Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Neovrysiphe sechii* Causing Powdery Mildew on *Sechium edule* in San Luis Potosí, Mexico

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From 2018 to 2020, powdery mildew-like signs and symptoms were observed on chayote (*Sechium edule* var. *virens levis*) in a commercial field located in Santa María del Río, San Luis Potosí, Mexico. Signs appeared as whitish powdery masses on both sides of leaves and stems. Disease incidence was about 30% and signs covered up to 70% of leaf surface. Ten samples were collected and analyzed. Mycelium was amphigenous, persistent, white, in dense patches. Hyphal appressoria were lobed and solitary. Conidiophores ($n = 30$) were hyaline, erect, straight, and 62 to 101 μm long. Foot cells were cylindrical and straight, followed by 1 to 3 shorter cells, and forming conidia in short chains. Conidia ($n = 100$) were hyaline, surface striate, cylindrical-ellipsoid, doliform or ovoid, 25.7 to 37.6×11.9 to $18.4 \mu\text{m}$, without fibrosin bodies, and with germ tubes terminal or subterminal. Conidial appressoria were lobed. Chasmothecia were not observed. The morphological characters were

consistent with those of the anamorphic state of *Neovrysiphe sechii* (Gregorio-Cipriano et al. 2020). A voucher specimen was deposited in the Herbarium of the Department of Agricultural Parasitology at the Chapingo Autonomous University under accession number UACH192. To confirm the identification of the fungus, genomic DNA was extracted from conidia and mycelium, 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 parsimony and maximum likelihood methods, including ITS and 28S sequences of isolates of *Neovrysiphe* spp., were performed and confirmed the results obtained in the morphological analysis. The isolate UACH192 grouped in a clade with isolates of *N. sechii*. The ITS + 28S sequence was deposited in GenBank under accession number MZ468642. Pathogenicity was confirmed by gently dusting conidia from infected leaves onto 10 leaves of healthy chayote plants. Five noninoculated leaves served as controls. The plants were maintained in a greenhouse at 25 to 30°C, and relative humidity of 60 to 70%. All inoculated leaves developed similar symptoms to the original observation after 8 days, whereas control leaves remained disease free. Microscopic examination of the fungus on inoculated leaves showed that it was morphologically identical to that originally observed. The pathogenicity test was repeated twice with similar results. Based on morphological data and phylogenetic analysis, as well as pathogenicity test, the fungus was identified as *N. sechii*. This pathogen has been previously reported causing powdery mildew on *S. edule* and *S. mexicanum* in Veracruz, Mexico (Gregorio-Cipriano et al. 2020). However, to our knowledge, this is the first report of *N. sechii* causing powdery mildew on chayote in San Luis Potosí (central Mexico). This pathogen represents a serious threat to chayote production and disease management strategies should be developed.

References:

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