Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Flower Rot Caused by *Fusarium luffae* and *F. asiaticum* on White Kiwifruit in China

Jiuming Yu,¹ Zixian Zhao,¹ Jing Sheng,¹ Wenpeng Song,¹
Lu Huang,¹ Qianwen Liu,¹ 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, Sichuan University, Chengdu 610064, China

J. Yu and Z. Zhao contributed equally to this work.

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As an important cultivated germplasm, kiwifruit cultivar ‘White’ (*Actinidia chinensis*) is appreciated for its long shelf life, richness in ascorbic acid and peelable skin. In May 2020, blighted flowers were observed on 1 to 3% of cultivated ‘White’ plants at farms in Hefei (117°25'E, 31°46'N) and Lujiang (117°27'E, 31°48'N), in Anhui Province of China. The infected flowers were yellowish at first; gradually turned brown, withered, and shrunk; and died without blossoming. Infected flowers were surface sterilized in 70% alcohol for 30 s and 1% NaOCl for 3 min, then washed five times with double distilled water (ddH₂O), and incubated on potato dextrose agar (PDA) at 25 ± 2°C in the dark. Twenty fungal isolates were obtained. Colonies from Hefei (HF1 to HF9) were pale yellow, and those from Lujiang (LJ to LJ11) were purplish-red on PDA. Both types of colonies were flat with little aerial hyphae on oatmeal agar. On carnation leaf agar (CLA), the HF1 isolates produced slightly curved macroconidia with three to six septa that measured 4.3 to 5.5 × 20.7 to 42.5 μm (*n* = 100). Microconidia and chlamydospores were not observed. Macroconidia derived from the LJ1 isolate were straight to slightly curved with three to five septa, measuring 4.0 to 6.5 × 21.7 to 71.0 μm (*n* = 100). It produced chlamydospores that were globose to subglobose (5.0 to 9.5 μm) on CLA. Pathogenicity

tests were performed on ‘White’ flowers. Thirty microliters of a conidia suspension (10⁵ spores/ml) from isolate HF1 or LJ1 was separately applied to each flower (*n* = 100). Control flowers were treated with ddH₂O. Two weeks postinoculation, all flowers inoculated with HF1 and LJ1 isolates turned brown and withered, but no symptoms were observed on the control. This experiment was repeated three times. All isolated and reisolated pathogens from diseased flowers were molecularly identified using the nuclear ribosomal internal transcribed spacer region (*ITS*), translation elongation factor (*TEF-1α*), calmodulin (*CaM*), RNA polymerase II subunit 1 (*RPB1*) gene, and RNA polymerase II largest subunit (*RPB2*) gene (O'Donnell et al. 1998, 2012; White et al. 1990). Based on sequence analysis, the reisolated strains were identical to those inoculated. Sequences of HF1, HF2, LJ1, and LJ2 were deposited in GenBank under accession numbers OK310710 to OK310713 (*ITS*), OK334291 to OK334294 (*TEF-1α*), OK412973 to OK412976 (*CaM*), OK412977 to OK412980 (*RPB1*), and OK484317 to OK484320 (*RPB2*). BLAST searches of sequences from HF1 and HF2 showed 99 to 100% identity with *ITS* (NR_164594), *TEF-1α* (MK289601), *CaM* (MK289698), *RPB1* (HM347158), and *RPB2* (MK289754) of *Fusarium luffae*. The LJ1 and LJ2 sequences also revealed 99 to 100% identity with *ITS* (NR_121320), *TEF-1α* (AF212452), *RPB1* (JX171459), and *RPB2* (MW233412) of *F. asiaticum*. *Fusarium asiaticum* species-specific primers were used to detect LJ isolates (Yin et al. 2009), and the correct fragments were amplified. Phylogenetic trees were inferred from the nucleotide sequences. Both morphological and molecular criteria supported identification of HF as *F. luffae* and LJ as *F. asiaticum*. *Fusarium* spp. cause flower rot on many hosts (Elmer et al. 2019; Liu et al. 2021), but this is the first report of *F. luffae* and *F. asiaticum* on ‘White’ kiwifruit in China.

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[†]Indicates the corresponding author.
W. Tang; tangweitw@aliyun.com