Azole exposure within 90 days	11 (19)	10 (21)	1 (9)	0.367
Chronic wounds	48 (81)	38 (79)	10 (91)	0.367
Indwelling devices	52 (88)	44 (92)	8 (73)	0.080
Vascular access*	35 (59)	30 (63)	5 (45)	
Percutaneous endoscopic gastrostomy	25 (42)	22 (46)	3 (36)	
Indwelling urinary catheter	29 (49)	26 (54)	3 (36)	
Other	16 (27)	14 (29)	2 (18)	
Tracheostomy within 30 days	22 (37)	18 (38)	4 (36)	0.944
Mechanical ventilation within 30 days	34 (58)	29 (60)	5 (45)	0.365
Abdominal surgery within 30 days	8 (14)	7 (15)	1 (9)	0.631
Gastrointestinal tract leak/perforation	8 (14)	6 (13)	2 (18)	0.620
***C. auris* characterization, n (%)**				
Specimen source				
Axilla/groin	41 (70)	41 (85)	0	
Blood	9 (15)	0	9 (82)	
Wound	4 (7)	2 (4)	2 (18)	
Respiratory	4 (7)	4 (8)	0	
Urine	1 (2)	1 (2)	0	
Testing Location				0.071
Acute care hospital	36 (61)	25 (52)	11 (100)	
Long-term acute care	14 (24)	14 (29)	0	
Skilled nursing facility	4 (7)	4 (8)	0	
Susceptibility available	6 (10)	1 (2)	5 (45)	
Antifungal treatment	11 (19)	2 (4)	9 (82)	<0.001
Echinocandins	10 (17)	2 (100)	8 (88)	
Azoles	1 (2)	0	1 (11)	
Treatment duration				0.187
1 week	1 (2)	1 (2)	0	
2 weeks	7 (12)	1 (2)	6 (55)	
>2 weeks	3 (5)	0	3 (27)	
30-day mortality, n (%)	10 (17)	8 (17)	2 (18)	0.904

*Central venous catheter, midline, peripherally inserted central catheter

were treated with echinocandins (88%); among the colonized, two (4%) were treated with echinocandins but had persistent colonization. Thirty-day mortality was not significantly different among the two groups and was nearly 20%. **Conclusions:** In this large cohort study, a history of healthcare exposure, drug-resistant organisms, use of broad-spectrum antibiotics, indwelling devices, and chronic wounds were common risk factors among C. auris patients. Limiting the use of broad-spectrum antimicrobials and invasive devices, adherence to infection prevention and control practices, and interfacility transfer communication are important mitigating strategies to reduce the incidence and spread of C. auris.

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Clinical and Genomic Characteristics of Candida auris in Central Ohio: An Insight into Epidemiological Surveillance

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Background: Candida auris is an emerging threat to hospitalized patients and invasive disease is associated with high mortality. This study describes clinical and microbiological characteristics of nine patients identified with C. auris at Ohio State Wexner Medical Center discovered through active surveillance or clinical investigation and uses whole genome sequencing (WGS) to compare isolates. **Methods:** In November 2022, an active C. auris surveillance program was implemented to screen patients admitted to high-risk units (intensive care units and progressive care units). Bilateral axilla and groin swabs were obtained upon unit admission and, if positive, were submitted for C. auris polymerase chain reaction (PCR) with culture and sensitivity testing. Patients with a positive screening or clinical isolate from November 2022 to November 2023 underwent chart review for clinical characteristics, microbiologic data, and index admission information. For each isolate, DNA was extracted and WGS was performed. Core single nucleotide polymorphism (SNP) variation identified from the sequence data was used to infer genetic relationships among the isolates. **Results:** Nine patients were identified between November 2022 and November 2023. The clinical and microbiologic characteristics are summarized in Table 1. All patients were hospitalized at various acute care facilities across the state at least once in the preceding 12 months. C. auris was determined to be present on admission for 6 patients. For 5 of these patients, it was their first interaction with our healthcare system. Three patients were not in contact isolation for >3 days before C. auris was identified. Unit wide point-prevalence screening was completed in these cases and no evidence of transmission was found. WGS showed eight of the nine isolates were related with 28 or less core SNP differences between isolates (Figure 1). One isolate (8) was genetically distinct with >45000 core SNP differences. Five isolates were highly related with a range of 4-15 SNP differences. No temporal or spatial overlap at our institution was identified among these five patients. **Conclusions:** The active surveillance program identified several patients colonized with C. auris in addition to those found through clinical testing. Multiple risk factors for C. auris were identified with high patient mortality (67%). Majority of the isolates were closely related without association with a known outbreak or epidemiologic link, suggesting a possible diffuse common reservoir. Next steps with surveillance in acute care and long-term care facilities will be critical for early detection to halt transmission of this organism.

Table 1. Clinical and Microbiological Characteristics of *C. auris* Isolates

	Clinical Specimen	Screening Specimen
Total (N=9)	4	5
Sex, M	4 (100%)	5 (100%)
Median Age, years (range)	66 (33-72)	63 (48-71)
Site of *C. auris*		
Blood	2	0
Respiratory	2	1
Urine	3	0
Axilla/Groin Screen	1	5
Multiple sites	3	1
Present on admission (<hospital day 4)	2 (50%)	4 (80%)
Admission origin		
Hospital transfer	1	1
SNF	1	1
Long term acute care/acute rehab	1	2
Home	1	1
Travel Interstate	1	0
Travel Abroad	0	0
History of MDRO colonization	4 (100%)	2 (40%)
Indwelling Medical Device	3 (75%)	2 (40%)
Immunosuppressed	3 (75%)	1 (20%)
Antibiotic use in past month	4 (100%)	5 (100%)
Antifungal use in past month	3 (50%)	0 (0%)
Presence of chronic wound	4 (100%)	2 (40%)
Discharge status		
alive	1(25%)	2 (40%)
deceased	3 (75%)	3 (60%)
Isolate Resistance		
Fluconazole R	4	4
Echinocandin S	4	4

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Figure 1: Dendrogram for *C. auris* isolates using core SNPs