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LETTUCE POWDERY MILDEW CAUSED BY *Golovinomyces orontii* IN BRAZIL. C.S. CABRAL¹; M.D.M. SANTOS¹; R.C.F. BORGES¹; M.E.N. FONSECA²; A. REIS²; L.S. BOITEUX². Universidade de Brasília¹; Embrapa Hortaliças². E-mail: clea.86@gmail.com

Lettuce (*Lactuca sativa* L.) is one of the most important leafy vegetable crops in Brazil and worldwide. In 2015, lettuce powdery mildew (LPM) was observed under greenhouse commercial crops of the cultivar 'Caipira' (100% disease incidence) in Brasília-DF, Brazil. Typical white cottony fungal growth was observed on leaves and stems. The fungal infection caused leaf distortion, localized chlorosis, and reduced growth. Morphological analyses of the isolates revealed straight and hyaline conidiophores (100.81 to 268.87 × 10.37 to 13.62 μm) with cylindrical foot cells measuring 56.17 to 63.35 × 7.9 × 8.60 μm. Conidia were also hyaline, ellipsoid to ovate (27.66 –35.14 μm × 13–14 μm) and produced 2 to 6 immature conidia in chains. No chasmothecia were observed. Pathogenicity assays were performed under greenhouse by inoculating via leaf-to-leaf contact seedlings of the lettuce cv. 'Caipira'. Four non-inoculated plants served as controls. Initial colony development was observed 4 days after inoculation. The fungus from these symptomatic plants was morphologically identical to that from diseased greenhouse plants. To confirm the fungal identification at species level, total genomic DNA of tree LPM isolates (named as 'Gollac1', 'Gollac2' and 'Gollac3') was extracted from conidial suspensions using a modified CTAB protocol. Purified DNA was used as template in PCR assays with the ITS (internal transcribed spacer) rDNA region prime pair ITS1 (5'-TCG-GAC-TGG-CCY-AGG-GAA-GA-3') and ITS2 (5'-TCA-CTC-GCC-GTT-ACT-GAG-GT-3'). BLASTn alignments of the tree lettuce isolates (KY984064 to KY984066) shared 100% similarity with the ITS sequence of *G. orontii* isolate reported on *Cirsium arvense* in Italy (KJ438822). An analysis by Bayesian inference was carried out (Geneious R8) with the sequences obtained, along several others references from GenBank (NCBI), and *Arthrocladiella mougeotii* (AF073358) as outgroup. The phylogeny revealed clustering of them with other *G. orontii* isolate (KJ438822), with 0.98 of posterior probability. On the basis of the morphological characteristics of the anamorph and the ITS sequence data, the isolates were identified as *G. orontii*. To our knowledge, this is the first report of LPM caused by *G. orontii* in Brazil.

Palavras-chave: Lettuce, Phylogenetic analysis, powdery mildew, *Golovinomyces orontii*.
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