Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Powdery Mildew Caused by *Podosphaera xanthii* on *Cucurbita argyrosperma* in Mexico

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Cucurbita argyrosperma, commonly known as winter or cushaw squash, is highly sought-after for its seeds, which have important uses in culinary arts. During the autumn of 2021, powdery mildew-like signs and symptoms were observed on cushaw squash in several commercial fields in Cocula, Guerrero, Mexico. Signs initially appeared as whitish powdery patches on both sides of leaves, which then covered entire leaves and caused premature senescence. The disease incidence was estimated to be 80% in about 1,000 plants in two fields. The mycelium was amphigenous, persistent, white, and occurred in dense patches. A voucher specimen was deposited in the Herbarium of the Colegio Superior Agropecuario del Estado de Guerrero under the accession number CSAEG22. For morphological characterization by light microscopy, fungal structures were mounted in a drop of lactic acid on a glass slide. Microscopic examination showed nipple-shaped hyphal appressoria. Conidiophores ($n = 30$) were straight, 100 to 190 $\times$ 10 to 12 μm , and produced two to six conidia in chains. Foot-cells were cylindrical, 41 to 78 μm long, and were followed by one to two shorter cells. Conidia ($n = 100$) were ellipsoid-ovoid to barrel-shaped, 29.5 to 39.1 $\times$ 19.4 to 22.7 μm , and contained conspicuous fibrosin bodies. Germ tubes were produced from a lateral position on conidia. Chasmothecia were not observed during the growing season. The morphological characters were consistent with those of the anamorphic state of *Podosphaera xanthii* (Braun and Cook 2012). For further confirmation,

total DNA was extracted from conidia and mycelia following the CTAB method (Doyle and Doyle 1990), and the internal transcribed spacer (ITS) region and part of the 28S gene were amplified by 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 likelihood method including the ITS and 28S sequences of isolates of *Podosphaera* spp. were performed and confirmed the results of the morphological analysis. The isolate CSAEG22 grouped in a clade with isolates of *P. xanthii*. The ITS and 28S sequences were deposited in GenBank under accession numbers OL423329 and OL423343, respectively. Pathogenicity was confirmed by gently dusting conidia from infected leaves onto 10 leaves of healthy *C. argyrosperma* plants. Five noninoculated leaves served as controls. The plants were maintained in a greenhouse at 25 to 35°C and a relative humidity of 60 to 70%. All inoculated leaves developed similar signs to the original observation after 10 days, whereas control leaves remained symptomless. Microscopic examination of the fungus on inoculated leaves showed that it was morphologically identical to that originally observed on diseased plants, fulfilling Koch's postulates. *P. xanthii* has been previously reported on *C. maxima*, *C. moschata*, and *C. pepo* in Mexico (Farr and Rossman 2021; Yañez-Morales et al. 2009). To our knowledge, this is the first report of *P. xanthii* causing powdery mildew on *C. argyrosperma* in Mexico. This pathogen is a serious threat to *C. argyrosperma* production in Mexico, and disease management strategies should be developed.

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