IDENTIFICATION OF PATHOGENIC FUNGI FROM BLOOD CULTURE BOTTLES USING DNA MICROARRAY

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Invasive fungal infections are associated to high mortality, especially, in the immunocompromised patients. The microbiologic diagnosis of fungemia relies in the fungal growth in blood cultures followed by the identification of the fungi. After the growth in blood culture, the identification of a fungal agent can take 24 to 72hs leading to a delay for the appropriate treatment. DNA microarray has been a promising technique for the rapid diagnosis of several microorganisms including fungi. The aim of this study was to evaluate the performance of a naked-eye visual DNA microarray platform designed for identification of pathogenic fungi. Fungal DNA was extracted from blood samples from blood cultures bottles and microarray was compared with the identification of microbiologic and DNA sequencing results. Sixty-six blood culture bottles that resulted positive for fungi were selected. The blood cultures were performed by Bact/ALERT (Biomerieux) equipment. The identification was done by morphological analysis and by Vitek 2 system (Biomerieux). The study included: 12 samples positive for *Candida krusei*, 14 *C. albicans,* 3 *C. glabrata*, 3 *C. dubliniensis*, 5 *C. tropicalis*, 2 *C. parapsilosis*, 1 *C. lusitaniae*, 1 *Aspergillus niger*, 19 *Cryptococcus neoformans*, 1 *Histoplasma capsulatum*, 2 *Saccharomyces cerevisiae*, 1 *Rhodotorula* spp. and 2 *Fusarium* spp.. Thirty negative blood cultures bottles and 93 positive bottles for bacteria were collected as negative controls. The DNA microarray was performed on a platform designed to identify 12 genera and 32 species of pathogenic fungi based on the internal transcribed spacer region (ITS). DNA sequencing of the ITS region was performed as the molecular gold standard. DNA microarray showed concordant results with microbiology in 63 of 66 positive blood cultures (95.5%). DNA microarray could not identify one *C. parapsilosis,* that was identified by DNA sequencing as *C. orthopsilosis* (*C. parapsilosis complex*), and *S. cerevisiae* and *Rhodotorula* spp., which probe sequences were absent from the platform. For negative controls, the DNA microarray identified one *C. albicans* in a bottle that was positive for coagulase negative *Staphylococus.* The results demonstrated high concordance among DNA microarray platform, microbiology techniques and DNA sequencing. The DNA microarray took a faster time for diagnosis and showed a high performance on visual identification of fungal species direct from blood cultures.

Keywords: DNA microarray, blood culture, fungal infection

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