Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Leaf Spot Caused by *Alternaria alternata* on *Yucca gloriosa* in China

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Yucca gloriosa L. was introduced to China as a garden plant because of its attractive tubular flowers (Ding et al. 2020). In 2020 and 2021, a foliar disease occurred on approximately 10% of the *Y. gloriosa* plants in the campus of Henan Institute of Science and Technology, Xinxiang (35°18'N, 113°54'E), Henan Province, China. At the early stages, symptoms appeared as small brown spots on the tips of the leaves. As the disease developed, the spots gradually expanded and turned into necrotic tissue with a clear brown border. The length of lesions ranged from 1 to 3 cm. Infected tissue samples were cut into small pieces, surface sterilized with 75% ethanol for 30 s followed by 0.5% NaClO for 2 min, rinsed three times with sterile water and plated on potato dextrose agar (PDA). After incubation at 25°C for 3 days, five fungal isolates were collected and purified using the single-spore isolation method. Morphological observations were made on the 7-day-old cultures. Colonies on PDA were white at first and then turned to dark olive or black along with profuse sporulation. Conidia were borne on branched conidiophores, light brown to dark brown, ellipsoidal to obpyriform, and 20.5 to 43.6 × 7.5 to 15.4 μm in size, with 2 to 6 transverse septa and 0 to 3 longitudinal septa ($n = 50$). The morphological characteristics of the five isolates were consistent with the description for *Alternaria alternata* (Simmons 2007). One representative isolate (ZQ20) was selected for molecular identification.

The internal transcribed spacers (ITS)-rDNA, translation elongation factor-1 alpha (TEF-1α), *Alternaria* major allergen (Alt a1), and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene regions were amplified with primer pairs ITS1/ITS4 (White et al. 1990), EFL-728F/EFL-986R (Carbone and Kohn 1999), Alt-for/Alt-rev (Hong et al. 2005), and gpd1/gpd2 (Berbee et al. 1999), respectively. Their sequences were submitted to GenBank (ITS, MW832377; TEF-1α, MW848791; Alt a1, MW848792; GAPDH, MW848793). BLAST searches showed ≥99% nucleotide identity to the sequences of *A. alternata* (ITS, 100% to KF465761; TEF-1α, 100% to MT133312; Alt a1, 100% to KY923227; GAPDH, 99% to MK683863). Thus, the fungus was identified as *A. alternata* based on its morphological and molecular characteristics. To confirm its pathogenicity, 25 healthy leaves of five 2-year-old *Y. gloriosa* plants were used. Leaves were wounded with one sterile needle and inoculated with 5-mm-diameter fungal agar disks obtained from 5-day-old cultures. Sterile PDA disks of the same size were used as the controls. Treated plants were covered with a plastic bag at 12 to 25°C for 48 h to ensure a high level of moisture. After 15 days, the inoculated plants developed symptoms similar to those observed in naturally infected plants, whereas the control plants were symptomless. The fungus was reisolated from the symptomatic leaves with the same morphological and molecular characteristics as the original isolates, fulfilling Koch's postulates. Leaf spot caused by *A. alternata* in *Yucca* plants has been reported in India (Pandey 2019). To our knowledge, this is the first report of *A. alternata* causing leaf spot on *Y. gloriosa* in China. Identification of the cause of the disease is important to developing effective disease management strategies.

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