

Morphological and molecular characterization of *Colletotrichum* causing anthracnose in ripe avocado (*Persea americana* Mill.)

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Anthracnose is a major disease in ripe avocados (*Persea americana* Mill.) worldwide which, while limiting the shelf life and marketing potential, incurs significant fruit losses. Avocado anthracnose has long been believed to be caused by *Colletotrichum gloeosporioides* and *C. acutatum*, both of which are presently regarded as species complexes, comprising many closely related species. *Colletotrichum* was isolated on PDA, from anthracnose lesions in twenty ripe avocados collected in Sri Lanka. Morphometric analysis, using eleven characters including colony, conidial and appressorial morphology, divided the twenty isolates into two main clusters. The conidial size has largely contributed to cluster separation. All the twenty isolates were subjected to DNA sequence analysis using internal transcribed spacer (ITS), β -tubulin 2 (TUB2) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) regions. Species affiliations and identities of the resulting sequences were determined through similarity-based searches of the NCBI GenBank Database. Considering >96% similarity in the three gene regions, nine and eleven isolates were identified as *C. siamense* and *C. endophytica* respectively, both belonging to the *C. gloeosporioides* complex. This is the first report of association of *C. endophytica* and *C. siamense* with avocado anthracnose. ITS region contributed in placing the taxa within *C. gloeosporioides* while TUB2 and GAPDH have successfully resolved their identity to species level. The results of multivariate statistical analysis did not agree with the molecular sequence analysis hence the present study has also shown that the morphological characters are not reliable for identification of *Colletotrichum* up to species level. The information that the present study has unveiled would help rectify the incorrect and insufficient understanding of the *Colletotrichum* species causing avocado anthracnose in Sri Lanka. This will also encourage design of similar identification techniques for determination of anthracnose pathogens in other fruit types in Sri Lanka. Moreover, accurate identification of the causal organisms is vital for designing meaningful disease management strategies.