

Abstract No: BS-31

Morpho-molecular characterization of *Lasiodiplodia* and *Diaporthe* species infecting *Solanum melongena* L. (brinjal) in Gampaha district

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Solanum melongena L. (brinjal) is a vegetable belonging to the family *Solanaceae* and a popular commodity among consumers. Brinjal plants are infected by numerous fungal pathogens causing a wide range of diseases such as anthracnose by *Colletotrichum* sp., stem and leaf lesions by *Phomopsis vexans* (anamorph of *Diaporthe*), and early blight by *Alternaria solani* which significantly reduce the yield. The objective of this study was to isolate and identify the fungal pathogens associated with leaves of *S. melongena* in the Gampaha district. Necrotic or prematurely wilted leaves of *S. melongena* were collected and associated fungi were isolated onto PDA medium. Pathogenicity was confirmed by wounded and non-wounded inoculation of a seven-day old isolate onto healthy *S. melongena* leaves and the confirmed fungal pathogens were identified using their morphological, cultural characteristics and analysis of the internal transcribed spacer region (ITS1-5.8S-ITS2). Fifteen fungal isolates were isolated from necrotic leaves of *S. melongena*. Three fungal isolates (Isolates H32A, H32B and U11) were identified to be pathogenic on leaves of *S. melongena* based on the pathogenicity test. A necrotic leaf spot was initiated at the site of inoculation with isolates H32A and H32B in both wounded and non-wounded inoculations, which later developed into wilting and premature falling of the leaf. Leaf blight was observed with non-wounded inoculation of isolate U11. Morphological characters of isolates H32A and H32B were similar, with fluffy, blackish-grey, septate mycelia and dark brown oval shape spores with a septum in the middle. Both had similar growth rates of 2.25 cm/day. They were morphologically identified as *Lasiodiplodia* sp. Yellowish grey color pigmentation was observed in the isolate U11 which produced aseptate hyphae but could not be identified by its morphological characteristics. The nucleotide sequence of ITS region confirmed the morphological identification of isolates H32A (MT990527) and H32B (MT990528) as *Lasiodiplodia theobromae* with 99.81% sequence similarity to *L. theobromae* (IRNKB244) at NCBI database. Further, isolate U11 (MT990529) showed 99.82% sequence similarity with *Diaporthe eugeniae* (ASHM304) at NCBI database. *L. theobromae* is reported to cause fruit rot in brinjal, while *Diaporthe* sp. has caused stem and leaf lesions. *L. theobromae* and *D. eugeniae* were confirmed to be pathogenic on *S. melongena* L. (brinjal) plants in the Gampaha district and further studies will be conducted to develop an environmentally friendly strategy to manage above mentioned diseases.

Keywords: *Diaporthe*, *Lasiodiplodia*, *Solanum melongena*

Acknowledgment

This work was supported by World Bank AHEAD project under the research grant AHEAD DOR, Faculty of Science, University of Kelaniya