Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Pestalotiopsis lushanensis* Causing Brown Leaf Spot on *Sarcandra glabra* in China

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Sarcandra glabra is a species of Chloranthaceae family, and members of this family grow in the southern part of China, Japan, and Southeastern Asia. (Li et al. 2019). It is a kind of precious Chinese herbal medicine, which occupies an important position in traditional Chinese herbal medicine. It plays an effective role in the treatment of cancer, rheumatism, pneumonia, digestive tract inflammations, traumatic injuries and fractures, antiviral, antibacterial, antioxidant, and so on (Li et al. 2019; Zheng et al. 2003; Zhou et al. 2013). Since June 2020, we discovered a serious leaf disease in the *S. glabra* planting base of Shibing County (108.12E, 27.03N), in Guizhou Province, with an incidence rate of 60% and yield losses of 40%. Initially, the symptoms developed as small specks, and the spots were purple with a dark brown halo margin and were round or oval. In later stages, the spots gradually expanded and became dry, causing severe whole leaf loss. To identify the pathogen, we collected the diseased leaves from *S. glabra* fields in Shibing County. Small tissue pieces from the edges of lesions were disinfected in 75% ethyl alcohol for 30 s and 1% hypochlorite for 1 min, rinsed five times in sterile water, plated on potato dextrose agar (PDA), and incubated at 28°C in a lighted incubator for 3 days. Fungal colonies were consistently isolated and transferred to PDA for morphological characterization (Fang 2007). Pathogenicity tests of the novel isolate HGUP CSH-2 were conducted by spraying spore suspensions with a concentration of 1.6×10^8 conidia/ml on surface-disinfected (70%

ethyl alcohol, 30 s) leaves, whereas sterile distilled water was used as the control. Plants with inoculated leaves (three per treatment) were placed in lighted growth chambers at 28°C for 5 days and watered as needed (light to dark ratio, 1:1; 90% relative humidity). Symptoms on inoculated leaves were similar to those described previously in the field. The same pathogenic fungus was reisolated from the infected leaves but not from the noninoculated leaves. Colonies on PDA attained 70-mm diameter after 7 days at 28°C, with pale honey-colored, sparse aerial mycelia on the surface with black, gregarious conidiomata. Conidiogenous cell discrete or integrated, ampulliform, clavate or subcylindrical, hyaline, smooth-walled, wide at base. Conidia fusoid, ellipsoid, straight to slightly curved, four-septate, slightly constricted at septa, 22.26 to 27.17×6.9 to 8.22 μm (average $\pm$ SD: $24.68 \pm 1.57 \times 7.68 \pm 0.38$ μm ; $n = 30$). According to the colony and conidia characteristics, the isolate was initially identified as *Pestalotiopsis* spp. (Liu et al. 2017). The pathogen was confirmed by amplification and sequencing of the internal transcribed spacer region (ITS) gene, the translation elongation factor-1 (TEF1) gene, and the β -tubulin (TUB2) gene (Liu et al. 2017) using ITS1/ITS4, Bt2a/T1, and EF1-526F/1567R primers, respectively. The sequences of the PCR products were deposited in GenBank with accession numbers MT919215 (ITS), MT939300 (TUB2), and MT939299 (TEF1). BLAST results of the obtained sequences of the ITS, TUB2, and TEF1 genes revealed 97.16% (479/493 nucleotides), 99.56% (675/678 nucleotides), and 99.89% (890/891 nucleotides) homology with those of *Pestalotiopsis lushanensis* in GenBank (MG726538, KY464157, and KX895223). The maximum likelihood method was used for phylogenetic analysis. The result showed that HGUP CSH-2 was together with *P. lushanensis* with a support rate of 100%. According to the morphological characteristics and molecular phylogenetic analysis, the pathogen was identified as *P. lushanensis*. So far as we know, our research is the first report of brown leaf spot of *S. glabra* caused by *P. lushanensis* in China. Thus, identification of *P. lushanensis* for this disease is important for the advancement of effective prevention and control practices as future prospects.

References:

- Fang, Z. D. 2007. Research Methods of Plant Diseases, 3rd Ed. China Agriculture Press, Beijing, China.
- Li, H., et al. 2019. Int. J. Biol. Macromol. 123:957.
- Liu, F., et al. 2017. Sci. Rep. 7:866.
- Zheng, W., et al. 2003. Talanta 60:955.
- Zhou, H., et al. 2013. Food Chem. 138:2390.

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