Candida auris is an emerging global healthcare-associat ed pathogen. During July–December 2018, four patients with C. auris were identified in Victoria, Australia, all with previous overseas hospitalization. Phylogenetic analysis revealed putative transmission between 2 patients and suspected overseas acquisition in the others. Vigilant screening of at-risk patients is required.

The fungal pathogen Candida auris is an emerging global health threat associated with a range of invasive infections, most commonly candidemia; it is often resistant to multiple antifungal drugs (1). First identified in Japan in 2009, C. auris has been reported across all 6 populated continents with outbreaks in healthcare settings, particularly intensive care and high-dependence units (1,2). Four genetic lineages of C. auris with phylogeographic variation have been identified (3).

Before July 2018, only 1 case of C. auris had been reported in Australia, none in the state of Victoria (population 6.5 million) (4); no centralized surveillance or mandatory reporting has been implemented on a state or national level, and local screening policies are limited. However, Victoria has experienced large interfacility and intrafacility healthcare-associated outbreaks of other multidrug-resistant organisms (5) and has increasingly implemented genomics in both the investigation of outbreaks and routine surveillance (C.R. Lane et al., unpub. data, https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3498431).

In July 2018, C. auris was cultured from a patient hospitalized in a Victoria healthcare facility. In response, the Victoria Department of Health and Human Services (DHHS) convened an incident management team and issued a Chief Health Officer alert to all health services and laboratories recommending admission screening for patients with recent overseas hospitalization. Also recommended was consideration of C. auris in patients with cultured non–C. albicans species and risk factors for fungal infection, including diabetes mellitus and recent antimicrobial drug use. The alert specified that all C. auris and nonspeciated non–C. albicans isolates from high-risk patients be referred to Victorian Public Health laboratories for speciation and characterization and reported to the DHHS (6). We report on the use of genomics to investigate putative transmission of C. auris in Victoria during July 1–December 31, 2018.

Isolates of C. auris were referred to the Victorian Infectious Diseases Reference Laboratory, where they underwent species identification and antimicrobial susceptibility testing. All isolates were then referred to the Microbiological Diagnostic Unit Public Health Laboratory for DNA extraction, whole-genome sequencing, and bioinformatic analysis.

Incursions of Candida auris into Australia, 2018

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During July–December 2018, we identified C. auris in 4 patients. Three patients (patients 1, 2, and 4 chronologically) were identified through clinically indicated samples, whereas patient 3 was screened on transfer from an overseas healthcare facility. Patients 1 and 2 were admitted to the same hospital at specimen collection, and patients 3 and 4 were admitted to different facilities. All patients reported previous overseas hospitalization (Figure).

We obtained 7 C. auris isolates from these 4 patients and performed core genome phylogenetic analysis on all isolates (Appendix, https://wwwnc.cdc.gov/EID/article/26/6/19-0936-App1.pdf). We downloaded publicly available C. auris sequences and included those meeting quality control metrics (Appendix Table 1). Phylogenetic analysis revealed all 7 isolates fell within the previously described South Asian clade (Figure, panel A).

We identified putative transmission during a concurrent hospital stay between patients 1 and 2 (Figure, panel B); transmission was epidemiologically validated and reported elsewhere (7). Because both patients reported overseas hospitalization, it is unclear which constituted the index case. Isolates from patients 3 and 4 were not closely related to each other, or any other included isolates, consistent with independent overseas acquisition.

**Figure.** Maximum-likelihood phylogenetic trees of Candida auris isolates from Victoria, Australia, in the context of international publicly available genomes. A) Complete tree; B) South Asian clade. Isolates from 4 patients in Victoria are indicated by colored dots on the inset tree; isolate details and patient travel history are provided in the key. Scale bars indicate substitutions per site.
We reported results of phylogenetic analyses prospectively and concurrently to the incident management team and affected facilities. Because all patients reported overseas hospitalization, the combined analysis of genomic and epidemiologic data enabled assessment of alternative hypotheses, identifying putative local transmission between patients 1 and 2 and excluding patients 3 and 4 from the outbreak. These results justified targeted infection control measures.

In late 2015, Victoria introduced combined phylogenetic and epidemiologic surveillance for carbapenemase-producing *Enterobacteriales*, a similar low-prevalence multiresistant organism (8). Using a search-and-destroy approach, this method enabled early identification of local transmission and complemented standard laboratory, screening, and outbreak control measures across the state. Leveraging from this work, a similar system was introduced for the control of *C. auris* in September 2019, with statewide mandatory notification of *C. auris* introduced in December 2019 (9,10). These measures address limitations in the current study, such as the inability to identify patients with *C. auris* because of noncompliance with screening recommendations, nonreporting, or decreased sensitivity of laboratory methods for the detection of *C. auris*.

A representative sample of international isolates enables inference of local transmission through local cluster identification and can indicate the source of local strains. The emergence of *C. auris* highlights the need for greater surveillance of nonbacterial multiresistant organisms and international data sharing. Sequences from our study were submitted to GenBank.

Our findings demonstrate the importance of proactive screening programs and of strict isolation and containment actions. Despite Australia’s geographic isolation, vigilance is necessary to ensure that patients hospitalized overseas are identified and screened for the presence of multiresistant organisms such as *C. auris* upon hospital admission.

**About the Author**

Ms. Lane is an epidemiologist and PhD candidate at the University of Melbourne. Her primary research interest is the use of genomics in the surveillance of antimicrobial resistance and pathogens of public health concern.

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Incursions of *Candida auris* into Australia, 2018

Appendix

Methods

Identification and Antifungal Susceptibility Testing

We confirmed isolates as *C. auris* by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF; Bruker Biotyper, https://www.bruker.com), and performed antifungal susceptibility testing by broth microdilution (Sensititre YeastOne, https://www.thermofisher.com).

DNA Extraction and Whole-Genome Sequencing

We performed DNA extraction and whole-genome sequencing (WGS) of study isolates at the Microbiological Diagnostic Unit Public Health Laboratory at the University of Melbourne. Genomic DNA was extracted from a single colony using a QIAsymphony DSP DNA Mini Kit (QIAGEN, https://www.qiagen.com) according to manufacturer’s instructions, and WGS was performed on an Illumina NextSeq 500 platform (Illumina, https://www.illumina.com) with 150 bp paired-end reads or Illumina MiSeq platform with 75 bp paired-end reads. We resequenced isolates that had sequencing depth \( \geq 50\times \) and a minimum Phred quality score of 30. Reads are available from the NCBI Sequence Read Archive (BioProject, https://www.ncbi.nlm.nih.gov/bioproject).

All *C. auris* sequences available on public databases were downloaded and assessed against the quality metrics above; we excluded sequences not meeting these targets.

SNP and Phylogenetic Analysis

We initially compared study genomes and publicly available genomes with *Candida auris* strain B8441 using Snippy version 4.3 (https://github.com/tseemann/snippy). We performed alignment using BWA MEM version 0.7.17-r1188 (1) and called single nucleotide polymorphisms (SNPs) using Freebayes version 1.2.0 (E. Garrison et al., unpub.data,
https://arxiv.org/abs/1207.3907), requiring a minimum read coverage of 10, minimum base quality of 13 and 90% read concordance at a site to report SNPs. The resulting core SNP alignment consisted of 151,484 sites. We inferred maximum likelihood (ML) phylogenetic trees using RAxML version 8.2.12 with 100 pseudo-bootstrap replicates and using a generalized time-reversible model, a Gamma distribution to model site-specific rate variation (the GTR + \( \Gamma \) substitution mode: GTRGAMMA in RAxML).

We performed subanalysis of the identified South Asian clade, including all locally sequenced isolates, using the methods above. The resulting core SNP alignment consisted of 103 sites.

We filtered these alignments for phage regions identified using Phaster (2) and recombination regions identified using Gubbins version 2.3.4 (3), and extracted core SNPs using SNP-sites (4). The resulting trees were midpoint-rooted with phangorn (v2.3.1) (5) and rendered using ggplot2 (1.8.1) (6). We calculated pairwise SNP distances using harrietR (https://github.com/andersgs/harrietR).

### Appendix Table 1. Publicly available *Candida auris* isolates included in phylogenetic analysis, Victoria, Australia

| Accession number | Year | Country      | Accession no. | Year | Country      |
|------------------|------|--------------|---------------|------|--------------|
| ERR2299885       | Unknown | United Kingdom | ERR2300789    | Unknown | Unknown |
| ERR2299874       | Unknown | United Kingdom | ERR2300809    | Unknown | Unknown |
| ERR2299886       | Unknown | United Kingdom | ERR2300771    | Unknown | Unknown |
| ERR2299870       | Unknown | United Kingdom | ERR2300797    | Unknown | Unknown |
| ERR2299877       | Unknown | United Kingdom | ERR2300772    | Unknown | Unknown |
| ERR2299887       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299892       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299893       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299891       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299882       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299884       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299881       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299872       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299883       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299871       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299869       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299873       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299875       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299886       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299880       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299878       | Unknown | United Kingdom | ERR2300796    | Unknown | Unknown |
| ERR2299889       | Unknown | United Kingdom | ERR2300796    | Unknown | United Kingdom |
| ERR2299890       | Unknown | United Kingdom | ERR2300796    | Unknown | United Kingdom |
| ERR2299876       | Unknown | United Kingdom | ERR2300796    | Unknown | United Kingdom |
| ERR2299888       | Unknown | United Kingdom | ERR2300796    | Unknown | United Kingdom |
| SRR3883466       | 2012 | Venezuela | ERR2300796    | Unknown | Unknown |
| SRR3883468       | 2012 | Venezuela | ERR2300796    | Unknown | Unknown |
| SRR3883464       | 2013 | Venezuela | ERR2300796    | Unknown | Unknown |
| SRR3883465       | 2012 | Venezuela | ERR2300796    | Unknown | Unknown |
| SRR3883467       | 2012 | Venezuela | ERR2300796    | Unknown | Unknown |
| SRR7140043       | 2016 | Colombia | ERR2300796    | Unknown | Unknown |
| SRR7140042       | 2016 | Colombia | ERR2300796    | Unknown | Unknown |
| SRR7140052       | 2016 | Colombia | ERR2300796    | Unknown | Unknown |
| Accession number | Year | Country    | Accession no. | Year | Country   |
|------------------|------|------------|---------------|------|-----------|
| SRR7140069       | 2016 | Colombia   | SRR7976608    | 2017 | United Kingdom |
| SRR7140058       | 2016 | Colombia   | SRR7976553    | 2017 | United Kingdom |
| SRR7140059       | 2016 | Colombia   | SRR7976587    | 2017 | United Kingdom |
| SRR7140010       | 2016 | Colombia   | SRR7976584    | 2016 | United Kingdom |
| SRR7140009       | 2016 | Colombia   | SRR7976543    | 2017 | United Kingdom |
| SRR7140022       | 2016 | Colombia   | SRR7976001    | 2017 | United Kingdom |
| SRR7140020       | 2016 | Colombia   | SRR7976112    | 2017 | United Kingdom |
| SRR7140076       | 2016 | Colombia   | SRR7976576    | 2017 | United Kingdom |
| SRR7140008       | 2016 | Colombia   | SRR7976605    | 2017 | United Kingdom |
| SRR7140044       | 2016 | Colombia   | SRR7976590    | 2017 | United Kingdom |
| SRR7140025       | 2016 | Colombia   | SRR7976547    | 2017 | United Kingdom |
| SRR7140063       | 2016 | Colombia   | SRR7976586    | 2017 | United Kingdom |
| SRR7140032       | 2016 | Colombia   | SRR7976602    | 2017 | United Kingdom |
| SRR7140007       | 2016 | Colombia   | ERR2300804    | Unknown | Unknown |
| SRR7140001       | 2016 | Colombia   | ERR2300783    | Unknown | Unknown |
| SRR7140035       | 2015 | Colombia   | SRR7976596    | 2016 | United Kingdom |
| SRR7140039       | 2016 | Colombia   | SRR7976583    | 2017 | United Kingdom |
| SRR7140045       | 2016 | Colombia   | SRR7976564    | 2017 | United Kingdom |
| SRR7140061       | 2016 | Colombia   | SRR7976600    | 2017 | United Kingdom |
| SRR7140004       | 2015 | Colombia   | SRR7976552    | 2017 | United Kingdom |
| SRR7140054       | 2016 | Colombia   | SRR7976609    | 2017 | United Kingdom |
| SRR7140033       | 2015 | Colombia   | SRR7976610    | 2017 | United Kingdom |
| SRR7140038       | 2016 | Colombia   | SRR7976541    | 2017 | United Kingdom |
| SRR7140046       | 2016 | Colombia   | SRR7976572    | 2017 | United Kingdom |
| SRR7140040       | 2016 | Colombia   | SRR7976544    | 2017 | United Kingdom |
| SRR7140030       | 2016 | Colombia   | SRR7976617    | 2017 | United Kingdom |
| SRR7140082       | 2015 | Colombia   | SRR7976598    | 2017 | United Kingdom |
| SRR7140017       | 2016 | Colombia   | SRR7976545    | 2017 | United Kingdom |
| SRR7140024       | 2016 | Colombia   | SRR7976555    | 2017 | United Kingdom |
| SRR7140047       | 2016 | Colombia   | SRR7976573    | 2017 | United Kingdom |
| SRR7140003       | 2015 | Colombia   | SRR7976585    | 2017 | United Kingdom |
| SRR7140068       | 2016 | Colombia   | SRR7976582    | 2015 | United Kingdom |
| SRR7140074       | 2016 | Colombia   | SRR7976540    | 2017 | United Kingdom |
| SRR7140041       | 2015 | Colombia   | SRR7976567    | 2017 | United Kingdom |
| SRR7140029       | 2015 | Colombia   | SRR7976546    | 2017 | United Kingdom |
| SRR7140080       | 2016 | Colombia   | SRR7976548    | 2017 | United Kingdom |
| SRR7140056       | 2015 | Colombia   | SRR7976615    | 2017 | United Kingdom |
| SRR7140015       | 2015 | Colombia   | SRR7976561    | 2017 | United Kingdom |
| SRR7140012       | 2015 | Colombia   | SRR7976557    | 2016 | United Kingdom |
| SRR7140071       | 2015 | Colombia   | SRR7976568    | 2017 | United Kingdom |
| SRR7140077       | 2016 | Colombia   | SRR7976574    | 2017 | United Kingdom |
| SRR7140062       | 2016 | Colombia   | SRR7976592    | 2017 | United Kingdom |
| SRR7140002       | 2016 | Colombia   | SRR3883473    | 2015 | Pakistan |
| SRR7140055       | 2015 | Colombia   | SRR3883439    | Unknown | India |
| SRR7140075       | 2016 | Colombia   | SRR3883437    | Unknown | India |
| SRR7140008       | 2015 | Colombia   | SRR3883451    | Unknown | India |
| SRR7140078       | 2016 | Colombia   | SRR3883436    | Unknown | India |
| SRR7140066       | 2016 | Colombia   | ERR899743     | Unknown | Unknown |
| SRR7140065       | 2016 | Colombia   | SRR3883434    | Unknown | India |
| SRR7140026       | 2016 | Colombia   | ERR1519358    | Unknown | Unknown |
| SRR7140026       | 2016 | Colombia   | ERR1519357    | Unknown | Unknown |
| SRR7140049       | 2016 | Colombia   | SRR3883435    | Unknown | India |
| SRR7140073       | 2016 | Colombia   | SRR3883440    | Unknown | India |
| SRR7140027       | 2016 | Colombia   | SRR3883449    | 2014   | Pakistan |
| SRR7140027       | 2016 | Colombia   | SRR3883429    | 2015   | Pakistan |
| SRR7140014       | 2016 | Colombia   | SRR3883471    | 2015   | Pakistan |
| SRR7140037       | 2016 | Colombia   | SRR3883430    | 2015   | Pakistan |
| SRR7140024       | 2015 | Colombia   | SRR3883438    | 2014   | Pakistan |
| SRR7140064       | 2016 | Colombia   | ERR1519359    | Unknown | Unknown |
| SRR7140036       | 2015 | Colombia   | SRR1664628    | 2013   | India |
| SRR7140067       | 2015 | Colombia   | SRR1664626    | 2013   | India |
| SRR7140016       | 2016 | Colombia   | SRR1664627    | 2013   | India |
| SRR7140031       | 2015 | Colombia   | SRR3883460    | 2014   | Pakistan |
| SRR7140011       | 2016 | Colombia   | SRR3883470    | 2014   | Pakistan |
| SRR7140028       | 2016 | Colombia   | SRR3883426    | 2014   | Pakistan |
| SRR7140034       | 2016 | Colombia   | SRR3883432    | 2015   | Pakistan |
| SRR7140051       | 2016 | Colombia   | SRR3883474    | 2015   | Pakistan |
| SRR7140019       | 2016 | Colombia   | SRR3883427    | 2014   | Pakistan |
Appendix Table 2. Antimicrobial susceptibility profile of isolates of *Candida auris* identified in Victoria, Australia, July–December 2018

| Patient | Collection date | Specimen source | Minimum inhibitory concentration (μg/mL) |
|---------|----------------|----------------|------------------------------------------|
|         |                |                | Amphotericin B | Fluconazole | Voriconazole | Micofungin | Anidulafungin |
| 1       | 10-Jul-18      | Urine          | 0            | 256         | 1            | 0.12      | 0.12         |
| 2       | 12-Aug-18      | Urine          | 4            | 256         | 2            | 0.25      | 0.25         |
| 3       | 5-Sep-18       | Groin swab     | 2            | 256         | 1            | 0.12      | 0.12         |
| 4       | 29-Nov-18      | Ear swab       | 0.5          | 16          | 0.5          | 2         | 0.5          |

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