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DISEASE NOTES

Description of *Golovinomyces orontii* as the Causal Agent of Lettuce (*Lactuca sativa*) Powdery Mildew in Brazil

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About the Cover

Gray mold on kiwifruit leaves cau

Lettuce (*Lactuca sativa* L.) is the most important leafy vegetable crop in Brazil, being affected by a number of fungal diseases. Severe powdery mildew (PM) symptoms (100% incidence) were observed in commercial lettuce cultivar 'Caipira' plantings in Formosa, Goiás State (2015) and 'Milena' in Planaltina, Federal District (2018) under hydroponic conditions in Central Brazil. Typical whitish fungal colonies were observed on both leaf surfaces. PM infection induced leaf distortion, chlorosis, necrosis, and reduced plant growth. Morphological analyses of fungal isolates revealed straight and hyaline conidiophores (100.8 to 268.9 × 10.4 to 13.6 μm) with cylindrical foot cells ranging from 56.2 to 63.3 × 7.9 to 8.6 μm. Conidia ($n = 30$) were hyaline, ellipsoid to ovate (27.7 to 35.1 × 13 to 14 μm), and produced two to six conidia in sinuous chains. Chasmothecia were not observed. Pathogenicity assays were performed under greenhouse conditions by inoculating seedlings of cultivar Caipira via leaf-


to-leaf contact with already-infected lettuce plants. Noninoculated plants served as controls. Only inoculated plants displayed conspicuous PM colonies 7 days after inoculation. The fungus from the inoculated plants was morphologically identical to that from the original isolates. The fungus was tentatively identified as *Golovinomyces orontii* (Braun and Cook 2012). To confirm this classification, the total genomic DNA of three lettuce-infecting isolates (named as Gollac1, Gollac2, and Gollac3) was extracted from conidial suspensions using a modified cetyltrimethylammonium bromide protocol (Boiteux et al. 1999). Purified DNA was used as a template in polymerase chain reaction assays with a pair of primer targeting the internal transcribed spacer (ITS) rDNA region: PM ITS1 (5'-TCGGACTGGCCYAGGGAGA-3') and PM ITS2 (5'-TCACTCGCCGTTACTGAGGT-3') (Cunnington et al. 2003). BLASTn alignments of the ITS sequences from the Brazilian lettuce isolates (KY984064 to KY984066) indicated 100% identity among themselves and also with *G. orontii* isolates reported infecting *L. sativa* and *L. scariola* in Japan (AB769447 and AB077688) and *Cirsium arvense* (L.) Scop. (Asteraceae) in Italy (KJ438822). A Bayesian inference analysis (Geneious R8) was carried out with several PM-inducing isolates from the GenBank. *Arthrocladiella mougeotii* (AF073358) was employed as outgroup. All lettuce-infecting isolates from Brazil clustered (0.98 posterior probability) with isolates of *G. orontii* 'group 3' (Takamatsu et al. 2013). *G. orontii* has been reported on a wide range of botanical families (Braun and Cook 2012). Infection of lettuce by *G. orontii* was already reported in European countries, North America, South Africa, Chile, Argentina, Australia, Israel, Japan, and Korea (Farr and Rossman 2018) and now in Brazil. Breeding for resistance is one of the few sustainable strategies for PM management in this crop.


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