Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium commune* Causing Stem Rot of Tobacco (*Nicotiana tabacum*) in Hunan Province, China

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Tobacco (*Nicotiana tabacum* L.) is a leafy, annual, solanaceous plant grown commercially for its leaves. It is one of the most important cash crops in China. In April of 2020, tobacco stems in commercial tobacco fields developed a brown to dark brown rot, in the Hunan Province of China. Almost 20% of the plants were infected. Symptoms appeared as round water-soaked spots and then turned dark black and developed into brown necrotic lesions, leading to the stem becoming girdled and rotted. Diseased stem tissue was cut and sterilized with 70% ethanol for 10 s followed by 0.1% HgCl₂ for 2 min, rinsed with sterile distilled water three times, plated on potato dextrose agar (PDA), and incubated at 26°C in the dark. Six isolates with similar morphology were obtained. Colonies cultured on PDA have morphological characteristics of *Fusarium* spp., producing white to orange-white, densely aerial mycelium with magenta to dark violet pigmentation. Macroconidia were produced on carnation leaf agar plates (Xi et al. 2019), which were slightly curved, with apical and basal cells curved, and usually contained three or five septa, 25.50 to 41.50 × 3.55 to 5.80 μm (*n* = 50). Microconidia were cylindrical, ovate-oblong, straight to slightly curved, aseptate, and 5.80 to 13.75 × 3.10 to 4.10 μm (*n* = 50). For molecular identification, the translation elongation factor 1-α (*EF1-α*), the largest subunit of RNA polymerase II gene sequences (*RPB2*), and the mitochondrial small subunit rDNA (*mtSSU*) of representative isolate CZ3-5-6 were amplified using the primer

pairs *ef1/ef2* (O'Donnell et al. 1998), *5F2/7Cr* (O'Donnell et al. 2010), and *NMS1/NMS2* (Li et al. 1994). The obtained *EF1-α*, *RPB2*, and *mtSSU* sequences (GenBank accession nos. MT708482, MT708483, and MW260121, respectively) were 99.70, 100, and 100% identical to strains of *Fusarium commune* (HM057338.1 for *EF1-α*, KU171700.1 for *RPB2*, and MG846025 for *mtSSU*). Moreover, *Fusarium*-ID database searches revealed that the *EF1-α* and *RPB2* were 100% identical to *F. commune* strains (FD_01140_EF-1a and FD_02411_RPB2). Based on the morphological and molecular characteristics of the representative isolate, the fungal species was identified as *F. commune*. Pathogenicity testing of a representative isolate was performed by inoculating tobacco plants, which were grown for 2.5 months in a sterile pot with autoclaved soil. Each tobacco stem was injected with 20 μl of conidial suspension (10⁵ spores/ml). Plants inoculated with sterilized water served as a control. The pathogenicity tests were performed twice using three replicate plants, and all plants were kept in humid chambers (80 × 50 × 80 cm) at 26°C with a 12-h photoperiod. After 10 days, dark brown necrotic symptoms around the inoculated site, similar to those observed in the natural field, had developed in all inoculated plants, whereas no symptoms were observed on the control plants. The pathogenic fungus was reisolated from symptomatic tissue and identified as *F. commune* but was not recovered from the control plants. *F. commune* has been reported to cause root rot or stalk and stem rot on some plants, such as sugarcane (Wang et al. 2018), *Gentiana scabra* (Guan et al. 2016), and maize (Xi et al. 2019). However, to our knowledge, this is the first report of *F. commune* causing stem rot on tobacco in China. Identification of *F. commune* as a stem rot-causing pathogen might provide important insights for disease diagnosis on tobacco caused by different *Fusarium* species. Overall, this disease might bring a threat to tobacco production, and appropriate control measures should be adopted to reduce losses in tobacco fields.

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