Molecular epidemiology and antifungal resistance of Candida pathogens

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ABSTRACT:
Invasive candidiasis (IC) is a major cause of morbidity among immunocompromised adults and very low birth weight neonates. IC is of major public health importance because it is associated with increased mortality, higher health care costs, and increased patient length of stay compared with other common healthcare-associated infections. This problem is compounded by the progressive increase in antifungal resistance among most clinically relevant *Candida* spp. such as *C. albicans, C. parapsilosis, C. glabrata, C. tropicalis*, and *C. auris* driven primarily by the widespread use of antifungal drugs in human healthcare. Whole genome sequencing (WGS) has been demonstrated to be a powerful tool in the identification of mycoses and in deciphering molecular mechanisms responsible for antifungal resistance. Also, genome-wide SNP profiles can provide finely resolved genotypes that correlate with their phenotypes. This study uses WGS data to determine the molecular epidemiology and the drug resistance mutations from emerging *C. auris* in Qatar. Over one hundred samples isolated from the patients, including those infected with SARS-CoV-2, and the hospital environment were sequenced by Illumina NextSeq. Genomic SNPs revealed that all isolates belonged to the Indian lineage, which could be originated from the expatriate labour from South Asia. The genetic variability among the isolates was low but comprised of more than one genetic cluster. The environmental isolates were identical to the clinical isolates, and the isolates from patients of different hospitals/outbreaks clustered together, suggesting the transmission of *C. auris* could be linked to infected/colonized patients and the hospital environment. Mutations in *ERG11* and *TAC1b* associated with azole and other mutations related to echinocandin resistance are also discovered.

KEYWORDS:
Genomics; candidiasis; antimicrobial resistance; epidemiology; azoles variants