Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium xylarioides* Causing Root and Stem Rot on *Aloe vera* in China

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Aloe vera (L.) Burm.f. is a perennial herb belonging to the family Liliaceae. It is widely grown for medicinal, cosmetic, and vegetable use. In 2018 and 2019, a root rot disease occurred on potted *A. vera* plants in a nursery in the Hunan Province of China. Symptoms of the disease included water-soaked lesions and brown spots on the taproot or basal part of the stem. The plants were easy to pull out when the taproot was rotten or necrotic. As the disease progressed upward, leaves in the basal part of stems became red-brown and gradually fell off. In severe cases, the whole plant became rotten and wilted. For isolation purposes, diseased tissues were excised from the lesion margins, surface disinfested with 70% ethanol for 10 s followed by 0.1% HgCl₂ for 2 min, rinsed with sterile water thrice, and then placed on potato dextrose agar (PDA) and incubated at 26°C for 3 days in the dark. When cultured on PDA, fungal strains with similar morphology were consistently isolated and purified by single-spore isolation. Colonies showed thick, pink aerial mycelium with a growth rate of 1.3 cm/day. The pigmentation was more intense in the colony center and became pale orange and white at the edge of colony. When cultured on Spezieller Nährstoffarmer agar, the fungus showed less pigmentation and thinner hyphae. Microconidia were abundantly produced, clavate, oval to kidney shaped, and 7.1 to 15.2 × 2.5 to 5.1 μm, with zero to one transverse septa. Macroconidia were sickle shaped, slender, slightly incurved in apical cell and foot-shaped in the basal cell, measured 27.9 to 53.2 × 2.5 to 3.5 μm, with three to five septa. These morphological characteristics were similar with those of *Fusarium* spp. (Booth 1971). For molecular identification, genomic DNA of the fungus was extracted by the cetyl trimethyl ammonium bromide

method. A portion of translation elongation factor 1-α (EF-1α) and the largest subunit of RNA polymerase (RPB1) genes were amplified and directly sequenced using the EF-1/EF-2 and Fa/G2R primers (O'Donnell et al. 2010). The EF-1α and RPB1 were deposited in GenBank (MT755386 and MT755387). The EF-1α and RPB1 had 97.14% (ID FD_01334) and 99.62% identity (FD_03853), respectively, to *Fusarium xylarioides* strains in the *Fusarium*-ID database (Geiser et al. 2004). In addition, the EF-1α showed 96.825% identity to *F. lateritium* CBS 119871(AM295281) (a synonym of *F. xylarioides*), and the RPB1 showed 99.623% identity to the *F. xylarioides* NRRL 25486 (JX171517.1). Accordingly, the fungus was putatively identified to be *F. xylarioides*. For the pathogenicity assay, *A. vera* seedlings were pot planted using sterilized nursery soil and inoculated with conidia suspension (1 × 10⁵ conidia/ml), which was eluted from 7-day-old PDA cultures with sterilized water, according to the method described previously (Vakalounakis et al. 2015). The collar of each potted plant received 20 ml of conidia suspension poured over it. Plants mock inoculated with sterile water were used as a control. All the inoculated plants were placed in a growth chamber at 25°C under a 12-h/12-h light/dark cycle. The inoculation assays were carried out twice, and each one had three replicated plants. After 30 days, rot symptoms seen from the roots and basal part of stems were observed on the inoculated plants, but no visible symptoms were observed on control plants. The fungus was reisolated from the inoculated plants and identified to be *F. xylarioides* by morphological and molecular characteristics, thus confirming Koch's postulates. As we know, many *Fusarium* species have been reported to cause root and stem rot disease in *A. vera*, such as *F. oxysporum* (Ji et al. 2007) and *F. solani* (Vakalounakis et al. 2015). However, to the best of our knowledge, this is the first report of *F. xylarioides* causing root and stem rot disease of *A. vera* in China. The identification of the pathogen fungus might provide a foundation for taking appropriate control strategies for this disease.

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