Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Fruit Canker Caused by *Nothophoma quercina* on Chinese Quince in South Korea

Elham A. Kazerooni,¹ Sajeewa S. N. Maharachchikumbura,^{2,†} Sang-Mo Kang,¹ and In-Jung Lee^{1,†}

¹School of Applied Biosciences, Kyungpook National University, Daegu 41566, Republic of Korea

²School of Life Science and Technology, University of Electronic Science and Technology of China, Chengdu 15 611731, People's Republic of China

Funding: This research was supported by Basic Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2017R1D1A1B04035601). Plant Dis. 105:3760, 2021; published online as <https://doi.org/10.1094/PDIS-12-20-2583-PDN>. Accepted for publication 2 April 2021.

The Chinese quince (*Pseudocdonia sinensis* [Thouin] CK Schneid.) is a tree that is commonly distributed in all regions of South Korea and other Asian countries. The ripened yellow fruit contains medically active compounds (Hamauzu et al. 2005). It has been consumed as tea and candies and used in traditional medicine for treating asthma, cough, influenza, harsh throat, and tuberculosis and for liver protection (Chun et al. 2012). In the Kyungpook National University campus (Daegu, South Korea), fruit canker on Chinese quince was ubiquitously observed during May to August 2020. The average disease incidence was around 30 to 40%, which caused significant yield loss. Initially, minute, brown-to-rust-colored, unbroken, circular, necrotic areas appear, and in the advanced stage of infection, the epidermis tears open and tube- or aecia-like white structures are formed. Successively, the affected areas become necrotic and gradually enlarge to reach 3 to 5 cm in diameter. To isolate the causative pathogen, symptomatic tissues obtained from diseased fruits were surface sterilized for 1 min with 70% ethanol, rinsed in sterile distilled water, and plated onto potato dextrose agar (PDA). The inoculated plates were incubated for 7 days at 25°C. Successively, pure cultures were obtained by transferring hyphal tips to new PDA plates. A total of 15 isolates were obtained across 20 fruit trees investigated. The colonies on the PDA plates reached a diameter of 60 to 70 mm after 7 days at 25°C, spreading with a regular margin, aerial mycelium covering the entire colony, compact, white to pale gray in color, and solitary and globose pycnidia were produced after 10 days. Conidiogenous cells were phialidic, hyaline, simple, smooth, doliform to ampulliform, and 3 to 5 × 3 to 4 µm; conidia were subglobose to oval or obtuse, thin-walled, smooth, aseptate, minute guttules, brown, and 5.5 to 8 × 4 to 7 µm. These morphologies corresponded to those

of *Phoma*-like species. Sequence data for the 28S nrDNA, the internal transcribed spacer, β-tubulin, and RNA polymerase II subunit (Aveskamp et al. 2009; Liu et al. 1999; White et al. 1990) were obtained randomly for one of the pure isolates (EAH 2), which resulted in the GenBank accession numbers MW325675, MW325676, MW330391, and MW330390, respectively. RAxML analysis (Stamatakis 2014) was run on the CIPRES Science Gateway portal of the combined sequence data of the isolate EAH 2 and the reference sequences obtained from GenBank. Analyses for the combined datasets were conducted with RAxML-HPC2 on XSEDE version 8.2.10 using a GTR+GAMMA substitution model with 1,000 bootstrap iterations. Results demonstrated that the isolate EAH 2 formed a strongly supported clade with the type isolates of *Nothophoma quercina* (Syd.) Q. Chen & L. Cai (basionym: *Ampelomyces quercinus*), which has been found on *Quercus* sp. in Ukraine (Chen et al. 2015). The procedure for Koch's postulates was followed to confirm fungal pathogenicity using 3-day-old mycelial disks. A total of 15 same-aged healthy fruits were divided into three groups, and each group received a different treatment. Artificial wounds were created on one group of fruits using a sterile pin, and a 5-mm mycelial plug of the fungus was placed on the injured tissues. Mycelial plugs were also placed on the surfaces of the sets of unwounded fruits. The remaining fruits were maintained as a control and inoculated with sterile PDA plugs. The test was repeated three times. The wounded fruits exhibited symptoms after 8 to 10 days identical to those observed in the field. The control group remained asymptomatic, and the morphology of the fungus reisolated from the inoculated fruits was similar to that of *N. quercina*. The phylogeny, together with morphological identification and inoculation results, confirmed the identity of the fungus as *N. quercina* (Chen et al. 2015). A previous study had also reported shoot canker caused by *N. quercina* in Chinese quince (Yun and Oh 2016). However, to our knowledge, this is the first report of fruit canker caused by *N. quercina* in Chinese quince.

References

- Aveskamp, M. M., et al. 2009. Mycologia 101:363.
- Chen, Q., et al. 2015. Stud. Mycol. 82:137.
- Chun, J. M., et al. 2012. Appl. Biol. Chem. 55:335.
- Hamauzu, Y., et al. 2005. J. Agric. Food Chem. 53:928.
- Liu, Y. J., et al. 1999. Mol. Biol. Evol. 16:1799.
- Stamatakis, A. 2014. Bioinformatics 30:1312.
- White, T. J., et al. 1990. Page 315 in: PCR Protocols: A Guide to Methods and Applications. Academic Press, San Diego, CA.
- Yun, Y. H., and Oh, M. H. 2016. Plant Dis. 100:2533.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: Didymellaceae, fungal disease, molecular identification, *Nothophoma quercina*

[†]Indicates the corresponding authors.

S.S.N. Maharachchikumbura; sajeewa83@yahoo.com, and I.-J. Lee; ijlee@knu.ac.kr