Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Geotrichum candidum* Causing Postharvest Sour Rot on Kiwifruits in China

Hao Cheng,¹ Wei Tang,^{2,†} Hanyang Wang,² Qianwen Liu,² Huanhuan Li,³ and Yongsheng Liu^{1,2,†}

¹Ministry 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

²School of Horticulture and State Key Laboratory of Tea Plant Biology and Utilization, Anhui Agricultural University, Hefei 230036, China

³North Minzu University, Yinchuan 750021, China

H. Cheng and W. Tang contributed equally.

Funding: This work was supported by grants from the National Natural Science Foundation of China (31972474 and 31700266), Leading Talent Group Funding of Anhui Province (WRMR-2020-75), key project from the Government of Anhui Province (1808085MC57), and key project from the Government of Sichuan Province (2019YFSY0037). Plant Dis. 105:1566, 2021; published online as <https://doi.org/10.1094/PDIS-09-20-1923-PDN>. Accepted for publication 24 December 2020.

Kiwifruit (*Actinidia* spp.) has been extensively cultivated (about 165,728 hm² recorded in 2017), and postharvest rot diseases have caused severe damage in China. In October 2019, fruits ($n = 60$) of cultivar Xuxiang (*Actinidia deliciosa*) were obtained from a farm (120.62°E, 28.92°N) in Pan'an county (a hot and humid area during the growth season), Zhejiang province, China. After the fruits were stored at 24°C and 70% relative humidity (RH) for 10 days, soft lesions (20 to 45 mm in diameter) with a sour odor and white mold were observed on ~20% of fruits. The lesions of infected flesh were off-white to pale yellow and irregular. Small pieces (4 × 4 mm) of lesion margins were excised, surface disinfested in 70% ethanol for 1 min and 10% NaOCl for 5 min, washed, dried, plated on potato dextrose agar, and incubated at 25°C for 7 days. In total, seven isolates were obtained, including two previously reported *Nigrospora sphaerica* strains (Li et al. 2018) and five unknown isolates. The five isolates appeared thin, flat, white to cream, and feathery. Hyphae were hyaline, septate, dichotomously branched, and broken into chains of subglobose to cylindrical arthrospores. The dimension of arthrospores varies from 4.11 to 12.55 × 2.54 to 5.84 μm ($n = 100$). To identify these isolates to species, the internal transcribed spacer (ITS), 26S rDNA, and translation elongation factor-1 alpha regions (TEF-1α) were amplified and sequenced (Ma et al. 2018). Sequence analysis showed no difference in

26S rDNA and TEF-1α, except ITS placed the isolates into two groups. Isolates gx2-2 and gx3-1 representing group one (gx2-1, gx2-2, and gx5-1) and group two (gx3-1 and gx4-1), respectively, were employed for further studies. Based on BLASTn analysis, ITS sequences for gx2-2 (MT946912) and gx3-1 (MT946913) isolates had 100 and 98.40% identity, respectively, with *Geotrichum candidum* accessions KY103452 and KY103455. Nevertheless, 26S rDNA sequences (MT981194; MT981195) showed 99.82% identity with *G. candidum* accessions JN974268 and KF112070. Consistently, their TEF-1α (MT981184; MT981185) had 100% identity with *G. candidum* accession MT346370. Phylogenetic trees were constructed using the neighbor-joining method with a dataset of ITS and 26S rDNA sequences, respectively. Based on morphology and phylogenetic analysis, the pathogens gx2-2 and gx3-1 were identified as *G. candidum* (De Hoog et al. 1986). To test pathogenicity, healthy and mature cultivar Xuxiang were surface sterilized. Wounded and unwounded fruits were inoculated with each conidial suspension derived from the two isolates (10⁷ conidia/ml, 30 μl for each fruit) and stored at 24°C under 90% RH. Control fruits were treated with sterile distilled water. Each treatment consisting of 20 fruits was evaluated daily for 10 days and repeated once. The symptom resembled the naturally infected fruits. The pathogen could develop into the inner pericarp after 7 days while cultivar Jinyan (*A. chinensis*) was used as a host. However, the control group remained disease-free. The fungus could penetrate into fruit peel and produce spores that were visualized by scanning electron microscope. For both isolates, the incidence rates for wounded fruit were 100% but for unwounded fruit were about 80%. The fungi were reisolated from diseased tissues and identified as *G. candidum* based on morphology and sequence analyses. *G. candidum*-caused sour rot on many hosts with similar symptom have been previously reported (Bourret et al. 2013; Halfeld-Vieira et al. 2020; Horita et al. 2016; Khan et al. 2019; Ma et al. 2018; Pennycook et al. 1989; Zhang et al. 2018), but this is the first report of *G. candidum* on kiwifruit in China.

References:

- Bourret, T. B., et al. 2013. N. Am. Fungi 8:1.
- De Hoog, G. S., et al. 1986. Stud. Mycol. 29:1.
- Halfeld-Vieira, B. A., et al. 2020. Plant Dis. 104:1537.
- Horita, H., et al. 2016. J. Gen. Plant Pathol. 82:65.
- Khan, M. F. R., et al. 2019. Plant Dis. 103:3278.
- Li, L., et al. 2018. Plant Dis. 102:1666.
- Ma, W., et al. 2018. Plant Prot. Sci. 54:92.
- Pennycook, S. R., et al. 1989. Plant Diseases Recorded in New Zealand. Plant Diseases Division, DSIR, Auckland, New Zealand.
- Zhang, L., et al. 2018. Plant Dis. 102:2640.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: kiwifruit, fungi, disease management, *Geotrichum candidum*

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