

TITLE: MOLECULAR EPIDEMIOLOGICAL INVESTIGATION OF HUMAN AND ANIMAL SPOROTRICHOSIS OUTBREAKS DRIVEN BY EMERGING *SPOROTHRIX* SPECIES.

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ABSTRACT:

Sporotrichosis is a neglected mycosis of clinical relevance that occurs in mammals after a traumatic inoculation of *Sporothrix* propagules. The disease is caused by thermodimorphic fungi embedded in a clinical clade composed of *S. brasiliensis*, *S. schenckii*, *S. globosa*, and *S. luriei*. Sporotrichosis is widely distributed, although the species causing outbreaks differ according to geographic location. Among the species in the clinical clade, *S. brasiliensis* is causing widespread epizootics and zoonotic outbreaks in Brazil and expanding into neighboring countries. Outbreaks due to *S. brasiliensis* gained notoriety in the 1990s, with the entry of the domestic cat into the disease transmission chain, especially in the southeast region of Brazil. Recently, reports of the disease expanding to Northeast Brazil raise questions about the dissemination of the fungus. To have a more trustworthy view of the dynamics of outbreaks, structure, and origin of genetic variation within and among populations of *Sporothrix*, we applied three sets of discriminatory AFLP markers and mating-type analysis to an extensive collection of isolates (n=188) spanning the major endemic areas. A total of 451 polymorphic fragments were amplified from *S. brasiliensis*, *S. schenckii*, and *S. globosa*. Dendrograms (Jaccard index, UPGMA) constructed using software Bionumerics v7.6 were able to differentiate between species of the clinical clade with well-supported branches (cophenetic values >86%). According to the genetic diversity analysis calculated from the generated fragments, we detected high levels of genetic diversity in *S. brasiliensis*, *S. schenckii*, and *S. globosa*. The population structure refers from paucity to regular sexual recombination, and molecular evidence suggests heterothallism as the unique mating strategy. The distribution of *MAT1-1* and *MAT1-2* in *S. brasiliensis* and *S. schenckii* were 1:1, supporting random mating, while in *S. globosa*, we observed a predominance of *MAT1-1*. The AFLP and mating-type markers developed in this study were key to track the emergence of *Sporothrix* during outbreaks. The content of this study provides an essential contribution to the epidemiology of the disease, which will assist further studies on the expansion of *Sporothrix* species.

Keywords: *Sporothrix*, sporotrichosis, genetic diversity, AFLP, epidemiology

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