

Study of new molecular markers for Phylogenetic reconstruction of the black fungus in humans

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Melanized hyphomycetes, or black fungi, are the etiological agents of opportunistic infections diseases, grouped into three classes: chromoblastomycosis, mycetoma and phaeohyphomycosis. Recently PCR methods (Polymerase Chain Reaction) have been successfully used for fungi identification, including melanized fungi of medical importance. Phylogenetic inferences, or taxonomic, organize knowledge on biological diversity, from the relationships among groups and knowledge of evolution of morphological, behavioral, physiological, cytogenetic, and molecular organisms. For the realization of phylogenetic analysis is necessary to choose a method to use, there are several statistical methods to carry out the phylogenetic analyzes each according to need analysis, specificity, and targets. Addition to the method is necessary to select a molecular marker to be used in phylogenetic analyzes. In fungi the ITS1 and ITS2 domains (Internal transcribed space) of the small subunit of the ribosome (18S-rDNA) can be well used in comparative analysis between species, as these regions are transcribed, but not translated, which allows these domains accumulate mutations, turning highly variable regions. Some authors have characterized two kinases of *Paracoccidioides brasiliensis*, responsible for inhibition of the Translation Initiation factor eIF2, EIF2AK1 and EIF2AK2, in response to cellular stress, such as temperature change, shortage of amino acids and stress Osmotic. Given the importance of these proteins, this research project aims to compare sequences of the kinases in different fungal classes, in order to design molecular markers for identification of species and even to aid in diagnosis of diseases caused by fungi. Through the analysis of sequences deposited in GenBank was observed the occurrence of genes kinases EIF2AK1 and EIF2AK2 in black fungi that are human pathogens. The result of the preliminary phylogenetic analysis confirms the results seen by Caligiorne and collaborators, in which *Fonsecaea* genus are part of a phylogenetic arm in relation to other gender, *Cladophialophora*, *Phialophora*, *Rinocladiella*. The results that can come with discovered new markers can help bring new information related to the classification, to demonstrate the diversity of etiologic agents of chromoblastomycosis, phaeohyphomycosis and mycetoma.