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CLINICAL BRIEF

Emerging fungal pathogen: *Candida auris*

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Fungal infections cause over 1.5 million deaths per year, and a quarter million of these deaths are caused by the genus *Candida* [1]. The mortality rate of invasive candidiasis (infections by *Candida*) can be greater than 40% due to limited treatment options and increased antifungal resistance [1].

Since 2009, *Candida auris* emerged across six continents and evolved simultaneously as five distinct geographic clades [2, 3]. *Candida auris* has become a global threat as it can colonize the skin, medical devices and hospital environments, causing nosocomial outbreaks of blood and urinary tract infections worldwide (Fig. 1) [2].

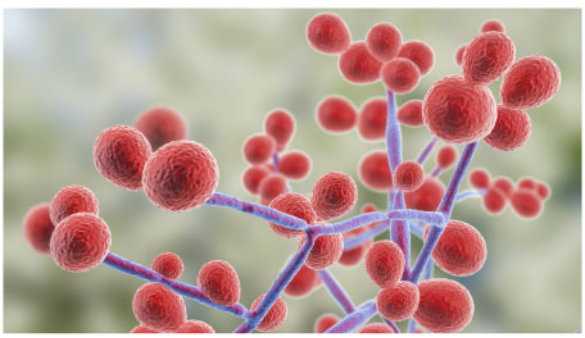

Figure 1. Illustration of yeast pathogen *Candida auris*

Evolutionary perspectives

Most fungal pathogens of humans and other mammals are opportunistic pathogens. Mammals are endothermic and have a high basal body temperature relative to the surrounding environment that limits infections by the majority of environmental fungi. *Candida auris* is distinct from most environmental fungi in that it thrives at mammalian body temperatures, enabling its rapid adaptation to mammalian hosts [4, 5]. Rising global temperatures due to anthropogenic climate change may have selected for thermotolerant strains of *C. auris*, leading to its emergence as a pathogenic fungus in humans across a wide geographic range [4–6]. *Candida auris* was recently identified in a salt marsh and sandy beach, a plausible reservoir in which it may have adapted to a warm, high salinity environment [7]. Adaptation to such an environment may have enabled *C. auris* to persist on the skin due to its thermal and salt tolerance.

Candida auris can spread among patients in hospitals and is intrinsically resistant to one or more classes of antifungals, which makes it particularly difficult to treat in health care settings [8]. The acquisition of multi-drug resistance could be due to the mis/overuse of antifungal drugs [8]. Comparative genomics demonstrated that *C. auris* has expanded families of transporters and lipases as well as mutations and copy number variants in genes/enzymes linked to increased resistance and virulence [2]. Investigating the fitness trade-offs in traits that confer resistance and virulence in *C. auris* would be beneficial to understanding the evolutionary potential of pathogenic strains.

Future implications

Pathogenic fungi pose a great threat to immunocompromised individuals, such as people living with human immunodeficiency virus (HIV) and solid organ transplant recipients [7]. Clinical evidence suggests that patients receiving novel immunotherapies for cancer may also be particularly susceptible to fungal infections [9], and secondary

fungal airway infections, such as candidiasis and aspergillosis, have been documented in COVID-19 patients [10]. Understanding the evolution of emerging fungal pathogens like *C. auris* will be useful for the design of antifungal drugs and therapies for susceptible patients, potentially improving clinical outcomes.

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