Abstract No: 89 ***Life Sciences***

MORPHOLOGICAL CHARACTERIZATION OF ANTHRACNOSE CAUSING PATHOGENS ISOLATED FROM COMMERCIALLY AVAILABLE PAPAYA IN THE KANDY DISTRICT

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Anthracnose, caused by *Colletotrichum* species, is a major post-harvest disease affecting tropical fruits, including papaya (*Carica papaya* L.). Pathogen variability can impact responses to fungicides and control methods, emphasising the crucial need to understand their diversity better. Despite identifying the causative pathogens, a knowledge gap remains regarding their morphological and biological traits in Sri Lanka. This study aimed to bridge this gap by isolating and characterizing *Colletotrichum* species from infected papaya fruits in the Kandy district, Sri Lanka. Representative samples of three commercially available papaya varieties of Red Lady (RL), Rathna (R), and Horana Hybrid (HH) were used in the study. Nine fungal pathogens from the diseased papaya fruits were isolated on Potato Dextrose Agar (PDA), and their single spore isolates were preserved for subsequent experiments. Pathogenicity tests were then conducted following Koch's postulates. Colony morphological characters were observed on seven-day-old cultures on PDA medium. Slide cultures of the isolates were prepared for observations of micro-morphological characters. The colonies of all the isolates were white, with an entire margin and flat elevation. All isolates exhibited a circular form except for one RL isolate, which displayed an irregular form. The colour of the colonies at sporulation varied, displaying black, brown, yellow and orange hues. The growth rate of seven-day-old isolates ranged from 0.48 – 0.83 cm/day. All conidia were hyaline and cylindrical with bluntly rounded ends, ranging in length from 9.7 to 16.5 μm and width from 1.8 to 5.2 μm. All hyphae were hyaline, with no significant variations. Based on the analysis of micro-morphological data and colony morphology, all isolates were identified as *Colletotrichum* spp., and the pathogen exhibited four distinct morphotypes. The findings suggest that further molecular research is needed to gain a more comprehensive understanding of the pathogen.

Financial assistance from the Faculty of Natural Sciences of the Open University of Sri Lanka is highly acknowledged

Keywords: Anthracnose, *Carica papaya*, Morphological characterization