Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Curvularia plantarum* Causing Leaf Spot on Sweet Potato (*Ipomoea batatas*) in China

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Sweet potato (*Ipomoea batatas* [L.] Lam) is an extremely versatile vegetable that possesses high nutritional values. It is also a valuable medicinal plant having anticancer, antidiabetic, and anti-inflammatory activities. In July 2020, leaf spot was observed on leaves of sweet potato in Nanchang, China (28°45'51"N, 115°50'52"E), which affected the growth and development of the crop and caused tuberous root yield losses of 25%. The disease incidence (total number of diseased plants/total number of surveyed plants × 100%) was 57% from a sampled population of 100 plants in the field. Symptomatic plants initially exhibited small, light brown, irregular-shaped spots on the leaves, subsequently coalescing to form large irregular brown lesions, and some lesions finally fell off. Fifteen small pieces (each 5 mm²) of symptomatic leaves were excised from the junction of diseased and healthy tissue, surface sterilized in 75% ethanol solution for 30 s and 0.1% mercuric chloride solution for 2 min, rinsed three times with sterile distilled water, and incubated on potato dextrose agar (PDA) plates at 28°C in darkness. A total of seven fungal isolates with similar morphological characteristics were obtained as pure cultures by single-spore isolation. After 5 days of cultivation at 28°C, dark brown or blackish green colonies were observed, which developed brown, thick-walled, simple, or branched, and septate conidiophores. Conidia were 18.28 to 24.91 × 7.46 to 11.69 μm (average 21.27 × 9.48 μm, *n* = 100) in size, straight or slightly curved, middle cell unequally enlarged, brown to dark brown, apical, and basal cells slightly paler than the middle cells, with three septa. Based on morphological characteristics, the fungal isolates were suspected to be *Curvularia plantarum* (Raza et al. 2019). To further confirm the identification, three isolates (LGZ1, LGZ4, and LGZ5) were selected

for molecular identification. The internal transcribed spacer region (ITS), glyceraldehyde-3-phosphate-dehydrogenase (GAPDH), and translation elongation factor 1-α (EF1-α) genes were amplified and sequenced using primers ITS1/ITS4 (Peever et al. 2004), gpd1/gpd2 (Berbee et al. 1999), and EF-983F/EF-2218R (Rehner and Buckley 2005), respectively. The sequences of the ITS region of the three isolates (accession nos. MW581905, MZ209268, and MZ227555) shared 100% identity with those of *C. plantarum* (accession nos. MT410571 to 72, MN044754 to 55). Their GAPDH gene sequences were identical (accession nos. MZ224017 to 19) and shared 100% identity with *C. plantarum* (accession nos. MN264120, MT432926, and MN053037 to 38). Similarly, EF1-α gene sequences were identical (accession nos. MZ224020 to 22) and had 100% identity with *C. plantarum* (accession nos. MT628901, MN263982 to 83). A maximum likelihood phylogenetic tree was built based on concatenated data from the sequences of ITS, GAPDH, and EF1-α by using MEGA 5. The three isolates LGZ1, LGZ4, and LGZ5 clustered with *C. plantarum*. The fungus was identified as *C. plantarum* by combining morphological and molecular characteristics. Pathogenicity tests were conducted by inoculating a conidial suspension (10⁶ conidia/ml) on three healthy potted *I. batatas* plants (five leaves wounded with a sterile needle of each potted plant were inoculated). In addition, 15 wounded leaves of three potted plants were sprayed with sterile distilled water as a control. All plants were maintained in a climate box (12 h light/dark) at 25°C with 80% relative humidity. All the inoculated leaves started showing light brown flecks after 7 days, whereas the control leaves showed no symptoms. The pathogenicity test was conducted three times. The fungus was reisolated from all infected leaves of potted plants and confirmed as *C. plantarum* by morphological and molecular identification, fulfilling Koch's postulates. To our knowledge, this is the first report of *C. plantarum* causing leaf spot on sweet potato in China. The discovery of this new disease and the identification of the pathogen will contribute to the disease management, provide useful information for reducing economic losses caused by *C. plantarum*, and lay a foundation for the further research of resistance breeding.

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