Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Root Rot on *Dendrobium officinale* Caused by *Fusarium incarnatum-equiseti* Species Complex in Zhejiang Province, China

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Dendrobium officinale Kimura et Migo is a rare and valuable Chinese herb cultivated in Zhejiang and Yunnan Provinces, China, which is known for its functions as an antineoplastic and for lowering the blood sugar (Cheng et al. 2019). In September and October of 2018 and 2019, symptoms of root rot on *D. officinale* were observed with an incidence of 15 to 20% in Wuyi County, Zhejiang Province, China. The pathogen mainly infected roots, causing severe root rot, which resulted in significant economic losses. At the early stage of this disease, the stalk turned brown, and then the whole plant rotted from bottom to top within a few days. Symptomatic roots were cut into small pieces (1.0 × 1.0 cm) and disinfected successively by submersion in 75% ethanol for 30 s and 1% NaClO for 30 s under aseptic conditions. After rinsing with sterile water three times and air drying, segments were placed on potato dextrose agar. After incubation at 25°C for 5 days in the dark, white to pale cream-colored colonies were produced. The average mycelial growth rate was 15.2 to 18.5 mm/day at 25°C. Macroconidia were falciform with three to

five septa and 18.0 to 32.0 × 3.0 to 5.0 μm in size. Microconidia were fusiform with two to three septa and 7.0 to 10.0 × 2.1 to 3.0 μm. Based on morphological characteristics of macroconidia and microconidia, isolates were identified as *Fusarium incarnatum-equiseti* species complex (FIESC) (Avila et al. 2019). The internal transcribed spacer (ITS) region, translation elongation factor (*EF-1α*), RNA polymerase largest subunit (*RPB1*), and RNA polymerase second largest subunit (*RPB2*) gene were amplified and sequenced using ITS1/ITS4, EF1/EF2, Fa/G2R, and 5f2/7cr primers, respectively (O'Donnell et al. 2010). BLASTN analysis of *FUSARIUM-ID* using ITS (accession no. MW172977), *EF-1α* (accession no. MW172978), *RPB1* (accession no. MW172979), and *RPB2* (accession no. MW172980) showed 99.8, 100, 99.74, and 98.63% identity to FIESC isolates NRRL43619, NRRL34059, NRRL32864, and NRRL32175, respectively. To verify pathogenicity, ten 1-year-old healthy *D. officinale* plants were used for inoculation tests. One milliliter of a conidial suspension (10⁶ conidia/ml) was pipetted onto the soil around the base of *D. officinale* plants per pot. Ten plants that were treated with sterile water were used as the control. All plants were maintained in a climatic chamber (26 ± 1°C, 70 to 80% relative humidity, and a photoperiod of 16-h/8-h light/dark). Seven days later, all inoculated plants showed typical symptoms of root rot identical to those observed in the fields. Control plants remained symptomless and healthy. The pathogenicity analysis was repeated three times. Pathogens reisolated from symptomatic plants were identified as FIESC species by morphology observation and sequence analysis. To our knowledge, this is the first report of root rot caused by FIESC species on *D. officinale* in Zhejiang, China.

References:

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