Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Didymosphaeria rubi-ulmifolii* Brown Spot Infection of Chinese Quince Fruit in South Korea

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Chinese quince (*Pseudocarya sinensis* [Thouin] C.K. Schneid.), a deciduous tree in the family Rosaceae, is native to China, Japan, and South Korea; the fruit is known as mogwa in South Korea. The ripened yellow fruit has been used as a traditional therapeutic for respiratory ailments and as an additive in health products such as syrups, tea, and candies (Sawai et al. 2008). From May to August 2020, Chinese quince trees showing symptoms of brown spots were observed on the Kyungpook National University premises, Daegu, South Korea, with an incidence of 30 to 40%. The disease first appeared as small, round, yellow specks on the fruits, which necrotized over time and gradually enlarged to 0.7 to 2.7 cm in diameter. To isolate the 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 at 25°C for 7 days. Successively, pure cultures were obtained by transferring hyphal tips to new PDA plates. Twenty isolates were obtained from 25 fruits. Colonies on PDA reached a diameter of 30 to 40 mm. After incubation for 7 days at 25°C, spreading with an even, colorless-to-buff glabrous margin, a submarginal ring of conidiomata developed from day 5 to 12 and was visible as scattered dots on either side of the plate. Conidiogenous cells were discrete (3.5 to 6 × 3.5

to 5 µm); conidia were ellipsoid to short-cylindrical (3 to 5 × 2.1 to 3.5 µm [$n = 60$]) and olivaceous in color. These conidial dimensions corresponded to those of *Didymosphaeria rubi-ulmifolii* Ariyaw., Camporesi & K.D. Hyde (basionym: *Paraconiothyrium brasiliense*), which has been found on *Rubus ulmifolius* in Italy (Ariyawansa et al. 2014). Sequence data for the rDNA internal transcribed spacer (ITS), large subunit ribosomal RNA (LSU), and partial translation elongation factor 1- α (TEF) (Rehner and Buckley 2005; White et al. 1990) were obtained for one of the pure isolates (BT1), resulting in the GenBank accession numbers MW020087, MW020060, and MW027220, respectively. The sequences of BT1 isolate using a BLASTn analysis showed 100% identity with the ex-type MFLUCC 14-0023 of *D. rubi-ulmifolii* in ITS and LSU portions (accession nos. MT310602 and MT214555, respectively) and 99% identity in TEF portion (accession no. MT394734). The procedure for Koch's postulates was followed to confirm fungal pathogenicity using 3-day-old mycelial discs. Fifteen healthy fruits were divided into three groups of five fruits each, with each group receiving a different treatment. One group of fruits was wounded by puncturing with a sterile pin and inoculated using 5-mm mycelial discs of the fungus on the wounds. Mycelial discs were also placed on the surfaces of five unwounded fruits. The remaining five fruits were maintained as a control and inoculated with sterile PDA plugs. The pathogenicity test was replicated thrice. The wounded fruits showed symptoms similar to those observed in the field. The control group remained asymptomatic, and the morphology of the fungus reisolated from the inoculated fruits was the same as that of *D. rubi-ulmifolii*. The phylogeny, together with the morphological identification and inoculation results, confirmed the identity of the fungus as *D. rubi-ulmifolii* (Ariyawansa et al. 2014). To the best of our knowledge, this is the first report of *D. rubi-ulmifolii* causing brown spot in Chinese quince.

References:

- Ariyawansa, H. A., et al. 2014. Fungal Divers. 68:69.
- Rehner, S. A., and Buckley, E. 2005. Mycologia 97:84.
- Sawai, R., et al. 2008. J. Ethnopharmacol. 118:108.
- White, T. J., et al. 1990. Page 315 in: PCR Protocols: A Guide to Methods and Applications. Academic Press, San Diego, CA.

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