

**TITLE:** COMPARATIVE ANALYSIS OF MALDI-TOF AND MOLECULAR IDENTIFICATIONS OF CLINICAL STRAINS OF *FUSARIUM* FROM SAO PAULO STATE, BRAZIL.

**AUTORS:** PAZIANI, M. H. <sup>1,2</sup>; SANTOS, C. <sup>2</sup>; DE ALMEIDA, M. T. G. <sup>3</sup>; MELHEM, M. S. C. <sup>4</sup>; KRESS, M. R. Z. <sup>1</sup>.

**INSTITUTION:** 1. FACULDADE DE CIÊNCIAS FARMACÊUTICAS DE RIBEIRÃO PRETO, UNIVERSIDADE DE SÃO PAULO – FCFRP/USP, RIBEIRÃO PRETO – SP (Av. do Café, s/n. Ribeirão Preto – SP. CEP: 14040-903.) – Brasil; 2. DEPARTMENT OF CHEMICAL SCIENCE AND NATURAL RESOURCES, UNIVERSIDAD DE LA FRONTERA, TEMUCO - CHILE; 3. FACULDADE DE MEDICINA DE SÃO JOSÉ DO RIO PRETO/SP, SÃO JOSÉ DO RIO PRETO – SÃO JOSÉ DO RIO PRETO – SP – BRASIL; 4. INSTITUTO ADOLFO LUTZ, SÃO PAULO – SP – BRASIL.

## **ABSTRACT**

*Fusarium* species are filamentous fungi from Ascomycota phylum and isolated from a wide variety of substrates such as soil, plant remains and water, mainly in tropical regions. Most of the species are phytopathogens, but are additionally related to animal infections. In humans, fusariosis may progress to invasive infection, with high mortality rate. The occurrence of fusariosis is mainly in superficial mycoses. However, with the growing number of immunocompromised patients, the subcutaneous fusarioses have increased at alarming levels. *Fusarium* genus is divided into 22 species complexes by the differences in morphology, host associations, and mainly by molecular features. Members of the species complexes *F. oxysporum* (FOSC), *F. solani* (FSSC), *F. fujikuroi* (FFSC) and *F. dimerum* (FDSC) have emerged as potential pathogens to humans. Here it was proposed the identification and characterization of clinical strains of *Fusarium* spp. from Sao Paulo State by both DNA sequence analysis (internal transcribed spacer - ITS region of the ribosomal DNA and elongation factor 1 alpha - ET1 $\alpha$  gene) and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). The results indicate that FSSC is the most frequent isolated clinical strain in Sao Paulo state, followed by FOSC, FDSC, and FFSC. The molecular method identified 98 clinical strains as FSSC, and 91 (92.8%) of them match with the MALDI-TOF MS results. On the other hand, 7 and 2 clinical strains in the FSSC were identified only by ITS region sequencing and MALDI-TOF MS, respectively. Among the FOSC clinical strains, the ITS region sequencing was able to identify 8 clinical strains in which 4 (57,1%) matched with MALDI-TOF MS results. However, 4 and 3 clinical strains of FOSC were identified only by ITS region sequencing and MALDI-TOF MS, respectively. For FFSC and FDSC, both methodologies matched the identification of the clinical strains. Nevertheless, 6 clinical strains were not identified by MALDI-TOF MS. Concluding, despite the need for a more enriched MALDI-TOF MS database, the sequencing of ITS region and the MALDI-TOF MS mass-spectra were able to identify and group most of the *Fusarium* clinical strains at species complex.

**Keywords:** *Fusarium* species complex, mycoses, molecular identification, MALDI-TOF MS.

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