Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Postharvest Stem End Rot of Mango Fruit (*Mangifera indica*) Caused by *Lasiodiplodia theobromae* in China

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Funding: Funding was provided by the National Key Research and Development Program of China (2019YFC1604502). Plant Dis. 105:2715, 2021; published online as <https://doi.org/10.1094/PDIS-01-21-0168-PDN>. Accepted for publication 11 April 2021.

China is the second largest producer of mango in the world, a fruit that has high nutritive value and is a rich source of fiber (Kuhn et al. 2017). In late June 2019, a postharvest stem-end rot disease was observed in different local fruit markets (39°48'42.1"N, 116°20'17.0"E) of the Fengtai district of Beijing, China. Black rot symptomatic lesions were observed on the fruit surface, which initially started from the stem end of the mango fruit. Approximately 45% of mango fruits were affected with the disease. Symptomatic portions from collected fruit samples ($n = 40$) were cut into small pieces (2 mm²), rinsed with 1% NaClO for 20 s, and then washed three times with sterilized distilled water (SDW) for surface disinfection. The disinfected pieces were then placed on sterilized filter paper for drying. Later, these pieces were placed on potato dextrose agar plates and incubated at 28°C for 7 days. The resulting fungal colonies were purified by the single-spore isolation technique. The isolated fungal colonies were initially greenish to gray in color, later turning olive-black to black. Conidia were dark brown in color, oval-shaped, two-celled, and measured 22.4 to 25.7 (24.06 ± 0.15) µm in length and 10.2 to 12.8 (11.3 ± 0.13) µm in width ($n = 36$). Based on the symptoms, culture morphology, and microscopic characters, *Lasiodiplodia theobromae* was suspected as the causal agent, and similar results were reported by Pavlic et al. (2004) and Burgess et al. (2006). For molecular identification, a multilocus sequence analysis approach was used. The internal transcribed spacer (ITS) region, elongation

factor 1 alpha (EF1-α), and β-tubulin genes were amplified and sequenced using ITS1/ITS4 (White et al. 1990), EF1-728F/EF1-986R (Carbone and Kohn 1999), and Bt2a/Bt2b (Glass and Donaldson 1995) primers, respectively. The sequences of isolate MFT9 were deposited in GenBank (MW115977 [ITS], MW118595 [EF1-α], and MW118596 [β-tubulin]). All sequences showed more than 99.5% similarity with reported sequences of *L. theobromae* isolate IBL340 with accessions numbers KT247466 (ITS), KT247472 (EF1-α), and KT247475 (β-tubulin). Phylogenetic reconstruction based on maximum likelihood, using Mega X (Kumar et al. 2018), grouped isolate MFT9 with isolates representing *L. theobromae*. Pathogenicity testing was performed on 18 fresh, healthy, medium-sized mango fruits for each treatment to fulfill Koch's postulates. The fruits were disinfested with 1% NaClO and punctured with a sterilized needle to create approximately 2-mm² wounds for inoculation. Fruits were inoculated with 15 µl of fresh inoculum (10⁷ spores/ml) from isolate MFT9. Control fruits were inoculated with 15 µl of SDW, and both the inoculated and control fruits were incubated at 28°C for 7 days postinoculation. The rot lesions appeared at the point of inoculation and gradually spread on the fruit surface. The symptoms were similar to the symptoms observed on the original fruit samples. This experiment was conducted three times under the same conditions, with control fruits remaining asymptomatic each time. The reisolated fungus was identified as *L. theobromae* based on symptoms and morpho-molecular analysis, described above. *L. theobromae* is also reported as a causal agent responsible for a postharvest stem-end rot on coconut in China (Zhang et al. 2019). To our knowledge, this is the first report of *L. theobromae* causing postharvest stem-end rot of mango fruit in China. This finding suggests that *L. theobromae* is a potential problem for mango fruit production in China.

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The author(s) declare no conflict of interest.

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Keywords: fungi, fruit, pathogen detection

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