Diseases Caused by Fungi and Fungus-Like Organisms

First Report of a Leaf Blight Caused by *Pyricularia pennisetigena* on *Cenchrus echinatus* in Paraguay

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The genus *Pyricularia* contains several fungal species known to cause diseases on plants in the Poaceae family (Klaubauf et al. 2014; Wang et al. 2019). While sampling for *P. oryzae* during March 2015 and April 2018, the common weed *Cenchrus echinatus* L. was observed with leaf lesions in and around experimental wheat fields in the departments of Canindeyú and Itapúa. *C. echinatus* samples from both locations displayed similar leaf lesions, varying from small light brown pinpoint to elliptical brown lesions with a greyish center. Symptomatic leaves were surface disinfested and cultured on potato dextrose agar (PDA) amended with 1% gentamicin at 25°C. Two monospore isolates were obtained, one from Itapúa (ITCeh117) and the other from Canindeyú (YCeh55). The isolates were subsequently grown on oatmeal agar (OA) and PDA under a 12-h photoperiod at 25°C and evaluated after 10 days for colony diameter, sporulation, and macroscopic and microscopic features. Colonies on OA reached up to 4.8 cm in diameter and were light gray, whereas colonies on PDA reached up to 5.3 cm in diameter and were brown with gray centers, with cottony mycelium and broad white rims. Mycelium consisted of smooth, hyaline, branched, septate hyphae 4 to 4.5

µm in diameter. Conidiophores were erect, straight or curved, unbranched, medium brown, and smooth. Conidia were solitary, pyriform, pale brown, smooth, granular, two-septate, 32 to 33 × 9 to 10 µm, truncated with protruding hilum, and varied in length from 1.0 to 1.5 µm and diameters from 2.0 to 2.2 µm. Both isolates were similar and identified as *Pyricularia pennisetigena*, according to morphological and morphometric characteristics (Klaubauf et al. 2014). Subsequently, genomic DNA was extracted from each isolate using the primers described in Klaubauf et al. (2014) to amplify and sequence the internal transcribed spacers (ITS), partial large subunit (LSU), partial RNA polymerase II large subunit gene (RPB1), partial actin gene (ACT), and partial calmodulin gene (CAL). Sequences from each isolate (YCeh55/ITCeh117) were deposited in GenBank with the following submission IDs: MN947521/MN947526 (ITS), MN984710/MN984715 (RPB1), MN944829/MN944834 (LSU), MN917177/MN917182 (ACT), and MN984688/MN984693 (CAL). Phylogenetic analysis was conducted using the software Beast version 1.10.4. The results obtained from the concatenated matrix of the five loci placed these isolates in the *P. pennisetigena* clade. To confirm pathogenicity, each isolate was adjusted to 5 × 10⁴ conidia/ml of sterile water, and *C. echinatus* plants were sprayed with the conidial suspension for isolate YCeh55, isolate ITCeh117, or sterile water using an oilless airbrush sprayer until runoff. The three treatments were kept in the greenhouse at 25 to 28°C and about 75% relative humidity under natural daylight. Each treatment included three to five inoculated plants, and 10 leaves were evaluated per treatment. Symptoms were observed 8 to 15 days after inoculation and were similar to those originally observed in the field for both isolates, whereas the control plants remained asymptomatic. *P. pennisetigena* was reisolated from the inoculated leaves, fulfilling Koch's postulates. To our knowledge, this is the first report of leaf blight on *C. echinatus* caused by *P. pennisetigena* in Paraguay. The occurrence of *P. pennisetigena* in the region and its ability to infect economically important crops such as wheat and barley (Klaubauf et al. 2014; Reges et al. 2016, 2018) pose a potential threat to agriculture in Paraguay.

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