

Poster (Painel)**415-2 Analysis of ribosomal RNA intergenic spacer (IGS) in *Colletotrichum gossypii* and *Colletotrichum gossypii* var. *cephalosporioides***

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Resumo

The main fungal diseases of the cotton plant (*Gossypium hirsutum*) are anthracnose and ramulosis caused by *Colletotrichum gossypii* (GC) and *C. gossypii* var. *cephalosporioides* (GCC), respectively, which are agents that cause severe yield loss. Both species are transmitted by seeds and morphology, growth habit and reproductive structures are very similar. Therefore, the use of molecular techniques is an alternative for identification of these pathogens. Ribosomal DNA regions, such as the intergenic spacer (IGS), show high inter and intra-specific polymorphism and for this reason are often used in phylogenetic analysis. The variations between CG and CGC can be detected through the analysis of the IGS region enabling including the development of diagnostic method between the pathogens. Thus, the present work aims to evaluate polymorphisms length of IGS region from isolates of *C. gossypii* and *C. gossypii* var. *cephalosporioides*. Were analyzed five isolates of *C. gossypii*, and five of *C. gossypii* var. *cephalosporioides*. The microorganisms were cultured on PDA (Potato Dextrose Agar) culture medium, the DNA extraction was performed by CTAB method. For the amplification of the IGS region, we used the CLN12 CNS1 primers. The results obtained reveal striking differences in the size of the IGS region between *C. gossypii* and *C. gossypii* var. *cephalosporioides* who presented respectively ~ 3.0 kb and ~ 2.6 kb. In addition, all isolated from CG presented two fragments corresponding to IGS region unlike isolated from CGC that showed only one fragment. These results indicate the existence of two IGS regions in CG and the possibility of occurrence of two nucleus in this species. Differences in the IGS region between *C. gossypii* and its variant *cephalosporioides* may help explain the evolution between these pathogens and the more notable polymorphism of length can be used for molecular diagnosis.