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Editorial

Candida auris: An Emerging Challenge in Clinical Mycology and Public Health in Latin America

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ABSTRACT

Candida auris is an emerging fungus that poses a critical challenge in clinical mycology and global public health. Identified in 2005, this pathogen has caused hospital outbreaks due to its resistance to multiple antifungals and ability to persist in hospital settings. In Latin America, *C. auris* has been reported since 2012 in several countries, including a case in Ecuador in 2024. Its emergence has been linked to climate change and the excessive use of antifungals, which could be favoring its proliferation. The diagnosis of *C. auris* is complex and requires advanced methods such as MALDI-TOF mass spectrometry and molecular techniques due to its phenotypic variability. Another factor to be relevant to public health is resistance to conventional treatments. In addition, genomic surveillance is essential to understand the epidemiology of this pathogen and control its spread in hospital settings. Urgent prevention, detection, and treatment measures are necessary to limit the spread of *C. auris* in the region and minimize its impact on public health. Implementing comprehensive strategies, including genomic surveillance and advanced diagnostic techniques, is crucial to address this emerging problem in Latin America.

Keywords: *Candida auris*, Fungal infections, Antifungal resistance, Clinical mycology, Genomic surveillance, Latin America.

INTRODUCTION

Candida auris is an emerging fungus that has garnered global attention due to its significant impact on clinical mycology and public health. First identified in Japan in 2005 [1], this pathogen has been responsible for numerous hospital outbreaks worldwide, notable for its resistance to multiple antifungal agents[2–4]. Its ability to colonize hospital environments and cause severe infections in vulnerable patients has raised serious concerns within the medical community. The high mortality rate associated with these infections, combined with the challenges in diagnosis and treatment, underscores the need for rigorous epidemiological surveillance and effective control strategies [2,3,5,6]. In Latin America, the rapid and concerning spread of *C. auris* highlights the importance of addressing this issue from a regional and global perspective [7,8]. This editorial explores the

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epidemiology, risk factors, clinical presentation, diagnosis, treatment, genomic surveillance, and phylogeny of *C. auris*, emphasizing the urgent need for comprehensive measures to manage it in the region.

Phylogeny and Global Distribution of *Candida auris*

Candida auris has emerged as a globally concerning pathogen, exhibiting a complex phylogeny that highlights its remarkable ability to adapt and spread in diverse environments. Phylogenetically*, C. auris* is closely related to species like *Candida haemulonii,* yet it is distinctly characterized by significant genetic variations that justify its classification as a separate species (Table 1A) [9,10].

Four main lineages of *C. auris* have been identified, each associated with a distinct geographic region: the South Asian clade, the East Asian clade, the African clade, and the South American clade [10,11]. These lineages demonstrate the genetic diversity within the species and reflect geographic dispersal patterns that may influence both virulence and antifungal resistance. Additionally, recent studies have identified new lineages linked to regions such as Iran (fifth clade) and Singapore/Bangladesh (sixth clade), suggesting greater complexity in the genetic structure of this species [10].

The global spread of *C. auris* is alarming, with reports of cases in over 40 countries since its identification in Japan in 2005. Its presence across multiple continents, including outbreaks in Venezuela, Colombia, India, South Africa, and more recently Ecuador, underscores its ability to persist in hospital environments and resist conventional antifungal treatments. Its nosocomial transmission and ability to colonize inert surfaces facilitate this widespread distribution. Understanding the phylogeny and global distribution of *C. auris* is crucial for developing effective control strategies. Different lineages may exhibit variations in antifungal resistance, making it essential to tailor therapeutic and preventive interventions according to the pathogen's genetic diversity [6,7,10].

Superkingdom	**Eukaryota**	**Identification Method**	**Fungal misidentification**
Reino	Fungi	Vitek 2 YST	*Candida haemulonii* *Candida duobushaemulonii*
Kingdom	*Ascomycota*	API 20C	*Rhodotorula glutinis* *Candida sake*
Class	*Saccharomycetes*	API ID 32C	*Candida intermedia* *Candida sake* *Saccharomyces kluyveri*
Order	*Saccharomycetales*	BD Phoenix yeast	*Candida haemulonii* *Candida catenulata*
Family	*Metschnikowiaceae*	MicroScan	*Candida famata* *Candida guilliermondii* *Candida lusitaniae* *Candida parapsilosis*
Genus	*Candida or Metschnikowiaceae*	RapID Yeast Plus	*Candida parapsilosis*
Species	*auris*		
A) Information adapted from taxonomy, National Library of Medicine.		B) Misidentification by different automated methods for *Candida auris*, according to Center for Disease Control and Prevention (CDC) data.	

Table 1.- *Candida auris* taxonomy and automated or semi-automated microbiological identification methods.

Epidemiology of *Candida auris* in Latin America

Since its first outbreak in Venezuela in 2012, *Candida auris* has rapidly spread across Latin America. Countries such as Colombia, the United States, Panama, Canada, Chile, and Costa Rica have reported subsequent cases, with a recent outbreak in Ecuador in February 2024, according to an unpublished epidemiological bulletin [7,8]. This fungus is known for its ability to persist on inanimate surfaces and resist disinfection, facilitating its transmission in hospitals. Its resistance to multiple antifungal agents complicates outbreak control and increases associated mortality. Furthermore, limited infrastructure and resource constraints in some countries hinder the implementation of effective surveillance and control measures. The rapid dissemination of *C. auris* in the region highlights the need for a coordinated response that includes epidemiological surveillance, healthcare worker training, and access to advanced diagnostic tools to prevent and control the spread of this emerging pathogen [8].

Climate Change and the Emergence of *Candida auris*

Climate change has been identified as a critical factor in the emergence of *Candida auris* [7]. Changes in climate, such as rising temperatures, may have created more favorable conditions for the proliferation of *C. auris*. This fungus has shown a remarkable ability to survive at elevated temperatures, suggesting a possible thermal adaptation linked to climate change. Furthermore, the extensive use of antifungals in agriculture and medicine has exerted selective pressure on various fungal species, promoting the emergence of resistant strains. *C. auris* has demonstrated resistance to multiple antifungals and an ability to persist in hospital environments, increasing its potential for nosocomial transmission. These dynamics highlight the need to consider climate change as a contributing factor in the evolution and emergence of fungal pathogens and underscore the urgency of integrating human, animal, and environmental health into mitigation strategies [12,13].

Infection Risk Factors

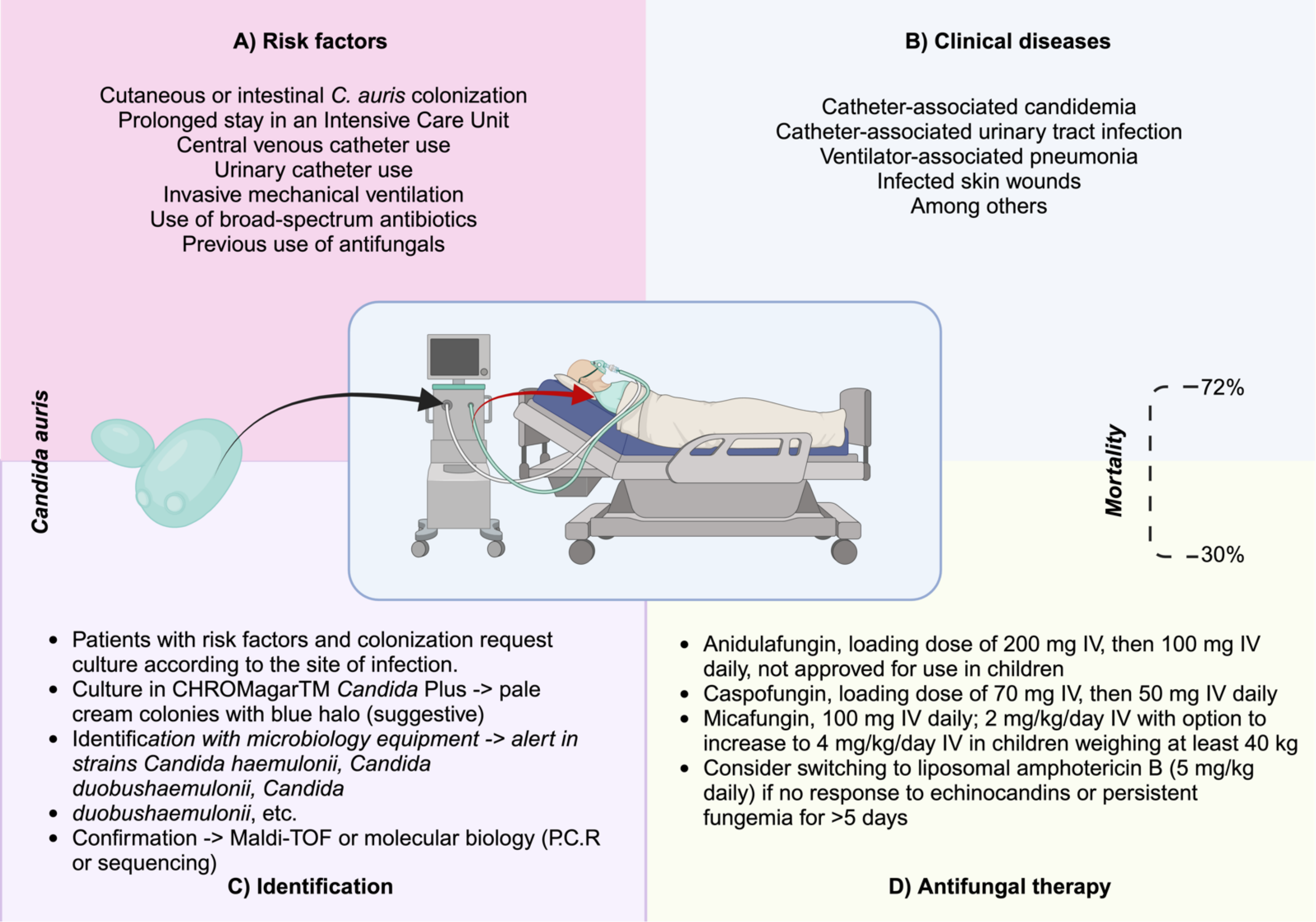
Key risk factors include prior colonization, prolonged stays in intensive care units, and invasive medical devices such as catheters and ventilators [4,6,13]. Immunosuppression, recent surgeries, and previous exposure to antibiotics and antifungals also significantly increase the risk of infection (Figure 1A). Patients in intensive care, especially those with multiple comorbidities, are particularly vulnerable. The ability of *C. auris* to persist on surfaces and medical devices facilitates its spread in hospital environments, making infections caused by this fungus a significant challenge in managing healthcare-associated infections (HAIs). Identifying and managing these risk factors is crucial to reducing the incidence of *C. auris* infections and improving hospital preventive measures [2,14].

Clinical Presentation

Infections caused by *Candida auris* present with nonspecific clinical symptoms, complicating both diagnosis and treatment [2,9,13–15]. Patients typically experience fever and chills that do not respond to conventional antimicrobial therapy (Figure 1B), potentially delaying appropriate diagnosis [2,14]. *C. auris* can cause severe invasive infections in the bloodstream, wounds, and other organs and is particularly dangerous due to its high mortality rate [2]. Its ability to form biofilms on medical devices such as catheters and ventilators contributes to its persistence and resistance to treatment [13]. Since *C. auris* infections can mimic other fungal infections, it is crucial to consider this pathogen in patients not responding to antibiotic and antifungal treatments.

Diagnosis and Treatment of *Candida auris*

Diagnosing *Candida auris* is complex due to its tendency to be misidentified as other *Candida* species using conventional methods (Table 1B) [5,9]. Advanced techniques such as MALDI-TOF mass spectrometry and Polymerase Chain Reaction (PCR) are essential for accurate identification (Figure 1C). These tools facilitate faster diagnosis and are crucial for guiding appropriate treatment. *C. auris* is resistant to multiple classes of antifungals, making treatment challenging [3,9,14]. An antifungal susceptibility test is critical to determine the fungus's resistance profile and guide treatment choices [2,3]. Resistance to azoles, echinocandins, and amphotericin B is standard, limiting therapeutic options (Figure 1D). However, the drug ibrexafungerp has shown *in vitro* efficacy against *C. auris*, offering a promising new treatment option [3,4,13–15]. Ongoing research is necessary to develop new therapies and address the growing antifungal resistance.



A) Risk factors

Cutaneous or intestinal *C. auris* colonization
Prolonged stay in an Intensive Care Unit
Central venous catheter use
Urinary catheter use
Invasive mechanical ventilation
Use of broad-spectrum antibiotics
Previous use of antifungals

B) Clinical diseases

Catheter-associated candidemia
Catheter-associated urinary tract infection
Ventilator-associated pneumonia
Infected skin wounds
Among others

- Patients with risk factors and colonization request culture according to the site of infection.
- Culture in CHROMagarTM *Candida* Plus -> pale cream colonies with blue halo (suggestive)
- Identification *with microbiology equipment -> alert in strains Candida haemulonii, Candida duobushaemulonii, Candida*
- *duobushaemulonii*, etc.
- Confirmation -> Maldi-TOF or molecular biology (P.C.R or sequencing)

C) Identification

- Anidulafungin, loading dose of 200 mg IV, then 100 mg IV daily, not approved for use in children
- Caspofungin, loading dose of 70 mg IV, then 50 mg IV daily
- Micafungin, 100 mg IV daily; 2 mg/kg/day IV with option to increase to 4 mg/kg/day IV in children weighing at least 40 kg
- Consider switching to liposomal amphotericin B (5 mg/kg daily) if no response to echinocandins or persistent fungemia for >5 days

D) Antifungal therapy

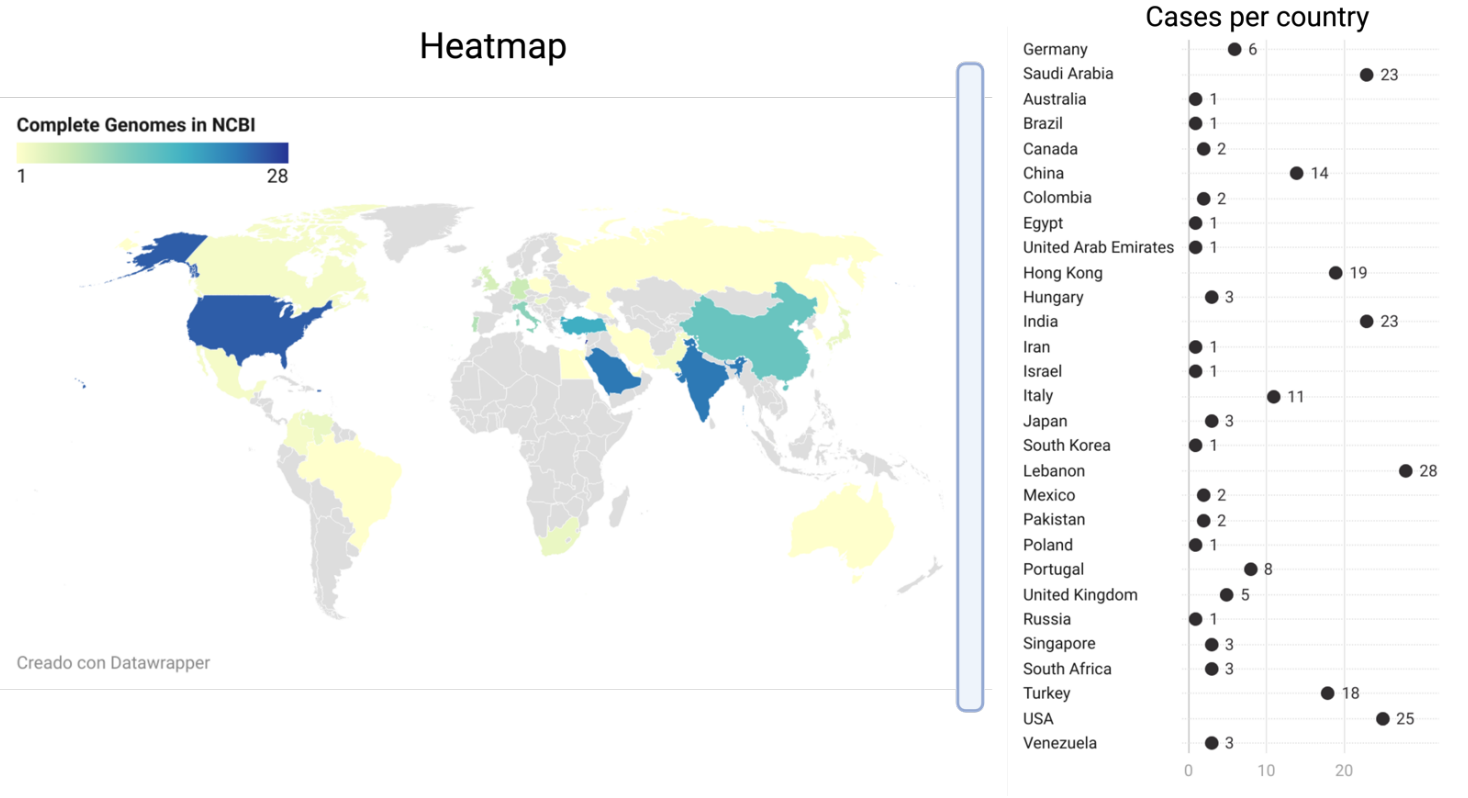
Figure 1. Evidence-based depiction of *Candida auris* infection. A) Risk factors for *C. auris* infection. B) Most common clinical diseases. C) Laboratory identification recommendations. D) CDC-recommended therapy. The budding yeast of *C. auris* is green and can colonize hospital environments and medical devices such as ventilators, central venous catheters, and urinary catheters. The red arrow indicates transmission from these devices to the patient with risk factors, facilitating invasion and infection—image created in Biorender.

Importance of Genomic Surveillance

Genomic surveillance is a vital tool in controlling *Candida auris*. Whole-genome sequencing allows for the identification of genetic variants and antifungal resistance genes, which is crucial for understanding the epidemiology of *C. auris* and its capacity to spread [16]. It also aids in identifying specific lineages and tracking outbreaks in hospital settings, enabling a rapid and effective response to new cases and helping to mitigate its impact on global health [16].

Currently, the NCBI (National Center for Biotechnology Information) database contains 212 complete *C. auris* genomes from 29 countries (Figure 2), emphasizing the importance of global genomic surveillance. This approach allows for a detailed analysis of the pathogen's epidemiology and more effective therapeutic strategies based on the early identification of antifungal resistance genes [16, 17].

Integrating genomic surveillance into *C. auris* diagnostic and treatment protocols are critical for strengthening control measures and improving available therapies. By leveraging the growing accessibility of nextgeneration sequencing technologies, public health systems can anticipate the pathogen's evolution and reduce its impact on human health, especially in increasing antifungal resistance. Therefore, genomic surveillance represents an advanced and comprehensive strategy for preventing and treating infections caused by this pathogen [16, 17].



Distribution by Country of 212 Complete *Candida auris* Genomes Uploaded to the NCBI Database (National Center for Biotechnology Information). Update Date: September 4, 2024.

Figure 2. Heatmap of Complete *Candida auris* Genomes in NCBI by Country.

CONCLUSIONS

The spread of *Candida auris* in Latin America represents a critical challenge for public health and clinical mycology. Its resistance to multiple antifungals and its ability to persist in hospital environments and cause severe infections underscores the need for a comprehensive response that includes epidemiological surveillance, advanced diagnostics, appropriate treatment, and genomic monitoring. Climate change and the overuse of antifungals have contributed to the emergence of this pathogen, reinforcing the need to consider these factors in mitigation strategies. Accurate identification of *C. auris*, combined with understanding its phylogeny and implementing new therapies, is crucial to controlling its spread and reducing its impact on human health. Collaboration between health systems and ongoing research is essential to address this emerging challenge and protect public health in the region.

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NCBI database, created the heatmap, included perspectives on genomic surveillance, and reviewed and approved all manuscript versions.

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