Diseases Caused by Fungi and Fungus-Like Organisms

Powdery Mildew Caused by *Erysiphe sedi* on *Crassula capitella* in China

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Crassula capitella Thunb. is a succulent used ornamentally in gardens and landscapes. In August 2019, severe powdery mildew infection was observed on *C. capitella* in a plant nursery, 1,000 m² in area, in Xining (36°42'44.39"N, 101°44'50.50"E, altitude 2,330 m), China. Approximately 35% of the leaves on a plant were symptomatic, and 80% of the plants were affected. The disease seriously reduced the ornamental value. A voucher specimen was deposited in the Herbarium of Plant Pathology at Qinghai University under accession number QHU2019150. The pathogen formed superficial mycelia on leaves and stems, producing conspicuous white colonies followed by necrosis of the leaf tissues and defoliation. Mycelia were amphigenous, white, effuse or in patches, persistent, with lobed appressoria. The pathogen produced conidia singly on two- to three-celled conidiophores occurring on the ectophytic hyphae. Conidia were subcylindrical, measured 22 to 41 × 10 to 16 ($n = 50$) µm, and were produced singly on the tip of conidiophores. Conidiophores were erect and up to 110 µm long, foot cells straight, cylindrical, and 22 to 53 × 8 to 10 ($n = 50$) µm, followed by one to three shorter cells. Chasmothecia were not found. The fungus was identified as *Erysiphe sedi* based on morphology (Braun and Cook 2012). To confirm identification, the ITS region was amplified. The ITS5/P3 and PM5/ITS4 primers were used to amplify the ITS region by

nested PCR, and the cloned fragments were sequenced (Takamatsu and Kano 2001). The aligned ITS region sequences were deposited in GenBank (accession no. MT178769). A BLAST search analysis of the two sequences revealed 99.84% identity with *E. sedi* infecting *Sedum aizoon* in Russia (LC010045). A phylogenetic tree was constructed in MEGA6 with 15 ITS sequences using the neighbor-joining method with the Kimura two-parameter substitution model. The sequence retrieved from powdery mildew on *C. capitella* in China clustered together with the sequences obtained from *E. sedi* on *Sedum* spp. with nearly 100% concordance, placing it in the *Erysiphe aquilegiae* complex as defined by Takamatsu et al. (2015) and recently critically discussed by Shin et al. (2019). This complex comprises numerous *Erysiphe* spp. insufficiently resolved, especially when based only on ITS data. However, for the time being we follow Götz et al. (2019) and recognize *E. sedi* as a species of its own and identify the Chinese collection on *C. capitella* as *E. sedi* because of the morphological agreement and concordant ITS data. Pathogenicity tests were completed by gently pressing infected leaves onto five healthy leaves of *C. capitella*. Inoculated and noninoculated plants were maintained separately in different rooms of a greenhouse at 22 to 25°C. Inoculated plants developed signs and symptoms after 12 days, whereas control plants remained symptomless. The morphology of the fungus on inoculated leaves was identical to that originally observed on diseased plants. To our knowledge, this is the first report of powdery mildew caused by *E. sedi* on *C. capitella* in China and worldwide, although *E. sedi* is reported to infect many crassulaceous or Crassulaceae hosts (Cho et al. 2012; Götz et al. 2019).

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