Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Southern Blight on *Aloe vera* Caused by *Athelia rolfsii* in China

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Aloe vera (L.) Burm f., which belongs to the family Aloaceae, is a perennial succulent plant cultivated for its medicinal, cosmetic, vegetable, and ornamental uses. In the summer of 2021, about 15% (60 of 400 surveyed plants) of *A. vera* (= *A. barbadensis*) plants in two gardens in Lishui, Zhejiang Province, China, showed symptoms of southern blight disease. Symptomatic plants primarily exhibited slightly sunken, water-soaked, dark brown lesions on the taproot and basal part of the stems. As the disease progressed, leaves in the basal part of stems and subsequently the whole plant rotted and withered, with white mycelial mats occurring on infected stems and leaves. Numerous brown, spherical sclerotia were observed on the colonized tissues and soil surfaces around the infected plants. Mycelial fragments and sclerotia from symptomatic leaves were plated directly to potato dextrose agar (PDA) amended with 100 µg/ml of streptomycin and incubated at 26°C in the dark. Using the hyphal-tip method, five pure isolates were obtained from five diseased leaf samples. When cultured on PDA at 26°C for 3 days, colonies showed thick, white aerial mycelium, with a radial growth rate of 23.7 mm/day. Typical clamp connection structures were observed microscopically after 3 days and numerous globoid,

rapeseed-shaped sclerotia, measuring 1 to 2 mm in diameter ($n = 50$), formed after 6 days. These sclerotia were initially white and gradually turned dark brown with age. On the basis of morphological characteristics, the fungal isolates were identified as *Athelia rolfsii* (Curzi) C.C. Tu & Kimbr (anamorph *Sclerotium rolfsii* Sacc) (Mordue 1974). The internal transcribed spacer (ITS) and translation elongation factor 1- α gene (TEF1) regions of a representative isolate LHB2-4 were amplified and sequenced using the primers ITS4/ITS5 (White et al. 1990) and EF1/EF2, respectively (accession nos. MZ956758 and OL365370). A BLASTn search showed that the amplified ITS and TEF1 sequences had 99.71% (680/682 bp) and 99.80% (498/499 bp) identity with the *A. rolfsii* isolates CBS 115.22 (MH854711.1) and Sr_286 (JF267815), respectively. A neighbor-joining phylogenetic tree based on the ITS sequences revealed that LHB2-4 clustered with *A. rolfsii* isolates. For a pathogenicity test, three potted *A. vera* plants (~30 cm tall) were inoculated by placing a 0.5-cm mycelial plug of isolate LHB2-4 (3 days old) at the base of each plant. Three *A. vera* plants inoculated with sterile PDA plugs served as controls. All the inoculated plants were placed in a growth chamber at 27°C under a 12/12 h light/dark cycle. The inoculation assays were carried out twice. After 5 to 7 days, stem bases of the inoculated plants showed brown lesions that were similar to those observed in the field. However, control plants remained symptomless. *A. rolfsii* was reisolated from all the inoculated plants and identified using morphological and molecular method described above, thus confirming Koch's postulates. Although *A. rolfsii* has been reported to cause disease on *A. vera* in India (Dubey and Pandey 2009), to the best of our knowledge, this is the first report of *A. rolfsii* causing southern blight on *A. vera* in China. Because *A. rolfsii* has a wide host range and is difficult to control (Punja 1985), occurrence of southern blight in China might be a serious threat for *A. vera* production and appropriate management strategies should be developed to control this disease.

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