

MOLECULAR AND MORPHOLOGICAL CHARACTERIZATION OF *COLLETOTRICHUM* CAUSING MANGO ANTHRACNOSE IN SRI LANKA

Ishani Komala Vithanage, Nimal Adikaram* and Deepthi Yakandawala

Department of Botany, Faculty of Science, University of Peradeniya, Sri Lanka

**n.k.b.adikaram@gmail.com*

Anthracnose disease in ripe mango (*Mangifera indica* L.) has long been known to be caused by *Colletotrichum gloeosporioides*. More recently *C. acutatum* was also reported to be associated with the disease. Identification of species within the genus *Colletotrichum* using morphological features is difficult because of the lack of well-defined criteria for distinguishing species. Recent studies combining morphological and molecular data have grouped *Colletotrichum* into two complexes i.e. *C. gloeosporioides* complex and *C. acutatum* complex, each comprising a large number of species requiring further studies. In the present study, *Colletotrichum* was isolated from anthracnose lesions of ripe mangoes belonging to cultivars; 'Ambalavi', 'Karthakolomban', 'Malwana' and 'Willard'. Thirty eight isolates of *Colletotrichum* were studied for colony appearance and growth rate, conidia size and morphology, appressoria morphology, production of setae and teleomorph on culture and resistance to Benlate[®] (Benzimidazole group). Morphological features among isolates were overlapping. Cultures on PDA were white to grey, cottony and consisting of concentric markings and the growth rate ranged 6.7 - 12.4 mm/day. Six isolates produced salmon-pink colour conidia masses. Length and width of conidia varied greatly ranging from 12 - 19 μm and 3 - 5 μm respectively. The isolates were divided based on conidial morphology into 3 groups i.e. with (i) fusiform conidia resembling *C. acutatum*, (ii) cylindrical conidia resembling *C. gloeosporioides*, and (iii) conidia with intermediate morphology. Growth of all isolates was retarded in Benlate at 3 $\mu\text{g/ml}$ and <10% of isolates exhibited retarded growth at 1 $\mu\text{g/ml}$. Eighteen isolates representing all three conidia morphology groups were subjected to molecular analysis for two nuclear gene regions, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [308 bp] and β -tubulin 2 (TUB2) [716 bp]. An isolate from anthracnose in orange was used as the type specimen for *C. gloeosporioides*. Earlier distinction of *Colletotrichum* spp. based on conidial morphology did not agree with molecular identification. None of the sequences from 18 isolates matched with *C. gloeosporioides* epitype. Considering >95% similarity in TUB2 and GAPDH gene regions, the 18 isolates were identified as *C. asianum*, *C. siamense*, *C. fructicola* and *C. tropicale* under Musae clade of *C. gloeosporioides* complex. *C. gloeosporioides* and *C. acutatum* were not among the 18 isolates examined from mango anthracnose in Sri Lanka.