Genetic relatedness of Candida albicans bloodstream infection clinical isolates in Malaysia

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Received March 9 2015; Received in revised form 6 April 2015; Accepted 8 April 2015

ABSTRACT

Aims: The aim of this study was to investigate the genetic relatedness of the most prevalent Candida bloodstream infection (BSI) species 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 (SAh) value 0.733±0.172]. Following in-depth analysis, five of the 14 isolates were observed to be identical (SAh values of 1.00 each), four isolates had SAh values of 0.80-0.99, indicating that they are highly similar, but are non-identical, while five isolates are unrelated (SAh 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, leukenemia, organ transplantation and patients undergoing chemotherapy) has heightened the need for more 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; Hata, 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