TITLE: INVESTIGATION OF A POSSIBLE OUTBREAK OF ASPERGILLUS SPP. AND FUSARIUM SPP. IN A HEMATOLOGIC UNIT OF A UNIVERSITY HOSPITAL.

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ABSTRACT
Opportunistic fungal infections are responsible for high rates of morbidity and mortality in immunocompromised patients, mainly those with hematologic malignancies. The identification of the etiologic agent is the key for the early and appropriate use of antifungal therapy. Thus, it is important to study the epidemiology, the microbiologic identification and the potential environmental factors and sources of contamination. *Aspergillus* and *Fusarium* are among the main causes of nosocomial fungal infections, in immunocompromised individuals. During March and April 2016, four patients from the Hematology division, hospitalized at the Clinical Hospital of the University of Campinas, developed invasive aspergillosis and fusariosis. Clinical samples of the four patients were analyzed and air samples were collected from the patient's rooms to study a potential environmental source of infection. Fungal DNA from 27 *Aspergillus* sp. and 29 *Fusarium* sp. was extracted and sequenced using Big Dye Terminator kit (Applied Biosystems). Primers for EF-1α gene were used for sequencing of *Fusarium* spp., while ITS region of the ribosomal DNA and β-tubulin gene were used for sequencing of *Aspergillus* spp. Fungi identification was performed by alignment of the gene sequences in gene databases (NCBI, CBS, *Fusarium*ID). The molecular relationship between clinical and environmental isolates was evaluated in the MEGA7 program with phylogenetic tree construction by Maximum Likelihood method with 1,000 replicates. Clinical isolates were as follow: *A. flavus* (n=2) and *A. nomius* (n=2), and in the air: *A. fumigatus* (n=10), *A. parasiticus* (n=6), *A. flavus* (n=3), *A. arachidicola* (n=3) and *A. sojae* (n=1). For *Fusarium* spp. clinical samples: *F. incarnatum* (n=2), *F. verticillioides* (n=2) and F. sacchari (n=1), and in the air: *F. verticillioides* (n=7), *F. incarnatum* (n=7), *F. equiseti* (n=3), *F. proliferatum* (n= 2), *F. solani* (n=2), *F. sacchari* (n=1), *F. subglutinans* (n=1) and *F. bactridioides* (n=1). The phylogenetic analysis showed the some air isolates of *Fusarium* spp. and *Aspergillus* spp. were grouped in the same species of the clinical isolates. These findings might contribute to the alert that the air could be a potential source of invasive fungal infection for these patients. The strategy of identification of species by similarity in the databases, followed by the phylogenetic tree was consistent. Multilocus sequence typing (MLST) and antifungal sensitivity tests are being studied.

Keywords: Aspergillus spp., Fusarium spp., molecular identification, hospital infection

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