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References

1. World Health Organization. Avian influenza A(H7N9) virus [cited 2014 Apr 8]. http://www.who.int/influenza/human_animal_interface/influenza_h7n9/en/index.html
2. Chen E, Chen Y, Fu L, Chen Z, Gong Z, Mao H, et al. Human infection with avian influenza A(H7N9) virus re-emerges in China in winter 2013. Euro Surveill. 2013;18. pii: 20616.
3. Gao R, Cao B, Hu Y, Feng Z, Wang D, Hu W, et al. Human infection with a novel avian-origin influenza A (H7N9) virus. N Engl J Med. 2013;368:1888–97. http://dx.doi.org/10.1056/NEJMoa1304459
4. Wu A, Su C, Wang D, Peng Y, Liu M, Hua S, et al. Sequential reassortments underlie diverse influenza H7N9 genotypes in China. Cell Host Microbe. 2013;14:446–52. http://dx.doi.org/10.1016/j.chom.2013.09.001
5. Lam TT, Wang J, Shen Y, Zhou B, Duan L, Cheung CL, et al. The genesis and source of the H7N9 influenza viruses causing human infections in China. Nature. 2013;502:241–4. http://dx.doi.org/10.1038/nature12515
6. Cui L, Liu D, Shi W, Pan J, Qi X, Li X, et al. Dynamic reassortments and genetic heterogeneity of the human-infecting influenza A (H7N9) virus. Nat Commun. 2014;5:3142. http://dx.doi.org/10.1038/ncomms4142
7. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. MEGA5: Molecular Evolutionary Genetics Analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol. 2011;28:2731–9. http://dx.doi.org/10.1093/molbev/msr121

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Carbapenem-Resistant *Enterobacter cloacae* Isolates Producing KPC-3, North Dakota, USA

To the Editor: Carbapenem-resistant *Enterobacteriaceae* (CRE) continue to emerge as a serious public health threat throughout the world (*1*). CRE infections in the United States are often mediated by acquisition of *Klebsiella pneumoniae* carbapenemase (KPC) expressed by *Klebsiella* spp., although KPC is also found in other genera (*2*). The spread of KPC-producing, gram-negative bacteria in hospitals has been linked to severity of illness, co-existing medical conditions, exposure to antimicrobial drugs, and need for chronic care (*3*).

After reporting of CRE ifections to the North Dakota Department of Health became mandatory in 2011, a total of 20 CRE cases were noted in 12 of 53 counties (2.9 cases/100,000 population [*4*]). Most cases involved infection with *Enterobacter cloacae* and occurred in Cass County, where the state's largest city, Fargo, is located. We describe an outbreak of clonal carbapenem-resistant *E. cloacae* in a health care system in Fargo.

Sanford Health is a 583-bed, acute-care facility, representing ≈70% of acute-care beds in Fargo. The hospital handles ≥27,000 admissions/year and serves as a referral center for a large area of the state, and the only long-term acute-care (LTAC) facility in the eastern half of the state operates on its campus. During December 2011–December 2012, all isolates of *Enterobacteriaceae* with reduced susceptibility to ertapenem (MIC ≥1 μg/mL) identified at the hospital's clinical microbiology laboratory were screened for carbapenemase production by using the modified Hodge test (mHT), according to Clinical and Laboratory Standards Institute recommendations (*5*). Identification and susceptibility testing were done with the MicroScan system (Siemens Healthcare Diagnostics, Tarrytown, NY, USA); MICs of carbapenems were confirmed with Etest (bioMérieux, Durham, NC, USA). Three carbapenem-resistant *E. cloacae* isolates from documented cases of CRE infection at the hospital during 2010 were analyzed for comparison.

To characterize carbapenem-resistant and mHT-positive isolates, we used PCR to amplify and sequence the carbapenemase genes bla_{IMP}, bla_{NDM}, bla_{VIM}, and bla_{KPC} by using established methods (*6*). The upstream sequence of bla_{KPC}-positive strains was analyzed to determine the isoform of the transposon Tn*4401* that harbored bla_{KPC} (*7*). We investigated genetic similarity among isolates by repetitive sequence-based PCR; isolates with >95% similarity were considered clonal (*6*). We also sequenced the highly conserved *hsp60* gene (*8*) and attempted conjugative transfer of the bla_{KPC} gene by growing KPC-producing *E. cloacae* along with sodium azide–resistant *Escherichia coli* J-53. As part of the study, we examined records of patients from whom carbapenem-resistant *E. cloacae* was isolated. The study was approved by the Institutional Review Board at Sanford Health.

During December 2011–December 2012, a total of 19 single-patient *E. cloacae* isolates and 1 *E. aerogenes* isolate had positive mHT results. bla_{KPC} was detected in 17 of the 19 *E. cloacae* isolates and in the 3 carbapenem-resistant *E. cloacae* isolates from 2010. For all 20 of those isolates, sequencing revealed bla_{KPC-3} in association with isoform d of the transposon Tn*4401*, and all isolates were clonally related (Figure). All 20 isolates also had an identical *hsp60* sequence belonging to cluster VI in the Hoffman and Roggenkamp scheme (*8*). Conjugation of a bla_{KPC}-containing plasmid into *E. coli* J-53 was successful for 1 strain.

All 20 of the patients from whom KPC-producing CRE isolates were obtained (17 from this study, 3 from 2010) had been hospitalized at Sanford Health during the 3 months before CRE isolation; 13 (65%) were admitted to intensive care. In addition, 13 (65%) patients had been admitted to the LTAC during the year before CRE isolation. Co-colonization with multidrug-resistant bacteria was documented in 16 (80%) patients, including extended-spectrum β-lactamase–producing and carbapenem-resistant organisms in 4 and 2 patients, respectively. Seven (35%) patients died; 3 (15%) deaths were attributed to CRE infection. One of the patients was a neonate 30 days of age.

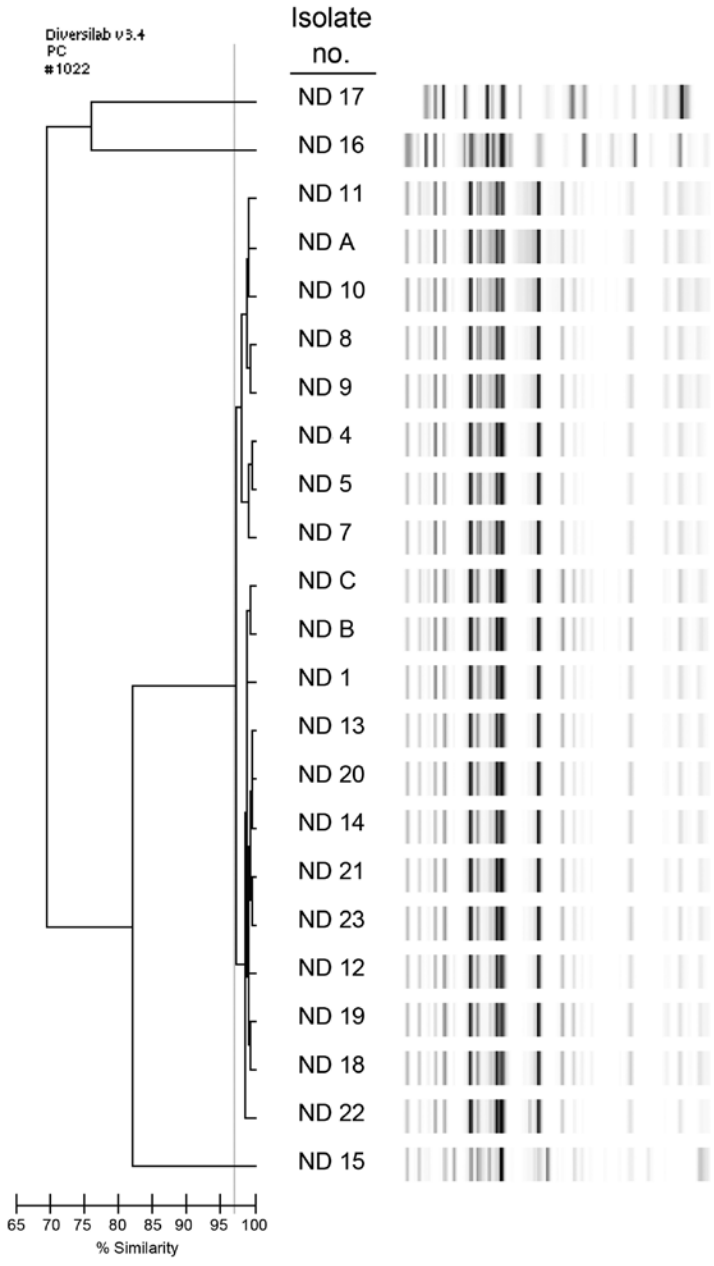

Figure. Genetic typing of carbapenem-resistant *Enterobacter cloacae* identified from patients at Sanford Health in Fargo, North Dakota, USA. Repetitive sequence–based PCR was used. The dendrogram at left displays the percentage similarity among band patterns shown at right. Isolate numbers ND 1, ND 4–5, ND 7–14, and ND 18–23 indicate *Klebsiella pneumoniae* carbapenemase (KPC) 3–producing *E. cloacae* isolates isolated during December 2011–December 2012; ND A–C indicate KPC-3–producing *E. cloacae* isolated during 2010. All KPC-3–producing *E. cloacae* isolates share >97% similarity, indicating a clonal strain. ND 15 and 16 are *E. cloacae*, and ND 17 is *E. aerogenes*, genetically distinct and without carbapenemases.

The finding of KPC-3–producing *E. cloacae* in North Dakota contrasts with the predominant epidemiology of CRE across the United States. Most CRE cases nationwide are caused by KPC-producing *K. pneumoniae* (*2*). KPC-type β-lactamases were previously identified in diverse strains of *Enterobacter* spp. from an urban health care system in Detroit, accounting for ≈15% of CRE (*9*). In contrast, our genetic analysis reveals a uniform genetic background among KPC-producing *E. cloacae*, which suggests horizontal dissemination of an outbreak strain.

Because active surveillance programs do not exist at our facility, this study probably underestimates the extent of CRE spread. We found that patients with KPC-producing *E. cloacae* in this sample were exposed to an LTAC and concomitantly were colonized or infected with other multidrug-resistant organisms (*9*). Although the spatio-temporal origin of the outbreak (acute care vs. LTAC) remains undefined, these findings likely reflect longer exposure to the continuum of care and higher rates of co-existing conditions within the LTAC population. This outbreak of KPC-producing *E. cloacae* infections in a health care system in North Dakota highlights the infection control challenges of long-term care facilities and the potential role they play in CRE dissemination.

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References

1. Munoz-Price LS, Poirel L, Bonomo RA, Schwaber MJ, Daikos GL, Cormican M, et al. Clinical epidemiology of the global expansion of *Klebsiella pneumoniae* carbapenemases. Lancet Infect Dis. 2013;13:785–96. http://dx.doi.org/10.1016/S1473-3099(13)70190-7
2. Kitchel B, Rasheed JK, Patel JB, Srinivasan A, Navon-Venezia S, Carmeli Y, et al. Molecular epidemiology of KPC-producing *Klebsiella pneumoniae* isolates in the United States: clonal expansion of multilocus sequence type 258. Antimicrob Agents Chemother. 2009;53:3365–70. http://dx.doi.org/10.1128/AAC.00126-09
3. Swaminathan M, Sharma S, Poliansky Blash S, Patel G, Banach DB, Phillips M, et al. Prevalence and risk factors for acquisition of carbapenem-resistant *Enterobacteriaceae* in the setting of endemicity. Infect Control Hosp Epidemiol. 2013;34:809–17. http://dx.doi.org/10.1086/671270
4. North Dakota Department of Health. Carbapenem-resistant. *Enterobacteriaceae* (CRE) including *Klebsiella pneumoniae* carbapenemase (KPC) producers [cited 2014 Jan 20]. http://www.ndhealth.gov/disease/cre
5. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 19th informational supplement. Wayne (PA): The Institute; 2009.
6. Perez F, Endimiani A, Ray AJ, Decker BK, Wallace CJ, Hujer KM, et al. Carbapenem-resistant *Acinetobacter baumannii* and *Klebsiella pneumoniae* across a hospital system: impact of post-acute care facilities on dissemination. J Antimicrob Chemother. 2010;65:1807–18. http://dx.doi.org/10.1093/jac/dkq191
7. Naas T, Cuzon G, Villegas MV, Lartigue MF, Quinn JP, Nordmann P. Genetic structures at the origin of acquisition of the b-lactamase bla_{KPC} gene. Antimicrob Agents Chemother. 2008;52:1257–63. http://dx.doi.org/10.1128/AAC.01451-07
8. Hoffmann H, Roggenkamp A. Population genetics of the nomenspecies *Enterobacter cloacae*. Appl Environ Microbiol. 2003;69:5306–18. http://dx.doi.org/10.1128/AEM.69.9.5306-5318.2003
9. Marchaim D, Chopra T, Perez F, Hayakawa K, Lephart PR, Bheemreddy S, et al. Outcomes and genetic relatedness of carbapenem-resistant *Enterobacteriaceae* at Detroit medical center. Infect Control Hosp Epidemiol. 2011;32:861–71. http://dx.doi.org/10.1086/661597

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Urethritis Caused by Novel *Neisseria meningitidis* Serogroup W in Man Who Has Sex with Men, Japan

To the Editor: We report a case of urethritis caused by a novel multilocus sequence type (ST), 10651, of the ST11/electrophoretic type (ET)–37 complex *Neisseria meningitidis* serotype W. The patient was a man who has sex with men. We also report on the patient's male partner, who was colonized with the same bacteria.

In March 2013, a 33-year-old Japanese man sought medical care at Shirakaba Clinic (Tokyo) after experiencing a urethral discharge for 4 days. The man was HIV positive (CD4 count 649 cells/mL) but was not receiving antiretroviral therapy. Physical examination showed a mucous urethral discharge. Gram staining of a sample revealed many gram-negative diplococci phagocytosed by polymorphonuclear leukocytes. Eleven days before seeking care, the patient had oral and anal intercourse with his male partner. A diagnosis of suspected urethritis caused by *Neisseria gonorrhoeae* was made, and a sample of the urethral discharge was sent for culture and testing (Strand Displacement Amplification) for *N. gonorrhoeae* and *Chlamydia trachomatis*. The patient was intravenously administered a single dose of ceftriaxone (1 g) (intramuscular administration of ceftriaxone is not approved in Japan). He was also given a single dose of azithromycin (1g orally) for possible *C. trachomatis* urethritis (*1*).

Six days after receiving treatment, the patient showed improvement. Results of the Strand Displacement Amplification test were negative for *N. gonorrhoeae* and *C. trachomatis*. Eight days after the patient received treatment, the culture for the urethral discharge sample was shown