

The Microarray Technology in Yeast Identification Directly from Positive Blood Cultures

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INTRODUCTION

The incidence of opportunistic fungal infections has increased dramatically in the past few decades, especially in immunocompromised hosts. In these patients, colonization of mucosal surfaces by endogenous *Candida* spp. is often followed by invasion of the vascular space, which carries a high risk of disseminated candidiasis. Fungemia is, in fact, one of the most feared complications in these patients, and their survival is strictly dependent on early antifungal treatment. In the majority of patients, the fungemia is caused by *Candida albicans*, although in the last 10 years there has been an increase in the incidence of infection with a non-*C. albicans Candida* etiology. Although considerable progress in the detection of fungemia has recently been made, conventional fungal blood cultures still require 1 to 2 weeks of incubation. Thus there is a need for a rapid and accurate means of identifying fungal species from patient samples.

The *Candida* microarray chip technology is designed to detect and discriminate between medically important yeasts in blood.

PURPOSE

To evaluate the diagnostic performance of MycArray™ Yeast ID, Myconostica, 80 blood cultures positive for yeasts at Gram staining and identified by classical testing, were processed with this technique.

METHODS

The “MycArray Yeast ID” kit is a DNA hybridisation assay which detects 18 *Candida and yeast species including; C. albicans, C. glabrata, C. krusei, C. parapsilosis, C. tropicalis, Histoplasma capsulatum, and Cryptococcus neoformans*. Multiple probes are present to cover intra-species genetic variation, and controls, including an internal amplification control, are included. The initial PCR stage can be carried out on DNA extracted from blood cultures or on “tooth-picks” of colonies, and the assay can be completed in under 6 hours.

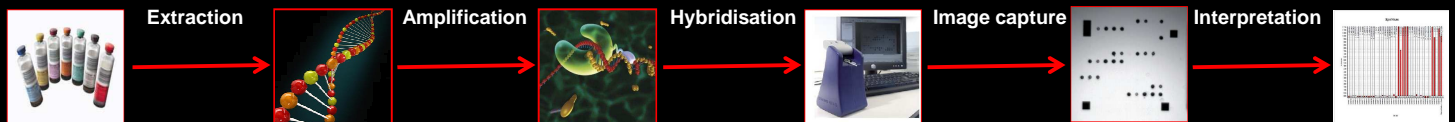


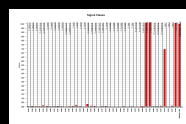
Fig.1 Summary of MycArray™ Yeast ID workflow

RESULTS

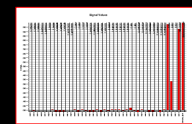
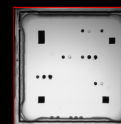
40 *Candida albicans*, 11 *C. parapsilosis*, 10 *C. Glabrata*, 2 *C. Tropicalis*, 1 *C. guilliermondii*, 1 *C. Krusei*, 3 *Cryptococcus neoformans*, 7 mixed cultures (*C. albicans* + *C. glabrata*) and 1 mixed cultures (*C. Tropicalis* + *C. glabrata*) were correctly identified, but 2 *C. lusitanae* has not been detected. Discrepancies in identification are summarized:

Classical methods	Microarray
<i>C. albicans</i>	<i>C. albicans</i> + <i>S. cerevisiae</i>
<i>C. tropicalis</i>	<i>C. tropicalis</i> + <i>S. cerevisiae</i>

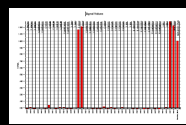
Cryptococcus neoformans



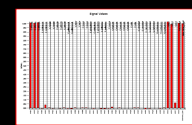
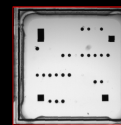
Candida lusitanae



Candida krusei



Candida albicans



Example data from a yeast-positive blood culture clinical sample

Example data from a yeast-positive blood culture clinical sample

CONCLUSIONS

Distinguishing which fungus is implicated in fungemia, and whether the infection is caused by multiple species, is important for the selection of antifungal therapy. A quick identification method is fundamental for the clinical management. The technical time for positive species identification directly from blood samples with the MycArray was 6 hrs, much quicker than classical methods. The microarray is a promising approach although not all *Candida/yeast* present in our clinical samples were included on the array and double identification including *S. cerevisiae* needed confirmation by culture.