Poster (Painel)

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Molecular phylogenetic analysis confirms taxonomic reavaluation of Colletotrichum guaranicola, causal agent of guarana anthracnose

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Resumo

Colletotrichum genus presents about 66 species described on the basis of morphology and sequence analysis of multiple genes. Among these species, there are pathogens of many economically important crops. In the Amazon region, the anthracnose of Guarana (*Paullinia cupana* var. *sorbilis*), caused supposedly by *Colletotrichum guaranicola* is a major disease in guarana plantation. Identification within the genus *Colletotrichum* is complicated because this species have few distinguishing morphological characters, and teleomorphic stages are rarely formed. Furthermore, identification based only in morphological data can lead to errors. The aim of this study was to analyze the molecular phylogenetic relationships of *C. guaranicola*, causal agent of guarana anthracnose by GS intron (Glutamine Synthetase). Phylogenetic analysis of *C. guaranicola* was carried out based on the aligned dataset of 25 sequences from eleven different *Colletotrichum* species from GenBank. Phylogenetic trees were constructed from GS nuclear regions with maximum likelihood (ML) and a Bayesian framework with the Markov Chain Monte Carlo (BMCMC) algorithm. Gaps were treated as missing data. The ML analysis was run in MEGA. Nonparametric bootstrapping was conducted with 1000 replicates. The BMCMC analysis was run in MrBayes 3.1.2 and Bayesian posterior probabilities were generated from 10^7 and 10^8 generations, respectively, sampling every 1000th generation. *C. guaranicola* is morphologically closely to several species in the *C. gloeosporioides* complex and phylogenetic analysis using ITS sequences could not confidently resolve its systematic placement because low nucleotide diversity among *Colletotrichum* species. A phylogeny approach by GS intron was therefore employed to infer interspecific relationships. The species relationships are well defined with all the major clades supported by parsimony bootstrap support and Bayesian posterior probabilities (equal or above 95%). In the phylogenetic tree, *C. guaranicola* does not group with *C. gloeosporiodes*, but clusters as a sister clade to *C. truncatum* (PP=1.0 and bootstrap=100), although conidial morphology is completely different between both. The result reported here confirms *C. guaranicola* as a new specie of *Colletotrichum* genus. Financial support: CNPq and Embrapa

Palavras-chave: anthracnose, GS, phylogeny