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Investigation of a *Candida auris* outbreak in a skilled nursing facility — Virginia, United States, October 2020–June 2021

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Abstract

Candida auris, an emerging multi-drug resistant organism, is an urgent public health threat. We report on a *C. auris* outbreak investigation at a Virginia ventilator skilled nursing facility. During October 2020–June 2021, we identified 28 cases among residents in the ventilator unit. Genomic evidence suggested 2 distinct *C. auris* introductions to the facility. We identified multiple infection and prevention control challenges, highlighting the importance of strengthening multi-drug resistant organism prevention efforts at ventilator skilled nursing facilities.

Keywords

Emerging infectious disease; Ventilator skilled nursing facility; Multidrug resistant organism; Infection prevention and control

BACKGROUND

Candida auris is a multi-drug resistant organism (MDRO) with rising international burden and propensity for transmission in healthcare settings, especially ventilator-capable skilled nursing facilities (vSNFs).^{1–3} During the COVID-19 pandemic, *C. auris* outbreaks have occurred in healthcare facilities across the Mid-Atlantic region of the United States.^{4–7} There are 5 clades of *C. auris*, with clade I predominant within the Mid-Atlantic region.⁸ Before 2020, Virginia Department of Health (VDH) only observed 2 *C. auris* cases. After a year without new cases, VDH identified its third clinical case in June 2020 in acute care hospital A. We performed an investigation at vSNF A, which is in the same healthcare transfer network as hospital A, to identify the potential source of the index case, understand the facility's *C. auris* burden, and implement prevention measures.

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Conflicts of interest: None to report.

METHODS

VDH assisted with case finding and conducted infection prevention and control (IPC) assessments. A case was a resident with a clinical or screening specimen positive for *C. auris* and at the vSNF from October 2020 to June 2021.⁹ Screening cases were residents with *C. auris* groin/axilla swabs that were collected on admission or during biweekly/monthly point prevalence surveys (PPSs) on ventilator and step-down units and were positive via PCR or culture.¹⁰ Clinical cases were residents with clinical specimens positive for *C. auris*. Using laboratory and medical records, data were collected on: positive specimens, patient characteristics, facility location, antifungal susceptibility testing (AFST), and whole genome sequencing (WGS). SAS 9.4 was used to calculate frequency of case characteristics.

RESULTS

VDH identified 39 *C. auris* cases during June 2020 to June 2021, 28 of which were found during the vSNF A investigation from October 2020 to June 2021. Most (93%) vSNF A cases were screening cases (Fig 1). Three clinical cases were identified: 2 from urine and 1 from blood. One clinical case was initially identified as a screening case, but had a positive urine specimen 7 months later. Most cases (93%) were identified in the 46-bed ventilator unit, and 3 of these cases were later transferred to the step-down unit (Table 1). Half of cases changed beds during their stay, but most bed changes were within the same unit. Both units have mostly double-occupancy rooms. Nearly all cases had respiratory failure (96%) and prior colonization/infection with a Carbapenemase-producing organism (89%). No cases had recent health care stays abroad or in other regions.

AFST results were available for 15 isolates; all were resistant to fluconazole. WGS results were available for 8 cases: 5 clade I (average difference of 8 single nucleotide polymorphisms [SNPs]) and 3 clade III (average difference of 11 SNPs). The average difference between clade I and III was 43,523 SNPs. Among cases with WGS results, all 8 were screening cases identified in the ventilator unit, where all were originally admitted. Three cases (2 clade I, 1 clade III) had stays in the same room. Two cases occupied the same bed at different times, but these cases were identified as different clades. Four clade I and 1 clade III cases were male, with average age of 61 and 68, respectively. All 8 had respiratory failure and co-colonization with a Carbapenemase-producing organism.

We identified several IPC breaches, including failure to: implement appropriate contact precautions, cohort residents by MDRO status, and use personal protective equipment. Despite alcohol-based hand sanitizer availability throughout the facility, lapses in staff hand hygiene compliance were observed. The vSNF used *C. auris*-appropriate disinfection products from EPA's List P, but bioburden testing indicated that disinfection was not thorough for high-touch surfaces. The facility lacked a designated infection preventionist for over 6 months.

DISCUSSION

This investigation found 28 cases among residents of 2 high acuity units that were screened. Most cases occurred among residents with risk factors like respiratory failure

and colonization with another MDRO. On-site assessments identified IPC gaps contributing to *C. auris* transmission.^{3-5,10} The facility continues to identify cases and suspected transmission, likely a result of unresolved IPC deficiencies and lack of an infection preventionist.

Cases belonged to 2 identified clades, demonstrating that this facility, specifically the ventilator unit, experienced multiple *C. auris* introductions with subsequent spread of both clades. There is no evidence of cases introducing *C. auris* acquired abroad or in other US regions. The *C. auris* risk factors among cases reflect residents who frequently transfer between facilities, increasing likelihood of introductions from other facilities. Before this cluster, clade I was predominant in the Mid-Atlantic region.⁸ Clade III isolates have recently been identified at other Mid-Atlantic facilities (unpublished CDC data), so clade III may have been introduced by a local resident, not necessarily by a resident from another country or US region. Within each clade, isolates were highly related to others in the region, further suggesting spread between facilities.⁸ Patient characteristics among clade I and clade III cases appeared similar, though few cases had WGS data available. Future research should examine how multiple *C. auris* clades spread in the context of an outbreak.

LIMITATIONS

This investigation was subject to several limitations. Data on room history and domestic healthcare exposures were incomplete. Cases that were not screened could have been missed. WGS results were only available for a subset of cases, so conclusions based on comparisons between clades are limited. Screening cases identified on admission were not distinguished from those during PPS, which would allow for a better understanding of how often *C. auris* was introduced from other facilities and degree of internal transmission.

CONCLUSIONS

Given the persistent *C. auris* burden, vSNF A must prioritize MDRO prevention strategies. The local health department continues to assist with PPSs, admission screenings, addressing IPC barriers, and interfacility communication.¹⁰ VDH routinely communicates with regional partners, as Virginia residents commonly receive care in surrounding jurisdictions. Strong IPC practices in vSNFs are crucial to prevent transmission from known cases and mitigate the risk of unidentified introductions given the high prevalence of *C. auris* in the Mid-Atlantic region.^{3,4,6,7} Future public health education will emphasize that MDRO prevention strategies must remain a priority to control the spread of *C. auris*.

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DISCLAIMER

The findings and conclusions of this paper are those of the authors and do not necessarily represent the official position of the US Centers for Disease Control and Prevention (CDC).

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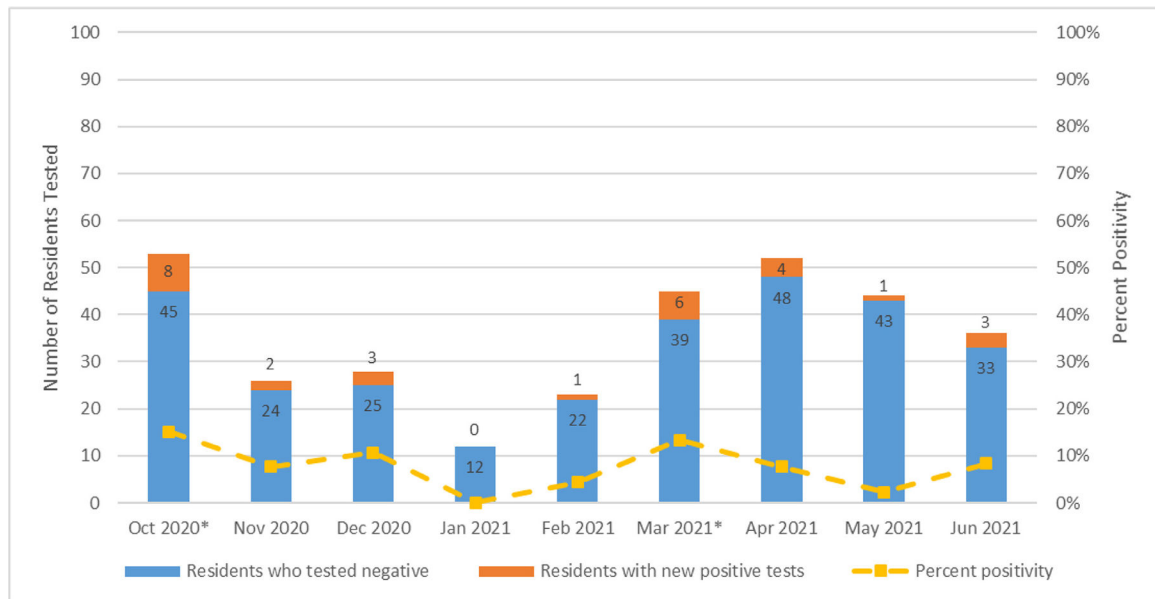


Fig 1.

C. auris colonization screening results^{^†} in vSNF A by month, October 2020-June 2021.

*Designates 1 clinical case identified during the month. One clinical case was identified through a blood specimen and one was identified through a urine specimen.

[^]Includes colonization swabs collected during point prevalence surveys and admission screening.

[†]Percent positivity was calculated based on results from all point prevalence surveys (PPSs), admission screenings, and clinical cases in a given month.

Table 1

Demographic and clinical characteristics of patients colonized or infected by *C. auris* in vSNF A, October 2020 - June 2021 (n = 28)

Characteristic		Count (%)
Male sex		15 (54)
Age, mean (Std dev)		59 (15)
Race/ethnicity	NH Black *	14 (50)
	NH White	9 (32)
	Hispanic	4 (14)
	NH Asian	1 (4)
Comorbidities and risk factors	Total number of underlying comorbidities, average (std dev)	24.0 (9)
	Acute or chronic respiratory failure	27 (96)
	Type 2 diabetes	15 (54)
	Unresponsive wakefulness syndrome †	14 (50)
	Infection/colonization with Carbapenemase-producing organism	25 (89)
Location of residents with <i>C. auris</i> case	Identified in the ventilator unit	26 (93)
	Identified in the step-down unit	2 (7)
	Changed beds during their stay	14 (50)
	Changed units during their stay	3 (11)
AFST results (n = 15)	Resistant to fluconazole	15 (100)
	Resistant to amphotericin B	0 (0)
	Resistant to echinocandins	0 (0)
WGS results (n = 8)	Clade I	5 (63)
	Average SNPs between clade I isolates (range)	8 (5–13)
	Clade III	3 (38)
	Average SNPs between clade III isolates (range)	11 (8–16)

* Non-Hispanic (NH) Black includes one resident who was multiracial, Black/other.

† Previously referred to as vegetative state.