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Rapid Assessment and Containment of *Candida auris* Transmission in Postacute Care Settings–Orange County, California, 2019

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Abstract

Background: *Candida auris*, a multidrug-resistant yeast, can spread rapidly in ventilator-capable skilled-nursing facilities (vSNFs) and long-term acute care hospitals (LTACHs). In 2018, a laboratory serving LTACHs in southern California began identifying species of *Candida* that were detected in urine specimens to enhance surveillance of *C auris*, and *C auris* was identified in February 2019 in a patient in an Orange County (OC), California, LTACH. Further investigation identified *C auris* at 3 associated facilities.

Objective: To assess the prevalence of *C auris* and infection prevention and control (IPC) practices in LTACHs and vSNFs in OC.

Design: Point prevalence surveys (PPSs), postdischarge testing for *C auris* detection, and assessments of IPC were done from March to October 2019.

Setting: All LTACHs ($n = 3$) and vSNFs ($n = 14$) serving adult patients in OC.

Participants: Current or recent patients in LTACHs and vSNFs in OC.

Intervention: In facilities where *C auris* was detected, PPSs were repeated every 2 weeks. Ongoing IPC support was provided.

Measurements: Antifungal susceptibility testing and whole-genome sequencing to assess isolate relatedness.

Results: Initial PPSs at 17 facilities identified 44 additional patients with *C auris* in 3 (100%) LTACHs and 6 (43%) vSNFs, with the first bloodstream infection reported in May 2019. By October 2019, a total of 182 patients with *C auris* were identified by serial PPSs and discharge testing. Of 81 isolates that were sequenced, all were clade III and highly related. Assessments of IPC identified gaps in hand hygiene, transmission-based precautions, and environmental cleaning. The outbreak was contained to 2 facilities by October 2019.

Limitation: Acute care hospitals were not assessed, and IPC improvements over time could not be rigorously evaluated.

Conclusion: Enhanced laboratory surveillance and prompt investigation with IPC support enabled swift identification and containment of *C auris*.

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C*andida auris*, an emerging multidrug-resistant yeast and antimicrobial-resistant threat (1, 2) first reported in Japan in 2009 (1, 3, 4), has since been reported in dozens of countries and more than 20 U.S. states since 2016 (1, 5–7). Whole-genome sequencing (WGS) has identified 4 distinct clades of *C auris*, suggesting concurrent emergence of *C auris* in 4 geographically diverse regions (3, 4). Although most patients with *C auris* are asymptomatic and identified through skin colonization testing, 5% to 10% of patients colonized with *C auris* subsequently develop invasive infections, with an all-cause mortality rate of 30% to 60% (4, 8, 9). The rapid emergence of *C auris* has shifted the epidemiology of candidemia worldwide; in South Africa, *C auris* has now become the major candidal pathogen (4), and in India, *C auris* is the responsible pathogen in 5% of candidemia cases (3). Most *C auris* isolates are resistant to fluconazole, and resistance to amphotericin B and echinocandins has already been identified in *C auris* strains globally and in the United States (3, 4, 10), making *C auris* a multidrug-resistant organism (MDRO) of concern.

Candida auris persists in health care environments and readily colonizes patients' skin and medical devices, facilitating patient-to-patient transmission and requiring transmission-based precautions to prevent spread, similar to other MDROs (4, 11, 12). Outbreaks of *C auris* have occurred in intensive care units internationally (5) and in long-term acute care hospitals (LTACHs) and ventilator-capable skilled-nursing facilities (vSNFs) in the United States (13–15). Long-term acute care hospitals, which support patients with prolonged ventilator weaning requirements and other acute complex medical needs requiring hospital-level care (9, 16), and vSNFs, which provide nursing care for patients with ventilator dependence and chronic comorbidities but lower acuity medical conditions (9), serve medically vulnerable patients, have high rates of colonization for MDROs, and face substantial infection prevention and control (IPC) challenges (16–19).

Most clinical laboratories do not routinely perform species identification of *Candida* detected in nonsterile body site specimens (for example, urine) because it usually represents colonization not requiring clinical intervention. However, because *C auris* frequently colonizes nonsterile body sites (14, 20), species identification of *Candida* from these sites can enable detection of *C auris* and facilitate implementation of measures to prevent transmission. In September 2018, to proactively enhance surveillance of *C auris*, state and local health departments (LHDs) in Orange County (OC) and Los Angeles, California, requested that a laboratory affiliated with 9 local LTACHs begin species identification of *Candida* isolated from urine specimens. After performing species identification on 271 *Candida* isolates in urine specimens from 3 LTACHs in OC and 6 LTACHs in Los Angeles between September 2018 and February 2019, the laboratory detected the first case of *C auris* in southern California in February 2019 in urine from a patient in an OC LTACH (21). The patient had not recently traveled, making the finding concerning for local acquisition. Further investigation identified additional *C auris* screening cases at 3 facilities that received patients who were discharged from the LTACH. Given rapid transmission of *C auris* through patient networks at LTACHs and vSNFs in other states and the risk for invasive infections (13–15, 20), the Orange County Health Care Agency (OCHCA), the California Department of Public Health, and the Centers for Disease Control and Prevention (CDC), investigated every adult vSNF and LTACH in OC to aggressively detect and contain *C auris*. The aims were to determine the local epidemiology and spread of *C auris*, evaluate for ongoing

transmission, assess relatedness of strains, and evaluate and strengthen IPC practices to contain the outbreak.

Methods

Study Population, Setting, and Design

Orange County is a large, metropolitan county in southern California (population, 3.2 million), with an acute and postacute health care network comprising 27 ACHs, 3 adult LTACHs (labeled A to C), and 14 vSNFs (labeled A to N). From 1 March to 1 October 2019, public health personnel and facility staff actively conducted surveillance for *C auris* in OC; CDC staff were deployed to assist from April to May 2019.

The population of interest was patients currently or recently residing in an OC vSNF or LTACH. Cases were classified by method of identification. A screening case was defined as detection of *C auris* by real-time polymerase chain reaction or culture testing from a composite axilla–groin or nasal screening swab. A clinical case was defined as detection of *C auris* by culture from a specimen obtained for a patient's clinical care, including urine, respiratory, wound, drain, or blood. A screening and clinical case could occur in the same patient if the patient had *C auris* detected by screening swab before a positive clinical culture was collected.

Surveillance of *C auris* was implemented primarily through point prevalence surveys (PPSs) facility-wide at LTACHs and in ventilator-capable units at vSNFs. Point prevalence surveys were first done at the initial LTACH where *C auris* was detected and 3 vSNFs that received patients who were discharged from that LTACH; surveillance subsequently broadened to all LTACHs and vSNFs in OC. Initial PPSs involved collecting both axilla–groin and nasal screening swabs from all patients without known *C auris* who were residing in the facility , including new admissions.

Any facility with a PPS that identified 1 or more new *C auris* screening cases had subsequent PPSs performed every 2 weeks with axilla–groin screening swab to detect new *C auris* positivity among patients with a previously negative result or among patients who were newly admitted. Ongoing facility-based transmission of *C auris* was presumed if 2 or more sequential PPSs identified new screening cases in patients without known *C auris* exposure at another facility.

For secondary surveillance of *C auris*, patients discharged from OC LTACHs or ventilator units of vSNFs with ongoing transmission were considered at increased risk for *C auris* colonization and placed on empiric transmission-based precautions with admission screening for *C auris* by the receiving facility or provider.

The OCHCA notified all ACHs, LTACHs, and vSNFs in OC weekly about facilities with ongoing transmission. Facilities with ongoing transmission were required to report patient discharges to the OCHCA, which contacted receiving OC facilities or the receiving LHD to encourage transmission-based precautions and admission screening.

Facilities with 2 negative PPSs within 1 month transitioned to monthly PPSs. Facilities with no cases on initial PPS repeated a PPS at 6 months.

Focused medical chart review to determine risk factors was done during the CDC deployment period. Chart review was done using a standardized form that included patient demographic characteristics, medical devices, and common medical conditions. The charts reviewed included those of the index patient and any patients identified with *C auris* during the investigation from March to May 2019.

Laboratory Methods

Swabs were shipped to CDC's Mycotic Diseases Laboratory and the Antibiotic Resistance Laboratory Network regional laboratories in New York, Maryland, Washington, and Minnesota for real-time polymerase chain reaction (22) and reflex culture (23) testing with identification using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. When resources permitted, antifungal susceptibility testing (AFST) by broth microdilution (24) using custom-prepared frozen panels (TREK Diagnostics, Thermo Fisher Scientific) for echinocandins and azoles, and by ETEST (bioMérieux) for amphotericin B, was done on *C auris* screening and clinical isolates. Results of AFST were interpreted using CDC's tentative susceptibility breakpoints (25). Whole-genome sequencing was done on DNA extracts using either the Illumina HiSeq 2500 platform or the MiSeq platform. Single nucleotide polymorphism (SNP) analysis was done using a reference genome assembly from GenBank; phylogenetic analysis was also done (26–31). Isolates were compared with 51 publicly available genomes of control *C auris* isolates representing the 4 clades (3, 7, 32). The control set included representative genomes of isolates: 16 controls of clade I from India, Pakistan, and the United States (northern California, Connecticut, Massachusetts, Maryland, New Jersey, New York, and Oklahoma); 3 controls of clade II from Japan and the Republic of South Korea; 16 controls of clade III from Canada, Kenya, South Africa, the United Kingdom, and the United States (Indiana and Maryland); and 5 controls of clade IV from Venezuela and the United States (Illinois).

IPC Assessments

The IPC teams, including certified infection preventionists or trained public health personnel, did assessments at all facilities. Comprehensive assessments were done at facilities with identified *C auris*, and limited assessments were done at facilities where *C auris* was not detected on the initial PPS. Written and verbal feedback and recommendations were provided to facility staff. All assessments included quantification of the presence of alcohol-based hand sanitizer (ABHS) inside and immediately outside of patient rooms and evaluations of hand hygiene (HH) and environmental cleaning. Hand hygiene was assessed by observing staff during patient care or environmental cleaning, recording the number of times that HH was done, and dividing by the total number of times it was indicated. At vSNFs, the quality of environmental cleaning was evaluated by discreetly placing fluorescent marker on high-touch surfaces before environmental cleaning and using black light after cleaning to verify marker removal. Environmental cleaning at LTACHs was assessed using a checklist that evaluated disinfectant type used, recommended wet contact time, procedures for mixing disinfectant solutions, personal protective equipment

use, and environmental service staff cleaning protocols. Comprehensive assessments also included a facility tour and interviews with infection preventionists, environmental service managers, and respiratory therapy leads to evaluate staff competency with IPC practices. In addition, processes and responsibilities for cleaning environmental surfaces and shared medical equipment and chart labeling for patients with known MDROs were assessed. Repeated IPC assessments were done at facilities with 2 or more positive PPSs to evaluate for improvements in HH, environmental cleaning, and overall IPC practices.

Data Analyses

Patient data were entered into CDC's Data Collation and Integration for Public Health Event Responses database and extracted into Excel (Microsoft) for descriptive analyses. Patient characteristics were assessed in aggregate and by facility type.

This investigation was a public health outbreak response. This activity was reviewed by CDC and was conducted consistent with applicable federal law and CDC policy (for example, 45 CFR part 46.102[l][2], 21 CFR part 56, 42 USC §241[d], 5 USC §552a, and 44 USC §3501 et seq).

Role of the Funding Source

The authors completed this work in the course of their regular duties for their affiliated institutions and received no additional funding. CDC provided funding to support the overall public health response to *C auris*, particularly laboratory testing. The funding was not specific to this investigation and was independent of its design; collection, analysis, and interpretation of the data; and the decision to submit the article for publication. The corresponding authors had full access to all of the data in the investigation and had final responsibility for the decision to submit for publication.

Results

From 1 March to 17 April 2019, initial PPSs at the initial LTACH (B) and 3 associated vSNFs (A, B, and D) identified 20 patients with *C auris*. From 17 April to 30 May 2019, initial PPSs at the remaining 11 adult vSNFs and 2 LTACHs identified 24 additional patients with *C auris* at 3 of 11 vSNFs and both LTACHs. Eight vSNFs had negative initial PPSs. Thus, in total, initial PPSs identified 44 patients in 9 OC facilities: 6 vSNFs ($n = 19$) and 3 LTACHs ($n = 25$) (Figure 1). Only 1 patient was identified solely by nasal swab. The highest initial *C auris* prevalence was at vSNF A (13 of 30 [43%] residents) and LTACH A (18 of 94 [19%] residents).

By 1 October 2019, a total of 182 OC patients with screening cases of *C auris* were identified through serial PPSs at the 3 OC LTACHs and 6 vSNFs with known *C auris* ($n = 169$) or on admission screening by a receiving facility or provider ($n = 13$). Most were associated with LTACH A ($n = 100$ [55%]) and vSNF A ($n = 34$ [19%]), where repeatedly positive PPS results indicated ongoing *C auris* transmission (Figure 1). Seven of 9 facilities with *C auris* identified on initial PPSs successfully limited transmission (Figure 1) by October 2019. The 6-month follow-up PPSs for 8 vSNFs with negative initial PPSs were done after October 1 and are not included in this report.

Clinical Cases and Outcomes

Of 182 patients with screening cases of *C auris*, 14 (8%) were subsequently diagnosed with clinical cases. The 14 clinical cases were diagnosed through positive culture results from blood (*n* = 6 [43%]), urine (*n* = 3 [21%]), respiratory specimens (*n* = 2 [14%]), wounds (*n* = 2 [14%]), or abdominal abscesses or drains (*n* = 2 [14%]); 1 patient had both positive blood and abdominal drain culture results. The first patient with a positive blood culture result was identified in May 2019 in LTACH A. As of 1 January 2020, of 182 patients, 22 (12%) died within 30 days of *C auris* identification; 47 (26%) died within 90 days. One of 47 deaths was attributed to *C auris*.

Demographic and Clinical Information

Fifty-two patients had a clinical or screening case of *C auris* identified by clinical sample, initial PPS, or subsequent PPS by May 2019; their medical charts were reviewed by the CDC team. Thirty (58%) patients were male; the median age was 72 years (range, 29 to 93 years). Thirty-eight patients (73%) required full assistance with mobility. Of 32 patients in LTACHs, chronic lung disease (69%), gastrostomy tube dependence (69%), and cardiovascular disease (66%) were common; of 20 patients in vSNFs, chronic lung disease (95%), tracheostomy dependence (95%), and gastrostomy tube dependence (80%) were common (Table 1). After the departure of the CDC team, further in-depth chart review was discontinued due to limitations in public health resources.

Whole-Genome Sequencing

Eighty-one isolates were selected for WGS analysis (representing all 9 OC facilities with *C auris* identified), compared with the 4 known *C auris* clades, and identified as clade III. (Figure 2, A). In comparison to control strains (and the *C auris* B11221 reference genome from South Africa [GenBank accession number PGLS00000000.1]), OC isolates differed by 29 to 102 SNPs from clade III strains previously reported in Indiana, Maryland, Kenya, South Africa, and the United Kingdom (Figure 2, B). Isolates from OC were also more than 1000 SNPs different from clade III strains from Canada (Figure 2, B). All investigation isolates from OC were clonal and differed by fewer than 11 SNPs (Figure 2, C).

Antifungal Susceptibility Testing

A total of 137 OC isolates that were tested had AFST. All were azole resistant (minimum inhibitory concentration (MIC) of fluconazole ≥32 μg/mL) and echinocandin susceptible (MIC of micafungin or anidulafungin <4 μg/mL) by AFST (Table 2). Amphotericin B resistance testing, done on 136 of these isolates, identified that 10 (7.4%) were resistant (MIC ≥2 μg/mL, with MIC = 1.5 μg/mL on ETEST, rounded up to 2) and, therefore, multidrug resistant (Table 2).

IPC Assessments

Before IPC intervention, HH rates at all 9 facilities with *C auris* were below 80%; 5 (56%) facilities (1 LTACH and 4 vSNFs) had HH rates below 65% (Table 3). Seven (78%)facilities had ABHS available inside 70% or more of patient rooms; 2 (22%) had ABHS available immediately outside 70% or more of patient rooms. Several gaps in

environmental cleaning (Table 3) and disinfection were identified. At several facilities, staff responsibilities for cleaning computers, hospital carts, and bed alarms were unclear, and the frequency of cleaning of mobile medical equipment was unspecified. Inadequate disinfectant concentration was identified at LTACH A. Signs for transmission-based precautions at several facilities did not specify what personal protective equipment was required for room entry. Five of 9 (56%) facilities did not have a chart labeling system to identify patients colonized with MDROs.

After intensive support at facilities with IPC gaps or ongoing transmission, repeated assessments showed improved HH and qualitative improvement in environmental cleaning at several facilities (Table 3). By October 2019, only 2 of 9 (22%) facilities with *C auris* identified on initial PPS (LTACH A and vSNF A) had ongoing transmission; both had the highest initial prevalence of *C auris*.

Regional Notifications

The OCHCA provided notification for 113 patients who were discharged from OC to any facility type in Long Beach ($n = 54$), Los Angeles ($n = 48$), other California LHDs ($n = 8$), and other states ($n = 3$). Fourteen patients had known *C auris* screening cases and 99 patients who had no known history of *C auris* but were discharged from facilities with ongoing transmission and thus considered at increased risk for *C auris*. Three receiving LHDs in California instituted admission screening at a few receiving facilities; 4 of the 99 patients who had no known history of *C auris* but were discharged from OC facilities with ongoing transmission tested positive at the receiving facility.

Discussion

The novel use of an enhanced *C auris* laboratory surveillance method in LTACHs identified *C auris* in OC 3 months before routine detection methods identified the first *C auris* bloodstream infection. Rapid public health intervention, with initial PPSs at all LTACHs and vSNFs, and serial PPSs with intensive IPC support at the 9 facilities with *C auris* identified, contained the outbreak in 7 facilities. The investigation improved IPC practices across facilities and likely mitigated transmission of *C auris* within and outside OC.

Previous studies have identified vSNFs and LTACHs as high risk for *C auris* transmission through patient transfer networks (9, 14). Consequently, although the initial investigation focused on discharge patterns from the index LTACH, once *C auris* was identified at receiving facilities, the investigation expanded to all vSNFs and LTACHs in OC. Expanding beyond directly linked facilities enabled comprehensive assessment for *C auris* and intensive IPC intervention countywide while the outbreak was limited, which contained transmission. The investigation also prompted regional containment efforts within southern California. Neighboring LHDs began admission screening and PPSs in a few receiving facilities to assess for *C auris* transmission during patient transfers from OC. Our findings support using enhanced laboratory surveillance and a rapid assessment of high-risk facilities immediately after *C auris* is identified in a highly connected postacute care network.

Our investigation identified substantial IPC challenges in vSNFs and LTACHs that likely contributed to *C auris* and other MDRO transmission yet improved with public health IPC oversight. Previous literature describes limited IPC resources and oversight in these facilities that hinder effective IPC implementation, leading to similar challenges during the COVID-19 pandemic (17-19, 34). Most facilities that received intensive, onsite IPC support had improved practices on follow-up assessments. Public health oversight of interfacility communication during patient transfers also enabled proactive attention to IPC practices at receiving facilities and limited the risk for transmission.

This outbreak likely resulted from a single introduction to the region followed by undetected transmission in local facilities before the first case was identified through enhanced laboratory surveillance. All OC isolates analyzed by WGS were within clade III, with fewer than 11 SNP variations between isolates, like variations seen within a single patient (7) and suggestive of recent transmission. Isolates in OC were distinct from the first *C auris* isolate in California (7) and those found in other states and countries (6). Antifungal susceptibility testing found universal fluconazole resistance and 7% amphotericin B resistance, but no echinocandin resistance. As more patients develop invasive infections requiring echinocandin treatment, resistance could develop, necessitating ongoing antifungal susceptibility monitoring in OC (10). Furthermore, clusters of pan-resistant or echinocandin-resistant *C auris* strains without clear epidemiologic linkages or history of prior echinocandin exposure have already been identified in the United States, most recently in Texas and in Washington, DC (35). This raises concern for ongoing transmission of resistant *C auris* in health care settings and the need to invest in greater prevention efforts nationwide.

Our investigation has several limitations. Despite extensive epidemiologic investigation, medical chart review, and WGS analysis, we could not identify the patient who first introduced *C auris* to OC. We prioritized assessments of vSNFs and LTACHs rather than short-stay acute care settings, although transmission of *C auris* may have also occurred in these settings. Whereas intensive IPC support seemed to improve facility practices, the investigation was not designed to rigorously assess qualitative IPC improvements over time. In addition, replicating this intensive investigation in regions with fewer resources, a larger population, or a more complex health care network may be challenging.

Although the outbreak was controlled during this investigation, with sustained containment through December 2019, *C auris* screening and clinical cases increased in OC and surrounding areas in southern California during the COVID-19 pandemic (36, 37). Similar to health care facilities in other states, pandemic-related resource constraints, conservation practices of personal protective equipment (36, 38), and staffing shortages likely impaired overall IPC adherence, surveillance, and oversight. Gaps in IPC that likely contributed to *C auris* transmission included use of ABHS on gloved hands; inadequate HH; and contamination of the local environment, shared medical equipment, and computers due to extended use of gowns and gloves (38). In response to the severe COVID-19 outcomes in California SNFs, California legislation (39) required each SNF, including vSNFs, to support a trained, full-time, dedicated infection preventionist as of January 2021; have a plan for IPC quality control; and have annual IPC training for all health care personnel.

Within this framework, and building on the connections created with facilities for *C auris* containment before the pandemic, the California Department of Public Health and several southern California LHDs are collaborating to provide ongoing testing and additional IPC support to LTACHs and SNFs to address the resurgence of *C auris* and have continued robust interjurisdictional communication when patients who have been exposed to or have *C auris* are transferred between facilities and across LHD.

Despite the limitations and challenges, implementing enhanced laboratory surveillance and rapid, countywide investigation to assess the burden of *C auris* and strengthen IPC practices in high-risk facilities limited transmission in OC through 2019. Our approach can inform future containment efforts for *C auris* and other emerging MDROs, in California and nationwide.

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Disclaimer:

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the CDC.

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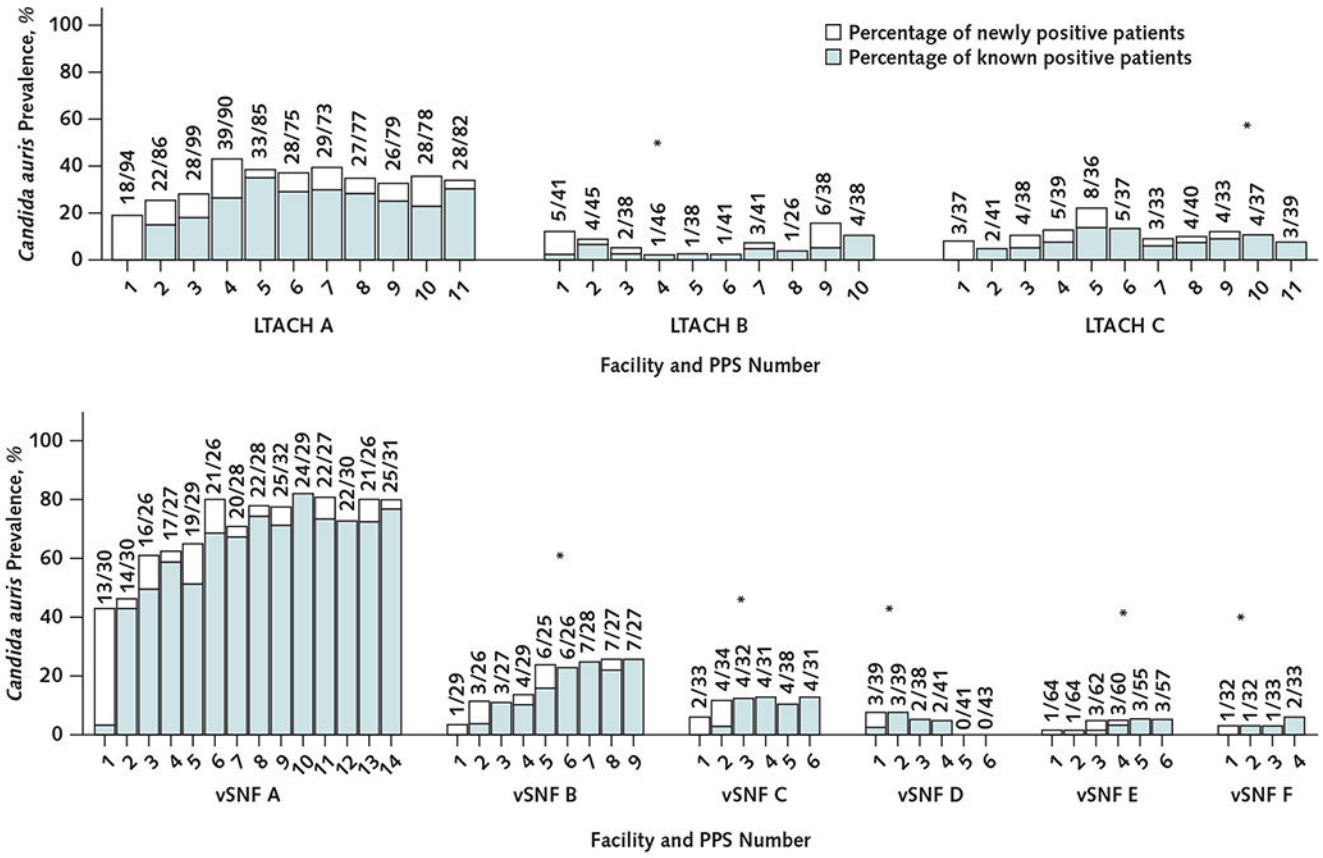

Figure 1.

Prevalence of *Candida auris* and the total number of screening cases (new and known) among total facility census, identified on serial PPSs within all OC LTACHs and 6 vSNFs (A to F), by PPS number–OC, California, March to October 2019.

LTACH = long-term acute care hospital; OC = Orange County; PPS = point prevalence survey; vSNF = ventilator-capable skilled-nursing facility.

* First facility instances of 2 consecutive PPSs with no new positive detections.

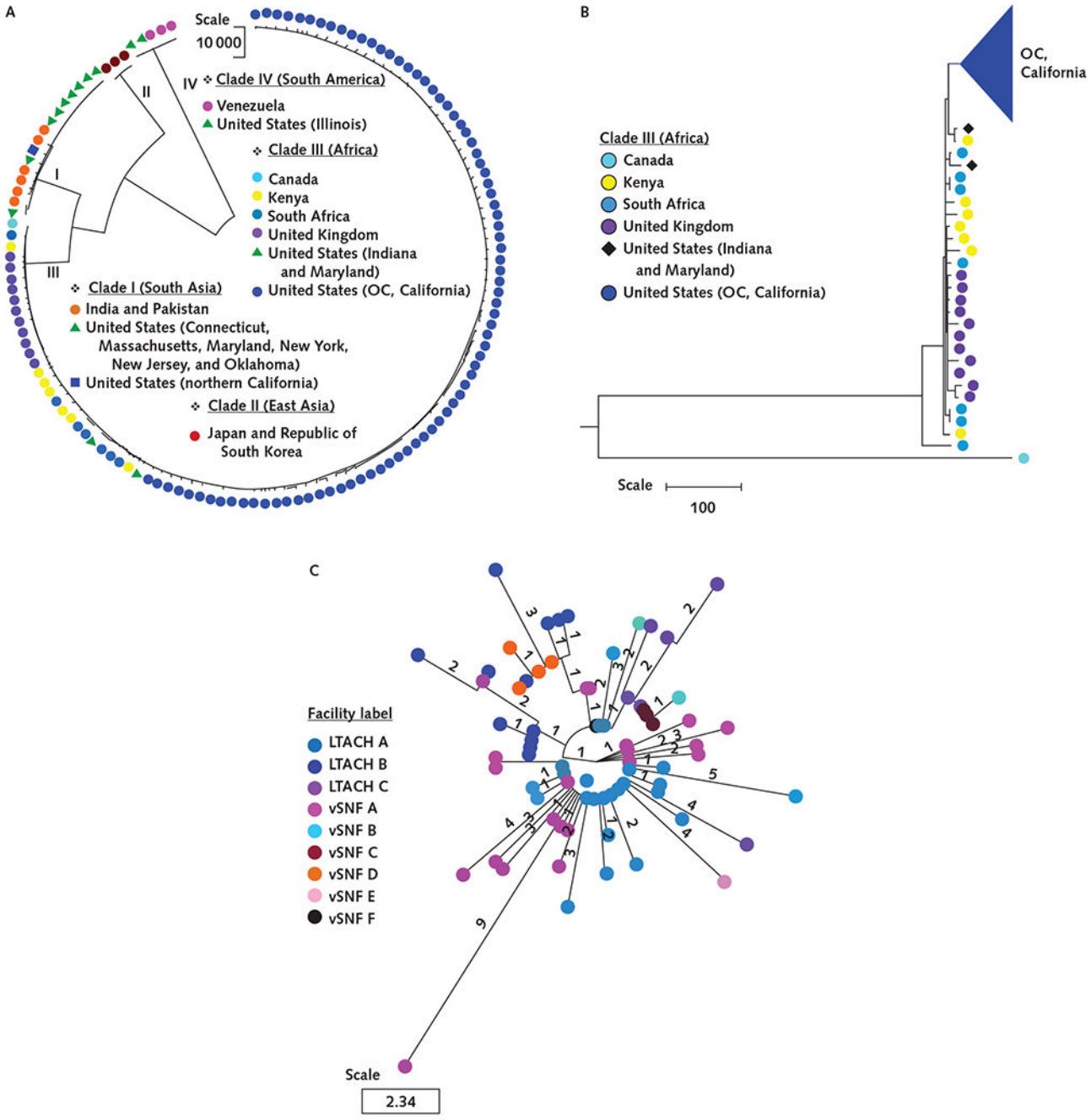

Figure 2.

Whole-genome sequencing results of *Candida auris* isolates, OC, California, 2019.

The scale bars shows pairwise SNPs. LTACH = long-term acute care hospital; OC = Orange County; SNP = single nucleotide polymorphism; vSNF = ventilator-capable skilled-nursing facility. **A**. Maximum parsimony tree showing the phylogenetic relationships among 133 *Candida auris* isolates representing all 4 clades constructed using 157 384 SNPs called against the *C auris* B11221 reference genome from South Africa (GenBank accession number PGLS00000000.1). All OC isolates clustered with clade III isolates and are

represented by a blue circle. Evolutionary analyses were done in Molecular Evolutionary Genetics Analysis (MEGA X) (31). Visualizations were done using Microreact (33) (https://microreact.org/project/qo5WqozYyKCxDyezFXeEC5/fb86da3b). **B**. Phylogenetic sub tree clade III (Africa) representing genetic diversity among *C auris* isolates from different countries, including the United States (Maryland; Indiana; and OC, California). All 81 isolates from OC are clustered together and represented by a large blue triangle. **C**. Genetic variations among *C auris* isolates from 9 facilities in OC, California and the LTACHs or vSNFs where they were identified. All 81 OC investigation isolates clustered together. Visualizations were done using Microreact (33) (https://microreact.org/project/bQtzYm3JqYghYkFWsUMhMv).

Table 1.

Demographic Characteristics, Underlying Conditions, and Medical Device Dependence Among Patients With Candida auris Identified by 30 May 2019, by Facility Type (n = 52)

Demographic Characteristics and Conditions of Interest	LTACH (n = 32), n (%)	vSNF (n = 20), n (%)	Total (n = 52), n (%)
Male	20 (63)	10 (50)	30 (58)
Medical conditions			
Any neurologic disease *	13 (41)	11 (55)	24 (46)
Cerebrovascular disease (cerebro-vascular accident/intracerebral hemorrhage/transient ischemic attack)	11 (34)	11 (55)	22 (42)
Chronic lung disease †	22 (69)	19 (95)	41 (79)
Cardiovascular disease ‡	21 (66)	6 (30)	27 (52)
Heart failure	7 (22)	2 (10)	9 (17)
Chronic kidney disease	18 (56)	2 (10)	20 (38)
Wound	16 (50)	9 (45)	25 (48)
Illness acuity			
Full assistance with mobility	21 (66)	17 (85)	38 (73)
Hospitalization within 6 mo	28 (88)	11 (55)	39 (75)
Documented antibiotic exposure	8 (25)	1 (5)	9 (17)
Medical devices			
Tracheostomy	14 (44)	19 (95)	33 (63)
Gastrostomy tube	22 (69)	16 (80)	38 (73)
Mechanical ventilation	12 (38)	11 (55)	23 (44)
Dialysis	9 (28)	0 (0)	9 (17)

LTACH = long-term acute care hospital; vSNF = ventilator-capable skilled-nursing facility.

* Any neurologic disease includes seizure disorders, Alzheimer disease, Parkinson disease, altered mental status, cerebrovascular accident, intracerebral hemorrhage, and transient ischemic attack.

† Chronic lung disease includes chronic obstructive pulmonary disease and chronic respiratory failure.

‡ Cardiovascular disease includes history of myocardial infarction, angina, arrhythmia, and heart failure.

Table 2.

Antifungal Susceptibility Testing Results for Candida auris Isolates From Orange County, California, 1 February to 1 October 2019 (*n* = 137)

Antifungal Medication	Isolates Tested, *n*	MIC Range, *μg/mL*	MIC_{50}, *μg/mL*	MIC_{90}, *μg/mL*	MIC Breakpoint, *μg/mL**	Resistant, *n* (%)
Fluconazole	137	64 to >256	256	>256	≥32	137 (100)
Voriconazole	134	0.5 to 8	2	4	-	-
Itraconazole	137	0.06 to 1	0.25	0.5	-	-
Isavuconazole	137	0.03 to 0.5	0.12	0.25	-	-
Posaconazole	137	0.03 to 0.5	0.12	0.25	-	-
Caspofungin	134	0.03 to 0.5	0.12	0.25	≥2	0 (0)
Anidulafungin	137	0.06 to 2	0.25	1	≥4	0 (0)
Micafungin	127	0.016 to 1	0.25	0.5	≥4	0 (0)
Amphotericin B	136	0.12 to 2	1	1	≥2	10 (7.4)

MIC = minimum inhibitory concentration; MIC_{50} = the MIC at which 50% of isolates were inhibited; MIC_{90} = the MIC at which 90% of isolates were inhibited.

* Minimum inhibitory concentration breakpoint/resistant: Using the Centers for Disease Control and Prevention tentative breakpoints (fluconazole MIC ≥32 mg/mL; caspofungin MIC ≥2 mg/mL; anidulafungin MIC ≥4 mg/mL; micafungin MIC ≥4 mg/mL; and amphotericin B MIC ≥2 mg/mL). No tentative breakpoints exist for the remaining azoles because the azole tentative breakpoint is based on fluconazole.

Table 3.

Results of Hand Hygiene and Environmental Cleaning Assessments[*] Before and After Infection Prevention and Control Interventions at LTACHs A to C and vSNFs A to F-Orange County, California, March to October 2019

Facility	Hand Hygiene		Environmental Cleaning	
	Observed Adherence/Hand Hygiene Opportunities, *n/n* (%)		Observed Adherence/Environmental Cleaning Opportunities, *n/n* (%)	
	Before	After	Before	After
LTACH				
A	4/6 (67)	10/10 (100)	11/18 (61)	15/17 (88)
B	12/18 (67)	Unknown[†] (64)	6/10 (60)	Unknown (90)
C	6/14 (43)	16/20 (80)	5/6 (83)	12/12 (100)
vSNF				
A	2/18 (11)	9/10 (90)	16/25 (64)	12/20 (60)
B	8/24 (33)	10/11 (91)	19/25 (76)	18/24 (75)
C	Unknown (33)	10/13 (77)	7/13 (54)	Unknown (83)
D	6/7 (86)	-[‡]	13/25 (52)	-[‡]
E	4/16 (25)	12/14 (86)	13/20 (65)	14/19 (74)
F	9/12 (75)	-[‡]	15/24 (63)	-[‡]

LTACH = long-term acute care hospital; vSNF = ventilator-capable skilled-nursing facility.

[*] Using environmental cleaning checklists at LTACHs and fluorescent marker on high-touch surfaces at vSNFs.

[†] ""Unknown"" is used when infection preventionists recorded only percentage adherence in final report without the total number of observations.

[‡] No assessment was done because there was no ongoing transmission detected at these facilities on PPS.