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Genetic relatedness of *Candida albicans* bloodstream infection clinical isolates in Malaysia

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ABSTRACT

Aims: The aim of this study was to investigate the genetic relatedness of the most prevalent *Candida* bloodstream infection (BSI) species in in a Malaysian population via Randomly Amplified Polymorphic DNA-Polymerase Chain Reaction (RAPD-PCR) fingerprinting.
Methodology and results: The genomic DNA of 43 *Candida* BSI blood culture samples obtained from Universiti Malaya Medical Centre (UMMC) was isolated, after which species identification was carried out using PCR with *ITS-1* and *ITS-4* pan-fungal primers in conjunction with CHROMagar™ *Candida*. The predominant *Candida* species in the BSI samples is *Candida albicans* (14 out of 43 isolates). RAPD-PCR on these 14 *C. albicans* clinical isolates was performed using *PST* as the arbitrary primer. Data analysis using MEGA found an overall non-relatedness of these 14 clinical isolates [average similarity coefficient (S_{AB}) value 0.733±0.172]. Following in-depth analysis, five of the 14 isolates were observed to be identical (S_{AB} values of 1.00 each), four isolates had S_{AB} values of 0.80-0.99, indicating that they are highly similar, but are non-identical, while five isolates are unrelated (S_{AB} lower than 0.80). This suggests that microevolution might have occurred and that these clinical isolates may possibly belong to different strains.
Conclusion, significance and impact of study: A fair degree of genetic heterogeneity was found among the 14 *C. albicans* isolates from UMMC. To our knowledge, this is the first report on the genetic profiles of *C. albicans* bloodstream infection isolates from Malaysia, warranting further studies in the possible evolutionary trends within this *Candida* species in Malaysia.

Keywords: Randomly Amplified Polymorphic DNA PCR (RAPD-PCR), *Candida albicans*, *Candida* bloodstream infections, Genetic relatedness, DNA fingerprinting

INTRODUCTION

In the last decade, the emergence of nosocomial bloodstream fungal infections in persons with challenged immune systems (such as those with extensive burns, HIV infections, leukopenia, organ transplantation and patients undergoing chemotherapy) has heightened the need for more extensive research, especially in the genetics aspect of the causative pathogen. One such fungal infection is *Candida* bloodstream infections (BSIs), which is caused predominantly by *Candida albicans* (Nguyen *et al.*, 1996; Pfaller *et al.*, 1998; Trtkova and Raclavsky, 2006; Moretti *et al.*, 2013). The primary origin of *Candida* BSIs has been the subject of debate (endogenous- or exogenous-acquired). Endogenous acquisition of bloodstream infections, from existing colonization of *Candida* from one's own gastrointestinal flora is the major source of *Candida* BSIs (Nucci and Anaissi, 2001; Magill *et al.*, 2006; Miranda et *al.*, 2009). The exogenous origin of *Candida* BSI is implied when the causative pathogen is acquired nosocomially. The transmission may occur through direct contact or indirectly via hospital personnel (hand carriage of *Candida* strains of healthcare worker, intravascular catheters and parenteral hyperalimentation) (Hedderwick *et al.*, 2000; Hota, 2004).

Candida BSIs occur when *Candida* spp. opportunistically penetrates the bloodstream through breaks or cuts in the skin or mucinous membranes. When *Candida* cells enter the bloodstream, they easily spread

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