

Abstract

Colletotrichum species cause anthracnose in various postharvest tropical and subtropical fruits. The disease in postharvest fruits of guava, mango and papaya has being reported causing by *C. gloeosporioides*, and in citrus by *C. acutatum*. The aim of this study was to compare isolates of guava, mango, papaya and citrus, through pathogenicity, morphological, cultural and rDNA sequencing. PCR amplifications of the rDNA gene fragment of all isolates were performed using ITS4 and ITS5 primers. Each PCR product was sequenced using ITS4 as a primer. The sequence data was aligned using CLUSTAL W and a phylogenetic tree was constructed. The results showed that through inoculation was observed that *C. acutatum* is pathogenic to guava, papaya and mango and morphologically isolates of mango and papaya were similar to *C. gloeosporioides* and isolates of guava and citrus were similar to *C. acutatum*. The tree constructed by rDNA sequencing showed that mango and papaya were similar and, guava and citrus were more close related.