Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose on ‘Purple Dream’ *Solanum melongena* in Malaysia Caused by *Colletotrichum siamense*

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‘Purple Dream’ eggplant (*Solanum melongena*) is widely grown for its edible fruit in Malaysia. In July 2021, anthracnose symptoms were observed on fruit with a disease severity of approximately 80% and an incidence of 10% in a field (14.6 m²) (5°56′50.9″N, 116°04′31.9″E) in the Penampang district of Sabah province. The symptoms initially appeared as irregular light brown spots. As the disease progressed, the spots enlarged and merged into extensive lesion patches that appeared in concentric circles. Symptomatic fruit tissues (5 × 5 mm) were surface sterilized based on Khoo et al. (2022b), plated onto potato dextrose agar (PDA), and incubated at 25°C in the dark. Colonies with gray-white fluffy mycelia developed after 7 days, and the reverse of the colonies was dark brown. A representative isolate named Penampang was characterized morphologically and molecularly. The conidia were one-celled, cylindrical, blunt at the ends, hyaline, smooth, and 13.3 to 16.1 × 3.9 to 6.0 µm (*n* = 20). Appressoria ranged in size from 7.6 to 9.3 × 5.5 to 6.6 µm (*n* = 20) and were spherical to irregular in shape and dark brown. Genomic DNA was extracted from fresh mycelia of isolate Penampang based on Khoo et al. (2022a, b). The ITS1/ITS4, CL1C/CL2C, ACT-512F/ACT-783R, CHS-79F/CHS-354R, and GDF1/GDR1 primer pairs were used to amplify the isolate’s internal transcribed spacer region (ITS), and partial calmodulin

(*CAL*), actin (*ACT*), chitin synthase (*CHS-1*), and glyceraldehyde-3-phosphate dehydrogenase genes (*GAPDH*) (Weir et al. 2012). PCR products were sequenced by Apical Scientific Sdn. Bhd. (Selangor, Malaysia). Sequences were deposited in GenBank under the accession numbers OL957466 (ITS), OL953035 (*CAL*), OL953032 (*ACT*), OL953038 (*CHS-1*), and OL953041 (*GAPDH*). They were 99 to 100% identical to the *Colletotrichum ti ITS* (NR_120143) (515 out of 519 bp), and *C. siamense CAL* (JX009714) (729 out of 731 bp), *ACT* (JX009518) (282 out of 282 bp), *CHS-1* (JX009865) (299 out of 299 bp), and *GAPDH* (JX009924) (276 out of 277 bp) sequences. ITS sequences do not reliably resolve relationships within the *C. gloeosporioides* complex (Weir et al. 2012). The phylogenetic maximum likelihood analysis using the combined ITS, *CAL*, *ACT*, *CHS-1*, and *GAPDH* sequences indicated that the isolate was part of the *C. siamense* clade (100% bootstrap value) that also contained the type isolate ICMP 18578 of this species. Morphological and molecular characterization matched the description of *C. siamense* (Huang et al. 2022; Ismail et al. 2021). Koch’s postulates were performed similarly to the description by Chai et al. (2017) but using spray-inoculation (10⁸ spores/ml) of three healthy Purple Dream eggplant fruit with isolate Penampang. Water was sprayed on three additional fruits that served as controls. All the fruits were incubated at 25°C and >90% relative humidity. Symptoms similar to those observed in the field developed 5 days after inoculation. No symptoms occurred on controls. The experiment was repeated two more times. The reisolated fungi were identical to the pathogen morphologically and molecularly. To our knowledge, this is the first report of *C. siamense* causing anthracnose on fruit of Purple Dream *S. melongena* in Malaysia as well as worldwide. Our findings expand the host range of *C. siamense* and indicate that the pathogen could potentially limit Purple Dream eggplant production in Malaysia.

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