Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Soft Rot on *Dendrobium officinale* Caused by *Epicoccum sorghinum* in China

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Dendrobium officinale Kimura L. is a traditional Chinese orchid herb with both ornamental and human therapeutic values (Wang et al. 2020; Wu et al. 2020). During the field surveys of 2019 to 2020, a disease of stem rot and root soft rot was observed in *D. officinale* in Xingyi, Guizhou Province, China. Disease incidence ranged from 10 to 20% in the greenhouse and was more than 35% in the field. Brown or black water-soaked, pale chlorotic spots appeared on the leaves; stems had abnormal soft shrinkage and dark brown wilting symptoms. Small pieces of infected tissue were cut from the margin of necrotic lesions, surface disinfected with 1% sodium hypochlorite solution for 3 min followed by 75% ethanol for 30 s and rinsed with sterile distilled water five times. The tissues were then dried on sterilized filter paper and placed on potato dextrose agar (PDA). After incubation at 25°C in the dark for 7 days, fungal colonies with similar cultural morphology were consistently obtained from repeated isolations. The colonies were white and round with entire margins; the reverse side of colony was yellowish. The hyphae were white, dense, without stratification. The conidia were hyaline, ellipsoidal, unicellular, aseptate, and ranged from 3.67 to 6.12 × 1.0 to 1.35 μm in size. The chlamydospores were light brown, unicellular or multicellular, nearly spherical. These morphological characteristics were consistent with the characteristics

described for *Epicoccum* sp. (Zhou et al. 2018). To identify the fungus, DNA of two isolates was extracted using Plant Genome DNA Extraction Kit (Hangzhou Bio Medical Technology Co., Ltd.). The rDNA internal transcribed spacer (ITS), RNA polymerase II (RPB2), and β-tubulin (TUB) genes were amplified and sequenced using the primers ITS4/ITS5 (White et al. 1990), 5F2/7cR (Villani et al. 2016), and Bt-1/Bt-2 (Glass and Donaldson 1995), respectively. The RPB2 sequence of isolate XY1J (MW899504) was 99.89% identical to that of *E. sorghinum* (MW446946.1). The TUB primers amplified a fragment isolate XY1J (MZ043757) that was 100% identical to that of *E. sorghinum* (MN512426.1). A pathogenicity assay was conducted on *D. officinale*. Stems were stab inoculated with 5 × 5 mm colonized agar discs of strain XY1J by piercing at three points using a 1-mm sterile needle; the stems that were mock inoculated with sterile PDA served as the controls. Each stem was inoculated with three agar disks. Treated stems were maintained in a growth chamber with 90% relative humidity at 26°C, and a daily 12-h photoperiod (Zhou et al. 2018). After 3 days, sunken lesions, similar to those observed in the field, appeared on the inoculated stems. Typical symptoms developed at 8 days after inoculation. No symptoms were observed on the control stems. The experiment was repeated twice with similar results. *E. sorghinum* was reisolated from infected tissues and confirmed by sequence analysis. To our knowledge, this is the first report of *E. sorghinum* causing soft rot of *D. officinale* in China. This research will be helpful to monitor the distribution of the disease and develop management recommendations.

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