Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Golovinomyces orontii* Causing *Hydrangea macrophylla* Powdery Mildew in Qinghai-Tibet Plateau, China

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Funding: Funding was provided by National Natural Science Foundation of China (31600513). Plant Dis. 105:2730, 2021; published online as <https://doi.org/10.1094/PDIS-11-20-2359-PDN>. Accepted for publication 5 February 2021.

Hydrangea macrophylla (Thunb.) Ser. (Hydrangeaceae) is the most popular hydrangea species grown in home gardens and landscapes in China. Plants of *H. macrophylla* with symptoms of powdery mildew were found in a commercial wholesale nursery in Huzhu, Haidong (36°49'11.87"N, 101°57'03.36"E, altitude 2,490 m), in May 2020, with disease incidence reaching 80%. Symptoms included yellowing and necrosis of leaves. Upon microscopic observation, masses of conidia and mycelium were observed covering the symptomatic tissues. Fungal isolates displayed nipple-shaped hyphal appressoria, often poorly developed, conidiophores erect, arising laterally or from the upper surface of hyphal mother cells, and positioned almost centrally or toward one end of the cells, up to about 160 µm long ($n = 30$), with foot cells straight or flexuous, 32 to 86 × 8 to 13 µm ($n = 50$), followed by one to three shorter cells about 11 to 24 × 10 to 15 µm ($n = 50$), forming catenulent conidia in usually predominantly chains, conidia doliform to limoniform, hyaline, and 24 to 35 × 13 to 25 µm ($n = 50$). Conidial germination was of the *Euoidium* type. Chasmothecia were not observed. To confirm fungal classification, single spores were isolated and cultured on a detached leaf bioassay following the

protocol described in Farinas et al. (2019). Total DNA was extracted directly from single-spore cultures using a Chelex extraction method (Walsh et al. 1991). The rDNA internal transcribed spacer (ITS) regions were amplified by polymerase chain reaction (PCR) utilizing the universal primer pairs ITS1/ITS4 (White et al. 1990). The sequences (726 to 727 bp) were deposited in GenBank (accession nos. MT568633, MT757924, and MT757925). The ITS sequences showed 99.9 to 100% identity with a sequence of *Golovinomyces orontii* reported on *Papaver rhoeas* (AB769466) in Switzerland. Based on the ITS rDNA phylogenetic tree, the sequences retrieved from the specimen clustered within a strongly supported clade with *G. orontii* (AB769466), confirming the identity of the pathogen (Takamatsu 2013). Cladistic trees were constructed using the neighbor-joining method with the Kimura two-parameter substitution model in MEGA 6.0. Branch robustness was assessed via bootstrap analysis with 1,000 replicates. To confirm pathogenicity, eight *H. macrophylla* plants were sprayed until run-off with a suspension containing 1×10^5 conidia/ml. Four plants were used for fulfilling Koch's postulates, and four plants were used as mock-inoculated controls sprayed only with sterile distilled water. Inoculated and noninoculated plants were covered with plastic bags separately and maintained overnight in a greenhouse at $25 \pm 2^\circ\text{C}$ and 50 to 60% relative humidity. Typical powdery mildew colonies developed on inoculated plants 10 to 15 days after inoculation, which were morphologically identical to those originally observed on the diseased plants, whereas the control plants remained symptomless. To our knowledge, this is the first report of powdery mildew caused by *G. orontii* on *H. macrophylla* in the Qinghai-Tibet Plateau, China (Braun and Cook 2012).

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The author(s) declare no conflict of interest.

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Keywords: Qinghai-Tibet Plateau, powdery mildew, *Golovinomyces orontii*, *Hydrangea macrophylla*

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