Diseases Caused by Fungi and Fungus-Like Organisms

Powdery Mildew of Tall Verbena Caused by *Podosphaera xanthii* in China

Quanchun Hong,[†] Mengyao Tao, and Zhenfeng Zhao

Key Laboratory of Plant-Microbe Interactions, College of Biology and Food, Shangqiu Normal University, Shangqiu, Henan 476000, China

Plant Dis. 105:3297, 2021; published online as <https://doi.org/10.1094/PDIS-02-21-0315-PDN>. Accepted for publication 12 April 2021.

Tall verbena (*Verbena bonariensis*) is widely used in landscape layout in sparse forests, botanical gardens, and villa areas, and it is also a kind of Chinese herbal medicine. The flower and bud are used as Chinese herbal medicine causing heat-clearing and detoxification. In August 2019, symptoms of white fungal growth were observed on both sides of fresh and mature leaves of tall verbena grown on the campus of Shangqiu Normal University (SQNU), Henan Province, China. More than 60% of plants were infected by this fungus, and infected plants were observed to shed leaves early. One representative voucher specimen was deposited at the herbarium of SQNU, under the accession number Vb01. Conidiophores of the fungus contained five to six cells and measured 102.0 to 142.9 μm (mean 126.2 μm , $n = 30$) long, with foot cells of conidiophores measuring 36.5 to 46.9 μm (mean 42.9 μm , $n = 30$). Conidia produced in chains were variable in shape, ellipsoid to ovoid, and measured 24.8 to 30.7 $\times$ 12.0 to 17.9 μm (mean 27.35 $\times$ 15.08 μm , $n = 50$), with a length/width ratio of 1.4 to 2.3. Fibrosin bodies were observed in the conidia. No chasmothecia were found. The morphological characteristics were consistent with the genus *Podosphaera*. To identify the above

powdery mildew fungus at species level using molecular markers, the complete ITS region of rDNA from the representative specimen was amplified with universal primer pair ITS1/ITS4 and directly sequenced. The resulting sequence of 567 bp was deposited in GenBank (accession no. MT864007). A BLAST search of this sequence showed more than 99% sequence identity with *Podosphaera xanthii* isolates (AB046985, AB462804, AB936277, and KM260741) on various hosts (Hirata et al. 2000; Meeboon and Takamatsu 2015; Tam 2016). Phylogenetic analysis revealed that the ITS sequence from Vb01 isolate was grouped into a clade with *P. xanthii sensu lato* (*s.l.*). A pathogenicity test was conducted through inoculation by gently pressing a diseased leaf onto five healthy leaves of a potted tall verbena. Five noninoculated seedlings were used as controls. The plants were maintained in a greenhouse at 26 to 28°C and relative humidity of 60 to 65%. Inoculated leaves developed symptoms after 9 days, whereas the control plants remained symptomless. The fungus presented on the inoculated plant was morphologically identical to that originally observed on diseased plants, fulfilling Koch's postulates. *P. xanthii s.l.* has been reported on several hosts in China (Braun and Cook 2012). This is the first report of *P. xanthii s.l.* on *V. bonariensis* outside of Japan (Meeboon and Takamatsu 2015).

References:

- Braun, U., and Cook, R. T. A. 2012. Taxonomic Manual of the Erysiphales (Powdery Mildews). CBS Biodiversity Series No. 11. CBS, Utrecht, the Netherlands.
Hirata, T., et al. 2000. Can. J. Bot. 78:1521.
Meeboon, J., and Takamatsu, S. 2015. Mycoscience 56:243.
Tam, L. T. T., et al. 2016. Plant Dis. 100:216.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: *Podosphaera xanthii*, *Verbena bonariensis*, powdery mildew

[†]Indicates the corresponding author.

Q. C. Hong; hongquanchun@163.com