Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Maize Ear Rot Caused by *Exserohilum rostratum* in Hainan Province in Southern China

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Maize (*Zea mays* L.) is one of three major grain crops in China, with production reaching 261 million tons in 2019 (NBS 2020). Some fungi cause maize ear rot, which leads to significant yield and quality losses. In 2016, about 5% of maize ears were dark brown and covered with a white mold in seed production fields in Lingshui, Hainan Province, China. These ears were brought back to the laboratory for analysis. Molded kernels were surface sterilized in 75% ethanol for 3 min and in 10% sodium hypochlorite for 3 min, subsequently rinsed three times in sterile distilled water, placed onto potato dextrose agar (PDA), and incubated at 28°C in the dark for 3 days. Mycelia tips grown from kernels were transferred into fresh PDA plates. Seven fungal isolates with similar morphology characteristics were obtained, and three of them were identified by morphology and molecular identification. The colonies grew rapidly. The aerial mycelia turned white to black with age. Conidia were straight to slightly curved, oval, pyriform or geniculate, brown to dark brown, and had two to seven septa, with both basal and caudal septa thicker and darker than others, 39.47 to 78.66 × 13.96 to 22.78 μm, with a distinctly protruding hilum swelled from the basal cell. Conidiophores were dark brown, with geniculate tip and many septa. For molecular identification, genomic DNA of isolate was extracted from mycelia. The internal transcribed spacer (ITS), 1,3,8-trihydroxynaphthalene reductase (*Bm*), and glyceraldehyde-3-phosphate dehydrogenase-like (*Gpd*) genes were amplified with primers ITS1/ITS4 (White et al. 1990), Bm01/Bm02 (Shimizu et al. 1998), and *gpd1/gpd2* (Berbee et al. 1999), respectively. BLASTn analysis showed high identities with *Exserohilum rostratum* (ITS, LT837845.1, 100%; *Bm*, AY621165.1, 99.87%; *Gpd*, LT882543.1, 99.75%). Sequences

of ITS, *Bm*, and *Gpd* were deposited in GenBank with accession numbers MW362495, MW363953, and MW363954, respectively. Based on morphological characteristics and molecular analysis, the isolate was identified as *E. rostratum* (Hernández-Restrepo et al. 2018). Koch's postulates were completed by using ears of maize inbred line Huangzaosi and Chang7-2 growing in the experimental field of Baoding, Hebei Province. Three days post silk emergence, each of the four maize ears was injected with 2 ml of conidial suspension (1×10^6 conidia/ml) of isolate ZBSF005 through the silk channel. In the control groups, three ears were inoculated with an equal amount of sterile distilled water. The inoculated ears grew under natural conditions for 30 days; the diseased kernels and ear tips were black-brown and the surface covered with a white or gray-black mildew layer. The kernels with severe infection were wizened. But the bract could not be infected by the pathogen. Meanwhile, the control remained asymptomatic. The same fungus was successfully reisolated from the inoculated kernels, and its identity was confirmed by morphological and molecular biology approaches, thus fulfilling Koch's postulates. *E. rostratum* has been reported to cause leaf spots in a wide range of hosts, such as *Calathea picturata*, *Lagenaria siceraria*, *Saccharum officinarum*, *Ananas comosus*, *Hevea brasiliensis*, *Zea mays*, and so on (Ahmadpour et al. 2013; Chern et al. 2011; Choudhary et al. 2018), and it was also reported to cause root rot in *Lactuca saliva* (Alamri et al. 2019). To our knowledge, this is the first report of *E. rostratum* causing maize ear rot in China. The pathogen was simultaneously inoculated to eight maize inbred lines in Hebei Province, but the disease only occurred in some varieties and the incidence area was large. Therefore, attention should be paid to the ear rot caused by this pathogen in the breeding process.

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