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Poster (Painel)

415-1 LENGTH POLYMORPHISM IN THE RIBOSOMAL DNA INTERGENIC SPACERS FROM Colletotrichum SPECIES

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Resumo

The genus Colletotrichum is one of the most important groups of plant pathogenic fungi in the world, including important crops in tropical and subtropical regions. Accurate identification of species of this genus is essential to understand the epidemiology of anthracnose and to development or improvement of practices to disease control. Several regions of genomic DNA have been used to characterization of microorganisms, including the Internal Spacers (ITS) and Intergenic Spacers (IGS) are variable portions of rDNA cistrons. IGSs frequently present sufficient variation to allow the analysis of the genetic relationships between closely related species, populations or varieties and simple techniques like PCR-RFPL can be applied to detect to intra-and interspecific polymorphism. This study aimed to assess the intra-and interspecific variability of Colletotrichum from different species by IGS PCR-RFLP of the rDNA region. Were analyzed the species Colletotrichum gossypii (CG), Colletotrichum gossypii var. cephalosporioides (CGC), Colletotrichum gloeosporioides, Colletotrichum brasiliense, Colletotrichum fragariae and Colletotrichum fructicola. The microorganisms were grown on PDA (potato, dextrose and agar) culture medium, DNA extraction was performed by the CTAB method. For amplification of the IGS region were used CLN12 and CNS1 primers, PCR products were digested by Hae III at 37 ° C for 3 hours. The IGS PCR-RFLP results indicate that HaeIII digest was able to differentiate the five Colletotrichum species axaminated here and also to distinguish C. gossypii and C. gossypii var. cephalosporioides each other. Polymorphisms among isolates of the same species but of different hosts were observed in C. gloeosporioides and C. fragariae isolate from guaraná tree (Paullinia cupana) and isolate reference from Fugal Biodiversity Centre (CBS-Centraalbureau voor Schimmelcultures).