## Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Lasiodiplodia brasiliensis Causing Crown Rot on Banana in Brazil

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Postharvest diseases compromise the quality of banana and cause high economic losses in Brazil. Crown rot is one such disease, and its causal agents are distinct fungal species such as Colletotrichum musae (Berk. & Curt.) von Arx, Fusarium spp., and Lasiodiplodia theobromae (Pat.) Griff. & Maubl. (Griffee and Burden 1976; Ploetz et al. 2003). Symptoms of crown rot were observed on banana fruits of cultivar Williams in a commercial area in Assu, Rio Grande do Norte, Brazil (4°54'0.06"S, 37°22'6.02"W) in 2017. The samples were collected, superficially disinfected with NaClO (2%), and incubated in a wet chamber at 25°C with a 12-h photoperiod for approximately 3 days. After the emergence of disease symptoms and pathogen structures, mycelia were transferred from the lesions to potato dextrose agar (PDA) medium to obtain pure cultures. Then, a monosporic culture was obtained (isolate BAN82). The fungus produced pycnidia with conidia on potato carrot agar culture medium containing pine needles after 4 weeks of incubation at 28°C. The conidia were hyaline when immature and brown with a central transverse septum when mature. The presence of conidiogenous cells, paraphyses, and conidiophores was also observed. The conidia were ovoid, measuring 20 to 28 × 11 to 14  $\mu$ m (n = 50). The fungal colony produced abundant aerial mycelia with mouse gray coloration, progressing to dark mouse gray (Rayner 1970), on PDA for 15 days at 28°C. The growth rate was 29.3 mm/day on PDA. The genomic DNA was extracted, amplified using PCR with the primers TEF1-688F/TEF1-1251R, ITS1/ITS4, and Bt2a/Bt2b, and sequenced in both directions. The TEF1 and TUB2 sequences showed 100% identity and the ITS sequence showed 93.06% identity with the sequences of Lasiodiplodia brasiliensis (GenBank accession nos.: ON623895, TEF1; ON623896, TUB2; and ON599012, ITS). Multiple alignments of the combined dataset of the isolate and representative sequences obtained from GenBank were submitted to phylogenetic analyses based on Bayesian inference (BI) with posterior probabilities of 10,000,000 generations. The morphological characteristics together with multigenic analysis of the three genomic regions made it possible to identify the BAN82 isolate as L. brasiliensis, showing bootstrap support with a posterior probability of 0.98 in the BI analysis. Pathogenicity was evaluated on 16 banana fruits from cultivar Prata Catarina at the point of harvest. For inoculation, the bananas were disinfected with water, soap, and NaClO (2%). Then, the fruits were wounded on both ends, followed by the deposition of 5-mm-diameter mycelial plugs from the fungal culture after 3 days of growth. After the inoculation, the fruits were placed in plastic boxes and incubated in a wet chamber at 25°C with a 12-h photoperiod for 3 days. To fulfill Koch's postulates, the isolate was inoculated again into another 16 banana fruits from cultivar Prata Catarina. The negative control fruits were not inoculated with the pathogen but only with PDA discs. The BAN82 isolate was pathogenic to the banana cultivar Prata Catarina. In northeast Brazil, in 2014, L. brasiliensis was reported to be associated with papaya stem rot. Until now, there have been no reports of L. brasiliensis as the causal agent of crown rot on bananas from Brazil (Farr and Rossman 2022; Netto et al. 2014). Thus, this work is the first to report L. brasiliensis causing crown rot on banana fruits of cultivar Prata Catarina in Brazil

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