Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Sawadaea polyfida* Causing Powdery Mildew of *Acer palmatum* in China

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Acer palmatum Thunb. is an important, colorful leaf ornamental tree species widely distributed in Japan, Korea, and China (Stuepp et al. 2016). In October 2019, powdery mildew was observed on leaves of *A. palmatum* planted at Qixia Mountain Park and the campus of Nanjing Forestry University, Nanjing, Jiangsu, China. The powdery mildew infected and colonized leaves, covering both leaf surfaces with white mycelia, giving affected plants an unsightly appearance. Nearly 17.4% of the plants (87 of 501) exhibited these signs and symptoms. Fresh specimens were collected and examined for the identification of the pathogen. Photos were taken with a ZEISS Axio Imager A2m microscope and a scanning electronic microscope. Chasmothecia were scattered or aggregated on the upper and lower surfaces of the leaves, blackish brown, oblate, 157.5 to 238.1 by 152.3 to 217.8 μm ($n = 30$), with numerous appendages (100 to 200). Appendages were often (1–) 2 to 3 times branched from the middle of the stalk, uncinately circinate at the apex, hyaline, aseptate, 30.0 to 70.8 by 4.1 to 8.2 μm ($n = 30$). Asci were 11 to 21 per chasmothecium ($n = 30$), long oval, oval, oblong, with short stalk or sessile, 80.6 ± 8.6 by 40.3 ± 4.0 μm ($n = 30$) in length, 6 to 8 spored ($n = 30$). Ascospores were ovoid, 18.2 ± 1.6 by 11.1 ± 1.2 μm ($n = 30$). Microconidiophores were 25 to 50 by 4.0 to 5.5 μm , producing microconidia in chains. Microconidia were ellipsoidal, subglobose, 8.7 ± 0.6 by 7.2 ± 0.6 μm ($n = 30$). Macroconidia were not observed. Based on the morphological characteristics, the fungus was identified as *Sawadaea*

polyfida (C. T. Wei) R. Y. Zheng & G. Q. Chen (Zheng and Yu 1987). To confirm the causative species identity, a representative voucher specimen collected and deposited at Nanjing Forestry University was used for a molecular analysis. Mycelia and conidia were collected from diseased leaves, genomic DNA of the pathogen was extracted, and the internal transcribed spacer (ITS) region was amplified with primers ITS1 and ITS4 (White et al. 1990). The resulting sequence of 461 bp was deposited in GenBank (accession no. MW255383). BLAST result showed that this sequence fully agreed with a sequence of *S. polyfida* (AB193381.1 [ITS], identities = 461 of 461 [100%]). A maximum-likelihood phylogenetic analyses using IQtree v. 1.6.8 with the ITS sequence placed this fungus in the *S. polyfida* clade. Based on the morphology and phylogeny, the fungus was identified as *S. polyfida* (Hirose et al. 2005; Zheng and Yu 1987). Pathogenicity was tested through inoculation by gently pressing the naturally infected leaves onto healthy ones of three potted *A. palmatum* seedlings with five leaves. Healthy leaves from three other seedlings served as the control. Inoculated and control seedlings were placed in separate growth chambers maintained at $20 \pm 2^\circ\text{C}$, 70% humidity, with a light and dark period of 16 and 8 h, respectively. Symptoms developed 8 days after inoculation. The powdery mildew developing on the inoculated seedlings was sequenced and confirmed as *S. polyfida*. The control leaves did not develop powdery mildew. *S. polyfida* has been reported on *A. catalpifolium* in China (Zheng and Chen 1980); *A. amoenum*, *A. australe*, *A. japonicum*, *A. palmatum*, *A. shirasawanum*, and *A. sieboldianum* in Japan (Hirose et al. 2005; Meeboon et al. 2015); as well as *A. takesimensis* in Korea (Lee et al. 2011). To the best of our knowledge, this is the first report of powdery mildew caused by *S. polyfida* on *A. palmatum* in China. These results form the basis for developing effective strategies for monitoring and managing this disease.

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