

**GENOMIC AND PATHOGENICITY VARIATIONS OF
COLLETOTRICHUM ISOLATES ASSOCIATED WITH BANANA
ANTHRACNOSE**

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Present study was conducted to determine genomic and pathogenicity variations of sixteen different *Colletotrichum* isolates obtained from dessert banana varieties grown in Sri Lanka, infected with anthracnose, crown rot and blossom end rot. Pathogenicity variation of the isolates was determined on different varieties of banana (i.e. *Anamalu*, *Embon*, *Embul*, *Kolikuttu*, *Puwalu* and *Rathkehel*) and cross-infectious ability on fruits other than banana (i.e. papaya and guava) was determined by inoculating the fruits with aliquots of spore suspensions of each isolate. Lesion development was highest or second highest on variety *Kolikuttu* when infected with 12 isolates and lesion development was highest or second highest on variety *Embon* when infected with 10 isolates out of the 16. Isolate Cm7, the most frequently isolated isolate and identified as *Colletotrichum musae*, developed the largest lesion area on varieties *Kolikuttu*, *Rathkehel*, *Embul* and *Puwalu* whereas, isolates Cm2 and Cm21 produced the largest lesion area on varieties *Anamalu* and *Embon* respectively. Isolate Cm10 produced the largest lesion area on papaya while isolates Cm18, Cm19, Cm6 and Cm7 did not develop lesions on papaya. None of the tested isolates developed lesions on guava, indicating that guava is a non-host for the tested isolates. Genomic variation among 16 isolates was determined by PCR and PCR-RFLP, targeting ITS1 and ITS2 regions of rDNA unit. Genomic DNA was extracted from each isolate and subjected to PCR. The isolates produced PCR products of 170 bp and 156 bp for ITS1 and ITS2 regions, respectively. As the PCR products for these regions did not give a clear polymorphism, the region between ITS1 – ITS2 was amplified and restricted with *MspI* for PCR-RFLP analysis. However, PCR-RFLP of ITS1-ITS2 region was not successful to give a clear genomic polymorphism among the *Colletotrichum* isolates tested.

Key words: Banana varieties, *Colletotrichum musae*, Genomic and pathogenicity variation, ITS1 and ITS2 region, PCR-RFLP