Rubella is of global public health concern; >100,000 cases of congenital rubella syndrome (CRS) are reported annually worldwide (*1*). An immunization program resulted in rubella elimination in the United States during 2004 (*2*). Currently, the Centers for Disease Control and Prevention (CDC) estimates that <10 persons are reported to have rubella annually in the United States (*2*). During the 8 years after rubella was eliminated (2004–2012), 79 of rubella cases were reported, including in case-patients with no travel history (*3*). For the same period, 6 CRS cases were reported to CDC, 5 of which were likely imported (*3*). The sixth case was the infant of a US-born vaccinated mother without known risk factors (*4*). During the next 4 years (2013–2016), 5 confirmed CRS cases were reported to CDC, indicating a relative increase in the total number of new cases in the United States. The 5 cases were reported by three states, Illinois (2 cases), New York (2 cases), and Maryland (1 case); infections were likely acquired in Algeria, Pakistan, Yemen, and Nigeria (US Centers for Disease Control and Prevention, pers. comm, March 2017) (*5*).

During early pregnancy, the mother of the case-patient likely acquired acute rubella infection in Saudi Arabia, which increased its rubella vaccine program in July 2017 to meet control needs (*6*). Maternal immunization records and rubella titers were not available. The infant had positive rubella IgM, cataract, congenital heart disease, microcephaly, unilateral hearing loss, and radiolucent bone disease, meeting criteria for CRS. Screening for rubella titers in early pregnancy is standard in the United States. The presence of positive maternal rubella serology at delivery does not always reflect maternal immunization but can be the result of a rubella infection in early pregnancy. A similar scenario was misleading in a case that was recently reported and resulted in late diagnosis of CRS and subsequent multiple exposures (*6*).

Rubella-like illness in early pregnancy warrants testing for acute rubella infection, which offers parents an opportunity to decide about pregnancy outcome. For confirmed cases, maternal counseling and pregnancy termination may be considered. Testing for CRS is critical for early disease confirmation, implementation of appropriate infection control, timely reporting, and possible epidemiologic investigation. Infants with CRS shed large quantities of virus from bodily secretions for up to 1 year and can transmit rubella virus to susceptible persons (*7)*. The presence of unimmunized persons in the United States (for age, personal, or medical reasons) and entry of persons from rubella-endemic countries enable potential circulation of the virus. Despite rubella elimination in the United States, the presence of birth defects compatible with CRS warrants consideration of rubella in addition to other congenital infections.

**Acknowledgments**

We thank the parents of the reported patient for providing the photograph that is included in this manuscript and consent to publish the case.

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# *Candida auris* Infection Leading to Nosocomial Transmission, Israel, 2017

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DOI: https://doi.org/10.3201/eid2404.171715

A patient transferred from South Africa to Israel acquired a *Candida auris* infection. Phylogenetic analysis showed resemblance of *C. auris* to isolates from South Africa but not Israel, suggesting travel-associated infection. *C. auris* infection occurred weeks later in another patient at the same hospital, suggesting prolonged environmental persistence.

*Candida auris* is a multidrug-resistant yeast that has emerged over the past 3 years to cause nosocomial outbreaks in multiple countries. *C. auris* can cause serious invasive infections, may spread between patients, and can survive for months on hospital room surfaces (*1*). Whole-genome sequencing has determined the presence of country-specific clades, which differ from one another by thousands of single-nucleotide polymorphisms (*2*). The mode of spread between countries remains unclear. We present a case of international *C. auris* transmission related to a medically repatriated patient.

A previously healthy 25-year-old Israeli man (patient A) was admitted to a hospital in Johannesburg, South Africa, after a motor vehicle accident on July 24, 2016. He had severe limb injury and underwent open reduction and internal fixation on both femurs, complicated by fat emboli, acute respiratory distress syndrome requiring mechanical ventilation, and ventilator-associated pneumonia. He was empirically treated with broad-spectrum antimicrobial drugs and caspofungin. Three weeks after the accident, he was transferred to the intensive care unit (ICU) of Sheba Medical Center, Tel Hashomer, Israel. Ten days after his arrival, a deep surgical-site infection developed in his left thigh. We initiated debridement and broad-spectrum antimicrobial drugs. After cultures obtained during surgery grew extended-spectrum β-lactamase–producing *Klebsiella pneumoniae* and meropenem-resistant *Pseudomonas aeruginosa,* we initiated contact isolation. Two of 3 deep-wound cultures grew *C. auris*. Two days later, 1 blood culture grew *C. parapsilosis*. We administered amphotericin B and appropriate antibacterial drugs, discontinuing amphotericin B after 10 days due to increased creatinine. The surgical site healed, and the patient was transferred to a rehabilitation unit. Rectal and skin surveillance cultures obtained 4 weeks after the first isolation of *Candida* were negative for *C. auris*. Routine ICU environmental disinfection included daily bleach cleaning of surfaces and quaternary ammonium wipes of sensitive medical equipment.

In January 2017, we isolated *C. auris* from a urine culture obtained through a catheter of a 70-year-old patient (patient B) who was admitted to the Sheba Medical Center ICU 6 weeks after the discharge of patient A. Patient B had not traveled abroad recently. Surveillance cultures (urine, axilla, perineum) of patients in the ICU at the time of *C. auris* isolation of either patient A or B were negative for *C. auris*. One environmental sample from the floor next to patient B's bed in proximity to the urinary catheter bag was positive for *C. auris*. All other environmental samples were negative. We removed the urinary catheter without further antimicrobial therapy. Strict environmental cleaning was performed in the ICU.

We performed drug susceptibility testing using broth microdilution in accordance with Clinical Laboratory Standards Institute methods (https://clsi.org/standards/products/microbiology/documents/m27/) and reported results with preliminary breakpoints as published by the US Centers for Disease Control and Prevention (*3*). The study was approved by the Sheba Medical Center institutional review board.

We identified isolates as *C. auris* by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (Bruker Daltonik, Bremen, Germany) and as *C. parapsilosis* by the Phoenix system (Becton Dickinson, Franklin Lakes, NJ, USA). Sequence alignment with *C. auris* type strain CBS10913T produced similarity scores of 98% for internal transcribed spacer and 100% for large subunit ribosomal DNA segments for all 4 strains. Internal transcribed spacer and large subunit sequences of isolates from both patients were 100% identical to strains for MRL293 and MRL208 from South Africa (*4*) and distinct from sequences of strains previously isolated in our hospital and in Tel Aviv (Figure) (*5*).

*C. auris* isolates from patients A and B were resistant to fluconazole and susceptible to anidulafungin and had high MICs to voriconazole (≥8 μg/mL). One isolate was resistant to amphotericin B (MIC 2 μg/mL) (*3*), although a recent study suggested a higher epidemiologic cutoff that defines the isolate as susceptible (*6*).

Nosocomial outbreaks associated with *C. auris* were reported from several countries and continents including India, South Africa, Venezuela, Pakistan, and the United States (*2*,*7*,*8*). Sporadic cases were reported from Israel (*5*). Echinocandin exposure, which preceded *C. auris* infection in patient A, was also reported in South Africa (*2*). Environmental contamination appears to be a common mode of *C. auris* spread within medical facilities (*1*); it is the suspected cause for the 2 cases reported here, despite the time between them. The use of quaternary ammonium compounds, which are less effective than bleach, for disinfecting equipment might contribute to persistence of *Candida* (*9*).

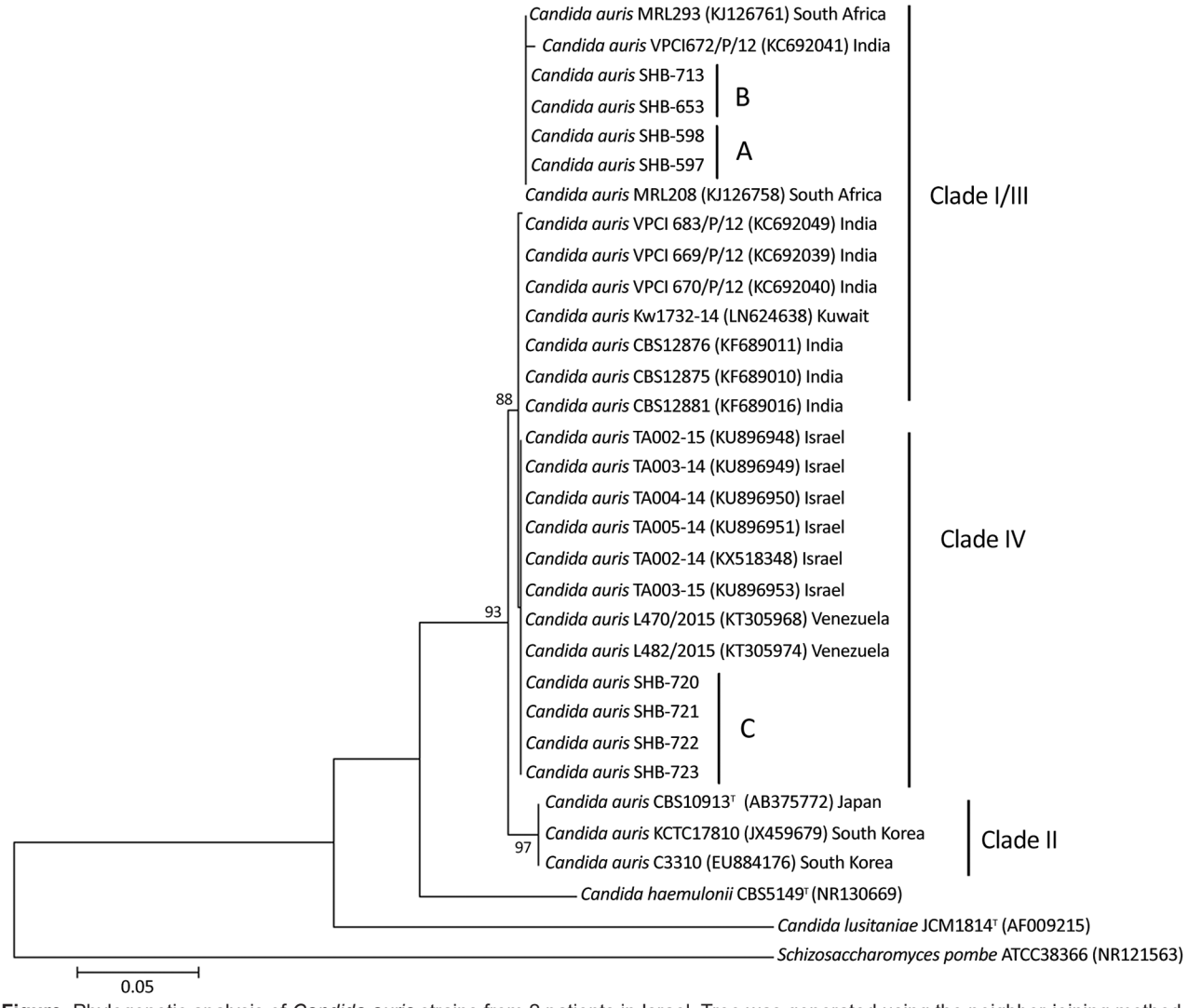


**Figure.** Phylogenetic analysis of *Candida auris* strains from 2 patients in Israel. Tree was generated using the neighbor-joining method. Internal transcribed spacer sequences of *C. auris* strains were aligned with the *C. auris* type strain CBS5149$^T$, strains previously isolated in Tel Aviv (TA002-TA005), and additional clinical strains available from GenBank. A indicates isolates from patient A, who was transferred from South Africa to Sheba Medical Center in Israel in late 2016. B indicates isolates from patient B, who was admitted to the same unit 6 weeks after the discharge of patient A, in January 2017; SHB-713 is an environmental sample from the floor near patient B's bed. C indicates isolates from sputum and urine from 2 different patients infected with *C. auris* in Sheba Medical Center during 2017 (SHB-720–723). The percentages of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches. GenBank accession numbers are given in parentheses, and countries of origin are listed. *C. lusitaniae* JCM1814$^T$ and *Schizosaccharomyces pombe* ATCC38366 were used as outgroups. Scale bar indicates nucleotide substitutions per site.

International travel is an increasingly recognized risk factor for infection with drug-resistant pathogens. Our investigation underscores the potential role of international travel and especially the transportation of patients between countries as a mode of *C. auris* dissemination. The wide genetic gap between country-specific clades allows the use of ribosomal DNA typing as a tool for identifying the geographic origin of specific isolates (*2*,*5*). A similar approach was used to demonstrate multiple transmission events into the United Kingdom (*10*).

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# Cephalosporin-Resistant *Neisseria gonorrhoeae* Clone, China

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DOI: https://doi.org/10.3201/eid2404.171817

Cephalosporin-resistant *Neisseria gonorrhoeae* is a major public health concern. *N. gonorrhoeae* of multiantigen sequence type G1407 and multilocus sequence type 1901 is an internationally spreading cephalosporin-resistant clone. We detected 4 cases of infection with this clone in China and analyzed resistance determinants by using *N. gonorrhoeae* sequence typing for antimicrobial resistance.

Gonorrhea, the second most prevalent sexually transmitted infection (STI) globally, remains a major public health concern in China. From 2015 to 2016, the reported cases of gonorrhea in China increased by 14.7% (100,245 to 115,024) (*1*). The extended-spectrum cephalosporin ceftriaxone has been recommended as monotherapy to treat gonorrhea in China since 2007 (*2*), but resistance to this drug emerged almost at the same time (*3*). Presently, the transmission of internationally spread cephalosporin-resistant clones in China has become a threat to effectively controlling gonorrhea (*4*). Strains with *N. gonorrhoeae* multiantigen sequence type (NG-MAST) G1407 and multilocus sequence type (MLST) 1901 have been successful clones associated with cephalosporin resistance and have caused clinical treatment failures in France and Spain (*5*,*6*); these strains have also became the predominant clones in the United Kingdom (*7*) and Japan (*8*) and among US men who have sex with men (*9*). Here we report 4 cephalosporin-resistant NG-MAST G1407/MLST 1901 clones identified out of 2,038 isolates collected through China's Gonococcal Resistance Surveillance Program during 2015–2016.

Demographic and clinical information for the 4 case-patients are summarized in online Technical Appendix Table 1 (https://wwwnc.cdc.gov/EID/article/24/4/17-1817-Techapp1.xlsx). All case-patients were adult men; gonococcal isolates were obtained from urethral swab samples. The 4 men had obvious urethral discharge and were diagnosed with acute urethritis. Gram staining and culture of the urethral swabs were positive for gonococcal infection. One of the 4 patients self-reported being a man who has sex with men. One of the infections, occurring in Zhejiang Province, was treated with a single-dose regimen of spectinomycin (4 g); the other 3 infections, occurring in the municipality of Chongqing, were treated with a 2-dose regimen of ceftriaxone (1 g) administered over 2 days. Test-of-cure follow-ups were not performed.

All strains were transferred to the reference laboratory at the National Center for Sexually Transmitted Disease Control, Chinese Center for Disease Control and Prevention. Gram staining, a rapid oxidase reaction test, and a carbohydrate utilization test confirmed the identification of *N. gonorrhoeae*. We determined antimicrobial susceptibility to ceftriaxone (CRO), cefixime (CFM), spectinomycin (SPT), azithromycin (AZM), ciprofloxacin (CIP), and