Distribution and antifungal susceptibility profile of four medically important *Candida* species isolated from blood cultures in a tertiary medical centre in Kuala Lumpur

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ABSTRACT

Objectives: To investigate the distribution and antifungal susceptibility patterns of major Candida species causing candidemia in HCTM. **Methods:** Sixty-six *Candida* isolates were obtained from blood cultures between March 2021 and January 2022. Identity of species were determined by VITEK 2 YST and confirmed by PCR amplification of the internal transcribed spacer regions 1 (ITS1) and 2 (ITS2), including the 5.8S rRNA. Antifungal susceptibility was determined by Sensititre YeastOne YO-10. **Results:** Out of 66 isolates, non-albicans *Candida* (NAC) species were the most prevalent (66.7%). However, as a single species, *C.albicans* was still the most common organism (n = 22, 33.3%), followed by *C.glabrata* (n = 17, 25.8%), *C.tropicalis* (n = 15, 22.7%) and *C.parapsilosis* (n = 12, 18.2%). In comparison with *C.albicans* which had only one isolate showing resistance (only to flucytosine), NACs were far more resistant. *C.glabrata* had only one isolate susceptible to itraconazole, none to fluconazole and 94.1% to echinocandins. *C.tropicalis* showed low susceptibility to azoles, with 33%, 20% and 60% to voriconazole, itraconazole, and 83% to fluconazole. All isolates remained susceptible to amphotericin B with minimum inhibitory concentrations of 0.25-1 µg/ml. **Conclusions**: Majority of candidemia cases were caused by the more resistant NAC species. C.albicans remained susceptible to antifungal agents, while *C.glabrata* and *C.tropicalis* showed resistance to triazoles at a concerning rate. This may warrant the usage of echinocandins as empirical treatment for NACs before finalisation of antifungal agents.

Keywords: candidemia, antifungal susceptibility, non-albicans Candida species