Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Maize Stalk Rot Caused by *Fusarium nelsonii* in China

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Maize (*Zea mays* L.) is one of the main crops in Ningxia Province, China, and stalk rot has become a serious disease of maize in this area. Infected plants showed softening of the stalks at lower internodes, which lodged easily and died prematurely during grain filling, and the pith tissue internally appeared to be disintegrating and slightly brown to reddish. In September 2018, symptomatic tissue was collected from 17 locations in Ningxia. The incidence ranged from 5 to 40% in surveyed fields, reaching as high as 86% in certain plots. The discolored stalk pith tissues from the lesion region were cut into small pieces (approximately 0.5 × 0.2 cm), superficially disinfected with 75% ethanol for 1 min and rinsed three times with sterile water before plating on potato dextrose agar (PDA) medium with chloromycetin. The purified strains were obtained by single-spore separation and transferred to PDA and carnation leaf agar (CLA) medium. Morphological and molecular characteristics confirmed the presence of nine *Fusarium* species in these samples, including *Fusarium graminearum* species complex and *F. verticillioides*. Four isolates of *F. nelsonii* were recovered from samples collected in Shizuishan and Wuzhong. On PDA plates, the floccose to powdery, white to rose-colored aerial mycelia were produced and covered plates after 8 days of incubation, producing abundant mesoconidia and chlamydospores. Mesoconidia were fusiform or lanceolate until slightly curved with 0 to 3 septa, and chlamydospores were initially

smooth and transparent, and became verrucous and light brown. Macroconidia produced in CLA were straight or curved and falcate, usually having 3 to 5 septa, with beak-shaped strongly curved apical cells and foot-shaped basal cells. Two isolates (SS-1-7 and ZY-2-2) were selected for molecular identification, and the total DNA was extracted using a fungal genomic DNA separation kit (Sangon Biotechnology, Shanghai, China). Sequence comparison of *EF-1α* (GenBank accession nos. MW294197 and MW294198) and *RPB2* (MW294176 and MW294177) genes showed 97% homology with the sequences of *F. nelsonii* reported in GenBank (MN120760 for *TEF* and MN120740 for *RPB2*). Pathogenicity tests with two isolates (SS-1-7 and ZY-2-2) were performed by individually inoculating five 10-leaf stage maize plants at between the second and third stem nodes from the soil level with 20 µl conidial suspension at a concentration of 10⁶ conidia/ml as described by Zhang et al. (2016). Five maize plants inoculated with sterile water were used as controls. The inoculated plants were kept at 25 ± 0.5°C in the greenhouse with a photoperiod of 12 h. After 30 days, all plants inoculated with the conidial suspension formed an internal dark brown necrotic area around the inoculation site, whereas the control plants showed no symptoms. The pathogen was reisolated from the necrotic tissue of the inoculated plants and identified by morphological characteristics as *F. nelsonii*. This species was first described by Marasas et al. (1998), and it is expanding its host range, having been isolated from sorghum, Medicago, wheat, and cucumber (Ahmad et al. 2020). The pathogen should be paid more attention owing to a serious risk of trichothecene and aflatoxin contamination (Astoreca et al. 2019; Lincy et al. 2011). To our knowledge, this is the first report of maize stalk rot caused by *F. nelsonii* in China.

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