Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Postharvest Fruit Rot Disease of Hardy Kiwifruit Caused by *Diaporthe eres* in China

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Hardy kiwifruit (*Actinidia arguta*), an economically important fruit crop growing in Northeast China with thin, hairless, smooth skin, is susceptible to postharvest decay. In September 2018, infected cultivar Kwiwlv fruits were obtained from a commercial farm in Liaoning Province, northeastern China. The incidence of the rot disease varied from 20 to 90% according to the number of fruit in each box during a 7-day-long storage at room temperature, and the initial symptom included a small, soft, chlorosis to light brown lesion followed by watery brown lesions. Pure cultures of the same characteristics were obtained from the isolated strains in four rotten fruits on potato dextrose agar (PDA) medium. The isolates grew into transparent radial mycelium on PDA in the first 2 days followed by abundant white, fluffy aerial mycelium. After 14 days, colonies formed white to light brown aerial mycelial mats with gray concentric rings, and they produced gray and embedded pycnidia. Alpha conidia of 4.4 to 8.8 $\mu\text{m} \times 1.4$ to 3.3 μm ($n = 50$) were abundant in culture, hyaline, aseptate, ellipsoidal to fusiform, while beta conidia at 20.5 to 28.6 $\mu\text{m} \times 1.0$ to 1.4 μm ($n = 50$) were hyaline, long, slender, curved to hamate. These morphological characteristics were similar to *Diaporthe* spp. (anamorph: *Phomopsis* spp.) (Udayanga et al. 2014a). For identification, DNA was extracted from three single isolates respectively, and the internal transcribed spacer (ITS) region, β -tubulin (BT), and histone (HIS) H3 gene were amplified using primers ITS1/ITS4 (White et al. 1990), T1/T22 (O'Donnell et al. 1997), and HIS1F/HISR (Gao et al. 2017), respectively. The three isolates produced identical sequences across all three gene regions, which

were submitted to NCBI (GenBank accession numbers MT561361, MT561360, and MT855966). Nucleotide BLAST analysis revealed that the ITS sequence shared 99% homology with those of ex-type *Diaporthe eres* in GenBank (MG281047.1 and KJ210529.1), the BT sequence had 98% identity to *D. eres* (MG281256.1 and KJ420799.1), and the HIS had 99% identity to *D. eres* (MG28431.1 and MG281395.1) (Hosseini et al. 2020; Udayanga et al. 2014b). Pathogenicity was tested by wound inoculation on the cv. Kwiwlv fruits. Five mature and healthy fruits were surface-sterilized with 1% NaClO solution, rinsed in sterile distilled water, and dried. Every fruit was wounded by penetrating the peel 1 to 2 mm with a sterile needle and inoculated with mycelial plugs (5 mm in diameter) of the isolate on PDA, with five inoculated with sterile PDA plugs as controls. Treated fruits were kept in sterilized transparent plastic cans separately under high humidity (RH 90 to 100%) at 28°C. After 5 days, the same rot symptoms were observed on all fruits inoculated with mycelium while the control remained symptomless. The fungi was reisolated from the lesions of inoculated fruits and identified as *D. eres* by sequencing, thus fulfilling Koch's postulates. The pathogenicity experiment was reperformed using *D. eres* conidial suspension (10^7 conidia/ml) in sterile distilled water in October 2019 and the same results were obtained. *D. eres* was recently reported to cause European pear rot in Italy (Bertetti et al. 2018). To our knowledge, this is the first report of *D. eres* causing a postharvest rot in hardy kiwifruit in China, leading to severe disease and thus huge economic losses in Northeast China. Accordingly, effective measures should be taken to prevent its spreading to other production regions in China.

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