

MOLECULAR CHARACTERIZATION OF *SPOROTHRIX* CLINICAL ISOLATES INVOLVED IN SPOROTRICHOSIS EPIDEMIC IN RIO DE JANEIRO, BRAZIL

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Sporotrichosis is a subcutaneous mycosis with a global distribution, with areas of high endemicity in Latin America. This infection is caused by the dimorphic fungus *Sporothrix schenckii*, which is associated, in the environment, with plants and soil. Recently, it was suggested through a combination of phenotypic and genetic features that *S. schenckii* should not be considered a single taxon, but a complex of several related species comprising three new species: *Sporothrix brasiliensis*, *Sporothrix globosa*, and *Sporothrix mexicana*. We recently demonstrated the genetic polymorphisms of *S. schenckii* isolates from humans and associated cats from the sporotrichosis epidemic in state of Rio de Janeiro (RJ), and demonstrated the zoonotic character of the epidemic. Since the delineation of such species could be of importance from a clinical point of view, and just 25 isolates from the endemic occurring in Rio de Janeiro were included in previous study reported in the specialized literature, a total of 247 *Sporothrix* isolates from this endemic obtained during the period of 1998 and 2008 was studied for us. The phenotypic characterization was based on the morphology of conidia, growth rates at 30°C and 37 °C, ability to grow at 37 °C, and auxonographic method. According to the key features for species differentiation, the predominant species found was *S. brasiliensis* (83.4%), which confirms previous data that strains of *S. brasiliensis* are associated with Rio de Janeiro sporotrichosis endemic. Molecular analysis with the primers CL1 and CL2A, a fragment of 785 base pairs (bp) of gene calmodulin of 25 isolates that showed inconclusive results on phenotypic studies enabled the formation of a clade composed by 24 isolates with 100% similarity with the species *S. brasiliensis* demonstrating again the importance of analysis at the level of genotype to identify species. Also, a new molecular methodology, PCR fingerprinting using primer T3B differentiated among the three new species, and is a promising molecular methodology to classify the *Sporothrix* complex.