

AS/OP/12

First Report of *Curvularia chiangmaiensis* on *Oryza rufipogon* (wild *Oryza* spp.) in Sri Lanka

Disanayaka DMSA¹, Fernandez HS¹, Yapa PN¹, Wijesinghe MM¹, Manamgoda DS²

¹Department of Biological Sciences, Faculty of Applied Sciences, Rajarata University of Sri Lanka

²Department of Botany, Faculty of Applied Sciences, University of Sri Jayewardenepura

Background: *Curvularia* spp. are typically associated with the poaceous crops, including rice (*Oryza sativa* L.). Sri Lanka is known for its diverse rice genetic resources. *Oryza rufipogon* is the most closely related to *O. sativa*, among the five (05) wild *Oryza* spp. found in Sri Lanka. According to the previous studies, wild *Oryza* spp. are genetically stronger than the cultivated rice varieties. Therefore, fungal pathogens associated with *Oryza rufipogon* can become potential pathogens to *O. sativa* as well. To date, no studies have been conducted to characterise the *Curvularia* spp. associated with wild *Oryza* spp. in Sri Lanka.

Objective: To collect *Curvularia* spp. associated with *Oryza rufipogon* and accurately identify them using morphological and molecular data.

Methods: Fungal pure cultures were obtained using the single spore isolation technique. Colony characters were observed on three different culture media: Potato Dextrose Agar (PDA), Corn Meal Agar (CMA), and Malt Extract Agar (MEA). Fungal isolates were characterised based on micro-morphological and molecular data. During this study, 15 samples with leaf spots, leaf blight, diseased panicles, and dead plant materials were collected. Collected *Oryza rufipogon* samples were authenticated by the National Herbarium, Peradeniya. Isolates were initially identified as *Curvularia* based on morphological and microscopic characteristics. The internal transcribed spacer 1 and 2 with 5.8S region (ITS) partial sequence and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) loci were sequenced and used in multi-locus phylogenetic analysis following the DNA extraction using a sodium dodecyl sulphate (SDS) method, polymerase chain reaction (PCR), and gel electrophoresis. Molecular phylogenetic analyses were performed using both maximum parsimony (MP) and maximum likelihood (ML) criteria for the fresh collections from this study, together with the available ex-type and reference sequences.

Results: The resulted phylogram revealed that the fungal isolate obtained was closely clustered with the ex-type sequences of the *Curvularia chiangmaiensis*.

Conclusion: *Curvularia chiangmaiensis* isolated from *Oryza rufipogon* updates a novel host-fungal association from Sri Lanka herein.

Keywords: *Curvularia*, GAPDH, ITS