

Phenotypic and genotypic diversity of yeast isolated from cancer patients and their environment and their antifungal sensitivity pattern

ZAHRAA DAWOOD GATEA AL-DARRAJI^{1*}, MOHANAD KHALAF MOHAMMED-AMEEN²

¹Department of Biology, College of Science, University of Basrah, Basrah, Iraq. Tel.: +964-7712598464, *email: hm992069@gmail.com

²Department of Biology, College of Science, University of Basrah, Basrah, Iraq

Manuscript received: 31 May 2023. Revision accepted: 30 July 2023.

Abstract. Al-Darraj ZDG, Mohammed-Ameen MKM. 2023. Phenotypic and genotypic diversity of yeast isolated from cancer patients and their environment and their antifungal sensitivity pattern. *Biodiversitas* 24: 4166-4174. This study aimed to investigate yeast diversity and their antifungal susceptibility patterns in 853 samples collected from cancer patients, their apparently healthy companions, their beds, their tables, and indoor hospital air. The samples were cultured and identified using classical phenotypic characteristics and a molecular method utilizing amplification of ITS conservative regions of rRNA. The sum of phenotyping and genotyping identification revealed that 102 yeast isolates included 6 genera and 14 species. *Candida* sp. was the most dominant genera (84.31%), followed by *Naganishia* sp. (10.78%). *Candida albicans* (24.50%) and *C. krusei* (16.66%) were the most prevalent yeast species. Fluconazole, caspofungin, and voriconazole exhibited potent antifungal activities against the most yeast species with low minimum inhibitory concentration (MIC) values compared with high MIC (64 µg/mL) values against *Meyerozyma guilliermondi*, *Naganishia difflunes*, and *C. tropicalis*. To conclude, the antifungal activity was isolate- and species-specific and the higher antifungal concentrations led to a more-rapid expression of activity. The high isolation rate of yeasts from beds and tables, advocated the use of various monitoring systems to ensure thorough cleaning and consistent disinfection of surfaces around patients and health care providers. The study findings showed that the molecular method was superior to the phenotyping technique in identifying yeast isolates. While similar research has been performed in different locations, the current project represents a unique milestone for this particular institution, and offers an opportunity to advance research in this area.

Keywords: Antifungal, cancer patients, environment, genotyping, phenotyping, yeasts

INTRODUCTION

A diverse variety of biological contaminants, including bacteria, fungus, viruses, algae, insects, and their byproducts, including endotoxins, mycotoxins, volatile organic compounds, etc., can be found in the indoor air environment (Moldoveanu 2015; EPA 2020). Biological pollutants have been divided into groups based on their potential to cause allergic, infectious, poisonous, or inflammatory reactions in people. Biological contamination in the interior environment and its possible origins in the development of various illnesses are currently not well known (Kumar et al. 2021). Bioaerosols are biologically produced aerosols such as metabolites, poisons, or microbe fragments that are widespread in the environment. International interest in bioaerosols is increasing quickly in order to further develop the comprehension of their identification, quantification, distribution, and health implications (e.g., infectious and respiratory disorders, allergies, and cancer) (Kim et al. 2018). Bioaerosols may contain pathogenic and/or non-pathogenic dead or alive microorganisms (e.g., viruses, bacteria, and fungi) (Karimpour Roshan et al. 2019). Bioaerosols have a tiny size and light weight; therefore, they are easily transported from one habitat to another (Van Leuken et al. 2016).

Microorganisms are commonly found everywhere in the environment, including hospital wards, and they are critical for human health. As a result, it is critical to

analyze microorganisms in hospital air both quantitatively and qualitatively (Montazeri et al. 2020). The exposure to a high inoculum of fungi in their natural habitat is another key socioeconomic and geocological factor that affects the prevalence and incidence of fungal infection globally (Bongomin 2017). The incidence of fungal infections has increased in the last decade, owing in part to recent medical advances such as increased survival of immunocompromised patients, widespread use of antibiotics, immunosuppressors, or medical devices such as catheters (Gabaldón and Carreté 2016; Rayens and Norris 2022).

Yeasts are becoming more prevalent, especially for those suffering from cancer, immune deficiency syndrome, renal failure, or who take immunosuppressive medications (Calderone and Fronzi 2001). For instance, there are over 30 different species among the etiological causes of invasive Candidiasis (Gabaldón et al. 2016), while more than half are regarded as extremely uncommon (i.e., 0.1% of cases). As a consequence, the concept of emerging fungal pathogens is now prevalent (Papon et al. 2013). Clinical diagnosis of nosocomial *Candida* infections is challenging, and treatment is ineffective. As a result, it's critical to obtain a quick and correct laboratory diagnosis in order to administer the proper antifungal therapy (Sharma and Aggarwal 2013). Opportunistic yeasts are highly similar related species, and due to the numerous limitations of traditional yeast identification methods, they are frequently misidentified or reported as unknown yeast