

DNA microarray based on arrayed-primer extension technique for identification of pathogenic fungi responsible for invasive and superficial mycoses.

Campa D, Tavanti A, Gemignani F, Mogavero CS, Bellini I, Bottari F, Barale R, Landi S, Senesi S (2008) DNA microarray based on arrayed-primer extension technique for identification of pathogenic fungi responsible for invasive and superficial mycoses. *J Clin Microbiol* 46(3), 909-915.

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Abstract

An oligonucleotide microarray based on the arrayed-primer extension (APEX) technique has been developed to simultaneously identify pathogenic fungi frequently isolated from invasive and superficial infections. Species-specific oligonucleotide probes complementary to the internal transcribed spacer 1 and 2 (ITS1 and ITS2) region were designed for 24 species belonging to 10 genera, including *Candida* species (*Candida albicans*, *Candida dubliniensis*, *Candida famata*, *Candida glabrata*, *Candida tropicalis*, *Candida kefyr*, *Candida krusei*, *Candida guilliermondii*, *Candida lusitanae*, *Candida metapsilosis*, *Candida orthopsilosis*, *Candida parapsilosis*, and *Candida pulcherrima*), *Cryptococcus neoformans*, *Aspergillus* species (*Aspergillus fumigatus* and *Aspergillus terreus*), *Trichophyton* species (*Trichophyton rubrum* and *Trichophyton tonsurans*), *Trichosporon cutaneum*, *Epidermophyton floccosum*, *Fusarium solani*, *Microsporum canis*, *Penicillium marneffeii*, and *Saccharomyces cerevisiae*. The microarray was tested for its specificity

with a panel of reference and blinded clinical isolates. The APEX technique was proven to be highly discriminative, leading to unequivocal identification of each species, including the highly related ones *C. parapsilosis*, *C. orthopsilosis*, and *C. metapsilosis*. Because of the satisfactory basic performance traits obtained, such as reproducibility, specificity, and unambiguous interpretation of the results, this new system represents a reliable method of potential use in clinical laboratories for parallel one-shot detection and identification of the most common pathogenic fungi.

Beteiligte Forschungseinheiten

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