

Genetic Divergence and Morphogenic Analysis of Sugarcane Red Rot Pathogen *Colletotrichum falcatum* under South Gujarat Condition

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Abstract : In the present study, nine strains of *C. falcatum* obtained from different places and cultivars were characterized for sporulation, growth rate, and 18S rRNA gene sequence. All isolates had characteristic fast-growing sparse and fleecy aerial mycelia on potato dextrose agar with sickle shape conidia (length x width: varied from 20.0 X 3.89 to 25.52 X 5.34 μ m) and blackish to orange acervuli with setae (length x width: varied from 112.37X 2.78 to 167.66 X 6.73 μ m). They could be divided into two groups on the base of morphology; P1, dense mycelia with concentric growth and P2, sparse mycelia with uneven growth. Genomic DNA isolation followed by PCR amplification with ITS1 and ITS4 primer produced ~550bp amplicons for all isolates. Phylogeny generated by 18S rRNA gene sequence confirmed the variation in isolates and mainly grouped into two clusters; cluster 1 contained CoC671 isolates (cfNAV and cfPAR) and Co86002 isolate (cfTIM). Other isolates cfMAD, cfKAM, and cfMAR were grouped into cluster 2. Remaining isolates did not fall into any cluster. Isolate cfGAN, collected from Co86032 was found highly diverse of all the nine isolates. In a nutshell, we found considerable genetic divergence and morphological variation within *C. falcatum* accessions collected from different areas of south Gujarat, India and these can be used for the breeding program.

Keywords : *Colletotrichum falcatum*, ITS, morphology, red rot, sugarcane

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