

Current Trends in Sporotrichosis

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Sporotrichosis is a sub-acute or chronic infection that affects the dermis and subcutaneous tissue, with a worldwide distribution, being more common in tropical and subtropical areas. In South America, the incidence is 48 to 60 cases per 100,000 inhabitants [1]. The classification schemes of several clinically important fungi have suffered major modifications in recent decades, due to advancement of molecular techniques, which allows easier access to sequences of DNA. However, in 2006, modifications occurred in the Sporothrix classification. [2] Marimon has suggested that *S. schenckii* could not be considered the only species, causing sporotrichosis. They described four new species of Sporothrix complex: *S. globosa*, *S. brasiliensis*, *S. Mexicana*, and *S. luriei*, formerly *S. schenckii* var. *luriei*.

Currently, the available data seems to indicate that the new species have different geographic distributions. *S. globosa* has a worldwide distribution [3], *S. brasiliensis* related epidemics of sporotrichoses in Rio de Janeiro, Brazil [4] and *S. Mexicana* appears limited to Mexican territory [2]. Only the correct identification of these new species will allow us to address the question, that the different clinical manifestations of Sporotrichosis, are produced by different species. Until now, the different species composing the complex have different susceptibility rates to antifungal drugs [5,6].

Molecular studies have demonstrated the existence of a high level of intraspecific variability, in which isolates are mainly grouped according to their geographical origin established [7-9], on the basis of Internal Transcribed Spacer (ITS) region sequence analysis, that more than one species could exist, within *S. schenckii*.

Several researches on the genomic DNA base composition rendered an average guanine and cytosine content, of about 54.7 mol% [10]. *S. schenckii* presents six to eight chromosomes of 460 to 6,200 kb, at a total genome size of about 28 Mbp [11]. Maybe such differences regard to either the different species recently described [2], or to underestimation in the methods adopted for genome size determination. It has also been reported that *S. schenckii*, a diploid organism, bearing around 50 fg DNA per cell, in both the filamentous and yeast phases. Aneuploidy, a state in which most of the chromosomes are disomic, cannot be excluded though [12]. Diploidy is considered as essential for thermal dimorphism in *Cryptococcus neoformans*, and similarities in life cycle between this fungus and other dimorphic fungi, including *S. schenckii*, might happen [13].

Mitochondrial DNA (mtDNA) analysis of Restriction Length Polymorphisms (RFLP) with the restriction enzyme Hae III, is usually the basis for studies on identification, typing, and epidemiology of sporotrichosis. It has been initially cited 24 mtDNA types [14], and more recently, 25 to 30 [15] and 31 to 32 [16] were introduced. Such analyses have been adopted in several studies, with *S. schenckii* strains from different geographical origins and also environmental isolates [17,18] being deposited to date in Gene Bank, nucleotide sequences of these fungi 914 being the most observed species *S. schenckii*, followed by *S. brasiliensis*, *S. globosa*, *S. mexicana*, *S. Schenkivarluriei* among others, respectively.

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