Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Powdery Mildew on *Zinnia elegans* Caused by *Podosphaera xanthii* in Northeast China

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Zinnia (*Zinnia elegans* L.) is a common garden flowering plant in China, which can also grow well in the cold regions of northeast China. In August 2020, powdery mildew on zinnia was observed in the garden of the International Agricultural Science and Technology Innovation Center of Heilongjiang Province (126°30' N, 45°47' E), Harbin, Heilongjiang Province, China. More than 95% of plants were affected in the garden. Powdery mildew colonies began as small white spots on the upper surface of the older leaves and then spread to entire leaves. Subsequently, younger leaves developed rapid symptoms, resulting in premature senescence of the plants. Conidia collected from infected plant tissues were ellipsoid-ovoid to barrel-shaped, with distinct fibrosin bodies visible in their cytoplasm, and measured 20 to 28 × 14 to 19 µm with a length/width ratio of 1.5 to 2.0. Conidiophores were unbranched, straight, 95 to 230 × 9 to 16 µm in size, and produced four to six immature conidia in chains. Foot cells of conidiophores were cylindrical and 35 to 70 µm long, with light constriction at the basal septum, and followed by one to three short cells. Fungal hyphae were septate, branched, flexuous to straight, and up to 5 µm wide with indistinct to slightly nipple-shaped appressoria. Chasmothecia were absent in the collected infected samples. Partial

sequence of small subunit ribosomal RNA gene, internal transcribed spacer 1 (ITS1), 58S ribosomal RNA gene, internal transcribed spacer 2 (ITS2), and partial sequence of large subunit ribosomal RNA gene were amplified from conidia collected from infected leaves of four individual plants using primers ITS1/ITS4, respectively (White et al. 1990). Four ITS region sequences were deposited in GenBank (accession no. MW142496 [538 bp], MZ348457 [538 bp], MZ348458 [540 bp], and MZ348459 [540 bp]). All the amplicons exhibited more than 99% sequence identity (MW142496 [536/538], MZ348457 [536/538], MZ348458 [538/540], MZ348459 [537/540]) with those sequences of *P. xanthii* isolates (accessions no. MT568609 to MT568611) on *Z. elegans* in Taiwan (Xiao et al. 2021). Based on these morphological characteristics and molecular analysis, this pathogen was identified as *P. xanthii* (Braun and Cook 2012). The phylogenetic trees were constructed using the neighbor-joining method in MEGA 7.0. Based on the ITS rDNA phylogenetic tree, the sequences retrieved from the specimens clustered within a strongly supported clade with *P. xanthii* (MT704550, MT864007, MN818562, and MW692364), confirming the identity. A pathogenicity test was performed by dusting conidia from an infected leaf onto young leaves of five healthy plants in the greenhouse with five noninoculated plants as a control. Powdery mildew symptoms were observed on inoculated leaves after 5 days of inoculation at 18/25°C (night/day) and 75% relative humidity, whereas control plants remained asymptomatic. The fungus on inoculated leaves was morphologically identified as that observed on the original diseased leaves. Powdery mildew on zinnia caused by *P. xanthii* has been identified in Taiwan (Xiao et al. 2021), and by *Golovinomyces cichoracearum* in Turkey (Soylu et al. 2011). To our knowledge, this is the first report of powdery mildew caused by *P. xanthii* on *Z. elegans* in northeastern China.

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