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IDENTIFICATION OF *CANDIDA* SPECIES ISOLATED FROM PATIENTS IN 'HOSPITAL DE SÃO MARCOS'

M. C. Henriques[1]*, A. Costa*[1]*, F. Silva*[2]*, J. Azeredo*[1]*, A. Faustino*[2]*, R. Oliveira*[1]*; [1]University of Minho, Braga, PORTUGAL, [2]Hospital de São Marcos, Braga, PORTUGAL.*

Candidiasis is increasing as one of the major hospital infections. Most of these infections have been attributed to *Candida albicans*. However,

recently non-*Candida albicans Candida* (NCAC) species have been increasingly identified as candidiasis agents. Thus, it is of utmost importance to identify these new species in order to control the dissemination of infection. Moreover, these NCAC species are acquiring resistance to the antifungal agents more commonly used. The main aim of this study, carried out in the Clinical Pathology Laboratory of Hospital de São Marcos (Braga, Portugal), was to evaluate the prevalence and distribution of *Candida* spp. among clinical specimens. Moreover, this work also aimed at the comparison of three biochemical methods (Auxocolor, ID32C and Vitek) with a molecular method (PCR), for *Candida* species identification. Samples were collected from different origins, namely, sputum/bronchial wash/bronchoalveolar lavage, vaginal swab, hemoculture, catheter tip and urine, among others. This clinical isolates (229) were identified by Auxacolor and ID32C manual systems and by Vitek, an automated system. The results were compared with a molecular identification performed by Polymerase Chain Reaction (PCR) and gel agarose electrophoresis. From the results obtained it was possible to observe that *C. albicans* and NCAC species were detected in an equivalent percentage. Among NCAC species, *C. parapsilosis* was found in a higher percentage (13.9%), followed by *C. tropicalis* (10.5 %), *C. glabrata* (9.1 %), *C. krusei* (0.9 %), *C. dubliniensis* (0.4 %) and other unidentified *Candida* species (14.8 %). The biochemical methods used in the identification differed significantly from molecular identification, especially the ID32C system. This manual method was the less accurate and, therefore, should be replaced by Auxacolor, which offered better results. Moreover, the molecular method is a promising technique for the rapid and accurate identification of *Candida* species in clinical routine. This study highlights the importance of *Candida* epidemiological studies, since, maybe due to the new methodology for yeast identification or to the emergence of new species, the prevalence of *Candida albicans* is changing.