

Phylogenetic species and biological characteristics of mango anthracnose pathogens in Taiwan

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Purpose: The study was aimed to identify phylogenetic species of mango anthracnose pathogens in Taiwan, and to compare their morphology, virulence and fungicides sensitivity.

Methods: Ninety-six *Colletotrichum* isolates were collected from diseased fruits, asymptomatic twigs and peduncles of Irwin, Jin-Hwang and native cultivars. Isolates of *C. gloeosporioides* species complex (CGSC) and *C. acutatum* species complex (CASC) were analyzed. Representative isolates of CGSC and CASC were further identified by phylogenetic analyses with concatenated sequences of multiple genes. Irwin mango fruits and leaves inoculations were used to compare the virulence of phylogenetic species. Eight fungicides media were used to assay the fungicide sensitivity of phylogenetic species.

Results and conclusions: *C. asianum* is a dominant species from diseased fruits, asymptomatic twigs and three mango cultivars. *C. fructicola* and two minor species were also identified. A possible new species (temporarily named Casp) of CASC was dominant in peduncles. In virulence assays, *C. asianum* and *C. fructicola* caused significantly bigger lesions than the other phylogenetic species on fruits, but only *C. asianum* significantly caused bigger lesions on leaves. In fungicide sensitivity tests, all species except MML025 and Casp showed high resistance to thiophanate-methyl and carbendazim. All species were resistant to azoxystrobin and kresoxim-methyl, but sensitive to tebuconazole, difenoconazole and prochloraz. To accelerate the identification, a specific primer, Casia-F2 / Casia-R2 was designed to amplify a band of about 300 bp. from *C. asianum*. This study may provide the basis for exploring the biological differentiation among phylogenetic species, and for studying the ecology of the mango pathogens.