Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Golovinomyces sonchicola* Causing Powdery Mildew on *Sonchus oleraceus* in Mexico

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Funding: This research was financially supported by the National Council of Science and Technology of Mexico (CONACYT), project INFRA-2019-302117, and the Autonomous University of the West (UAdeO), project PIFIP-2019. Plant Dis. 105:3306, 2021; published online as <https://doi.org/10.1094/PDIS-01-21-0117-PDN>. Accepted for publication 25 April 2021.

Sonchus oleraceus, common sow thistle, is native to Europe, Northern Africa, and Western Asia. This plant has become a common weed throughout the world. In Mexico, this weed has become widely naturalized by replacing indigenous plants and invading many agricultural areas. During the spring of 2018 and 2019, common sow thistle plants showing typical symptoms and signs of powdery mildew were collected from agricultural fields in Ahome, Sinaloa, Mexico. As much as 30% of plants were diseased, and 60 to 95% of the foliage was affected. Mycelium was conspicuous and white-gray and was on stems and both surfaces of leaves. Appressoria were nipple-shaped to crenulate. Conidiophores ($n = 30$) were hyaline, cylindrical, erect, and up to 150 μm long. Foot cells ($n = 30$) were distinctly curved, 47 to 75 $\times$ 10 to 13 μm , slightly constricted, followed by one to three shorter cells and formed conidia in chains. Conidia ($n = 100$) were ellipsoid to doliform to subcylindrical, 28 to 37 $\times$ 14 to 19 μm , lacked fibrosin bodies, and germinated from the apex. Chasmothecia were not observed. The morphological characters were consistent with those of the anamorphic state of *Golovinomyces sonchicola* (Braun and Cook 2012; Jakše et al. 2019). A voucher specimen (accession no. FAVF215) was deposited in the Herbarium of the Faculty of Agriculture of El Fuerte Valley at the Autonomous University of Sinaloa (Juan Jose Rios, Sinaloa, Mexico). To

confirm the morphological identification, genomic DNA was extracted from mycelium and conidia, and the internal transcribed spacer (ITS) region and part of the 28S gene were amplified by polymerase chain reaction (PCR) and sequenced. The ITS region of rDNA was amplified using the primers ITS5/ITS4 (White et al. 1990). For amplification of the 28S rRNA partial gene, a nested PCR was performed using the primer sets PM3 (Takamatsu and Kano 2001)/TW14 (Mori et al. 2000) and NL1/TW14 (Mori et al. 2000) for the first and second reactions, respectively. Phylogenetic analyses using the maximum parsimony and maximum likelihood methods (Braun et al. 2019), including ITS and 28S sequences of isolates of *Golovinomyces* spp., were performed and confirmed the results obtained from the morphological analysis. Isolate FAVF215 grouped in a clade with the other isolates of *G. sonchicola*. The ITS and 28S sequences were deposited in GenBank under accession numbers MW425872 and MW442972, respectively. Pathogenicity was demonstrated by gently dusting conidia from infected leaves onto leaves of 20 healthy plants and covering with plastic bags for 24 h. Ten noninoculated plants served as controls. All plants were maintained in a greenhouse at 25 to 35°C. All inoculated plants developed similar symptoms to those observed in the field from natural infections after 12 days, whereas powdery mildew symptoms and signs were not observed on control plants. The morphology of asexual structures of fungus on inoculated plants were identical to those on naturally infected plants, fulfilling Koch's postulates. Inoculation tests were repeated twice with identical results. Based on the morphological data and phylogenetic analysis, the fungus was identified as *G. sonchicola*. This fungus has been reported causing powdery mildew on *S. oleraceus* in Germany, the Netherlands, Slovenia, and the United Kingdom (Farr and Rossman 2021). To the best of our knowledge, this is the first report of *G. sonchicola* causing powdery mildew on *S. oleraceus* in Mexico. This powdery mildew pathogen may represent an option for the biological control of common sow thistle.

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The author(s) declare no conflict of interest.

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Keywords: fungi, pathogen detection, phylogeny

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