Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Root Rot on Kiwifruits Caused by *Athelia rolfsii* in Hefei, China

Qianwen Liu,¹ Hanyang Wang,¹ Wenpeng Song,¹ Jiuming Yu,¹ Lu Huang,¹ Hao Cheng,² Jianbing Lan,³ Lixin Zhang,⁴ Yongsheng Liu,^{1,2,†} and Wei Tang^{1,†}

¹ School of Horticulture and State Key Laboratory of Tea Plant Biology and Utilization, Anhui Agricultural University, Hefei 230036, China

² Ministry of Education Key Laboratory for Bio-resource and Eco-environment, College of Life Science, State Key Laboratory of Hydraulics and Mountain River Engineering, Sichuan University, Chengdu 610064, China

³ College of Landscape Architecture and Life Science, Chongqing University of Arts and Sciences, Yongchuan 402160, China

⁴ School of Plant Protection, Anhui Agricultural University, Hefei 230036, China

Q. W. Liu and H. Y. Wang contributed equally.

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Kiwifruits (*Actinidia* spp.), known as the “king of vitamin C”, have been widely cultivated. In August 2020, about 15% of *Actinidia deliciosa* (cv. Xuxiang) and *A. macrosperma* (rootstock) plants displayed symptoms typical of root rot at a farm in Hefei (117.25°E, 31.86°N), Anhui Province of China. Symptoms first appeared at the root and stem junction, which was covered by cottony white mycelium during the warm and humid summer. Then, the infected tissues became rotted, and subsequently the whole plant withered. Tan to brown sclerotia were observed on the basal stem epidermis and soil surface surrounding the stem. Infected plant tissues and sclerotia were collected for isolating the fungal pathogen. The samples were surface sterilized in 70% alcohol for 30 s, followed by 2% sodium hypochlorite for 3 min, washed five times with sterile double-distilled water (ddH₂O), dried, placed on potato dextrose agar, and incubated at 25°C in the dark. In total, 12 fungal isolates were obtained. The mycelia of all the isolates were white with a fluffy appearance. Sclerotia that formed after 7 days were initially white and gradually turned to dark brown, measuring 0.67 to 2.03 mm in diameter (mean = 1.367 ± 0.16 mm; *n* = 30). Hyphae were hyaline, septate. Some cells

possessed multiple nuclei and clamp connections. No spores were observed. For species-level identification, ITS1/ITS4 and EF1-983F/EF1-2218R primers were used to amplify the internal transcribed spacer regions (ITS) and translation elongation factor-1 alpha regions (TEF-1α), respectively (Rehner and Buckley 2005; White et al. 1990). Based on ITS and TEF-1α sequence analyses, all 12 isolates were categorized into two groups, group 1 including isolates NC-1 and NC-6 to 10, and group 2 containing NC-2 to 5 and NC-11 to 12. The length of the ITS sequence for NC-1 (MW311079) was 684 bp, and it was 99 to 100% similar to *Athelia rolfsii* (MN610007.1, MN258360.1). Similarly, the ITS sequence for NC-2 (MW311080) was 99 to 100% similar to *A. rolfsii* (MH858139.1, MN872304.1). Also, TEF-1α sequences of NC-1 (MW322687) and NC-2 (MW322688) were 96 to 99% similar to sequences of *A. rolfsii* (MN702794.1, GU187681.1, MN702789.1). Based on morphology and phylogenetic analyses, the isolates NC-1 and NC-2 were identified as *A. rolfsii* (anamorph *Sclerotium rolfsii*) (Mordue 1974; Punja 1985). To fulfill Koch's postulates, 10 sclerotia of NC-1 were incorporated into the soil near stems of healthy Xuxiang plants. Similar treatments were also used for plants of *A. macrosperma* or *A. arguta*. Each control group had the same number of plants (*n* = 3) for inoculating with ddH₂O. The plants were kept in an incubator with a relative humidity of 80% and temperature of 28°C with a 16-h/8-h light/dark photoperiod. After 20 days, the pathogen-inoculated plants developed similar symptoms of root rot as were observed in the field. Similarly, 4 days after inoculation with sclerotia, leaves developed water-soaked lesions. No significant difference in pathogenicity was observed between NC-1 and NC-2. Noninoculated control plants remained disease-free. The pathogenicity experiments were repeated three times. The pathogen was reisolated from infected tissues and sclerotia, and isolates were confirmed as *A. rolfsii* by the ITS sequences. *A. rolfsii* has been reported to cause root rot in kiwifruit in the United States (Raabe 1988). To our knowledge, this is the first report of *A. rolfsii* causing root rot on kiwifruits in China.

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[†]Indicates the corresponding authors.
Y. S. Liu; liuyongsheng1122@ahau.edu.cn, and
W. Tang; tangweitw@aliyun.com