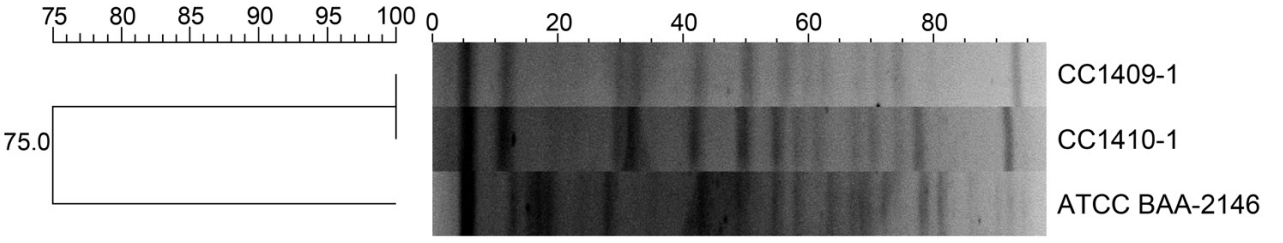

Figure. Dendrogram of pulsed-field gel electrophoresis patterns showing the genetic relationship between 2 *Klebsiella pneumoniae* isolates co-producing New Delhi metallo-β-lactamase 5 and oxacillinase 181 carbapenemases, South Korea, 2014. ATCC BAA-2146 indicates New Delhi metallo-β-lactamase 1 *K. pneumoniae* used as a reference strain. Scale bar indicates percentage genetic relatedness.

reported in India but has been sporadically detected in the United Kingdom, the Netherlands, France, New Zealand, Oman, and Singapore (*8*). It has also been found to be associated with other carbapenemase genes, such as the $bla_{\text{NDM-1}}$ and $bla_{\text{VIM-5}}$ genes, and particularly in isolates with a link to the Indian subcontinent.

In the cases we describe, the first *K. pneumonia*e isolate was recovered from a patient transferred from the UAE. Recent studies suggest that the Middle East, a region with close ties to the Indian subcontinent that hosts a large expatriate population, may act as another reservoir of OXA-48 and NDM producers (*9,10*). The emergence of extremely drug-resistant isolates carrying multiple carbapenemase genes is of concern because of limited treatment options and the possibility of global dissemination by means of cross-border transfer. A collaborative interdisciplinary strategy, including active surveillance for high-risk patients and adequate infection control measures against spread of such highly transmissible multidrug-resistant strains in health care settings, is necessary.

References

1. Cantón R, Akóva M, Carmeli Y, Giske CG, Glupczynski Y, Gniadkowski M, et al. Rapid evolution and spread of carbapenemases among *Enterobacteriaceae* in Europe. Clin Microbiol Infect. 2012;18:413–31. http://dx.doi.org/10.1111/j.1469-0691.2012.03821.x
2. Nordmann P, Naas T, Poirel L. Global spread of carbapenemase-producing *Enterobacteriaceae.* Emerg Infect Dis. 2011;17:1791–8. http://dx.doi.org/10.3201/eid1710.110655
3. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. Twenty-fourth informational supplement. M100-S24. Wayne (PA): The Institute; 2014.
4. European Committee on Antimicrobial Susceptibility Testing (EUCAST). Clinical Breakpoints version 3.0. EUCAST; 2013 [cited 2015 Jan 8]. http://www.eucast.org/clinical_breakpoints/
5. Diancourt L, Passet V, Verhoef J, Grimont PA, Brisse S. Multilocus sequence typing of *Klebsiella pneumoniae* nosocomial isolates. J Clin Microbiol. 2005;43:4178–82. http://dx.doi.org/10.1128/JCM.43.8.4178-4182.2005
6. Matushek MG, Bonten MJ, Hayden MK. Rapid preparation of bacterial DNA for pulsed-field gel electrophoresis. J Clin Microbiol. 1996;34:2598–600.
7. Hornsey M, Phee L, Wareham DW. A novel variant, NDM-5, of the New Delhi metallo-β-lactamase in a multidrug-resistant *Escherichia coli* ST648 isolate recovered from a patient in the United Kingdom. Antimicrob Agents Chemother. 2011;55:5952–4. http://dx.doi.org/10.1128/AAC.05108-11
8. Poirel L, Potron A, Nordmann P. OXA-48-like carbapenemases: the phantom menace. J Antimicrob Chemother. 2012;67:1597–606. http://dx.doi.org/10.1093/jac/dks121
9. Zowawi HM, Sartor AL, Balkhy HH, Walsh TR, Al Johani SM, AlJindan RY, et al. Molecular characterization of carbapenemase-producing *Escherichia coli* and *Klebsiella pneumoniae* in the countries of the Gulf cooperation council: dominance of OXA-48 and NDM producers. Antimicrob Agents Chemother. 2014;58:3085–90. http://dx.doi.org/10.1128/AAC.02050-13
10. Sonnevend A, Al Baloushi A, Ghazawi A, Hashmey R, Girgis S, Hamadeh MB, et al. Emergence and spread of NDM-1 producer *Enterobacteriaceae* with contribution of IncX3 plasmids in the United Arab Emirates. J Med Microbiol. 2013;62:1044–50. http://dx.doi.org/10.1099/jmm.0.059014-0

Address for correspondence: Doo Ryeon Chung, Division of Infectious Diseases, Samsung Medical Center, Sungkyunkwan University School of Medicine, Irwon-ro 81, Gangnam-gu, Seoul 135-710, South Korea; email: iddrchung@gmail.com

Salmonella enterica Paratyphi A Infections in Travelers Returning from Cambodia, United States

Michael C. Judd, Julian E. Grass, Eric D. Mintz, Amelia Bicknese, Barbara E. Mahon

Author affiliations: Centers for Disease Control and Prevention, Atlanta, Georgia, USA (M.C. Judd, J.E. Grass, E.D. Mintz, A. Bicknese, B.E. Mahon); Atlanta Research and Education Foundation, Atlanta (M.C. Judd)

DOI: http://dx.doi.org/10.3201/eid2106.150088

To the Editor: Health authorities from Cambodia and European Union member states recently described a pronounced increase in *Salmonella enterica* serotype Paratyphi A infections in Cambodia resulting from an ongoing outbreak

(*1*,*2*). To further characterize this outbreak, we analyzed 2013–2014 data on Paratyphi A infections associated with travel to Southeast Asia that were reported to the Centers for Disease Control and Prevention (CDC) National Typhoid and Paratyphoid Fever Surveillance (NTPFS) system and the CDC National Antimicrobial Monitoring System (NARMS).

NTPFS began tracking *Salmonella* Paratyphi A infections in 2008. During 2008–2012, ten cases were reported in patients who had traveled to Southeast Asia within 30 days before illness onset; only 1, who also reported travel to Sri Lanka, Nepal, and Nigeria, reported travel to Cambodia. During January 1, 2013–August 22, 2014, however, NTPFS received 19 reports of laboratory-confirmed Paratyphi A infection in travelers returning from Southeast Asia; 13 traveled to Cambodia, and 8 of them reported travel only to Cambodia (Table). Of the 7 patients who traveled only to Cambodia and reported reason for travel, all cited "visiting friends and relatives." Six (75%) of the 8 patients who traveled only to Cambodia were hospitalized (median duration 7 days, range 2–10 days), and all recovered. Cases occurring in 2014, especially later in the year, might not yet have been reported, so the 2014 data most likely are an underestimate. Although many cases reported to health authorities in Cambodia and the European Union clustered in the Phnom Penh region (*1*,*2*), we lack information about destinations within Cambodia for US patients.

Paratyphi A isolates from southern Asia (e.g., India, Pakistan, Bangladesh) often are resistant to the quinolone nalidixic acid or are multidrug resistant (i.e., resistant to ampicillin, chloramphenicol, and trimethoprim/sulfamethoxazole) (*3*), but little is known about antimicrobial drug resistance among Paratyphi A strains from Southeast Asia. However, most outbreak-associated isolates from Cambodia reported by others have been pansusceptible (*1*,*2*). CDC NARMS characterized the antimicrobial susceptibility of isolates from all patients who reported travel only to Cambodia; 7 (87.5%) were pansusceptible, and 1 (12.5%) was resistant to nalidixic acid and had reduced susceptibility to the fluoroquinolone ciprofloxacin. CDC NARMS also tested isolates from all patients who reported travel to Cambodia and other countries in Southeast Asia and from 2 patients who reported travel to other countries in Southeast Asia only; all were pansusceptible.

The Paratyphi A outbreak in Cambodia appears to be large and ongoing. To our knowledge, information about possible sources and risk factors that could help inform prevention activities is not yet available. This outbreak highlights the urgent need for a paratyphoid fever vaccine; although typhoid fever vaccines exist, persons living in and visiting regions of active Paratyphi A transmission have no alternative to relying exclusively on close attention to food and water safety to mitigate risk (*4*). Furthermore, although most isolates from this outbreak appear to have been pansusceptible, antimicrobial drug resistance has emerged quickly among Paratyphi A strains in southern Asia (*5*–*7*). More comprehensive surveillance of antimicrobial resistance among Paratyphi A strains is warranted in Southeast Asia to determine the extent of geographic expansion of resistant strains from southern Asia and to inform treatment options for management of patients. We recommend a systematic outbreak investigation to determine source and routes of transmission.

Table. Characteristics of patients with *Salmonella enterica* serotype Paratyphi A infection returning to the United States from Southeast Asia, NTPFS, 2013–2014*

Characteristic	Cambodia only, n = 8	Cambodia and other countries in Southeast. Asia, n = 5†	Other countries in Southeast. Asia only, n = 6‡
Travel history§			
Reason for travel, no (%)			
Business	1 (14)	0	3 (60)
Tourism	0	3 (60)	3 (60)
Visiting friends and relatives	7 (100)	3 (60)	0
Missionary work	0	1 (20)	0
Immigration	0	0	1 (17)
Unknown	1 (<1)	0	0
Demographics			
Age, y, median (range)	23 (9–50)	21 (18–59)	39 (25–52)
Female sex, no. (%)	5 (63)	4 (80)	4 (67)
Clinical			
Hospitalized, no. (%)	6 (75)	3 (60)	2 (33)
No. days, median (range)	7 (2–10)	6 (4–7)	3 (1–4)
Recovered, no. (%)	8 (100)	5 (100)	6 (100)
Specimen source, no. (%)			
Blood	7 (88)	4 (80)	4 (67)
Feces	1 (12)	1 (20)	2 (33)

*Cases occurring in 2014, especially later in the year, might not yet have been reported to NTPFS. NTPFS, National Typhoid and Paratyphoid Fever Surveillance system.
†In addition to Cambodia, patients also visited Vietnam (2 patients) and Laos (1 patient).
‡Other countries in Southeast Asia included Indonesia (4 patients) and Thailand (2 patients).
§Of patients with known reason for travel. Some patients listed multiple reasons.

Acknowledgments

We thank our local and state public health partners for submitting typhoid and paratyphoid case report forms and NARMS laboratory personnel for isolate testing.

References

1. Vlieghe E, Phe T, De Smet B, Veng C, Kham C. Increase in *Salmonella enterica* serovar Paratyphi A infections in Phnom Penh, Cambodia, January 2011 to August 2013. Euro Surveill. 2013; 18:20592.
2. Tourdjman M, Le Hello S, Gossner C. Unusual increase in reported cases of Paratyphoid A fever among travellers returning from Cambodia, January to September 2013. Euro Surveill. 2013;18:20594.
3. Newton AE, Mintz ED. Infectious diseases related to travel: typhoid & paratyphoid fever. CDC health information for international travel [cited 2014 May 11]. http://wwwnc.cdc.gov/travel/yellowbook/2014/chapter-3-infectious-diseases-related-to-travel/typhoid-and-paratyphoid-fever
4. Mahon BE, Newton AE, Mintz ED. Effectiveness of typhoid vaccination in US travelers. Vaccine. 2014;32:3577–9. http://dx.doi.org/10.1016/j.vaccine.2014.04.055
5. Akhtar S, Sarker MR, Jabeen K, Sattar A, Qamar A, Fasih N. Antimicrobial resistance in *Salmonella enterica* serovar typhi and paratyphi in South Asia—current status, issues and prospects. Crit Rev Microbiol. 2014;7828:1–10. http://dx.doi.org/10.3109/1040841X.2014.880662
6. Parry CM, Threlfall EJ. Antimicrobial resistance in typhoidal and nontyphoidal salmonellae. Curr Opin Infect Dis. 2008;21:531–8. http://dx.doi.org/10.1097/QCO.0b013e32830f453a
7. Sahastrabuddhe S, Carbis R. Increasing rates of *Salmonella* Paratyphi A and the current status of its vaccine development. Expert Rev Vaccines. 2013;12:1021–31. http://dx.doi.org/10.1586/14760584.2013.825450

Address for correspondence; Michael C. Judd, Centers for Disease Control and Prevention, 1600 Clifton Rd NE, Mailstop C09, Atlanta, GA 30329-4027, USA; email: mjudd@cdc.gov

Candida auris Candidemia in Kuwait, 2014

Maha Emara, Suhail Ahmad, Ziauddin Khan, Leena Joseph, Ina'm Al-Obaid, Prashant Purohit, Ritu Bafna

Author affiliations: Al-Sabah Hospital, Shuwaikh, Kuwait (M. Emara, I. Al-Obaid, P. Purohit, R. Bafna); Faculty of Medicine, Kuwait University, Jabriyah, Kuwait (S. Ahmad, Z. Khan, L. Joseph)

DOI: http://dx.doi.org/10.3201/eid2106.150270

To the Editor: Recent reports from Asia (*1*–*4*) have highlighted the increasing incidence of the fungus *Candida auris* as a nosocomial bloodstream pathogen affecting persons of all age groups. We report a case of *C. auris* candidemia in a 27-year-old woman in Kuwait with a long history of chronic renal failure. On May 9, 2014, the patient was admitted to the intensive care unit with symptoms of septic shock secondary to lobar pneumonia and complicated by acute renal failure. The patient was known to have immotile cilia syndrome (primary ciliary dyskinesia) and bronchiectasis with recurrent episodes of sinusitis. Beginning on day 1, she received treatment with different courses of a wide range of broad-spectrum antimicrobial drugs. However, despite treatment, the patient's condition continued to deteriorate. On day 12 after admission, a blood culture yielded yeast growth that was identified with 99% probability as *C. haemulonii* by using the Vitek 2 yeast identification system (bioMérieux, Marcy l'Etoile, France). As part of routine patient care, we sent the isolate (Kw1732/14) to the Mycology Reference Laboratory at Kuwait University for further identification and antifungal susceptibility testing. The isolate was resistant to fluconazole (MIC of ≥256 μg/mL), but it appeared susceptible to amphotericin B (MIC of 0.064 μg/mL), voriconazole (MIC of 0.38 μg/mL), and caspofungin (MIC of 0.064 μg/mL) by using the Etest (bioMérieux, Marcy l'Etoile, France). The patient was started on liposomal amphotericin B (150 mg/day), but the next day, she died from multiorgan failure.

On MAST ID CHROMagar Candida medium (Mast Group Ltd., Bootle, UK), the isolate formed pink colonies, which grew well at 42°C but not at 45°C. The isolate did not grow on BBL Mycosel Agar (BD, Sparks, MD, USA) containing 0.4 g cycloheximide per liter of medium. As with *C. auris* isolates from India and South Africa, this isolate assimilated *N*-acetyl glucosamine (*2*,*5*). Because the isolate showed reduced susceptibility to fluconazole, it was further characterized by sequencing of internal transcribed spacer and D1/D2 domains of ribosomal DNA. Genomic sequences for the internal transcribed spacer and D1/D2 regions (EMBL accession nos. LN624638 and LN626311) shared 99%–100% identity with sequences for corresponding regions of several *C. auris* strains (identification nos. CBS12874, CBS12875, CBS12876, CBS12880, CBS12882, CBS12886, and CBS12887, and several isolates from India).

C. auris was isolated in 2009 from the ear canal of a woman in Japan (*6*). The species has attracted attention because of its reduced susceptibility to azoles and amphotericin B (*2*,*5*) and its misidentification as *C. haemulonii* or *Rhodotorula glutinis* by commercial yeast identification systems (*1*,*4*). Because there are no reliable phenotypic methods for the rapid identification of *C. auris* and because molecular methods are not yet widely available, it is reasonable to infer that *C. auris* may be a more frequent cause of candidemia than previously recognized, particularly in Asian countries. A recently published multicenter study from India supports this view (*7*). In that study, a significantly higher occurrence of *C. auris* candidemia was re-