**Objectives**

The aim of this study is to characterize Uruguayan clinical and environmental isolates of *Sporothrix spp*. by using end-stage PCR and to analyze their phylogenetic relationships.

**Methods & Materials**

Isolates

The laboratory of the Department of Parasitology and Mycology (Institute of Hygiene, Udelar) receives clinical samples of fungal infections and environmental isolates for identification. Since 1960, we have collected and preserved isolates of *Sporothrix* *spp*., continually adding new strains to our collection. Currently, we maintain 38 preserved *Sporothrix spp*. strains, all identified based on phenotypic characteristics. Each strain was cultured on potato dextrose agar (PDA), with purity verified and identification confirmed through both macroscopic and microscopic morphological analysis.

Characterization by PCR at end-time.

DNA was extracted from the mycelial phase using the Quick-DNA Fungal/Bacterial Miniprep Kit protocol (Zymo Research, USA). Following extraction, DNA concentration was measured using a NanoDrop spectrophotometer, yielding a final concentration of 100 ng/μL. Subsequently, a fragment of the calmodulin (CAL) gene was amplified using primers CL1 (5′-GARTWCAAGGAGGCCTTCTC-3′) and CL2A (5′-TTTTTGCATGAGTTGGAC-3′), as outlined by O’Donnell. The PCR products were then sent to Macrogen Inc. (Korea) for purification and sequencing. Upon receiving the sequences, they were compared with those deposited in GenBank using the Basic Local Alignment Search Tool (BLAST; http://blast.ncbi.nlm.nih.gov/Blast.cgi). Finally, phylogenetic analysis was performed using Molecular Evolutionary Genetics Analysis software (MEGA), version 6.0.

**Results**

A total of 20 *Sporothrix spp.* isolates were studied, the majority of which were of clinical origin (16 clinical and 4 environmental). The species characterized included *Sporothrix schenckii, S. variecibatus, and S. mexicana* (Table 1). Notably, no *S. brasiliensis* strains were identified in this study. Furthermore, phylogenetic analysis was conducted using the maximum likelihood method, comparing the Uruguayan isolates (Figure 1) with sequences deposited in GenBank.

**Conclusion**

In summary, we successfully genetically characterized several of our isolates, thereby obtaining the first results of *Sporothrix* characterization and genetic analysis for Uruguay. To date, there have been no reports of *non-schenckii* species from our environment. In the phylogenetic analysis, we observed significant genetic divergence among our isolates, even within *S. schenckii.* Moreover, no *S. brasiliensis* strains were detected, consistent with the absence of reported cases of feline sporotrichosis in Uruguay.