

2nd Annual Congress on MICROBIOLOGY AND MICROBIOLOGISTS

& 6th International Conference on MYCOLOGY AND FUNGAL INFECTIONS

October 07-08, 2019 | Madrid, Spain

Molecular and morphological identification of isolated fungal pathogens from infected *Nephelium lappaceum* L. (RAMBUTAN)

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Mephelium lappaceum L. (Rambutan) is a staple, seasonal tropical fruit that has both economical and medicinal value. It is a fragile fruit that is sensitive to environmental and pathologic conditions. Considering the factors involved, the primary reason for fruit rot is due to pathogenic fungi which cause infection and diseases. This study identified the fungi isolated from the symptomatic leaves and fruits of rambutan. Infected plant samples were collected from a farm in San Juan, Sta. Cruz, Laguna. Symptomatic tissues from leaves and fruits were cultured in potato dextrose agar and then transferred to malt extract agar to aid sporulation. The fungal isolates, after subjecting for pathogenicity test, were characterized using the partial Internal Transcribed Spacer (ITS) region and morphological analysis. DNA sequences of the isolates were subjected to phylogenetic analysis using Mega v.7 software with reference sequences from the GenBank. The fungal pathogens were identified as *Aspergillus aculeatus, Fusarium fujikuroi, Lasiodiplodia theobromae, Neopestalotiopsis clavispora, Pestalotiopsis microspora,* and *Trichoderma afarasin.* The latter was found to be not pathogenic but exhibits biocontrol potential in plant host. Phylogenetic findings showed that there is a high correlation of each isolated species to the published identified sequences in GenBank. The use of multilocus analysis which may strengthen the species identification as well as testing the pathogenicity of the fungal isolates to rambutan fruit is highly recommended.

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