characteristics of *Fusarium* were transferred to fresh PDA (Leslie and Summerell 2006). Single-sporing was conducted to purify the putative *Fusarium* colonies. A total of 120 isolates belonged to 16 *Fusarium* species were determined, and *Fusarium meridionale* was the dominant species. Five isolates from Huaxi district of Guiyang City were identified as *Fusarium miscanthi* (Gams et al. 1999). Colonies on PDA were white and floccose, and pigmentation as viewed from the underside of the Petri dish was violet. The average growth rate was 7.5 to 8.0 mm/day at 28°C in the dark. In cultures grown on PDA, zero- to one-septate microconidia were produced in slimy heads. Microconidia were clavate to fusiform with a truncate base and a broadly rounded tip, 4.8 to 13.3 × 1.8 to 3.3 μm (*n* = 110). In cultures grown on half-strength

carboxymethyl cellulose (CMC) broth (Xu et al. 2010), macroconidia were mostly three-septate, almost straight for most of the length, with a slightly foot-shaped basal cell and curved apical cell that gradually tapered, 17.8 to 71.3 × 2.0 to 4.3 μm (*n* = 78). The identity of the fungus was confirmed by sequence comparison of the partial translation elongation factor-1α (*TEF-1α*), RNA polymerase II subunit (*RPB2*), mitochondrial small subunit rDNA (*mtSSU*), and β-tubulin genes (Mirete et al. 2004; O'Donnell and Cigelnik 1997; O'Donnell et al. 2010). BLASTn searches of GenBank, using the partial *TEF-1α* (MN750829), *RPB2* (MN750834), *mtSSU* (MT594104), and β-tubulin (MT584781) sequences of representative isolate GYHXB03 as the queries, revealed 99.84, 99, 100, and 100% sequence identity, respectively, to *F. miscanthi* NRRL 26231 accessions AF324331, JX171634, AF060371, and AF060384. Inoculum of isolate GYHXB03 was prepared (Xu et al. 2010), and a pathogenicity test was conducted on maize hybrid ‘Shundan7’ and repeated twice. A 10⁶/ml spore suspension (2 ml) or sterile water was injected into each of eight maize ears through the silk channel at the blister stage of reproductive development in the field (Duan et al. 2019). After 3 weeks, typical *Fusarium* kernel rot symptoms the same as those previously shown in the field were observed on all pathogen-inoculated plants, whereas the controls were asymptomatic. The pathogens reisolated from two diseased kernels were identified as *F. miscanthi* based on morphology and *TEF-1α* and *mtSSU* analyses. *F. miscanthi* was first isolated from *Miscanthus sinensis* in Denmark (Gams et al. 1999) and also identified from *M. × giganteus* rhizomes in Belgium (Scaufflaire et al. 2013). To our knowledge, this is the first report of *F. miscanthi* causing maize ear rot in China. This disease should be monitored in Guizhou due to its threat to maize production.

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