Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum scovillei* Causing Anthracnose on Watermelon (*Citrullus lanatus*) in Malaysia

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Production of watermelon (*Citrullus lanatus*) in Malaysia was 150,000 tons in 2020 (Malaysian Department of Agriculture 2021). In November 2019, nine locally produced watermelon fruit (red flesh, seedless) from five local stores in the states of Kelantan, Terengganu, and Penang exhibited sunken, circular, brown lesions that enlarged to 1.5 to 10 cm in diameter with scattered orange masses of conidia. Lesions coalesced to cover approximately 50% of the fruit surface. Lesions were surface sterilized by spraying 70% alcohol onto the fruit followed by drying with sterilized paper towels. A total of 153 tissue segments (1 × 1 cm) were excised from the rind, immersed in 1% sodium hypochlorite for 3 min, rinsed twice for 1 min in sterilized distilled water, air-dried, transferred to potato dextrose agar (PDA) plates, and incubated at 25 ± 1°C for 7 days. Single-spore transfers produced pure cultures, resulting in 12 isolates. Colonies on PDA were initially white and turned pale gray with age. Conidia were hyaline, one end round and the other narrowly acute, aseptate, smooth walled, straight, cylindrical to clavate, 10.5 to 16.5 × 3 to 4.5 μm (*n* = 30). Observed morphological characters matched a published description of *Colletotrichum* spp. (Damm et al. 2012). Internal transcribed spacer (ITS) and glyceraldehyde-phosphate

dehydrogenase (*GAPDH*) genes were amplified using primer sets ITS1/ITS4 and GDF1/GDF2, respectively. All sequences were deposited in GenBank (MW856808 for ITS; MZ219296 for *GAPDH*). A BLASTn search of both sequences on GenBank showed 99% identity with *C. scovillei* along with other closely related *Colletotrichum* species. Phylogenetic analysis of ITS and *GAPDH* alignments, using maximum likelihood along with reference strains of closely related species from MycoBank, confirmed species identity as *C. scovillei*. A pathogenicity test was conducted on two healthy watermelon fruit (red flesh, seedless). A 6-mm-diameter mycelial plug of a colony on PDA was positioned on a 0.5-cm-long wound on each fruit; a sterile PDA plug placed on a similar wound on the opposite side served as a control. Fruit were incubated at 25 ± 1°C for 7 days in plastic-wrapped trays above distilled water to maintain high humidity. Small, sunken, circular brown lesions appeared and expanded at inoculation sites within 7 days. Symptoms were identical to those produced by natural infections, and the controls were asymptomatic. Isolates from the lesions at the inoculation sites were confirmed as *C. scovillei* based on morphological characteristics, fulfilling Koch's postulates. The pathogenicity test was conducted four times with a total of eight fruit. Many species in the *C. orbiculare* complex cause watermelon anthracnose (Keinath, 2018). To our knowledge, this is the first report of *C. scovillei* (*C. acutatum* species complex; Damm et al. 2012) causing anthracnose on watermelon in Malaysia. Anthracnose caused by *C. scovillei* has been confirmed on other crops such as pepper (Toporek and Keinath, 2021), banana (Zhou et al. 2017), and chili (Oo et al. 2017). This insight will inform efforts to improve management of watermelon anthracnose in Malaysia.

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