

Genomic Surveillance of *Candida auris*, Aga Khan University Hospital

Quarter 4 (Oct – Dec), 2024

Too few isolates to render phylogenetic tree

Too few isolates to render map

All Candida auris isolates were cultured from diagnostic clinical specimens at The Aga Khan University Hospital mycology laboratory in the indicated time period. All isolates are first specimens collected from separate individuals. The phylogenetic tree represents a midpoint-rooted maximum likelihood analysis from whole genome sequences. All sequenced C. auris isolates to date belong to Global Clade 1. Circle colors indicate region of residence for the individual from which the isolate was cultured, also shown on the map. Squares indicate the hospital, each assigned a random two-letter code, where the specimen was collected. Triangle colors indicate the origin of the specimen. Hexagon colors indicate phenotypic antifungal susceptibility to fluconazole (FLU), amphotericin B (AMB) or to one or more of the echinocandin class of antifungals (ECH). Minimum inhibitory concentration breakpoints as per US CDC (<https://www.cdc.gov/candida-auris/hcp/laboratories/antifungal-susceptibility-testing.html>). If an isolate is resistant to one or more of the echinocandin antifungal medications anidulafungin, caspofungin, or micafungin, it is considered resistant to the echinocandin class. Supported by US CDC award NUH3HCK000007 to the Center for Pathogen Genomics and Microbial Evolution at Northwestern University (Chicago, USA), Lurie Children's Hospital (Chicago, USA), and The Aga Khan University (Karachi, Pakistan).