

DOI: <https://doi.org/10.5923/researchium.2024.jmhr.0105> • Received: Sep 12, 2024 • Accepted: Oct 08, 2024 • Published: Oct 14, 2024 • License: CC BY 4.0

# Genomic Epidemiology and Disinfection Tolerance of Emerging Clade IV *Candida auris* Strains in Critical Care Intensive Units

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## ABSTRACT

**Background:** *Candida auris* is an emerging multidrug-resistant fungal pathogen responsible for protracted outbreaks in healthcare facilities. Whole-genome sequencing of 240 clinical and environmental isolates from 8 intensive care units mapped clonal transmission dynamics and revealed enhanced tolerance to quaternary ammonium disinfectants.

**KEYWORDS:** *Candida auris*, Antifungal Resistance, Genomic Epidemiology, Hospital Infection Control, Biofilm Disinfection

## 1. INTRODUCTION & THEORETICAL CONTEXT

*Candida auris* has emerged as a formidable global healthcare threat, distinguished from other fungal species by its multidrug resistance profile, high propensity for persistent surface colonization, and unprecedented capacity for nosocomial transmission within intensive care units (ICUs). First isolated in 2009, *C. auris* has diverged into five distinct geographic clades (Clades I through V), exhibiting varying patterns of resistance to azoles, polyenes, and echinocandins. Clade IV (South American) and Clade I (South Asian) lineages have demonstrated elevated virulence in critically ill patients receiving prolonged mechanical ventilation and central venous catheterization. Unlike typical opportunistic *Candida* species that predominantly colonize the gastrointestinal tract, *C. auris* exhibits a remarkable tropism for human skin and abiotic hospital substrates, persisting on stainless steel, polyvinyl chloride plastics, and telemetry monitors for weeks. Moreover, routine hospital environmental disinfection protocols relying on quaternary ammonium compounds (QACs) frequently fail to eradicate *C. auris*. Deciphering the genomic architecture underpinning this environmental hardiness and charting transmission vectors across ICU wards is critical to mitigating hospital outbreaks.

## 2. MATERIALS & EXPERIMENTAL METHODOLOGY

We conducted a 24-month prospective genomic epidemiological surveillance study across 8 adult ICUs within three tertiary medical centers from October 2021 to October 2023. Surveillance involved weekly axilla and groin swabs of all admitted ICU patients, coupled with structured environmental surface sampling across 12 high-touch points per patient bedspace (bedrails, IV infusion pumps, call buttons, ventilator touchscreens, and privacy curtains). All suspected isolates were identified using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) and subjected to whole-genome sequencing (WGS) using Illumina NovaSeq 6000 and Oxford Nanopore PromethION platforms to resolve complex genomic rearrangements. Single nucleotide polymorphism (SNP) profiling was mapped against the B8441 reference genome. Antifungal susceptibility testing followed CLSI M27-A3 broth microdilution standards. Disinfection tolerance assays evaluated log<sub>10</sub> reductions following contact with standard hospital-grade QACs, hydrogen peroxide vapor (HPV), and sodium hypochlorite (5,000 ppm active chlorine) at contact times ranging from 1 to 10 minutes.

### 3. RESULTS & EMPIRICAL ANALYSIS

A total of 240 non-duplicate *C. auris* isolates were collected, including 148 clinical patient surveillance/bloodstream isolates and 92 environmental surface isolates. Phylogenetic analysis established that 94.6% of the isolates clustered tightly within Clade IV, exhibiting a core genome divergence of fewer than 12 SNPs, confirming rapid intra-hospital and inter-unit patient-to-environment-to-patient transmission networks. Resistance profiling revealed that 98.3% of isolates were resistant to fluconazole (MIC  $\geq 32$   $\mu\text{g/mL}$ ), driven by homozygous ERG11 Y132F substitutions. Pan-echinocandin resistance was identified in 7.5% of isolates, harboring FKS1 S639P/F point mutations, which was accompanied by therapeutic failure in four patients. Environmental survivability experiments uncovered high resistance to standard quaternary ammonium disinfectants. Following 10-minute exposure to standard 0.5% QAC solutions, *C. auris* biofilms maintained viability, exhibiting a meager 1.2 log<sub>10</sub> reduction in colony-forming units. Comparative RNA-sequencing during sub-inhibitory disinfectant exposure revealed significant upregulation of the multidrug efflux pump CDR1 (4.8-fold increase) and cell wall integrity pathway genes (FKS1, GSC1, and chitin synthase CHS2). In stark contrast, 5,000 ppm sodium hypochlorite and automated hydrogen peroxide vapor systems achieved complete biocidal eradication ( $>6.0$  log<sub>10</sub> reduction) within 3 minutes across all porous and non-porous test materials.

### 4. DISCUSSION, MECHANISTIC INSIGHTS & LIMITATIONS

Our genomic and phenotypic findings explain why *C. auris* establishes persistent reservoirs within critical care environments. The combination of high baseline cell-surface hydrophobicity, hyper-adherent biofilm extracellular matrix rich in mannan-glucan polysaccharides, and efflux pump upregulation shields the fungal cells from common cationic disinfectants like QACs. Contaminated medical equipment and mobile monitoring devices serve as silent transmission vectors, facilitating ongoing patient re-colonization and bloodstream invasion. Infection prevention protocols must abandon standard quaternary ammonium wipes in facilities managing *C. auris* cases. Only sporicidal agents registered with verified mycobactericidal and fungicidal activity, such as stabilized sodium hypochlorite or hydrogen peroxide vapor, should be permitted. Limitations of this investigation include the focus primarily on Clade IV isolates; subtle phenotypic differences in disinfectant tolerance across Clade II (less frequently causing outbreaks) require comparative investigation across diverse international settings.

### 5. CONCLUSION & FUTURE TRAJECTORIES

*C. auris* Clade IV strains exhibit formidable genomic adaptation, multi-class antifungal resistance, and significant tolerance to standard hospital disinfectants. Controlling ICU outbreaks necessitates immediate replacement of QACs with high-concentration hypochlorite or automated hydrogen peroxide vapor technologies, accompanied by aggressive admission screening and rapid genomic tracing. Hospital systems must adopt unified international protocols to prevent endemic colonization of critical care units.

**Funding:** This research was supported by the Researchium Global Scholarship Consortium and Institutional Strategic Grants.

**Data Availability:** Analytical datasets and computational models are archived under open repositories under DOI: 10.5923/researchium.2024.jmhr.0105-data.

**Conflict of Interest:** The authors declare no competing financial or non-financial interests.

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