Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Athelia rolfsii* Causing Southern Blight on *Sarcandra glabra* in China

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Sarcandra glabra, belonging to the family Chloranthaceae, is a Chinese medicinal plant. The whole dry plant can be used as a medicine; it is rich in bioactive phytochemicals that possess antibacterial, anti-inflammatory, antioxidant, and antitumor properties (Xie et al. 2020). The current market price of *S. glabra* is around US\$5/kg, and the annual demand is ~3,500,000 to 4,000,000 kg in China (Pan et al. 2007). To meet consumer demand for safe and high-quality herbal products, the artificial cultivation of *S. glabra* has been vigorously promoted. In 2020, it was observed that a plant disease affected *S. glabra* growth in Hunan Province. The disease symptoms included constriction at the base of the stem, with decay and a white mycelium covering. The plants finally died with a disease incidence ranging from 15% to 20%. Using our previously published methods (Yi et al. 2019), one fungal isolate was isolated from the cultured symptomatic stem tissue on potato dextrose agar (PDA) medium and was named as Kb. The isolate was subsequently transferred into 70% glycerol for preservation. The Kb colony varied in color from white to light yellow. The septate hyphae grew rapidly on PDA medium, at approximately 25 mm/day, at 28°C. On the fifth day, rhizomorphs were formed at the edge and on the center of the PDA plate. On

the sixth day, sclerotia developed into a rapeseed shape (diameter = ~1.2 to 2.3 mm) with a smooth surface, and with white, yellow, or chestnut brown coloring. Morphologically, Kb was similar to *Sclerotium rolfsii* (Sun et al. 2020). Vigorously growing aerial hyphae were selected for molecular identification. The internal transcribed spacers (ITS) were amplified using the primer pairs ITS1/ITS4 (Glass et al. 1995). BLAST searches against GenBank indicated that Kb's ITS sequence shared 97% similarity with that of *Athelia rolfsii* (MN696630.1). Based on morphological and molecular characteristics, Kb was identified as *A. rolfsii*. The sequence was deposited in GenBank (MW288292). Pathogenicity tests were carried out using the following procedures. Three healthy *S. glabra* seedlings were inoculated at the stem base with a PDA plug (5 mm in diameter) covered with 5-day-old fungal mycelium cultured at 28°C, while the remaining three seedlings were inoculated with distilled water only, as the control. Plants were incubated in a greenhouse at 28°C. At 7 days post inoculation, the inoculated sites infected with the putative pathogen displayed identical constrictions as previously observed in the field. In contrast, the controls remained symptomless. The pathogen was reisolated from these infected seedlings, and its culture showed the same morphological and molecular traits as the original isolates. No pathogens were isolated from the control plants. Pathogenicity tests were repeated three times. Koch's postulates were fulfilled. Although *S. rolfsii* has been previously reported to cause southern blight on mung bean crops in China (Sun et al. 2020), this is the first report on *A. rolfsii* causing similar symptoms of southern blight on *S. glabra* in Hunan Province, China. Identification of the pathogens causing each disease is important for the development of effective disease management strategies and for extensive artificial cultivation.

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