

***Candida auris*: A global health threat identified in Malaysian Hospitals**

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ABSTRACT

Introduction: *Candida auris* has emerged as a formidable global health threat, characterized by its multi-drug resistance, high transmissibility, and significant mortality rates. In this study, we aiming to understand characteristics, genetic relatedness and resistance profiles of local *C. auris* isolates. **Materials and Method:** A total of seven suspected *Candida auris* isolates were isolated from clinical specimens and subjected to various identification methods such as conventional, biochemical and molecular methods. Molecular analysis using polymerase chain reaction (PCR) targeting specific fungal genes (ITS and LSU regions). The DNA was extracted and amplified, followed by Sanger sequencing for species identification. Additionally, phylogenetic analysis was employed to study genetic relatedness among *C. auris*, reference and other genetically related isolates. Antifungal susceptibility testing was performed to assess the susceptibility profile of *C. auris* isolates against commonly used antifungal agents. **Results:** Utilizing various identification techniques, we accurately identified seven *C. auris* isolates and differentiate them from other closely genetic related species. Phylogenetic analysis showing the genetic relationships between our local, global and type strains of *C. auris* isolates, as well as genetically closely related species. Our antifungal susceptibility pattern highlights a concerning prevalence of antifungal resistance, particularly to commonly used treatments such as fluconazole and amphotericin B. **Conclusion:** This study highlights the critical importance of improving diagnostic tools and developing new antifungal treatments to address the growing threat of *C. auris* in Malaysia. Phylogenetic analysis suggests that Malaysian isolates may be connected to global clonal lineages, indicating potential cross-border transmission. These findings stress the need for rigorous infection control and effective surveillance to prevent the spread of this pathogen.